Agenda has been moved!

Due to large history + slow Google Docs (lots of lag/delay while typing), the meeting minutes for 2024 meetings have been moved to the following link:

https://docs.google.com/document/d/10txnlVrX3roF-VYP3yYUVLk7KmeL-43-ppKMKJ1BCpE/edit

If you have arrived at this document from another page, please update the link accordingly.

SCT Meetings

When: See slack announcement and NeuroPoly's calendar
Where: https://polymtl-ca.zoom.us/j/81029425251?pwd=NytHVHN4YVlvQWdiUC9nSm5TdVlhUT09
Repository: https://github.com/spinalcordtoolbox/spinalcordtoolbox
Website: https://spinalcordtoolbox.com/

Roles

Each week we rotate the roles of Moderator/Minutes-taker.

Moderator: Role is to moderate/chair the meeting. The moderator is also responsible for ensuring that the agenda has been filled out prior to the meeting.
Minutes: Role is to take minutes of the meeting.

Please fill the agenda before the meeting with points you would like to discuss. Don't be shy!

Use this empty agenda to copy-paste and create new agendas.
(Don’t fill this template page!)

Template

Attendees:
Not yet arrived: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Naga Karthik, Rohan Banerjee, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Simon Queric, Benjamin De Leener, Maxime Bouthillier, Baptiste Taverne, Katerina Krejci, Arthur Toulouse, Samuelle St-Onge, Thomas Dagonneau,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: TBD

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared

Check last meeting’s action items

☐

Software Development

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Research

-

Action Items

☐

2024-09-06

Attendees: Joshua Newton, Mathieu Guay-Paquet, Julien Cohen-Adad, Jan Valosek, Pierre-Louis Benveniste, Arthur Toulouse, Samuelle St-Onge, Nathan Molinier, Thomas Dagonneau,
Not yet arrived: Sandrine Bédard, Naga Karthik, Rohan Banerjee, Nilser Laines Medina, Simon Queric, Benjamin De Leener, Maxime Bouthillier, Baptiste Taverne, Katerina Krejci
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: TBD

Miscellaneous items

- Welcome Arthur!! 🎉
    - Exchange student, axondeepseg/mri project to be decided
- Change SCT time to accommodate classes. Suggestion: Tuesday 3pm. (9 votes in favour so far)
    - TODO: Double-check on slack for people who are missing today
- JN: Trying phone audio (in lieu of good wifi connection), apologies if it doesn't work well!

Check last meeting's action items

- ☑ ~~MathieuGP: open an issue to consider merging API functions between `sct_analyze_lesion` and `sct_extract_metric` and `sct_process_segmentation` SCT#4624~~
- ☑ ~~Sandrine & MathieuGP try installing SCT on compute canada~~
    - Sandrine ended up switching back to Joplin due to many R/W operations on files
    - Potentially try arbutus VMs if we need this (rather than CC jobs)
    - Wait to see what Sandrine/others' needs are…
- ☐ All: check `sct_analyze_lesion` tutorial PR (#4586)
    - Jan: Sandrine, Naga and PL reviewed the tutorial
    - Jan: I addressed reviewers comments
    - Jan: I added a new section covering atlas/template analysis (`sct_analyze_lesion -f` link)
    - TODOs:
        - Add example data – not easy as we need MS and SCI patients
        - Here is a comment discussing MS data from the ms-challenge-2021
            - ☐ our internal dataset (data.neuro.polymtl.ca/msseg_challenge_2021) contains FLAIR images covering both the brain and spinal cord
            - ☐ However, kaggle/isbi-ms-dataset contains only brain images.
            - ☐ Consider faking a lesion?
            - ☐ Canproco data: Add mention
        - Confirm with collaborators (Andrew, Dario) figures and refs used at this tutorial page

        - Tutorial as-written may be obsoleted by contrast-agnostic lesion segmentation model
            - ☐ This is OK though, as the skeleton is still very useful as a first draft

Software Development

- 6.4 was successfully released! 🎉

- JN: Status updates for in-progress work:
    - #4602: TSNR `-qc`
        - Joshua: 95% reviewed, just needs a check to ensure `-m` is mandatory for `-qc`.
    - #4611: Suspicious MOCO softmask (fix: convert soft to binary)
        - Joshua: Needs review.
    - #4617: Lesion length and width for the midsagittal slice
        - Jan: Mathieu reviewed (and help me fix) the angle correction logic
        - PR is now ready for full review
    - #4618: Install arbitrary `sct_deepseg` .zips (to test unreleased models)
        - WIP.
    - #4622: Fix coordinate orientation in output `.csv` of `sct_get_centerline`
        - We (Joshua, MathieuGP, AlexD) had a very clarifying zoom call this morning to figure it out, summarized at the end of the PR.
        - Possible issue: user scripts silently changing results?
        - Feature question: NIFTI standard is that all **physical/world** coordinates are RAS+ (aka LPI-). Should we implement conversion functions to other physical/world orientations?
            - Advertise the breaking change in the changelog

- Upcoming release: SCT v6.5/v7.0 (Milestone: October 24th, 2024)
    - **SCT Course:** Will we be having one in November?
        - If so, then we should prioritize course material updates during this release cycle.
        - JCA: Let’s have one - end of november-ish. :)
            - Keep 2 days
            - Jan: I’m on holidays in Europe (+6h) November 20 - December 4
            - <Nov 20 (too little time), so instead >Dec4 —> Dec 9/10? 👍

    - **sct_deepseg:** If we are doing an SCT Course, then JN is interested in these issues:
        - JCA: +1 for this as a focus for JN in preparation for the SCT course
        - #4318: Sub-commands for sct_deepseg tasks
        - #4532: Move `sct_deepseg_{sc,lesion,gm}` to `sct_deepseg`
        - #3767 : Improve advertising for `sct_deepseg` models
            - (Including updating the segmentation tutorial to introduce `sct_deepseg -task contrast_agnostic`)
        - #3095: Split command-line tools into 1 page per script.

        - This would let us have a single-page “hub” for `sct_deepseg` information that we can link to from the tutorials/course.
    - If we want to do the above tasks, then perhaps we could release SCT v7.0 instead of SCT v6.5, then make a big push to advertise the suite of `sct_deepseg` models?
        - This was already covered!

Research

-

Action Items

- ☐ MathieuGP: Double-check on slack for people who are missing today to check if Tuesday 3pm works– then let’s secure schedule by today latest
- ☐ `sct_analyze_lesion` tutorial PR (#4586)
    - ☐ Thomas Dagonneau: try the `sct_analyze_lesion` tutorial PR (#4586)
    - ☐ Jan: create fake lesion
    - ☐ Jan: remove * from paper REFs
    - ☐ Jan: make sct_deepseg_lesion fig
    - ☐ PL: improve STIR/PSIR canproco fig for the tutorial
    - ☐ Jan: merge “before starting this tutorial” sections
    - ☐ Jan: confirm the fig with Andrew
- ☐ Check whether Sandrine is available for SCT course early december
- ☐ PL: speaker for the next meeting Research part

2024-08-22 (canceled)

2024-08-08

Attendees: Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Abel Salmona
Not yet arrived: Julien Cohen-Adad, Naga Karthik, Rohan Banerjee, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Simon Queric, Benjamin De Leener, Maxime Bouthillier, Baptiste Taverne, Katerina Krejci
Moderator: Mathieu Guay-Paquet
Developer Minutes: Joshua Newton
Research Minutes: Jan Valosek

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared

Check last meeting's action items

☑ ~~Jan: open an issue to create tutorial for `sct_analyze_lesion`~~
  - Done: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4575
  - WIP PR: #4586

Software Development

- Sandrine Bédard: issue installing SCT on compute canada: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4593
  - Try to install everything manually pip no--install
  - Mathieu: Compute Canada does not allow conda installations
  - See also the "install with pip" instructions that SCT maintains: https://spinalcordtoolbox.com/user_section/installation/linux.html#option-3-install-with-pip-experimental
    - Not sure if this is compatible with CC though

    Side note: The motivation is re-running old analysis scripts that requires Python3.7, so the scripts will need to be updated first (and if they can't be updated, then the CC installation is moot)

- Jan Valošek: `lesion-analysis` tutorial: #4586
  - Ready for first feedback - built website here
  - The tutorial has two sections:
    - lesion-segmentation - this section covers SCI lesion segmentation (sct_deepseg -task seg_sc_lesion_t2w_sci) and MS lesion segmentation (sct_deepseg_lesion)
    - lesion-statistics - this section covers sct_analyze_lesion
  - Open access data is needed
  - Should we include a `-f` section? (Needs template registration – but we could always pregenerate the warping fields and just include those, then start the tutorial with the

sct_warp_template command to generate the warped atlas files)

- SCT 6.4 release: almost there! project board
    - Should be ready to announce by today!
    - Jan is working on the last PR #4597
    - Joshua fixed up the changelog PR and double checked manual steps

Research

- Jan Valošek : implementing SCT in the clinical workup
    - https://github.com/sct-pipeline/balgrist-sci
    - Idea: create easy to use repo for clinicians
        - The plan is to create a single script to run several SCT commands (SC seg, vert labeling, lesion seg, lesion analysis) + QC
        - Input images will be DICOMs downloaded from PACS → we need to take care about dcm2nii conversion
            - → I'll to install dcm2niix or dcm2bids → I'll probably install it into SCT conda env instead of creating a new env, what do you think?
            - Joshua: FYI, make sure to not use conda dcm2niix package, use pip dcm2niix package. See: https://www.anaconda.com/blog/using-pip-in-a-conda-environment)
            - Note that dcm2niix also has standalone executables: https://github.com/rordenlab/dcm2niix?tab=readme-ov-file#install
            - Discussion:
                - Use bash script for installation
                - Use bash/python script for the analysis; python might be more robust to human errors as it provides more robust arg parser

- Sandrine Bédard : update on TSNR qc

Action Items

☐ MathieuGP: open an issue to consider merging API functions between `sct_analyze_lesion` and `sct_extract_metric` and `sct_process_segmentation`

☐ Sandrine & Mathieu try installing SCT on compute canada

☐ All: check `sct_analyze_lesion` tutorial – Jan: tag Naga and PL as they're working with lesions

2024-07-25

Attendees: Joshua Newton, Mathieu Guay-Paquet, Jan Valosek, Rohan Banerjee, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Simon Queric, Katerina Krejci, Abel Salmona, Sandrine Bédard, Samuelle St-Onge, Julien Cohen-Adad,
Not yet arrived: Naga Karthik, Benjamin De Leener, Maxime Bouthillier,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: Nathan

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared

- Welcome Abel Salmona! 🎉 He just started a 10-month internship at the lab

Check last meeting's action items

☑ ~~Next time: Simon: artifact detection artefact-detection_2024-06-13 → stand by project~~
    - Not relevant anymore

Software Development

- MathieuGP: I pushed back the 6.4 release by a week to finish the QC refactor
    - Everything else seems to be on-track!
    - TODO: Test suite doesn't check the visual aspects – manual testing would be appreciated. (PL is available to help)

- JN: `sct_analyze_lesion -f` forum post
    - Background:
        - `-f` allows you to compute percentage distributions for "{lesion in ROI}" across GM/WM atlas (tracts, etc.)
        - Currently `-f` only considers individual tracts, and aggregates by vertebral level
    - Feature requests from forum post
        - Consider `CombinedLabels` (e.g. WM labels 0:29, GM labels 30:35, etc.) from info_label.txt
        - Per-slice instead of per-level (Add `-perslice` option?)
        - Treat multiple lesions as a single lesion (Add `-single-lesion` option?)
            - NB: I recommended to the user that they should perform QC/manual correction if they are getting multiple labels for a single lesion.
    - Q: Should I try to fit these feature requests into SCT v6.4? (I think I should have time, with the deadline pushed back 1wk.)
    - Bigger picture: Overlap between sct_analyze_lesion and sct_process_segmentation
        - Issue: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3378

    - sct_analyze_lesion: Contains volume calculation (lesion seg only), but also lesion-specific calculations (require lesion seg + spinal cord seg): https://github.com/spinalcordtoolbox/spinalcordtoolbox/blob/625f62e449000f8822b3a59dd9b6bb8dd96f4a7d/spinalcordtoolbox/scripts/sct_analyze_lesion.py#L470-L474
    - Consider deduplicating functionality between sct_analyze_lesion and sct_process_segmentation on the API level (mophometrics.py)
  - Takeaway: sct_analyze_lesion has become more lesion-specific, so keep the existing

Research

- Sandrine Bédard : sct_qc TSNR issue #4290
  - Make sct_qc work for motion correction (new feature)
  - Overlap with qc of sct_register_multimodal ?
  - TSNR qc: sometimes 1, sometimes 2
    - 1: Single image (sct_fmri_compute_tsnr qc?)
    - 2: Compare before/after TSNR images (moco, denosing, etc.)
  - TSNR qc is basically the same as the sct_register_multimodal qc (before/after compare) with a different colormap
  - Discuss about the way we call sct_qc to not constraints it to specific functions

Action Items

☑ ~~Jan: open an issue to create tutorial for `sct_analyze_lesion`~~
  - Done: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4575

☐ Someone: open an issue to consider merging API functions between `sct_analyze_lesion` and `sct_extract_metric` and `sct_process_segmentation`

2024-07-11

Attendees: Julien Cohen-Adad, Mathieu Guay-Paquet, Sandrine Bédard, Rohan Banerjee, Nathan Molinier, Nilser Laines Medina, Simon Queric, Benjamin De Leener, Baptiste Taverne, Katerina Krejci, Naga Karthik

Not yet arrived: Jan Valosek, Pierre-Louis Benveniste, Maxime Bouthillier,
Moderator: Mathieu Guay-Paquet
Developer Minutes:
Research Minutes: XXX

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared
- Away this week: JoshuaN and JanV

Check last meeting's action items

☑ ~~MathieuGP: allow "bypass branch protections" for admins of spine-generic/data-multi-subject~~
☐

Software Development

- Next release (6.4) is July 25, in 2 weeks.
    - Are there any features that really need to go in?
        - In progress: multiple operations in sct_maths
        - In progress: qc refactor
        - In review: mid-sagittal tissue bridges
        - In review: replace seg_ms_lesion_mp2rage model with nnUnet
        - Anything else? → No
            - Do we want to publish the dog template – https://github.com/spinalcordtoolbox/template-dog/releases/tag/r20240709 as a part of the release? -> yes

    - If need be, can we push it back by a week? → yes

- Some questions came up while refactoring sct_maths (SCT#4557)
    - Q1: Does it make sense to do mean/rms/std for a dimension other than time?
        - code link
            - Remove dimension only if it is the time dimension
            - No need for an option to keep axis ?
            - What happens to the affine matrix ?
        - This turns an image from 4D -> 3D, or from 3D -> 2D, but if it's not the last dimension, then the later dimensions don't match the affine matrix anymore.

        - The easy fix would be to re-add an axis of length 1, so that 4D -> 4D and 3D -> 3D, but this is not backwards compatible.
        - The other easy fix would be to only allow the time dimension.

    - Q2: Does it make sense to do laplacian or smooth for a 4D image?
        - It’s not clear whether the current code wants to handle 4D images or not
        - For 3D images, we normalize the sigmas with the voxel sizes, so that everything is in millimeters. But the time dimension is in seconds, so normalization isn’t really possible
        - Easy fix: only allow 3D images, but is this ok? → yes and generate an error for 4D images

-

Research

- PLB: We should advertise the fact that `sct_register_multimodal -identity 1` can be very useful for data curation and bidsification
    - Has to be used when labels and images are not in the same space

  (Sorry I am not available to discuss it today)
  Issue related: here
- Simon: registration and segmentation: https://github.com/ivadomed/ivadomed/issues/659

Action Items

☑ ~~Next time: Simon: artifact detection artefact-detection_2024-06-13 → stand by project - not relevant anymore~~

☐

2024-06-27

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Jan Valosek, Naga Karthik, Maxime Bouthillier, Baptiste Taverne, Katerina Krejci, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Benjamin De Leener, Samuelle St-Onge
Not yet arrived: Sandrine Bédard, Rohan Banerjee, Simon Queric,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: Naga Karthik

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared
- New feature: Insert -> Building Blocks. Wow! Nifty!
  - Maybe it's worth updating the calendar invites? 🤔

Check last meeting's action items

☑ ~~PL: discuss the tissue bridges during the Canproco meeting: issue 100 opened~~
  - Meeting did not occur because of a holiday

☑ ~~Jan: email Jason Talbott and CC Julien and Benjamin~~
  - Follow-up: wait for Jason Talbott to reply by email

☑ ~~JanV/SandrineB: Follow up on conflicts between #275 / #276 + release creation~~
  - Jan: #275
    - Code from this PR was published within a release
    - `process_data.sh` has conflicts (naming convention update (#276))
    - → closing #275 without merging; details in this comment
  - Jan: #276 - already merged

☑ ~~Julien: contact Mohamed Feroze to get more data for the rootlets (so far 25 subj)~~

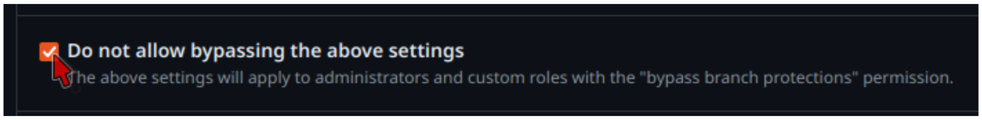
☑ ~~Note: Points from last week's meeting have been carried over to "Research" section~~

Software Development

- Design question: move the caching logic inside `sct_straighten_spinalcord`? (instead of the individual callers)
  - Original PR: #4537
  - Followup issue: #4540
  - Reusing *just* the straightened spinal cord warping fields.
    - There were previous discussions – straightening is highly dependent on the input segmentation, so we need to make sure the exact segmentation itself is taken into account. (We do!)
  - Do we want to cache other results? (Are there other expensive intermediate operations where we use the same inputs for each step?)

        - Not a high priority, probably not other candidates.

- NathanM: spine-generic is blocked on this old pull request data-multi-subject#159
    - MathieuGP: the testing CI pipeline has been buggy and outdated for a long time, but now its dependencies don't install anymore. And branch protections are currently non-bypassable (settings link).
    - JoshuaN has offered to help ♥
        - JN: PR Opened! #168
        - The checks have found a number of ERRORS/WARNINGS. (Q: Which of these need to be fixed, and which can be safely ignored?)
            - The validator can raise only WARNINGS, not ERRORS
            - The check script relies on the old naming scheme (naming has been updated in #159)
    - JN: Should we temporarily bypass these protections, just to unblock the PR?



☑ Do not allow bypassing the above settings

The above settings will apply to administrators and custom roles with the "bypass branch protections" permission.

- JN: New "**GitHub Project for SCT Issues**"
    - JN: I have been privately testing this for about 2 months (to evaluate GitHub Projects)
    - Features:
        - Auto-adds new issues from SCT repo (they appear in the **Categorization** tab)
        - Provides a more useful view of the **6.4 Milestone** than the actual milestone page (which I find confusing, since it mixes issues + PRs).
        - Gives a nice overview of **your assigned issues**, as well as the **team's assigned issues**.
        - It lets us sort our **backlog of issues** by priority and/or scope (to figure out what to work on next).

- JN: 6.4 Milestone Progress
    - There are quite a few in-progress issues/PRs
        - JN: I need to respond to PR feedback! I'll do this after the meeting.
    - Apart from these in-progress items, the only things left are QC-related.
    - I think we're on track for a late July (25) release? (2 meetings left before release)

- Jan: tissue bridges: #4489
    - Working on addressing comments from collaborators: comment
    - Ideally finish to be ready for 6.4 (July 18, 2024)
    - Version referenced in a paper to be published

- Jan: two minor help/argument description clarifications
    - #4547: add example command for `sct_qc -p sct_detect_pmj`
    - #4550: clarify that `sct_label_utils -disc` does not involve orthogonal projection
        - "Projection onto the spinal cord centerline within the axial plane"
        - Don't use the word "orthogonal"

Research

- Items added from the last meeting that we did not get to (I think? Pls remove if it was covered)
    - Simon: artifact detection artefact-detection_2024-06-13
        - On holiday, bring to next meeting
    - Julien: Brain/spine MS lesion segmentation, and module in 3D Slicer
        - Already discussed?
        - Maxime working on manual seg with 3D slicer – widely used by clinical community – Customizable with modules as extension
        - Goal: create a module that could be an Slicer extension, unify several disjoint manual correction efforts
        - Nathan: manual_correction is not just doing seg. but also labeling
        - Need for a strategy to decide who will lead/work on the project. Reach out to other researchers to see what's needed
            - Requires 2-3 part-time devs to work/maintain the modules
        - Jan has been maintaining the `manual_correction.py` script.
        - Maxime: Slicer workflow is better than with FSLeyes
            - Segmentation
            - Classification
            - Self-assessment

    - Julien: PACS-AI
        - Started by Robert Avram, Cardiology institute
        - Mainly for running inference on cardiology images (for now)
        - Use case: inference of MS lesions on MRI scans.
        - Workflow: Manual correction → model development → integrating into PACS AI
        - Requirements? → Models have to be PyTorch and served with TorchServe. MONAI models can also be converted to TorchServe
        - Hospital runs on its own system (inference can be run within the hosp.)
        - Really good way to test our models on a large timeframe

Action Items

☐ Simon: artifact detection artefact-detection_2024-06-13

☑ ~~MathieuGP: allow "bypass branch protections" for admins of spine-generic/data-multi-subject~~

2024-06-13

Attendees: Joshua Newton, Mathieu Guay-Paquet, Jan Valosek, Simon Queric, Maxime Bouthillier, Nathan Molinier, Nilser Laines Medina, Baptiste Taverne, Katerina Krejci, Katerina Krejci, Benjamin De Leener, Julien Cohen-Adad, Pierre-Louis Benveniste, Naga Karthik
Not yet arrived: Sandrine Bédard, Rohan Banerjee,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: Simon Queric

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared

Check last meeting's action items

- ☑ ~~Maxime: Document frustrations/improvements requests regarding manual correction to prepare the meeting — see manual_correction meeting here.~~
- ☑ ~~Maxime: organize meeting and create team for the Kaggle challenge~~
  - Simon will be the leader!
  - Simon, Baptiste, Katerina, (Maxime), Nilser
- ☐ JanV/SandrineB: Follow up on conflicts between #275 / #276 + release creation
  - Jan: Sorry, not done yet. I'll do it by the next meeting. → Move to next meeting
- ☑ ~~BaptiseT: Open issue on BIDSification repo to document/publish metadata-downloading with Datalad (see https://github.com/ivadomed/Bidsification/tree/Dataset_selection)~~
- ☐ MGP/Emma: Think about how to reorganize Gitea orgs / dataset permissions
  - Not yet!
  - Context
    - Big question, not specific to SCT.
    - Everything under "datasets" org, could be moved into histology vs. mri orgs
    - Standardizing dataset naming conventions
  - Should we take a few minutes to discuss in the next lab meeting? (Lab-wide meeting)
- ☑ ~~Make sure that folks know that lab meetings won't end for the summer (JCA -> Eva)~~

Software Development

- JN: Not much to discuss this week!
  - Things have been going smoothly – fixing issues as they come up.
  - Open PRs that need review:
    - #4484: Fix install_sct crash for `sct_download_data` failures
    - #4508: Fix sct_deepseg softsegs (-`thr 0`)

    - #4485: `sct_maths` multiple sequential operations
    - #4499: `sct_maths` 3D operations on 4D images

- Do we want to keep testing CentOS Stream 8 in CI? It has reached end-of-life.
  - Issue #3675, pull request #4517
  - We can drop it when a big issue comes up

- Jan: tissue bridges: #4489
  - Joshua, thanks for the initial review! 👍
  - Try the bridges on MS!

- PierreLouisB: Thresholding during image registration
  - issue #4504
  - JN: This is on my TODO list!

- What Julien mentioned: MONAI resampling / interpolation method
  - https://github.com/Project-MONAI/MONAI/issues/7836

Research

- Jan: A question from Jason Talbott (UCSF): pediatric template
  - PAM50 adult template ?
  - There is a pediatric dataset and we have a preliminary version developed by Nadia and now Samuel is following on this project

- Jan: ISMRM feedback from users
  - Some people use `sct_deepseg_lesion` (which is MS model) for SCI lesions
    - People use it for spinal cord injury lesion and don't read the documentation
    - Rename the model ? → use instead sct_deepseg -task segment_MS_lesion ?
  - Several people asked me whether there SCT contains tools for animal images
    - Mention animal models during the next SCT course
- Katerina: pediatric rootlets: Pediatric-spinal-rootlets-presentation_2024-06-13
  - Context : model for segmentation of spinal rootlets
  - What to do if there is more than one level in one slice ?
  - disc levels saved and pushed back to git-annex for Nathan?
- Julien: Brain/spine MS lesion segmentation, and module in 3D Slicer
  - Next time!
- Nilser: `sct_deepseg` nnUNet models implementation on Slicer: #4528 , #4531
  -
- Simon : artifact detection artefact-detection_2024-06-13

Action Items

☐ PL: discuss the tissue bridges during the Canproco meeting: issue 100 opened

☑ ~~Jan: email Jason Talbott and CC Julien and Benjamin~~

- ☐ Julien: contact Mohamed Feroze to get more data for the rootlets (so far 25 subj)
- ☐ Julien: discuss at next meeting about Brain/spine MS lesion segmentation, and module in 3D Slicer, and talk about PACS-AI
- ☐ Simon : discuss to next meeting about artifact detection artefact-detection_2024-06-13

2024-05-30

Attendees: Joshua Newton, Mathieu Guay-Paquet, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Simon Queric, Naga Karthik, Maxime Bouthillier, Katerina Krejci, Rohan Banerjee, Baptiste Taverne
Not yet arrived: Julien Cohen-Adad, Sandrine Bédard, Jan Valosek, Benjamin De Leener,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: TBD

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared
- Meeting time change: Wednesday → Thursday
    - Does this work for everyone? (Has Benjamin given confirmation that this is okay?)
        - Just go for it! 🚀

- Welcome Katerina!! 🎉
    - Use this meeting for discussing points + asking questions → brainstorming, etc.

Check last meeting's action items

- ☐ JV/SB: Follow up on conflicts between #275 / #276 + release creation
    - Still not here → Move to next meeting
- ☐ BT: Open issue on BIDSification repo to document/publish metadata-downloading with Datalad
    - Hacky script? Did not upload yet → Forgot, move to next meeting. :)
- ☐ MGP/Emma: Think about how to reorganize Gitea orgs / dataset permissions
    - Not yet!
    - Context
        - Big question, not specific to SCT.
        - Everything under "datasets" org, could be moved into histology vs. mri orgs
        - Standardizing dataset naming conventions
    - Should we take a few minutes to discuss in the next lab meeting?
        - Make sure that folks know that lab meetings won't end for the summer (JCA -> Eva)

Software Development

- v6.4 Milestone Progress update
    - Deadline: July
    - Most "6.4" issues have open, in-progress PRs 🎉
    - Joshua: I am looking for new things to work on…
        - Does anyone have any issues that are impeding their research?
            - None?

      - Contrast agnostic model → Doesn’t work for thick sagittal PSIR Toronto subjects
        - **(Is there an open issue? Examples of subjects? Link to issue?)** 🎉 🚀
          - 😀
          - https://github.com/ivadomed/canproco/pull/95
        - Not recommended to segment thick sagittal images
          - Resolution may be an issue no matter what?
          - Super-resolution
          - Before that, start with soft segmentation (use -thr 0 to turn off 0.5 thresholding!)
        - Compare with sct_deepseg_sc and report back?
        - WIP model for PSIR images that has not been released yet! (!!!)
          - We can release a new model!

      - “Straightening is not a bijective transformation” issue (#4477)
        - Mathieu is taking a look (physical vs. voxel coordinates)

    - If not, I will look into our issue backlog for bugs to fix. 🙂
      - Perfect!

- Naga: Should we think of maintaining a deployment server (or Cloud) that SCT users can use?
  - **Context:** CIFAR
    - CIFAR wants to find PIs who want to show models
    - PACS AI (Montreal Heart Institute) - PI: Dr. Robert Avram
    - Inference server → Link to webpage? Not yet, wait for it to be deployed
  - Pros: Don’t have to rely on local systems (i.e. having/not having GPUs) and instead the cloud (which we configure) will have the required GPUs and the performance will be the same for all users
    - Execution time is not a good motivation
    - But, getting to avoid installation would be a big Pro.
  - Cons: Users have to upload their data to the cloud (?)
  - JN: There is already a (very old) SCT web UI (looking for it now) – Can’t find… definitely not up to date, not relevant :P

- Adapt our models for DICOM inputs/PACS connection?
  - PARADIM project for SCT models? → https://paradim.science/
    - Another inference platform + data management
    - PACS AI is just inference (for comparison)
  - Add additional decorator that allows DICOM → NIFTI conversion
    - image.py :: `Image` constructor (since we pass a filepath to Image)
      - Since we already detect .nii vs. nii.gz, can we detect .dcm? → File extensions can vary quite a bit.
      - Header filetype detection?
    - Detail: Inputting DICOM folder vs. DICOM file (SCT is largely single-image)

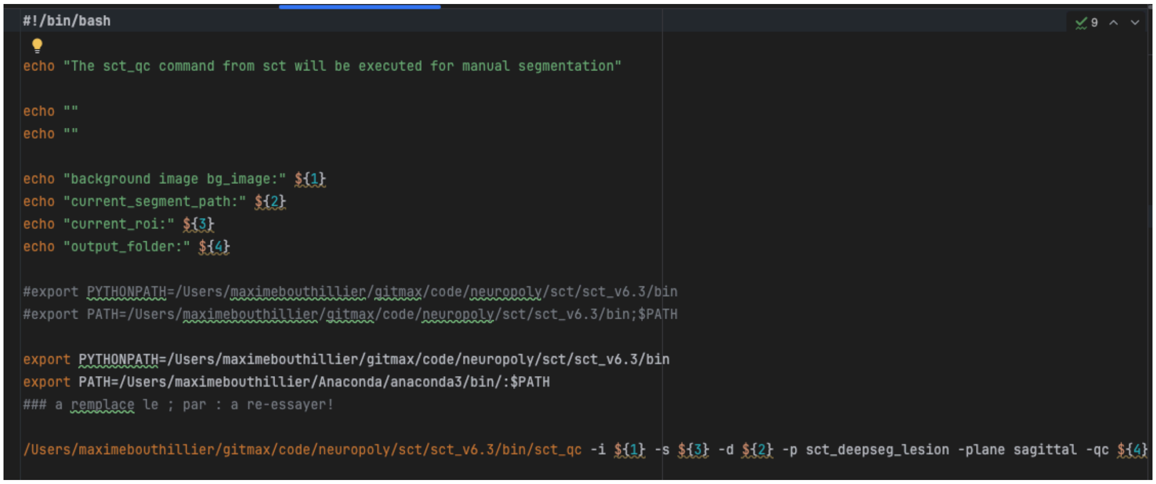
    - Dependencies: pydicom? pydicomseg?
    - But, right now we're outputting Nifti files, and that would be *much* harder to change, since I think we hardcode `.nii.gz` all throughout SCT
  - Ultimately, not a high priority, need a strong usecase before moving ahead

Research

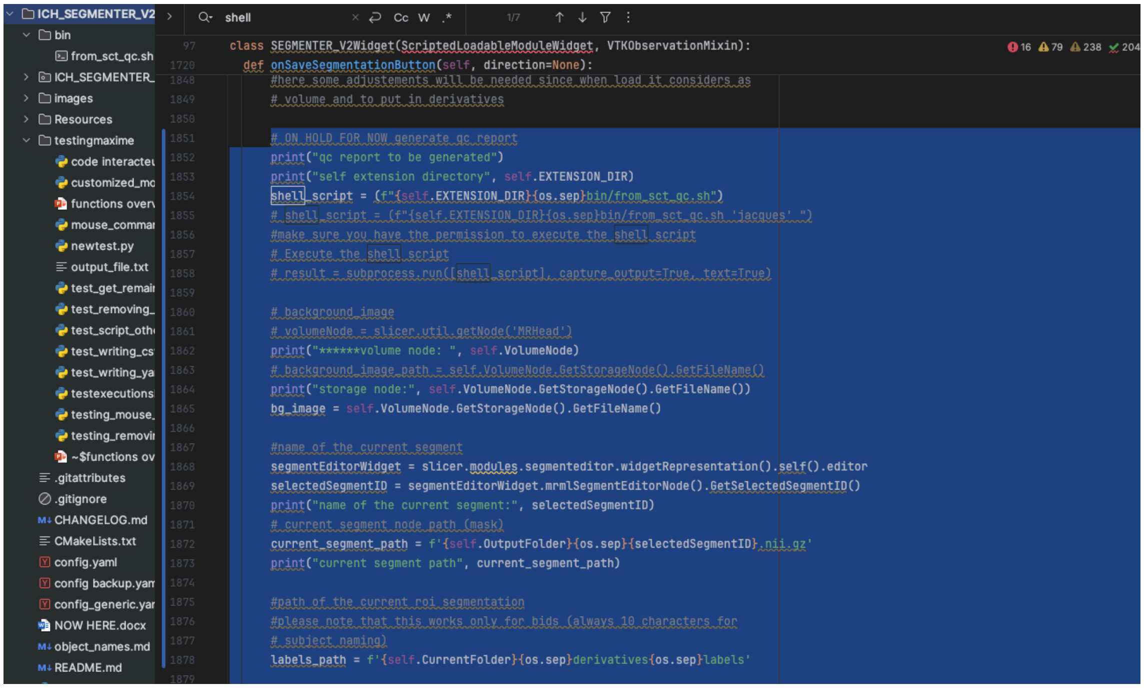
- Nilser:
  - RSNA 2024 Lumbar Spine Degenerative Classification
    - Data: Open 1975 subjects T1w_sag, T2/STIR_sag and T2w_axial lumbar images
    - Annotation: Coordinates XYZ of stenosis on .csv file
    - Deadline: 2024-10-01
    - Internship project?
    - Very interesting + challenging project
    - Active forum
    - Max registration: 5
    - Project Leader : Maxime
  - Release of `seg_ms_lesion_mp2rage` model on `sct_deepseg` #82
    - For SCT 6.4 ?

- Maxime:
  - Google docs for organization created. Link here for RSNA 2024 Lumbar Spine Degenerative Classification — team leader: Maxime
  - sct_run_batch not robust to variation in BIDS format. #4500. Fixed (#3415).
    - But, maybe that could be implemented automatically without adaptations?
    - JCA: wouldn't recommend automatization, instead document the script better to let people know to "adapt the script"
  - Manual_correction update meeting: to come on monday June 10th, 3h30 pm to 4h30 pm
  - E.g. (working on) — generating a qc report from 3DSlicer python script executable function (my plan; creating a shell script (.sh file) that is executed when a function (python script) is called from the 3DSlicer interface (save segmentation button)
    - Anticipated issue : 3DSlicer has its own version of python and it may cause troubleshooting by trying to execute it
    - Nathan: Why not, not integrating QC in 3DSlicer ?
    - Problem from environments python version
    - MGP: try to run the command "env" and capture the output (list the variables and overwrite from the shell script the variable that are incorrect in the 3dslicer python interactor)
      - Worst case; run slicer from terminal, then run sct_qc from the terminal – it will generate QC (can perform a print of the output folder that would have the qc and copy it in the therminal)
    - We need to discuss what to will happen with "manual correction"

        - JCA: Need to document your frustrations and the desired improvements to prepare the meeting



```bash
#!/bin/bash

echo "The sct_qc command from sct will be executed for manual segmentation"

echo ""
echo ""

echo "background image bg_image:" ${1}
echo "current_segment_path:" ${2}
echo "current_roi:" ${3}
echo "output_folder:" ${4}

#export PYTHONPATH=/Users/maximebouthillier/gitmax/code/neuropoly/sct/sct_v6.3/bin
#export PATH=/Users/maximebouthillier/gitmax/code/neuropoly/sct/sct_v6.3/bin;$PATH

export PYTHONPATH=/Users/maximebouthillier/gitmax/code/neuropoly/sct/sct_v6.3/bin
export PATH=/Users/maximebouthillier/Anaconda/anaconda3/bin/:$PATH
### a remplace le ; par : a re-essayer!

/Users/maximebouthillier/gitmax/code/neuropoly/sct/sct_v6.3/bin/sct_qc -i ${1} -s ${3} -d ${2} -p sct_deepseg_lesion -plane sagittal -qc ${4}
```



```python
class SEGMENTER_V2Widget(ScriptedLoadableModuleWidget, VTKObservationMixin):
  def onSaveSegmentationButton(self, direction=None):
        #here some adjustements will be needed since when load it considers as
        # volume and to put in derivatives

        # ON HOLD FOR NOW generate qc report
        print("qc report to be generated")
        print("self extension directory", self.EXTENSION_DIR)
        shell_script = (f"{self.EXTENSION_DIR}{os.sep}bin/from_sct_qc.sh")
        # shell_script = (f"{self.EXTENSION_DIR}{os.sep}bin/from_sct_qc.sh 'jacques' ")
        #make sure you have the permission to execute the shell script
        # Execute the shell script
        # result = subprocess.run([shell_script], capture_output=True, text=True)

        # background image
        # volumeNode = slicer.util.getNode('MRHead')
        print("******volume node: ", self.VolumeNode)
        # background_image_path = self.VolumeNode.GetStorageNode().GetFileName()
        print("storage node:", self.VolumeNode.GetStorageNode().GetFileName())
        bg_image = self.VolumeNode.GetStorageNode().GetFileName()

        #name of the current segment
        segmentEditorWidget = slicer.modules.segmenteditor.widgetRepresentation().self().editor
        selectedSegmentID = segmentEditorWidget.mrmlSegmentEditorNode().GetSelectedSegmentID()
        print("name of the current segment:", selectedSegmentID)
        # current segment node path (mask)
        current_segment_path = f'{self.OutputFolder}{os.sep}{selectedSegmentID}.nii.gz'
        print("current segment path", current_segment_path)

        #path of the current roi segmentation
        #please note that this works only for bids (always 10 characters for
        # subject naming)
        labels_path = f'{self.CurrentFolder}{os.sep}derivatives{os.sep}labels'
```

- Simon : Automatic motion artifact detection :
    - Presentation : https://docs.google.com/presentation/d/1oyHYMKwj_ReGz5AquS6c_trKRbAr4qfDrTyID_x8Ngk/edit?usp=sharing
    - JCA: need to discuss more the different types of artifacts with people in the lab
    - JCA: have more diversity in the dataset ? Maybe not
    - JCA: create an artifact.yml in each dataset
    - PL: Should I leave the artifacted images when doing DICOM to BIDS ? yes

Action Items

- ☐ Maxime: Document frustrations/improvements requests regarding manual correction to prepare the meeting
- ☐ Maxime: organise meeting and create team for the Kaggle challenge
- ☐ JV/SB: Follow up on conflicts between #275 / #276 + release creation
  - ☐ Still not here → Move to next meeting
- ☐ BT: Open issue on BIDSification repo to document/publish metadata-downloading with Datalad
  - ☐ Hacky script? Did not upload yet → Forgot, move to next meeting. :)
- ☐ MGP/Emma: Think about how to reorganize Gitea orgs / dataset permissions
  - ☐ Not yet!
  - ☐ Context
    - ☐ Big question, not specific to SCT.
    - ☐ Everything under “datasets” org, could be moved into histology vs. mri orgs
    - ☐ Standardizing dataset naming conventions
  - ☐ Should we take a few minutes to discuss in the next lab meeting?
- ☐ Make sure that folks know that lab meetings won’t end for the summer (JCA -> Eva)

2024-05-15

Attendees: Joshua Newton, Mathieu Guay-Paquet, Nilser Laines Medina, Maxime Bouthillier, Simon Queric, Julien Cohen-Adad, Baptiste Taverne, Naga Karthik,
Not yet arrived: Sandrine Bédard, Jan Valosek, Rohan Banerjee, Nathan Molinier, Pierre-Louis Benveniste, Benjamin De Leener,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: TBD

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared
- Trying new system: Minutes taker controlling the agenda

Check last meeting's action items

☐ JV/SB: Follow up on conflicts between #275 / #276 + release creation
  - Not here -> Push to next meeting

☑ ~~MGP: Change milestone dates to be quarterly~~

☑ ~~SimonQ: Try out the latest SCT course material~~
  - Straightforward! Good to hear 🎉

☑ ~~BT/MGP: Improve the process of fetching OpenNeuro data/metadata (using "official" Datalad tools/scripting to make things faster/more reproducible)~~
  - OpenNeuro datasets are hosted on Amazon S3, and we were able to use standard command-line tools to fetch only the nifti header (HTTP range requests, gzip, head)
  - Just a few command line tools piped together (no code)
  - Faster but not instantaneous
  - 700 down, 200 to go
  - Sometimes crashes, unclear why, but still fast enough → doesn't interrupt shell commands
  - Useful tool → Document/publish/etc. → Action item: Open an issue for BIDSification repo?

Software Development

- Sidecar functionality for sct_deepseg is implemented!
  - Please try it out!
  - Huzzah! 🎉
  - JSON schema can still be changed, so please try this with manual correction package and provide feedback if necessary.

- #4477: Straightening is not bijective
  - This is pretty technical to try to explain mid-meeting

  - Should we save until the end of the meeting? (Chat between JCA/MGP/JN)
  - MGP is on it → suspicion re: qforms and/or centerline tilt/alignment
  - Benjamin replied on Slack (no github access?)
    - Should we grant Benjamin github reply access?

- #4484: Not blocking SCT installation for failed downloads
  - Issue: How do we emit a useful error message
  - Potentially check for missing packages not at the end of the install script, but in sct_check_dependencies
  - List of "default" data could be stored in the SCT package

- #4481: Postprocessing functionality for monai/nnunet (i.e. non-ivadomed) models
  - This issue is because ivadomed has specific postprocessing functionality, but the new MONAI/nnUNet models do not get this functionality
  - Naga: working on it.
    - "keep largest" option needs to be adapted to be opt-in OR model-specific
  - JCA comments:
    - Moving away from ivadomed → Still working on it, taking time,
    - Jeanne working on moving 1 model to MONAI
    - Motivation: Ease burden of import time
      - Lazy imports! → JN has proof of concept already
      - Typically, import will be moved inside the function
      - But, standard library has "lazy importing" alternative tool that allow you to put the lazy imports at the top of the file
        - Example: lazy_import("ivadomed")
        - Only really useful for CLI scripts where different arguments have different import requirements

Research

- Nilser: GM contrast-agnostic segmentation
  - 4/6 collaborators have accepted to share data/masks
    - Goal : train robust model to have better performance on sct_deepseg_gm and lumbar
    - (sct_deepseg_gm currently only works on t2s images, I believe?)
    - (dilated? pyramidal?) convolution could be the best approach?
    - Dilated convolutions, atrous convolution → some keywords

- Nilser: new lumbar dataset #313
  - Name? → mri-histology
  - General dataset conventions
    - Check wiki (of ivadomed) → https://github.com/ivadomed/ivadomed/wiki/repositories#data
    - Underscores aren't great? (instead, replace _ by -)
    - Not set in stone → Redecide then document on the intranet wiki? (Ivadomed Wiki obsolete)
      - Axondeepseg examples : having 2 dataset s(one for pathology, one for MRI)
      - Pathology and/or region and/or species?
      - Ex of how organizing datasets could be : pathology-site-
        - Ex ms-canproco
      - Attention! To have issues, it must be associated to a repository — makes more difficult to address conventional naming of datasets
        - To correct: copy issue and save it in data management, then save
  - Organizing Gitea orgs/datasets?
    - We can have multiple orgs!
    - Emma/MGP → Think about how to organize Gitea
      - histology, mri

- MGP: Added instructions for connecting to data server when on the VPN (or eduroam at Poly) (if on wired connection, it is not needed)
  - https://intranet.neuro.polymtl.ca/data/git-datasets.html#connecting-from-wifi-or-off-campus
  - Now that Gitea is usable, we can do PR workflows off GitHub (no need to use GitHub for data management anymore?)
  - PSA: Use GUI for management/creation of new repos + templates
    - Need to repeat this in the general meeting
  - How to divide the workload between platforms…
    - GitHub: Public-facing, can discuss issues with outside collaborators
    - Gitea: What pros are there to doing issue tracking here?
    - Are there any bots that can sync comments between GitHub and Gitea?
    - Division of work:
      - Issues: GitHub
      - PRs: Gitea
  - Who gets notified on Gitea?
    - Julien/MGP/Nathan/anyone with write access to the repo
    - Use GUI for management/creation of new

Action Items

☐ JN: Finish lazy importing to limit the burden of importing ivadomed, etc.

- ☐ BT: Open issue on BIDSification repo to document/publish metadata-downloading with Datalad
- ☐ MGP/Emma: Think about how to reorganize Gitea orgs / dataset permissions
- ☑ ~~MGP: update intranet docs about issues being on github, pull requests on neurogitea~~
- ☐

2024-05-02 (Moved to Thursday)

Attendees: Julien Cohen-Adad, Joshua Newton, Nilser Laines Medina, Simon Queric, Mathieu Guay-Paquet, Pierre-Louis Benveniste
Not yet arrived: Sandrine Bédard, Jan Valosek, Naga Karthik, Rohan Banerjee, Nathan Molinier, Jeanne Malécot, Benjamin De Leener
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: TBD

Miscellaneous items

- Zoom setup: 1) Double-check audio 2) Zoom on screen 3) Meeting agenda screen-shared
  - JN: Looks and sounds good!
- Small group this week!
- Welcome Simon Queric 🎉
  - Internship (5mo)
  - Subject: TBD – medical image processing, AI, etc.

Check last meeting's action items

- ☐ JV/SB: Follow up on conflicts between #275 / #276 + release creation
  - Not here – follow up when they return. :)

Software Development

- SCT v6.3 has been released! 🎉🎉🎉
  - Good luck at ISMRM!
  - Posters/stickers will be distributed – ISMRM advertisement :D

- JN: Future release milestone dates
  - We originally did not schedule v6.3 around ISMRM, resulting in a last-minute scramble.
  - So, we should work around any future deadlines where SCT will be referenced:
    - ISMRM conference: **May**
    - SCT Course / ISMRM submission deadline: **November**
    - Are there any other important dates we should work around?
      - ISMRM workshops? (There's one in Quebec City!)
      - Any other conferences?
  - Release date proposals:
    - Biannual: **April** / **October** release dates (e.g. SCT v6.4: October)
    - Quarterly: **April** [July] **October** [January] (e.g. SCT v6.4: July)
      - Stick with existing plan (every 3mo)

- JN: Priorities for SCT v6.4 (Milestone)
  - QC report rework

        - sct_deepseg JSON sidecars (PR opened! #4466)
            - Current format is inaccurate (2 “GeneratedBy” entries should be 1 entry)
            - Feedback
                - Don’t store all of the mirrors – only store the one that was actually used.
                - Add exact command that was used to the sidecar output
                - Can add custom fields (for SCT version, model version, etc.)
                - Should we scrub the personal information from the JSON sidecars?
                    - We aren’t doing this currently for sct_run_batch/QC
                    - But, that doesn’t mean we shouldn’t start trying this now…
                    - Pros vs. cons – we care more about the parameters than the exact command
                - BIDS standard for “Name” “Version” “etc.”
                    - Name → Pipeline (sct_deepseg) or software (spinalcordtoolbox)?
                    - Should “CLI args” be a separate entry? Or, should we combine them (e.g. (“spinalcordtoolbox”)
                - Should we use the specific git reference in `CodeURL` → Yes!
        - If you think of any other “high priority” issues, please assign them to the v6.4 milestone
            - I use the milestone link as a “TODO list”/backlog, so if there’s an issue that you want my attention on, tagging it with the milestone is the best way to do it!
        - Next release -> July! 🎉

- JN: Status of the `sct_compute_flow` PR (#4302)
    - This PR has been pushed from 6.2 -> 6.3 -> 6.4
    - Can we spend a moment to look it over in this meeting? (Or, 1 on 1 after the meeting ends?)

Research

- JN/Naga: a dataset for benchmarking different SC seg methods?
    - Context: Testing contrast agnostic softseg on SC compression: Source
    - Model worked well on individual images, but do we want to test a benchmark dataset?
        - JCA: Outside the scope of SCT maintainers

- Nilser: Contact collaborators for GM contrast-agnostic segmentation (3T and 7T)?
    - Roland Henry (sp?) → PSIR data
    - Contrasts:

- Baptiste: BIDSifications contrast classifier project
    - **Context**: Extend existing contrast classifier (done in first weeks of internship)
        - 2-contrast initial version performs poorly
        - Want to expand to analyze all possible contrasts (T2 , T2*, etc.)
        - Application: BIDSification (to automate automate renaming with contrast)
        - MGP can help with BIDS-specific details
    - 750 OpenNeuro subjects, Several days/weeks to download

    - Think about scaling / data storage / future revision
    - Is this CSV creation involving a lot of manual work? Can anything be automated sped up?
    - How can we get the metadata while speeding up the process?
    - MGP will offer to help make this process easier/faster 🎉
    - Can we partially download the files (to fetch just the header information?)
      - Nii vs. nii.gz may be a quirk to work around
      - HTTP download method → only download the first N bytes
    - Datalad community is active and may suggest solutions, too!
  - Training is currently running
  - Detail: 4D vs 3D
    - Multiple classifiers, no need to have a "universal" 4D/3D classifier
  - Related: Praxis project
    - What contrast?
    - What orientation? (Axial/sagittal)
      - We can tell via anisotropic (e.g. X*Y*Y → just look at "Y", no need for AI)

Action Items

☐ JV/SB: Follow up on conflicts between #275 / #276 + release creation
☐ MGP: Change milestone dates to be quarterly
☐ SQ: Try out the latest SCT course material
☐ PLB/MGP: Improve the process of fetching OpenNeuro data/metadata (using "official" Datalad tools/scripting to make things faster/more reproducible)

2024-04-17

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Naga Karthik, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Jeanne Malécot, Maxime Bouthillier
Not yet arrived: Rohan Banerjee, Benjamin De Leener,
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: Pierre-Louis

Miscellaneous items

- PSA: Your PolyMtl address grants GitHub Education benefits
  - JN: Non-student faculty can apply under “Teachers”, mine was approved in 5m
  - How to preserve your polymtl account? → Need to log in every 3m?
    - Unsure how uni defines “active”/”inactive” after graduation
- Jan: SCT stickers are now printed!
  - Everyone going to ISMRM can take a few from me :-D
- Jan: New fliers
  - Last minute update → release v6.3 before ISMRM?
  - We may need to update the fliers if we’re releasing v6.3
  - Link is independent of release – only the text changes (2 → 3)

Check last meeting’s action items

☑ ~~JN: Investigate possible convention mismatch between -getorient and -setorient~~
  - The two commands seem to agree?
  - Pick any image -> -setorient RPI -> -getorient (returns RPI)
  - SB: In a past project, they didn’t agree. (Which data/repo?)
    - MTS → spine-generic data-multi-subject, mt-on→ Follow up later once we find the data

☑ ~~JN: Add more visible documentation for how to use SCT with GPUs.~~
  - The exact steps depend on what gets merged, but the PR still needs to be reviewed. EDIT: Has been reviewed by Naga!
  - I’ve added updating documentation as an action item on the PR, though.
  - Jan has to review; sorry for the delay

☑ ~~JN: Write test for GPU usage that works alongside MGP’s new mouse data testing~~
  - JN: I’m not sure if I can access data.neuro.polymtl.ca remotely (via VPN), so I don’t seem to be able to access sct-testing-release… I think there was an SSH-based workaround, though? I’ll need to look into this.
  - MGP: repo created sct-testing-release
  - MGP: issue created SCT#4441
  - We’ll do this as part of the imminent release 😉

☐ JV/SB: Follow up on conflicts between #275 / #276 + release creation

- Release branch first, then merge important parts in master!

Software Development

- PLB :
    - ~~issue with `sct_image -copy-header` : issue 4424 : resolved~~
    - Lisa Lee: How to use the canproco nnunet model for lesion segmentation using SCT ? Time-sensitive issue…
        - PL: How to release canproco lesion seg model into SCT
        - Should be relatively easy as we already have nnUNet wrapper under SCT (for SCIseg and rootlets models)
        - PL : to do: Create a new branch/PR, add the model and tell Lisa how to git clone SCT and use it

- Julien: packaging of manual-correction script
    - Goals
        - Making it easier to install (e.g. PyPI → pip install)
        - Making it more generic
        - Making it easier to use (too many options)
            - Discussion from SB re: fetching segmentation from derivatives
            - QC yaml doesn't specify the segmentation name directly
            - Lot of tricky usages + tedious manual labor involved in current usage
        - Add missing use-cases (fMRI, branches are open?)
    - Packaging as part of SCT (previously discussed as part of #3353)
        - We said no previously, due to the heavy SCT dependency (when some users do not need this – install manual correction separately)
        - However, if manual-correction is pip-installable, then SCT could fairly easily integrate the script as-is by pip installing it into the SCT conda, then lightly wrapping it in an SCT command (`sct_manual_correction` → directly exposing the manual-correction argparse)
    - Sandrine:
        - Has a branch for fMRI (because there several tasks for each fMRI task)
    - MGP: Out-of-the-box idea
        - Separate QC from SCT and have it be a common dependency of both SCT and manual-correction?
            - Great idea!
            - People could use it for brain

- Jan: manual-correction issues:
    - `-path-out` #83
    - Modification of the config file #86
    - Latest convention adoption #87

Research

- `Contrast-agnostic` model → how easy is it to update the model in SCT? Is it as simple as updating the url pointing to the release? → JN: Yes!
    - New version of SCT (i.e. v6.2.1)? Is it worth it?
    - Maybe we can wait until the last week before ISMRM for a new release? Still training models so before May 1st there will be a better model
    - Mathieu: Do a release a week before May 4th (beginning of ISMRM)
    - **✋ Joshua**: As far as coordinating SCT release + contrast agnostic release, we could create a placeholder release name for the contrast agnostic model (e.g. **“ISMRM 2024 release”**) and commit that URL to SCT. Then, if Naga wants to update the model again in the next two weeks, then we can just change the upload associated with this placeholder release tag (that way, we don’t have to worry about updating SCT at the last minute)
    - April 25th – create SCT release.

- Jan: `SCIseg` model → the same as the previous point
    - Should be added in release 6.3

- Nathan: packaging SPINEPS and cGAN
    - Nathan: maybe we don’t want to add SPINEPS as a dependency (too large, as previously discussed + Python 3.10 conflict)
    - Nathan: Adding SPINEPS is relatively easy (pip install -e .)
    - Mathieu: SCT command can check if the SPINEPS command exist : temporary solution
    - To be continued

- Jan: Discuss the compression labeling approach
    - How many slices to label etc.
    - Model training:
        - At least one point of compression, how much it spans is less relevant?
        - Is the extent relevant?
        - Distance between compression?
        - For trauma, not at the disc?
            - Less clean about compressions?
    - Jan: Compressions are detected in the sagittal view and in the axial slice, we segment one voxel.
    - Naga: Problem: too much context (class imbalance)
    - Julien: one solution: classification task on axial slices : this requires to update the labels. Start on a 2D axial classification model and see how it performs

- Nilser: GM contrast-agnostic segmentation (3T and 7T)
    - Collect data: axial GRE T2s, PSIR, AMIRA, MP2RAGE, SWI, ex-vivo
    - Nilser: request more data (more contrast) to train and improve the performance of the model

Action Items

- ☑ ~~Jan: update the flyer to SCT 6.3 (the QR code is still the same as it points to SCT Release page)~~
- ☑ ~~PLB : for Lisa Lee : Create a new branch/PR, add the canproco model and tell Lisa how to git clone SCT and use it. Add milestone 6.3 to the issue related~~
- ☑ ~~Naga: open PR to update URL for spine-generic (SCIseg, right?)~~
- ☑ ~~Next meeting: May 2 (many people will not be present, but keep the date)~~

2024-04-03

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Naga Karthik, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Jeanne Malécot, Samuelle St-Onge, Baptiste Taverne
Not yet arrived: Rohan Banerjee, Benjamin De Leener
Moderator: Julien Cohen-Adad
Developer Minutes: Joshua Newton
Research Minutes: Jan

Miscellaneous items

- Welcome Baptiste Taverne
  - Possible project: Segmentation tasks, generalization, superresolution, etc.!
  - Welcome! 🎉
- Jan: sent a request to print SCT stickers!

Check last meeting's action items

- ☑ ~~JN/MGP: Add T1w mouse testing image to a new dataset + fix the datatype. (MGP: I forgot, sorry! JN: Me too, sorry!)~~
  - WIP: MGP has started it. (Thank you!)
- ☑ ~~JCA: Follow up with person who asked for video of SCT course (MGP: done)~~
  - Too late for sending a large email
- ☐ JCA: Look into seeing if we can delete the \`sct_testing/large\` dataset (comment)
  - It already exists on git-annex → need to double-check if all data has been moved
- ☑ ~~JN: Summarize for Hendrik discussion about SPINEPS integration~~
  - On the issue → see this comment
- ☐ NM/NK: Schedule separate meeting with Hendrik → discuss availability?
  - SPINEPS is not doing labeling → wait to figure out how we want to use it
- ☑ ~~JN: Add link to review paper to SCT readme/introduction~~
  - See #4418.

Software Development

- JN: Progress update: I have mainly been working through my backlog of new bugs and user reports that have been discovered in recent weeks.

- JN: sct_deepseg GPU inference support (#4360)
  - I have been working on a prototype for this here.
  - ~~It is almost ready for testing, but I was interrupted by a user forum post this morning. 😅~~
    - It is now ready for testing! 🎉
    -
      ```
      CUDA_VISIBLE_DEVICES=X SCT_USE_GPU=1 sct_deepseg -task
      seg_sc_lesion_t2w_sci -i t2.nii.gz
      ```

      - `X` can the no. of GPUs e.g. `CUDA_VISIBLE_DEVICES=0,1,2` to use GPUs 0, 1 and 2
    -
  - Are there any research folks who want to test this out when it's ready? (Ideally on a large sct_run_batch job for romane/rosenberg)
    - Jan: Yes, I'll be happy to test the PR!
    - Naga: Even I volunteer to test! (Thank you! 🎉)

  - Test on new automatic release repo?
    - Follow-up with what MGP will do to test the "manual" data

  - Add documentation so that this "hidden environment variable"
    - Dev wiki?
    - GPU clusters page on intranet?
    - Make sure to document the resource calendar too (so that people will know which GPU IDs to select with CUDA_VISIBLE_DEVICES)

  - Jobs (i.e., number of subjects) vs. "CUDA_VISIBLE_DEVICES"
    - jobs=4 → single GPU is OK → in this case, 4 subjects will be processed on a single GPU (it won't crash, assuming the GPU has enough memory)
    - jobs=4 + CUDA_VISIBLE_DEVICES=1,2,3,4 = ??? (do the jobs get spread out across the GPUs that were made available to PyTorch?)
      - Yes, for e.g: say `jobs=2` in `sct_run_batch` args and inside the script we specify the GPUs as follows:
        - `CUDA_VISIBLE_DEVICES=1 SCT_USE_GPU=1 sct_deepseg -task seg_sc_lesion_t2w_sci -i t2.nii.gz`
        - `CUDA_VISIBLE_DEVICES=2 SCT_USE_GPU=1 sct_deepseg -task seg_sc_lesion_t2w_sci -i t2.nii.gz`
      - Then, jobs *do* get split across the GPUs. See [this example]() of how it can be used within a run_batch script.
      - JN: Does `=1,2` not split them up, too? (Like, will PyTorch automatically distribute the jobs to the "least used" available GPU among a group of GPUs?)
        - Ah that might be! I have only clubbed GPUs (i.e. "=1,2") when I needed to run the same process on multiple GPUs (i.e. one process on 2 gpus instead of 2 processes on 2 separate GPUs)
        - Ah, gotcha! 👍
  - https://monitor.neuro.polymtl.ca

- NM: Question about orientation convention ([#4419]())
  - We use a different convention: Us: LPI, nibabel: RAS (we say the opposite)
  - Important: +/- is necessary for clarifying the ambiguity, but we don't really use this?
  - Action item: -getorient may not match -setorient (is this true?)
  - Is it worth changing the convention? (BIg change, we'd have to relearn our default conventions)

    - `sct_image` supports: `-header [{sct,fslhd,nibabel}]`

- MGP: For the mouse testing image, I got the image from Joshua and am currently setting up `datasets/sct-testing-release` on data.neuro.polymtl.ca for large/private/manual tests.

Data Management

- Jan & Sandrine:
    - spine-generic/#275 - update from Rene Labounek
        - conflicts for the `process_data.sh` script caused by the update of the naming convention done in #276
        - Script has also diverged in other ways (slightly different extract metric steps, etc.) → JN: I recommend using https://diffchecker.com to view difference (rather than "resolve conflicts") if there is no good automatic diff view already available
        - Publish a release from his branch (i.e., do not merge to `master`)

Research

-

Action Items

☑ ~~JN: Investigate possible convention mismatch between -getorient and -setorient~~
☐ JN: Add more visible documentation for how to use SCT with GPUs.
☐ JN: Write test for GPU usage that works alongside MGP's new mouse data testing
☐ JV/SB: Follow up on conflicts between #275/#276 + release creation

2024-03-13

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Naga Karthik, Rohan Banerjee, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Jeanne Malécot, Benjamin De Leener
Not yet arrived:
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

-

Check last meeting's action items

- ☑ ~~JN: Don't crop QC in SI axis for `sct_deepseg_lesion` → context is important~~
- ☑ ~~JN: Discourage usage of existing duke datasets in SCT Wiki~~
  - Done: Wiki page here
- ☑ ~~JN: Communicate GM/WM angle correction to Benjamin (Zurich)~~
  - Email sent + updates provided in the relevant issues.
- ☑ ~~JN: Record the change in scope for the JSON sidecar feature in the relevant issue + link to manual correction PR for reference ("GeneratedBy")~~
  - Done: Comment here.
- ☐ JN/MGP: Add T1w mouse testing image to a new dataset + fix the datatype.
  - I forgot to add this as an action item last week → I will follow up this week.
- ☐ JCA: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides (will do by Friday Jan 26) → TBD
  - Too late for sending a large email? → OK!
  - Follow up for the person who has asked.
- ☐ JCA: Look into seeing if we can delete the `sct_testing/large` dataset
  - Julien had made a self-comment: https://docs.google.com/document/d/1ItApJQfajO2IRzOU2yenWbeRg6alfsdut3J4AVVdo78/edit?pli=1&disco=AAABG1JB-Bg
  - Can it be removed? (It already exists on git-annex → need to double-check if data has been duplicated correctly)
- ☑ ~~JV: Update poster to advertise v6.2 + SCT mailing list 🙂~~
  - Discussed in a post to the #sct_dev channel
- ☑ ~~NM: Provide updates on the superresolution segmentation paper (How do they do it?)~~
  - Point added under research.

Miscellaneous items

- Next meeting
    - 3pm on Wednesday is tricky (conflict with flight?)
    - Skip next week's meeting then do 3 weeks from now, April 3rd. ✅
    - Hendrik meeting → Side meeting, not main SCT meeting, need to chat about availability.

Software Development

- JN: Status update on SCT development
    - Note: I don't really have anything that needs meeting input/discussion.
    - Many of the in-progress issues/PRs have been approved and are close to merging:
        - QC fixes:
            - ✅ #4383: Fix coloring for full-spine label QC
            - ✅ #4393: Sagittal mosaic SI-axis padding
            - 🚧 #4389: PSIR data contrast bug (fix in-progress)
        - ✅ #4395: SCT repo broken link detector
        - ✅ #4396: Use mean magnitude for `moco_params.tsv`
        - 🚧 #4332: Fix dependency conflicts between ivadomed/nibabel/numpy/dipy.

    - Right now, the biggest bottleneck for development is #4400 (macOS GHA limits)
        - Only 5 macOS runners can be active (even on paid plans!), causing delays.
        - I will try to address this ASAP (today) so that we can begin merging all of the approved PRs in sequence.

- MGP: QC fixes in backlog, will work on it soon (once IT/data management tasks are resolved)
    - Which fixes / QC report hacks (#4166) are going to be added?
        - Future meeting → Check which ones are still relevant!
    - QC refactor is needed first. Prototype looks good, but needs a little more work.

    - NK: Would a spinal cord contouring option (Fig 4 in this paper) for QCing with `sct_qc` be useful?
        - Mention of difficulty for generating this (why?). Reliability, etc.
        - How to display? (Less than one voxel, etc.)
        - Mention of whether this should be a checkbox in the QC reports, or a flag in the QC command…
        - Hacky possible implementation: dilate the SC by a single voxel and then subtract.
        - Nilser: QC contourning/region : nisnap

    - Sandrine: Resampling in QC can be tricky for identifying exact voxels for correction
        - Nearest neighbor vs. linear.

Research

- NM: SPINEPS integration into `sct_label_vertebrae` → issue
  - Joshua Newton : **Context:** `spineps` is a large Python package (heavy dependencies, heavy models) that does much more than just disc detection. (Vertebrae labeling, endplate, sacrum, etc.). It also requires Python 3.10. ❌
    - So, integration into SCT would require simplifying the output and/or processing.

  - NM: Fork with a script doing a simple run
    - I added a function to extract the point labels for the discs (3 → 25) (see labeling convention)
    - Still need to add point 1 and probably 2 but how should I compute it?
    - JN: Label extraction needs to be optimized → not that fast? (Profiling, fast numpy array operations, etc.)

  - SPINEPS maintainer (Hendrik Moller) joined Slack! Very receptive to feedback, too. 🎉
    - → Discuss how we can isolate the output we want without necessarily installing the heavy dependencies.
    - “Ease of user install” vs. “maintenance burden” → Tricky to balance
    - Can we extract the “inference code” separate from the training code?

  - Note about ANTs vs. ANTsPy in SCT
    - Hard to reduce size since ANTsPy comes with _everything_ but we only need 4 functions for normal SCT usage.

  - Large model file → 3-fold vs. 1-fold
    - We could reduce that size by isolating only the input we need?

  - Integrating into SCT v6.3.
    - Long-term rewrite of SPINEPS → Might be more involved.
    - Full SPINEPS processing might be *very* long.
    - Separate the tasks into two parts:
      - “Disc label extraction” → light, easy to implement, part of sct_label_vertebrae?
        - Brainstorming right now…
        - Morphometrics (skeletonization)
        - Computing bisecting plane (focus on just the anterior-posterior / right-left axes)
      - “Full SPINEPS segmentation” → Heavy, needs work, part of sct_deepseg?

- JV: A new review about SCT just came out 🎉
  - Congrats on the publication! (A little strange to review our own tool!)
  - Should we link to this on the “citing SCT” page or something along those lines?

    - Not on citing SCT
    - Not on studies using SCT
    - But… maybe Tutorials? Introduction? “Usage on README”
  - Good for advertising SCT → Add QR code to conference posters?
    - Maybe? No? QR already includes a landing page anyway! (Always up to date)

- JCA: Robert Graf on superresolution paper → application to lesion seg?
  - Colleague of Hendrik → Naga is going to visit! Going to talk next week…
  - Could it be applied to lesion segmentation?
    - Dataset would need to meet requirements of the superresolution paper → multiple sessions/contrasts/etc.

Action Items

☐ JN: Summarize for Hendrik how we can integrate SPINEPS → lots of ideas (Potentially schedule a meeting?)
☐ JN: Add link to review paper to SCT readme/introduction
☐ Schedule separate meeting with Hendrik → discuss availability?

2024-02-21

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Benjamin De Leener, Nilser Laines Medina, Rohan Banerjee, Jeanne Malécot
Not yet arrived: Naga Karthik
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

- Joshua Newton : Congrats on the release of SCT v6.2! 🎉
  - New models are now available in a stable release.
  - v6.3 Milestone is scheduled for June 20th, 2024.
- Jan Valošek :
  - Do we want to prepare a flyer for the following conferences (ACTRIMS/CSS/ ISMRM/OHBM) promoting SCT v6.2 (and potentially also the next SCT course)?
  - The previous flyer (v6.0 + SCT Course) + Stickers? 👍
    - Above conferences are happening next week / 3 months (!!!)
    - Screenshot of how models work? (for advertising sct_deepseg)
    - Have we settled on a date for the next SCT course? (Do we know in advance?)
      - Maybe point to the general SCT Course page on the website?
      - Or, subscribe to the mailing list! (Good idea!)
      - Mention rough estimate of when the next course may be (~Nov 2024)
    - Jan will prepare. (Thank you! 🎉)

Check last week's action items

- ☐ JCA: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides (will do by Friday Jan 26) → TBD
- ☑ ~~PL: crop a mouse image and make it available for model testing in continuous integration~~
  - Further discussion later on
- ☐ JN: Don't crop QC in SI axis for `sct_deepseg_lesion` → context is important
  - Not done yet, my apologies! But there is an open issue :)
- ☑ ~~v6.3: Prioritize QC refactor – more and more popular, we're pushing its limits~~
  - Added to v6.3 milestone.

Software Development

- Joshua Newton : T1 mouse data for testing
  - **Context:** Mouse image is too large for `sct_testing_data`, and also private (is this true?)
    - sct_testing_data -> 7MB
    - Mouse image -> 10MB (todo: look into dtype/cropping/etc. to reduce size)

    - So, we planned to store the mouse image outside of `sct_testing_data`, and only run the test locally if the image is present on disk.
        - Consider "optional group of tests" explicitly (pytest.mark) 👍
    - Where should we store this image?
        - We have some existing duke datasets:
            - `sct_testing/large`: Large collection of sample datasets
                - JCA: This is outdated, side note: do not use anymore!!
                - JN: Update SCT Wiki to discourage usage of sct_testing/large
            - `sct_testing/issues`: Private user data
            - ^ these were just provided for context. Neither of these are suited to the purpose of "hand-picked images used in specific `pytest` tests"
        - Some suggestions for storage given by Mathieu in this comment.
        - Ideally, the storage folder would be set up to be easily downloaded and extracted to the existing `sct_testing_data` folder (to enable local testing)
            - Conclusion: Create a separate dataset

- Joshua Newton: Computing angle-corrected CSA for GM/WM masks
    - **Context**: `-angle-corr 1` does not work for GM/WM masks (Issue #4367)
    - Julien suggested a workaround: Multiplying by the cosine factors from SC -angle-corr 1
    - However, multiplying by the cosine factors produces slightly different results compared to -angle-corr 1 (Issue #4378)
    - How should we do angle correction for GM/WM masks?
        - Follow up offline?
        - JCA: Differences are not significant for the kind of research they are doing.
    - Side question: Orthogonal area vs. axial area + angle correction
        - MGP: Is this not just equivalent to straightening + normal method?
            - JCA: Not necessarily → Additional imprecision/discretization errors?
        - Something to consider: Orthogonal area → does not add to the total volume of the cord (voxels may be duplicated, so would be an entirely different method compared to our current angle correction)
        - BDL: Orthogonal vs. corrected axial → Not an issue. Past discussion (years ago) we concluded that the different methods result in negligible area → a lot of work for not much difference
            - (JN: 👍)
        - JCA: Depends on what we want to do with the CSA → people have very different needs, maybe just focus on BFCombes use case for now?

- JCA side note: `sct_label_vertebrae` also struggles with orthogonal/axial projection of vertebral disc labels when there are highly curved cords → Relevant for Nathan?
    - Do we already have this feature?
    - sct_label_utils -project centerline is already added! (QC?)
        - But we don't consider LR/AP in the current projection? TODO?

- Joshua Newton: Follow-up on "Averaged Moco Params" feature request (#4344)
    - Quite a lot of back and forth discussion! (Some confusion?)

  - It seems like the suggestion was narrowed to 2 different metrics:
    - One summary value: Average RMS → sum(sqrt(xx+yy))/n
    - Two summary values: sum(abs(x))/n and sum(abs(y))/n
    - Which should we implement?
      - It is clear in the discussion thread!

- Joshua Newton : Are there any high-priority issues that I should focus on for 6.3?
  - **Context**: Many new issues (small bugs/enhancements) have been opened during the 6.2 development period. (Thank you to everyone who has opened new issues!)
  - To the students in the lab: Are there any issues in particular that are specifically hindering your research?
    - Sandrine: QC report!
    - PL : MS lesion segmentation multi-contrast? → Link to issue?
    - EPI segmentation model (Rohan)
    - JV: JSON sidecar / Compatibility with BIDS?
      - Useful for `sct_run_batch` + full pipelines (e.g. manual correction)
        - Temporary solution was added for manual correction.
      - MGP: Not necessarily useful for individual functions?
      - JCA: Create json sidecars just for `sct_deepseg` to start?
        - Much easier in scope!
    - If there are no other high priority, I can continue to triage issues on my own. 🙂

Research

- Jan Valošek :
  - Talk about "Modeling the acquisition shift between axial and sagittal MRI for diffusion superresolution to enable axial spine segmentation" paper
    - Naga not present → Make sure we bring this up again
    - Paper mentions 2 open access lumbar datasets
      - MRSpineSeg → Where to download? (Yehuda might have it!)
      - Might be useful to store alongside the Spider dataset (bidsify, annex?)
    - JCA's comments
      - We are currently collaborating with the authors! 🎉
      - How do they do the segmentation? (Model architecture details, Python frameworks, etc.)
      - Could this be integrated into SCT?
        - Speak with collaborators about this idea!

Action Items

☐ JN: Don't crop QC in SI axis for `sct_deepseg_lesion` → context is important
☑ ~~JV: Update poster to advertise v6.2 + SCT mailing list 😃~~
☐ JN: Discourage usage of existing duke datasets
☐ JN: Communicate GM/WM angle correction to Benjamin (Zurich)
☐ NM: Provide updates on the superresolution segmentation paper (How do they do it?)

- ☐ JN: Record the change in scope for the JSON sidecar feature in the relevant issue + link to manual correction PR for reference (“GeneratedBy”)
- ☐ JCA: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides (will do by Friday Jan 26) → TBD
- ☐ JCA: Look into discouraging/retiring the `sct_testing/large` dataset

2024-02-07 (moved to 2:00PM EST)

Attendees: Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Nilser Laines Medina, Samuelle St-Onge, Jeanne Malécot, Julien Cohen-Adad, Pierre-Louis Benveniste,
Not yet arrived: Naga Karthik, Rohan Banerjee, Benjamin De Leener
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

- MGP: During these meetings, please speak up loud enough so that the remote attendees can follow the conversation

Check last week's action items

- ☑ ~~JN: Close discussion thread about crop size, make separate issue~~
  - Done: Issue #4349
- ☑ ~~PL : open an issue in SCT about zurich mouse nnUNet model integration in SCT's future release~~
  - Done: Issue #4348
- ☑ ~~JV: find a subject with "lesion" for the SCIseg model CI/CD~~
  - Done: spine-generic/sub-fslPrisma05_T2w.nii.gz
- ☑ ~~JV: Open an issue with a summary about the "Slice I->S" column in sct_process_segmentation and sct_compute_compression - values are always reported for axial slices (I-S) even though the input images have different resolutions → will open an issue~~
  - Column only applies to the reoriented image (RPI) – agnostic of input image orientation.
  - Does this still apply when the IS axis is actually SI? (e.g. RPI -> RPS, AIL -> ASL)
    - TODO: Check reorientation before/after sct_process_seg
      - ☐ Done in #4363
  - TLDR: No SCT bug, just about making this more intuitive. (Orientations are confusing!)
- ☐ JCA: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides (will do by Friday Jan 26)

Software Development

- SCT v6.2 release is scheduled for next Thursday (2024-02-15)
  - Milestone link (issues + PRs) (link to just issues: link)
  - Which issues are 100% necessary for 6.2, and which ones can be pushed back?
  - Should we delay the releas e a week or two to make time for the remaining issues/PRs?
    - If need be, sure

- Joshua Newton : Status update on MONAI/nnUnet PR #4345:

    - Has been reviewed multiple times, and most review comments have been resolved!
    - Outstanding issues:
        - Models need `long_descriptions` (training data description, etc.)
        - SCI model lesion automated testing
            - Manual testing == ✅
            - Automatic testing == cropped images with hyperintensities don't segment at all, which is a problem for our testing dataset (since we want to keep the file size down)
            - Are we okay with just using manual testing for now? Or, should we try to modify some voxels to add a fake lesion?
                - Discussed earlier: Don't try to create realistic lesions, just try to create a false positive to test the output.

- Joshua Newton : Zurich mouse model integration
    - Good news! It was simple to add it to the existing nnUNet PR: [#4345 (comment)]
    - Issue: Segmentation time and RAM requirements (>20m, OOM crashes)
        - Will work on adding GPU inference capabilities to address this.
        - But, right now it is difficult to test this model without proper data + computing capabilities.
        - MGP: Create tests that are skipped on CI but can be run locally
          Should have test images that can be referenced by url
        - Should we roughly estimate when inference will take a long time? (e.g. post resampling to 0.1mm isotropic, done by mouse model)
            - Something to discuss in future

- Joshua Newton : "internal" GPU inference for `sct_deepseg`
    - Issue opened here: #4360
    - Discussion points:
        - How to install dependencies? (Manual steps vs. Adding an option to `install_sct`)
        - How to enable GPU inference? (CLI option? Environment variable?)
    - Suggestion:
        - Make a prototype for the simplest implementation (manual dependency installation, select GPU # using an environment variable)
        - Then, later on we can consider changing this into a more public implementation (install script, CLI option) once we've tested it internally

- PL : Adding QC feature for full inferior-superior view of spinal cord segmentation
    - Issue here : #4362
    - Joshua Newton : There should be a short-term workaround for now? (creating dilated SC mask)
    - Request: Lesion QC: Don't crop in the IS direction
        - (or at least add padding?)
    - Long-term brainstorming: QC revamp with updated views

    - Don’t use function-based views (e.g. `-p sct_deepseg_lesion`), specify the view itself
    - But we will still need to specify the function for QC fail categorization purposes!!!
      - Side note: `FILES_SEG` is not specific enough, as a single image can have multiple segmentations.
      - Spinal canal seems to be particularly problematic.
    - So, tl;dr, function + view should be separate options, not one or the other.
    - Side note: yaml vs json
      - Yaml is more human-friendly
      - Supports comments
      - JN: Yaml has a lot of footguns, software devs like to roast it :P
      - Add tsnr (sandrine, on going, but to be continued)
  - PL: Feature request: Seeing image and seg side by side for longitudinal data
  - SB: Feature request: Zooming
    - Requires web dev skills qq

- JV:
  - PAM50 rootlets - #29
  - SCIseg and rootlets models released 🎉– both models can be now accessed by `sct_deepseg`
    - SCIseg: r20240130
    - Rootlets: r20240129

Research

- JM:
  - Unboarding completed! → Spent some time exploring the data
    - model_seg_exvivo_gm-wm_t2_unet2d-multichannel-softseg
      Found a corresponding dataset on git annex, but few data
      (model’s description:
      "../duke/projects/ivadomed/gm_t2_exvivo__20210331_223156")
    - Started exploring how we could train this model using **MONAI**; nothing to present this week
  - Still focusing on issue #4234
    - Isolation of the inference code from the rest of ivadomed’s code and integrate into SCT
      - JM is referring to JN’s old “short-term” september suggestion here: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4234#issuecomment-1741515489
      - However, retraining models with MONAI is a separate “long-term” effort, with the goal of getting rid of ivadomed’s code entirely.
    - Should be able to try it on existing models by the end of the week
    - Question about integration
      - Feel free to post in #sct_dev on Slack for questions, and joshuacwnewton (or anyone else) would be happy to help

Action Items

- ☑ ~~All: Remember to write full names – We have a lot of J names!! (JCA, JN, JV, JM…)~~
- ☑ ~~JV: Check reorientation before/after sct_process_seg to make sure IS accurate - issue open: #4363~~
- ☑ ~~MGP: Add next milestone proactively (6.3)~~
- ☑ ~~PL: crop a mouse image and make it available for model testing in continuous integration~~
- ☐ JN: Don’t crop QC in SI axis for `sct_deepseg_lesion` → context is important
- ☐ v6.3: Prioritize QC refactor – more and more popular, we’re pushing its limits

2024-01-24

Attendees: Julien Cohen-Adad, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Benjamin De Leener, Joshua Newton, Jeanne Malécot
Not yet arrived: Naga Karthik, Rohan Banerjee
Moderator: Mathieu
Minutes: Joshua Newton

Miscellaneous items

- Naga: I will not be able to attend today's meeting (too late in my timezone (1:30 am), sorry!). I have been (briefly) assisting Joshua/Mathieu on the nnunet/monai integration PR. Excited with the progress there! Nothing much on my side, have a nice meeting y'all! 🙂

Check last week's action items

- ☑ ~~JN: make a note to add poll results for next course~~
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4303
- ☐ JCA: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides (will do by Friday Jan 26)
- ☑ ~~JCA: we should submit the poll to a larger crowd (maybe sct_mailing list) → not relevant anymore (won't do it)~~
- ☑ ~~JV: Finish sct_compute_compression slice numbering #4326~~
    - Merged! 🙂
- ☐ JV: Open an issue with a summary about the "Slice I->S" column in sct_process_segmentation and sct_compute_compression - values are always reported for axial slices (I-S) even though the input images have different resolutions → will open an issue

Software Development

Joshua Newton :

- Progress Update:
    - I have mainly been working through my backlog of assigned issues + reviewing open PRs (e.g. Flow PR - #4302)
    - In the next two weeks, I will focus on getting the nnUNet/MONAI PR merged, with any remaining time spent fixing important bugs.

- Preprocessing in `sct_deepseg` (MONAI inference: #4345 (discussion))
    - Currently, softseg model has hardcoded center crop size `(64, 192, -1)`
    - Should we add an option to change the center crop size?
        - Current preprocessing order: Reorient -> Resample -> Crop
        - Since we currently crop **after** reorientation/resampling, how will the user know what crop size to specify for their specific data? (Will likely be unintuitive for users… past discussion cross-ref)

-
    -
        - Maybe we could make the behavior modal? i.e. if the user specifies nothing, then do cropping last (as is currently done). But, if the user specifies a crop size, do cropping first?
    - JCA: If we do add an option, then maybe put it in “advanced” section
        - alternatively: propose to input the center crop in the space of the input image, and in the code we adapt the crop box to the 1mm reoriented image to be cropped before nnUnet inference
    - TODO: Review past discussions to see why we chose the order of operations we did.
    - Doesn’t need to hold up the current PR, can be amended later on 🙂

- SCI lesion seg testing
    - Currently we are testing the multiclass SCI seg model (SC+lesion) on the existing `t2.nii.gz` in `sct_testing_data`
        - This works well enough for the SC seg output, but the lesion seg output is empty, and we have no ground truth
        - Should we add lesion data to `sct_testing_data`? If so, which image?
            - Can we manually create a fake lesion for testing purposes?
                - ANS: Not easily done!!! Copy-pasting into healthy subjects doesn’t look realistic
            - Find an SCI image, manually segment, compute DICE?
                - Problem: Data is publicly available, so we can’t use private data
                - Cropping does not get around agreements sadly :(
                - OpenNeuro → See what’s there?
        - Or, is it fine to treat the model as a “black box” when it comes to lesion outputs?
            - Given the difficulty of finding appropriate data, it’s OK to just use the existing data, since we’re mostly just testing for crashes

Jan Valošek :

- Will nnUNet (and MONAI) be integrated into SCT before the v6.2 release? PR #4345
    - I am asking because I plan to submit a preprint in 1-2 weeks and I want to specify in which SCT version the rootlets model will be available
        - ANS: Joshua Newton This is the plan! Jan: Great 🎉

PL :

- Integration of zurich mouse nnUNet model in SCT : link to repo
    - Joshua Newton : ~~Is there a link to the repo? Added above~~ I can try to see whether it’s compatible with the changes from the in-progress nnUnet PR.
    - Depends on how this project was implemented relative to the other nnunet projects -> Investigation is needed -> TODO for Joshua/Mathieu
        - ANS: Inference script has a different name but looks remarkably similar! (`test.py` vs. `run_inference_single_subject.py` → compare methods)
    - Does this need to be in v6.2? -> No

Research

- Intern projects - TODO: list the projects GBM3100
    - Catherine Spino : CanProCo spinal cord MS lesion detection : issue
- Jeanne Malécot:
    - Working on migrate some ivadomed models
    - Still waiting for access to data, but have stuff to do in the meantime
    - First focussing on the ivadomed inference code, will look at monai versus nnunet later
    - The goal is to port the most useful models

Action Items

- ☑ ~~JN: Close discussion thread about crop size, make separate issue~~
- ☑ ~~PL : open an issue in SCT about zurich mouse nnUNet model integration in SCT's future release~~
    - Done : issue here
- ☑ ~~JV: find a subject with "lesion" for the SCIseg model CI/CD - spine-generic/sub-fslPrisma05_T2w.nii.gz~~

2024-01-11

Attendees: Julien Cohen-Adad, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Naga Karthik, Nilser Laines Medina
Not yet arrived: Benjamin De Leener, Joshua Newton, Rohan Banerjee,
Moderator: Julien Cohen-Adad
Minutes: Mathieu Guay-Paquet

Miscellaneous items

- Welcome Jeanne Malécot! 🎉 Will be working on porting the models used by SCT out of Ivadomed

Check last week’s action items

- ☑ ~~JN: SCT_Course_2023-11-20 -> “Make a Copy” -> Move to new folder~~
    - Please make all future changes to: SCT_Course_2024
- ☑ ~~Julien: reuse poll results for brainhack talk~~
- ☐ JN: make a note to add poll results for next course
- ☐ ?: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides
- ☐ we should submit the poll to a larger crowd (maybe sct_mailing list)
- ☑ ~~MGP: Open an issue to prototype sct_deepseg subcommands SCT#4318~~

Software Development

- Pull request questions
    - Can we merge #4326 (slice numbering in `sct_compute_compression`)?
        - Wait for Sandrine's review?
        - Slice ordering: should it always match RPI (I->S)? Or the original orientation? What would the user expect? Need to open a followup issue for discussion
        - Note: I->S means "zero is the Inferior-most slice", not "the rows in this file are ordered"
        - Jan will summarize the discussion on the issue
    - Can we merge #4317 (save QC records in browser local storage)?
        - MGP should review one unresolved comment

- Something to be aware of: Numpy v2 is coming soon, will probably need to restrict our dependency to `numpy<2` for some time (see this blog post)

- Next release (SCT v6.2, milestone link) is coming up on 2024-02-15 (~1 month from now)
    - Are we happy with the release date? Sure why not
      Do we need to coordinate with any conferences or papers coming out or collaborations? Not really

        - What are the main priorities?
            - Integration of nnUnet and monai models (issue #4182)
                - Rootlets segmentation is re-trained, relies on nnUnet
                - The two integrations can be at a separate time
            - Improvements to QC reports (issue #4204)
            - ~~Changing the `sct_deepseg` CLI to use subcommands for the different models (like `git add/commit/etc`) instead of "`-task seg_`" (issue #4318)~~
            - Anything else?

- New contrast-agnostic SC segmentation model: how to switch to it?
    - People will want to still use sct_deepseg_sc command, not break their pipelines, not "sneakily" use a different model
    - Maybe both models (old one and contrast-agnostic) should be available at time same time, for comparison?

- sct_deepseg: we don't want old, unused models to clutter the interface
    - Idea: maybe have sub-sub-commands, to first specify what structure is being segmented (SC, WM, GM, etc.), then second to specify which model/variant
    - The main concern is to avoid overwhelming the user while searching
    - Idea: have a different sct_deepseg_* functions such as sct_deepseg_sc, sct_deepseg_lesion, etc. for each structure, and flags for which model
    - Idea: print which model and the citation in the terminal output every time
    - On-going discussion!

- What date should we set for SCT v6.3? 3-4 months later? Sure
  Coordinate with Jeanne Malécot's end of internship? Not really

- PLB: group in Zurich has difficulties with the new nnUnet model (mouse GM and WM), because nnUnet is difficult to install. So, having it "just work" as part of SCT would be great

Research

- Laurine (GBM3100) working on a lumbar T2*w GM/SC segmentation with nnUnet- supervised by Nathan
    -

Action Items

☐ JN: make a note to add poll results for next course

☐ JCA: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides

☐ JCA: we should submit the poll to a larger crowd (maybe sct_mailing list)

☑ ~~JV: Finish sct_compute_compression slice numbering #4326~~

- ☐ JV: Open an issue with a summary about the “Slice I->S” column in sct_process_segmentation and sct_compute_compression

2023-12-15 (canceled)

Attendees:
Not yet arrived: Benjamin De Leener, Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Rohan Banerjee, Naga Karthik, Nilser Laines Medina
Moderator:
Minutes:

Miscellaneous items

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Check last week's action items

- ☑ ~~JN: SCT_Course_2023-11-20 -> "Make a Copy" -> Move to new folder~~
    - Please make all future changes to: SCT_Course_2024
- ☐ Julien: reuse poll results for brainhack talk
- ☐ JN: make a note to add poll results for next course
- ☐ ?: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides
- ☐ we should submit the poll to a larger crowd (maybe sct_mailing list)
- ☑ ~~MGP: Open an issue to prototype sct_deepseg subcommands SCT#4318~~

Software Development

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    -

Research

-
    -

Action Items

- ☐
- ☐

2023-11-30 (SCT Course postmortem)

Attendees: Mathieu Guay-Paquet, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Julien Cohen-Adad, Naga Karthik, Sandrine Bédard,
Not yet arrived: Joshua Newton, Benjamin De Leener, Rohan Banerjee,
Moderator: Julien Cohen-Adad
Minutes: Mathieu Guay-Paquet

Miscellaneous items

-

Check last week's action items

☑ ~~JV: Find the original reference for the Cadotte figure~~
☑ ~~MGP: Send a follow-up email (re: PAM50 → BIDS BEP) making it explicit that they have feedback to consider → maybe schedule meeting (only if needed)~~
☑ ~~Sandrine: Respond to forum post saying it is C2-C3~~

Software Development

- SCT Course postmortem
    - Create new slide deck for all edits for the future course
        - SCT_Course_2023-11-20 -> "Make a Copy" -> Move to new folder
        - This will make sure that any future changes we make will not break the course material for past attendees
    - Review of exit survey results (link)
        - Significant minority of Windows users, others split evenly macOS / linux
        - We would like to convince people with custom bash/python to use sct_run_batch
        - Should include a link in an email to the course attendees
        - Generally interesting feedback
    - Integrate changes from SCT course slides into web tutorials (SCT#4311)
        - Can also tag Julien if feedback is needed

- Jan: nnUNet model packing under SCT and function names (SCIseg, rootlets)
    - We want to ship these models to users outside the lab as quickly as possible
    - Reimplementing the models in monai can be time consuming, and the performance (accuracy may change, but speed is faster with monai)
    - Would really like to integrate nnUnet under SCT
    - Maybe add as a dependency to SCT? Pip install is ~400MB, reasonable, but does it work reliably to install it on Windows? We can always roll this back in another SCT release
    - Proposed names:

        - `sct_segment_rootlets`
        - `sct_deepseg_lesion -patho sci` (and `sct_deepseg_lesion -patho ms`)
    - JN: Should this be done under the more “general” sct_deepseg?
    - Maybe sct_deepseg should accept sub-commands (like git) instead of an annoying “-task” flag, eg:
        - sct_deepseg rootlets
        - sct_deepseg ms-lesions
        - sct_deepseg sc-mp2rage
        - sct_deepseg sc-mouse
    - We could consider folding the various sct_deepseg_* commands into sct_deepseg as a single entry point?
    - Current proposal for these 2 new models: let’s include them into sct_deepseg
    - We want to avoid doing pip install after the initial installation (so, not during sct_download_data)
    - This is a high priority item
    - nnUnet may be annoying as a dependency because of its requirement on a recent version of torch
    - Aim for SCT v6.2

- PLB: There’s another nnUnet model to integrate
    - Segmentation of mouse SC white and grey matter
    - Link to code : here
    - Should it work on monai? Let’s stick to nnUnet for now

- Possible future ability to run GPU inference:
    - Maybe limited to internal or power users
    - Should work with a simple pip install command to change the torch version flags
    - Would be very useful for nnUnet
    - But for general usage, it would be a significant burden of support for the lab

Research

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    -

Action Items

☐ JN: SCT_Course_2023-11-20 -> “Make a Copy” -> Move to new folder
☐ Julien: reuse poll results for brainhack talk
☐ JN: make a note to add poll results for next course
☐ ?: make a postmortem email to the course attendees with: poll results (anonymous), link to video/slides
☐ we should submit the poll to a larger crowd (maybe sct_mailing list)
☐ MGP: Open an issue to prototype sct_deepseg subcommands

2023-11-17

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina
Not yet arrived: Benjamin De Leener, Rohan Banerjee, Naga Karthik,
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

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Check last week's action items

- ☑ ~~JN: Change presenter note text size~~
- ☑ ~~JN: Add stitching slide to `sct_image` section~~
- ☑ ~~JN: Test space in slide titles (edit slide template template?)~~
    - Unfortunately, formatting cannot be re-applied to all slides without resetting all of the carefully chosen formatting that has been already done. So, this needs to be done manually.
- ☑ ~~JN: Update TOC with "Conclusion" section~~

Software Development

- SCT Course Prep
    - Jan & Sandrine:
        - Presentation of the Shape-based analysis section
            - Tricky to switch screen-sharing, etc. during virtual meeting
            - Keep Julien's screen shared but keep the mic?
            - But, there are some command-line sections… → Still OK, because Julien can run the commands while Sandrine/Jan present. ✅

    - JN: Review open comments
        - 1. Pick best SCIseg figure → Done!
        - 2. Compressed cord "try at home" slide (broken)
            - Slide shows compressed MT1, but MT section has non-compressed MT1 file?
        - 3. Double-check rootlets figure ref
            - → Action item for JV
        - 4. Google Forms exit poll for participants
            - → Come back to this point at the end of the meeting

    - JCA: Update schedule to identify 'Future features and feedback from users'

        - JN: We had already blocked out some time on Day 2 (see: https://spinalcordmri.org/2023/11/20/sct-course.html) → Done! ✅

- PR #4300: Order of “Reorientation → Resampling” during registration
    - Before: 1. Resampling → 2. Reorientation (caused bug)
    - After: 1. Reorientation → 2. Resampling (fixes bug)
        - Side effect: batch_processing.sh results change slightly
        - This is probably to be expected, though?
        - Confirmed that reorientation first is desired behavior! ✅

- JCA: PAM50 template → BIDS BEP (PAM50#11)
    - Prior discussion: PAM50#11 (comment)
    - Feedback was given, ball is sort of in their camp now
    - We can try to prompt the discussion again and make it explicit that they need to act → maybe organize a meeting if need be?

Research

- paper csa pmj see forum post didibed99@gmail.com
    - Sandrine: I saw it quickly, will respond tonight!

Action Items

☐ JV: Find the original reference for the Cadotte figure
☐ MGP: Send a follow-up email making it explicit that they have feedback to consider → maybe schedule meeting (only if needed)
☐ Sandrine: Respond to forum post saying it is C2-C3
☑ ~~JN: Send out another reminder email to install SCT~~

2023-11-01

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Rohan Banerjee, Naga Karthik, Nilser Laines Medina
Not yet arrived: Pierre-Louis Benveniste, Benjamin De Leener
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

- Future meeting scheduling
  - Nov 1: This meeting (was moved from Thur Nov 2 to Wed Nov 1 2pm)
  - Nov 16: Next #sct_dev meeting
    - Spinal Cord Workshop in Boston
    - Cancel → Reschedule to Nov 17th 3pm (Friday)
  - Nov 20-21: SCT Course
- Do we want to add another meeting for doing a dry run of the SCT Course material?

Check last week's action items

- ☑ ~~All: Complete assigned SCT Course slides~~
  - If you have completed any "What's next?" or "New Features" slides, please make sure to close the corresponding issues listed in #4186.
- ☐ JN: Change presenter note text size
- ☐ JN: Add stitching slide to `sct_image` section
- ☐ JN: Test space in slide titles (edit slide template template?)
- ☐ JN: Update TOC with "Conclusion" section

Software Development

- 6.1 is almost ready for release
  - New last minute issue: #4280
    - PR opened: #4281
    - Will create 6.1 release after this PR is merged
  - Proposed timeline
    - ~Nov 3: Create release
    - ~Nov 3-5: Ask lab members to install the release + test the course steps
    - ~Nov 7: Make announcement + send email to course participants?

- SCT Course Prep (#4186 + SCT_Course_2023-11-20)
  - Go through open comments

Research

- Sandrine:
  - Structural analysis of patients with cervical radiculopathy
    - Consider adding symmetry computation?

Action Items

☑ ~~JN: Create next meeting’s agenda~~

2023-10-26 (SCT Course planning)

Attendees: Joshua Newton, Julien Cohen-Adad, Sandrine Bédard, Jan Valosek, Nathan Molinier, Pierre-Louis Benveniste, Nilser Laines Medina, Naga Karthik
Not yet arrived: Rohan Banerjee, Benjamin De Leener, Mathieu Guay-Paquet
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

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Check last week's action items

- ☑ ~~Sandrine: add slide on contrast-agnostic in SCT course and on sct_compute_compression~~
  - See Slide 82: SCT_Course_2023-11-20
- ☑ ~~JN: Consider "Seg -> Vert -> Shape Analysis" and *then* "Registration"~~
  - Issue #4264.
- ☑ ~~JN: Add "What's next?" section to TOC~~
- ☑ ~~Mathieu: Try steps in lumbar tutorial~~
- ☑ ~~Jan: Update shape analysis figure – Combine the best of both figures (see feedback above)~~
  - PR Merged: #4262; new figure: #5
- ☑ ~~JCA: Regenerate PAM50/template/label 14 (originally generated in 2019) to be in line with updated spinal levels~~
  - PR Merged: #18
- ☑ ~~JCA: respond to feedback in lumbar tutorial PR~~
  - Show all 3 methods, don't settle on a specific one – "Learning moment"
  - JCA didn't spend too much time on the parameters, just tested + recommended
  - Default ones might not perfect – need to test
- ☐ All: Fill out assigned pages for new/upcoming features

SCT Course discussion

- JN: Review new course structure (#4264)
  - **Reordered:** 1. Seg -> 2. Labeling -> 3. Shape Analysis -> 4. Registration
    - Originally, labeling section was written entirely for registration
      - But, now the labeling section has been split up:
      - "Using sct_label_vertebrae to label cord" **(2. Labeling)**
      - "Extracting labels for use in registration" **(4. Registration)**
    - Also, shape analysis section was previously written for registration, too:
      - Shape analysis now comes before registration
      - So, we simply reuse the previously labeled spinal cord for `-vertfile`, rather than the warped PAM50 template file (which doesn't exist yet)
    - We should double-check speaker notes to make sure they make sense.

        - If this looks good, I can mirror the SCT Course changes to the web tutorials.
    - **New:** “What’s next?” section
        - Jan:
            - Add SCIseg slide no 161
            - Add Rootlets segmentation slide no 162
            - Contrast agnostic has been moved to What’s Next too

- JCA: Going over “General Considerations” section
    - Moving individual pages into other sections
    - Turning “General considerations” into a “Conclusions” section in the TOC

- JN: Segmentation section rewrite (#4263)
    - SCT_Course_2023-11-20
        - sct_propseg theory condensed into one page
        - sct_propseg hands-on section removed (sct_deepseg_sc now comes first)
        - “What to do if segmentation fails?” rewritten for sct_deepseg_sc
        - Speaker notes rewritten to match new structure

- Go over remaining open comments
    - Done! 🎉
    - TODO: Create action items from newly opened comments

- SCT Course Dry Run (Do we have time?)
    - Sandrine: since the course is spread over 2 days, how do we want to split it?
        - JN: Proposal
            - Day 1, individual tools
            - Day 2, sct_run_batch + “try on your own data” / Q&A from day 1?
                1. I think it might be good to start day 2 with the “sct_run_batch” section, since it’s really important, but putting it at the end of the day makes people not pay enough attention
                2. Do we need to bulk up the sct_run_batch section to be able to make good use of the time? (e.g. add tips about reproducibility)
    - JCA: Who is going to present what?
        - Shape-based analysis → Sandrine/Jan?
        - What’s next? → Individual students (Sandrine/Naga/Jan/Nathan/etc.)

Action Items

☑ ~~JN: Prepare agenda for next week’s meeting (copy over last week’s points)~~
☐ JN: Change presenter note text size
☐ JN: Add stitching slide to `sct_image` section
☐ JN: Test space in slide titles (edit slide template template?)
☐ JN: Update TOC with “Conclusion” section

2023-10-19 (v6.1 Release planning)

Attendees: Mathieu Guay-Paquet, Jan Valosek, Nathan Molinier, Julien Cohen-Adad, Naga Karthik, Nilser Laines Medina, Joshua Newton, Sandrine Bédard, Pierre-louis Benveniste
Not yet arrived:, Rohan Banerjee, Benjamin De Leener
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

- Congrats on (upcoming?) contrast agnostic sc seg submission! 🎉
- NeuroLibre paper (https://neurolibre.org/papers/10.55458/neurolibre.00017)
    - Fancy reproducible preprint built as HTML website using Jupyter Book!

Check last week's action items

- ☑ ~~JN: Complete first checkbox on PAM50 PR #18 (remove option -s from sct_warp_template)~~
    - Merged: PR #4252
- ☑ ~~JN: Generate new release of PAM50 + update URL for SCT~~
    - Temporary release has been created (to help review lumbar tutorial)
    - Waiting for JCA's changes in PR #18 to create "final" PAM50 release for 6.1
- ☑ ~~JN: Fix TOC for sct_compute_compression PR~~
    - Merged: PR #4162
- ☑ ~~JN: Fix course slides/tutorials to add distinct vertebral labeling section~~
    - Added new TOC entries: Vertebral labeling, shape analysis, "other registration approaches"
    - Moved part of the PAM50 theory section to the beginning of course. That way, we can frame the seg/label steps as being motivated by template registration.
    - Where to put sct_compute_compression? (After shape analysis?)
    - Add "What's next?" section to TOC
- ☑ ~~JN: Look into permalinks to specific slides that aren't dependent on page numbers~~
    - Added hyperlinks to TOC 🎉
- ☐ JCA: Update PAM50 template (SCT Issue #4215 - PAM50 PR #18)
    - PR 18 → info_label.txt: 14 file (point labels) → add spinal levels (cord) as file 15
        - First question: Is having both files okay?
            - Sandrine → Keep both, point labels useful for registration
            - Need to regenerate point level labels from new levels files (centre of mass?) → added as task on PR
        - info_label numbering (missing file in the middle → 8?)
            - Removed files are okay! (Users will not care/know in most cases)
            - Is Yehuda using some of these files for total segmentator?
            - Don't change the IDs for existing files, then.
- ☐ JCA: Update documentation + SCT course for PAM50 PR #18

    - Documentation has been approved by JN but not PL/SB, but SCT course is still WIP
- ☐ PL & SB: give feedback on new documentation of PAM50 (PR #4249)

Software Development

- SCT v6.1 postponed (October 12th → Friday, November 3rd)
    - Nov 3 is the last weekday before we ask course participants to install SCT on Nov 6.
        - Is this too "last minute"?
        - Nov 6 is conservative already, so November 3rd is fine.
    - Remaining tasks:
        - #4250: Lumbar tutorial (needs re-review → subject matter experts)
            - Trying the steps → Mathieu (will do!)
        - #4215: PAM50 spinal level update
            - JN: Do other PAM50 issues (e.g. GM/WM seg update) need to be completed before we can create a new PAM50 release?
            - Needs to be updated, but not enough time
            - 6.1 will have a PAM50 with mismatched cord + gm/wm

- Reminder: #4186 – Help finalize SCT Course material
    - Create issues for any remaining items in task list, and assign them as action items
        - Note: "Coming soon" feature pages were assigned to lab members.
            - Just a reminder :)
        - Action item: Create poll / think of questions we want to ask
            - What questions?
            - Yes/no questions only
        - "Needs discussion"
            - spinal-rootlets#13
            - Is discussion needed internally, or from the participants?
                a. Participant feedback would be good → Add to "Discussion section" → WIP, no "yes/no" questions
        - "If you need help connecting" email
            - Should we use sct_developers@googlegroups.com?
            - If so, we should prune membership (remove ex-developers) so that only current people get the email notifications
    - Resolve remaining open comments on slides
        - sct_deepseg section organization
            - Issue opened: #4263 (needs assignee)
        - **Above: Finish up offline / next meeting (Course discussion)**

    - Jan:
        - update "Shape analysis" slide no 78
            - Lovely! ♥
            - New figure feedback
                a. Reorganize the figure so that pairs of graphs and cord diagrams are side by side

                b. Consider adding dashed lines for the “compression point” – resolve issue with overlapping/transparency?
                c. Remove x-axis labels (since they can’t be seen anyway)
                d. Extra blue line and blue highlighting – Better convey what these features mean (“deviation from spine-generic norm”)
                e. Compression ratio is shown in figure but not computed by sct_process_segmentation
                f. Increase size of schematics
            - **Action item: Combine the best of both figures!! Haha :-D**
        - Add SCIseg slide no 158
        - Add Rootlets segmentation slide no 159

- Jan Valošek :
    - Update figure in the "Other shape metrics" tutorial #4183
        - PRs: #4262 and #4

- Naga & Sandrine:
    - Packaging contrast-agnostic in SCT (https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord)
        - Put code into repository, then put model as a release asset
            - Upload code to GitHub repo
            - Create release, then add model as a release asset to the model repo
            - Additional idea: Should we add it as an asset to SCT?
                a. Makes more sense to link it with the model code/repo, since everything will be together
        - Before or after the course?
            - Would be nice to have course feedback on as-is model
            - End of segmentation section → New model coming out soon, please help us test!
            - Plan B: Doesn’t *need* to be integrated into SCT to advertise it. As long as there are basic instructions for performing inference in the repo.
        - TODO: Prepare some slides → Issue created + assigned

Research

- Jan Valošek :
    - Registering sagittal PSIR/STIR CanProCo images to the PAM50 template
        - All discs: `sct_register_to_template -ldisc`
        - Versus two mid vert labels (C3 and C7): `sct_register_to_template -l`
        - You could also do 2 discs
        - **Above: Finish up in next regular meeting (2 wks from now)**

Action Items

- ☐ Sandrine: add slide on contrast-agnostic in SCT course and on sct_compute_compression
- ☐ JN: Open issue for considering “Seg -> Vert -> Shape Analysis” and *then* “Registration”
- ☐ JN: Add “What’s next?” section to TOC
- ☐ JCA: Regenerate PAM50/template/label 14 (originally generated in 2019) to be in line with updated spinal levels
- ☐ JCA: respond to feedback in lumbar tutorial https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/4250#pullrequestreview-1665309612
- ☐ Mathieu: Try steps in lumbar tutorial
- ☐ Jan: Update shape analysis figure – Combine the best of both figures (see feedback above)
- ☐ All: Fill out assigned pages for new/upcoming features

2023-10-05

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Rohan Banerjee, Naga Karthik, Nilser Laines Medina,
Not yet arrived: Benjamin De Leener, Nick Guenther, Julian McGinnis,
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

-

Check last week's action items

- ☑ ~~JN: Explore ways to fix dependency compatibility between ivadomed and monai.~~
    - Ivadomed can install torch>=2.0.0 without issue. 🎉
- ☐ JCA: High priority on updating PAM50 template (SCT Issue #4215 - PAM50 PR #18)
    - Reached out to Rob, Nawal, Ilaria, Raphaelle, Christian (email)-- no answer – should not expect answer
    - Currently do not have the time
    - Would love to get help
        - Updating docs, figures → Action items created
- ☑ ~~All: Review course material~~
    - Lots of good discussion happening!
- ☑ ~~Naga: Move wiki page from ivadomed to SCT~~
    - Done! Check here
- ☐ JN: Look into installing GPU torch into the SCT environment to speed up (internal, lab-only) inference on ivadomed/MONAI models
    - Lumbar reg tutorial took priority (6.1 deadline)
- ☑ ~~Nilser: Replace tab with space in info_label.txt https://github.com/spinalcordtoolbox/template_AMU7T/blob/nl/AMU7Tv3/atlas/info_label.txt~~
- ☑ ~~Nilser: Double-check a priori subgroup assumptions → Hardcoded in sct_extract_metric?~~
- ☑ ~~Nilser: Make sure that the migration from single labels (30:35) to the combined labels works as expected (no extra logic, e.g. partial volume compensation, etc.) https://github.com/spinalcordtoolbox/template_AMU7T/issues/7~~
    - Follow-up will happen in the issue

Software Development

- 6.1 Milestone
    - JN: Lumbar registration tutorial is now WIP
        - JN: PAM50 Spinal levels → Generate PAM50 release + URL + SCT
    - Finalizing course material is in progress as well

        - SCT_Course_2023-11-20 – Review comments
        - Action items: Pages to add as TODOs #4186

- Sandrine: sct_compute_compression tutorial:
    - Joshua, can you check the TOC to remove subsections of CSA? https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/4162#issuecomment-1747419520
    - JN: Yes, I'd be happy to check this out! Thanks for the tag on the PR :)

- Naga: Next steps in the monai → SCT integration after this update?
    - TODO: Add dependencies + inference script to sct_deepseg
    - Do postprocessing in sct_deepseg CLI? Or in the monai inference script?
        - ANS: Inference script should be isolated, with pre/processing done on the SCT side of things.
        - Question to answer offline: Is the existing sct_deepseg postprocessing calling ivadomed functions? Or, is the postprocessing code included in SCT libraries?
    - Need a user-accessible version of the contrast-agnostic model in SCT for the paper
        - TODO: Create repo, create release, upload the model to the release
        - Upload size quotas should be fine for 500MB model: https://docs.github.com/en/repositories/releasing-projects-on-github/about-releases#storage-and-bandwidth-quotas

Research

- JCA/Jan: get spinal levels from nerve rootlets segmentation (#13) – check if NURBS code can be applied for registering a cloud of labels – see issue

Action Items

☐ JN: Complete first checkbox on PAM50 PR #18 (remove option -s from sct_warp_template)
☐ JN: Generate new release of PAM50 + update URL for SCT
☑ ~~JN: Fix TOC for sct_compute_compression PR~~
☐ JN: Fix course slides/tutorials to add distinct vertebral labeling section
☐ JN: Look into permalinks to specific slides that aren't dependent on page numbers
☐ JCA: Update documentation + SCT course for PAM50 PR #18
☐ PL & SB: give feedback on new documentation of PAM50

2023-09-21

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Naga Karthik, Nathan Molinier, Nilser Laines Medina, Rohan Banerjee
Not yet arrived: Jan Valosek, Benjamin De Leener, Nick Guenther, Julian McGinnis
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

- Audio test: Both the Yeti and the Jabra (with updated firmware) work perfectly! 🎉

Check last week's action items

- ☑ ~~MGP: Try upgrading Jabra firmware using a Windows machine~~
- ☑ ~~JCA: Bring Yeti from home to test setup with TV audio~~
- ☐ JCA: High priority on updating PAM50 template
- ☑ ~~MGP: Open a new milestone for 6.2, move some of the 6.1 issues to it (link)~~
- ☑ ~~MGP: Open a tracking issue on SCT for PAM50 update in 6.1 release SCT#4215~~
- ☑ ~~All: think about copy-pasting from course slides (pdf generated from keynote) and/or syncing up SCT#2407~~
- ☑ ~~JN: Open an issue for updating the processing script to reproduce `results.zip` for the future data-multi-subject#149~~
- ☑ ~~Jan: send email to Colorado about sci-colorado data - email sent~~

Software Development

- JN: Ideas for improving SCT course presentation + copy-paste
    - Good news: Keynote → Google Slides conversion was easier than expected!
        - We can now share SCT_Course_2023-11-20 with participants
        - It should be able to be opened even when logged out/incognito, and participants can easily copy and paste without any weird formatting bugs.
        - Plus, the slides are editable by anyone who has NeuroPoly drive access.
        - No more need to rely on Keynote! 🎉
    - Other brainstormed ideas are still possible, but Google Slides seems like the simplest/most straightforward solution. (I think we can close the issue?)
    - For access from China, make sure to have an OSF link (or other?)

- JN: Updating outdated slides
    - We should proofread the slides and removed outdated info (e.g. "Windows (via WSL)")
    - Should we devote some meeting time to proofreading as a group?

    - Or, should we do this offline using Google Slides comments (since anyone in the lab can add suggestions now)?
        - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4186

- JN: sct_compute_compression tutorial
    - Needs re-review (see: this comment)
    - After merge, we can add a new slide to the SCT Course Google Slides. :D

- MGP: early draft of QC report refactoring on SCT#4224, would love to get feedback

- Naga/MGP: would it be possible to support GPUs for `sct_deepseg`?
    - See SCT's `requirements.txt`, we only install pytorch with CPU support
    - Maybe this could be a pip-installable "extra", for example

  Suggestions:
    - Having GPU support for advanced users
    - Write a set of instructions for internal usage to start

Research

- Naga: Feedback on the inference procedure for the contrast-agnostic model
    - Inference script (still a work in progress 80% done)
        - Still need to add post-processing to keep largest component
    - Inference instructions
        - TODO: Convert script from inputting full datasets to inputting a single image

- Need to integrate into SCT - How to do?
    - Requirements file for the monai model
    - Ongoing issue on monai integration
    - Current stalemate as per Joshua's comment:
        - ivadomed requires torch<=1.11.0 but monai and nnunet use torch>=2.0.0
            - JN: I am happy to test expanding ivadomed's torch restrictions!
        - Look into onnx? (instead of using torch's .pt/.ckpt models)
            - Unfortunately we are dependent on ivadomed + torch: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3396#issuecomment-1407213807

- Move this to SCT wiki?
    - 👍
- Nilser: AMU7T info_label.txt IDs numbering for use sct_extract_metric (PAM50 compatibility):
    - #7
    - Feedback: See action items below

- Padding single-slice images?

    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4223

Action Items

- ☑ ~~JN: Make next meeting's agenda immediately~~
- ☑ ~~JN: Explore ways to fix dependency compatibility between ivadomed and monai.~~
- ☐ JCA: High priority on updating PAM50 template
- ☐ JCA: Review course material
- ☐ NM: Review course material
- ☐ PL: Review course material
- ☐ RB: Review course material
- ☐ NL: Review course material
    -
- ☐ MGP: Review course material
- ☐ Naga: Move wiki page from ivadomed to SCT
- ☐ JN: Look into how to install GPU torch into the SCT environment
- ☐ Nilser: Replace tab with space in info_label.txt
- ☐ Nilser: Double-check a priori subgroup assumptions → Hardcoded in sct_extract_metric?
- ☐ Nilser: Make sure that the migration from single labels (30:35) to the combined labels works as expected (no extra logic, e.g. partial volume compensation, etc.)

2023-09-07

Attendees: Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nilser Laines Medina, Joshua Newton, Nathan Molinier, Julien Cohen-Adad, Pierre-Louis Benveniste
Not yet arrived:, Nadia Blostein, Naga Karthik, Rohan Banerjee, Maxime Bouthillier, Theo Mathieu, Benjamin De Leener, Nick Guenther, Julian McGinnis
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

- Welcome back Julien! 🎉
- Julian will (probably) visit next SCT meeting!
- Note: Next meeting Jan will be away on holidays (as per holiday calendar)
- *(MGP)* Meeting audio:
    - Output:
        - Jabra audio output is bad/unreliable (maybe hardware issue), even when plugged in through USB cable
        - TV audio output through HDMI works great
        - MGP's laptop speaker is an acceptable temp solution
    - Input:
        - Jabra audio input is good but unreliable (maybe firmware issue?), even when plugged in through USB cable → Action item (firmware upgrade)
        - MGP's laptop microphone is an acceptable temp solution
    - Echo cancellation:
        - If the input and output are both attached to the same computer, there doesn't seem to be any feedback or echo
    - Next attempt:
        - Buy a USB microphone?
        - Tom's guide 2023 reviews suggests Blue Yeti brand, or JLab Talk
        - JLab Go Talk (slightly more basic model, same company) available at Best Buy for ~½ the price of all other options. Try that one first?

Check last week's action items

☑ ~~JN: Apply a fix for Yehuda's 3+ labels registration issue (SCT#4206)~~
☑ ~~JN: Update sct_tutorial_data to include new .zip archives (sct_tutorial_data#16)~~
☑ ~~JN: Look into preventing future forum email outages (~~
☑ ~~Sandrine: Look into forum post: https://forum.spinalcordmri.org/t/registration-tips/1102/22~~
  - Registration advice was given, and there was follow-up from JCA (thanks!!)

☐ MGP/Jan: Look into resolving remaining issues for redefaced spine-generic (see Data Management heading below)
☑ ~~Sandrine/Jan: Apply wording clarification feedback for sct_compute_compression tutorial~~

~~(SCT#4162)~~

Software Development

- JN:
    - Update on preventing future SCT forum email outages (#83)
        - For past outages, error log mention SSL certificate expiry
        - However, I was able to confirm that the SSL certificates are correctly being auto-renewed by the Discourse setup
        - My theory: The forum's mail server is not loading the renewed certs
        - I have a plan in place for testing this theory and fixing the underlying problem

    - Apart from this, I have been helping review PRs, as well as helping Julian McGinnis with a request re: his brain lesion segmentation project (LST).
    - Next tasks: I will be looking at the 6.1 issues (discussed further below)

- MGP:
    - Working on QC refactoring to enable new features: #4204

- Next SCT release (v6.1) is scheduled for October 12 (milestone), coming up soon!
    - In time for SCT courses (see issue #4186)
        - @Joshua can we merge the list below with this list: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4186
            - Can do! EDIT: Done!
        - Take the opportunity to poll SCT userbase at course. Questions:
            - Ask about regressors? Provide context about the current state of interoperability with FSL
    - Which projects are must-have, versus nice-to-have?
        - High priority: PAM50 update (JCA)
        - Sidecar files → Not a high priority for the "SCT Course"-related release
        - QC report/sct_run_batch teaching may be more important
            - Current tutorial: https://spinalcordtoolbox.com/user_section/tutorials/analysis-pipelines-with-sct.html
            - Important to not put the sct_run_batch at the end of a long day where people are tired and not paying close attention
            - Really emphasize this feature at the start of the course
            - Current "analysis pipeline" tutorial perhaps doesn't apply to real-world projects (starting from scratch, using the QC reports, encourage to specifying the same path)
        - How to present the SCT Course? https://github.com/spinalcordtoolbox/sct_tutorial_data/issues/7
            - Mix Slides + Tutorials? → Too complicated.
            - Some participants print slides (presumably to write notes on)
                - Tutorials presumably don't print as nicely

        - Assuming we keep using slides, how should we make it easier for users to follow commands on their own/copy paste?
            - Editing iCloud presentation to make it easier to double-click and copy the whole command

Data management

- *(MGP, Jan)* Question about `sci-colorado`: what to do with the `af/fix_data` branch? data-management#258
    - It changes some image files, some JSON sidecars, substantially
    - No one seems to have much context on this old PR
    - Can/should we contact the original external collaborators? If so, who contacts who?

- *(MGP, Jan)* Spine-generic documentation has failed to update for ~2 years spine-generic#268
    - Quick fix available in spine-generic#269 and spine-generic#270, needs review because it would pin `results.zip` to an old release of `data-multi-subject`
        - JCA: this is fine, we can update it next time we generate a `results.zip`
    - Would unblock a docs update about filename conventions for MTS spine-generic#267, used by external collaborators

- *(MGP, Jan)* Re-defaced images for spine-generic (data-multi-subject#148)
    - New images produced by Rene Labounek are visually identical (apart from defacing), but have different intensity. Should we rescale? Not necessary, but document in changelog (no dtype change, intensities rescaled for some images)

Research

- Anyone?

Action Items

☑ ~~MGP: Try upgrading Jabra firmware using a Windows machine~~
☑ ~~JCA: Bring Yeti from home to test setup with TV audio~~
☐ JCA: High priority on updating PAM50 template
☑ ~~MGP: Open a new milestone for 6.2, move some of the 6.1 issues to it~~
☑ ~~MGP: Open a tracking issue on SCT for PAM50 update in 6.1 release~~
☑ ~~All: think about copy-pasting from course slides (pdf generated from keynote) and/or syncing up~~
☑ ~~JN: Open an issue for updating the processing script to reproduce `results.zip` for the future~~
☑ ~~Jan: send email to Colorado about sci-colorado data - email sent~~

2023-08-24

Attendees: Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nilser Laines Medina, Joshua Newton, Nathan Molinier
Not yet arrived: Nadia Blostein, Naga Karthik, Theo, Julien Cohen-Adad, Rohan Banerjee, Etienne, Daniel, Maxime Bouthillier, Theo Mathieu, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

Check last week's action items

- ☑ ~~Jan: reorient re-defaced images from Rene Labounek (issue #146)~~
    - images reoriented and pushed PR #148 - but there are some other problems with the image headers (likely introduced during the de-facing?)
    - In the future, suggest to external collaborators to preserve metadata/orientation/data type/etc. to save us work in the future.
    - We could have re-defaced it ourselves? ANS: No, since it is private data.
    - Original defacing – one large box that cut out part of the brain
    - New defacing – smaller boxes that preserve the brain
    - Not yet ready to be merged – need answers about intensity values changing.
        - Manual rescaling + compare → less than 1% difference
- ☑ ~~Jan: open PR about the clarification of sct_run_batch -script-args (#4187)~~
    - merged in #4190
- ☑ ~~Sandrine: open issue ses in sct_run_batch (filtering for ses/sub)~~
- ☑ ~~Sandrine: continue with sct_compute_compression tutorial~~
- ☑ ~~MGP and JN: test out new settings for meeting audio~~
    - MGP bought some USB extensions so that the Jabra Speak can stay plugged in
    - The Jabra Speak microphone seems to be working mostly fine
    - If the microphone stops working, the Jabra Speak can be rebooted
    - The Jabra Speak audio output, however seems to be broken
    - But we can use the HDMI output, and echo suppression works fine

Software Development

Joshua Newton:

- I haven't had much time to start any new efforts. (So, I don't have much to discuss today!)
- I have mainly been helping with new requests from others:
    - Forum email outage (#79 (comment))
        - Need to debug failed SSL cert renewal → Action item
    - Fixing registration for 3+ labels (#4085)
        - Still need to apply a fix for this! → Action item
    - Sandrine/Jan's tutorial PR (#4162)
        - Need to update sct_tutorial_data. → Action item
    - Co-decode's Docker installation PR (#4196)
    - Rohan's template PR (#75)
    - Julian McGinnis's LST tool (private message)
    - Forum posts (#1102, #1115, #1116, etc.)

Mathieu Guay-Paquet:

- I've been working on QC refactoring to enable new features: #4204
    - Part 2 should address the front-end code problems!
    - Make it possible to upload a YML file to resume a long QC analysis - #3619 ♥

Jan Valošek :

- raise error if `sct_run_batch` config file has wrong suffix (e.g., .sh instead of json/yml) - merged PR #4201

Data management

Jan Valošek :

- rename MTS suffix in spine-generic.rtfd.io Documentation - PR #267
    - BIDS spec updated, and we updated the files in data_multi_subject a while ago
    - But, the documentation is still out of date (confusing for collaborators)
    - So, this PR is updating the Documentation to match the BIDS spec

Research

- Fewer people than usual (interns are leaving) + Julien not present = Less to talk about!
- sct_compute_compression PR
    - Clarifications needed for the steps
    - Add the data
    - Waiting for Julien's feedback

Action Items

- ☐ JN: Apply a fix for Yehuda's 3+ labels registration issue
- ☐ JN: Update sct_tutorial_data to include new .zip archives

- ☐ JN: Look into preventing future forum email outages
- ☐ Sandrine: Look into forum post: https://forum.spinalcordmri.org/t/registration-tips/1102/22
- ☐ MGP/Jan: Look into resolving remaining issues for redefaced spine-generic
- ☐ Sandrine/Jan: Apply wording clarification feedback for sct_compute_compression tutorial

2023-08-10

Attendees: Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nilser Laines Medina, Nadia Blostein, Joshua Newton, Nathan Molinier, Naga Karthik, Theo
Not yet arrived: Julien Cohen-Adad, Rohan Banerjee, Etienne, Daniel, Maxime Bouthillier, Theo Mathieu, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

Check last week's action items

- ☑ ~~MGP: open issues for the SCT feature requests from this meeting SCT#4179, SCT#4180, SCT#4181, PAM50#16, SCT#4182~~
- ☑ ~~MGP: shop for a new meeting microphone (Will try a USB extension for the existing speakerphone)~~
    - ○ JN: Sounds good this week! :)
- ☑ ~~(Whose action item is this?) Add tutorial for SCT Course about registration of lumbar images using two labels (issue is opened, link: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/4180)~~

Software Development

- JN: I don't have much to talk about today. Very sorry!
    - Still adjusting after time away + my recent move on August 1st
    - Have been working on some registration-related issues that were assigned to me by Julien from the forums (e.g. #4184, #4085)
    - I plan to look into Naga's QC issue (#4178) and Rohan's straightening issue (#65) soon
    - I'm also aware of the recent issues created last meeting, and will start triaging them as well. :)

- Jan:
    - #4187 - Clarification of `sct_run_batch -script-args` input flag help
    - #4185 - `sct_compute_compression` fails when processing several subjects in parallel
        - Possible solution from Mathieu: output several individual files (one for each subject) and then merge them
        - Also possibly applies to `sct_process_segmentation`
        - Requirements:
            - Ability to run processing in parallel
            - Final output should be combined, all subjects and metrics, correct header line

        - #4174 - `sct_label_vertebrae` does not raise error when `-discfile` is empty

- Sandrine:
    - Add option to include or exclude ses in sct_run_batch
        - Need to open an issue about that
        - Try using ses in include
    - Working on sct_compute_compression tutorial, still work and progress
        - Jan: Thanks 🎉
- MGP: There are several current issues and feature requests for QC, but the code needs some overhaul, but this is becoming high priority

Data management

Jan:

- `spine-generic/data-multi-subject` - issue #146
    - Some of T1w re-defaced images from Rene Labounek are now RPI (instead of original LPI), see this comment
    - Solution: reorient images back to LPI using `sct_image -setorient LPI`

Nadia

- Working with Mathieu Guay-Paquet on adding the philadelphia-pediatric derivatives to the git-annexed dataset – Issue #248
    - Reran the neuropoly/template pipeline step 1
        - SC mask + disc labeling (README steps 1.1 to 1.5)
        - Straightening + normalizing to template space (README steps 1.6 and 1.7)
    - Gradually adding derivatives folders with to nb/add-labels branch
    - Next: rerun template generation neuropoly/template (README step 2) on beluga

Research

Theo: Larger FOV for the rootlets QC reports - #4177

    - Is it possible to add slice number, display different color like in sct_label_vertebrae
        - Both feature requests are documented in the second part of this comment

Action Items

- ☑ ~~Jan: reorient re-defaced images from Rene Labouneck (issue #146) - done here~~
- ☑ ~~Jan: open PR about the clarification of sct_run_batch -script-args (#4187) - done in #4190~~
- ☑ ~~Sandrine: open issue ses in sct_run_batch~~
- ☑ ~~Sandrine: continue with sct_compute_compression tutorial~~

2023-07-27

Attendees: Julien Cohen-Adad, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nilser Laines Medina, Rohan Banerjee, Etienne, Daniel, Theo, Nadia Blostein
Not yet arrived:, Joshua Newton, Nathan Molinier, Maxime Bouthillier, Naga Karthik, Theo Mathieu, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Julien Cohen-Adad
Minutes: Mathieu Guay-Paquet

Miscellaneous items

- Joshua is away for a few days

- Christian Kündig and Rob Barry are visiting NeuroPoly today! Both interested in spinal cord MRI, 7T, lumbar

Check last week's action items

- ☑ ~~Jan: Review sct_image -stitch PR - done ♥~~
- ☑ ~~Joshua: Merge PR, then create changelog PR + start release procedure~~
- ☑ ~~Joshua: Try prototyping sidecar generation → launcher.py~~
- ☐ Mathieu: Try prototyping sidecar generation → image saving functions
    - In the backlog, not started yet
- ☑ ~~Mathieu: Mail stickers to Joshua (Thank you!!!!!! :D)~~
- ☑ ~~Nilser: Respond to JCA's feedback on AMU7T issue (discussion starting at this comment)~~

Software Development

- 6.0 Release done! (release page)
    - OHBM feedback: this year there were a lot of posters using SCT! ~95% of 15-20 posters which were about the spinal cord

- Questions from Christian Kündig's talk this morning:
    - Make it easier to use motion regressors from `sct_fmri_moco` in FSL
        - Rob: NEPTUNE calling AFNI

    - Add explicit tips in SCT tutorials and course about registration of lumbar images using 2 labels: lumbar enlargement and SC tip – forum post
        - Add to SCT Course
        - Ilaria was very happy with SCT support!

    - `sct_maths` does not support operations on 4D images

        - Users have to split the 4D volume into individual 3D volumes, apply an operation (e.g. applying smoothing kernel) on each 3D volume, and then concatenate the volumes back into a single 4D volume
        - Would it cause memory problems? Worth investigating

    - Could SCT be more useful (or easy to use) for slice-wise metrics?
        - This is more about improving Christian's existing scripts, to be discussed

- Are there any specific priorities for 6.1?
    - Target date: before the course and Rob's workshop, so mid-end of October?
    - New features?
        - Outputting BIDS-compliant (or BIDS-inspired) JSON sidecars with images
        - Applying 3D image manipulations to 4D time-series volume-wise
        - Common feedback from lots of posters: spinal segments from PAM50 are inaccurate: Frostell
        - Contrast-agnostic segmentation model? (Sandrine)
            - Early experiments are giving nice results
        - EPI segmentation model? (Rohan)
            - Interesting results so far, currently validating them
    - Bug fixes?
        - Not particularly, as comes up
    - Architectural changes?
        - Not planned
    - Packaging/installation changes?
        - We're OK for now, with the Windows installer

- Julien: package monai inference (related to contrast-agnostic project)
    - Need an update of the sct_deepseg API so that it can be run under Monai (in addition to the current ivadomed-based workflow)
    - Need to coordinate with the contrast-agnostic project
    - Should discuss with Naga
    - Rohan: also need to discuss packaging nnunet – used as a part of the fMRI EPI SC segmentation project.

-

Research

- Etienne du Fayet: compression detection through regression on morphometric parameters (Compression detection)
    - Julien: how was the train-test split done? On subject or slice level?
        - Etienne: subject level

- Sandrine: OHBM feedback

    - Project from Nawal and Caroline on functional spinal levels → inaccuracies in PAM50 (link to abstract)
    - Users are looking forward to having an automatic segmentation method for fMRI EPI data (of the lumbar cord too!)

- Nadia: neuropoly/template (link to branch)
    - Works with SCT 6.0 (commit a11e9f1f5675fe6f25f3aceda4ceb5d13ad07c59)
    - Currently:
        - Adapting to the new SCT manual-correction module
            - E.g. adapting nomenclature, link to issue
        - Investigating how to adapt the pipeline such that users can control the discs within which the template will be generated
            - `sct_straighten_spinalcord` cannot seem to straighten a spinal cord that is too short and/or uses less than 14 disc labels → link to issue (will open issue on SCT repo once I understand the problem)

Action Items

☑ ~~MGP: open issues for the SCT feature requests from this meeting SCT#4179, SCT#4180, SCT#4181, PAM50#16, SCT#4182~~
☐ MGP: shop for a new meeting microphone
☐ Add tutorial for SCT Course about registration of lumbar images using two labels

2023-07-13 (v6.0 Release)

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Nilser Laines Medina, Maxime Bouthillier
Not yet arrived: Rohan Banerjee, Naga Karthik, Nilser Laines Medina, Theo, Nadia Blostein, Benjamin De Leener, Nick Guenther, Nilser Laines Medina, Julian McGinnis, Adrian El Baz, Theo
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

-

Check last week's action items

- ☐ Rohan: Post-Brainhack: Dig about bagging
    - Is this still relevant? (Unsure)
- ☑ ~~Jan: Send SCT flyer to Armand~~
- ☑ ~~Jan/Sandrine: Look into SCT v6.0/SCT Course stickers for OHBM~~
- ☑ ~~Jan/Joshua/Mathieu: Look into implementing sidecar files~~
    - See discussion under "Dev" heading
    - Further investigation will be done offline after v6.0
- ☑ ~~Joshua/Mathieu: Keep eyes on PAM50 PR for 7T template/atlas, consider implementation~~
    - See discussion under "Research" heading

Software Development

- 6.0 Release! (milestone)
    - Due: July 14th
    - Jan printed some stickers for OHBM 🎉
    - Remaining tasks for 6.0:
        - #4157: `sct_image -stitch` QC issues
            - QC report has two issues:
                a. #4152: Image path in YML files is incorrect
                b. #4051: Layout is confusing (need to toggle to see stitched image)
            - We can only solve 1 at a time, because they both depend on order of the images that are passed to the QC function
            - Which issue is more important to solve before the 6.0 release?
                a. YML filepaths → Then we merge PR #4157
                    - More important!
                b. QC layout → Then we keep things as-is
        - We're good to go? ANS: Apart from the above issue, yes we are!

- Jan: Output JSON sidecar files together with label files (SC seg, vert. labeling, etc.) - #3394
    - Without sidecar, impossible to know which algorithm generated for example SC seg
        - Also provides a space for people to record who is manually adjusting the segmentations, etc.
    - Consider "BIDS-ifying" the output in the future, but either way, "beside" the output data.
    - JN: I plan to try out a "launcher.py" refactor (as soon as 6.0 is over)
    - Mathieu: Looked into BIDS `dataset_description.json`
        - Pipeline-specific, ~~rather than SCT function-specific~~
        - Derivative folder should have their own dataset_description.json!!
        - Includes "GeneratedBy" field, too
        - Jan: We are currently using this template, which does not include GeneratedBy
        - Jan: for derivatives, we are using "DatasetType": "derivative"
        - to get inspiration: fmriprep
    - Related discussion (very recent): manual-correction#34
    - Reach out to users? To know what they would like to have in the files
        - SCT course is an opportunity for this as well
    - Current use-case?
        - Manual labeling → First generated by sct_deepseg_sc and others, edited later
    - So, json file from SCT script nudges folks to edit the existing files when manually correcting
    - Other possible places:
        - Launcher.py
        - Image class (saving code)
        - "View results" message in the terminal

- Étienne: Missing PMJ in PAM50 template
    - In April 2018, PMJ labels (49 and 50) were added to `PAM50_label_discs.nii.gz`
    - In December 2018, PAM50 template was cropped just above the C1 level, causing the PMJ labels to be removed (since the PMJ is cut out of the FOv and is no longer seen)
        - Not high
    - Was this intentional? (JCA authored the "crop out" commit)
        - Yes! Reason for the cropping in 2018 – Wanted to not overlap with MNI brain template, since labels are already present there
        - Label is mentioned in the tutorial? (!!!)
            - Labeling convention page → Separate from PAM50
    - What are the problems with not having PMJ labels?
        - Not able to compute distance to PMJ using the PAM50 labels
        - Motivation: Anat images didn't have PMJ, so the idea was to use PAM50's PMJ label
        - Might not actually be relevant? (Complicated approach: PAM50 is straightened, brain template isn't straightened.)
        - Just a brainstorming idea – not worth revisiting the lack of PMJ labels

Research

- Welcome Maxime 🎉
- Nilser: AMU7T template
  - Plan for integrating into SCT has been proposed here
  - Nilser has been investigating the performance using `-t` option with AMU7T template
  - Feedback: JCA is commenting on issue #4

Action Items

- ☑ ~~Jan: Review sct_image -stitch PR - done ♥~~
- ☐ Joshua: Merge PR, then create changelog PR + start release procedure
- ☐ Joshua: Try prototyping sidecar generation → launcher.py
- ☐ Mathieu: Try prototyping sidecar generation → image saving functions
- ☐ Mathieu: Mail stickers to Joshua (Thank you!!!!!! :D)
- ☐ Nilser: Respond to JCA’s feedback on AMU7T issue

2023-07-06

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Rohan Banerjee, Naga Karthik, Nilser Laines Medina, Theo
Not yet arrived: Nadia Blostein, Benjamin De Leener, Nick Guenther, Nilser Laines Medina, Julian McGinnis, Adrian El Baz
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

- Welcome back Sandrine and Mathieu! 🎉

Check last week's action items

- ☑ ~~Nilser: Post-Brainhack: Check what is pseudo dice~~
- ☑ ~~Nilser: Post-Brainhack: What fold is slide 7~~
    - Already discussed – can continue offline
- ☐ Rohan: Post-Brainhack: Dig about bagging

Software Development

- 6.0 Release! (milestone)
    - Due: July 14th
    - Previous advertisement done for new release + workshop (Nov 20-21)
        - Future advertisement: UCL?
        - We have a website: https://spinalcordmri.org/workshops.html
        - We also have a flyer (Jan send to Armand)
        - Stickers → Bring to OHBM (Jan?)
            - Plastic vs. paper etc.

    - Remaining tasks for 6.0:
        - #4003: `sct_compute_compression`
            - Done, but could use one last review from Sandrine to look over the recent refactor (2 metric_ratio columns → 3 metric_ratio columns)

        - #4060: 6.0 installation docs
            - Done, waiting until release to merge

        - #4009: `sct_label_utils -create-viewer 1,1,1`
            - Discussion: Do we even need this feature?
                a. ANS: Not urgent for 6.0

        b. **Pros:** In tutorial, users can try out sct_compute_compression pipeline without needing to download/learn FSLeyes.
        c. **Cons:** Compression labeling is very difficult to do accurately with only a sagittal image, so this feature might not even be useful.
        d. In the tutorial, should we describe both methods ([e.g.](e.g.))? Or, should we stick to recommending just FSLeyes for labeling?
            - Should compression labeling be done by radiologists, instead? In other words, really emphasize that the compression labeling tutorial step needs to be done with a lot of care. (More tricky than disc labeling)
            - Tricky to ask a radiologist to go into FSL, label the images, etc.
            - Check with radiologist if they have questions.
        e. How should the tutorial be written?
            - → Emphasis the use of FSLeyes, or other viewers if they like

    - Release checklist
        - Manual testing (FSLeyes plugin, PyQT) → Done (by Joshua)
            a. Plugin still works with upgrade from FSLeyes v1.5.0 → v1.7.0
        - Testing installation on Windows →TODO (by MathieuGP)

  - Does anything else need to be done for the 6.0 release?
    - Advertisement for OHBM?
        - Discussed earlier → Flyer/stickers
        - Mention 6.0 on the posters specifically

- Jan: Output JSON sidecar files together with label files (SC seg, vert. labeling, etc.) - #3394
  - Without sidecar, impossible to know which algorithm generated for example SC seg
    - Also provides a space for people to record who is manually adjusting the segmentations, etc.
  - Possible to do in the launcher? To avoid repeating the same sidecar-generating code in each and every script
  - Would have to take into account the `-ofolder` option, though, so maybe not the launcher…
  - Consider "BIDS-ifying" the output in the future, but either way, "beside" the output data.
  - → Jan, Joshua, Mathieu

Research

- NL: integration of AMU7T template/atlas in PAM50 #14
  - Include in PAM50 or separate download?
  - Keep in mind the usage of this template with sct_warp_template and further functions (e.g. sct_extract_metric)

Action Items

- ☑ ~~Sandrine: Look over new changes to sct_compute_compression~~
- ☐ Jan: Send SCT flyer to Armand
- ☐ Jan/Sandrine: Look into SCT v6.0/SCT Course stickers for OHBM
- ☐ Jan/Joshua/Mathieu: Look into implementing sidecar files
- ☐ Joshua/Mathieu: Keep eyes on PAM50 PR for 7T template/atlas, consider implementation

2023-06-01

Attendees: Julien Cohen-Adad, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Theo, Nilser Laines Medina
Not yet arrived: Joshua Newton,Nathan Molinier, Rohan Banerjee, Naga Karthik, Nadia Blostein, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Mathieu Guay-Paquet
Minutes: Julien Cohen-Adad

Miscellaneous items

-

Check last week's action items

- ☑ ~~Jan: (prepare to) advertise SCT 6.0 at ISMRM, and November course date~~
    - Poster and website page created (Slack message, pdf, apple keynote)
        - If you agree, I will print it!
        - How many copies? 10 should be enough, bring tape or sticky tack
- ☑ ~~Nadia: advertise SCT at QBIN, and at the highlights party at ISMRM~~
- ☑ ~~JCA (and others): figure out the exact dates for the November course~~
- ☑ ~~MGP: adjust release dates on github (July 15 for v6.0)~~
- ☑ ~~JN: Update dev wiki and submit PR to normalize the headers in CLI scripts~~
    - Done by Mathieu (Thank you! 🎉)
- ☐ Nilser: Share progress in 2 weeks after brainhack
    - Added to Research section
- ☐ Rohan: Share progress in 2 weeks after brainhack
    - Added to Research section

Software Development

- Update on PAM50 spinal levels effort
    - Meeting yesterday – How did it go? It went OK. No hard feelings.
    - New atlas won't be included.

- Next steps for sct_compute_compression PR
    - High priority - Needed for 6.0
    - What's left?
        - (Finishing up script (PR #4003), adding a tutorial, adding to batch processing?)
        - Modifying the arguments description
    - What would be application
        - Jan: apply on SCI subjects?
    - Start on this after PAM50 level effort is resolved/dropped?

        - Yes, now! 🙂

- Resampling on QC report
    - QC includes resampling to 0.6mm by default to help keep the display size reasonable.
    - However, resampling has caused multiple display issues
        - #3625: Missing/doubled centerline voxels
        - #4125: Distorted lesion softsegs
    - Temp solution: Turn resampling off (e.g. PR #3626)
        - Secondary issue: Images may appear too large / too small without resizing.
    - Should we try using a different resizing solution, rather than resampling?
        - Brainstorm ideas here
        - Jan: maybe we can keep the original sagittal resolution? (ie: slice thickness R-L dim)
            - the 0.6mm resampling should be done on the in-plane image
        - JCA: documenting the possible culprit on the issue
    - Jan: resampling should maybe not add new slices in the sagittal mosaic

Research

- Nilser: Post-BrainHack progress report
    - Link

- Rohan: Post-BrainHack progress report
    - link

Action Items

☑ ~~Sandrine: continue PR sct_compute_compression~~
☑ ~~JN: Troubleshoot + fix the improper binarization + resampling on wrong axes~~
☐ Nilser: check what is pseudo dice
☐ Nilser: what fold is slide 7
☐ Rohan: dig about bagging

2023-05-31 (Phillips + PAM50 spinal levels)

Attendees:

- Update on using the rostral- caudal rootlet to the intervertebral foramen distance
    - We identified the rostral- caudal rootlets of levels C2 to C5
    - We computed the distance rostral- caudal rootlet to the intervertebral foramen
    - We computed a ratio for rostral and caudal distance in PAM50 vs Mendez paper
    - Placed the distances of Mendez using the ratio
- Results:
    - Location is bad already at C8…
- Discussion:
    - Could be because of the distortion caused by straightening in the PAM50
    - The further you are from the spinal cord, the higher are the distorsions
- Next steps:
    - JCA: It would not be more reliable then what we currently have
    - Aaron:
        - there is no clear solution to improving the accuracy
        - Approach serve the purpose of knowing where the epidural location

2023-05-18

Attendees: Sandrine Bédard, Jan Valosek, Nilser Laines Medina, Nadia Blostein, Rohan Banerjee, Mathieu Guay-Paquet, Julien Cohen-Adad, Joshua Newton, Theo, Nathan Molinier
Not yet arrived:, Naga Karthik, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

-

Check last week's action items

- ☑ ~~Sandrine/Théo: prepare presentation for meeting with Igor about the PAM50~~
- ☑ ~~Sandrine/Nathan : look at PAM50 data~~
- ☑ ~~Joshua/Mathieu/Jan: Collaborate on lesion QC~~
  - Sagittal QC added here: #4102
  - JN: Look into whether the resampling (in QC) is creating a "partial volume effect"-type visualization.
- ☑ ~~Jan: Check if soft lesion can be provided to sct_analyze_lesion~~
  - Context: "Does volume calculation account for weighted volume soft masks?"
  - Jan: sct_analyze_lesion supports only binary lesions - I opened issue #4120
    - Julien comment: be aware that some calculations can require binary mask
- ☐ Naga: Look into training data for sct_deepseg_sc (Charley, repos, subject list in .pkl file, etc.)
  - Not present in the meeting – In another meeting.

Software Development

- PAM50 Calgary level file updates
  - Meeting with Igor (May 8th)
    - How did the meeting go?
      - Igor didn't have any new ideas / explanations.
    - Next steps?
      - Label rostral/caudal + compare to paper data
      - First levels = good results, lower levels = poorer results
      - Not confident with results
  - Future meeting with Aaron Phillips/Julien Rimok
    - Scheduled for: → Taken care of by Julien Rimok
    - JulienR has other ideas: Vertebral length… (Sandrine: This wouldn't be reliable)

- JN: Timeline for releasing v6.0/v6.1
    - Previously, we had planned releases around the compression OHBM submission
    - Old timeline:
        - 6.0: Release in mid-late April
        - 6.1: 2.5 month development (May-July), release July 15th
        - OHBM: Mention v6.1 in submission

    - However, given the delays from the PAM50 template updates, the development time for 6.1 is shortening (Currently: ~1.5 months – Late May to July 15th)
    - Perhaps a new timeline is now necessary?
        - 6.0: Release closer to OHBM (and include sct_compute_compression)
        - OHBM: Mention v6.0 in submission
        - 6.1: Some later date post-OHBM, perhaps focusing v6.1 on the upcoming November SCT course?

    - Should PAM50 be included in the 6.0?
        - 90% chance of dropping, will require a separate project/future release

    - Advertising new release of SCT + SCT Course
        - 2 big conferences (ISMRM, OHBM) + QBIN
            - QBIN: Small slide presentation
            - ISMRM: June 3rd to 8th Toronto
            - OHBM: July 22th to july 26th Montréal
        - Announcement at the party, too? June 8th
        - Advertising information
            - Coming soon? July? Specific date?
            - July 15th! → Change 6.0 milestone, too.

    - Determining date of workshop
        - Martinos hybrid workshop, November 13th-15h
        - SCT not formally a part of the Martinos workshop, but we can time it soon after
        - 1 day vs 2 half days? Latter allows for fixing installations, digesting content, etc.
            - 2 half days: (Mon/Tues) 20th and 21st of November, in the morning for timezone purposes
            - Past years: In-person active participation, not possible now (full online)
            - 2020 SCT workshop page, all previous workshops

- JN: Postmortem for SCT Forum email outage
    - TLDR: SSL certificate expired, email jobs were failing, wasn't caught for ~2 months
        - For what it's worth, Discourse's certs should be auto-renewed, in theory?
        - But, I found I had to restart the `systemd-openstmpd` service for the changes to propagate.
    - Ideas on how I can better catch email failures in the future?
        - JN: Make a point to check the admin dashboard regularly.
            - Easy to forget… 😓

        - JN: Send out a daily automated email to the forum admin’s email (i.e. my email)
            - Would act as a canary in the coal mine
            - If the emails stop, then I know that something has broken, and I can address it.
        - Any other ideas?
            - Have a second agent that can send an alert email when emails stop being received
            - Mention to the new IT specialist (Nathan #2)

- Jan:
    - Drop segmentation/centerline requirement for `sct_analyze_lesion` - PR [#4112](#) ready for review

    - What to keep in script headers - issue [#4117](#)
        - Julien’s comment: also include cross-ref to license?
        - LICENSE.txt -> LICENSE

spinalcordtoolbox/spinalcordtoolbox/scripts/sct_analyze_lesion.py
Lines 5 to 7 in `822d1a3`

```
5    # Copyright (c) 2014 Polytechnique Montreal <www.neuro.polymtl.ca>
6    # Author: Charley
7    # Modified: 2023-05-16 by Jan Valosek
```

Research

- Théo:
    - Model for automatically segment the nerve rootlets
- Nathan:
    - Comparing 3 different (sct_label_vertebrae and 2 DL-based) methods to identify the disc labels
    - The best method will be integrated into SCT to replace/complement the C2/C3 finder + iterative probability-matching level approach
- Nilser:
    - Project for Brainhack
    - Automatic MS lesion segmentation from CanProCo dataset
    - Share in 2 weeks 🎉
- Rohan:
    - Spinal cord segmentation from fMRI data (gradient echo EPI) (multi-center dataset)
        - The dataset will be published at OpenNeuro
        - Manual GT available
        - Test contrast-agnostic model
        - Once the model is ready, segment SC from individual fMRI volumes to do motion correction
        - https://github.com/sct-pipeline/fmri-segmentation
        - Share in 2 weeks 🎉

- Contrast-agnostic model
    - Does not include MToff → problem for CanProCo
    - Link to MICCAI submission: https://drive.google.com/drive/folders/1LIKw8pNA8G9gYgqwFy00fiPORXgBrT3H
    - Just an idea - include also artificially augmented lesions?

Action Items

☑ ~~Jan: (prepare to) advertise SCT 6.0 at ISMRM, and November course date~~
☐ Nadia: advertise SCT at QBIN, and at the highlights party at ISMRM
☐ JCA (and others): figure out the exact dates for the November course
    - Was this determined earlier in the meeting?
☐ MGP: adjust release dates on github (July 15 for v6.0)
☐ JN: Update dev wiki and submit PR to normalize the headers in CLI scripts
☐ Nilser: Share progress in 2 weeks after brainhack
☐ Rohan: Share progress in 2 weeks after brainhack

2023-05-08 (Igor + PAM50)

Link to presentation and follow up notes: P presentation_pam50_spinal_levels_2023-05-08.pptx

2023-05-04

Attendees: Mathieu Guay-Paquet, Jan Valosek, Théo Mathieu, Sandrine Bédard, Nilser Laines Medina, Naga Karthik, Samuelle Saint-Onge, Nathan Molinier, Julien Cohen-Adad, Étienne Du-fayet, Joshua Newton,
Not yet arrived: Rohan Banerjee, Nadia Blostein, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Miscellaneous items

- JN: Will be away for Mondays in May (using remaining days off for the year)
    - Still, feel free to ping me if you need anything!

- Welcome Samuelle, Théo and Pierre-Louis! 🎉
    - Samuelle: Spinal cord imaging, pediatric populations (may be using SCT)
    - Theo: Internship, detection of nerve rootlets with DL
    - Pierre-Louis: Internship

Check last week's action items

- ☑ ~~Invite Aaron, Julien, and others to #sct-spinal-level-calgary for discussion~~
- ☐ Sandrine/Theo: Implement proposed vertebral landmark-based approach
    - Work being done in Jupyter notebooks (spine_level_theo_sandrine_STD.ipynb) in PR PAM50/#3.
- ☐ Sandrine/Theo: Figure out a way to validate the new level approach given the lack of visibility of rootlets in PAM50 template
- ☑ ~~Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has idea~~
    - Nadia had first version of the template
    - Abstract for QBIN is submitted :) 🎉

Action items copied from last meeting due to absence

- ☑ ~~Jan: Contact Philippe (Ottawa) team to start labeling traumatic SCI lesions. (PRAXIS database)~~
    - Re: Automated lesion segmentation tool + feedback from clinical standpoint
    - Add new dataset to training dataset
- ☐ Naga: Try torch.io data augmentation to downsample 3D images to simulate highly-anisotropic sagittal images in the context of DL-model training
    - Haven't had a chance to try this yet
- ☐ Naga: Compare resampling during augmentation vs during preprocessing

Software Development

- v6.0 release
    - Progress on Phillips PAM50 level file adjustment?
        - Sandrine Bédard : https://github.com/spinalcordtoolbox/PAM50/issues/12
            - We are meeting the group from the Mendez 2021 paper next monday to see how the intervertebral foramen to rostral/caudal rootlet was computed. The measures in the PAM50 space don't seem right.
            - During meeting, we'll also be able to validate the current work, because a neurosurgeon from the Calgary group will be present
            - Possible conclusion: We may not be able to use their methods.
            - Re: v6.0 inclusion – If we can't include, then release v6.0? Yes.
        - Question: Axial slices rotated by 45°? – Just for visualization, to make sure that we're in the right spot
            - Show axial, sagittal and coronal

- JN: Python 3.9 support (#3367)
    - **Context:** 3D Slicer uses Python 3.9, but SCT uses Python 3.8 (Slack thread)
        - So, upgrading SCT to 3.9 may aid with Slicer/SCT integration
        - NB: We would have to do this anyway by October 2024.
    - **Blocker:** PyQt5 v5.14.2 wheel issues
        - A viable solution has been found (downgrading PyQt5 to 5.12-5.13)

- 3D Slicer integration
    - Slicer seems to be importing SCT through our Python API
    - However, they're importing `run_proc`, which is a roundabout way of calling the SCT CLI anyway
    - So, we should discuss whether they need to be accessing SCT's Python API at all

- JN: Update on other work
    - Until v6.0 is released, I am currently working on small, easy-to-review bug fixes.

- Jan: lesion QC (issue #3803)
    - Axial QC implemented (draft #4102)
        - Axial alone is not enough to analyze lesions
    - Sagittal QC implementation is more complex → will take more time; help from SW devs would be appreciated 🙂
        - The QC code is very complex + difficult to understand (decorators, etc.)
            - Sync with Mathieu + Joshua
        - Want to be able to show several sagittal slices → how would that UI look? 🤔
            - How many slices do we want to show?
            - Use centerline to select a few relevant slices
    - Do we want to always show both? Or do we want to choose Axial *OR* Sagittal?
        - Potentially offer a CLI argument to specify which view you want

    - Naga: Comment about specific type of data (I missed the details, sorry!)
        - Add as a command line flag

- Jan: `sct_analyze_lesion` requires segmentation/centerline to do angle correction (issue canproco #27)
    - → Refactor the function to not require the centerline for lesion volume calculation - draft #4112
    - I.e. if seg/centerline is not provided, then skip angle correction and just compute volume (i.e. # of voxels * voxel size)
    - Question: Does volume calculation account for weighted volume soft masks?
        - ANS: Atlas can be provided to compute for specific tracts
        - Is possible with sct_process_segmentation
        - Jan: check if soft lesion can be provided

- NM: data management #235 issue regarding the large FOV data used for PAM50 → where is the data ?
    - Requires Benjamin's input → Not here?
    - NM: Can't find T1/T2 data
    - Sandrine: Marseilles → DICOM → Present on sct_testing_large
        - Issue: Missing FOV
        - participants.tsv contains relevant patients
        - More than 50 subjects, but T2* (The 50 in "PAM50" → 50 T1/T2 images)
    - Follow-up: Talk to Sandrine to go through NeuroPoly

- Naga: Where can I find the training data used for sct_deepseg_sc?
    - Paper (Gros et al., 2019) mentions that there are 12 sites + over 500 patients
    - Should be in sct_testing_large
    - Get in touch with Charley Gros → Still on slack?
    - Past SCT Issue #4046.
        - May be better to close the SCT issue and open an issue in the deepseg_sc_models repo?
    - Info about subject list might be in the .pkl file here

Research

- Pierre-Louis: Working on:
    - https://github.com/ivadomed/model_seg_mouse-sc_wm-gm_t1
    - Try using 3D nnUnet (v1, v2) to retrain, perhaps integrate into SCT

Action Items

☐ Sandrine/Théo: prepare presentation for meeting with Igor about the PAM50
☐ Sandrine/Nathan : look at PAM50 data
☐ Joshua/Mathieu/Jan: Collaborate on lesion QC

2023-04-21 (Aaron Phillips)

Attendees: Aaron Phillips, Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Nadia Blostein, Sandrine Bédard, Julien Rimok, Nathan Molinier, Victor Baillet
Not yet arrived: Rohan Banerjee, Naga Karthik, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz, Julien Cohen-Adad, Jan Valosek, Nilser Laines Medina
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

PAM50 level file discussion

- Discussion of Issue #10
    - Old spinal levels (PAM50) vs. New levels (Phillips' lab)
        - C3 – Mid-slice is the same
        - C4 – Shifting in the mid-slice
        - Further down:
            - Much greater shifting
            - Cannot see the spinal nerve rootlets

    - Mendez paper: Linear scaling
        - May not be accurate
        - May be better to use vertebral landmarks

    - Aaron Phillips/Julien Rimok's motivations:
        - Existing PAM50: Conus location is not consistent with Mendez paper/Aaron+Julien's clinical observations/"dogmatic view", so Calgary side was motivated to update the PAM50 to improve locations in line with Mendez paper
        - However, they agree that linear scaling is likely suboptimal
        - Landmark-based approach sounds good + worth a try

    - How to validate the new approach?
        - Can't see rootlets very well in PAM50 overall → Mainly in top section
        - But, inaccuracies were primarily in lower levels. So, how to validate?

    - Would we still do any scaling?
        - Perhaps scaling per-level
        - Perhaps rely on Mendez data
        - Could depend on differences – experimental approach?

    - Which side should devote the effort? (Collaborative effort?)
        - Neuropoly’s side:
            - Sandrine?
            - Yes, but unsure about the difficulty of labeling foramen
        - Calgary side:
            - Julien Rimok
            - Neurosurgeon team → Stefano?
            - Collaborative effort? → Yes!
        - Revisiting paper? → Should be accurate as possible, Aaron’s side is happy to pause until the updated results

    - Timeline on NP’s end: Release date of SCT v6.0?
        - Relatively high priority on our end – ASAP.
        - Julien: Seems like a few days worth of work (?)
        - Hopefully we can release SCT v6.0 by the end of the month.

    - JN: NeuroPoly Slack channel for this? Invite Julien + Aaron + collaborators?
        - Yes!

Action Items

☑ ~~Create a Slack channel for this effort~~
    - #sct-spinal-level-calgary

☐ Invite Aaron, Julien, and others to #sct-spinal-level-calgary

☐ Determine a way to validate the approach given the lack of visibility of rootlets in PAM50 template

2023-04-17 (3D Slicer)

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Jonathan Chu, Michael Hardisty, Philippe Phan, Hediyeh Toufani, Raj Ranabhat, Etienne Du Fayet, Victor Baillet, Nadia Blostein, Jan Valosek, Nick Guenther, Sandirne Bedard, Nathan Molinier, Rohan Banerjee
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Introduction

- Round table 👋
    - Montreal: Many! (NeuroPoly folks)
    - Ottawa: Philippe + Hediyeh
    - Toronto: Michael, Raj, Jonathan

- Background on collaboration with Philippe
    - Hediyeh's PhD project topic: Potentially visualizing 3D spinal cord segmentation/lesions

- Background on SCT Slicer Plugin
    - SCT has an issue with context; Bitbucket repo
    - Collab between Julien (NeuroPoly) and Michael
    - Work largely done by Michael's team
    - Q: How has the plugin evolved?
        - Interest primarily in surgical planning (MRI tractography)
        - SCT + Slicer == Spinal cord tractography
        - Dataset was created
        - Slicer's extension language → Python wrappers around SCT's CLI
        - SCT was updated to make it easier to call from Slicer
        - Challenges: ITK/VTK version incompatibilities between SCT and Slicer
            - Froze at specific versions of SCT/Slicer to avoid these issues
            - Build SCT against Slicer's version of ITK/VTK
    - Q: Current users and use of the plugin?
        - Quite modest – not many outside of Michael's group
        - Mainly used for segmentation/tractography
        - SCT plugin isn't the only plugin being used
        - Runs inside of a docker container (VNC/web interface) – clunky?
            - Aside: Possibly SCT inside of docker, making interfacing easier?
    - Demo (Raj)
        - Docker container running
        - VNC viewer → Connect to docker container, run Slicer
        - Viewing a 3D mesh of the spinal cord!

Questions

- Julien: Can we try to move away from Docker? (hard to maintain updated image, etc.)?
  - More context about “difficult maintainability” SCT issue comment
  - Reason for Docker is ITK/VTK compatibility
  - Might be possible to avoid the incompatibilities through other ways
    - ANTsPy
  - Michael: Hesitant to move away from Docker
    - Reason: Engineer had already tried and failed due to ITK/VTK collisions
    - Requires a lot of expertise re: Slicer and SCT’s build
    - Joshua: Side note: I’m not sure that our binaries rely on shared libraries anymore, and thus I’m not sure there would be collisions anymore.
      - Nick and I recently redesigned the build process via GHA
    - Action item: Try installing the most recent version of SCT to see if there are still collisions.
    - Action item: Create slack channel for discussing this collaboration

- Philippe: What aspect of surgical planning has it been used for; who are the surgeons that have used it so far?
  - ANS: Haven’t had surgeons using this Slicer or this plugin
    - Medical students, undergraduates, software engineers
    - Use more geared towards VR-based planning
    - There is a learning curve that is a barrier to entry

- Philippe: Interest (re: Hediyeh’s PhD topic) is more geared towards making software easier/more accessible for clinician usage
  - qMRI analysis, but missing the simple/accessible tools to apply pipelines
  - ANS: Slicer in general is flexible + powerful → hence all of the buttons
    - “Slicelets” make the Slicer interface cleaner/simpler
    - Pipelines are much simpler → one button runs the full pipeline

- Philippe: Progress on Praxis national database of SCI patients?
  - Lesion labeling needs to be done of these images
  - Objective 1: Use SCT to compute biomarkers
  - Objective 2: Train model to segment lesions/edemas
  - Objective 3: Potentially develop Slicer pipeline to make the above tasks easier for clinicians

- Philippe: Desire to extra FA
  - Julien: `sct_extract_metric` command would be used for that purpose
  - Michael: `sct_extract_metric` not currently in Slicer plugin

Action items

- ☑ ~~Julien: Create slack channel for collaboration (For questions about new versions of SCT)~~
- ☑ ~~Michael: Share Docker plugin/documentation with Hediyeh to test/try~~
- ☑ ~~Michael/Julien: Try upgrading to the most recent version of SCT to see if there are still collisions~~

2023-04-06 (Philippe/Hediyeh)

Attendees: Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Nadia Blostein, Nathan Molinier, Victor Baillet, Nilser Laines Medina, Julien Cohen-Adad, Philippe Phan, Hediyeh Toufani
Not yet arrived: Jan Valosek, Rohan Banerjee, Naga Karthik, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz,
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Welcome Philippe and Hediyeh! 🎉

- Previous meeting context: 2023-03-23

- Updates to SCI ground truth labeling
    - How has contacting various sites gone? (Re: availability of site personnel to create new ground truth)
        - Naga/Jan are not here
        - Follow up offline → will be the responsibility of those students

    - PP: How many subjects do we have so far?
        - JCA: ~350 subjects were requested
            - Currently, we have 2 sites, 30 subjects (not enough for meaningful analysis)
                - 2 sites have agreed to data sharing agreements
            - PP: Praxis → A lot of sites are behind?
            - But we can set up the pipeline using this initial dataset, then use the pipeline once we have the full ground truth

    - Discussion about the research proposal (what work will be contributed)
        - Ongoing projects/deliverable:
            - Cross sectional area
            - Spinal cord compression metrics
        - Future work:
            - Lesion segmentation
            - PP's lab: Ground truth identification of edema (?) region?
                - To be separated into training/testing database
        - Platform for hosting/sharing the data?
            - Still needs to be worked out → https://spineimage.ca/
            - Mathieu/Jan are working on hosting/pipeline respectively

- Updates to “Web SCT” PhD proposal
    - How did the 3DSlicer integration go?
        - HT: Not designed for the spinal cord…?
        - Correction: Hasn’t been tried yet
        - NB: 3DSlicer integration is not contained in the SCT source code
        - There is a 3DSlicer plugin that includes SCT functionality
            - **Action item:** Provide a link to this plugin as well?
    - How did the FSLeyes plugin go?
        - HT: Just a visualization tool – can’t do analysis?
            - This is just vanilla FSLeyes
            - The plugin is separate
            - **Action item:** Provide a link to the specific FSLeyes plugin page.
    - PP: Potential miscommunication?
        - JCA: SCT is integrated into 3DSlider/FSLeyes

- Next steps
    - Restructuring of Hediyeh’s PhD Focus → 3D Spinal cord visualization
        - I.e. inspecting the spinal cord features in 3D, rather than SI/AP/LR planes
        - Does this exist already?
            - JCA: FSLeyes does not have 3D viewer
            - JCA: 3DSlicer has a 3D viewer already
                - JN: What about using SCT to compute SC/GM/WM segmentations, then viewing that segmentation file in a 3D viewer such as 3DSlicer?
            - PP: It feels as though clinicians aren’t aware of the 3DSlicer, so the PhD goal is to improve accessibility
                - JCA: Some clinicians are aware and do use it

    - Alternate project proposals, if 3D spinal cord visualization is not feasible
        - JCA: Perhaps automatic edema segmentation, which does not exist yet

    - PP: NDA/Data agreements
        - What tasks can the Praxis data be used for? What restrictions do the NDAs apply?
        - → Follow up outside of this meeting

    - PP: What is the best quality example dataset we have access to?
        - JCA: Depends on what qualities we’re looking for
            - MRI → Can’t see tracts
            - Diffusion imaging → Can distinguish tracts
            - Example: https://spine-generic.readthedocs.io/data-acquisition.html#example-of-datasets
        - JCA: There is one online

If there is any remaining time left in the meeting:

Check last week's action items

- Action items assigned last week
    - ☑ ~~JV/MGP: Open issue in manual correction repo about JSON sidecar discussion~~
    - ☑ ~~JN: Update 6.0/6.1 milestone dates~~
    - ☑ ~~JN: Assign sct_compute_compression PR to 6.1 instead of 6.0~~
    - ☑ ~~Julien/JN/SB: Upload processing code to PAM50 repo (make new `code/` folder)~~
        - Done by SB in this commit.
    - ☑ ~~JN/JV: Merge histology changes, close issue #7/#8, and update old SCT PR~~
    - ☑ ~~JN/MGP: Close C8-related disc level discussion on "Code Cleanup" PR (But, make sure that the proper language is used ("spinal" vs "vertebral" levels)~~
    - ☑ ~~JN: Unlink JV's `labelize` PR from sct_label_vertebrae issue~~

- Action items copied from last week due to absence
    - ☐ Naga et al.: Contact Philippe (Ottawa) team to start labeling SCI lesions.
    - ☐ Naga: Try torch.io data augmentation to downsample 3D images to simulate highly-anisotropic sagittal images in the context of DL-model training
    - ☐ Naga: Compare resampling during augmentation vs during preprocessing
    - ☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
        - Nadia: Finally started → Trying to get analysis running on Beluga (CC?)
        - JN: Why is this being run on CC?
            - Not enough cores on Nadia's personal laptop
            - Issues with minc-toolkit on lab computers
            - Benjamin used CC to generate previous templates
    - ☑ ~~Nadia: Try using ANTs instead of MINC~~
        - Too time-consuming to explore ANTs right now → perhaps after conference season
        - JN: This is potentially a solution for the minc-toolkit issues?
            - Messy Python dependency issues (SCT, minc, etc.)

Software Development

- v6.0 Progress
    - All is complete except Phillips level file PR
        - Meeting will be held on April 10th
        - Once concerns are resolved:
            - A new PAM50 release can be created
            - The PAM50 release can be merged alongside the Histology file PR
            - We can release SCT v6.0 🎉

  - JN: One last issue to sneak into new PAM50 release, since we’re already making changes
    - #3256: Change q/sform codes of the PAM50 (2/1 → 4)
    - May be more complicated than it looks → Make sure to check that this doesn’t break any existing pipelines (e.g. perhaps open a quick PAM50 PR then use the temp branch in an SCT PR to check.)

- JN: In lieu of SCT v6.0 tasks, I have been helping Mathieu with fixing the data-multi-subject CI (see issue https://github.com/spine-generic/spine-generic/issues/264)

Research

-
  -

Action Items

☑ ~~Send links to SCT plugins to Hediyeh~~

2023-03-30

Attendees:
Not yet arrived: Rohan Banerjee, Naga Karthik, Nadia Blostein, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz, Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek (holidays), Nathan Molinier, Philippe Phan, Nilser Laines Medina, Hediyeh Toufani,
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Miscellaneous items

- Welcome Victor Baillet! 🎉

Check last week's action items

- ☑ ~~Julien: get Naga et al. to contact Philippe (Ottawa) team to start labeling SCI lesions.~~
    - Related to meeting from last week → Need training data for model
    - Not urgent.
- ☑ ~~Sandrine & Matthieu: Centerline extrapolation - ParamCenterline(minmax)~~
- ☑ ~~JN: Delete SourceForge site~~
- ☑ ~~JN: Review Sandrine's sct_compute_compression PR~~
    - Reviews in progress, see more in "Software Development" section
- ☑ ~~Julien + Jan: Examine resampling + file size of histology files - PAM50/#8~~
    - Mostly done, discuss further in "Software Development" section
- ☑ ~~MGP: Advertise next week's in-between meeting~~
- ☑ ~~Jan: compression labels should be located in the middle of SC → update #3984 and maybe open also separate issue about compression labeling procedure~~
    - Done in this comment - feedback welcome
- ☑ ~~Nathan: Continue to explore the "next steps" following the presentation~~
    - Continued to work on hourglass approach
    - Benjamin is not here (on holidays) → Wanted to ask about projecting coordinates on the spinal cord (doesn't exist → create from scratch?) → PR to add this projection feature on SCT
    - Discuss further in "Research" section soon

Action items moved from a previous meeting due to absence

- Nadia/Naga not present at this meeting

☐ Naga: Try torch.io data augmentation to downsample 3D images to simulate highly-anisotropic sagittal images in the context of DL-model training
☐ Naga: Compare resampling during augmentation vs during preprocessing
☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
☐ Nadia: Try using ANTs instead of MINC

Data Management

- Jan Valošek and MGP:
    - Should `derivatives/labels` be compatible with BIDS (pass bids-validator)?
        - If so, how do we handle suffixes?
        - `sub-001_T2w_seg.nii.gz` is not BIDS compatible because `seg` is not a valid suffix.
            - → _T2w considered as the suffix ←
            - The extra "_seg" is not considered by BIDS
            - New filename convention has been established?
                a. _T2w_label-SC_mask-manual.nii.gz
                b. Link to intranet?
            - But this problem is often introduced by SCT scripts
            - Not fixing in this meeting → Consider for the future
        - Example mistake that might have been caught: data-management#224

    - What to include in JSON sidecars for automatically generated and visually inspected files (like outputs of `sct_deepseg_sc`)
        - Empty JSON is not allowed by BIDS
        - Maybe something like:
```
{
    "VerifiedBy": "Generated automatically and visually checked by JV",
}
```
        - In the intranet, it says to include:
            - Author/date (when creating the file)
            - But what about when checking the files (different author/date)?
                - Add the new names/dates to the same JSON, or a separate JSON?
                - List of authors/dates/author-date pairs
                - → Action item: Add discussion issue in manual correction repo?

Software Development

- JN: 6.0 Release Progress
    - #3: PAM50 level files
        - In-progress discussion about “sharp” vs. “gradient” mean level locations
        - ~~Waiting on further response from Aaron Phillips about their methods~~
            - Update: We received an email literally the night before the meeting! (Again!)
            - We will need some time to review all of the new information/files/code/etc.
            - Unsure if we agree with method, but need to run the code and investigating the approach
            - We should host the scripts / code somewhere (PAM50/PR#3)
                1. Right now processing code is in README
                2. But we can create a code folder now that we have more than one processing script
                3. Do we have permission to re-host the code?
                    - → Action item: Need precise clarification

    - #2179: PAM50 histology files
        - Remaining open issues that need to be resolved:
            - #7: Including the histology atlas in PAM50 upon installation
                1. File size reduced to 31M!
                2. JN: Very reasonable to include upon installation, I think?
            - #8: Histology atlas has inconsistent dimensions
                1. Jan: if we are fine with `0.199074x0.198795x0.5` resolution (which we probably are), #9 can be merged
                    - Pad and crop → More effort than is worth
        - Once resolved, a new release needs to be created, then added to:
            - #3444: Add new `-histo` option to warp the PAM50 histology files

    - #3531: Wrong behavior of `fitseg` algorithm: the output centerline is not extrapolated
        - Fixed in #4079

    - #4003: sct_compute_compression PR
        - JN: Reviews are going well (there is a lot to review, 1-2 reviews per day)
        - Discussion about default value of `-normalize`
            - Choose default now? (Normal MSCC vs. PAM50-normalized)
                1. Set no default so that people know what they’re doing when they’re turning on PAM50 normali
            - Or do we wait to release until 6.1 so that we can fully test the script + fully perform analysis, then decide later.
            - Waiting lets us save an important feature for a 6.1, since 6.0 has plenty of new features already.

                - No need to make this decision now?
            - What do we mean by the flag `-normalize`?
                - There’s multiple definitions of normalization
                    a. Levels above and below (done in both cases)
                    b. Normalize with attributes of control database
                - We can maybe just clarify this using help descriptions in the argparse of the script.

- MGP: What’s the target/expected release date for 6.0 now?
    - Just dependent on Phillips Lab
    - Tentatively set for April 15th

- MGP: Next release milestone is created for 6.1, set for July 31 arbitrarily.
    - Should 6.1 be out for OHBM → Before July 22nd? (Yes!)
    - Change the milestone deadline to July 15th-ish (i.e. a week before).

- NM: #4080: sct_label_utils -project-centerline:
    - What should we do when points have the same projection coordinate ? (Highly unusual for discs labels)
        - Return an error ? Overwrite the last projection ?
            - If there is an error, what recourse does the user have to even fix things?
            - We should let things continue to run → warning
                a. Which label should “win out” (first, last, biggest, smallest)
                b. Can be decided offline → not a huge deal

- MGP: Question for a subject matter expert during refactoring #4075 (comment):
    - In types.py, in the Centerline class, there are various spinal region dicts where the regions go directly from C6, C7 to T1, T2 (i.e. no C8)
        - NB: These spinal region dicts are used in Centerline methods such as `compute_vertebral_distribution`
    - However, in PAM50/spinal_levels, the levels include C8 as well
    - Is this a bug? Maybe BDL or JCA knows?
        - Response from Sandrine:
            - vertebral level don’t have C8, but spinal levels do
            - C8 is “aligned” with C7 vertebrae
            - Would be good to clarify between “spinal level” and “vertebral level”

- JN: Issue #3395: Improve sct_label_vertebrae by skipping straightening
    - There are currently 2 open PRs linked to this issue:
        - #4072: JV: Improving `labelize_from_discs` function
            - This is just a quick fix for the DCM project → Shouldn't close the issue
            - Maybe unlink this PR because Nathan's is the more important PR
            - Still relevant, keep this work!
            - NB: This is only relevant to sct_label_utils, unrelated to other methods such as sct_label_vertebrae
                1. (There are multiple ways of getting labeled segmentations)
        - #4080: NM: Adding `project_discs` option
            - This is the "real" solution → Keep the link to the issue

    - Q: Is this duplicated effort? Or are both enhancements needed to fix #3395?
        - Not duplicated effort, entirely separate efforts

Research

-

Action Items

☑ ~~JV/MGP: Open issue in manual correction repo about JSON sidecar discussion~~
☑ ~~JN: Move Nadia/Naga action items to next week's meeting~~
☑ ~~JN: Update 6.0/6.1 milestone dates~~
☑ ~~JN: Assign sct_compute_compression PR to 6.1 instead of 6.0~~
☑ ~~Julien: Contact Aaron Phillips about permission to re-host processing code~~
☑ ~~Julien/JN/SB: Upload processing code to PAM50 repo (make new `code/` folder)~~
☑ ~~JN/JV: Merge histology changes, close issue #7/#8, and update old SCT PR~~
☑ ~~JN/MGP: Close C8-related disc level discussion on "Code Quality" PR~~
- But, make sure that the proper language is used ("spinal" vs "vertebral" levels)

☑ ~~JN: Unlink JV's `labelize` PR from sct_label_vertebrae issue~~

2023-03-23

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Nathan Molinier, Philippe Phan, Nilser Laines Medina, Hediyeh Toufani,
Not yet arrived: Rohan Banerjee, Naga Karthik, Nadia Blostein, Benjamin De Leener, Nick Guenther, Julian McGinnis, Adrian El Baz
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Miscellaneous items

- Welcome Philippe Phan and Hediyeh (and perhaps Eve?)! 🎉
  - Philippe: Neurosurgeon at Ottawa Hospital
  - Collaborating with NeuroPoly on the Praxis Pan-Canadian database of SCI patients
    - Mathieu + Jan are familiar
    - https://spineimage.ca
  - Meeting purpose: Strategy around training an SCI DL lesion segmentation model
    - Developing ground truth for training → Emails resulted in this meeting
      - Ottawa can produce ground truth for their own data
      - Uncertain of available people to produce ground truth for other sites
    - Analysis: Pre vs. post-surgery; post-surgery images contain metal implants → induce severe image artifacts, consider that decompression was performed → changes the purpose
    - Emails re: online version of SCT (would help clinicians)
      - Which functions are most useful? → Hediyeh's presentation?
      - Webdev discussion re: frontend/backend, database, api design, etc. (django, heroku, mongoDB), cloud hosting
    - Questions about presentation from Hediyeh
      - What SCT features would be useful
      - API/models: SCT is not only DL models
      - host/server, maintenance, etc.
      - possibility to use cloud instance from compute canada?
      - FL: very ambitious,
        - coda: QC-based initiative, JM Mac Thiong involved–
      - Other solution: 3D Slicer plugin (see Michael Harditsty)
      - Visualisation: HUGE work. Many solutions already exist. eg Slicer
    - Conclusion:
      - Ottawa team will review FSLeyes and Slicer3d plugins and will come back to us with feedback, what is needed, etc.

Check last week’s action items

- ☑ ~~Joshua: Follow up by posting the Phillips PAM50 email responses to the discussion threads in the issue. (Mark completed threads as resolved)~~
  - ○ Discuss further in “Software Development” section
- ☑ ~~Joshua: Review sct_compute_compression PR~~
  - ○ Review in-progress, but was blocked by ongoing discussion/rewrites
  - ○ Discuss further in “Software Development/Research” sections
- ☑ ~~Julien: Create a new release for the MP2RAGE models that resolves the PR issues~~
  - ○ MP2RAGE/ensemble PR has been merged!
- ☑ ~~Nathan: Test out Windows installer update PR~~
  - ○ Installer was tested and PR was merged!
- ☑ ~~Jan: Explore strategies how to bring histological atlas to PAM50 - WIP~~
  - ○ Discuss further in “Software Development” section
- ☐ Nathan: Continue to explore the “next steps” following the presentation
  - ○ Continued to work on hourglass approach
  - ○ Benjamin is not here (on holidays) → Wanted to ask about projecting coordinates on the spinal cord (doesn’t exist → create from scratch?)
  - ○ Discuss further in “Research” section
- ☑ ~~Rohan/Nathan: Review changes to the installer documentation PR (#4060)~~
  - ○ Received a review from Mathieu instead

Action items moved from last meeting due to absence

- ☐ Naga: Try torch.io data augmentation to downsample 3D images to simulate highly-anisotropic sagittal images in the context of DL-model training
- ☐ Naga: Compare resampling during augmentation vs during preprocessing
- ☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
- ☐ Nadia: Try using ANTs instead of MINC

Data Management → Move to next week

- Jan Valošek and MGP:
    - Should `derivatives/labels` be compatible with BIDS (pass bids-validator)?
        - If so, how do we handle suffixes?
        - `sub-001_T2w_seg.nii.gz` is not BIDS compatible because `seg` is not a valid suffix.
    - What to include in JSON sidecars for automatically generated and visually inspected files (like outputs of `sct_deepseg_sc`)
        - Empty JSON is not allowed by BIDS
        - Maybe something like:

```
{
    "VerifiedBy": "Generated automatically and visually checked by JV",
}
```

Software Development

- JN: 6.0 Release Progress
    - #3: PAM50 level files
        - In-progress discussion about “sharp” vs. “gradient” mean level locations
        - Waiting on further response from Aaron Phillips about their methods
            - Is there anything we can do to make progress in the meanwhile?

    - #2179: PAM50 histology files
        - Remaining open issues that need to be resolved:
            - #7: Including the histology atlas in PAM50 upon installation
            - #8: Histology atlas has inconsistent dimensions
        - Once resolved, a new release needs to be created, then added to:
            - #3444: Add new `-histo` option to warp the PAM50 histology files
            - NB: New PAM50 release would ideally contain Phillips level files, too?

    - #4003: `sct_compute_compression`
        - Undergoing a rewrite to include calls to sct_process_segmentation
        - Is this ready for review?
            - YES 🎉

    - #4040: Fix flake8 lints
        - In-progress by Joshua (See PR #4074)

    - #3531: Wrong behavior of `fitseg` algorithm: the output centerline is not extrapolated
        - Easy fix: Update the help description to remove mention of “extrapolation”
        - Hard fix: Add extrapolation to `fitseg`
            - Not called “extrapolation”, called “min/max”
            - Might not be an available CLI parameter, but is an API function argument!! Very very good to know.

      - Q: How difficult is this to implement?
      - Should it be included in 6.0?
        a. Needs close review, examine the algorithm, interface design, etc.
        b. May be better to exclude from 6.0 to not try to juggle too many tasks? We have a lot going on right now and this seems like a large task! → Not too complicated, 6.0 is reasonable.

- JN: Do we need to push the 6.0 release back → Yes
  - There are several in-progress issues that need further work/discussion/correspondence.
  - If we push back the release by 1-2 weeks (March 31st -> April 7th/14th), then we can fit in one more SCT meeting to hammer out any remaining details.

- JN: Removing the old outdated SCT sourceforge documentation
  - Problem: Currently, the Sourceforge project outranks SCT's GitHub repo in Google Results, and could potentially confuse users as to the "correct" documentation page
    - Previously, we had set the project to a "Moved" state
    - But, after several years, I think most (all?) of our users know the new location of our documentation by now
    - So, I think we can finally close the SourceForge project once and for all?
  - Should we back anything up before deletion?
    - Documentation-related materials have already been migrated
    - However, there is some old user support discussion. (NB: This discussion only concerns SCT v3.2.7 and below (March 2019), so it's quite outdated.)

Research

- #4003: `sct_compute_compression`
  - Questions from ongoing discussion:
    - Which area to consider in averaging?
      - Vertebral body vs. Including extent (e.g. ~1cm) above and below
    - Do we need to use the spinal cord centerline?
      - POV: Orthogonal to cord
      - Just do 1cm in the PAM50 space?
    - 1cm: Hitting the center of a slice (Include or exclude?)
      - Julien: Use rounding; only include if >½ of slice is included
  - Has every question been resolved?
    - yes!!!!!!!!
  - What work is left to be completed?
    - Ready for review 🎉

- #3395: `sct_label_vertebrae` - skip straightening
  - Use orthotogonal projection?
  - Or the closest point? - should be same as the orthotogonal projection, right?
  - Use the same slice - not ideal

Action Items

- ☐ Julien: get Naga et al. to contact Philippe (Ottawa) team to start labelling SCI lesions.
- ☑ ~~Sandrine & Matthieu: Centerline extrapolation - ParamCenterline(minmax)~~
- ☑ ~~JN: Delete SourceForge site~~
- ☑ ~~JN: Review Sandrine's sct_compute_compression PR~~
- ☑ ~~Julien + Jan: Examine resampling + file size of histology files - PAM50/#8~~
- ☑ ~~MGP: Advertize next week's in-between meeting~~
- ☑ ~~Jan: compression labels should be located in the middle of SC → update #3984 and maybe open also separate issue about compression labeling procedure~~

2023-03-09

Attendees: Joshua Newton, Mathieu Guay-Paquet, Jan Valosek, Nathan Molinier, Benjamin De Leener, Nilser Laines Medina, Julien Cohen-Adad, Sandrine Bédard, Rohan Banerjee,
Not yet arrived: Nick Guenther, Nadia Blostein, Julian McGinnis, Adrian El Baz
Moderator: Julien
Minutes: Joshua Newton

Miscellaneous items

- Welcome back from reading week! :)

Check last meeting's action items

- ☑ ~~Team: Investigate email sent by Phillips Lab about PAM50 data → Check assumptions about data, interrogate methods, etc.~~
  - JN: With reading break/grant proposals/etc., I assume there wasn't much time for this?
  - Email didn't answer all of our questions…
  - Haven't had time to check
  - JN: There are a list of open questions in the PR: PR#3/comment
- ☐ Naga: Try torch.io data augmentation to downsample 3D images to simulate highly-anisotropic sagittal images in the context of DL-model training
- ☐ Naga: Compare resampling during augmentation vs during preprocessing
- ☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
  - NB: This action item was moved from last meeting
- ☐ Nadia: Try using ANTs instead of MINC
  - NB: This action item was moved from last meeting
- ☐ Jan: Explore strategies how to bring histological atlas to PAM50
  - Misalignment might be caused by the updated PAM50 header
    → Find the transformation between the "old" and "new" PAM50 - WIP

Software Development

- v6.0 Release Progress
  - JN: Newly opened PRs
    - #4060: Documentation PR opened for new installer changes
      - Can someone who is relatively new to SCT look over these changes?
      - (It would be nice to get some fresh eyes on our installation documentation, to make sure that it makes sense.)
        1. Rohan/Nathan? 🎉

    - #4061: Bring missing `install_sct` features to Windows installer
      - Can someone with a Windows machine try out the updated install script?

            - Nathan has a Windows machine

    - Progress on existing PRs
        - #3952/PR #3: PAM50 Phillips Lab Level Files
            - Resolved (From “Last Week’s Action Items)
        - #4042: Ensemble/bagging feature for sct_deepseg
            - Further development on MP2RAGE models is needed
            - Julien – Follow up on that (Generate new models)
        - Will we have enough time before the March 31st deadline?
            - We can revisit this question on the March 23rd meeting, too.
        - Histology template would be good to have for v6.0
        - #4003: Compression metrics normalization
            - Missing description or documentation
            - Julien and Jan already tested
            - Maybe Joshua you can review now
                1. Sure!!

Research

- Nathan: Quick presentation of the first comparison results of the disc labeling methods
    - Presentation: Slides
    - Next steps
        - Expanding dataset (beyond Spine Generic)
            - For both training and validation
        - Disc label numbers: Without c2-c3 detection, we currently can’t infer the disc number from the Hourglass model predictions
        - Model prediction coordinates – Centerline vs. posterior tip
            - Consider projecting both the ground truth and predicted discs onto the centerline (using the built-in functionality in SCT’s Centerline objects?
    - Aside: Julien’s thoughts about changes to sct_process_segmentation
        - Labeled segmentation → How it handles boundaries between vertebral levels. (Which voxels do we use to identify levels?)

Action Items

- ☐ Joshua: Follow up by posting the Phillips PAM50 email responses to the discussion threads in the issue. (Mark as resolved)
- ☐ Joshua: Review compression metric normalization PR
- ☐ Julien: Create a new release for the MP2RAGE models that resolves the PR issues
- ☐ Rohan/Nathan: Review changes to the installer documentation
- ☐ Nathan: Test out Windows installer update PR
- ☐ Nathan: Continue to explore the “next steps” following the presentation

2023-02-23

Attendees: Julien, Jan, Naga, Joshua, Nathan, Mathieu Guay-Paquet
Not yet arrived: Nick Guenther, Sandrine Bédard, Rohan Banerjee, Nadia Blostein, Nilser Laines Medina, Benjamin De Leener, Julian McGinnis, Adrian El Baz
Moderator: Jan
Minutes: Joshua Newton

Miscellaneous items

- Is 3pm a good meeting time? (Time has been changed a few times in the past few months.)
  - This meeting was only changed because Julien is in France
  - 3pm is a good time most of the time 👍

Check last week's action items

- ☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
  - Move to next meeting
- ☐ Nadia: Try using ANTs instead of MINC
  - Move to next meeting
- ☐ Jan: Explore strategies how to bring histological atlas to PAM50 - WIP
  - Follow up in next meeting
- ☑ ~~Sandrine: Open new repo on SCT organization to store generated CSV files, then access them via sct_download_data~~
  - Done here: PAM50-normalized-metrics
  - Integrated into morphometrics PR #4003
- ☑ ~~Sandrine: Update name of MSCC PR~~
- ☑ ~~Sandrine: update PAM50 spinal levels~~
  - PR has been opened: #3
- ☑ ~~Sandrine: send paper to nadia~~
- ☐ Julien: Look into emails, Google Drive for sdika 'optic' (isct_spine_detect, etc.) source code
  - Potentially not worth looking into, other priorities
- ☑ ~~Joshua: Close issue, then make note about Vanderbilt lab collaboration on pediatric template issue/PR~~
  - Note made here: pediatric-template/#4
- ☑ ~~Benjamin De Leener: Open issue about macOS 13.2 failure → #4035~~

Software Development

- Progress on v6.0 release (Currently Due: March 30th)
  - All issues with the 6.0 milestone have have open PRs (or have been addressed) 🎉
  - Are there any other "breaking changes" we want to introduce during this release cycle, given the optics of a new major release?
    - JN: Once existing PRs are merged, I'd like to spend more time unifying the install scripts for Windows/Linux before the v6.0 release (to make sure install experience is consistent between OSs)

- Phillips Lab PAM50 file PR (#3)
  - PR is dependent on input from Phillips Lab
  - ~~We have received no email response or PR commentary~~
    - Update: At 11pm last night, we received a response! 🎉
    - Since this is last minute, we will probably need more time to read the response and incorporate feedback into PR
    - More investigation is needed – not all questions have been addressed
      - Sandrine not here
      - More feedback/insight is needed from other SCT developers (Jan/Sandrine)

- `display_viewer_syntax()` colormap argument PR (#4037)
  - This function is responsible for "Open this image in FSLeyes" output command
  - PR introduces new argument \`im_type\` to specify colormaps
    - ('anat' maps to 'grayscale', 'seg' maps to 'red', etc.)
  - Should we keep the old \`colormaps\` argument, too? Or do a full replacement?
    - JN: In favor of replacing the old argument, because it ensures we keep our colormap usage consistent for a given image type (all segs will be automatically red, etc.)
    - NM: Is it for internal use only ? Should we implement a way to change those mapping (global variable) ?
  - Conclusion: Follow-up offline

- Nathan: Training datasets for sct deep learning models: issue
  - sct_label_vertebrae → isn't DL-based
  - sct_deepseg_sc → info should be in the GitHub issue
  - Follow up in GitHub issue

- Julien: relevance of centerline detection if SC seg is super-robust
  - Context: There was a proposal for DL-based centerline detection project?

        - Project put on pause because [contrast-agnostic DL model] doesn't need centerline to determine segmentation
        - If we really need the centerline, it can be obtained from the SC seg obtained by [contrast-agnostic DL model]
    - Naga: What's the rationale for using `get_centerline` in the first place?
        - Starting with the centerline improves the quality of the SC segmentation methods (at least for older methods, pre-DL)

- Julien: SCT course
    - Had a talk with Robert Barry (who organized the [last SCT workshop])
    - Wanted to do another one → [Organized by team at MGH]
        - Paid course :(
        - Doesn't fit the philosophy of SCT courses (free, open source knowledge, etc.)
        - Split the event → Have SCT course that is independent (hybrid)
        - Organize whenever we want! 🎉
    - We would like to organize a course → When?
        - Usually done right after ISMRM (This year → June 2023)
        - However, conflict with another workshop
        - So, a bit later → November?
        - Gives us time to return to the issues that have arisen since the last SCT course.

Research

- Naga: Diverse data for DL model training (accounting for sagittally-acquired highly-anisotropic images?)
    - Strategies for data augmentation step
        - Generate low resolution data from high resolution data
        - Resample during training (data augmentation)? → ANS: Is usually **done during preprocessing**
            - Actually, let's try it, and see how it goes.
            - Charley has tried it → Get in touch, maybe?

    - Strategies for preprocessing step
        - Accommodating different dimensions/resolutions → resampling?
        - Ivadomed has configs for resampling
        - Should we skip resampling during inference, and not assume anything about the image?
            - Comparison project: Lung? (Unsure) [insert link here]
            - ANS: In this case (spinal cords), we have specific priors – the range of possible resolutions is relatively constrained.
            - Comparison project: AxonDeepSeg (big range of voxel sizes/resolutions) → makes convergence harder

- Next meeting → 5-min presentation by Nathan?

Action Items

- ☐ Relevant point from Julien: try torch.io data augmentation to downsample 3D images to simulate highly-anisotropic sagittal images in the context of DL-model training
- ☐ Naga: compare resampling during augmentation vs during preprocessing
- ☐ Team: Investigate email sent by Phillips Lab → Check assumptions about data, interrogate methods, etc.
- ☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
  - ○ Move to next meeting
- ☐ Nadia: Try using ANTs instead of MINC
  - ○ Move to next meeting
- ☐ Jan: Explore strategies how to bring histological atlas to PAM50 - WIP
  - ○ Follow up in next meeting

2023-02-09

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Rohan Banerjee, Nadia Blostein, Benjamin De Leener, Nathan Molinier
Not yet arrived: Nick Guenther, Nilser Laines Medina, Julian McGinnis, Adrian El Baz, Jan Valosek
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~Nadia: Open issue in SCT for divide by zero problem with coordinates~~
    - Nadia: I think this could have been an error pertaining to the preprocessing of a specific subject, will get to this now that template generation works on N = 3 (thanks Rohan & Benjamin!)
    - Next action item (to replace one above): finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas) → Added as action item for next meeting
- ☐ Jan: explore strategies how to bring histological atlas to PAM50 → On holidays

Miscellaneous items

- New students? Introduction?
    - Nathan Molinier 🎉

Software Development

- Updates on in-progress PRs
    - ~~`-normalize-PAM50` (#3977):~~ Complete!
    - `sct_compute_mscc` (#4003): Draft PR, still WIP
        - Needs a name change + Update title of PR
            - `sct_compute_compression_metrics` → specific but long
            - `sct_compute_compression` → shorter
                a. Would match up better with sct_detect_compression, too
                b. Conclusion: Use shorter name!
        - Need a better way to distribute/store the normalized metric CSV files
            - Link to current folder? Is it GitHub-hosted?
            - Action item: Open new repo on SCT organization, add via sct_download_data
            - Question: Should we store inside the SCT repo?
                a. The CSV files may/will be updated in the future
                b. So, it will have its own history/releases, separate from SCT
                c. Would also want to be used outside of SCT, so it isn't SCT-specific

                d. Conclusion: Keep in separate repo for now, for storage purposes (to get them off of duke)
    - `-soft-centerline` (#4012): Almost complete, needs tests.
        - Are we using Mathieu's suggested method to compute the soft centerline?
            - Previous: Float -> Discrete coordinate
            - Current PR: 2x2 grid around the centerline
                a. Puts heavy weight on the location of the float coordinate
                b. E.g. 10.9,10.9 → most weight on 11,11
            - Suggestion: Gaussian around the centerline?
    - `_get_centerline` (#4010): Refactoring done! Needs review from non-Joshua dev.
        - If it's just for SCT code quality: MGP can do it

- Ivadomed development is being put on hold (Slack thread)
    - Upcoming meeting this Monday to discuss impact on SCT/ADS
    - Q: What should we do to prepare for this meeting?
    - A: Identify questions that need further investigation:
        - **How do we support SCT's usage of ivadomed long-term?**
            - SCT only uses inference method – so potentially repackage only those methods in a separate package?
            - Ivadomed frozen in time → Good for now
            - In the future (6 months) … Julien suggestion: remove Ivadomed entirely (and support for all existing sct_deepseg models??)
                a. Due to ivadomed having its own dependencies → Difficult to maintain, holding SCT back
                b. Ivadomed cannot just be replaced with ONNX → dependent on PyTorch preprocessing, so we can't do any sort of ONNX-only inference.
            - Could we migrate the ivadomed inference code inside of SCT to maintain only the "sct_deepseg"-relevant parts of SCT?
                a. This way we keep `sct_deepseg` while also removing the dependency on PyTorch

        - **How would MONAI integrate with SCT in the future (if at all)?**
            - Should SCT be a wrapper around MONAI?
            - Or should the MONAI-specific commands be packaged separately in its own separate project? (That people use alongside SCT, rather than inside SCT.)
                a. Interface is Python-developer specific → possibly not as user-friendly as SCT's CLI scripts, so wrappers might be useful

    - Julien: example scenario with new feature needed (Basel MP2RAGE project)
        - There is current, in-progress work – should we finish up the existing ivadomed projects?
        - Model trained by Nilser → Also ivadomed (Different? Calling other models?)
            - Check in with Nilser next meeting? - Perhaps same as the others

- Joshua: Philips Lab PAM50 levels (#3952)
    - Due for v6.0, but needs an assignee
    - Q: What steps are needed to integrate? (Is it similar to histological atlas, i.e. aligning in the same space?)
        - Quite different from the histological atlas
        - Just a simple modification to the existing levels → Only 1-2hr work to make sure the files are in the right space, use the same levels, etc.
        - Update link in sct_download_data
        - Possibly suited to Sandrine?

- Joshua: Cleanup of old issues involving external collaborators
    - #3438: Source code of optic functions
        - Task: Create private internal repo for source code
        - Q: Were we ever given the source code?
            - Julien: Need to dig into emails, google drive, etc.
    - #2530: Pediatric template
        - External party offered to create a pediatric template
        - They stopped responding, issue has stalled for 3 years
            - Sad that they stopped responding, due to the quality of their data.
            - But, connected to an ongoing project with Rohan/Benjamin/Nadia, so perhaps we should reach out to collaborate in the future!
            - Add a note somewhere to not forget about this collaboration:
                a. PR in this repo: https://github.com/neuropoly/template
        - Should we close? Or try to reach out again? (Is it too late by now?)
            - Conclusion: Close the issue

- Joshua: Call to action for "good first issues"
    - I went through old issues and marked easy tasks (~5-30m of work)
    - Good practice for using git, opening PRs, code reviews, etc.
    - There are 57 to choose from!
    - If you need a palate cleanser, one of these would be good to work on. 🙂

- Benjamin: installation failure on macOS Ventura 13.2
    - Experienced this morning, need to open issue
    - Q: Has anyone else experienced failures on 13.2?
        - A: No (on the fence about updating) → Open issue

Research

- Template update (Nadia & Rohan):
    - Preprocessing:
        - Rohan: done for full dataset (N = 5 out of 5)
        - Nadia: done for subset (N = 3 out of 22)
        - Next: Since we were working on this separately, the changes in the functions have to be unified and pushed into single PR for cleaner merging.

  - For config file, we will follow the BIDS convention decided on in Jan’s PR #94
    - derivatives/labels and derivatives/manual_labels according to naming convention described on the neuropoly dataset-curation page
    - Question: “labels” pluralized or not (conclusion unclear?)
      - Will ask this in PR
- Template generation: Pipeline currently being run on our local computers, have to transferred to rosenberg/compute canada
  - Rohan:
    - Got preliminary results for T1 and T2 for dog spinal cord template. can be found at: duke/projects/template_dog_virginiatech/template_initial_results.
    - Bug fix to be done: The size of the template doesn’t cover all the discs - the dog images have 26 disc levels and the template has 21. This is possibly due to a parameter/calculation in the template generation pipeline
    - Nadia: this is something that can be fixed in preprocessing I think
  - Nadia: Is there a reason why we can’t just use ANTS with NIFTI files? MNC packaging confusing, tough to troubleshoot; https://github.com/CoBrALab/optimized_antsMultivariateTemplateConstruction
    - Would be lovely to avoid depending on the MINC ecosystem
    - Currently used for data augmentation
    - We could implement flipping/symmetrize ourselves → just creating additional data files (julien: not the most elegant solution)
    - Nadia: Try using ANTs instead of MINC to minimize the dependencies

  - Method to use for averaging
    - MS Lesion project tried to handle this → Link?
    - Benjamin: Discontinuities?
    - Contrast-agnostic → map on 1 covering the field of view

- Nadia: Question about “ground truth” reference points
  - Very good paper with good abstract → Link
  - Do people normalize based on the length between the PMJ and the other point <name I did not catch>
  - Sandrine: We just talked about this an hour ago!
    - May not have the entire spinal cord length
    - Various spinal cord regions may have varying lengths – not exactly coherent between subjects, lots of individual variability that is not yet understood

Action Items

- ☐ Nadia/Sandrine: Finish preprocessing pediatric dataset (11 / 22 subjects failed with initial sc segmentation attempts, will fiddle with this / see if Sandrine has ideas)
- ☐ Jan: Explore strategies how to bring histological atlas to PAM50

☑ ~~Sandrine: Open new repo on SCT organization to store generated CSV files, then access them via sct_download_data~~
☑ ~~Sandrine: Update name of MSCC PR~~
☐ Sandrine: update PAM50 spinal levels
☐ Julien: Look into emails, Google Drive for sdika ‘optic’ (isct_spine_detect, etc.) source code
☐ Joshua: Close issue, then make note about Vanderbilt lab collaboration on pediatric template issue/PR
☑ ~~Benjamin De Leener: Open issue about macOS 13.2 failure → #4035~~
☐ Nadia: Try using ANTs instead of MINC
☑ ~~Sandrine: send paper to nadia~~

2023-01-26

Attendees: Nick Guenther, Joshua Newton, Sandrine Bédard, Jan Valosek, Rohan Banerjee, Nadia Blostein, Benjamin De Leener,
Not yet arrived:, Nilser Laines Medina, Julian McGinnis, Adrian El Baz, Julien Cohen-Adad, Mathieu Guay-Paquet,
Moderator: Rohan Banerjee
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~Sandrine Bédard & Jan Valošek: add all versions of manual correction that exists + package for correction: spinalcordtoolbox~~
- ☐ Nadia: Open issue in SCT for divide by zero problem with coordinates
  - Not done yet
  - Potentially data-dependent (specific to pediatric dataset)
  - Centerline issue/PR took up time this week

Miscellaneous items

- JCA/MGP/Nilser not present this week

Software Development

- JN: I don't have much to discuss this week
- Since last meeting, I have been primarily:
  - Cleaning up old issues (removing duplicates, investigating/reproducing bugs, adding present-day context to old issues, resolving small changes, etc.)
  - Reviewing PRs opened by Sandrine/Nadia/etc.

Research

- Jan Valošek:
  - PAM50/histology
    - Which steps to apply to bring the histology atlas to PAM50?
    - Landmarks (spinal levels, discs, etc. depends on what's available in histology)
    - Sct_register_multimodal
    - Warning: Spinal levels will be updated in parallel project – perhaps postpone until the Philips Lab update is complete?
    - Histology is higher resolution, but PAM50 is 0.5mm – we want to preserve the resolution of the histology files, so we may just need to update the qform/sform
  - Manual correction scripts - first draft available for testing
  - Centralize derivatives conventions for BIDS datasets - PR

    - sct_get_centerline -method fitseg - allow to output soft centerline - issue
        - ☐ Should be relatively simple – Update from nearest neighbor interpolation to linear interpolation

- BDL: Announcement: Paper has been accepted! (Which? I missed the name)
    - “Combining PropSeg and a convolutional neural network for automatic spinal cord segmentation in pediatric populations and patients with spinal cord injury”
    - By Colline Blanc

- JCA: Announcement: Basel/MP2RAGE data for lesion segmentation
    - 300 masks generate for segmentation of the spinal cord
    - Will be uploaded to git annex for use in future DL projects
    - Louis Bouchard – Ping on Slack?
        - ☐ Jan: Use for centerline generation → Deep learning centerline detection project
        - ☐ Contrast agnostic segmentation meeting

Action Items

- ☐ Nadia: Open issue in SCT for divide by zero problem with coordinates
- ☐ Jan: explore strategies how to bring histological atlas to PAM50
- ☐

2023-01-12

Attendees: Julien Cohen-Adad, Joshua Newton, Mathieu Guay-Paquet, Sandrine Bédard, Jan Valosek, Rohan Banerjee, Nadia Blostein, Benjamin De Leener,
Not yet arrived:, Nilser Laines Medina, Julian McGinnis, Adrian El Baz, Nick Guenther,
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JN: Investigate centerline method discrepancies between sct_deepseg_sc's default and sct_get_centerline's default methods~~
    - See: Issue #3993
    - Tl;dr:
        - `sct_deepseg_sc` **resamples** the input image (anatomical) to 0.5mm isotropic before passing it to `get_centerline()`
        - `sct_get_centerline` **does not resample** the input, however!
        - This difference results in different centerline output from 'optic', and thus different segmentations.
        - Should we try to unify these methods (to produce consistent centerline output)?
            - Probably safer to resample – no harm done for images with sufficient resolution, but there are benefits for low-resolution images.
            - So, potentially adding resampling to sct_get_centerline / get_centerline?
        - Julien: Perhaps not the highest priority – We have other priorities…
        - JN: Copy discussion to the issue.
- ☐ Nilser: Share the branch with the current work-in-progress code (re: sct_analyze_lesion issue #2667)
    - Not present.

Miscellaneous items

Jan Valošek :

- I'm configurating a new laptop (MacOS) → where to install SCT?
    - `/usr/local/share` vs `/opt` vs home `(~/)`
    - If i'm both user and "developer", should I install two versions? One for development, second one for using?
        - MGP: Single install, home directory, install using instructions on the dev wiki
        - JN: Single install, clone to ~/repos, install from master using `install_sct -iy`
        - Julien: single install, clone to ~/code, install with ./install_sct. When need to reproduce issues, i either checkout vx.y or i reinstall completely
        - Rohan: Home directory
        - Benjamin: "code/" directory with multiple versions
        - Nadia: Different conda environments for different versions

- Student needs are different than dev needs
    - For projects that result in papers, use a single version if possible (rather than using the bleeding-edge version of SCT)
    - JCA: Emphasize reproducibility using `sct_run_batch` scripts if possible, should be reproducible → using a specific version of SCT!

Software Development

- Not much to report
    - Next version (6.0) scheduled for March 31
    - Should include Calgary lab article related stuff (PAM50 levels update)
        - Update PAM50 spinal levels prior to March 31st
        - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3952
    - Should use conda for Windows installation
        - JN: Unifying installation methods between linux/windows has been a maintenance desire of mine

- Nadia: quick question about coordinate interpolation (SCT v 5.8) in spinalcordtoolbox.types → issue with division by zero (lines 661, 662, 573) → fixed it for template and will make create Github issue, wondering if this can cause downstream issues
    - E.g. 661: `weight_closest = abs(relative_position - relative_position_closest) / abs(relative_position_next - relative_position_closest)`

Research

- Manual correction script & package for correction:
    - #3353
    - SCT dependencies
        - Need for disc labeling, not for segmentation corr
        - Summarize all of the features desired (
        - Exclude list: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3971
        - JN: Double-check the mapping between sct_deepseg_lesion and file type: (FILE_SEG, FILE_ETC.)
    - Might be better off as a standalone repository to start, (i.e. not in SCT)
        - We already have several copies of the script
        - So, copy the most recent script to its own repository, then begin development in that repository
        - Name of repository? → neuropoly/manual_correction or **spinalcordtoolbox/manual_correction**
        - Public repository: https://github.com/spinalcordtoolbox/manual-correction
    - Aside: Choosing default licenses – Perhaps we should consider recommendations Neuropoly-wide? (SCT uses LGPL, some projects use MIT, etc.)

Action Items

- ☐ Sandrine Bédard & Jan Valošek: add all versions of manual correction that exists + package for correction: spinalcordtoolbox
- ☐ Nadia: Open issue in SCT for divide by zero problem with coordinates

2022-12-15

Attendees: Joshua Newton, Rohan Banerjee, Sandrine Bédard, Jan Valosek, Nick Guenther, Julien Cohen-Adad, Benjamin De Leener,
Not yet arrived: Julian McGinnis, Adrian El Baz, Nadia Blostein, Mathieu Guay-Paquet, Nilser Laines Medina,
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☐ JN: Investigate centerline method discrepancies between sct_deepseg_sc's default and sct_get_centerline's default methods
    - Not completed – My focus this week has been on the forum `discourse-solved` issues
- ☐ Nilser: Share the branch with the current work-in-progress code (re: sct_analyze_lesion issue #2667)

Miscellaneous items

- Reminder: there's **no meeting** in 2 weeks (December 29)

Software Development

- Jan: sct_run_batch - exclude.yml format - discussion here and here
    - Context: Cannot currently use an "exclude.yml" file alongside existing `-exclude` and `-exclude-list` options for sct_run_batch
    - Current proposal: Add new "`!include`" syntax to yaml parser: Comment here
    - Alternative: Switch `-exclude-list` to only accept config files (nudging users to put their exclusions into a file)
        - Should we rename the argument while we're at it?
            - -exclude-file? → Might be ambiguous "Are we excluding an [image] file?"
        - Or, is -exclude-list already a suitable name for this new behavior?
    - Make it compatible also with ivadomed?
        - Subject? Filename?
        - → Responsibility of ivadomed
    - QC Report compatibility
        - QC report currently list the filenames
        - For -exclude-list, artifact/error yml must output list of subjects instead (and the comment would indicate the file)
        - Do we want to be able to create both kinds of .yml files? (1. subject, 2. files)
            - No? - Stick with current QC report exporting (file-based)
            - Therefore, use this file-based exclusion via -script-args (i.e. make it the responsibility of the script itself)
            - Don't try to output subject-based exclusion file from QC report

- Joshua: Scheduling SCT Forum downtime
    - Context: `discourse-solved` plugin installation (Issue #403)
        - Previously, trying to install the plugin had been causing the forum to crash
        - To fix the issue, the forum software has been reinstalled from scratch on a separate "devforum" test server
    - Next steps:
        - Add an announcement post about the downtime, then set it as a banner topic
        - Put the “forum” production server into read-only mode
        - Decommission the “forum” production server
        - Promote the “devform” test server to be the new “forum” production server
    - When should we schedule the downtime?
        - We could schedule the downtime for 2 weeks from now (to give some heads-up to our users, and also to minimize disruption, as presumably our users will be busy with holidays on Dec 29th)
        - Or, we could do the migration immediately (seeing as the changes shouldn’t take too long, and the forum has seen little activity in the past few weeks anyway – maybe we don’t need to schedule?)
            - Can do this e.g. tomorrow night!

Research

- Heads Up: Conference OHBM → 13th january (Montréal)
    - Abstract 1: Contrast-agnostic project: model insensitive of the contrast for spinal cord seg
    - Abstract 2: Canproco - cross-sectional area computed from T2w images in multiple sclerosis (MS) patients and comparison to spine-generic normative data
    - Abstract 3: DCM (degenerative cervical myelopathy) normalization (normalized MSCC)
        - MSCC: maximum spinal cord compression (AP diameter of compression, level above and below)
    -

Action Items

☐ JN: Investigate centerline method discrepancies between sct_deepseg_sc’s default and sct_get_centerline’s default methods

☐ Nilser: Share the branch with the current work-in-progress code

2022-12-01 (v5.8 release)

Attendees: Sandrine Bédard, Nick Guenther, Mathieu Guay-Paquet, Joshua Newton, Rohan Banerjee, Nilser Laines Medina, Jan Valosek,
Not yet arrived: Julien Cohen-Adad, Julian McGinnis, Benjamin de Leener, Adrian El Baz, Nadia Blostein
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~RB: BIDSification of data~~
    - sub_ → sub-
    - anat should not contain folders– look at BIDS specs
    - use nii.gz instead of nii
    - scripts/ -> code/ (see here)
    - Changes done: duke/projects/template_dog_virginiatech/bids_data/
- ☐ JN: Investigate centerline method discrepancies between sct_deepseg_sc's default and sct_get_centerline's default methods
    - Not complete due to time spent on v5.8. Will prioritise for the next meeting.
- ☑ ~~JN: Add a warning message when images are too large to fit in RAM for algo=dl~~
- ☑ ~~JN and MGP: prepare the release, then advertise it right after the next meeting~~
- ☑ ~~Nilser: Take a quick look at #2677 and present some ideas, and perhaps play around with sct_analyze_lesion/sct_process_segmentation for analyzing lesions (get used to script, understand how it works, etc.)~~
    - JN: Share branch (once more work has been done) prior to next meeting?

Miscellaneous items

- Don't forget to mark your holiday hours in the NeuroPoly calendar!
    - Mathieu: Dec 26 - Jan 4th
    - Joshua: Dec 26 - Jan 3rd
- Next meetings
    - December 15th → OK
    - December 29th → Multiple people on holidays… Cancel this meeting? → Yes

Software Development

- SCT v5.8 is released! 🎉
  - Please retweet! https://twitter.com/SpinalToolbox/status/1598381122928447498

- Let’s pick a date for the next release and create a milestone for it
  - JN: Might be good to pick a Friday/Monday (for advertising/timing purposes, so that the release can be finished up at the end of the week, then announced at the start of the week)
  - Last milestone spanned ~4 months (Aug/Sept/Oct/Nov)
  - 4 months from now (Dec/Jan/Feb/Mar) would give us a late March/early April release
  - Friday, March 31st? (Then, announce on Monday, April 3rd?)

- Based on the discussion in issue #3952, would the next release be v6.0?
  - JN: I think v6.0 is sort of overdue? (many large changes in past v5.X versions) So, I’m in favor of a v6.0 release.

- Do we have any particular priorities for the next release?
  - Calgary Philips lab article → timeline?
    - Should be able to advertise it will be available in SCT v6.0
    - Publication vs. release, which comes first?
      - Ideally, SCT v6.0 should be available when the publication is released
      - It’s ok to include it in SCT early, it’s worse if it happens after paper publication
  - Research: Ongoing student projects?
    - Compression detection (#3946) → will be part of the metrics normalization project (https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3733)
    - New intern coming in Intervertebral disc labeling project →
    - Spinal cord segmentation (softseg??) (might not be ready for v6.0 though)
    - In general, depends more on upcoming papers, not sure if it will be necessary
  - Dev/maintenance: If we’re announcing v6.0, it might be nice to prioritize other large/breaking changes that we might have been putting off? (To further justify a “new major version”...)
    - E.g. using Miniconda for Windows (#3942),
    - Distributing `install_sct` as a release asset (#3545)
    - sct_analyze_lesion/sct_process_segmentation refactor?

- MGP: Is Sentry still relevant to SCT?
  - JN: Unused now, but easily fixed up.
  - We could trial it like we did code coverage, then make a decision based off of the experience of having it active for some months?

- JN: Reinstalling “discourse-solved” on the SCT forum
  - Last time, trying to install this plugin broke the Discourse forum.

  - To avoid downtime, it would be helpful to debug on a separate DigitalOcean droplet to leave our current forum instance untouched
  - For cost: If, for example, it takes 5 days, it would cost us approx. (5/30) * $6 = $1 (then the dev server would be shut down)
  - Is it alright if I use a separate droplet for debugging purposes?

Research

- Sandrine & Jan: Normalization of metrics for spinal cord compression ([#3733](#3733))
  - Where to implement? → sct_process_segmentation
  - 2022-12-01-normalization_compression_sct
    - sct_compute_mscc
    - Sct_process_segmentation
  - How to handle “incomplete levels” (superior/inferior)
    - Per-slice scaling factors are output
    - JCA: <very mathy approach that I didn’t catch>

- Rohan: Dog spinal cord segmentation update: link
  - Updated segmentation results for VISTA images
    - Centerline-based approach worked well for removing segmentation leakage
    - Segmentation is largely done 🎉
  - Labeling for VISTA images
    - Automatic segmentation (sct_label_vertebrae) did not work well
    - Manual disc labeling worked well for some subjects, though
    - One subject (3) is done, others are not done
      - QC is needed for subject 3
      - Some discs are not clearly visible for VISTA images
    - Why not use other contrasts (T1) for labeling?
      - T1 images also do not have visible discs…
      - Or, do they? Subject-dependent…?
    - FSLeyes → Multiple images with different spaces/resolutions/fields of view
      - For viewing/disc identification, each image should be opened on its own (without other images)

Action Items

- ☐ JN: Investigate centerline method discrepancies between sct_deepseg_sc’s default and sct_get_centerline’s default methods
- ☐ Nilser: Share the branch with the current work-in-progress code
- ☑ ~~JN: Copy over topics that weren’t covered today into next meeting’s minutes~~
  - I honestly think we covered everything?

2022-11-17

Attendees: Julien Cohen-Adad, Sandrine Bédard, Nick Guenther, Mathieu Guay-Paquet, Joshua Newton, Rohan Banerjee Jan Valosek, Rohan Banerjee, Nilser Laines Medina,
Not yet arrived: Julian McGinnis, Benjamin de Leener, Adrian El Baz,Nadia Blostein,
Moderator: Julian Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~MGP: Meeting logistics: try bringing the giant meeting TV~~
- ☑ ~~MGP → Update PMJ-specific usage locations (sct_process_segmentation, PMJ Tutorial, Citing SCT)~~
- ☑ ~~JN: Open issue to systemize location of references in argparse help usage~~
    - Issue #3949
- ☑ ~~JN: Open issue for new feature where QC reports (or another report, based on the batch analysis script), includes a text that says what processing was done, with appropriate references. See eg FSL report. It would look like this: "Analyses were done using SCT vX.Y.Z [REF]. T1w images were registered to the PAM50 template [REF], using sct_register_multimodal (command: XXX), etc."~~
    - ~~Jan: FSL provides a brief summary text how to cite individual functions, e.g., https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/topup#Referencing~~
    - ~~Issue #3950~~
- ☑ ~~RB: Try out new segmentation methods (propseg, deepseg)~~
    - Propseg has many parameters to play with! Try to explore if it doesn't work at first
    - Update: link
        - Action Item: Checking the BIDS-ified dog dataset (names, scripts, etc.)
        - sct_propseg did not yield any segmentations on dog dataset (Reason unknown)
        - "sct_deepseg_sc -file-centerline" + "sct_get_centerline" = better results?
            - sct_get_centerline has more options than sct_deepseg_sc's built-in centerline methods (optic vs. svm/cnn/etc.)
            - Should sct_deepseg_sc's default centerline method be updated to match sct_get_centerline's? → Action item
            - JV: `svm` vs `optic`
        - Segmentations on T1
            - Are the segmentations even needed for template generation pipeline?
                - Vertebral labeling can be done manually, rather than via SCT
                - What about straightening? → Slide 9
                - Register centerline of vista images T2 to T1, then use deepseg
                    - TODO: Tweak sct_register_multimodal parameters
                - NB: Segmentation is only needed for a high quality centerline
            - Observation: T1 images are quite poor in quality (seg is difficult)

- ☐ Nilser (Is this already done?): Take a quick look at #2677 and present some ideas, and perhaps play around with sct_analyze_lesion/sct_process_segmentation for analyzing lesions (get used to script, understand how it works, etc.)
    - Follow-up with a text comment on the issue itself
    - For next meeting → Ask participants to read comment
    - With ISMRM, no time for this meeting, add to next meeting

Miscellaneous items

- Advent of code signup: Slack link
    - Fun coding activity during December
    - MGP has created a team for the lab

Software Development

- Progress update on “stitching” PR (#3865)
    - Merged! 🎉
    - JN also fixed a post-merge issue (#3939)

- Would someone with knowledge about the algorithms behind ‘sct_propseg’ and ‘sct_deepseg’ like to volunteer to review the documentation PR #3941?
    - JCA: Can review?
    - JN: For context, this PR is specifically in response to issue #3627, so I might not have additional context from recent projects. (?)
    - Make sure to use language like “generally”, rather than absolute recommendations “should”

- MGP: Does JCA have some more context about this dice score test for ANTs?
    - This issue may no longer need input? We’ve decided to scrap this test.

- MGP: SCT v5.8: Are we still aiming for an early December release? (The current milestone is arbitrarily set to December 2)
    - The last big item we’re working on is #3232 (PR #3944) which deals with datatype/scaling issues when loading and saving NIfTI files, and is going to need careful thought.
        - Due to the complexity of the problem, I think discussing the solution might be better saved for offline (i.e. in the PR itself)
        - If anyone has an interest in how SCT handles the Nifti1Image format (via nibabel), your input on PR #3944 would be greatly appreciated!
        - Otherwise, JN, MGP and JV can perhaps work on this together over the next 2 weeks prior to the upcoming release?

- Are there any other issues that should be included in the upcoming 5.8 release?
  - Note: All recent (last ~6 mo) “User requested” issues and “High priority issues” have either been dealt with, or have open PRs to fix them.
  - However, there are some recent “bug” issues that have not been resolved
    - E.g. Issue #3867 (algo=dl abruptly stops with no error message when used on images that are too large)
      a. Should this issue be prioritized in the next 2 weeks?
      b. Should be relatively simple to fix, so Ans: Yes!
      c. Tangent: General discussion about algo=dl
        - Impressions: Too many degrees of freedom
        - Registration will be “perfect”, but not anatomically correct
        - Users should be careful when using this method
        - Paper coming out in OpenNeuro
  - Otherwise, I think we should be okay to finish up what’s currently open, then create a release. 🎉

Research

-

Action Items

☐ RB: BIDSification of data
  - sub_ → sub-
  - anat should not contain folders– look at BIDS specs
  - use nii.gz instead of nii
  - scripts/ -> code/ (see here)

☐ JN: Investigate centerline method discrepancies between sct_deepseg_sc’s default and sct_get_centerline’s default methods

☐ JN: Add a warning message when images are too large to fit in RAM for algo=dl

☐ Nilser: Take a quick look at #2677 and present some ideas, and perhaps play around with sct_analyze_lesion/sct_process_segmentation for analyzing lesions (get used to script, understand how it works, etc.)

☐ JN and MGP: prepare the release, then advertise it right after the next meeting

2022-11-03

Attendees: Mathieu Guay-Paquet, Joshua Newton, Nadia Blostein, Jan Valosek, Rohan Banerjee, Nilser Laines Medina
Not yet arrived: Julien Cohen-Adad, Julian McGinnis, Sandrine Bédard, Nick Guenther, Benjamin de Leener, Adrian El Baz
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~Rohan: Connect with Julian McGinnis → Dog segmentation project~~
    - Reached out to Joshua → Provided data
    - Working on segmentations → Will present next week
    - Slideshow is done!
- ☑ ~~Nadia: Connect with Benjamin regarding past template generation techniques~~
- ☑ ~~JCA/other members: Sort out getting keys on time for meeting to avoid issues~~
    - Someone else took the keys!!!
    - Other set was on the 6th floor!!! D:
    - In the past, unlock the door…? Get the key before, keep the key…?
    - How was getting keys this week?
        - This time: Went to Secrétariat (in the M corridor) and asked for the key, the secretary came and unlocked the room (without giving keys), but we only have the key starting at 3pm
        - Person unlocked for us

Miscellaneous items

    - Julien: Refs for PMJ-based CSA measurement (urgent)in sct_process_segmentatino usage
    - SCT example script
- website tutorials
    - Slack link: https://neuropoly.slack.com/archives/C03GA63LMA8/p1667401627372759
    - We received an email re: ECTRIMS poster
    - Action item: Open an issue for PMJ method specifically (SCT)
        - "If you use this, please cite …"
        - Add references to… where?
            - sct_process_segmentation usage (will require new version)
            - batch_processing example comment → too noisy
            - PMJ Tutorial pages → citation needs to be updated for Frontiers paper
                - Frontiers paper supersedes our existing preprint citations
            - "Citing SCT" page → add if not there
        - Which SCT versions are the PMJ methods included in? 5.7/5.6?

        - Backporting is low-priority

- General question: Where should we put references for scripts?
    - Should we consider adding another section at the very end of the help description?
    - Or, is it sufficient to put it at the end of the “Description” part (it would appear in the middle of the console output) ←yes this one
    - Can make an issue for systemizing location → TBD

- Pie in the sky idea →Automated collection of used citations
    - Spit out a copy-pastable summary of used citations
    - Issue → TBD

- Nadia: Small question about semantics (for naming conventions in .json files and all that): “disc” or “disk”? Okay to refer to t1w images as t1 for packages that don’t have a “t1w” contrast options?
    - Disc, I believe! (Julien had previously mentioned this in the context of SCT here: https://github.com/spinalcordtoolbox/spinalcordtoolbox/wiki/Programming%3A-Naming-conventions-(variables,-files))
    - Contrast name convention
        - T1 == T1w (equivalent)
        - T2 == T2w (equivalent)
        - T2s = T2s
        - What to use for BIDS dataset directory names?
            - From SCT’s perspective, it should work with either
            - SCT’s example datasets use both terms inconsistently
            - But, it would be good to harmonize on a specific convention
        - Add a section to the Naming Conventions page to clarify this?
        - Jan: Convection used by BIDS - https://bids-specification.readthedocs.io/en/stable/04-modality-specific-files/01-magnetic-resonance-imaging-data.html#anatomy-imaging-data
            - For example, BIDS uses a bit long suffix “T2starw” for T2*-w

Software Development

- Progress update on “stitching” PR (#3865)
    - It is basically done! All requested changes from recent PR reviews (Joshua, Mathieu) have been addressed.
    - There is one open question that needs to be answered by Julian McGinnis, but it is small and should not impede progress.

- Joshua: I have been away for a week, so I do not have much to bring up at this meeting
    - My recent work has been focused on debugging and dependency maintenance to address PyQt5 (#3928) and matplotlib (#3929) errors
    - I will have more to share (regarding progress on the header/dtype mismatch bug) at the next meeting → I’ll write a small summary and then share in advance of meeting

Research

- Rohan -> Present slideshow (link)
    - T1 segmentations have some issues (missing segmentations, leakages)
        - Next steps: Try alternative segmentation methods (sct_propseg, sct_deepseg -task)
    - VISTA segmentations are better, but show segmentation values outside of the slices with SC
        - Next steps: Manual correction for leakage

Action Items

- ☐ JN/MGP? → Update PMJ-specific usage locations (sct_process_segmentation, PMJ Tutorial, Citing SCT)
- ☐ JN: Open issue to systemize location of references in argparse help usage
- ☐ JN: Open issue for new feature where QC reports (or another report, based on the batch analysis script), includes a text that says what processing was done, with appropriate references. See eg FSL report. It would look like this: “Analyses were done using SCT vX.Y.Z [REF]. T1w images were registered to the PAM50 template [REF], using sct_register_multimodal (command: XXX), etc.”
    - Jan: FSL provides a brief summary text how to cite individual functions, e.g., https://fsl.fmrib.ox.ac.uk/fsl/fslwiki/topup#Referencing
- ☐ RB: Try out new segmentation methods (propseg, deepseg)
    - Propseg has many parameters to play with! Try to explore if it doesn’t work at first
- ☐ (Is this already done?) Nilser: Take a quick look at #2677 and present some ideas, and perhaps play around with sct_analyze_lesion/sct_process_segmentation for analyzing lesions (get used to script, understand how it works, etc.)
    - Follow-up with a text comment on the issue itself
    - For next meeting → Ask participants to read comment
    - → Leave as action item for next meeting?

2022-10-20

Attendees: Joshua Newton, Julien Cohen-Adad, Julian McGinnis, Sandrine Bédard, Nick Guenther, Rohan Banerjee, Nadia Blostein, Benjamin de Leener
Not yet arrived: Mathieu Guay-Paquet, Adrian El Baz, Jan Valosek,
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☐ Benjamin: When dog data are received, try generating a template
    - Has been an action item for several weeks (Is this still assigned to BDL, or is it now RB's responsibility?)
    - See also issue 2
- ☑ ~~Nilser: Present a plan moving forward for the segmentation project (data, etc.)~~
    - Informal summary to inform other lab members
    - 7T lesion segmentation
    - Preliminary multichannel model trained using 22 subjects
        - Preliminary results: Not so good in 2D, but better in 3D
    - Next steps:
        - 1. Manual correction
        - 2. Transferring existing masks to other modalities →
            - How to handle coregistration? Ans: 7T template needed.
            - What about the PAM50 template? (Missing DTI GM/WM masks…?)
        - 3. Synthetic images
        - 4. BIDS organization
        - 5. Training multi-contrast modal → IVADOMED, rather than SCT
- ☐ Nilser: Take a quick look at #2677 and present some ideas, and perhaps play around with sct_analyze_lesion/sct_process_segmentation for analyzing lesions (get used to script, understand how it works, etc.)
    - Follow-up with a text comment on the issue itself
    - For next meeting → Ask participants to read comment
- ☐ Rohan: Connect with Julian McGinnis → Dog segmentation project
    - Reached out to Joshua → Provided data
    - Working on segmentations → Will present next week
- ☑ ~~Joshua: Move the now-unnecessary isct_ scripts into spinalcordtoolbox-dev~~
    - Merged already
- ☑ ~~Joshua: Merge isct_test_ants functionality into sct_check_dependencies~~
    - Open PR → #3915
- ☑ ~~Julien CA: Next meeting → Book a room, as the majority of participants are local~~
    - How to handle video for remote participants, TBD
    - Sorted

Miscellaneous items

- Heads-up:
    - Mathieu is away this week at a Mathematics conference
    - Joshua will be away next week (October 22nd-29th)

Software Development

- Progress update on “stitching” PR
    - QC Report tested on Julian McGinnis’ bavaria_quebec dataset (9 subj)
        - Joshua: Demo
    - PR is almost ready to merge
        - Only a few small tweaks needed
        - Hoping for one last review from MGP when he returns
        - PR should be merged by next meeting

- Joshua: I don’t have much else to discuss due to MGP’s absence
    - Several PRs opened over the past week with no reviews (due to MGP’s absence)
    - To avoid creating a larger backlog of PRs, I’ve begun prioritized issues that involve investigations/debugging, rather than design decisions
        - Python 3.8 upgrade (Issue #3367, PR #3916)
        - Nibabel slope/intercept datatype issues (Issue #3843 and #3232)

Research

- Nadia on pediatric template
    - Trial run of `sct_register_multimodal` w/ recomposed T2w images (2 age and sex matched subjects), no parameter modification, seems to yield bad results.
        - Next: register both to PAM 50 (but deformation field errors tend to add up so best not to need to concat fields)
        - Q: PAM50 template registration pipeline? → Connect with JCA/BDL/Nadia about previous template generation efforts
    - Head removal: BEaST? (I’ve used it in minc-bpipe image preprocessing pipeline for skull stripping)
        - Other head removal techniques? →

- Nadia: Morphometry (just curious)
    - Since sct_propseg outputs a final surface mesh, is it possible to use the vertices of that mesh for a shape analysis? Or such metrics are not very robust?
    - Is there a way to adapt sct_deep seg to output a surface mesh too? Or the model was trained to only output labels (w/o deformation fields)?
        - sct_deepseg doesn’t estimate deformation fields / mesh
        - Mesh not needed, thankfully!
        - Template registration is based on:
            - SC segmentation

        - Vertebral labeling
    - In the future, softseg will be used over binary segmentations

Action Items

- ☑ ~~Nilser: present your project at next ivadomed meeting~~
- ☑ ~~Nadia: Connect with Benjamin regarding past template generation techniques~~
- ☑ ~~JCA/other members: Sort out getting keys on time for meeting to avoid issues~~
    - Someone else took the keys!!!
    - Other set was on the 6th floor!!! D:
    - In the past, unlock the door…? Get the key before, keep the key…?

2022-10-06

Attendees: Joshua Newton, Julien Cohen-Adad, Sandrine Bédard, Mathieu Guay-Paquet, Nick Guenther, Nadia Blostein, Nilser Laines Medina, Rohan Banerjee
Not yet arrived:, Julian McGinnis, Adrian El Baz, Benjamin de Leener, Jan Valosek,
Moderator: Nick Guenther
Minutes: Julien Cohen-Adad

Check last week's action items

- ☑ ~~JN + NG + MGP: Write up some background about sct_download_data in next meeting agenda~~
- ☐ BDL: When dog data are received, try generating a template
    - Not present at today's meeting

Miscellaneous items

- Welcome new lab members!!
    - Nadia Blostein
        - Research associate
        - SCT + VENUS (Vendor-Neutral Sequences)
            - Venus -> Control MR scanners regardless of manufacturers
            - Agah Karakuzu is working on this as well
            - Showcase -> Automated acquisition + analysis of spinal cord
            - Plugging SCT into this framework 🎉
        - Tutorial = <3, QC = <3
    - Nilser Laines Medina
        - Peru -> now in Marseille (France) working with Virginie Callot
        - PhD (April 2023)
        - Past contributor to SCT, multiclass model for 7T (PR #3527)
    - Rohan Banerjee
        - Master's student
        - Focusing on spinal cord segmentation & CSF seg, with possible application for motion correction

- JN: Heads-up about personal absence from October 24-28.
    - Next SCT meeting is October 20th, so I will be attending :)

- MGP: Heads-up about absence during next SCT meeting (October 20th)

Software Development

- From sct#3895: Is the script **isct_convert_binary_to_trilinear** used by anyone? It seems to have been totally broken for some time, maybe it should be moved to spinalcordtoolbox-dev?

  - I -> implies that it’s only used internally, not something that users are expected to user
    - Even though it’s available for users via ‘bin/’, they’re not *intended* to be used
  - Isct_convert_binary_to_trilinear
    - → Can be removed
  - What about other **isct_*** files in “scripts/” folder?
    - isct_test_ants → Does this need to be a standalone script? Could be integrated directly into sct_check_dependencies (which is the only place it’s invoked).
      - Definitely can be integrated into the API, rather than a standalone script
    - isct_minc2volume-viewer → ?
      - Context: MINC = McGill specific image format
      - Used in past projects to create a template that relies on minctools
      - Needed for Nifti->Minc conversion at the time
      - Can be removed now, though

- `sct_image -stitch` progress (PR #3865)
  - JN: Some small PR review fixes to QC report contribution.
  - JN: No progress to report as far as `stitching` evaluation. JCM messaged me saying that he hasn’t made much progress over the past 2 weeks, but will try to attend the next meeting to report findings.

- Follow-up on past triage (trickier issues)
  - Proposed changes to **sct_download_data** (#2959)
    - JN + NG + MGP had a good subcommittee meeting, some notes:
      - **TL;DR**: there’s no pressing need to change anything right now.
      - We should split #2959 into a few less-tangled issues.
      - We should open a (low-priority) issue to give **sct_download_data** an API layer (why? → because data downloading can only be run via run_proc calls to sct_download_data ATM).
      - We should eventually treat binaries and machine-learning models as dependencies rather than datasets.
    - More notes:
      - We don’t do install-on-demand, and we don’t want to.
      - The current script currently covers many use cases (maybe too many?):
        a. 1. **PAM50 and other templates**, which are data files, some of which are optional, the best use of **sct_download_data**.
        b. 2. **Course bundles**, also a good use of **sct_download_data**.
        c. 3. Various **machine-learning models**, which are more like dependencies than datasets, all of which are downloaded during installation. Could be replaced by *curl*.
        d. 4. **Binaries**, which are vendored dependencies, also downloaded during installation. Could be replaced by *curl*.
        e. 5. **Example/testing data**, for which integrity-checking is an actual concern, since our automated test suite might modify data in-place.

          - For more context, see also: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/2911
          - (Making sure that tests don’t modify the existing sct_testing_data dataset.)
          - Can be an issue for local runs of the test, because the tests don’t redownload the sct_testing_data each time anymore.
          - Proposed solution: Hide the testing data from the user, since they shouldn’t be accessing this; they should only be accessing sct_example_data.
      - For **example/testing data**, NG gave a nice demo of using *pip install* combined with a small *pip-integrity* script that leverages the existing metadata available to *pip* for integrity checking.
Unfortunately we want at least some of these files to be in a “user-friendly” directory, rather than the “site-packages” hierarchy used by *pip*.
      - For **binaries**, NG has a good prototype with ivadomed-anima-bin of how to distribute binaries as pip packages (originally for ms-challenge-2021#63).

  - Volume calculation CLI (#3378, #2707)
    - Already discussed last time
    - See also → https://docs.google.com/document/d/1ItApJQfajO2IRzOU2yenWbeRg6alfsdut3J4AVVdo78/edit#heading=h.ykwpdydqgjfk

  - Lesion statistics per slice (#2677)
    - Part of above morphometrics discussion
      - The issue is: sct_analyze_lesion does morphometric calculations on individual segmented blobs, but not slicewise calculations
      - sct_process_segmentation does slicewise calculations on spinal cord segmentations, but not necessarily individual segmented blobs
      - Can we somehow unify the underlying API, and align the features of both scripts?

- Future triage: there are currently 22 open issues with the needs discussion tag

Research

- Nadia: Question regarding dog spinal cord segmentation (value in this?)
  - Collaborator desires the creation of a dog template
  - We started with sets of separate (non-full-body) dog images, then stitched together

    - Addressed already during earlier part of the meeting

- Sandrine Bédard : Spinal nerve rootlets labeling/ PMJ project
    - PMJ-based CSA:
        - https://spinalcordtoolbox.com/user_section/tutorials/registration-to-template/shape-metric-computation/csa-pmj.html
        - Paper regarding this method is accepted 🎉
            - 🎉🎉🎉🎉🎉🎉
    - Continuing on Neck position analysis
        - Compares CSA based on spinal nerves, intervertebral discs and PMJ
        - Finishing up the manuscript
    - Next step:
        - Label spinal nerve rootlets on ex vivo spinal cord
            - Data only received yesterday, so this is a WIP
        - Measure position of each spinal segment vs the length of the spinal cord
        - Hypothesis: the relative position of the spinal segment to the total length is constant across subjects
        - Collaboration with Hugues Leblond, neuroanatomist at Trois-Rivière
        - *Next*: check the model in MRI images

Action Items

- ☐ BDL: When dog data are received, try generating a template
- ☐ NLM: Present a plan moving forward for the segmentation project (data, etc.)
- ☐ NLM: Take a quick look at #2677 and present some ideas, and perhaps play around with sct_analyze_lesion/sct_process_segmentation for analyzing lesions (get used to script, understand how it works, etc.)
- ☐ RB: Connect with Julian McGinnis (?) → Dog segmentation project
- ☐ JN: Move the now-unnecessary isct_ scripts into spinalcordtoolbox-dev
- ☐ JN: Merge isct_test_ants functionality into sct_check_dependencies
- ☐ JCA: Next meeting → Book a room, as the majority of participants are local
    - How to handle video for remote participants, TBD

2022-09-22

Attendees: Joshua Newton, Julien Cohen-Adad, Julian McGinnis, Rohan Banerjee, Sandrine Bédard, Mathieu Guay-Paquet, Nick Guenther
Not yet arrived: Noël Rignon, Adrian El Baz, Benjamin de Leener, Jan Valosek
Moderator: Mathieu Guay-Paquet
Minutes: Joshua Newton

Check last week's action items

- ☐ JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)
  - → Not done
- ☑ ~~JCA: Send dog data to Benjamin for template~~
  - done: raw nifti data on duke → duke/projects/template_dog_virginiatech
  - Julian/Joshua: stitching kind of done
  - next step: segment the cord
    - T+C+L stitched together
    - Rohan Banerjee → Talk to JCA
- ☐ BDL: When dog data are received, try generating a template
- ☑ ~~JN: Create a first draft QC report for the sct_image -stitch PR~~
- ☑ ~~TODO: Tag Rohan in CSF deep learning project idea (comment on #2277)~~

Miscellaneous items

- Welcome Rohan! :D
  - Master's @ Neuropoly!
- Welcome Julian! :D
  - Munich, Germany!

Software Development

- Follow-up on triage (trickier issues)
  - Discuss proposed changes to sct_download_data (#2959)
    - Postpone to next meeting
    - → JN + MGP + NG == Touch base before meeting so we have some background

  - Discuss potential API changes to sct_process_seg/sct_analyze_lesion
    - Overlap between sct_process_segmentation + sct_analyze_lesion ⇒ s
      - Do not remove the `sct_process_segmentation`
      - `sct_analyze_lesion` might be safer to deprecate down the line.
      - But, start, introduce a new function with a more intuitive name:
        a. sct_compute_morphometrics? _volumetrics?

                    - We already have sct_compute_* functions that users may be familiar with.
                    - “Morphometrics” is an accurate term, but that term may not be recognizable to people without the requisite background
                    - Is “volumetrics” more intuitive to understand? (“Volume” is a well-known term, etc.)
                b. Simpler names: sct_analyze_volume / sct_compute_shape_metrics / sct_compute_X_volume (...mask? label? blob?)
                c. Reaching out to users…? Survey, proposing choices, etc.
                    - NB: Combine with other questions that we’ve accumulated in the past and
                d. No consensus about the name of function
                    - → But, doesn’t necessarily need to be settled on before work can begin on the API side of things.
            - MGP: Shape calculations: Slice-by-slice vs. analyzing entire blobs/segmentations. What are typical workflows?
                a. Slice-by-slice: sct_deepseg -> SC segmentation -> **sct_process_segmentation** (based on same API as sct_extract_metric)
                b. Entire segmentation/blob: **sct_analyze_lesion**
        - Volume calculation CLI (#3378, #2707)
        - Lesion statistics per slice (#2677)

- `sct_image -stitch` progress (PR #3865)
    - First draft of QC report is complete
        - → JN: Demo?
        - → Others: Feedback?
            - Account for 1000voxel image
            - Browser zoom can control size if image is too big (to avoid scrollbar)
    - Over the weekend, JMG (Julian McGinnis) will be processing a small cohort (30-50 patients), to further evaluate the SCT PR/QC Report in its current state
    - C++ vs. Python stitching → Any updates?
        - No time to update Python version to match C++ version
        - If C++ version is working, is it necessary to work on the Python version?
        - Stick with C++ for now? (First PR, stay with C++ version)

- Are the scripts listed in #3884 unused? Can they be moved to spinalcordtoolbox-dev? Yes!
    - isct_check_detection -
    - isct_get_fractional_volume -
    - matlab_batcher.sh -
    - msct_base_classes -
    - msct_gmseg_utils -
        - Yes! Can be moved to spinalcordtoolbox-dev.

Research

- Nothing to report, see you next time!

Action Items

- ☐ Future triage: there are currently 22 open issues with the needs discussion tag
- ☐ JN + NG + MGP: Write up some background about sct_download_data in next meeting agenda

2022-09-08

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Nick Guenther
Not yet arrived: Noël Rignon, Adrian El Baz, Benjamin de Leener, Jan Valosek, Rohan Banerjee
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~Next time, continue the curation of "user request" GitHub issues (starting from: #3365)~~
- ☑ ~~Julien: Include Rohan in meetings~~
- ☐ JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)
- ☐ JCA: Send dog data to Benjamin for template
    - done: raw nifti data on duke → duke/projects/template_dog_virginiatech
    - Julian/Joshua: stitching kind of done
    - next step: segment the cord
- ☐ JCA/Mathieu: put Shinn (dog) data on git-annex
    - Data is fine to stay on duke for now
- ☑ ~~JN/NG: Benjamin De Leener does not currently have access to the spinal cord toolbox org~~
- ☐ BDL: When dog data are received, try generating a template

Miscellaneous items

- None

Software Development

- `sct_image -stitch` progress
    - PR #3865 progress
        - C++ binary build process is fully automated across Linux/macOS/Windows
        - A basic SCT test passes for all platforms
        - QC report still needs to be authored, though (JN: Can self-assign this task to give Julian McGinnis more time for algorithm evaluation, etc.)
    - However, a fellow PhD student has taken the time to rewrite the C++ stitching tool in Python
    - So, we are now waiting on Julian McGinnis to evaluate and compare the Python and C++ versions of 'stitching' to see which should be included in SCT

- Triaging "user requested" GitHub issues (Link here)
    - One page left (25 issues to triage) → 15m
    - We should probably do this last? (To best utilize meeting time, let non-devs leave early, etc.…)

  - 1 meaningful grouping of issues: Overlap between sct_process_segmentation + sct_analyze_lesion ⇒ sct_compute_morphometrics?
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3378
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/2707
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/2677

Research

- Sandrine Bédard : DCM metrics
  - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3733
  - There are 3 parts:
    - Normalize with PAM 50 template per-level, then compute MSCC
    - Compute CSA in the right part of the cord and left part of the cord
    - Characterize triangular compression
      - Perhaps there is a simpler metric already provided by e.g. scikit-image that
      - Proposed 3-step process: CSA scaling -> Reg with PAM50 -> Similarity metric
        - Registration step complicates things (do we reg before sct_process_segmentation? During? How do we display the reg metric alongside the non-reg metrics)
        - Make sure that this even characterizes triangular compression (e.g. outside of sct_process_segmentation) before adding it to SCT

Action Items

☐ JN: Create a first draft QC report for the sct_image -stitch PR
☐ JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)
☐ BDL: When dog data are received, try generating a template
☐ TODO: Tag Rohan in CSF deep learning project idea
☐ Next meeting: Discuss proposed changes to sct_download_data
☐ Next meeting: Discuss potential API changes to sct_process_seg/sct_analyze_lesion

2022-08-25

Attendees: Joshua Newton, Mathieu Guay-Paquet, Julien Cohen-Adad, Nick Guenther, Benjamin De Leener
Not yet arrived:, Sandrine Bédard, Noël Rignon, Adrian El Baz, Jan Valosek, Rohan Banerjee
Moderator: Julien Cohen-Adad
Minutes: Mathieu Guay-Paquet

Check last week's action items

- ☐ ~~JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)~~

Miscellaneous items

- JN: Back from vacation. :)

Software Development

- Triage the 40 open issues under user requested
  - Use "priority: HIGH/MEDIUM/LOW" labels?

- JN: Julian McGinnis's `stitching` contribution
  - `sct_image -stitch` PR: #3865
    - Julian has already completed a large % of the contribution
    - TODO: Cross-platform `stitching` builds, test writing, QC report
    - QC Report comment – Supporting: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3865#discussion_r955007206
      - Possibly lower priority than actually testing the functionality of the contribution and the usefulness of the
  - `stitching` C++ build PR: jqmcginnis/build_biomedia_stitching@pull/#1
    - Necessary for building `stitching` for Windows, macOS platforms
    - JN: Self-assigned, will be working on this in the coming week
  - Next meeting for bavaria-quebec project → Sept 7th

- MGP: Is there any objection to using more type hints in function signatures?
  - NG: Inconsistent code formatting, complicated typing
  - MG: The act of adding types is just as important as having the types themselves, so inconsistency isn't necessarily a bad thing
  - NG: mypy (strong typing) vs. type hints (enforcing vs. lighter suggestions/IDE warnings)

Research

- Julien: Richard Shinn dog template/atlas

        - Related Slack discussion regarding Shinn’s past publications that use SCT: https://neuropoly.slack.com/archives/CB27THD2T/p1658804369523129?thread_ts=1657252468.406629&cid=CB27THD2T
        - We got the data some time ago, where is it now?
            - Doesn’t seem to be on git-annex
            - Doesn’t seem to be on duke
        - Will need some resources from Compute Canada to do the heavy processing
        - Template doc:
            - https://github.com/sct-pipeline/exvivo-template
                - generated template: https://github.com/spinalcordtoolbox/exvivo-template
            - If by chance template code was in dev/ folder, then that now exists here: https://github.com/spinalcordtoolbox/spinalcordtoolbox-dev
                - 404
            - https://github.com/neuropoly/template

Action Items

- ☐ Next time, continue the curation of “user request” GitHub issues (starting from: #3365)
- ☑ ~~Julien: Include Rohan in meetings~~
- ☐ JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)
- ☐ JCA: Send data to Benjamin
- ☑ ~~JCA/Mathieu: put Shinn data on git-annex~~
- ☑ ~~JN/NG: Benjamin De Leener does not currently have access to the spinal cord toolbox org~~
- ☐ BDL: When dog data are received, try generating a template

2022-08-09

Attendees: Julien Cohen-Adad, Sandrine Bédard, Mathieu Guay-Paquet,
Not yet arrived: Joshua Newton, Noël Rignon, Nick Guenther, Evan Béal, Adrian El Baz, Benjamin de Leener
Moderator: Mathieu Guay-Paquet
Minutes: Julien Cohen-Adad

Check last week's action items

☑ ~~SCT v5.7 is released (github link) (forum link)~~

Miscellaneous items

- JN is still on vacation until Aug 12

Software Development

- SCT v5.7 release went well (thanks to the instructions by JN)
  - Advertised on forums (spinalcordmri, neurostars), twitter, slack (spinal cord mri group, brainhack)
  - Users notified of bugfixes on the forum
- Next release will be SCT v5.8 on December 2 (github link)
  - We may need a release before December, so that Sandrine's features can be included in a journal reference (TBD)
  - What are the priorities?
    - Anything that comes up with Julian McGinnis
    - Visitor in October (Yehuda Warszawer) for a few weeks, will probably do tutorials and have feedback, application in MS
    - Resident from Cornell university (Michelle Chen) will be here for a year starting September 1, will probably develop new models (application in MS)
    - Jan Valosek: postdoc, arrive early October
    - Specific new features?
      - #3432: Output csa perslice and distance from PMJ
      - #3857: citation statistics in sphinx-generated docs
      - #3809: looping over sub-* without ses-*
    - Specific cleanups?
      - #3854: deal with nibabel deprecations (and others?)
      - #2682: refactor sct_analyze_lesion
    - Maybe triage the 40 open issues under user requested

Research

- Nothing to report this week

Action Items

- ☐ JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)
- ☑ ~~Add to next meeting agenda: triage the 40 open issues under user requested~~

2022-07-26 (v5.7 release)

Attendees: Joshua Newton, Julien Cohen-Adad, Noël Rignon, Sandrine Bédard,
Not yet arrived: Mathieu Guay-Paquet, Nick Guenther, Evan Béal, Adrian El Baz, Benjamin de Leener
Moderator: Mathieu Guay-Paquet
Minutes: Julien Cohen-Adad

Check last week's action items

- ☐ JCA: Look into specifics of warp histology atlas PR file contents (question on #3444)
- ☑ ~~JN: Keep installing deepreg models by default~~
- ☑ ~~JN: Write tutorial for Evan's registration method~~
- ☑ ~~JN: Move optional dependencies section above mandatory dependencies~~

Miscellaneous items

- August vacation time (See "NeuroPoly - Holidays" calendar)
    - JN: Aug 1 - Aug 12
        - (Somewhat flexible – Basically just waiting until after SCT v5.7 is released.)
        - Should MGP handle the #sct_general citation alerts during this time?
            - Yes
        - Other tasks?
            - JN: Forum notifications, possibly? (For more dev-related user questions)
    - Anyone else? (Most people seem to have taken holidays in July?)

Software Development

- SCT v5.7 Release
    - 5.7 Milestone has 2 remaining PRs:
        - #3831: **Tutorial for Evan's contrast agnostic registration method.**
            - (Needs review: Just needs proofreading + confirming that these are indeed the steps that we want to recommend to users.)
        - #3840: **Rewording the sct_merge_images argparse help description.**
            - (Needs review: Very small PR that just needs proofreading.)

    - Potential last-minute bugfixes for user-requested issues
        - JN: I have gone through the list of user-requested bugs, and cleaned it up a little (closing stale issues, renaming issues, etc.)
        - IMO the remaining issues are low-priority, and not mandatory for the 5.7 release
        - Still, there are a few candidates for quick, easy fixes:
            - #3851: Small QC formatting issue – I suspect this will be easy to investigate and fix?

            - #3800: We can likely just close this one? (See discussion here, more input would be helpful, though.)
            - #3673: Likely just needs better error handling?
    - Apart from these points, the release could be created as soon as the end of this week?

- MGP: Are we still happy with the current set of OSes we're testing on? (workflow) Yes
    - archlinux
    - centos (7, stream 8)
    - debian (9, 10, testing, rolling)
    - ubuntu (18.04, 20.04)
    - macos (11, 12)
    - windows native (2019)
    - windows wsl ubuntu (2019 / 18.04, 2019 / 20.04)

Research

- Sandrine Bédard
    - For PMJ-based CSA project with different neck angle
        - Neck angle computation: https://jamboard.google.com/d/1R_GNuTkfWX0yar4dN0MfnrpL2UfhVW8Hn5T3fONbJoo/viewer?f=3
        - Problem:
            - Projection in R-L direction

Action Items

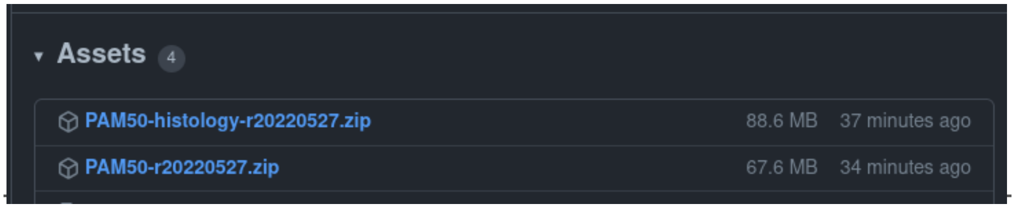
☐

2022-06-28

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Nick Guenther,
Not yet arrived:, Evan Béal, Adrian El Baz, Benjamin de Leener
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JN: Review Evan's PR after TF/Keras PR is merged~~
- ☑ ~~MGP: Review sct_maths `-add` bugfix PR~~
- ☐ JCA: Look into specifics of warp histology atlas PR file contents
- ☑ ~~JN: Revert PAM50 release to split warp histology atlas into separate download~~



▾ Assets 4

PAM50-histology-r20220527.zip	88.6 MB	37 minutes ago
PAM50-r20220527.zip	67.6 MB	34 minutes ago

Miscellaneous items

Software Development

- MGP: What to do with the dev/ folder?
  - It seems to have been used as a catch-all for developer-only scripts, not intended for inclusion in releases, and mostly obsolete.
    - Question for JCA: Is this true?
  - It's currently **partially** included in releases, because of the way we do releases. We're simplifying the release process in #3813, and need to decide whether to include it **completely** or **not at all**.
  - Including it would increase the release size from ~8MB to ~12MB.
  - JN dug up the history in this comment on #3813, and made a separate repository called dev-backup so we don't lose anything by removing it from the SCT repo.
    - Making sure that this dev folder is discoverable
    - Name repo `spinalcordtoolbox-dev` ← `dev-backup`

- JN: Remaining questions for EB's registration method PR
  - 1: Installing models by default vs. installing at runtime
    - Model files take up ~300MB space
    - Right now in the PR, the model files are being installed by default

        - Alternate suggestion: Check if files are present, then download if missing at runtime.
            - Pros: Only downloads files if necessary, saves 300MB installation space
            - Cons: Might cause double downloads in parallel sct_run_batch runs, makes SCT harder to use “offline”, more complicated to maintain, etc.
                a. Are these actually big cons?
            - (Similar dilemma to PAM50 histology files – optional vs. default installations, etc.)
            - ANS: Install by default for now, but can always return to decision

    - 2: Advertising the new registration method
        - Bare minimum: Adding a note in the new release announcement
        - Better: Adding a tutorial/SCT Course section for this new method
            - JN: I can self-assign this as an action item.
            - Tutorial == Good!
            - Include link to paper
        - Associated paper has been submitted!
        - Any other ideas?

- MGP: Brainstorm for wording for FSLeyes dependency check:
    - Current wording looks like an error message, even though FSLeyes is optional.
    - Proposed wording keeps the error message, but puts it under an “OPTIONAL DEPENDENCIES” heading.
    - Another suggestion: “Check for an image viewer (optional).....[None found] (127) / [FSLeyes] (1.4.3)”
    - Thoughts?
        - OPTIONAL DEPENDENCIES is good, especially if above

- Julien: deepseg_sc/deepseg_lesion: where is the processing script?
    - Model architecture code is known, but training scripts are missing
    - → Email Charley

Research

- N/A
    -

Action Items

☐ JCA: Look into specifics of warp histology atlas PR file contents
☑ ~~JN: Keep installing deepreg models by default~~
☐ JN: Write tutorial for Evan’s registration method
☑ ~~JN: Move optional dependencies section above mandatory dependencies~~

2022-06-14

Attendees:
Not yet arrived: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Nick Guenther, Evan Béal, Adrian El Baz, Benjamin de Leener
Moderator: Joshua Newton
Minutes: Noël Rignon

Check last week's action items

- ☑ ~~NR: Review of the 4 PR of JN to unblock pipeline until Mathieu came back~~
  - Did some reviews, but the PR are ongoing work so the workload will still be here
- ☑ ~~JN: Continue to clean up draft PRs~~
  - Only 2 remain, and both have assignees (Jan Valosek / Mathieu), so this looks to be resolved. :)
  - Jan's PR: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3172
  - about Jan joining the lab: Blocker for applying for visa → Resolved in 1-2 months
- ☑ ~~JN: Finish PR for template for packaging dependencies using pip~~
  - Put on hold for now. Rationale: #1526 (comment)

Miscellaneous items

- N/A

Software Development

- JN: Paired PR reviews
  - **Problem:** SCT PRs require a lot of background knowledge to be able to give useful feedback on the PR work
  - **Proposal:** Pairing with JN over Zoom so that JN can give walkthroughs of PRs and answer any background-knowledge questions in real time
  - Would that be helpful for you, @Mathieu/@Noel?
    - Depends on the PR + person, has worked well with prior PRs/people in the past.

- PR #3738: Replace Tensorflow/Keras with .ONNX
  - Update: This PR is now necessary for Evan's registration PR.
  - Noel has given approval, so this will be merged after this meeting, unless someone feels that we should get a 2nd approval (due to the size/complexity of the PR).
    - 1 review is probably enough → Better to unblock progress on Evan's PR

- PR #3444: Add warp histology atlas

    - JN: Since this is Alex’s work, I could only clean up the PR. I don’t know enough about the specific MRI knowledge to understand how to review it, or whether this is safe to merge.
    - Question raised in PR: Adding the histology microstructure atlas to the PAM50 template increases size on disk (from 68 MB to 156 MB, more than double). Is this acceptable?
        - Might not need to be included in the mainline PAM50 template – could be a separate sct_download_data download.

- Issue #3806: sct_maths bug for 4D data
    - New PR has been opened to fix this bug.
    - Mathieu → Action item

Research

- PR #3807: Integration of DL multimodal registration in SCT
    - PR opened today!
    - Installation conflict between VoxelMorph and Tensorflow, but this will be resolved once TF/Keras PR is merged.
    - JN: Will review this week. :)

Action Items

☐ JN: Review Evan’s PR after TF/Keras PR is merged
☑ ~~MGP: Review sct_maths `-add` bugfix PR~~
☐ JCA: Look into specifics of warp histology atlas PR file contents
☐ JN: Revert PAM50 release to split warp histology atlas into separate download

2022-05-31

Attendees: Joshua Newton, Julien Cohen-Adad, Noël Rignon, Nick Guenther,
Not yet arrived:, Sandrine Bédard, Mathieu Guay-Paquet, J Evan Béal, Adrian El Baz, Benjamin de Leener
Moderator: Noël Rignon
Minutes: Julien Cohen-Adad

Check last week's action items

- ☑ ~~JN: Assign moderators/minutes ahead of time (forgot after last meeting)~~
- ☑ ~~JN: Give an update on the onnxruntime/batch_processing.sh~~
    - Issue was resolved by talking to upstream ONNX devs and changing a default option (`enable_cpu_mem_arena=True`) to False (PR is ready for review)
- ☑ ~~EB: Investigate resource usage issues re: PyTorch vs. TF for VoxelMorph~~
    - https://github.com/voxelmorph/voxelmorph/issues/434
- ☐ NG: Contact upstream developers directly to request a new PyPI release
    - https://github.com/voxelmorph/voxelmorph/issues/432
- ☐ NG: Offer a helpful publishing script to speed up dependencies
    - https://github.com/voxelmorph/voxelmorph/pull/433
    - https://github.com/adalca/neurite/pull/56
    - https://github.com/adalca/pystrum/pull/8
- ☐ NG: Stop manually tracking torch versions
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3790

Miscellaneous items

Software Development

- JN: Availability of SCT reviewers
    - Mathieu → On vacation
        - Until June 12th
    - Noel → Filling in for Alexandru/Taowa's roles in other areas of NP
        - Noel is available to review PRs!
    - There are 4 open PRs in need of review that have yet to be reviewed.
    - I've also been hesitant to open new PRs, as I don't want to add to the backlog.
    - Should we consider temporarily merging PRs without review in SCT?
        - Ideally, avoid this!

- JN: Developer priorities

    - For now, I have been focusing on cleaning up past unfinished work (draft PRs, CI-built binaries, pip-installable SCT) and existing in-progress efforts (VoxelMorph resource usage issues) rather than starting new efforts
    - Reason: Progress can be made on these tasks without increasing the backlog of open PRs
    - I plan to continue working on these efforts in the short term (e.g. until Mathieu returns), unless there are higher priority tasks

Research

- JN: PyTorch memory usage for EB's model
    - No response from upstream VoxelMorph developers
    - I have been trying to profile the memory usage myself, and brainstorm ideas to fix this
    - But, I haven't found any obvious improvements
    - It's looking to me like the memory usage issues might be inherent to PyTorch
    - Good news: Cropping around the spinal cord (i.e. smaller input images) avoids memory issues – but is this sufficient?
        - For development, take things 1 step at a time
        - Start with implementing the PyTorch model as-is
        - Provide a usage example that uses cropped input images
        - If users run into issues with larger images, then we can cross that bridge when we get to it.

Action Items

- ☐ NR: Review of the 4 PR of JN to unblock pipeline until Mathieu came back
- ☐ JN: Continue to clean up draft PRs
- ☐ JN: Finish PR for template for packaging dependencies using pip

2022-05-17

Attendees: Joshua Newton, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Nick Guenther, Evan Béal
Not yet arrived: Sandrine Bédard, Adrian El Baz, Benjamin de Leener, Nick Guenther
Moderator: Julien Cohen-Adad
Minutes:

Check last week's action items

- ☐ None

Miscellaneous items

Software Development

- JN: Updates on work I've been doing
  - Less to report than usual, since onboarding issues took up time this past week
  - #2668: Use binaries that are packaged by the spinalcordtoolbox-binaries repo
    - Using GitHub Actions to build ANTs binaries, which should make future updates easier
    - Infrastructure is now in place in the build_ANTs repository
    - There is only a small change on SCT's end that needs review (just updating the binary links, no change in registration results)
  - #3738: Replace Tensorflow/Keras-based inference (.h5) with onnxruntime (.ONNX)
    - New batch_processing.sh test caught a resource issue on Windows
    - Happened right before the meeting – haven't had time to investigate
    - Will provide more details for next meeting

- Integrating Evan's registration approach (issue #3760)
  - Good news: PyTorch conversation was largely a success! (now publicly available)
  - Bad news: VoxelMorph model relies on upstream master features, but VoxelMorph devs haven't released a new PyPI version since Sept 2020
    - EB: Same problem may be observed with Neurite and Pystrum that are needed to use VoxelMorph but are not up-to-date with PyPI and so require to be cloned from GH (see issue #321 in VoxelMorph repo)
    - NG: If SCT wants to be pip-installable, our dependencies also have to be pip installable (i.e. published to https://pypi.org and nowhere else)
    - Step 1: Contact upstream developers directly to request a new PyPI release
    - Step 2: If they don't rely promptly, we may need to fork the packages and release things ourselves

    - EB: PyTorch models seem to require more computing resources than the TF ones → need further investigations and then open an issue on VoxelMorph repo to determine if this problem has been observed on their side
        - TODO: Ask upstream developers to see if they've encountered these resource usage discrepancies between PyTorch and TF versions of the model architectures

- NG: A better fix for the CPU pain point: #3790
    - Blocked on ivadomed#1129 but I have high hopes

Research

-
    -

Action Items

☐ JN: Assign moderators/minutes ahead of time (forgot after last meeting)
☐ JN: Give an update on the onnxruntime/batch_processing.sh
☐ EB: Investigate resource usage issues re: PyTorch vs. TF for VoxelMorph
    - https://github.com/voxelmorph/voxelmorph/issues/434
☑ ~~NG: Contact upstream developers directly to request a new PyPI release~~
    - https://github.com/voxelmorph/voxelmorph/issues/432
☑ ~~NG: Offer a helpful publishing script to speed up dependencies~~
    - https://github.com/voxelmorph/voxelmorph/pull/433
    - https://github.com/adalca/neurite/pull/56
    - https://github.com/adalca/pystrum/pull/8

2022-05-03 (v5.7 planning)

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Evan Béal
Not yet arrived: Nick Guenther,, Adrian El Baz, Benjamin de Leener
Moderator: Julien Cohen Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~5.6 was released! All action items taken care of.~~

Miscellaneous items

- Mathieu GP has some vacation coming up (end of may / start of june)

Software Development

- v5.6 Postmortem
  - Q1: Was 3 months enough time to produce significant enough changes?
  - Q2: Does a quarterly cycle mesh well enough with the lab's schedule?
    - Would it work better to release 3 times/year to line up with PolyMtl school terms? (Jan-Apr, May-Aug, Sept-Dec)
    - That way, the start/end of internships, summer vacations, etc. can coincide with SCT releases.
      - Internship time periods don't necessarily line up with school terms
      - So, trying to sync things up doesn't really make sense

- v5.7 Planning – What should our priorities be?
  - Ranking various efforts → See Issue #3765
  -

- [Noel] Currently stalled draft PRs
  - Should we unblock PRs from Nick that have been blocked since last year on SCT ? He put some effort into it and I'm afraid that we will lose it if we wait too long and that conflicts pile-up on it:
    - Three chained PRs waiting for the first one (#2666): #2666, #2667, #2668
    - A PR that was waiting for #3102 that is merged since: #3138

  - There are two draft PRs from Alexandru Foias waiting for review, should we re-assign them to finish the work ?
    - Automate SCT references: #3170
    - Add warp histology atlas: #3444

Research

- Sandrine Bédard : PMJ-based CSA, results neck position: 2022-04-27-Results_neck-position-distances
  - Nerve rootlet validation → 2022-05-02-Validation_label-nerfs
  - Next step: redo some labels!

- EB: Update on issue #3760

Action Items

☐

2022-04-19 (v5.6 release)

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Evan Béal,
Not yet arrived: Nick Guenther, Adrian El Baz, Benjamin de Leener
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☐ Julien Cohen-Adad : Review https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3541
    - Reminder added to review
- ☑ ~~Joshua Newton /EB: Try convert the Tensorflow VoxelMorph model into ONNX~~
    - Follow-up discussion has been going on in Issue #3760.
        - Idea 1: Weight transfer between Tensorflow and PyTorch
            - This is because we already depend on PyTorch for deepseg
        - Idea 2: ONNX-only model
            - Requires patch/block-based approach
            - Less accurate
        - Idea 3: Keep TensorFlow (2+) for new approach 9
    - Explore Idea 1, if not realistic, explore options 2/3
- ☑ ~~Joshua Newton : Move the installation instructions for native Windows into the main RTD (with the "light" warning that this is a new installation method)~~
    - PR opened here: #3761

Miscellaneous items

- JN: Planning out future meetings in advance based on tentative release schedule
    - I've added a rough outline to this document, so that we're not scrambling to create meeting agendas at the last second.
    - Thoughts?

- JN: Moderator / minutes rotation
    - We haven't been rotating as of recently, like we previously proposed.
    - Options:
        1. Assign these roles in advance? (e.g. Rotating order, Noel -> Mathieu -> Joshua -> Julien -> Sandrine -> Noel -> etc. added to future meeting agendas)
            - NB: Plus new students in the future
        2. Alternatively, we could stop rotation and assign dedicated people to moderate/take minutes.

Software Development

- JN: Pending work for April 30th v5.6 Release (5.6 milestone link)

  - #3541: Add a new flag sct_deepseg -list-description
    - Still needs review (Julien)
      - Covered already

  - #3761: Add Native Windows installation instructions to RTD
    - PR in need of a review. (Action item for… ____?)

  - #3703: ValueError w2 should be positive
    - PR #3771 has been opened and is being reviewed by JN.

  - #3673: Watch out for ‘negative’ discs
    - Preliminary PR #3774 opened – needs review
      - Noel? (If not, Joshua?)

  - 2 new important Windows-related issues:
    - #3762: Double-clicking install_sct.bat results in the CMD window disappearing
      - Assignee: Noel? (If not, Joshua?)
    - #3763: Update release workflow to add install_sct.bat as a release asset
      - Assignee: Noel? (If not, Joshua?)

  - Cut-off for new, non-urgent work
    - Suggestion: Any new work started after the end of this week (April 22nd) should be pushed to 5.7 release

- JN: Suggestion for the next meeting (May 3rd)
  - 5.6 release postmortem + feedback
  - 5.7 release planning (ranking priorities for larger efforts)

- JCA: overall feedback for newcomers
  - Noel: Cleaning up unfinished draft PRs will make finding work to contribute on easier (JN: see discussion item on next meeting agenda)
  - Noel: Timing for releases made starting on new work a bit awkward (administrative aspects got in the way until right before v5.6 release)

Research

- Sandrine Bédard : Just finished my bachelor degree!
  - Will get started on PMJ CSA project and new metric for degenerative cervical myelopathy (https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3733)

- incoming summer students:
  - Shu Ai, starting in may
  - Mortamet, Paul (might start in may, otherwise in sept: MSc)
  - Valosek, Jan (PDF, ~august 2022)

Action items

- ☐ All: Read through Issue #3765 to discuss at the next meeting.
    - NB: Intern projects may take priority over more dev-focused effort? (See above)

2022-04-05 (v5.6 prep)

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Nick Guenther, Evan Béal,
Not yet arrived: Adrian El Baz, Benjamin de Leener
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~SB: Write issue on SCT installation on windows~~
  - Ongoing discussion re: bugfixes happening @ Issue #3740
- ☑ ~~JN: Look more deeply into ITKSnap's Windows CLI~~
  - Opened PR#3754, almost ready (just needs a test written for it)
- ☑ ~~JN: Investigate processing time for ONNX/Keras model comparison~~
  - Current CI suite runs show that the ONNX PR improves test suite execution time by about ~1min (Before, After)
  - e.g. CentOS: 6m42s → 5m38s, macOS 9m48s → 8m23s, etc.
  - Re-trying these CI runs consistently produced similar improvements (with small variances depending on the VM given by GitHub)
  - A more thorough profiling could be performed (e.g. with better isolation of the specific inference functions), but this might not be worth the time, given cursory results.

Miscellaneous items

- N/A

Software Development

- Joshua Newton: 5.6 Release (Due date: April 30th)
  - Internal Windows testing
    - Is there anyone else internal to NeuroPoly with a Windows machine who we can ask to try out the Windows installation prior to the release?
      - Gaspard Cereza
      - Maybe from Ben's lab (maybe Colline?)
    - Any other ideas for how we can test typical usage?
      - e.g. running through the SCT Course materials
      - User feedback → Might be best to just release it out into the wild and get our testing that way. :)

  - How should we announce the "experimental" Windows installation?
    - Normal release, but with installation instructions in separate Gist, instead of main docs?

  - Normal release, with instructions in main docs + possibly an “experimental” warning?
    - Based on discussion, this looks like the best option (see notes below)
    - Users could react ^^^ “Oh there’s a beta, scary warning, might not be worth using”
    - Could dissuade people from trying out the software and finding said bugs in the first place
    - Users tend to be understanding of bugs, won’t necessarily be angry or distrustful if something doesn’t work
    - We might want to only give a light, friendly warning → “If you see a bug, don’t hesitate to contact us.”
  - Beta release instead of normal release, then push “full” 5.6 release to August?
    - Pros: Less chance people will try to seriously install native Windows to be used in their analyses (which, in its current state, might not give the best first impression if there are critical undiscovered bugs)
    - Cons: Probably less exposure, fewer people able to test?
    - Julien: “Beta” may not mean much to our users
      - → What’s the point of distinguishing a beta release if the current state of Windows (possibly buggy) is not all that different from the current state of SCT’s normal releases (possibly buggy)
  - Mathieu: Possibly a pilot “tester” program for directly connecting to users
    - Time commitment → May not have the ability to keep in constant contact

- Remaining work in 5.6 milestone:
  - PR #3541 - Add a new flag sct_deepseg -list-description
    - Old PR from external contributor (taken over by us) that has stalled
    - Would benefit from 2 different reviews:
      - Review of the feature design (argparse UI design, etc.) → Best suited for Noel or Mathieu?
      - Proofreading of the model/task descriptions (this involves details of past research projects) → Best suited for Julien?

  - Other pending issues have assignees already! Hoorah 🎉
    - #3703: ValueError: w2 should be positive (Mathieu)
    - #3673: Watch out for missing discs (Mathieu)
    - #3745: Add support for ITK-Snap in display_viewer_syntax (Joshua)

  - Are there any other issues/bugfixes that we should try to include?
    - For inspiration, see recent user-requested issues → here
    - Nothing super urgent / small is standing out…?
    - We can always focus on our current workload and come back to these issues if we have time.

- Wording question about isct_propseg on Windows

        - “Skipping PropSeg compatibility check (sct_propseg is not yet supported on Windows ‘Native’ installation (ie: without WSL))")
            - Would guide users to WSL if they truly need propseg over deepseg
        - Clarifying the tutorials is also a priority here (since they also prominently feature sct_propseg)

- Mathieu: Now that Noel is able to work with us (yay!), do we have any thoughts on who reviews what/when/etc.?
    - Pull requests probably don't need more than one reviewer, in general.
    - One possibility: the pull request opener semi-randomly assigns a reviewer. If the reviewer knows they won't get to it soon, they can re-assign.
    - Another possibility: the pull request opener leaves reviewer blank. Whoever starts the review first self-assigns (before doing the review, to avoid duplicated work).
        - “Awaiting review” is a status that can help with filters
        - Joshua Newton: I really like the “self-assign” convention for signaling commitment to PRs for reviewers
        - Instead of leaving the “request reviewer” field blank, we could also request both devs (e.g. Noel requests Mathieu+Joshua, Mathieu requests Noel+Joshua, etc.), maybe?
        - We already have “draft” status to signal “not ready for review”
        -
    - Other possibilities?

Research

- EB: Integration of cascaded deep learning registration models in sct_register_multimodal
    - repos of project
    - New function in register.py ?
        - Include preprocessing steps
        - Load the models weights and build the architecture (using VoxelMorph functions)
            - What is VoxelMorph? → Model architecture? (“SynthMorph” is the technique, package is VoxelMorph?)
            - .h5 → PyTorch or Tensorflow/Keras?
            - Needs investigation to see if model can be converted to ONNX, or if we need to depend on VoxelMorph directly
            - Something to explore further between EB+JN
        - Use the models to produce the warping field
        - Transform the warping field so it can be used with sct_apply_transfo
        - Call this function from the register function of sct_register_to_template
    - Re: Announcement about leaving the lab → ?
        - Not giving up the project this close to the integration
        - Still available to contribute!
    - Paper submitted to Aperture Neuro
        - Congratulations!! :) !

Action items

- ☐ Julien Cohen-Adad : Review https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3541
- ☐ Joshua Newton /EB: Try convert the Tensorflow VoxelMorph model into ONNX
- ☐ Joshua Newton : Move the installation instructions for native Windows into the main RTD (with the “light” warning that this is a new installation method)

2022-03-22

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Evan Béal
Not yet arrived:, Nick Guenther, Adrian El Baz, Benjamin de Leener, Alexandru Foias
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JN: Add support for ITKsnap (end of script "open in this viewer")~~
  - See discussion below
- ☑ ~~JN: Do some initial research into onnxruntime to see how much of an investment it would be~~
  - See discussion below
- ☑ ~~Mathieu: Set up Windows computer to help with Windows reviews~~
- ☑ ~~Sandrine/Noel/Mathieu: Test install_sct.bat installer + tools on windows~~
  - Sandrine: Installation failed (French error message?) → New issue?

Miscellaneous items

- Noel have some administration delay to onboard in the team (not able to be paid for the moment)

Software Development

- Joshua Newton : Windows PR updates
  - Progress is steady (8/10 PRs approved/merged, 2/10 need reviews)
  - Once all PRs are merged, we can tweak the WIP installation instructions to install SCT from master, instead of the jn/3682-support-native-windows-installation branch.
  - Potential next steps:
    - Attach install scripts to releases (downloading single script, not all source code)? (Related: Issue #3545)
    - Expand the test suite to more thoroughly cover all major CLI scripts?

- Joshua Newton : ITK-Snap support in scripts
  - ITKsnap's Windows package does not have a CLI interface (Can't launch viewer with specific images from command prompt) → See this help thread.
    - Actually, the CLI interface DOES work →
    -
  - Potential alternatives to try:
    - MRIcroGL: No Windows CLI interface
    - ImageJ: Has Windows CLI interface, but is very barebones compared to FSLeyes
    - Mango: No Windows CLI interface

        - Any others?
    - SB: For windows: here is an example: https://github.com/sct-pipeline/ukbiobank-spinalcord-csa/blob/04b9dd20bf2ad646e734e3e3effae174d4e451ca/pipeline_ukbiobank/cli/manual_correction.py#L134
        - Instruction for installation on Windows: https://github.com/sct-pipeline/ukbiobank-spinalcord-csa#dependencies

- Joshua Newton: Investigating .h5 -> ONNX model conversion
    - **Context:** SCT's Tensorflow-based models (sct_deepseg_X) have been a pain, Issue #3046 would require significant effort, so Issue #3735 could act as a short-term way to ditch TF/Keras.

    - Good news! PR #3738 would remove Tensorflow/Keras from SCT and replace them with the much lighter onnxruntime (.h5 models -> .ONNX models)
        - Identical performance between Keras/ONNX models for deepseg_sc / deepseg_lesion, and for deepseg _gm (large images only)

    - There is one issue: sct_deepseg_gm for small images
        - Predictions are *almost* identical to Keras models
        - However, some slices have 1-2 voxel differences
        - Is this enough of a concern to outweigh the benefits of removing TF/Keras?

    - ONNX vs Keras – Computation time? Potentially large images might be slow? Double check, though!
        - Discussion in ADS meeting (ONNX vs Pytorch)
        - Issue #961 in Ivadomed

- Mathieu: Cleaning labels → Issue #3702, PR #3739
    - May have found underlying issue for weird behavior during voxel cleaning
        - Dilation may have caused overlap between labels
    - What default behavior should we use between 0/1/2?
        - 1!

Research

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Action items

☑ ~~SB: Write issue on SCT installation on windows~~
☐ JN: Look more deeply into ITKSnap's Windows CLI
☐ JN: Investigate processing time for ONNX/Keras model comparison

2022-03-08

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon
Not yet arrived:, Evan Béal, Nick Guenther, Adrian El Baz, Benjamin de Leener, Alexandru Foias
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JN: Write a set of instructions for how to use the new Windows installation method.~~
    - JN: First draft of installation instructions here
- ☑ ~~JN: Verify that versions of ANTs/ITK for Win match the versions used for Linux/macOS~~
    - JN: Success! This was the cause of the moco/registration differences, and this has been fixed.
- ☑ ~~JN: Explore options for using sct_run_batch with Windows (bash on win? non-shell scripts?)~~
    - JN: Both Git Bash and Cygwin work perfectly. As long as there is a bash.exe in the PATH, I was able to run the sct_run_batch part of the SCT course just fine.)
- ☑ ~~JN: Investigate which Windows versions/CPUs we can say we support (32/64-bit processors? Win7 vs Win10? Different versions/updates?~~
    - JN: ML libraries (Tensorflow/PyTorch/ONNX) unsupported on 32-bit platforms.
- ☐ JN: Add support for ITKsnap (end of script "open in this viewer")
- ☐ JN: Do some initial research into onnxruntime to see how much of an investment it would be
- ☑ ~~Mathieu: Try Windows VM (from Slack thread) to help with Windows reviews~~
    - In progress: I'm setting up a Windows computer instead of a VM
    - But Windows reviews are going well anyway! (JN: Yes they are! :))

Miscellaneous items

-

Software Development

- Joshua Newton : Update on Native Windows installation
    - Barebones Windows installer PR has been merged to master!
        - However, many test failures still remain on master.
        - 11 new PRs have been opened to fix these test failures
        - Reviews wanted! (2 merged already, 9 remain)
    - Proposed (rough) timeline:
        - April release (5.6):
            - Finish merging first round of Windows bugfixes
            - Quietly advertise "experimental, use at your own risk" native Windows installation (for adventurous users, and people close to the lab)
        - July release (5.7, or perhaps 6.0):

            - Further testing between April-July (from users + expanded test suite)
            - Officially announce native Windows installation

Research

- EB: Inter-subjects registration (report)
    - comments:
        - jca: pmj not robust
        - BSplineSyn[3] -> Might have better performance with [didn't hear what was said]

Action items

- ☐ JN: Add support for ITKsnap (end of script "open in this viewer")
- ☐ JN: Do some initial research into onnxruntime to see how much of an investment it would be
- ☐ Mathieu: Try Windows VM (from Slack thread) to help with Windows reviews
- ☐ Sandrine/Noel: test installer on windows

2022-02-22

Attendees: Joshua Newton, Sandrine Bédard, Mathieu Guay-Paquet, Julien Cohen-Adad, Noël Rignon, Evan Béal, Nick Guenther
Not yet arrived: Adrian El Baz, Benjamin de Leener, Alexandru Foias,
Moderator: Julien Cohen-Adad
Minutes: Sandrine Bédard

Check last week's action items

- ☐ JN: Do some initial research into onnxruntime to see how much of an investment it would be
    - JN: Haven't looked into this yet due to prioritizing Windows
- ☑ ~~JN/others (for review): Prioritize improving Windows installation procedure~~

Miscellaneous items

-

Software Development

- Joshua Newton: Update on Native Windows installation
    - Good news! Majority of tests pass with Windows-built binaries + compatibility bugfixes
        - See #3699
        - Specifically, this CI run

    - Remaining 9 test failures require some discussion:
        - sliceReg test deviations: #3697
            - Could be due to discrepancies between ANTs/ITK versions
            - Consider rebuilding Linux/macOS binaries with newer versions, or Win binaries with older ANTs/ITK versions.

        - isct_propseg: #3694
            - Not as much of a priority (sct_deepseg_sc takes priority)

        - sct_run_batch: #3696
            - Needs to be explored further

    - Reviews needed:
        - Bare-minimum Windows installer PR: #3701
        - PRs for additional bug fixes will be created one-by-one. (See #3699)

    - Questions/discussions
        - how many windows version are we covering?
            - probably not 7
        - How do we install it?
            - Command prompt + running install_sct.bat
        - Image viewer: FSLeyes not available on Windows
            - ITKSnap?
        - Propseg?
            - Don't prioritize for the first windows release
        - 32-bit support? → Do we need to provide this?
        - Which shell to support?
            - Install_sct.bat is supported by both cmd and powershell -> No issue?

- Joshua Newton : April release
    - Are we confident enough in our test suite to want to advertise a Windows install by next release?
        - Many of the CLI script tests are run without validating results (holdover from sct_testing)
        - However, despite this, we can still merge the above changes without it affecting our macOS/Linux releases
        - So, it's possible for us to quietly improve the test suite + fix bugs, until we get to a point where we feel confident enough to make the big announcement. (e.g. August release instead of April)

- Mathieu Guay-Paquet : Working on bug fixes and refactoring:
    - Follow-up refactoring for sct_analyze_lesion (wrong lesion length/diameter #3633, output CSV instead of XSL #3691, general refactoring #2682)
    - Refactoring sct_label_vertebrae to find the cause of negative discs #3673, came across another bug (gaussian_std is ignored #3698)

Research

- Sandrine Bédard :
    - Starting a new project on metrics to quantify spinal cord compression in cervical myelopathy (in collaboration with neurosurgeon Allan Martin @UCDavis)
    - Will be integrated in sct_compute_mscc
    - An improvement would be to normalize the personalized measures with the PAM50 template.
    - Applications: degenerative cervical myelopathy and trauma

- Evan's project:
    - Registration of spinal cord images
    - Evaluation of the registration
        - Spinal cord segmentation of both images
        - Compare how they are overlapping before and after registration

        - QC report to visualize both segmentation and registration
    - Integration into SCT
        - `-param algo=evan_algo`?
        - Project dependent on SCT only
        - Is integrating the project into SCT necessary for the report?
            - For time management purposes -> return to this after report is finished

Action items

- ☑ ~~JN: Write a set of instructions for how to use the new Windows installation method.~~
- ☑ ~~JN: Verify that versions of ANTs/ITK for Win match the versions used for Linux/macOS~~
- ☑ ~~JN: Explore options for using sct_run_batch with Windows (bash on win? non-shell scripts?)~~
- ☐ JN: Add support for ITKsnap (end of script “open in this viewer”)
- ☐ JN: Investigate which Windows versions/CPUs we can say we support (32/64-bit processors? Different versions/updates?)
- ☐ JN: Do some initial research into onnxruntime to see how much of an investment it would be
- ☐ Mathieu: Try Windows VM (from Slack thread) to help with Windows reviews

2022-02-08 (v5.6 planning)

Attendees: Joshua Newton, Sandrine Bédard, Noël Rignon, Mathieu Guay-Paquet, Evan Béal, Julien Cohen-Adad,
Not yet arrived: Adrian El Baz, Benjamin de Leener, Alexandru Foias
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JN: Finish up with "ready to merge" PRs and release v5.5~~
- ☑ ~~JN/JCA: Take a closer look at MS Lesion PR (prediction suffix?)~~
- ☑ ~~JCA: Follow-up on email for SCT Course video recording~~
  - Alexandru has uploaded the SCT course recording to our YouTube channel
- ☑ ~~JN/JCA: Test different fMRI registration commands + verify the results~~
  - JN: I can no longer reproduce the original fMRI issue from the course, so I believe the underlying issue may have been fixed. (See: this comment for details.)
  - No need to change the fMRI command? If so, then we can export the course PDF now.

Housekeeping

- JCA: new students coming (image analysis: Nilser, Jan, DL: Adrian, Louis-Francois, Etienne, Sayan, Srikar)

Software Development

- Release v5.6 Development (Feb-Apr 2022)
  - Besides the usual bugfixes/improvements, which larger project should we prioritize next?
  - Google Doc ← Provides context on the following high-priority projects:
    - Writing missing tests for SCT scripts
    - Fixing reproducibility/numerical stability of our scripts
    - Improving Windows user experience
      - Highest priority
    - Adding sct_manual_correction
    - Porting Keras/TF models to ONNX
    - Packaging SCT using pip
      - Second highest (especially if it relates to improving the Windows user experience)

Research

- Evan's project integration in SCT.

    - Deep learning based image registration between contrasts. Would ‘replace’ sct_register_multimodal. → should we add a flag to sct_register_multimodal to use this approach?
    - https://github.com/ivadomed/multimodal-registration
    - Should this be included in SCT, or should it be a separate project?
        - Bigger than just registration, so keep separate

Action items

- ☐ JN: Do some initial research into onnxruntime to see how much of an investment it would be
- ☐ JN/others (for review): Prioritize improving Windows installation procedure

2022-01-25 (v5.5 release)

Attendees: Joshua Newton, Sandrine Bédard, Noël Rignon, Mathieu Guay-Paquet, Evan Béal, Julien Cohen-Adad, Adrian El Baz
Unable to attend: Nick Guenther, Benjamin de Leener, Alexandru Foias
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JCA: Ask Alex to follow up on forum, computers#259~~
- ☑ ~~Noel: #3618~~
- ☑ ~~Mathieu (actually, Noel): #3611~~
- ☑ ~~SB: #3643 (waiting for sct_tutorial_data#8~~)

Housekeeping

- Newcomer: Adrian! :tada:
  - PhD → deep learning + SCT will be a big part of research (for preprocessing)
  - Welcome!

Software Development

- Mathieu: How do people feel about using the "Assignees" field on github issues and/or PRs? That could make it easier to see which issues are up for grabs.
  - Sounds reasonable – very similar to what we've already been doing! :)
  - Possibly needs to be made explicit (dev docs, etc.)
  - Related to contributing guidelines!

- *From last meeting:* v5.5 release
  - **Proposal:** Quarterly release schedule (e.g. January/April/July/October)
  - In the short-term, does January (30-31st?) release give us enough time to finish pending work?
    - #3643: Replace sct_maths with sct_dmri_separate_dwi_and_b0
    - #3638: Convert input file to float32 before compute MTR.
      - Status: Ready to merge by today.
    - #3510: Adding Patch2Self Denoising to SCT
      - Status: Ready to merge by today.
        - However, I've made some new changes re: adding a citation for the preprint, so this could use one last quick look-over!
        - → JCA made a review comment
    - #3673: Added model for MS lesion segmentation
      - Status: Needs work re: the prediction suffix. JCA?

      - Might not be necessary for SCT to anything (taken care of by ivadomed)? → Requires looking at in more detail offline. Action item for JN/JCA/etc.

    - #3614: Fixing up SCT Course slides, then uploading to website
      - Status: Still needs a little more work to address raised comments.
        - Should we take a look at this together during today's meeting just to get it out of the way? (Link to slides for editing.)
        - Action item: Update "edited" date for notes.
        - Once complete, export with presenter notes (for uploading to spinalcordtoolbox.com)

  - This week: Finish up these PRs and release?
  - Next meeting: Follow up to discuss goals/timeline for April release (v5.6)

- *From last meeting:* SCT Course 2021
  - Did we receive permission to record the course? And, if so, are we able to upload the recording to our YouTube channel like we did in 2020?
    - Y/N? → Email send

Research

- Sandrine Bédard: Nerve rootlets identification: 2022-01-25-PMJ-based CSA - Update
  - Straightening of the spinal cord + denoising is a good solution!
  - Looking into detection of the cervical enlargement
- JCA: MS lesion segmentation to release asap
  - https://github.com/ivadomed/model_seg_ms_mp2rage
  - benchmarks:
    - lesion seg: https://github.com/ivadomed/model_seg_ms_mp2rage/issues/39
    - SC seg: https://github.com/ivadomed/model_seg_ms_mp2rage/issues/28
    - script with results: https://github.com/ivadomed/model_seg_ms_mp2rage/pull/40
  - Something to think about: What's the best way to share WIP models? Do we need to create a new release every time? (Alpha/beta/etc. pre-releases?)
    - Something to consider for the time period for Jan-Apr!

Action items

- ☐ JN: Finish up with "ready to merge" PRs
- ☐ JN/JCA: Test different FMRI registration commands + verify the results
- ☐ JN/JCA: Take a closer look at MS Lesion PR (prediction suffix?)
- ☐ JCA: Report back once we get a response for an email re: SCT Course video recording
- ☐ All: Read up on and brainstorm possible ideas for things to focus on for v5.6 (January-April timeline)
  - "High priority" label on GitHub is good to explore

    - Past meetings also have good ideas for things to work on! (Specifically, the “2021-12-15” meeting agenda has a list of “high priority” tasks that we can draw from.)

2022-01-11 (v5.5 prep)

Attendees: Joshua Newton, Sandrine Bédard, Noël Rignon, Mathieu Guay-Paquet, Evan Béal, Julien Cohen-Adad, Nick Guenther,
Unable to attend: Benjamin de Leener, Alexandru Foias
Moderator: Julien Cohen-Adad
Minutes: Sandrine Bédard

Check last week's action items

- ☑ ~~JCA: Verify that Tuesday 4pm time works with everyone's schedules~~
- ☑ ~~JCA/JN: Update p104 to replace sct_maths command with sct_dmri_separate_b0_and_dwi~~
    - JN: PR opened → #3643

Housekeeping

- Welcome to the lab, Noël and Mathieu! 🎉
- Schedule → Good for everyone :)

Software Development

- Joshua: Backlog of PRs in need of review (for v5.5 Release)
    - **Context:** At end of 2021, there was a lack of available reviewers, so unreviewed PRs had accumulated over the month of December
    - **Proposal:** Prioritize finishing currently pending work before starting new tasks
    - Double-check: Who will be available to review PRs in the coming weeks?
        - (Sandrine? Noël? Mathieu? Julien? etc.)
        - Sandrine Bédard I am 🙋
    - Open PRs in need of a reviewer (Assign each as an action item?):
        - Requires some conda/pip knowledge to review:
            - #3618 (Fixes a somewhat common installation error from a pip dependency)
        - Requires basic Python knowledge to review:
            - #3611 (Addresses an issue where sct_propseg would stall with user data)
        - Requires deeper understanding of SCT's background history:
            - #3643 (Replace sct_maths with sct_dmri_separate in course/tutorials)
            - #3605 (Bring back sct_testing command – soft approval already?)
            - #3541 (Extended descriptions for sct_deepseg models)
                - This one specifically needs an MRI background + knowledge of SCT/ivadomed's past models (Charley's work)

- SCT forum is down (expired certificate)
    - https://github.com/neuropoly/computers/issues/259

  - Alex will follow up on this

- Preparing for the next meeting: v5.5 Release
  - **Context:** In a previous meeting, we discussed + approved adopting time-based releases to better match our development workflow.
  - **Proposal:** Does a quarterly release schedule (e.g. January/April/July/October) sound reasonable?
    - Given an end-of-January cutoff for new work, is there any other (reasonably sized) pending work (besides the above PRs) that we want to fit into the release?
    - If not, then we can tentatively release v5.5 in the week following our next (Jan25) meeting, based on progress on action items.

- SCT Course 2021
  - **Context:** The lab provides a yearly workshop for researchers, physicians, etc. to learn how to use SCT. Our last workshop was in November 2021.
  - **1:** PDF Slides → Feedback from SCT Course
    - Some remaining feedback suggestions for presenter notes/warnings still need to be written (Action item for Julien? Joshua?)
    - Once this is finished, this task requires:
      - Someone with Desktop Mac + KeyNote to export the PDF with presenter notes
      - Upload to Google Drive
      - Create PR modifying Tutorials page with new link to drive
  - **2:** Did we receive permission to record the course? And, if so, are we able to upload the recording to our YouTube channel?
    - Y/N?

Research

- **Notice:** Upcoming SCT PMJ/CSA meeting: January 14, tentatively 5pm (Possibly 4pm?)

- Sandrine Bédard : PMJ CSA→ Overview of the project: 2022-01-11-PMJ-based CSA - Overview
  - **Context**: CSA, cross-sectional area
  - https://www.biorxiv.org/content/10.1101/2021.09.30.462636v1
  - **PMJ-based CSA tutorial**:
    - https://spinalcordtoolbox.com/user_section/tutorials/registration-to-template/shape-metric-computation/csa-pmj.html
  - **Aim of the project:**
    - Compare PMJ-based & Vertebral based vs Nerve rootlets
    - To do so, we need to identify nerve rootlets
    - Last fall, we acquired T2w 0,6mm resolution scans of 6 subjects with 3 different neck positions
    - Cervical enlargement

    - Nerve rootlets identification
    - Current manuscript: manuscript_csa_pmj

Action items

- ☐ JCA: Ask Alex to follow up on forum
- ☐ Noel: #3618
- ☐ Mathieu: #3611
- ☐ SB: #3643
- ☐ Next meeting: Preparing for the next meeting: v5.5 Release

2021-12-15

Attendees: Joshua Newton, Sandrine Bédard, Evan Béal, Julien Cohen-Adad,
Unable to attend: Nick Guenther, Benjamin de Leener, Alexandru Foias
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~JN: Create GitHub issues for any feedback items that don't already have them~~
  - SCT Course Feedback tracked in Issue #3612.
- ☑ ~~SB: Clean up notes to make sure they're easier to address in future meetings~~
  - JN: I transferred some of your notes to Issue #3612 ← Suggestion: We could use that issue as a place to keep the "cleaned up notes" so to speak.
- ☐ Everyone: Typos/changes in slides (Tracked in #3614)
  - JN: Some are complete, but other suggestions were a bit unclear to me

Housekeeping

- Next meeting (December 29th) is canceled due to holidays
  - First meeting of new year currently scheduled for January 12th
    - Sandrine Bédard : I may have a class at 4pm next semester
    - Meeting date is flexible, too!
  - Moved to -> Tuesday, 11th, 4pm

- Announcement: New software development intern hire for SCT
  - Youssef Benhissi - Student at ESPRIT, Tunisia
  - (Presumably) beginning with SCT after holidays, start of 2022
  - Ideas for starter tasks to help onboard new hires onto SCT?
    - Go through the tutorials
    - "Good first issues" ← Let them decide? Or hand-pick issues good for training?
    - Introductory MRI materials to read…? ANS: Avoid!

Software Development

- Sandrine Bédard : Follow up on SCT course:
  - I updated the issue with my notes, corrected some of the slides. (#3614)
  - Pending comments that need discussion:
    - ✅ P90: "Coverage of gray matter and MT scans for T2s, so there are less slices"
      - T2S covers fewer slices than MT, and so screws up slices from MT not covered by T2s
      - Warping field is undefined at edge -> Mention in presenter notes/comments

        - P104: “Replace `sct_maths` with `sct_dmri_separate_b0_and_dwi`”
            - JN: Why? The sct_maths command here is just meant to get a rough single-volume mage for creating a very approximate mask... I'm not sure I understand the point of separating the individual b0 and dwi volumes?
            - The script outputs the mean of just the dwi images, allowing us to exclude the b0 images

- Upcoming Release v5.5
    - Python 3.6 EOL is on December 23, 2021
    - JN: I think it could be good to wrap up some of the pending PRs and submit a release soon, so that future installs will be done using Python 3.7
    - Do we have enough time and people to review pending work before holidays? Or is it too close to be worth trying to rush?
        - Too rushed – wait until after the holidays.
        - Return –
    - If we want to try, which open PRs do we want to review, merge, and include in this release?
        - #3569: M1 Support (Mandatory)

- Difficulty finding reviewers for SCT PRs
    - JN: While I’m able to start new work, I can’t self-review my own work, so progress has stalled a little…
    - Also, many PR reviews have been quick “rubber stamp” approvals, rather than thorough reviews
    - Should we consider removing the requirement for reviews on SCT PRs?
        - Perhaps temporarily, e.g. only until new student hire in 2022

- Priorities for the future of SCT (v5.6 and beyond)
    - JN: SCT has many different tasks and ideas proposed from the past year:
        - General maintenance tasks (i.e. Small bugs, tweaks, etc. – there are many small issues that have been opened but not addressed yet.)
        - Reviewing currently open PRs…
        - #3612: Addressing SCT Course feedback **(High priority)**
            - Note: Not all of the comments need to be addressed
        - #3610: Improving the Windows user experience (WSL, Docker, native support)
            - Possibly addressed through other means ->
        - #3353: Adding manual correction script to SCT
        - #3046: Replacing Tensorflow scripts with new deepseg models **(High-priority)**
            - **Needs a student / JCA’s input**
            - **contrast-agnostic SC segmentation URL**
            - **MS lesion segmentation (mp2rage, other contrasts)**
            - **Uzay is not continuing as a MSc student**
            - **Nick wants to learn this**
        - #2979: Finishing the deep learning intervertebral disc labeling project **(High-priority)**

            - **See above**
        - #1526: Pip + packaging
            - Nick wants to finish this
        - #3194, #3597: Reproducibility/numerical stability of our existing scripts
        - Improvements to the test suite
            - (JN: This is a pet desire of mine – many scripts are woefully under-tested right now, and I wish I had the time to write new tests.)
    - For 2022, it would be helpful if we could pick just 1 or 2 areas we intend to address to make sure SCT can stay focused (without getting distracted by new developments on other issues).
        - Especially with new hires: Where do we want to direct their efforts?
    - TLDR from discussion:
        - **All** of these ideas are high priority in their own ways
        - But, as far as available staff go, each kind of task will fall to different people (devs vs grad students)
        - Devs can continue to work on maintenance + support tasks, while new research-oriented features can be handled by future grad students
        - There is pressure on

Research

- Evan's project → Becoming more linked with SCT as time goes on
    - Could it become an SCT feature in the future?
    - https://github.com/ivadomed/multimodal-registration

Action items

☐ JCA: Verify that 4pm time works with
☐ JCA/JN: Update p104 to replace sct_maths command

2021-12-01

Attendees: Joshua Newton, Julien Cohen-Adad, Evan Béal, Nick Guenther, Sandrine Bédard
Unable to attend:
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

SCT Course Debriefing

Link to the notes

- **High priority feedback items + ideas from course**
    - Joshua Newton
        - Dedicated Q&A time period
            - Some questions were basically "I have X data, how do I do Y?" which risks going on a tangent and losing the other participants
            - Maybe saving these questions for the end section ("try on your data") could help avoid derailing the discussion.
                - ANS: Was not enough time to get to the 4th section
            - Maybe we could collect questions ahead of time with a submission form put inside the initial email we send out?
                - Participants drained by end of day -- hard to do "try on your data" section anyway
    - Julien Cohen-Adad
        - *There are a lot of questions about manual corrections, when to do it, how , …*
            - Open issue -- higher priority given feedback from course
        - Video tutorials
            - Very helpful for newer users
        - *Recurring questions with WSL: where are my files??*
            - How do we want to support Windows?
                - Natively vs. WSL vs. Docker vs. VMs…
                - ANTs+propseg might be a blocker for native Windows support
                    - Needs exploration though -- halfway complete project from last year to build ANTs on Windows
                    - ANTsPy still needs to be explored (Perhaps easier to support Windows?)
    - Sandrine Bédard
        - We could add the correspondence of the line in the slides and in batch_single_subject.sh in the slide, would be easier to refer to for us and the users
            - Hard to stay in sync between the slides and the script (How to keep the page + line numbers in sync)
            - Add links between slides and script
                - Would these links break if the script/slides go out of date?

    - Literate programming tools from the R community: sweave/rknit;/rmarkdown, ported to python:
      - https://myst-nb.readthedocs.io/en/latest/
      - https://mpastell.com/pweave/
      - Simpler: https://pypi.org/project/mechanical-markdown/

  - A lot of of questions with WSL / terminal
    - Like can’t use my terminal when I run
      - xdg-open "/home/sabeda/qc_singleSubj_course/index.html"
      - For a WSL user, the window closes
      - We should add Add & at the end of this line “
    - I have a lot of tips & tricks that I learned. We could add a getting started with WSL page on the website.
    - JN: I very much agree! The windows experience needs to be tested more thoroughly, I think.
  - A lot of questions on registration → I felt like we lost some people with the specific questions sometimes
  - In my notes, I have a lot of issue to create or modifications in the slides (mistakes/typos)
  - More functional changes in the slides
    - 5.4-specific slides → Mark on each new feature?
    - fMRI motion correction params

- EB
  - People with an older version of SCT may not have downloaded the most recent version before the course → it would be good to clarify on the slides which version of SCT is associated with each feature or to point out when a feature is only available in the most recent version
  - Do you know if the (majority of) participants ran the various commands on their own computers ?
    - If not, I feel that it might be beneficial to take some time at the beginning of the day (for example with the SC segmentation) to make sure that SCT works on their computer and that they understand how to use it. Then, go a bit faster in presenting the different features to free up time at the end of the day to let the participants explore the features they are most interested in and try out those features on their own (potentially own data) with the help of the team.
    - JN: “make sure that SCT works” <- I very much agree with this!
      - Have a page that provides a set of test commands (e.g. “xdg-open”, “cmd.exe”, “fsleyes”, “sct_check_dependencies”, “sct_deepseg” etc.)
      - Then, help people with any issues before starting with the actual material, so we can minimize interruptions
    - Have the first break (or some kind of “checkpoint”) be immediately after the initial SCT setup so that we can make sure everyone is ready to run

commands.

Action items

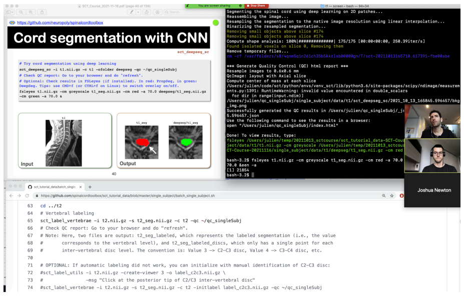
- ☑ ~~JN: Create GitHub issues for any feedback items that don't already have them~~
    - SCT Course Feedback tracked in Issue #3612.
        - JN: Make sure there are no iCloud links on spinalcordtoolbox.com
        - Explore manual correction issue (sct_manual_correction -- functionality from sister projects)
        - Consider creating video tutorials for difficult subjects
        - Explore better support for windows users (improving docs for existing solutions vs providing native support)
- ☐ SB: Clean up notes to make sure they're easier to address in future meetings
- ☐ Everyone: Typos/changes in slides (Tracked here) → Fix in iCloud link
    - Later on -> Export to PDF -> spinalcordtoolbox.com

2021-11-11

Attendees: Joshua Newton, Julien Cohen-Adad, Evan Béal
Unable to attend: Nick Guenther, Sandrine Bédard
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

SCT Course Material Runthrough #3

- Notes for presenting
    - Layout: (1) Slides top-left, (2) terminal top-right, (3) batch_single_subject.sh at bottom



Cord segmentation with CNN

sct_deepseg_sc

```
# Try cord segmentation using deep learning
sct_deepseg_sc -i t1.nii.gz -c t1 -ofolder deepseg -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Optional: Check results in FSLeyes (if installed). In red: PropSeg, in green:
DeepSeg. Tips: use CMD+f (or CTRL+f on Linux) to switch overlay on/off.
fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0 deepseg/t1_seg.nii.gz
-cm green -a 70.0 &
```

```
Segmenting the spinal cord using deep learning on 2D patches...
Reassembling the image...
Resampling the segmentation to the native image resolution using linear interpolation...
Binarizing the resampled segmentation...
Removing small objects above slice #174
Removing small objects above slice #174
Compute shape analysis: 100%|#############| 175/175 [00:00<00:00, 250.39iter/s]
Found isolated voxels on slice 0, Removing them
Remove temporary files...
rm -rf /var/folders/s8/4qnm5q1n261ch35b5kkclsb00000gn/T/sct-20211013165710.617391-fbe00abe

*** Generate Quality Control (QC) html report ***
Resample images to 0.6x0.6 mm
QcImage: layout with Axial slice
Compute center of mass at each slice
/Users/julien/code/sct/python/envs/venv_sct/lib/python3.6/site-packages/scipy/ndimage/measurem
ents.py:1391: RuntimeWarning: invalid value encountered in double_scalars
  for dir in range(input.ndim)]
/Users/julien/qc_singleSubj/single_subject/data/t1/sct_deepseg_sc/2021_10_13_165845.596457/bkg
_img.png
Successfully generated the QC results in /Users/julien/qc_singleSubj/_js
5.596457.json
Use the following command to see the results in a browser:
open "/Users/julien/qc_singleSubj/index.html"

Done! To view results, type:
fsleyes /Users/julien/temp/20211013_sctcourse/sct_tutorial_data-SCT-Cour
ject/data/t1/t1.nii.gz -cm greyscale /Users/julien/temp/20211013_sctcour
CT-Course-20211116/single_subject/data/t1/deepseg/t1_seg.nii.gz -cm red

bash-3.2$ fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0
70.0 &een -a
[1] 21854
bash-3.2$
```

```
cd ../t2
# Vertebral labeling
sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Note: Here, two files are output: t2_seg_labeled, which represents the labeled segmentation (i.e., the value
#       corresponds to the vertebral level), and t2_seg_labeled_discs, which only has a single point for each
#       inter-vertebral disc level. The convention is: Value 3 -> C2-C3 disc, Value 4 -> C3-C4 disc, etc.

# OPTIONAL: If automatic labeling did not work, you can initialize with manual identification of C2-C3 disc:
#sct_label_utils -i t2.nii.gz -create-viewer 3 -o label_c2c3.nii.gz \
#                -msg "Click at the posterior tip of C2/C3 inter-vertebral disc"
#sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -initlabel label_c2c3.nii.gz -qc ~/qc_singleSubj
```

-
    - Use Safari for QC, Chrome for Course Commands (For easy alt-tabbing)

- **LAST MEETING:** Ended during sct_run_batch multi_subject section
    - Link to newest copy of slides? ⇒

- **THIS MEETING:** Ended …

Action items

- Keynote presentation environment (for JCA)
    - ☐

- batch_single_subject.sh
    - ☐

- Slides
    - ☐ Presenter notes for sct_run_batch are out of date (parameters.sh -> parameters.yml)
    - ☐ BIDS datasets in sct_run_batch
        - Figure --
    - ☐ Showing git commit for dataset (spine-generic, etc.)
    - ☐ Sct_run_batch section is complicated -- “black box” -- bash scripting functions are difficult to explain on the spot.
        - Next course: Have “pure SCT” sct_run_batch script first
        -
    - ☐ Process_data.sh -> needs tweaking/verification

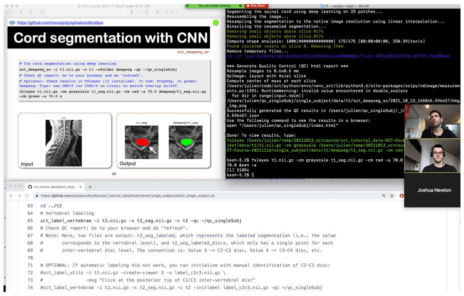
- SCT repo
    - ☐ Default value sct_run_batch jobs=1? Should be -1?

2021-11-08

Attendees: Joshua Newton, Julien Cohen-Adad, Evan Béal,Sandrine Bédard
Unable to attend: Nick Guenther ,
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

SCT Course Material Runthrough #2

- Notes for presenting
    - Layout: (1) Slides top-left, (2) terminal top-right, (3) batch_single_subject.sh at bottom



Cord segmentation with CNN

sct_deepseg_sc

```
# Try cord segmentation using deep learning
sct_deepseg_sc -i t1.nii.gz -c t1 -ofolder deepseg -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Optional: Check results in FSLeyes (if installed). In red: PropSeg, in green:
DeepSeg. Tips: use CMD+f (or CTRL+f on Linux) to switch overlay on/off.
fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0 deepseg/t1_seg.nii.gz
-cm green -a 70.0 &
```

```
Segmenting the spinal cord using deep learning on 2D patches...
Reassembling the image...
Resampling the segmentation to the native image resolution using linear interpolation...
Binarizing the resampled segmentation...
Removing small objects above slice #174
Removing small objects above slice #174
Compute shape analysis: 100%|##############| 175/175 [00:00<00:00, 250.39iter/s]
Found isolated voxels on slice 0, Removing them
Remove temporary files...
rm -rf /var/folders/s8/4qnm5q1n261ch35b5kkclsb00000gn/T/sct-20211013165710.617391-fbe00abe

*** Generate Quality Control (QC) html report ***
Resample images to 0.6x0.6 mm
QcImage: layout with Axial slice
Compute center of mass at each slice
/Users/julien/code/sct/python/envs/venv_sct/lib/python3.6/site-packages/scipy/ndimage/measurem
ents.py:1391: RuntimeWarning: invalid value encountered in double_scalars
  for dir in range(input.ndim)]
/Users/julien/qc_singleSubj/single_subject/data/t1/sct_deepseg_sc/2021_10_13_165845.596457/bkg
_img.png
Successfully generated the QC results in /Users/julien/qc_singleSubj/_js
5.596457.json
Use the following command to see the results in a browser:
open "/Users/julien/qc_singleSubj/index.html"

Done! To view results, type:
fsleyes /Users/julien/temp/20211013_sctcourse/sct_tutorial_data-SCT-Cour
ject/data/t1/t1.nii.gz -cm greyscale /Users/julien/temp/20211013_sctcour
CT-Course-20211116/single_subject/data/t1/deepseg/t1_seg.nii.gz -cm red

bash-3.2$ fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0
70.0 &een -a
[1] 21854
bash-3.2$
```

```
cd ../t2
# Vertebral labeling
sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Note: Here, two files are output: t2_seg_labeled, which represents the labeled segmentation (i.e., the value
#       corresponds to the vertebral level), and t2_seg_labeled_discs, which only has a single point for each
#       inter-vertebral disc level. The convention is: Value 3 -> C2-C3 disc, Value 4 -> C3-C4 disc, etc.

# OPTIONAL: If automatic labeling did not work, you can initialize with manual identification of C2-C3 disc:
#sct_label_utils -i t2.nii.gz -create-viewer 3 -o label_c2c3.nii.gz \
#                -msg "Click at the posterior tip of C2/C3 inter-vertebral disc"
#sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -initlabel label_c2c3.nii.gz -qc ~/qc_singleSubj
```

    - Use Safari for QC, Chrome for Course Commands (For easy alt-tabbing)

- **LAST MEETING:** Ended page 100-101 of SCT_Course_2021-11-16_copy
    - Action items almost all completed.
    - See also: sct_tutorial_data PR #4
- **THIS MEETING:** Ended during sct_run_batch multi_subject section

Action items

- Keynote presentation environment (for JCA)
    - ☐ Downloading files on Safari might be a bit of a hassle
    - ☐ QC demo → mark e.g. segmentations as fail (to demo scripts for manual correction)

- batch_single_subject.sh
    - ☑ ~~Provide "Check QC report" comment for dMRI moco registration~~

- Slides
    - ☐ Drop sct_propseg as first option and focus mainly on sct_deepseg + move sct_propseg as an alternative option for edge cases (eg: ex vivo extracted spine)
        - Q: Do we want to do this for this SCT Course, or wait until the next one?
    - ☑ ~~Fix old buggy Size[vox] values in MTR section (and verify they match online tutorial pages)~~
    - ☑ ~~Fix % error in presenter notes for "Extract MTR in white matter" p103 (67vox ==> ??% error?)~~

  - ☑ ~~Provide more details for new MOCO QC pages (~~
  - ☑ ~~Update p110 “Quality Control” (list of supported functions)~~
  - ☑ ~~Second QC page (p111) with edited screenshot to show “download QC Fails/Artifacts” buttons~~
  - ☑ ~~Update QC presenter notes to demo manual correction for failed sct_deepseg_sc~~
  - ☐ Live demo for FSLeyes -> Remember to switch to T2* folder (Add note in slides?)
  - ☑ ~~Create a dedicated section for FMRI :tada:~~
  - ☑ ~~sct_image/sct_maths pages -- are these up to date?~~
  - ☐ Live demo for demonstrating sct_run_batch using spine-generic project?

- SCT repo
  - ☐ QC resizing page → Overlapping images and buttons
  - ☐ QC reports -> Text overlapping
  - ☐ https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3353 -> Came up for manual correction demo in QC.
  - ☐ Reminder for text-wrapping caused by Python 3.7 upgrade (but, not an issue for the stable release -- v5.4, so this won’t be a problem).

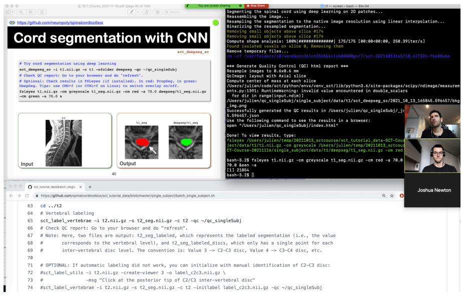
2021-11-04

Attendees: Joshua Newton, Julien Cohen-Adad, Evan Béal, Nick Guenther
Unable to attend: Sandrine Bédard,
Moderator: Julien Cohen-Adad
Minutes: Joshua Newton

SCT Course Material Runthrough #1

- Evan doesn't have edit access → In Google Group?
    - Fixed! Evan was in the NeuroPoly Google Group, but NP GG didn't have editing access to this document until now.

- Notes for presenting
    - Layout: (1) Slides top-left, (2) terminal top-right, (3) batch_single_subject.sh at bottom



Cord segmentation with CNN

sct_deepseg_sc

```
# Try cord segmentation using deep learning
sct_deepseg_sc -i t1.nii.gz -c t1 -ofolder deepseg -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Optional: Check results in FSLeyes (if installed). In red: PropSeg, in green:
DeepSeg. Tips: use CMD+f (or CTRL+f on Linux) to switch overlay on/off.
fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0 deepseg/t1_seg.nii.gz
-cm green -a 70.0 &
```

```
Segmenting the spinal cord using deep learning on 2D patches...
Reassembling the image...
Resampling the segmentation to the native image resolution using linear interpolation...
Binarizing the resampled segmentation...
Removing small objects above slice #174
Removing small objects above slice #174
Compute shape analysis: 100%|#############| 175/175 [00:00<00:00, 250.39iter/s]
Found isolated voxels on slice 0, Removing them
Remove temporary files...
rm -rf /var/folders/s8/4qnm5q1n261ch35b5kkclsb00000gn/T/sct-20211013165710.617391-fbe00abe

*** Generate Quality Control (QC) html report ***
Resample images to 0.6x0.6 mm
QcImage: layout with Axial slice
Compute center of mass at each slice
/Users/julien/code/sct/python/envs/venv_sct/lib/python3.6/site-packages/scipy/ndimage/measurem
ents.py:1391: RuntimeWarning: invalid value encountered in double_scalars
  for dir in range(input.ndim)]
/Users/julien/qc_singleSubj/single_subject/data/t1/sct_deepseg_sc/2021_10_13_165845.596457/bkg
_img.png
Successfully generated the QC results in /Users/julien/qc_singleSubj/_js
5.596457.json
Use the following command to see the results in a browser:
open "/Users/julien/qc_singleSubj/index.html"

Done! To view results, type:
fsleyes /Users/julien/temp/20211013_sctcourse/sct_tutorial_data-SCT-Cour
ject/data/t1/t1.nii.gz -cm greyscale /Users/julien/temp/20211013_sctcour
CT-Course-20211116/single_subject/data/t1/deepseg/t1_seg.nii.gz -cm red

bash-3.2$ fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0
70.0 &een -a
[1] 21854
bash-3.2$ 
```

```
63  cd ../t2
64  # Vertebral labeling
65  sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -qc ~/qc_singleSubj
66  # Check QC report: Go to your browser and do "refresh".
67  # Note: Here, two files are output: t2_seg_labeled, which represents the labeled segmentation (i.e., the value
68  #       corresponds to the vertebral level), and t2_seg_labeled_discs, which only has a single point for each
69  #       inter-vertebral disc level. The convention is: Value 3 -> C2-C3 disc, Value 4 -> C3-C4 disc, etc.
70
71  # OPTIONAL: If automatic labeling did not work, you can initialize with manual identification of C2-C3 disc:
72  #sct_label_utils -i t2.nii.gz -create-viewer 3 -o label_c2c3.nii.gz \
73  #                -msg "Click at the posterior tip of C2/C3 inter-vertebral disc"
74  #sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -initlabel label_c2c3.nii.gz -qc ~/qc_singleSubj
```

-
    - Use Safari for QC, Chrome for Course Commands (For easy alt-tabbing)

Action items

- Keynote presentation environment (for JCA)
    - ☐ Update local Keynote installation → Requires macOS 11.0 → cannot do :-(
    - ☐ Fix missing fonts

- batch_single_subject.sh
    - ☑ ~~Add new QC command to script, etc. → following what has been added on "new" slide 57~~
    - ☑ ~~Fix "Toggle overlay" comments for FSLeyes are actually for QC~~
    - ☑ ~~Use one line for commands that are optional/commented out (sct_label_utils, lines 72-73) optionally, see if it can be left uncommented without disrupting the pipeline~~
    - ☑ ~~Undo the commands that were split over several lines for readability~~

- Slides
    - ☑ ~~Add "-qc" for sct_label_utils 3,9 →~~
        - EDIT: Actually, don't add QC for this step because it doesn't show anat image (so it's hard to assess the quality of the labels)

        - But, we can provide instructions to generate a QC report using sct_qc
    - ☑ ~~Verify that the values are correct for sct_process_segmentation (using the registered template from the slide immediately previous) → compute CSA slides 66 →69~~
    - ☐ Drop sct_propseg as first option and focus mainly on sct_deepseg + move sct_propseg as an alternative option for edge cases (eg: ex vivo extracted spine)
    - ☑ ~~SCT forum link https://forum.spinalcordmri.org/c/sct/8~~
    - ☑ ~~Have a slide describing new QC reporting functionality (marking as pass/fail/etc.)~~
    - ☑ ~~“Next steps” slide -> add sct_deepseg (describe existing models), contrast agnostic, etc.~~

- SCT repo
    - ☑ ~~Voxel size in sct_extract_metric is incorrect (sum vs. average) -> urgent bugfix, necessitates v5.5~~
        - Actually the voxel size was OK! See this GitHub comment for explanation.
    - ☑ ~~Progress bar in “_gm” looks really good! Are we using it elsewhere? E.g. sct_deepseg~~
        - ANS: This is Keras’ progress bar. It appears when iterating through a batch. Specifically, sct_deepseg_gm runs slice-by-slice predictions on axial slices, so as a whole the slices are treated as a batch.
    - ☑ ~~Investigate warning given by PMJ-based QC~~

- STOP: page 100 - 101 (Follow-up meeting - Monday, Nov 8, 12:30pm)

2021-11-03

Attendees: Joshua Newton, Sandrine Bédard, Julien Cohen-Adad, Evan Béal, Nick Guenther
Unable to attend:
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~None~~

Software Development

- Joshua Newton : Quick updates for in-progress PRs
  - #3493: SCT Tutorials ⇒ Merged 🎉
  - #3361: Python 3.7 ⇒ Merged 🎉
  - #3510: Patch2Self denoising ⇒ Stalled (waiting on dipy release for upstream bugfix, ~Nov 7)
  - #3541: sct_deepseg -task-description ⇒ Work needed
    - Refactor to only output 1 task at a time
    - Long descriptions needed for older ivadomed models (see this slack thread.)
    - Will follow up when I have a little more time

- Joshua Newton : Harvard Course Preparation
  - THINKIFIC site (re: Harvard email)
    - Have we been granted access yet?
    - *"I will have set up the THINKIFIC site for that. And I'll make sure that whomever you wish will have access to that site, as if you were enrolled in the program, so you can see what the enrolled participants would see."*
  - Lab members providing course assistance
    - Any info on who will need to be present + how we will provide assistance? (Zoom, web chat, etc.)
    - Depends on THINKIFIC site -> Wait to hear back
  - SCT meetings are Nov 3 (today) and Nov 17 (i.e. after Nov 16 Harvard Course 😟)
    - Should we do another in-between meeting to prepare for the course?
      - Meeting 1: Plans to go over entire tutorial -> 3hr block?
        a. Thursday, Nov 4, 2-4pm (No conflict with Pizza :D)
      - Meeting 2: Depends on info about THINKIFIC site → plan more once we hear back
    - Sandrine Bédard : Nov 17 → I am assisting the workshop
      - Cancel SCT dev meeting
  - Evan: can you register?

Research

- Sandrine Bédard → Scanning for PMJ project
    - We acquired T2w scans at 0,7mm and 0,6mm, 0,6mm was better to see the spinal rootlets (🎉)
        - Rootlets -> true reference of spinal levels
        - Will be used for comparing level-based vs PMJ-based methods for predicting spinal levels
        - Preprint article: https://www.biorxiv.org/content/10.1101/2021.09.30.462636v1.full
    - We discussed also detect the cervical enlargement to normalize distance with the PMJ
        - To consider the spinal cord length variation between subjects
    - Maxime's involvement ⇒ Doesn't have access to scans yet
        - Action item?
    - Next scan on thursday
        - Only 1 participant
        - Survey ⇒ All have answer
        - Only 30m for scanning ⇒ focus on 0,6mm scan
    - Find a solution to… (? Didn't hear)
    - In the future, include Benjamin (de Leener?) in these discussions
        - Worked on similar data at end of PhD in Tokyo

- Joshua Newton : (Very short) update for DL-based vertebral labeling
    - What I've been working on:
        - sct-testing-large (finding suitable subjects for evaluation)
            -
        - Evaluation metrics (updating vertebral-labeling-validation)
            -
    - I hope to present preliminary evaluation results soon after the SCT Course has finished

- Maxime SCT install (julien)
    - https://neuropoly.slack.com/archives/C0135PQ0XGT/p1635967846006100?thread_ts=1635288906.002400&cid=C0135PQ0XGT
    - ⇒ Follow up on slack

Action Items

☐ Follow up about THINKIFIC site in emails ⇒ Email sent, waiting to hear back on repsonse
☑ ~~Cancel SCT meeting~~
☑ ~~Sandrine Bédard : Send Maxime recent PMJ scans~~
☐ Joshua Newton : Follow up on Maxime's failing SCT install

2021-10-21

Attendees: Joshua Newton, Sandrine Bédard, Julien Cohen-Adad, Evan Béal, Alexandru Foias
Unable to attend: Nick Guenther
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~Evan: Possibly try to run through the SCT tutorials (installing SCT, trying to run some commands, etc.)~~
- ☑ ~~JCA: Update Harvard agenda ("lecture" vs "demo" in time-block headers)~~
  - "Lecture + Hands-on" ×3 + "Process your own data"
- ☑ ~~JCA: Look into options for supporting users during SCT course (virtual, chatroom, etc.)~~
  - had a chat with rob+rob
- ☑ ~~JN: Fix sizing on images from earlier tutorials~~
- ☑ ~~JN: Open sct_deepseg issue for documentation~~
- ☑ ~~JN: Review Sandrine's new PMJ tutorial PR~~
- ☑ ~~JN: Try exporting iCloud presentation to e.g. Google Slides, PDF, etc. for distributing notes~~

Software Development

- Joshua Newton : Tutorial PR (#3493)
  - PMJ tutorial added + almost all review feedback has been addressed.
  - 2 review comments remain that need discussion (see this comment)
    - Addressed during meeting
  - Once those are done, ready to be approved/merged? (Assuming there are no big changes for the SCT Course PDFs.)

- Joshua Newton : SCT Course PDF
  - Google Slides version of Course PDF
    - iCloud -> PowerPoint -> Slides == ❌ (Formatting conversion did not work well)
    - resolution: export iCloud/keynote → PDF and share the PDF (host it in slideshare).
  - PMJ tutorial added (Page 69 of SCT Course iCloud)

- Joshua Newton : External contributions
  - Patch2Self denoising (#3510)
    - I've pinged one more time, and we've agreed for me to finish up the PR.
  - 7T deepseg model PR (#3527) has been merged! 🎉
  - sct_deepseg "extended description" PR (#3541)
    - Nilser3 has opened a second PR for this! :D

        - Feedback given on the weekend, waiting for response. (Nilser is generally quite responsive, though!)

- Evan Beal: Tutorial feedback
    - Large amount of tutorials ⇒ Information dense, taxing to get through in one session.
    - SCT Course is more information light ⇒ Can come back to tutorials afterwards to refresh memory + read further
    - RTD theme (Visual clarity/usability?)
        - Not much to say off the top of head ⇒ Compare with ivadomed?

Research

- Sandrine: PMJ project ⇒ Next (next) Friday, scanning!

Action Items

- ☐

2021-10-13

Attendees: Joshua Newton, Sandrine Bédard, Alexandru Foias, Evan Béal, Julien Cohen-Adad
Unable to attend:, Nick Guenther
Moderator: Joshua Newton
Minutes: Sandrine Bédard

Context for this extra meeting

- SCT tutorial webpages were difficult to present, due to wordy paragraph sections
- Idea (proposed last meeting): Use the slides for the text-heavy theory sections, but still use the webpages for the hands-on sections
- An action item from the last meeting was to try out this idea.
- This meeting is to discuss the progress made on the issue since the last meeting.

Check last week's action items

- ☐ JCA: Update Harvard agenda ("lecture" vs "demonstrations" in time-block headers)
- ☐ JCA: Look into options for providing support for users during the virtual SCT course (chatroom, etc.)

SCT Course planning

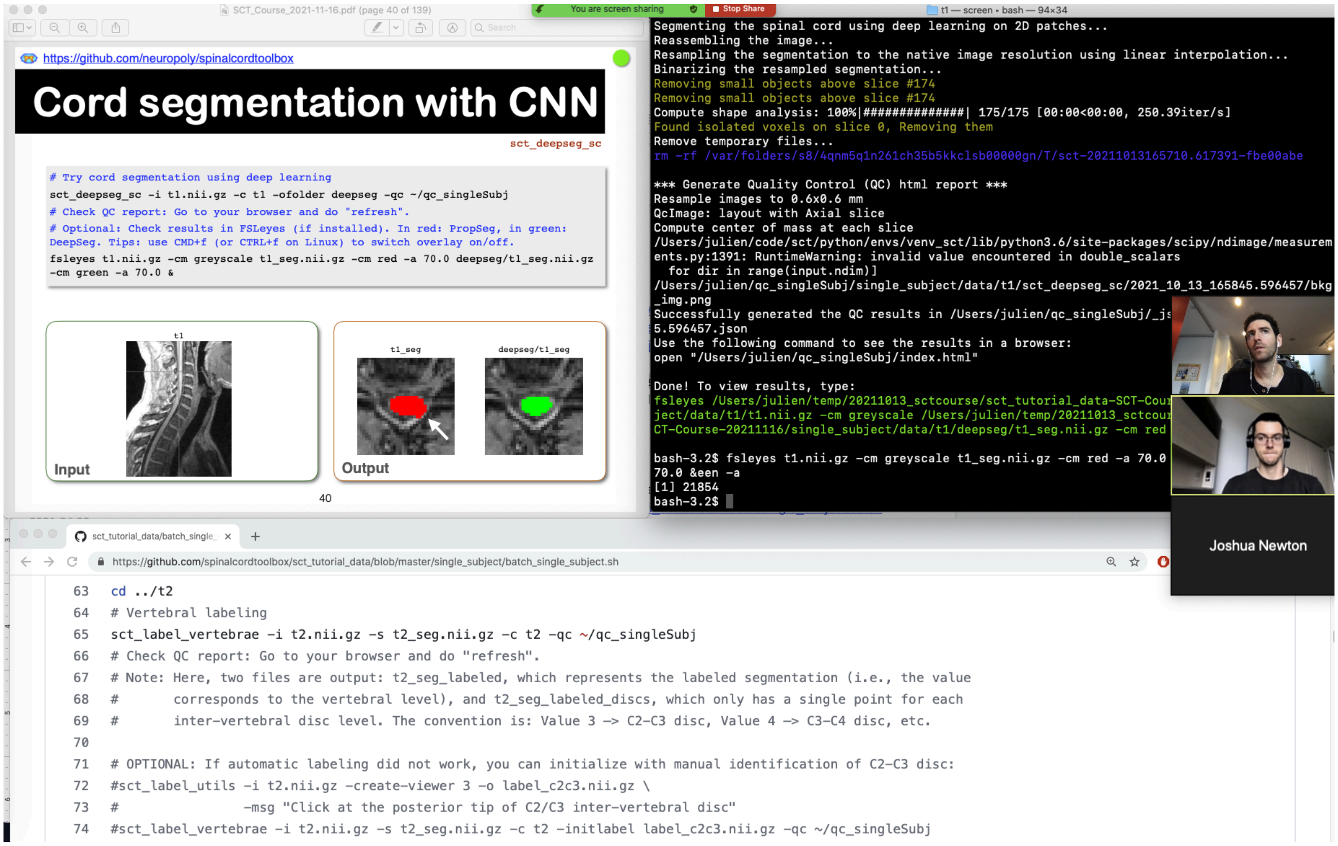
- Joshua Newton: Alternate idea proposal: Continue to use full slide deck for SCT Course
  - Reasoning: `sct_tutorial_data` can act as the "single source of truth" for both the webpage tutorials and the slide deck. (So, updating the slide deck each year should not be too much extra work, since we can just diff `batch_single_subject.sh` to see the new changes.)

  - Joshua Newton: SCT_Course_2021-11-16 (Updated from 2020-01-21)
    - Summary of changes so far.
    - TODOs
      - Update "What's next?" page with future roadmap for SCT…
        a. Skip page in presentation
      - Consider porting the new "How many labels should I use for registration?" page to slide deck (maybe just speaker notes are necessary though)
        a. Slide 59 → there is a warning about it
        b. We can specify at the start that there is a complete tutorial so that people can read up webpages after the course
      - Consider moving fMRI section into dedicated section (rather than "other features")
        a. +1

- Sandrine Bédard : PMJ-based tutorial: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3542
    - https://spinalcordtoolbox--3542.org.readthedocs.build/user_section/tutorials/registration-to-template/shape-metric-computation/csa-pmj.html
        - Side comment: Explicitly mention CSA in title of section
    - Todo for JN: Add command to `batch_single_subject.sh` as well
    - JN: Should we include it in the SCT Course (add to slide deck) as well?
        - Very much worth mentioning!!!
        - Between slide 68 and 69

- Notes from testing out iCloud slide deck presentation

    - iCloud link → can't access when there is too many people
    - iCloud link is not great for distribution. Migrate iCloud -> Google Slides? PDF?
    - Update commands to dataset
    - Copy/paste commands from batch_single_subject.sh to the terminal (see layout below)
    - Presentation layout:



https://github.com/neuropoly/spinalcordtoolbox

Cord segmentation with CNN

sct_deepseg_sc

```
# Try cord segmentation using deep learning
sct_deepseg_sc -i t1.nii.gz -c t1 -ofolder deepseg -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Optional: Check results in FSLeyes (if installed). In red: PropSeg, in green:
DeepSeg. Tips: use CMD+f (or CTRL+f on Linux) to switch overlay on/off.
fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0 deepseg/t1_seg.nii.gz
-cm green -a 70.0 &
```

40

```
Segmenting the spinal cord using deep learning on 2D patches...
Reassembling the image...
Resampling the segmentation to the native image resolution using linear interpolation...
Binarizing the resampled segmentation...
Removing small objects above slice #174
Removing small objects above slice #174
Compute shape analysis: 100%|##############| 175/175 [00:00<00:00, 250.39iter/s]
Found isolated voxels on slice 0, Removing them
Remove temporary files...
rm -rf /var/folders/s8/4qnm5q1n261ch35b5kkclsb00000gn/T/sct-20211013165710.617391-fbe00abe

*** Generate Quality Control (QC) html report ***
Resample images to 0.6x0.6 mm
QcImage: layout with Axial slice
Compute center of mass at each slice
/Users/julien/code/sct/python/envs/venv_sct/lib/python3.6/site-packages/scipy/ndimage/measurem
ents.py:1391: RuntimeWarning: invalid value encountered in double_scalars
  for dir in range(input.ndim)]
/Users/julien/qc_singleSubj/single_subject/data/t1/sct_deepseg_sc/2021_10_13_165845.596457/bkg
_img.png
Successfully generated the QC results in /Users/julien/qc_singleSubj/_js
5.596457.json
Use the following command to see the results in a browser:
open "/Users/julien/qc_singleSubj/index.html"

Done! To view results, type:
fsleyes /Users/julien/temp/20211013_sctcourse/sct_tutorial_data-SCT-Cour
ject/data/t1/t1.nii.gz -cm greyscale /Users/julien/temp/20211013_sctcour
CT-Course-20211116/single_subject/data/t1/deepseg/t1_seg.nii.gz -cm red

bash-3.2$ fsleyes t1.nii.gz -cm greyscale t1_seg.nii.gz -cm red -a 70.0
70.0 &een -a
[1] 21854
bash-3.2$
```

https://github.com/spinalcordtoolbox/sct_tutorial_data/blob/master/single_subject/batch_single_subject.sh

```
cd ../t2
# Vertebral labeling
sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -qc ~/qc_singleSubj
# Check QC report: Go to your browser and do "refresh".
# Note: Here, two files are output: t2_seg_labeled, which represents the labeled segmentation (i.e., the value
#       corresponds to the vertebral level), and t2_seg_labeled_discs, which only has a single point for each
#       inter-vertebral disc level. The convention is: Value 3 -> C2-C3 disc, Value 4 -> C3-C4 disc, etc.

# OPTIONAL: If automatic labeling did not work, you can initialize with manual identification of C2-C3 disc:
#sct_label_utils -i t2.nii.gz -create-viewer 3 -o label_c2c3.nii.gz \
#                -msg "Click at the posterior tip of C2/C3 inter-vertebral disc"
#sct_label_vertebrae -i t2.nii.gz -s t2_seg.nii.gz -c t2 -initlabel label_c2c3.nii.gz -qc ~/qc_singleSubj
```

Action Items

- ☐ JN: Review Sandrine's new PR
- ☐ JN: Try exporting iCloud presentation to e.g. Google Slides, PDF, etc. for distributing notes

2021-10-06

Attendees: Joshua Newton, Sandrine Bédard, Julien Cohen-Adad, Evan Béal
Unable to attend: Nick Guenther, Alexandru Foias
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~SB: Make an SCT issue for making Jupyter notebooks/other interactive tutorials~~
- ☑ ~~SB: Finish up help description for PR #3515~~
- ☑ ~~NG: talk to Joshua about what I can do with pytorch.~~
    - Also discussed at yesterday's ivadomed meeting
- ☑ ~~JN: Follow up with external contributor for denoise2patch PR~~
    - I pinged Shreyas last week, and they responded that they'll try to get to it "early next week" (i.e. right now). However, there have been no changes yet.
    - If there is no action by the end of this week, I could step in to help move the PR along.

Software Development

- Joshua Newton: SCT v5.4 released!
    - Next release (v5.5): December? (To address Python 3.6 EOL)
    - If so, then v5.4 will be used for the Harvard SCT course…
        - Sounds good for now!
        - Depends on what happens between now and then, of course (bugs, etc.)

- Joshua Newton: SCT Course tutorials
    - Srishti has given her review! (Working on this today.)
    - However, since she has left the lab, I can't discuss the feedback directly with her anymore 😅
        - Evan: Possibly run through the tutorials after feedback from Srishti has been addressed
    - @JCA -- Between now and the Harvard course (November 16), can you help with review and final approval to make sure that these tutorials are suitable for presenting?
    - Sandrine Bédard: I am planning to add the PMJ-based tutorial next week (reading week)
    - find a solution for presenting the course via the web browser-- pb: the "sliding" and the presence of a lot of text is not super audience-friendly. Ex of embedded slides to get inspiration from: https://inria.github.io/scikit-learn-mooc/ml_concepts/slides.html
    - Reworking the PAM50 template material to be "presentation friendly"
    - "Next" button no longer on the top of slides after theme change
    - Structure/categories do not make as much logical sense to people with a medical imaging background

        - Nix “4D”, “Antomical” categories, etc.
        - 4D → fMRI and dMRI
    - Missing context blurbs at the start of each tutorial
    - Sidebar doesn’t automatically seek to position from before (lots of unnecessary scrolling)
    - IDEA: Have theory in slides ⇒ Then put link to the “hands-on” pages of the tutorials from the slides.
        - Requires some restructuring -- separate theory/hands-on in tutorials
    - Introductory/context materials missing from spinalcordtoolbox.com documentation
        - Comparison with other MRI imaging software
        - “What SCT is capable of doing” -- Example projects/applications (5/10m)
        - “Lesson 00” -- IT prerequisites (“How to use the terminal”, etc.)
        - Updating links to installation
    - Image size for the first set of tutorials
    - ⇒ Schedule a separate SCT meeting to go through tutorials?
        - Next week same time
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3493

- Joshua Newton : External contribution -- 7T SC/GM `sct_deepseg` PR (#3527)
    - PR looks good!
    - To what extent should we test this new model, though? Ideas:
        - Treat new deepseg models like this as a black box and only run barebones test (i.e. test that the model can be downloaded and inference generates the expected output files without error, but don’t check any specific results)
        - Test specific results, checking that the segmentation looks good against ground truth
            - Is this necessary? We are already sort of presenting the model “as-is” to our users, and trusting that the model has been validated by external contributors.
        - Documentation does a long way → Linking to associated paper in the usage
            - Long description for sct_deepseg tasks? (A place to put more detailed information about each individual model.)

Research

- Joshua Newton : Intervertebral disc labeling update
    - I’m hoping to change priorities back to SCT dev issues
        - Disc labeling project was taking time away from SCT -- hence why I have not made much progress on pending issues (tutorials, recent bugs)
    - Current state of project:
        - HourglassNet was trained on straightened data using IMED #852
        - Both models (Countception, Hourglass) can now be tested using SCT #2679
        - Suitable test subjects selected from sct-testing-large using new metadata
        - vertebral-labeling-validation scripts now function properly

        - Remaining steps:
            - Perform a comparison between approaches
            - Try to improve performance of HourglassNet using hyperparameter tuning/data augmentation/etc.

- Sandrine Bédard :
    - Manuscript on CSA normalization submitted to NeuroImage 🎉

Action Items

☐ Evan: Possibly try to run through the SCT tutorials (installing SCT, trying to run some commands, etc.)
☐ JCA: Update Harvard agenda (“lecture” vs “demo” in time-block headers)
☐ JCA: Look into options for supporting users during SCT course (virtual, chatroom, etc.)
☐ JN: Fix sizing on images from earlier tutorials
☐ All: Think about how to present materials (slides vs. tutorials, avoiding maintaining 2 sources of truth)
☑ ~~JN: Open sct_deepseg issue for documentation~~

2021-09-22

Attendees: Nick Guenther, Joshua Newton, Sandrine Bedard, Julien Cohen-Adad, Alexandru Foias
Unable to attend:
Moderator: Nick Guenther
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~AF: Check if Ferguson would be suitable for testing AVX-less PCs (Python 3.7)~~
    - Ferguson has Intel(R) Core(TM) i5-4590 CPU @ 3.30GHz, which seems to have AVX capabilities
    - JN: Above CPU is "Haswell" microarchitecture, which does support AVX (unfortunately)
    - Tested using QEMU VM -- good enough for now. :)
    - QEMU link: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3509
- ☑ ~~JN: Come up with more concrete details re: next steps for intervertebral disc detection~~
    - Next steps are documented in the body of ivadomed PR #852
    - Current step: Fix issues in vertebral-labeling-validation repo to compare approaches
    - No results to report yet, though (still just "setting up" so to speak)
- ☑ ~~JCA: Respond into forum post~~
- ☑ ~~All: Brainstorm ideas for internship projects, propose at next meeting?~~

Software Development

- JN: **SCT Course Tutorials** (#3493)
    - Currently part-way through Srishti's reviews
    - Not much to report yet

- JN: Not much new has happened since the previous meeting
    - JN's efforts have been focused on intervertebral disc labeling project
    - No new contributions/updates from other contributors, either

- NG: Development velocity? (Knowledge of codebase, ease of making changes)
    - Suggestion 1: more people?
    - Suggestion 2: spend time training (me) on the methods
    - Suggestion 3: if possible, do internship projects as separate repos to reduce future complexity

Research

- **Internship project ideas**
    - JN: PyTorch-based replacements for `sct_deepseg_gm` and `sct_deepseg_lesion`
        - Rationale: The Keras/Tensorflow dependencies will still exist until we address the remaining two tools (See also: #3046)
        - Recreate the Keras/Tensorflow models to PyTorch could be a friendly and straightforward research project (since the methodologies for training the existing tools have already been established and published)
        - Aside: `sct_deepseg_gm` is currently restricted to T2* contrast, so perhaps an extended project goal could be to include other contrasts...
            - Is this feasible, though? (Available training data, manual GM ground truth segmentation effort, etc.)
            - https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord
        - Possibly a project for Nick?
    - Sandrine Bédard :
        - QC for sct_deepseg https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3325
            - For tumors, there could be other visualisation than axial only for example
        - Implement interactive tutorials
            - prerequisite: know HTML/JS
            - NG: something like https://replit.com/ ?
            - JCA: something on https://colab.research.google.com/ ?
                - example: https://mathieuboudreau.github.io/pipelines-jupyter-book/01/sct_mtsat.html
                - NG: runnable on https://binder.conp.cloud/
- Sandrine Bédard : CSA normalization
    - Discuss what description, info, warnings to include:
        - https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3515#pullrequestreview-751827014
- JCA: external contribution (denoise2patch)
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3234
    - PR: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3510
- JCA: future student MD resident in radiology (pizza tmr)

Action Items

☑ ~~SB: Make an SCT issue for making Jupyter notebooks/other interactive tutorials~~
☑ ~~SB: Finish up description of https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3515#pullrequestreview-751827014~~
☐ NG: talk to Joshua about what I can do with pytorch.
☐ JN: Follow up with external contributor for denoise2patch PR

- ☑ ~~All(ish): go to Pizza, meet Maxime~~

2021-09-08

Attendees: Julien Cohen-Adad, Sandrine Bedard, Joshua Newton, Alexandru Foias
Unable to attend: Nick? Paul?
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Check last week's action items

- ☐ JN: Keep in touch with SB re: PMJ-based CSA tutorial

Software Development

- Joshua Newton: Progress Updates
  - **Python 3.6 EOL** (#3361)
    - We should now be able to upgrade to Python 3.7, because users with old CPUs can install this alternate Tensorflow wheel. 🎉
      - ☐ Testing: Ferguson, older CPU? Potentially…
    - Question: How should we handle installing this wheel?
      - ☑ ~~Detect AVX error in `install_sct`, then install on behalf of our users~~
        - Newer users, not IT-proficient, easier to support
      - ☐ Let the user install Tensorflow manually
        - Possibly more viable once we're pip-installable

  - **SCT Course Tutorials** (#3493)
    - Waiting for review/approval. (Srishti has volunteered to run through the tutorials.)
    - Question: Is the Harvard SCT Course still scheduled for approx. November 15?
      - ☐ It is 😊 → https://education.martinos.org/home/martinos-spinal-cord-workshop/
      - ☐ <3 !

  - **Intervertebral disc labeling** (#2679)
    - I will be focusing more on this project in the coming weeks, and will try to provide more in-depth progress updates at future meetings.
      - ☐ TODOs ⇒ Documentation, Training model, Evaluation, Comparison with existing approach…
      - ☐ Internship project?
      - ☐ Project for Joshua? (Not time-limited by 3-4mo internship)
      - ☐ Details for next steps are somewhat vague -- Perhaps prepare something more concrete and propose at next meeting ⇒ JN TODO

- Unanswered SCT forum post: https://forum.spinalcordmri.org/t/some-questions-regarding-the-analysis-of-mri-data/740
    - Hard to help… Hm.

Research

- Sandrine Bédard : CSA normalization (#3515)
    - Question: Where to store model files? (2 small .csv weight files)
        - ☑ ~~Inside the SCT repo?~~
            - Data subfolder? Not in the repo initially, created by sct_download_data
            - ANS: Create a data folder in CSA PR
        - ☐ Hardcode the values themselves in the script?
        - ☐ In a separate repo?
            - Other models are stored this way
            - Good landing page for research links (README.md, fixed link)
            - Aside: Possibly write a guide for sct_download_data “How to add a new model”

    - Question: After this, release 5.4?
        - ☐ Any other PRs? ⇒ Nothing pressing

Other

- September -> New students -> New Internship project ideas
    - 3 students who have contacted Julien
        -
    - Similar in scope to Clara Giroux’s internship project (QC)
    - Issue label for potential ideas: https://github.com/spinalcordtoolbox/spinalcordtoolbox/labels/good%20internship%20project

Action items

- ☑ ~~AF: Check if Ferguson would be suitable for testing AVX-less PCs~~
    - Note: Viable CPUs include Core 2 or Nehalem/Westmere families of Intel CPUs
    - Sandy Bridge is too late (first CPU to support AVX)
    - ferguson has Intel(R) Core(TM) i5-4590 CPU @ 3.30GHz, which seems to have AVX capabilities
- ☐ JN: Come up with more concrete details re: next steps for intervertebral disc detection
- ☐ JCA: Respond into forum post
- ☐ All: Brainstorm ideas for internship projects, propose at next meeting?

~~2021-08-24~~

Attendees: Meeting cancelled due to lab members on vacation
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~NC: Review SB's data management PR~~
- ☑ ~~SB/PB: Check status of contrast agnostic softseg with Uzay, etc.~~
- ☑ ~~SB: Review tutorials PR~~
- ☑ ~~JN: Get reviews on SCT course tutorials PR~~
- ☐ JN: Keep in touch with SB re: PMJ-based CSA tutorial
- ☑ ~~JCA: Reschedule SCT meetings? (Bring up at next meeting when JCA returns from holidays?)~~

Software Development

-

Research

Other

- Sandrine Bédard : Reschedule SCT meetings?
  - ⇒ Wednesdays at 4PM

Action items

- ☐

2021-08-10

Attendees: Paul, Joshua, Sandrine, Nick
Moderator: Ainsleigh Hill
Minutes: Nick Guenther

Check last week's action items

☑ ~~None~~

Software Development

- Joshua Newton : PR for remaining SCT Course Tutorials (#3493)
  - First draft is ready for review!

Research

- Sandrine Bédard : Uk-Biobank CSA normalization
  - Intergrate normalization method in SCT → https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3483
    - Where to keep the models
      - Existing large models → separate repos (unrelated to this though)
      - Small coefficient files → put directly into SCT?
      - Current example of a small coefficient data file (in progress of porting to pip): https://github.com/spinalcordtoolbox/c2c3_disc_models/tree/ng/pip
        -
      - But we could just equally well create /data/ under spinalcordtoolbox; → (tag Nick when creating the PR)
    - In which API do we want to integrate this?
      - https://github.com/spinalcordtoolbox/spinalcordtoolbox/blob/master/spinalcordtoolbox/aggregate_slicewise.py
  - Manuscript: manuscript_csa_ukbiobank 🎉
  - PMJ-based CSA tutorial: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3496
- Sandrine Bédard :PMJ-based CSA : comparison with different neck positions
  - 2021-08-10-pmj-neck-positions
- Paul bautin: Comparaison Deepseg vs SoftSeg

Other

- Summer time-off scheduling heads-up ("NeuroPoly - Holidays" calendar)
  - August 15-21: Sandrine Bédard
  - August 15-21: Joshua Newton

    - ○ August 22-Sept 3: Nick Guenther
- Sandrine Bédard : heads up→ I have a class from 4 to 7 pm on tuesday this fall
    - ○ Conflicts with typical meeting time

Action items

- ☑ ~~NG: Review SB's data management PR~~
- ☑ ~~SB/PB: Check status of contrast agnostic softseg with Uzay, etc.~~
- ☑ ~~SB: Review tutorials PR~~
- ☑ ~~JN: Get reviews on SCT course tutorials PR~~
- ☐ JN: Keep in touch with SB re: PMJ-based CSA tutorial
- ☑ ~~JCA: Reschedule SCT meetings? (Bring up at next meeting when JCA returns from holidays?)~~

2021-07-27

Attendees: Joshua Newton,
Moderator: Sandrine Bédard
Minutes: Joshua Newton

Check last week's action items

- ☑ ~~Ainsleigh Hill Change font headings to different colour in TOC sidebar~~
- ☑ ~~Ainsleigh Hill Make font slightly smaller - font was the same size as original~~
- ☑ ~~Ainsleigh Hill Grey background, Lato font~~
- ☑ ~~Ainsleigh Hill Fix dark mode~~
- ☑ ~~Sandrine Bédard : Report issue 11 bug to SCT.~~

Software Development

- Joshua Newton : Proposal, release v5.4 after PMJ-related features are merged
    - PMJ CSA PR (#3478)
    - Are there any other features that are relevant for Sandrine's research that we want to include in the upcoming release?
    - e.g. Should we wait on the normalization method?
        - Yes wait for https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3483, shouldn't be that long
- Then, tentatively set the date of the next release for… when?
    - Important dates:
        - November: Harvard SCT course (Is this still planned?)
            - (Tutorial documentation needs to be finished by then.)
        - December: Python 3.6 EOL.
            - To upgrade to Python 3.7, we would need to finish up either:
                a. sct_deepseg as a replacement for Tensorflow-based segmentation methods (sct_deepseg_gm, sct_deepseg_sc, sct_deepseg_lesion) (issue #3046)
                    - Contrast-agnostic segmentation is only a replacement for sct_deepseg_sc (gm and lesion are more long-term), so we might be forced to go with the second option based on the timeline
                b. Upgrade Tensorflow, and come up with a plan for how to provide Tensorflow-based segmentation methods to users without AVX (PR #3361)
    - So, set v5.5/v6.0 for November (4mo from now) and try to finish both?

Research

- Sandrine Bédard : **Contrast-agnostic segmentation**
    - We have all the manual segmentations
    - I am generating the softsegs and checking the registration
- Sandrine Bédard : **CSA based on distance from PMJ**
    - Implementing this in Uk-Biobank → https://github.com/sct-pipeline/ukbiobank-spinalcord-csa
    - Implement normalization method: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3483
    - Stats results: https://docs.google.com/presentation/d/1P4XGTLIpa0t0X7jsBaJWbgWcmudaei-pJ3mYiqGoJRI/edit#slide=id.ge6631f8cdf_0_10
    -
- Paul Bautin : **simulate "realistic" scan-rescan variability with TorchIO**
    - How to choose artifacts to implement? https://github.com/sct-pipeline/csa-atrophy/issues/107#issuecomment-877283223
        - Compute results (scan-rescan variability) for one artifact at a time
        - Compute and implement an artifact occurrence rate

Other

- Next meeting? Yess :D

Action items

☐
☐
☐
☐
☐

2021-07-13

Attendees: Srishti Yadav, Julien Cohen-Adad, Sandrine Bédard, Joshua Newton, Ainsleigh Hill, Nick Guenther
Moderator: Nick Guenther
Minutes: Paul Bautin

Check last week's action items

- ☐ ✅ Ainsleigh Hill Prototype grey vs blue sidebar, B vs C headings in RTD
  - Blue background: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3355/commits/96a60ca168cbf28152b834b3f64bd7e733cc06da
  - Dark grey background: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3355/commits/d76783ce1962f1d6c26835577206ddb41a7c3266
  - Lato font: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3355/commits/6a5901b2585640f95ad519e60168d97ff4b7a2e6
  - RTD/Sphinx original font: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3355/commits/a00bdbabb020c429c2d9b03979fed236c21adfb1
  - RTD Build from GitHub: https://spinalcordtoolbox--3355.org.readthedocs.build/en/3355/user_section/installation/mac.html
    - Action Items: see below
    - SY: Are the ads always on RTD?
      - JN: https://docs.readthedocs.io/en/stable/advertising/ethical-advertising.html
- ☐ ✅ Ainsleigh Hill : Remove padding from code blocks on RTD: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3355/commits/6b457142dd317b68aed014779338210c0ad7817c

Software Development

- Joshua Newton : Next release? (5.4)
  - Has been open for several months now
  - SCT doesn't currently have a roadmap/plan for when to release
  - Proposal: Time-based releases (i.e. releasing on a set schedule)
    - e.g. 4x a year (March/June/Sept/Dec)
    - Possibly easier to coordinate for open-governance projects like ours [1] [2]

- We could go back to feature-based releases when SCT is pip-installable, because at that point major/minor/patch distinctions will become much more important (since people will be able to more easily update their existing SCT installations -- something they can't do right now).
- Compare: https://www.openbsd.org/papers/asiabsdcon2009-release_engineering/
- Sounds good! (?)

- Minor releases only? (Rarely reasons to release a major, and patch releases aren't as useful until SCT can be more easily updated.)

Research

- Sandrine Bédard : **Contrast-agnostic segmentation**
    - Edge effect : https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord/issues/11
    - Still missing some manual segmentations
- Sandrine Bédard : **CSA based on distance from PMJ**
    - 2021-07-05-PMJ_CSA_comparison_methods
    - For UK-Biobank, we're going to use interpolation from PMJ and centerline method and compare both methods in another project.
    - Implement QC report
    - PMJ detection → R-L position needs to be centered → https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3456

Action items

☑ ~~Look! Google Docs has checklists now.~~
☑ ~~Ainsleigh Hill Change font headings to different colour in TOC sidebar~~
☐ Ainsleigh Hill Make font slightly smaller
☑ ~~Ainsleigh Hill Grey background, Lato font~~
☑ ~~Ainsleigh Hill Fix dark mode~~
☑ ~~Sandrine Bédard : Report issue 11 bug to SCT.~~

2021-06-29

Attendees:
Moderator: Ainsleigh Hill
Minutes: Julien Cohen-Adad

Check last week’s action items

Software Development

- New admin role: Joshua

Research

- Sandrine Bédard : Contrast-agnostic seg (Update)
  - Issue: https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord/issues/2
  - https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord/pull/9
- Sandrine Bédard : Distance from PMJ - CSA → https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3429
  - QC assessment for centerline: issue #3431
  - context: https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3063

2021-06-15

Attendees: Sandrine, Julien, Paul, Nick, Alex Foias, Joshua, Ainsleigh
Moderator: Sandrine Bedard
Minutes: Charley Gros

Check last week's action items

- Alexandru Foias : AtlasRat and PAM50 microstructure upload
    - https://github.com/spinalcordtoolbox/atlas-rat/pull/1
    - https://github.com/spinalcordtoolbox/PAM50/pull/2
- ☐ Ainsleigh Hill : Prototype grey vs blue sidebar, and B vs C headings in RTD
    - will do next week (just wrapping up GitBook)
- ☐ Ainsleigh Hill : Remove padding from code blocks on RTD
    - will do next week
- ☐ ✅ Joshua Newton : Respond to feedback on tutorials

Software Development

- Joshua Newton : Discussion Q: **Should we be doing patch releases?** (e.g. 5.3.1)
    - Currently, users must delete their old SCT installations, then reinstall from scratch
        - This kind of defeats the purpose of patch releases (no way to directly upgrade)
    - So, might it be better to stick to minor/major releases (5.3, 5.4, 6.0) until SCT is pip-installable?
        - This would also let us avoid having to coordinate patch/minor releases around bugfix/feature PRs
        - See, for example, the situation with #3390

Research

- JCA: overview of current projects:
    - contrast-agnostic seg (SB)
        - https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord/pull/9
    - length between PMJ and location where to compute csa (SB)
        - https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3063
    - PB project → Paul pls fill in
        - article submitted to Neuroimage Clinical 🎉
            - version submitted
        - torchIO: data augmentation with artifact simulation
    - vert. labeling (RA),
        - URL https://github.com/ivadomed/ivadomed/pull/787
        - work: compare performance of new vs. old
            - spine-generic + uk biobank + others (sct-testing-large) baseline

Action Items

- ☐ Ainsleigh Hill : Prototype grey vs blue sidebar, and B vs C headings in RTD
    - will do next week (just wrapping up GitBook)
- ☐ Ainsleigh Hill : Remove padding from code blocks on RTD
    - will do next week

2021-06-01

Attendees:
Moderator: Alexandru Foias
Minutes: Nick Guenther

Check last week's action items

- ☐ ✅ Joshua Newton : Investigate presentation formats to display the information in an easy-to-follow way (compared to slide decks + projections)
- ☐ ✅ Joshua Newton : Get in touch with SB regarding tutorial command that needs updating
- ☐ ✅ Ainsleigh Hill /Paul give feedback on tutorials
  - see below
- ☐ ✅ Ainsleigh Hill : implement the font/colour/heading changes, get people to vote on them
  - will discuss below
- ☐ ✅ JCA/CG/SB/KN: Concrete plan for sct_deepseg → Meeting on monday 24th, 17h
  - https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord

Software Development

- Joshua Newton : SCT Course/Tutorials
  - RE: Last week's suggestion to split up long tutorials into multiple subpages
    - Pull request: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3094
    - WIP Demo: Old theme, New theme.
    - Wording + page names still need to be tweaked, so ignore that part for now svp.
    - **Q: Which page format is better?** (Voting poll: here)
      - Update: It looks like a majority prefer split pages -- Do we still need to discuss?
    - AH: smaller pages are a lot easier to follow.
    - SB: New theme, button is difficult to see
    - Header issue: 'Before starting this tutorial' on doesn't get a #header link
    - SB: Issue with TOC : goes up when clicking on it
    - DP: the new theme has too much empty space on the right
      - AH: some pages use the space to give a sub-TOC, e.g. here
      - JCA: we wanted to leave some margin to help readability
      - JN: In tutorial 1, left/right aligned images are too squished (e.g. this) for the new width -- refactor to have single-column images/text.
    - DP: The contrast between text and CLI commands (e.g. here) is low, especially on brighter monitors
    -
  - Ainsleigh Hill : Reviewed here: https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3094#pullrequestreview-673279230

        - tested all the tutorials
        - looks amazing Joshua Newton !
        - much prefer the split pages, it really helped me follow along

- Joshua Newton : 5.3.1 patch release
    - 5.3.1 PRs that still need review:
        - `MPLBACKEND` fix in __init__.py: #3401
        - `sct_register_multimodal` empty file: #3407
        - GH Actions workflow to automate releases: #3383

- Ainsleigh Hill : SCT Themes
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/pull/3355
    - SCT Themes
    - changed background to RTD background (slightly darker white)
    - AH:
        - extra padding code-blocks?
            - Vote: 2 yes, 5 no.
        - Left sidebar colour:
            - AH: The dark blue is the nicest
            - JCA: The dark grey is nice because it gives a sharp
            - Vote: split down the middle between blue and grey
        - Heading style:
            - Vote: 0 A, 7 B, 2 C
            - JCA: please prototype C
- Alexandru Foias : Review high priority PR
    - https://github.com/spinalcordtoolbox/spinalcordtoolbox/labels/priority%3AHIGH
    - JCA: python migration is blocked on tensorflow~=sct_deepseg_sc and torch~=sct_deepseg
    - JCA: label the forgotten GUI problem ‘good internship project’
    - JCA: label this extrapolation project ‘good internship project’
    - AtlasRat and PAM50 microstructure uploads -> Alex

Research

- Sandrine Bédard : Contrast-agnostic cord CSA → processing pipeline
    - Registration: https://spinalcordtoolbox.com/en/jn-2857-template-registration-tutorial/user_section/tutorials/2/2-9.html → very useful :)
    - SB: Explained the experiments run this week on combining datasets taken under different MRI settings
    - JCA: How do you average the image results?
- JCA: We have been conservative about our segmentation, leading to under-segmentation. Some related projects like GIN (?) are more eager about segmenting. Should we try to be more eager?

- Sandrine Bédard :
    - Adding some manual segmentations in spine-generic:
    - Need to update scripts for spine-generic and uk-biobank → Not ideal (ITK-SNAP vs FSLeyes, new yml format)
        - Re: ITK-SNAP vs FSLeyes, Include both via a flag
    - Would be great to address : https://github.com/spinalcordtoolbox/spinalcordtoolbox/issues/3353
        - This is about combining two scripts from related projects into an official SCT CLI
        -

Action Items

☐ Alex: AtlasRat and PAM50 microstructure upload
☐ Ainsleigh Hill : Prototype grey vs blue sidebar, and B vs C headings in RTD
☐ Ainsleigh Hill : Remove padding from code blocks on RTD
☐ Joshua Newton : Respond to feedback on tutorials

2021-05-18

Attendees: Ainsleigh, Sandrine, Julien, Alexandru Foias, Joshua, Nick, Charley, Paul
Moderator: Ainsleigh Hill
Minutes: Sandrine Bedard

Check last week's action items

- ☐ ✅ JN: Migrate spinalcordtoolbox repos to new org
- ☐ ✅ JN: Contact Alex regarding permission management on new org
- ☐ CG/JCA: come up with concrete plan for sct_deepseg
  - Talked about it in Ivadomed meetings, working on BIDS compatibility of datasets, spine generic, ukbiobank and sct_testing, start with T2*
  - Contrast_agnostic → need to clarify
    - One: a different model work with various contrasts
    - A model that generates the same segmentation
    - Need to manage and coordinate both
    - Meeting about this on monday 24, 17h (Julien, Sandrine, Charley and Konstantinos)
  - Sandrine/KN repos →https://github.com/sct-pipeline/contrast-agnostic-softseg-spinalcord
- ☐ Ainsleigh Hill : implement the font/colour/heading changes, get people to vote on them
  - Haven't had a chance yet, will add to action tasks for this week

Software Development

- ☐ SB: Strategy for tutorials
  - Joshua Newton : 2/3rd of tutorials handled by PR #3094.
    - Link to view tutorials
    - Very well done!!!
  - Only ~1hr duration of course material remaining:
    - 2:06:51: 5. Gray matter segmentation
    - 2:21:54: 6. Atlas-based analysis
    - 2:36:32: 7. Diffusion-weighted MRI
    - 2:53:03: 8. Other features
    - 3:01:53: 9. Analysis pipelines with SCT
    - 3:10:43: 10. General considerations
  - Julien Cohen-Adad discussion about the flow of the course: so far, EVERYTHING was on the slides, and slides were passed chronologically (slide 1, slide 2, etc.). If we move the course material to the RTD, it is unclear how the flow will look like (start from tutorial, then click on "concept pam50", then go back to tutorial, etc.), will that be difficult for participants to follow?

  - This guy uses GitBook to run his course (which is similar to RTD, perhaps this video might have some useful tips): https://youtu.be/yfbKXqRAgOA
    - Idea, switch from web browser and terminal, we need to show the terminal
  - If only RTD
    - Pros:
      - People can reference back
      - Easier to access than the PPT
      - Not duplicated
      - They look at it online, maybe better
      - Up to date
    - Cons
      - Scrolling
      - A lot of text → makes the class of making it more boring
  - R Markdown has option to turn markdown into a presentation: https://bookdown.org/yihui/rmarkdown/powerpoint-presentation.html
- Joshua Newton : To add to above, formatting differences (font size, paragraph-style content etc.) might make it difficult to project material in a classroom -- How do the pages look with page zoom? etc.
  - Nick: Find (or construct) a CSS theme where every section header displays as a slide. So long as the sections aren't too long, we can generate both readthedocs and presentation versions,
    - E.g. like prezi.com, https://revealjs.com/, https://impress.js.org/ , https://www.inwebson.com/css3/pure-css-slideshow-effect-for-presentation/ , https://webslides.tv/
    - We might need to create our own theme
    - Would address the scrolling theme
  - We could split up the existing pages to make them smaller and closer to slide-deck sized
  - Usually, for the course:
    - 30 people, additional people from the lab
    - 5 people that really struggle with the terminal, where are my directory, etc, things like that
    - 3h → way too short
    - We will have one day, or 2
    - Installation → more issues and questions
    - Questions at the end: people use their own data
  - We would upload the video recording on the course section of spinaltoolbox page
- Julien Cohen-Adad separating concept and tutorials (eg: https://spinalcordtoolbox--3094.org.readthedocs.build/en/3094/tutorials/pages/registration_to_template.html#labeling-conventions)
  - AH: Include the slides in RTD?
    - JCA: More difficult to link and copy paste, more difficult to redirect to a concept if it is all included in the tutorials, should we balance that?

  - JN: if we separate one page /script for the CLI
    - There could be some tutorials included with the CLI
    - We want to add a link to the script: both ways!
  - SCT concepts should we keep it seperate? With the new theme it will be easier to navigate with the table of content
- Let's continue the way we are doing
  - Maybe the concepts could be move to the tutorials

Research

-

Action Items

- Ainsleigh Hill : implement the font/colour/heading changes, get people to vote on them
- JCA/CG/SB/KN: Concrete plan for sct_deepseg → Meeting on monday 24, 17h
- Joshua Newton : Investigate presentation formats to display the information in an easy-to-follow way (compared to slide decks + projections)
- Joshua Newton : Get in touch with SB regarding tutorial command that needs updating
- Ainsleigh Hill /Paul give feedback on tutorials

2021-05-04

Attendees: Nick, Ainsleigh, Julien, Sandrine, Alexandru Jora, Alexandru Foias, Joshua, Charley
Moderator: Julien Cohen-Adad
Minutes: Nick Guenther

Check last week's action items

- ✅ JCA: interactive QC PR #3253
- ✅ NG: will create script for testimonial RST doc
- ✅ JCA: create PR for testimonial page with example entries
- All done.

Software Development

- Joshua Newton : Python 3.6 → Python 3.7 (#3227)
    - **Short-term:** Upgrade Tensorflow, then switch to `sct_deepseg` later on
        - Test suite is passing for Tensorflow 1.15 + Python 3.7. 🎉 (#3361)
        - **Problem:** Upgrading TF makes things harder for users without AVX capabilities.
            - Context: #2618
            - AVX was first introduced in 2011 -- How necessary is it to support 10+ year old CPUs? How prevalent are non-AVX users?
            - Since our user base is small, it may be easier to support users on a case-by-case basis by providing pre-compiled TF wheels without AVX. (See this link.)
            - NG: It should be possible to do this, but it will take some time and research. Do we want to just focus on dropping tensorflow instead?
            - JCA: Context: sct_propseg is our older tool that uses tensorflow; sct_deepseg_sc is newer and uses torch.

    - **Long-term:** Switch to `sct_deepseg` (#3046)
        - See CG's discussion points in "Research" section below.

- JCA: we want to construct a workflow for training models that version tracks the input training data and version tags the outputs.

- Joshua Newton : Moving SCT from the **neuropoly** org to the **spinalcordtoolbox** org
    - Related question: Should we keep "sct-data" org and "sct-pipeline" orgs, or merge them into the main "spinalcordtoolbox" org?
        - Having 1 org would make administering permissions easier.
        - We would gain org-level @mentions across projects (e.g. **@spinalcordtoolbox/developers** and **@spinalcordtoolbox/researchers**)
        - It might make discovering related projects easier. (e.g. Right now, how would someone learn about sct-pipeline projects if they are on the SCT main repo?)

        - NG: we had sct-data separate at least partially because we were paying Github for professional bandwidth.
            - JCA: but we switched off the paid plan, so there's no blocker anymore.
    - We can use teams and sub-teams instead of giving access to users one repo at a time. This will make maintaining permissions cheaper and more accurate in the long run.

- Julien Cohen-Adad : cool stuff: https://www.connectedpapers.com/main/1f9e0b7c8b24bf37dd978b8d7ef49460dc465022/SCT-Spinal-Cord-Toolbox-an-opensource-software-for-processing-spinal-cord-MRI-data/graph

- Ainsleigh Hill : https://github.com/neuropoly/spinalcordtoolbox/pull/3355
    - 👉 **https://spinalcordtoolbox--3355.org.readthedocs.build/en/3355/**
    - **current website: https://spinalcordtoolbox.com/**
    - new theme for docs; still in progress
    - feedback welcome!
    - similar to: https://torchio.readthedocs.io/index.html & https://pradyunsg.me/furo/quickstart/ (template)
    - font size of admonitions too small
    - background color -> too white?
    - slightly too big gap between h1 and h2
    - h1 all caps and font-weight change to match h2
    - python API page fonts change
    - different fonts under different browsers, OSes, browser extensions
    - check out different colors for the table of contents

- JCA: plan to have an SCT course at harvard
    - tentative dates ~15 nov (3-day course, 1 full day for SCT)

Research

- CG: sct_deepseg: model requirements → to be discussed before starting the trainings, linked to (#3046)
    - Proposal:
        - Top priority:
            - Model that are able to replace the sct_deepseg_sc, _gm, _lesion models
                - mono-channel input
                - SC models: “Contrasts”: ALL_TOGETHER, t2, t1, t2s, dwi
                - Lesion models: “Contrasts”: ALL_TOGETHER, t2_ax, t2_sag, t2_combined
        - SoftSeg vs. HardSeg:
            - SoftSeg
            - Threshold optimised on the training set so that can be used as post-processing with a specific flag
        - Objective: CSA constant across contrasts

        - Use visualisation tools from Konstantinos
        - CLI: sct_deepseg MODEL -i DATA
            - sct_deepseg seg-cord -i mydata.nii
            - sct_deepseg seg-gm -i data…
            - sct_deepseg seg-spinal-tumor -i …
            - currently: sct_deepseg -task seg-cord -i mydata.nii

Action Items

- ☐ For next meeting: discuss strategy for tutorials
- ☐ JN: Migrate spinalcordtoolbox repos to new org
- ☐ JN: Contact Alex regarding permission management on new org
- ☐ CG/JCA: come up with concrete plan for sct_deepseg
- ☐ AH: implement the font/colour/heading changes, get people to vote on them

2021-04-20

Attendees:
Moderator: Ainsleigh Hill
Minutes: Giselle Martel

- Last meeting action items
    - NG: https://github.com/neuropoly/spinalcordtoolbox/pull/3253 got taken over by Joshua (thank you)
    - NG: started gm_model https://github.com/neuropoly/spinalcordtoolbox/issues/3333
    - NG: no other progress on packaging this time
    -

Software Development

- JCA: Next release? (5.3.0)
    - JN: There are 2 remaining PRs that need reviews:
        - **Moco QC** (PR #3320): Approved by JN, but would like someone else to also take a look at it + approve (because UI design is more of a subjective thing)
        - **Interactive QC** (PR #3253): Approved by Julien, but it would be good for someone to quickly double-check on various browsers/platforms to make sure the most recent issues have been resolved
    - Once both are merged → Action item for JN to create the release.

- JCA: need money to pay salary → sponsors → testimonials → urgent
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3346
    - Move ahead with 530, take care of testimonials later
    - Should have a specific page for testimonials:
        - Could add another entry in the table of contents
        - Google form data scraping:
            - Maybe manual curation is better
            - Google form data requires monthly maintenance
        - Sphinx for automation

- JCA: good news from Chan-Zuckerberg foundation: LOI accepted--

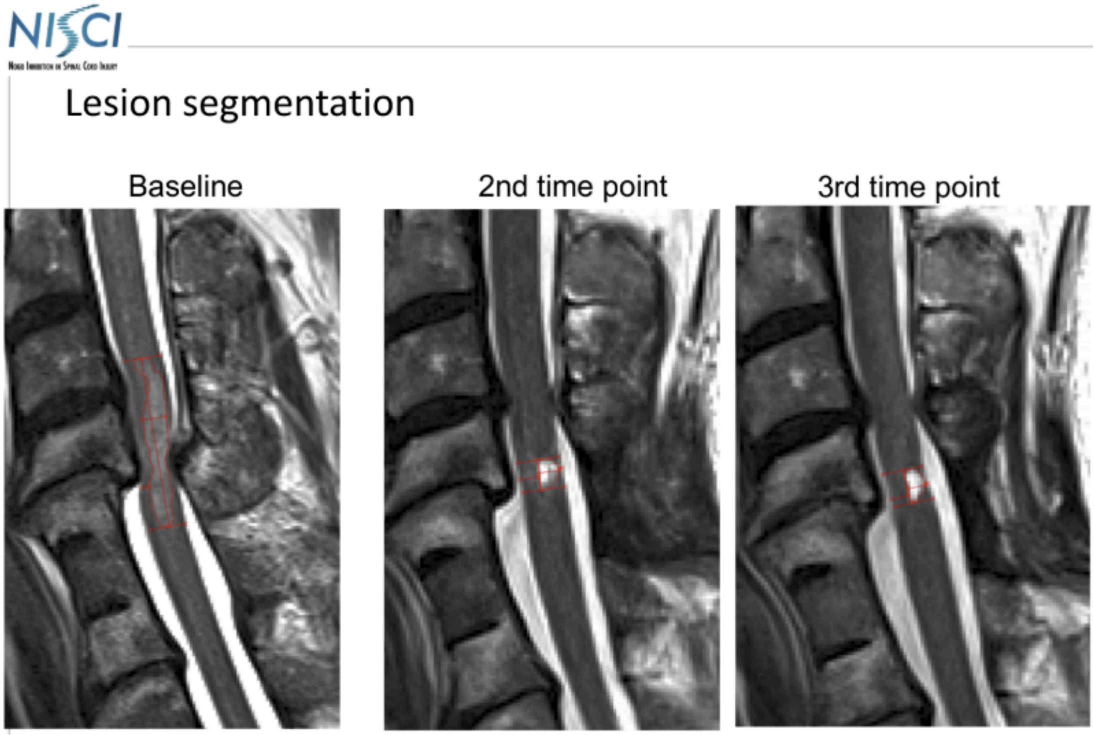
- JCA: QC report: status?
    - JN: This is covered by previous “Next Release” bullet point

- JCA: packaging SCT, data, models
        - Experimental to package with pip: https://github.com/neuropoly/spinalcordtoolbox/issues/1526

            - Dependencies with pip: https://github.com/neuropoly/spinalcordtoolbox/issues/2669#issuecomment-814099995
                - https://github.com/sct-data/spinalcordtoolbox-data-template/pull/1 + related PRs
                    - https://github.com/sct-data/PAM50/pull/1
                    - https://github.com/sct-data/pmj_models/pull/1
                    - etc
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3334
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3335
-

Research

- JCA: SCI lesion segmentation from Patrick Freund's group in Zurich



Lesion segmentation

  150 subjects, model to train and include in SCT. Great opportunity-- strong group, large visibility.
- Dog spinal cord template:
    - Richard Shinn, DVM, MS, Assistant Professor, Neurology & Neurosurgery, Virginia Tech | Department of Small Animal Clinical Science
    - Goal: Use our template creation pipeline for creating a dog spinal cord template

Action Items

- ✅ JCA: interactive QC PR #3253
- ✅ NG: will create script for testimonial RST doc

- ✅ JCA: create PR for testimonial page with example entries

2021-04-06

Attendees: Sandrine, Andreanne, Julien, Nick, Charley, Joshua
Moderator: Sandrine Bedard
Minutes: Andreanne Lemay

- Last meeting action items

Software development

- JCA: Timeline for v5.3.0? *(Link to check progress: 5.3.0 Roadmap)*
    - Almost all the issues are resolved, 2 issues still remaining
    - 1 PR is ready for review
    - Interactive QC: should be part of 5.3.0
- AJ: Interactive QC report: https://github.com/neuropoly/spinalcordtoolbox/pull/3253
    - Almost done, only minor things to address
    - Nick will take care of it
- NG: packaging: https://github.com/neuropoly/spinalcordtoolbox/issues/2669
    - Look into options for packaging
    - I understood pip finally and went on a roll turning *sct_download_data* into *pip install*:
        - https://github.com/sct-data/c2c3_disc_models/pull/1
            - (these are all pretty much identical patches)
        - https://github.com/sct-data/pmj_models/pull/1
        - https://github.com/sct-data/optic_models/pull/1
        - https://github.com/sct-data/deepseg_gm_models/pull/1
        - https://github.com/sct-data/deepseg_sc_models/pull/2
        - https://github.com/sct-data/deepseg_lesion_models/pull/1
        - https://github.com/sct-data/PAM50/pull/1
        - https://github.com/sct-data/sct_testing_data/pull/8
            - I plan to make this one an optional dependency, only installed when commanded with `pip install spinalcordtoolbox[tests]`
    - Includes CI to auto-package stuff just by clicking on "New Release":
        - https://github.com/sct-data/optic_models/releases/tag/2017.04.13rc1
        - https://test.pypi.org/project/spinalcordtoolbox-data-optic-models/2017.4.13rc1/
        - (and I migrated some incrementalism from this to ivadomed https://github.com/ivadomed/ivadomed/pull/753)
        - These lessons can help SCT too
    - Haven't started working on patching SCT to actually use these yet
    - `path.join(__data_dir__,'something/file.nii.gz')` will be replaced by `importlib.resources.path(spinalcordtoolbox.data.something, 'file.nii.gz')`
    - *sct_download_data* will be (partially) replaced by *install_requires* pointed at these packages
    - We should be able to get *sct_check_dependencies* to integrity-check our datasets.

- Please use https://github.com/sct-data/spinalcordtoobox-data-template in the future to make more packages like this (you can pick it from "New Repo" if you're a member of sct-data)
- **Bureaucracy issues**
  - sct-data is limited to 4 users because it was on a paid plan? Sorry :/. Maybe it will clear up?
  - we should have an organization-level Github pypi passwords.
    - currently: sct-data: TEST_PYPI_API_TOKEN - but it's in my name
    - currently: neuropoly: PYPI_PASSWORD - presumably this is https://pypi.org/user/neuropoly/
      - **Delete this one**?
    - wanted: change to neuropoly: PYPI_API_TOKEN - for consistency
      - get a new token at https://test.pypi.org/manage/account/token/
      - Give to https://github.com/organizations/neuropoly/settings/secrets/actions
    - wanted: sct-data: PYPI_API_TOKEN
      - add a new token at https://pypi.org/manage/account/token/
      - Give to https://github.com/organizations/sct-data/settings/secrets/actions
    - wanted: neuropoly: TEST_PYPI_API_TOKEN - in https://pypi.org/user/neuropoly/'s name
      - add a new token at https://test.pypi.org/manage/account/token/
      - Give to https://github.com/organizations/neuropoly/settings/secrets/actions
    - wanted: sct-data: TEST_PYPI_API_TOKEN - in https://pypi.org/user/neuropoly/'s name
      - add a new token at https://test.pypi.org/manage/account/token/
      - edit at https://github.com/organizations/sct-data/settings/secrets/actions
- **Feedback**!:
  - The installation layout I picked is spinalcordtoolbox/data/{deepseg/{sc,gm,lesion},svm/{optic,c2c3,pmj}}, are there aesthetic thoughts about this?
  - The model files, both SVM and deepseg, are not very open source:
    - they are opaque vectors
    - the equivalent of their source code would be the training set + training scripts (like source code + compiler)
    - Where are those and can we put them into the model's repos? Even if we can't provide the training data can we at least explain where the training data came from in their READMEs?
  - The datasets are missing license files
    - except for sct_testing_data, which is "MIT Neuropoly 2014"
    - Should Creative commons for data and MIT for code

- optic, c2c3 and pmj are very very tiny; they could be grouped into a single ‘svm’ package, or even just included directly in SCT. IMO the major benefit of splitting up packages is to make downloading them easier, and save people bandwidth when they do updates.
- Should we try to retain the multiple-mirrors feature of *sct_download_data* or just trust in PyPI?
    - These packages are all under 100MB; PyPI’s limit is 1GB.
    - It is possible to set up mirrors with *pip* but not super elegant
    - conversely, I’m not convinced *sct_download_data*’s mirroring system is working right now:
        - https://forum.spinalcordmri.org/t/installation-failed-in-ubuntu/610/6
        - https://forum.spinalcordmri.org/t/installation-failed-at-the-end/496
        - https://forum.spinalcordmri.org/t/installation-error-sct-4-3/451/2
    - Use Github instead of mirrors since mirrors need to be maintained
- Dead data?
    - *exvivo_template*
        - The repo is alive but SCT doesn’t seem to use it
        - Should be included inside SCT
        - https://github.com/neuropoly/spinalcordtoolbox/issues/3280
        - This is an optional dependency with sct_register_to_template, selected via `-t`
    - *gm_model*
        - Appears to be pre-deepseg, svm-based grey-matter model?
        - it was used by sct_segment_graymatter (dev: Sara Dupont)
        -
    - *sct_example_data*
        - Seems to be forgotten except for a couple of integration tests. Could this be merged into *sct_testing_data*?
        - JN: **Used in batch_processing.sh** (larger files, vs. sct_testing_data’s cropped files)
        - For users to learn how to use SCT (as a demo)
- An apparently entirely separate clone of *sct_download_data* inside the *deepseg* code. Are these likely to be good pip candidates as well? I just repackaged a bunch of *deepseg* related files above, but they were in a different file.
    - Should be handled with pip
    - Mostly optional datasets
- What about *tutorial* data?
    - https://github.com/sct-data/PAM50/pull/1#issuecomment-814253463
    - “pip isn't great for courseware like course_beijing or sct_example_data” because it hides the files away inside of install directories
    - That is:
        - *course_hawaii17, etc:*
        - *course_paris18*
        - *course_london19*

            - *course_beijing19*
            - possibly *exvivo_template → it is a template (similar to PAM50)*
            - possibly *sct_example_data*?
            - *MNI-Poly-AMU → it is a template (similar to PAM50)*
        - How should we handle these?
        - They're sort of like optional dependencies ;
            - I envisioned, say: `pip install spinalcordtoolbox[course_london19,exvivo_template]`, but again that will hide them away from the user!
            - Add a wrapper to not depend on a virtual environment
        - The current *sct_download_data* reminds me of Stata's '. net get' feature that downloads sample files associated with a package to your working directory. I've never seen this feature in another language, have you?
        - Keep *sct_download_data* for now
- USER ISSUES:
    - https://forum.spinalcordmri.org/t/segmentation-fault-core-dumped/660/18
        - NG: Interesting problem! Hard to reproduce.
            - Twisty little passages if you want to go on a wild and difficult computer journey: https://github.com/neuropoly/spinalcordtoolbox/issues/3308
            - 2 weeks ago I was hoping to use this to build tools to make reproducible Windows environments for us, like Github and Travis provide, but locally. Maybe like 5% of the way there.
        - User solved this issue (can be tagged as resolved)
    - https://forum.spinalcordmri.org/t/measure-data-for-corticospinal-tract/674
        - https://github.com/neuropoly/spinalcordtoolbox/issues/3328
        - 2-hour job (very trivial, knowledge of SCT / nibabel required)
        - internal deadline April 15th.
        - Nick will take care of it

Research

- JCA: Clara: moco QC → julien will do a demo
    - Part of a PI3 (projet integrateur 3) at Polytechnique
    - Tool to do QC motion correction
    - Will be part of the new release (will be merged soon)
    - https://github.com/neuropoly/spinalcordtoolbox/pull/3320
- JCA: vertebral labeling: where are we at?
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2679
    - https://github.com/ivadomed/ivadomed/issues/550
    - https://github.com/rezazad68/DeepSpine
    - Reza worked on a model that works well, but it is not included yet (completely independent)

Action Items:

- ✅ Julien review last PR before release

- NG: Include interactive QC in the release / finish related PR
- ❌ Joshua: release 5.3.0
- ✅ JCA: Add test pypi password and regular password for NeuroPoly and SCT org., see bureaucracy issues
- NG: Update packaging scripts to use new passwords
- ✅ JCA: delete extraneous https://github.com/neuropoly/spinalcordtoolbox-data-template/settings
- NG: move optic/pmj YML into SCT repos
- NG: open issue to deprecate gm_model
- NG: take care of packaging of deep learning models
- NG: package exvivo_template and *MNI-Poly-AMU as optional deps*
- ✅ JCA: tag as resolve: https://forum.spinalcordmri.org/t/segmentation-fault-core-dumped/660/18
- ✅ JN: fix this issue https://github.com/neuropoly/spinalcordtoolbox/issues/3328
- Reza: Implement vertebral labeling in SCT / ivadomed (sct_label_vertebrae)

2021-03-23

Attendees: Ainsleigh Hill, Julein Cohen-Adad, Charley Gros, Joshua Newton, Andreanne Lemay, Alexandru Jora, Alexandru Foias, Sandrine Bedard, Daniel Papp
Moderator: Julien Cohen-Adad
Minutes: Ainsleigh Hill

Software Development

High Priority Issues

- https://github.com/neuropoly/spinalcordtoolbox/issues/3280 -> -t flag doesn't work (sct_register_to_template)
  - issues with ghsplit
  - changed from float64 to fit GitHub requirements
- https://github.com/neuropoly/spinalcordtoolbox/issues/3261 (sct_register_to_template)
- https://github.com/neuropoly/spinalcordtoolbox/issues/3187
- https://github.com/neuropoly/spinalcordtoolbox/issues/2865
  - environment issues, difficult to debug
  - if pattern occurs, then we can look into it
  - time-consuming
- https://github.com/neuropoly/spinalcordtoolbox/issues/2768
  - think it was fixed in a PR?
  - AL: there was a workaround?
- https://github.com/neuropoly/spinalcordtoolbox/issues/2423
- https://github.com/neuropoly/spinalcordtoolbox/issues/1821
  - JN: try suggestion in issue and let JCA know how it goes

Other

- https://github.com/neuropoly/spinalcordtoolbox/pull/3253 -> can someone with JS knowledge help?
- Redirect job offers to Job Offers on forum (saw postdoc posting)
- Need to have discussion about LFS, large files
  - other servers that have LFS integrated (GitLab, GitKey), but wouldn't be on GitHub
  - currently we don't have data > 100mb
  - this would be relevant for > 100mb
  - splitting tool for users not ideal
  - can set up hooks, but only in GitHub Enterprise
  - warning for 50mb could be deprecation warning
  - not a top priority, can stay as-is for now

Research

- https://github.com/sct-pipeline/ukbiobank-spinalcord-csa/issues/31
    - maybe try installing in sct_venv?
    - gradunwarp can’t be installed in a virtual environment
- https://github.com/neuropoly/spinalcordtoolbox/issues/3200 <- gradunwarp issue

Action Items

- ☐ Moderator has additional task: role is to fill up the agenda in advance
- ☐ AH: take a look at JS issue:
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3187
    - https://github.com/neuropoly/spinalcordtoolbox/pull/3253
- ☐ Open issue for student project for Dash app
- ☐ ✅ AL: Find PR for https://github.com/neuropoly/spinalcordtoolbox/issues/2768 and close issue
- ☐ ✅ AF: pls add Sandrine SCT ggroup
- ☐ ✅ JN: Message SB re gradunwarp

2021-03-09

Attendees: Ainsleigh Hill, Giselle Martel, Yang Ding, Julien Cohen-Adad, Alexandru Jora, Nick Guenther, Andreanne Lemay, Sandrine Bedard, Joshua Newton, Lucas Rouhier, Alexandru Foias
Moderator: Ainsleigh Hill
Minutes: Giselle Martel

Software Development

- JN: SCT v5.2.1 Patch Release (Links: Slack Context, GitHub Milestone)
    - Should anything else be included? (Open PRs, Recent Issues, "priority:HIGH" Issues)
    - https://github.com/neuropoly/spinalcordtoolbox/pull/3247 <- Close to done, easy to add to 5.2.1

- YD: SCT-Data Mirror Up:
    - Context: SCT-Data ran out of bandwidth, issues resolved via paying GitHub and file splitting?
    - https://dev.azure.com/neuropoly/sct-data
    - Public accessible
    - No bandwidth limit; file size limit 5GB, no need for Git LFS
    - Can help with hosting a deep learning model zoo? https://github.com/neuropoly/spinalcordtoolbox/issues/2746
    - For now LFS not a major issue (can split data)
    - Motivation for LFS is to be able to download only subset of data that is needed
    - Could look into CDN, can be used with Git Annex
    - LFS is well integrated into github, might be worth paying for it

- YD: Discussion: Shared dependency management with IvadoMed for long term integration
    - Prototype Idea: Depend on specific version of IvadoMed LTS releases?
    - Agree on the sub/shared dependencies with IvadoMed LTS releases
    - Only upgrade between IvadoMed LTS releases in SCT

- YD: pipeline management for SCT
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2169
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2142
    - nextflow / nipype /
    - Luigi pipelines could help streamline process

Research

- JCA: Pipeline for MS lesion segmentation
    - https://github.com/ivadomed/pipeline-ms-lesion/
    - Idea: register contrasts, then train model using ivadomed
    - First step: processing pipeline

        - SCT batch used to run pipeline on different subjects
    - Can assess quality control via parameter tuning

Action Items

- ✅ If you want to add a new item to the next release 5.2.1, please message Josh on slack
- For future reference: if feedback is needed from team on an item (such as the case with the release discussion), send an email prior to the meeting
- Follow discussion threads for pipeline management
- ✅ MS lesion pipeline: Sandrine will check registrations for different modalities

2021-02-23

Attendees: Char, Alexandru, Joshua, Charley, Ainsleigh, Nick, Julien, Sandrine, Lucas, Andreanne, **Alexandru**
Moderator: Julien Cohen-Adad
Minutes: Char

- JCA: split meetings in half: 30min softdev, 30min research/applications
    - Restructuring; half are students, half are programming/adding features
    - Improve meetings by splitting this meeting into two; all are welcome to come to either or both

    - **Softdev Notes:**
    - **JN: v5.2.0 Release**
      - Anything extra to be included in the new version of SCT
      -Ainsleigh has documentation PR to be put in; relates to FLSEyes: https://github.com/neuropoly/spinalcordtoolbox/pull/3228
      -Ainsleigh has added an issue for FSLeyes to fix their dependencies; timeline looks like a few weeks
      -A new modeltype added to deepsag; does it warrant a minor version instead of a patch
      - Two minor PRS for inclusion, aim for tomorrow morning, and then continue with the release
    - **Python 36 EOL: on dec 2021**
      - Start python 3.6 end of life discussion
      - 3.7 is still supported, do not jump too far ahead on versions because 3.9 breaks the appl so far

      https://github.com/neuropoly/spinalcordtoolbox/issues/3227
      - sct_deepseg_X depends on Tensorflow 1.5.0 which depends on Python 3.6: https://github.com/neuropoly/spinalcordtoolbox/issues/3046

- **Move scattered testing files/folders into a central location:**
  https://github.com/neuropoly/spinalcordtoolbox/issues/3219
  Testing related code is scattered; reorganizing would be useful

- Lint Issue - Two competeing rules
  -LR: https://github.com/neuropoly/spinalcordtoolbox/issues/3235
  -https://www.flake8rules.com/rules/W503.html
  -https://www.flake8rules.com/rules/W504.html
  - Issue 3235: missing line break required but has to be before or after binary operator: we have to pick to test just one for lint checker (recently added) To be discussed offline

  Research Notes:

- Sandrine cord csa (cross-sectional area) doing a project using deepseg: goal is to find factors of the source of the variables in cord sca (Normalize spinal size)

- Two issues opened which would help this project:
  QC: https://github.com/neuropoly/spinalcordtoolbox/issues/3218
  https://github.com/neuropoly/spinalcordtoolbox/issues/3187
    - Context: SCT QC module generates HTML page, we can navigate with arrows to go across sections- it would be useful to identify if manual correction is needed; this is done on a piece of paper right now, but having it on the html page is requested
    - You would need a backend; it's static currently. Needs a webstack

- Use pontomedullary junction (PMJ) part of the central nervous system (not vertebrae), to find where you are on the spinal cord to make up for head tilting- something to consider as a feature to add
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3063
    - Could also use body of C1 and C2 to determine location in spinal cord
    - Ask students for manual defragmentation on slack - a lot of volunteers

-

- **Action items**
    - **AR to review Ainsleigh's documentation task (3228) ✅**
    - **New meeting reminder and day and time for each half of the meeting(needed?)**
    - **Ainsleigh to review 3240 ✅**
    - **AF: add Charlotte to ggourp ✅**
    - **Discuss issue 3235 offline ✅**
    - **Alexandru to look into backend data delivery for 3187**

2021-02-09

- Travis -> GH Actions Migration
    - JN: I've experienced intermittent Travis issues (jobs sometimes fail for non-code reasons, unable to restart). Q: Should we make migrating higher priority?
        - Eg1: Unable to find image 'centos:8' locally
        - Eg2: Misc connection issues
    - Update on concurrency blocker
        - Disable xdist: https://github.com/neuropoly/spinalcordtoolbox/pull/3212 -- Can this be approved?
        - If the above is merged, should we shelve the locking fix? https://github.com/neuropoly/spinalcordtoolbox/pull/3152
    - Migration PR: https://github.com/neuropoly/spinalcordtoolbox/pull/3125
        - Is there anything left that needs to be done?

- JCA: git-lfs max BW reached
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3214

- JCA: packaging discussion: recent forum issue: will we have *more* problems if we move to a more pythonic approach
    - NG: AFAIK pypi is not blocked in countries-- should be good-- in any case we can serve a pypi mirror
- JCA: Apple M1 chip
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3211
- JCA: WSL FSLeyes install
    - https://forum.spinalcordmri.org/t/fsleyes-installation-with-wsl/621/7
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3206
    - https://github.com/neuropoly/axondeepseg/pull/452

Action task:

- AJ: check this git-lfs thing on sct-data

2021-01-26

- Discussion: should we drop **xdist** in favour of something else (or nothing)?
  - Motivation: we have hit some limitations/issues with regards to concurrency issues (https://github.com/pytest-dev/pytest-xdist/issues/271#issuecomment-763402552, https://github.com/neuropoly/spinalcordtoolbox/pull/3152). This complicates the ongoing effort to port CI to github actions.
  - Other annoyances such as **xdist** disabling **-s** (capture) thus preventing the user from viewing the output of stdout which is confusing for users. (Relevant dev Wiki page about this issue.)
    - This issue specifically is causing Julien to disable xdist for local testing, for example.
  - Doesn't add value in CI since almost all VMs are single-core.
  - Alternatives:
    - **pytest-parallel**
    - Disabled by default config. People who know what they are doing can enable it (or it can be enabled in **ci.sh** only).
    - Strategies in https://github.com/neuropoly/spinalcordtoolbox/issues/2674, particularly split tests across jobs; but we also need to consider that each job needs to spend installation time (there is a sweet spot in terms of number of tests per job)
  - CI time on GH actions: total ~15min; on Travis: ~1hr
    - Largely dominated by waiting for the macOS VM to boot
- Vertebral labeling:
  - testing workflow of trying two pipelines sequentially was not working -- updating the pipeline-- ETA for results: next week
- Avoiding large files:
  - https://github.com/neuropoly/spinalcordtoolbox/issues/3100
  - Some small progress in our sibling project: https://github.com/shimming-toolbox/shimming-toolbox/issues/199#issuecomment-766397441

2021-01-12

- Next SCT release
  - Minor vs. patch? (5.0.2 vs 5.1.0)
    - Merged PRs since last release (**Note:** Many are missing “next release” milestone)
    - ANS: Minor
  - Should any open PRs also be included?
    - https://github.com/neuropoly/spinalcordtoolbox/pulls

- What should we do to put the new/old method side by side for sct_label_vertebrae ? (Lucas)
  - https://github.com/neuropoly/spinalcordtoolbox/pull/2679

- Automatize releases (JCA)
  - Current manual steps: https://github.com/neuropoly/spinalcordtoolbox/wiki/Misc%3A-Creating-a-new-release
  - condition: batch_processing → could we
    - Batch_processing during CI: https://github.com/neuropoly/spinalcordtoolbox/issues/2888
    - Talk to Drulex, as he was a part of that batch_processing issue? yup!!

- **Action items:**
  - Someone: Check merged PRs for “next-release” milestone (done Maybe double check)
  - JN: Review https://github.com/neuropoly/spinalcordtoolbox/pull/3081 ✅
  - JN: Address feedback from https://github.com/neuropoly/spinalcordtoolbox/pull/3156 ✅
  - JN: Follow up on https://github.com/neuropoly/spinalcordtoolbox/pull/2704 ✅
  - JCA: https://github.com/neuropoly/spinalcordtoolbox/pull/3050 ✅
  - JCA: https://github.com/neuropoly/spinalcordtoolbox/pull/2858 ✅
  - NG: Make an issue about automating releases (and/or talk to Drulex?)

2020-12-15

- AL: sct_deepseg model have two URL links (github and OSF). I need to update/add models -> Do we want the model duplication on github + OSF?
    - https://github.com/neuropoly/distriploy
    - resolution: for now, let’s trust GH and only upload on GH
    - NG: long term: we should use a more “package management” strategy and have this pkg management deal with data,
- AF: GH actions:
    - Free for public repos
        - nb jobs allowed for macOs → we might want to look into current limitations
    - Private repos per organization:
        - Free plan: 2,000 Actions minutes/month
        - Team plan (only neuropoly at the moment): 3,000 Actions minutes/month
- migration of neuropoly/spinalcordtoolbox → https://github.com/spinalcordtoolbox
- QT issues
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2865
    - Users on forum haven’t posted the necessary debugging information unfortunately, so taking a more proactive approach may be useful.
- Install issue:
    - https://github.com/neuropoly/spinalcordtoolbox/issues/3029
    - https://forum.spinalcordmri.org/t/installation-failed-problem-creating-launchers/562/10
    -

action tasks:

- AF: open issue about migration https://github.com/neuropoly/spinalcordtoolbox/issues/3096
- NG/JN: Discuss conda install issues #3029
    -

2020-12-01

- CI:
  - should we move to GH actions?
  - estimated cost if we stay with travis.com: https://github.com/neuropoly/spinalcordtoolbox/issues/3057#issuecomment-735281988
  - NG: suggests we move to GH actions, AJ agrees. GH actions supports adding external “runners” (e.g old macOs)
  - GH actions has a cost, so we need to adjust
    - nevermind: seems to be free for public repos -- however there might be limitations with nb of concurrent jobs → AJ will look into that → seems to be 20 jobs.
  - AJ: first step: we run the current ci script
  - AJ: platforms: linux: OK with docker, macOs: catalina/big sur,

- ~~Interaction with user’s Python environment: what’s our best strategy?~~
  - ~~context: https://forum.spinalcordmri.org/t/attributeerror-str-object-has-no-attribute-decode-v5-0-0/567/13~~
  - ~~issue tracker: https://github.com/neuropoly/spinalcordtoolbox/issues/3067~~
  - **Addressed by https://github.com/neuropoly/spinalcordtoolbox/pull/3070**

- JN: “Require branches to be up to date before merging” setting for SCT PRs
  - Recently changed during recent Slack discussion thread (see this screenshot https://files.slack.com/files-pri/T034UD4QN-F01G68WR1KK/image.png)
  - Possibly too strict a requirement? Whenever a new PR is merged then other PRs must be updated. (e.g. https://github.com/neuropoly/spinalcordtoolbox/pull/3060)
  - Could burn through our Travis credits too quickly
  - NG: suggests keeping it the way it is (ensures we don,t merge things with potentially a conflict). AJ: only cons is that it would trigger CI more.

LR: cannot merge PRs anymore-- same problem for AL.

Action tasks:

- AF: check billing / GH action + if this is per organization
- LR: check estimate for ivadomed GH actions
- AJ: start the move to GH actions
- NG: will check setting for GH about permissions to merge PRs

2020-11-17

- macOS Big Sur issues:
    - Outdated gcc: https://github.com/neuropoly/spinalcordtoolbox/issues/3049
        - Q: How does SCT use gcc? Is the check even needed?
            - issue with macOs Catalina: https://github.com/neuropoly/spinalcordtoolbox/issues/2492
        - A: If a python package doesn't have a wheel, and the sdist requires compiling C/C++ code
        - So, an alternate solution could be to enforce wheels for our dependencies -> Default behaviour is to prefer wheel and fallback to sdist. Can be forced to wheel only with **--only-binary** flag
    - macOS version parsing: https://github.com/neuropoly/spinalcordtoolbox/issues/3048

- JN: Beta/prereleases
    - Motivation: Recent 5.0.0 bugs (#3033, #3038) not caught by test suite, but caught by users
    - Lets collaborators try out new functionality without needing to create a stable release
    - Context, tried previously: https://github.com/neuropoly/spinalcordtoolbox/tags?after=4.0.0
    - Challenges: Time commitment, recruiting beta testers, collecting feedback

- Migration from travis.org -> travis.com: Status?

- Modality order for multiclass model (sct_deepseg): https://github.com/neuropoly/spinalcordtoolbox/pull/3041
    - Challenge: Communicating to the user which tasks require which modality orders
    - Alternate proposal 1: Add e.g. "Input Order" column to "sct_deepseg -list-tasks"
    - Alternate proposal 2: Subparsers (per-task/per-model parsers)
        - e.g. "sct_deepseg <task> <task-specific options>"
        - Would need to add a new subparser for each task
        - Possibly generate subparsers on the fly?

- Sct_run_batch parallelism: https://github.com/neuropoly/spinalcordtoolbox/issues/3036
    - variable: ITK_GLOBAL_DEFAULT_NUMBER_OF_THREADS
    - Q: Do we have the right default value?
    - "Right" value is context-dependent…
    - Q: Why '1'? Reproducibility? May affect randomization…
        - Possibly relevant re: reproducibility: https://github.com/neuropoly/spinalcordtoolbox/issues/3044
    - old SCT issue: https://github.com/neuropoly/spinalcordtoolbox/issues/201
    - Possible idea: Rough heuristic, choose value based on available RAM
    - Resolution: Keep '1' default, if more is needed then instruct user to change value

Action tasks:

- verify if gcc needed for mainstream platform (ie macOs)
- NG: look into the travis.com setup
- AL: open issue to describe subparser approach wrt. PR 3041

2020-11-03

- AF: forum notification failed due to ban of domain (polymtl.ca)
    - context: slack channel sct_dev
    - sendgrid got exploited by bots so now spamhaus has blocked some of their servers
    - solution: nick implementing local email server opensmtpd on droplets (where we host the forum)
    - WIP: should be ready soon
    - next steps: we need “good reputation” → AF check with Nick to know exactly what that means
        - NG: Not being on common blocklists like spamhaus (which is something of a protection racket but it’s what we’ve got) -- easy: just don’t send spam.
        - NG: Not sending spam to the big servers (Google, Outlook) where their machine learned models will start to peg us as spammy -- easy: only provide sending credentials to the forum bot, and don’t send spam.
        - NG: Having SPF and perhaps DKIM enabled.
        - NG: Extensive instructions at https://bridge.grumpy-troll.org/2020/07/small-mailserver-bcp -- but this is *very* extensive, we don’t need to do it all.
        -
- **AL:sct_deepseg:** https://github.com/neuropoly/spinalcordtoolbox/issues/2994
- AL:Collaborators in Beijing would like to use *sct_deepseg*: when can we expect a release?
- LR:Compute_mean_squared_error: slight changes
    - Issue: https://github.com/neuropoly/spinalcordtoolbox/issues/2986
    - PR: https://github.com/neuropoly/spinalcordtoolbox/pull/2992
- LR:Missing disc in output of sct_label_vertebrae:
    - Issue: https://github.com/neuropoly/spinalcordtoolbox/issues/2967
    - PR: https://github.com/neuropoly/spinalcordtoolbox/pull/2990
- JCA: v5.0 (https://github.com/neuropoly/spinalcordtoolbox/milestone/39)
- Travis slow:
    - Other projects reporting slowdowns on travis org domain, speed better on new .com domain: https://twitter.com/dwijnand/status/1321873017299939329
    - Travis .org ceasing as of Jan 1 2021, currently scaling back capacity.
    - https://docs.travis-ci.com/user/migrate/open-source-repository-migration
    - JCA: can we move to travis.com?

Action tasks (urgent: for v5.0)

- CH: look at migrating to travis.com (after v5.0)
- JCA: document https://github.com/neuropoly/spinalcordtoolbox/issues/2995
- AL: deepseg get rid of models
- LR: work on https://github.com/neuropoly/spinalcordtoolbox/issues/2172
- JN: https://github.com/neuropoly/spinalcordtoolbox/issues/2934
- AJ: revert commit about the performance imports + bug with output folder (2995)

2020-10-20

- **sct_download_data** and related data packaging concerns
  - https://github.com/neuropoly/spinalcordtoolbox/issues/2959
  - WIP requirements summary (feel free to edit): https://docs.google.com/spreadsheets/d/1EJZC1JXk_H0X9-X1pblcIfWfHzcfcWR9TpgYF2QTFuk/edit#gid=0
- Pip-only install proof of concept: https://github.com/neuropoly/spinalcordtoolbox/compare/master...Drulex:aj/pip-only-install
  - **install_sct** removed, customization done in **setup.py**
    - No conda environment
    - No injection of environment variables in user environment
    - One step install (**pip install -e .**) not compatible with wheels install.
    - Currently only works with python3.6 because of requirement **tensorflow==1.5.0**. If this is not a hard requirement it should work with the latest version of python as well.
  - Simpler install allows faster and more flexible CI. See example with github actions: https://github.com/Drulex/spinalcordtoolbox/actions/runs/311130106
  - Goal was to evaluate feasibility + effort -> definitely possible to have a pip-only development install with low-effort.
  - Next step: POC **.whl** install
- v5 release:
  - status of label vertebrae?
    - evaluation/validation needed.
    - testing pipeline: https://github.com/sct-pipeline/vertebral-labeling-validation
    - issue: https://github.com/neuropoly/spinalcordtoolbox/issues/2944
  - anything else?
- release management discussion
  - https://github.com/neuropoly/axondeepseg/pull/364
- ANTs doesn't initialize sform - what to do?
  - https://github.com/neuropoly/spinalcordtoolbox/pull/2858
  - https://github.com/neuropoly/spinalcordtoolbox/issues/2429

Action tasks

- Lucas: tag Julien once testing pipeline labeling is pushed-- so i can review
- AJ/NG: prototyping packaging approach for binaries/data
  - starting with binaries to be distributed as wheels
  - then, potentially moving data + models as wheels as well
  - ultimately, the goal is to get rid of sct_download_data

2020-10-06

- **SCT v5 release**: what needs to be done?
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2900
        - Nick reviewed, GTG
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2901
        - Nick reviewed, practically GTG
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2858
        - Chris mentioned not being able to make meeting
    - Anything else? https://github.com/neuropoly/spinalcordtoolbox/pulls
    - If not, then: https://github.com/neuropoly/spinalcordtoolbox/wiki/Misc:-Creating-a-new-release

- sct_testing vs. pytest for users (should we do the change before SCT v5?)
    - What is the easiest way to instruct users to run pytest inside the virtual environment?
- Discussions about packaging:
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2669
    - https://github.com/neuropoly/spinalcordtoolbox/issues/1526
- Epic features/implementation
    - packaging (not a priority)
    - datalad-type books for documentation (priority)
    - ANTsPy (not a priority)
- Labeling issues with priority
    - https://github.com/neuropoly/spinalcordtoolbox/labels?q=priority

2020-09-22

- 5.0.0 Release (Milestone: https://github.com/neuropoly/spinalcordtoolbox/milestone/39)
    - #1548: Replace usage of msct_parser with argparse
        - Some remaining internal uses of msct_parser, see this comment
    - #2858: Check qform and sforms match first
        - CI currently failing
    - #2901: sct_maths: Convert usage of convert_list_str to use list_type
        - Needs review
    - #2900: Convert argparse '0'/'1' options to be typed as ints rather than strings
        - Needs review
    - #2679: Sct_label_vertebrae: Disc detection and template matching using deep learning
        - Reviews currently in-progress
        - Should this PR be included in 5.0.0? May take some time for multiple passes of reviews
            - not included in 5.0.0. (too risky)

- https://github.com/neuropoly/spinalcordtoolbox/pull/2887 (Refactor sct_label_utils into proper API)
    - Need some help with CLI testing (common use cases).
        - Should functional tests be moved to unit_tests/test_cli_labels.py?
    - Need some help with some unimplemented unit tests
        - See TODO and skipped

- Testing discussion link: https://github.com/neuropoly/spinalcordtoolbox/issues/2893
    - Investigate a lightweight way of re-using existing sct_testing tests?

- Status of https://forum.spinalcordmri.org/t/installing-sct-4-3-fails-pycache-not-empty/493 ?

- git-annex internal repos
    - Currently: `git remote add internal git@132.207.65.204:datasets/your-data.git`; Julien or Nick can grant you an account.
    - Goal: `git remote add internal git@data.neuro.polymtl.ca:datasets/your-data.git`, and you will be able to auto-inscrire using your polygrames account.
    - VM: size (not big enough) 150GB-- will be increased
    - Remember: connect to polyvpn to get access.
    -

- cool new collaboration: https://forum.spinalcordmri.org/t/deepseg-lesion-not-working/490/4

2020-09-08

- Joshua
    - SCT Contributing docs
        - Moved from RTD to GitHub Wiki (see: PR #2885)
        - Alternate suggestion: Having a single DokuWiki Contributing page shared by each NeuroPoly project.
            - See also: this WIP DokuWiki page I made to demonstrate the idea.
    - SCT GitHub Wiki
        - GitHub Action workflow to automatically update the sidebar (see: PR #2861)
        - Thoughts on using the GH Wiki more often for internal developer documentation?
            - e.g. Decisions made in meetings/GH issue threads -> Added to Wiki
            - See also: Useful article on subject
    - Argparse conversion
        - AFAIK, the last PR (see: PR #2842) is blocking progress for some other PRs. Status?

- Alpha testing a new version?
    - Don’t have regular (predictable) users...
    - More thorough testing instead? Batch_processing.sh -> test on merge

- 5.0.0 Release
    - Remove “Sct_label_vertebrae: Disc detection and template matching using deep learning”

- **Action items**
    - Joshua: rename download -> Software, and continue populating contribution info there
    - Julien: send email/slack about moving lab contributing guidelines to dokuwiki

2020-08-24

- Wiki: https://github.com/neuropoly/spinalcordtoolbox/issues/2855
    - dev doc: https://github.com/neuropoly/spinalcordtoolbox/issues/2856
    - https://github.com/neuropoly/spinalcordtoolbox/wiki
- ~~CLI discussion: https://github.com/neuropoly/spinalcordtoolbox/pull/2819/files#r476002026~~
- 5.0.0 Release To-dos
    - Should anything else be added to https://github.com/neuropoly/spinalcordtoolbox/milestone/39?
- **Joshua**: What to work on once argparse/5.0.0 release is done
    - Would anyone like my help/involvement? (e.g. with reviews, datalad/annex, etc.)
- Render images for CLIs in RTD: should we embed links inside the docstrings (as in https://ivadomed.org/en/latest/scripts.html#ivadomed-visualize-transforms), or do it another way?
    - to consider: currently, RTD renders the literal output of the help
    - we would need to change it to render as “module” with sphinx (collateral damages?)
    - decision: go with the current approach (display help output) and add images above it (taken from the SCT course/sourceforge)
- Porting SCT course in RTD
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2857

2020-08-11

- welcome Joshua 👋
- new website: https://spinalcordtoolbox.com
    - suggestions? feedback?
    - should the forum have the address: https://spinalcordtoolbox.com/forum ? or https://forum.spinalcordtoolbox.com? is that a problem if this is already hosted under https://spinalcordmri.org → https://forum.spinalcordmri.org/c/sct/8 ?
- next release: major or minor?
    - arguments for major: new website
    - changes in CLI
    - change of license: LGPLv3 → any additional thoughts (see discussion on slack)
    - sct_deepseg → announcement of future deprecation of sct_deepseg_*
    - changes in binaries
    - **Joshua:** we've been using 4.3.1 (i.e. minor) for the GH milestone (https://github.com/neuropoly/spinalcordtoolbox/milestone/39) but could be changed
    - → ***we decided for major release!*** 🎉
- When?
    - current bottlenecks:
        - changes in CLI. (msct_parser -> argparse, verbosity, etc.) ETA?
        - RTD version.txt fix https://github.com/neuropoly/spinalcordtoolbox/issues/2832
        - "Parts of this page are note secure - use SSL for forum" fixed!
        - **Joshua:** Travis Windows builds are failing since Aug 11, see: https://github.com/neuropoly/spinalcordtoolbox/issues/2838
    - any other changes before release?
        - MPI: https://github.com/neuropoly/spinalcordtoolbox/issues/2806
- tagging releases: vX.Y.Z vs. X.Y.Z
    - Relevant PEPs: https://www.python.org/dev/peps/pep-0101/, https://www.python.org/dev/peps/pep-0440/
    - ***No strong opinion either way, so we keep status quo (i.e. XYZ)***

Action tasks

- AF: redirect https://forum.spinalcordtoolbox.com → https://forum.spinalcordmri.org/c/sct/8 → fixed
- Redirect www.spinalcordtoolbox.com -> spinalcordtoolbox.com (currently not working?) → fixed

2020-07-28

Data management

- welcome Joshua 👋
- original issue: https://github.com/neuropoly/spinalcordtoolbox/issues/2788
    - collateral issue: https://github.com/spine-generic/data-multi-subject/issues/13
    - conp: https://portal.conp.ca/about
- new ANTs binaries: https://github.com/neuropoly/spinalcordtoolbox/issues/2779

Decisions:

- we will move spine-generic data to a datalad/git-annex repos
    - why not openneuro: https://github.com/spine-generic/spine-generic/issues/97
    - Nick will help
    - where to host: osf → no (china, iran)
    - note: we cannot use github with git-annex
    - local server with JBOD: https://storehousetech.com/jbod?gclid=CjwKCAjwmf_4BRABEiwAGhDfSZ9RiqmyelaGs_vLOI-XGrsZU-UuLG6bIZBkPtNDLnIYYoewcxwa4RoC1hwQAvD_BwE
    - buy VPS space and put our server there:
        - companies: OVH (possibly unlimited BW), AWS

Action tasks:

- AJ: comparative table for VPS
- AJ/NG: will help setting up datalad/git-annex server for spine-generic

2020-07-14

- Script entry points: https://github.com/neuropoly/spinalcordtoolbox/pull/2759
- API doc: https://github.com/neuropoly/spinalcordtoolbox/pull/2781
- Data for pytest: https://github.com/neuropoly/spinalcordtoolbox/issues/2775
- Data version tracking: https://github.com/neuropoly/spinalcordtoolbox/issues/2788
    - scenario:
        - Testing
            - testing data is light and will not be changed moment to moment.
                - Light enough to be downloaded each use
        - Large data processed with sct_run_batch
            - Data is heavy
            - We will assume data will not be manipulated by the user or their tools
                - The data should be marked read-only (chmod -R -r dataset/)
                - Checksumming could be done on the archive
        - Training models with ivadomed
            - Model's json config file can include the URL of the data to use → approach compatible with distriploy-created list of URLs
            - The data used for these models are private medical data
                - So hosting them on Github, even on a private, paid, github account, is not ideal.
            - ***question: can distriploy work with private git server?*** Nick proposed a solution with local gitlab/gitea/`git archive` cli, which can generate release tarball, and with within-VPN http connection we could access those
            - ***private GH?***
                - privacy issues if hosted in the cloud
    - Solutions:
        - solution 1: tarball (via https://github.com/neuropoly/distriploy)
            - For each version of a dataset, we would version tag it *on Github*
            - Then we run distriploy which does `git archive` and uploads the resulting .tar.gz to github and to other mirror sites with the version tag in its filename
            - We would generate a checksum over the tarball and put it into our data downloading script (this is the same approach taken by https://wiki.archlinux.org/index.php/PKGBUILD)
            - For private datasets, we would either:
                - install a local Gitea/Gitlab server, and use it like Github, generating releases and uploading the tarball to them
                - Use `git archive`
            - PRO:
            - CON:

            - We need to add a way to embed the version tag into the tarball so that projects making use of the dataset can detect it automatically
            - There's no easy guarantee against corruption *once the tarball is in unpacked and in use*; the only prudent course is to reunpack it on every use. Perhaps making sure to unpack it with all the files set to read-only helps, though that is a weaker guarantee than per-file checksums or what git does.
    - solution 2: git clone
        - Each version of a dataset is automatically versioned, by git SHA IDs, or git tag (accessible by `git describe --always --dirty`, or whatever https://pypi.org/project/setuptools-scm/ does)
        -
        - CON:
            - Git has file size
                - Workaround: git clone --depth 1
                - Workaround: use git-annex, to support partial checkouts
                    - Con: the UI is difficult.
                - Workaround: use git-lfs, which is another way to support partial checkouts
                    - Con: only supports one download server, and it must be either Github (expensive) or Gitea/Gitlab (infrastructure we would have to maintain)
- things to consider
    - we have a data release system in place: https://github.com/neuropoly/distriploy for public data
        - we run distriploy, we get a list of URLs (incl. mirrors)
        - we copy those URLs in SCT code (or other projects)
    - for private data: Nick on it (local git server)
    - in SCT we have an API to download data (spinalcordtoolbox.download), where we can add checks for versions
        - problem with that: if we use data that were not downloaded by SCT, that's a problem (e.g. sct_run_batch applied to external data, e.g. data-spine-generic-single → currently on github) https://github.com/spine-generic/data-single-subject/releases/tag/v1.0.0
    - Manifest file could be added to the data
        - For inspiration: https://www.python.org/dev/peps/pep-0427/, defining .whl format

Action tasks

- Julien: move the scenario section to https://github.com/neuropoly/spinalcordtoolbox/issues/2788
  tmr 5pm
-

2020-06-30

- Data management: JCA/JC
    - update/roadmap
- spine generic: openneuro disaster (JCA)
    - issue: https://github.com/sct-pipeline/spine-generic/issues/97
    - new org/repos: https://github.com/spine-generic
    - recent problem: file >100MB on the multi-subject: https://github.com/spine-generic/data-multi-subject/issues/2#issuecomment-652010998
    - https://github.com/spine-generic/data-multi-subject/issues/3
- old PRs
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2682
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2679
- Jan Valosek
    - sct_run_batch parallel mode crashed when one certain process failed:
      https://github.com/sct-pipeline/spine-generic/issues/88
      https://github.com/neuropoly/spinalcordtoolbox/issues/2725
      issue opened: https://github.com/neuropoly/spinalcordtoolbox/issues/2767

2020-06-16

- Charley:
    - sct_deepseg with a two-step pipeline, ie 2 models run one before the other, ie input of the first one is used as additional input of the second one (second model's input = input image + first model's output): https://github.com/neuropoly/spinalcordtoolbox/issues/2744
    - sct_deepseg: how to deal with model versions: here we check if the model has been installed locally, but we are not checking if it is the latest version.
    - Small spine_generic dataset looking for a kind host.
        - context: https://ivadomed.org/en/latest/tutorials.html
- Git large file storage: https://git-lfs.github.com/
    - Potential solution for dealing with large models (more than 100MB) without having commits blocked by Github

Action tasks

- Saulo: work on solution for uploading large files with git-lfs, and propose a strategy for deepseg models for ivadomed projects.

2020-06-02

- Julien
    - CLI: after giving it additional thoughts, i’m backing off from the idea of changing the CLI to have non-boolean fields (see discussion on slack). So for now, let’s keep it as it is, and for new functions, we could adopt both conventions if it makes sense.
- Ajora
    - Quick intro
- Jan
    - Spine-generic - anything else to work on (I could help with)? https://spine-generic.readthedocs.io/en/latest/index.html
- Chris
    - Email/SMS notifications (Issue: **https://github.com/neuropoly/spinalcordtoolbox/issues/2726#issuecomment-633272263, PR: https://github.com/neuropoly/spinalcordtoolbox/pull/2732#issuecomment-636590807)**
- Julien
    - deepseg models hosting location https://github.com/neuropoly/ivado-medical-imaging/issues/269
    - Jerome is suggesting to have deepseg models into their own repos. Pros: GH accessible from China/Iran.
      Plan is to go along this direction: https://github.com/neuropoly/spinalcordtoolbox/pull/2733, only for “production” models. For “prototype” models, they could stay local in the lab.

Action Tasks

- Chris: Investigate just using sendmail and offering configuration instructions for email notification.

2020-05-19

Agenda (please add your name in order to know who added each item):

- Julien:
    - Git for dummies: from Nick: “Also, as you go, it helps to git rebase -i and use 'fixup' to hide undos. Then your conflicts will be minimized.” ; “And when you do submit the PR, make sure to rebase immediately on the PR branch as you take code review”
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2415
    - Discussion on CLI: https://github.com/neuropoly/spinalcordtoolbox/pull/2639#discussion_r426245434
- Charley
    - Segment_volume: retrocompatibility issues to come → linked to metadata update https://github.com/neuropoly/spinalcordtoolbox/issues/2695
    - Tests sct_deepseg: https://github.com/neuropoly/spinalcordtoolbox/issues/2714 → layers in ivadomed + SCT?
    - https://github.com/neuropoly/ivado-medical-imaging/issues/225 → due to old model implementation
- Alex:
    - Bids-neuropoly: https://pypi.org/project/bids-neuropoly/ → contact Christian to migrate package to neuropoly
        - Create release integration → https://github.com/neuropoly/bids_neuropoly/pull/13 (thanks Olivier for helping)

- Paul: openneuro: not able to condition import on subject and version at the same time

Minutes

- CLI: we decided to adopt the “linux” convention, i.e. “-v” instead of “-v 1”. To avoid breaking people’s pipeline, we will announce future deprecation. We could deprecate as of v5.0. For new functions, we can already adopt this new convention. Info needs to go in the contribution/wiki → https://github.com/neuropoly/spinalcordtoolbox/wiki/CLI
- pypi/GH packaging of binary
    - argument for *not* hosting on pypi is to avoid crowding pypi with additional namespaces from sct. We have ~10-20 packages, so that might be a bit abusive.
- segment_volume()
    - we need to track version of models → if ivadomed evolves, old models will break.
    - CI should be enough: https://github.com/neuropoly/spinalcordtoolbox/issues/2714
- Packaging models for sct_deepseg
    - Jerome suggestion: ONNX → https://pytorch.org/docs/stable/onnx.html
    - package would include:
        - model.pt (or onnx…)
        - training.json
        - inference.json

        - log.json
        - image.nii.gz
        - image_seg.nii.gz
- testing sct_deepseg vs. ivadomed
    - consensus is to test at both end, because models used by SCT are hosted on OSF-SCT and we don,t want to create SCT-dependency from ivadomed.
    - for facilitating testing, we could add an example image in the package, along with a segmentation (for dice comparison).
- Warning pytorch:
    - https://github.com/neuropoly/ivado-medical-imaging/issues/225
    - cause: old model implementation
    - potential solution (Jerome) incl. source code in model, and do the inference from the model itself (does not rely on ivadomed code anymore during inference).
    - Please document the issue 225
- openneuro: ask forum neurostar/openneuro if possible to use both subject and version to fetch data

2020-05-05

Agenda (please add your name in order to know who added each item):

- Paul: internship, early may → early sept
    - Possible project: CSA on rescaled images to check sensitivity to detect subtle atrophy
- Introducing Saulo
- Julien: single vs. double dash for flags vs. both
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2658#discussion_r413459855
- Andréanne: Add PEP8 + pylint check in Travis
    - Related to: https://github.com/neuropoly/spinalcordtoolbox/pull/2690
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2439
    - https://github.com/neuropoly/spinalcordtoolbox/issues/1538 (first issue)
- Charley: sct_analyze_lesion: https://github.com/neuropoly/spinalcordtoolbox/pull/2682
- Charley: http://forum.spinalcordmri.org/t/segmetation-centerline-errors/352/14
- Alex/Julien: Datalad status
- Nick: dependencies update:
    1. updating ANTS (https://github.com/neuropoly/spinalcordtoolbox/pull/2642), stalled out verifying and stabilizing the results, but it's stable and ready for review now.
    2. updating ctrDetect
    3. Adding license files
    4. Using direct CI builds
- Nick: testing more distros in CI https://github.com/neuropoly/spinalcordtoolbox/issues/2313
- Nick: but dropping centos6 https://github.com/neuropoly/spinalcordtoolbox/issues/2675
- Chris: Can someone with a mac look at: https://github.com/neuropoly/spinalcordtoolbox/pull/2685
-

Action tasks

- Single vs. double convention: we decided to stick with single dash long word
    - AF: pls document (in wiki)→https://github.com/neuropoly/spinalcordtoolbox/wiki/Dash-for-flags
- Verbose, boolean flags → we will use “-v”, “-vv” for more and more more verbose. And slowly remove all the explicit 0/1 boolean flags.
- NG: add PEP8 check with pylint
    - Ben: add instructions to get hooks to run pylint locally
- CG: when training new model pls add the datalad hashtag inside the json file
- AF: test PR 2685 → done

2020-04-21

Agenda (please add your name in order to know who added each item):

- Julien: Status of ANTs binaries
    - Nick: Freshly built in CI, published to https://github.com/kousu/ANTs/releases, but failing the tests on https://github.com/neuropoly/spinalcordtoolbox/pull/2642
        - 1. The DMRI motion correction test is giving different results; we need to assess visually what the differences are.
            - Reproducible ants results: https://github.com/ANTsX/ANTs/issues/976
            -
        - 2. OS X should be rebuilt with -mmacosx-version-min=10.12
- Julien: Status of sct_deepseg: https://github.com/neuropoly/spinalcordtoolbox/pull/2639
    - Julien: Travis failing
        - https://travis-ci.org/github/neuropoly/spinalcordtoolbox/jobs/677424561
        - If no easy solution, we will drop support for ubuntu 14.04
    - Julien: Integration of ivadomed: lighter pytorch for CPU-only?
        - Charley will open issue on ivadomed to check if pytorch-cpu only is sufficient for inferences
    - Julien: Discussion about postprocessing default fields: in json metadata or in SCT code.
        - Pros of json: external people can create models and set default values for postproc in the json without needing to touch sct code.
        - Cons of json: heavy maintenance (e.g. if we want to add a field, we need to download/edit/upload all models), less clear (having all fields in SCT code is convenient)
        - Nick: possibility to have CI package our models (and populate json fields)
- Julien: status of moco (Jan)
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2664
    - Create synthetic data for testing moco?
    - Info about moco in spinal dmri: http://forum.spinalcordmri.org/t/how-to-correct-for-distortions-in-spinal-cord-diffusion-mri-data/326
- Julien: sct_run_batch (Chris)
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2658
- Julien: status of sct logo in fsleyes (Jan):
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2657
    - Jan: I have just got answer from wxPython maintainer - https://github.com/wxWidgets/Phoenix/issues/1588#issuecomment-617420295
    - Another fsleyes plugin example: https://github.com/neuropoly/axondeepseg
        - https://github.com/neuropoly/axondeepseg/blob/master/ads_plugin.py#L59
- Nick: Packaging plan: https://github.com/neuropoly/spinalcordtoolbox/issues/2669
    - Julien: ctrDetect → @Nick, needs discussion?
        - https://github.com/neuropoly/spinalcordtoolbox/pull/2666

    - Julien: Status of binary CI-building (Nick)
        - https://github.com/neuropoly/spinalcordtoolbox/pull/2668
        - Purpose of latest uploads? https://osf.io/6zbyf/
    - Nick: new neuropoly repos?
        - neuropoly/ANTs (or neuropoly/spinalcordtoolbox-ants. or both?)
        - neuropoly/ctrDetect (it can be empty; we'll fill it when we get the code)
        - neuropoly/spinalcordtoolbox-dev or neuropoly/spinalcordtoolbox with a -dev release posted every so often?
        - neuropoly/spinalcordtoolbox-binaries
- Julien: “draft” feature on PR
    - Use instead of “WIP”
    - Need to update: https://github.com/neuropoly/spinalcordtoolbox/blob/master/CONTRIBUTING.rst#pr-title

2020-04-07

Agenda:

- Introduce Jan Valosek
- Julien: new button “sponsor”
    - WIP: Some errors were encountered when parsing the FUNDING.yml file:
- Charley: https://github.com/neuropoly/ivado-medical-imaging/pull/184
- Julien: sct_deepseg: https://github.com/neuropoly/spinalcordtoolbox/pull/2639
- Nick: cross-platform build bot for ANTs:
    - Follow up to http://forum.spinalcordmri.org/t/sct-fmri-moco-very-very-slow/365/5
    - Cross-platform via https://help.github.com/en/actions/configuring-and-managing-workflows/configuring-a-workflow#configuring-a-build-matrix
    - WIP: https://github.com/kousu/ANTs/pull/3/checks
    - Testing strategies?
        - Current strategy: run `./batch_processing.sh`; final summary archived to release notes on https://github.com/neuropoly/spinalcordtoolbox/releases for manual inspection.
    - Proposal: take on maintenance of official packages?
        - Motivation: vendoring makes builds very slow and poorly integrated with the systems they run on, or depends on distributing opaque binary blobs; it’s slower to get fixes published but can be more efficient worldwide to invest in making stable, canonical binary packages for each OS.
        - Debian/Ubuntu: https://tracker.debian.org/pkg/ants
            - Abandoned: https://tracker.debian.org/news/873587/ants-removed-from-testing/, and the support forums on http://neuro.debian.net/about.html#chap-contacts are missing
                - https://bugs.debian.org/cgi-bin/bugreport.cgi?bug=872741
                - https://bugs.debian.org/cgi-bin/bugreport.cgi?bug=909833
        - Arch: up to date but fragile
            - https://aur.archlinux.org/packages/ants/ which uses https://aur.archlinux.org/packages/insight-toolkit and https://aur.archlinux.org/packages/ants-git which builds ITK inline
        - OS X:
            - ANTS is not packaged but ITK is up to date (https://github.com/Homebrew/homebrew-core/blob/master/Formula/itk.rb)
        - CentOS:
            - Non-existent as far as I can tell.
        - NixOS:
            - https://github.com/NixOS/nixpkgs/blob/master/pkgs/applications/science/biology/ants/default.nix
            -

    - Counterproposal: declare the docker version the only supported version of SCT?

Action tasks

- JCA: follow up sponsorship info, blababla

2020-03-24

Agenda

- JCA: Introduce Paul
    - Starting date: beginning of early may → early sept
- JCA: schedule
- JCA: discussion on SCT install strategy: https://github.com/neuropoly/spinalcordtoolbox/issues/2622
- JCA: distros compatibilities https://github.com/neuropoly/spinalcordtoolbox/pull/2642 If centos6 doesn't work with python's libraries (TF), should we bother compiling ANTs for centos6?
- Ben: process of code review for larger PRs? + slack message
    - https://github.com/neuropoly/spinalcordtoolbox/pull/2634
- Lucas: WSL
- Alex:
    - sct_testing/large migration :
        - 1336/1574 → 238 subjects left to migrate
    - Develop tool to check contents of sct_testing/large based on discussions :
        - Loop across the subjects listed in the participants.tsv file --> check if nii image and its ground truths are available (nifti file). Run the inverse test as well (i.e. look for files physically present but not listed in the tsv
        - Regarding the .json --> we were checking if there were all present when we were playing with FiLM approach (use metadata --> use json files) --> we have not run this test for a while
        - A start point would be: https://github.com/neuropoly/bids_neuropoly/blob/master/bids_neuropoly/bids.py
- Charley: https://github.com/neuropoly/spinalcordtoolbox/pull/2639
    - sct_deepseg

Action tasks

- JCA: move meeting to 4:30pm + IVADO → Alex:changed time in calendar
- Chris+Alex (done - remarks: installation is slow ~45min)+Paul: try WSL SCT install: https://github.com/neuropoly/spinalcordtoolbox/wiki/SCT-on-Windows-10:-Installation-instruction-for-SCT-on-Windows-subsytem-for-linux

- Lucas: Installation: Update README to remove VM, replace Docker with this (only for ubuntu): https://github.com/neuropoly/spinalcordtoolbox/wiki/testing#run-docker-image and add a headings for WSL with link to wiki.
- JCA: centos6 compatibility: given that centos6 will drop support soon, we decided that if the ubuntu-compiled binaries work with centos7, we can drop the “centos6 case” and only maintain one set of binaries for linux.
- Alex: pybids, internal custom scripts
- Alex: contact basile to install datalad for managing our internal dataset → done

2020-03-10

Agenda

1. Introducing Nick
2. Bring the ivadomed code into production:
    a. USER request: http://forum.spinalcordmri.org/t/segmetation-centerline-errors/352
    b. https://github.com/neuropoly/spinalcordtoolbox/issues/2626
    c. https://github.com/neuropoly/ivado-medical-imaging/issues/154
    d. https://github.com/neuropoly/ivado-medical-imaging/pull/155/files
    e. Things to consider:
        i. Do a pipy release of neuropoly/medicaltorch
        ii. Upload ivadomed package to pipy
3. Olivier : Training of ivadomed on mice data
    a. https://docs.google.com/presentation/d/1XHCJtD4GMKUg9UidrxZQgMjySqPBZbLLmc7szqmlRVs/edit?usp=sharing
    b. Include only slices with GT (n=8)
    c. Issue with dice score=None but dice loss is fine
4. Testing itk->fsl: https://github.com/neuropoly/spinalcordtoolbox/pull/2529
    a. Lucas and Anthime tested both backward and forward deformations on the straightening and output of sct_register_to_template (only on the T2).
    b. Chris could test with another orientation.
5. Sct_utils refactor: https://github.com/neuropoly/spinalcordtoolbox/issues/2627
6. Parallel QC crash: https://github.com/neuropoly/spinalcordtoolbox/pull/2628
7. Parser error generation in scripts: https://github.com/neuropoly/spinalcordtoolbox/pull/2621
8. Change schedule wrt. Australia

Action tasks

- Lucas: add point on IVADOmed agenda about HEMIS for release
- Julien: add Nick in GH → done

2020-02-25

Agenda

1. ITK->FSL transforms update. Particularly discussions in https://github.com/neuropoly/spinalcordtoolbox/pull/2529#issuecomment-590359209 and below.
2. OHBM results
3. Count of SCT citations in abstracts: ISMRM + OHBM + MIDL
4. Windows User (Lucas): https://docs.google.com/presentation/d/1KWbTY1AEIoFYga_kFHO5sAXOAIYkigfp30qFQHWXRKw/edit?usp=sharing
    a. Plan is to drop docker in the long term.
    b. First: we want to check with our windows users if linux subsytem is a working solution
        i. Julien: will contact windows users
        ii. Lucas: will generate doc
5. Pb with *sct_crop_image* fixed.
    a. PR 2604: https://github.com/neuropoly/spinalcordtoolbox/pull/2604
6. Pre-processing **Spine Generic**:
    a. New version for Ivadomed
    b. New patients to exclude (sub-beijingXXXX)
        i. Yes, they should be excluded because MT data are missing
    c. Issue when running on Abbey/ Rosenberg as variables are not exported to the env (https://askubuntu.com/questions/53177/bash-script-to-set-environment-variables-not-working) - need to run source *./parameters.sh*
    d. Would be nice to add *GNU parallel* **option** to *sct_run_batch*.

2020-02-13

Agenda

- JCA: Welcome Chris + Ben
- JCA: PR-2529: we might want to close and re-open (contaminated by GH's repos fat removal)
    - Ben will do a rebase from master-- that should solve it
- JCA/Chris: Transforming ITK-style warping field to FSL/SPM-style produces error when used #2525. Status/discussions
- JCA: what to do with: https://github.com/neuropoly/spinalcordtoolbox/issues/1622
- CG: Atrophy: https://github.com/neuropoly/spinalcordtoolbox/issues/2590
- CG: CSA normalization: https://github.com/neuropoly/spinalcordtoolbox/issues/2543
- Ivado-medical-imaging: https://github.com/neuropoly/ivado-medical-imaging

Action tasks

- Ben will do a rebase from master in PR2529

2020-01-28

Agenda

- Debriefing after SCT's course in London (Julien)
  - 35 people at the course
  - Help: Olivier + Simon + Ferran
  - Important things to note: we saved time by making sure SCT was preinstalled in almost all users
    - 2 exceptions: 1: windows TRES lent , 2: OSX hardware too old (incompatiblity with TF)
  - Will redo in London 2021 -- maybe in MTL 2020 OHBM
    - Check brainhack/hackathon ppl-- ask for schedule-- how to submit, etc.
      - Lucas will do the follow-up
- Lucas:
  - sct docker .
    - https://github.com/neuropoly/sct_docker/pull/51
    - To generate a container with the new plugin we will need a new release.
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2587
- IvadoMed:
  - Anthime: Adaptative Learning + CSF Segmentation
    - https://docs.google.com/presentation/d/1_fpORSFh1qw4Wak5HjLgB_Tr7Y_te47JEhmrzNamvHI/edit?usp=sharing
  - Olivier : film on inter-rater : huge weight initialization variability (from 0.0 of dice to 10% better than U-net)
  - Charley:
    - OptiC for Tumour
    - Uncertainty, WIP: https://github.com/neuropoly/ivado-medical-imaging/pull/134

2020-01-14

Agenda

- SCT course : https://github.com/neuropoly/spinalcordtoolbox/projects/11
    - LR: check if permission to generate new container
- JCA: fsleyes integration
- AF: reminder to do the USB sticks on thursday
- Should we create a new presentation for future use ?
    - Option : https://docs.google.com/presentation/d/1EPld79JVwjrcD3G9rxUqJFByFH436e4bxGHlq5xwFGk/edit?usp=sharing

Minutes

- We decided to provide a gslide link for the course
    - We need to change the slide that says “open the batch processing”
    - We need to re-export by adjusting the master template of the gslide
    - We need to add the link to the README
        - Small link? → YES: AF can you check?
    - Create a pdf link (with comments) and make it available on OSF+neuropoly
        - AF: check if possible to use OSF API to get static version of gslide
    - The idea for each course is to freeze a gslide version and get the link
        - Anthime check how to do that

2019-12-18

Agenda

- Julien:
    - Release
    - Fat in repos, create new organization: https://github.com/neuropoly/spinalcordtoolbox/issues/1823
- SCT course : https://github.com/neuropoly/spinalcordtoolbox/projects/11
- Charley:
    - https://github.com/neuropoly/ivado-medical-imaging/pull/126
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2537
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2542
    - https://github.com/neuropoly/spinalcordtoolbox/issues/2543
    -

2019-12-05

Agenda:

- Julien: release 4.2.0
- Olivier : open source ivadomed? (to eventually implement RTD)
- Charley:
    - Ivadomed repo cleaning, WIP, todolist
    - Quantify cord atrophy & CSAn
    - SCT course: how can we help
- Lucas :
    - Update on vertebral labeling: https://docs.google.com/presentation/d/1yfex6qh3maGpOpA808mC3mYfTg5dBB78-_EHnCsYVxI/edit?usp=sharing