# bioc-teaching

# Bioconductor training group notes

(Bioconductor & Carpentries)

https://meet.jit.si/BioconductorTeaching

## Table of contents

**Table of contents**

### 2025-10-13, 3-4 pm CEST

**Attending**:
**Regrets**:

- Welcome and introduction of new attendees
- BiocHowTos
    - Suggestion from Ellis Patrick to restructure the single package into one package per HowTo

### 2025-09-08, 3-4 pm CEST

**Attending**: Charlotte, Izabela, Samuel, Jenny, Fabricio, Chioma, Laurent, Tim, Robert, Susan
**Regrets**:

- Welcome and introduction of new attendees
- Ethiopia workshop recap
    - blog post in progress
- Hacktoberfest planning
    - https://hacktoberfest.com/
    - Sweave -> Rmd vignettes
    - bioc-rnaseq

    - Bioc-project
    - Bioc-intro issues
    - core Bioc packages
    - Course translations
- Note/reminder on Bioc instructors independence as to who they teach for (Physalia, instats…)
- Bioc-intro still waiting for reviewers
- EuroBioC Carpentry workshops:
    - https://training.bioconductor.org/workshops/2025-09-EuroBioC/rna-seq/
    - https://training.bioconductor.org/workshops/2025-09-EuroBioC/scrna-seq/

## 2025-08-11, 3-4 pm CEST

**Attending**: Jenny, Wes, Hamdi, Susan, Maria, Fabricio
**Regrets**: Laurent, Charlotte, Fred

- Welcome and introduction of new attendees
- From Vince in #education-and-training: “Next request for NHGRI funding …”
    - 1) What are current practices related to assessing effectiveness of educational efforts?
        - Carpentries pre & post assessments (don’t use official one as that goes to Carpentries)
        - These are/aren’t tracked per individual pre & post, just aggregate.
        - Within workshop formative assessments
- 2) What are the methods for determining priorities for starting new training materials or courses? DO we want to have a formally committed/salaried individual who can help establish metrics and assemble information on needs and priorities?
        - Workshop requests in conferences and workshops
        - Whomever is willing to develop the workshop
            - Microbiome - Leo Lahti’s
            - S4 OO programing for package development
            - Epigenetics
            - CosMix/GeoMix
            - Flow Cytometry
        - Having a dedicated, paid person would help shepherd new workshops along. Also have this person get certified to run training workshops for new instructors?
            - But would need to expand duties to justify full time position - AI, coordinating, translation and new tools

        - Have CZI funding for 2 to go through Carpentries lesson development; need to be certified https://carpentries.org/lesson-development/
    - Updates on Ethiopian workshop - 160 applied, filtered to 42 but only have room for 25.
    - Will have one in Benin conducted in English with French material (and explanations)
    - EuroBioC workshops in September. First time to teach scrna-seq; 30 signed up so far between bulk and sc https://eurobioc2025.bioconductor.org/pages/carpentryworkshops.html
    - Hacktoberfest?
        - Internal-led push to make known changes in bulk workshop?
            - Pick 24-hr window
            - Have hackpad
            - Have real-time groups working on things
            - Wes volunteered to set this up
    - Plan for on-line versions of workshops in 2026?
        - One in each of the 3 major world timezones
        - Possibly record for YouTube
        - Free for participants; could get a lot more exposure.
    - BiocHowTo - try to get another push of new ones before EuroBioC? Charlotte will have poster there.
        - Need to get more on line to help LLMs get better training material
        - Use ChatGPT/Claude to give first outline of HowTo and then refine/correct
        - Come up with a "HowTo write a HowTo"

## 2025-07-14, 3-4 pm CEST

**Attending**: Trushar, Laurent, Izabela, Betty, Vasileios, Jenny, Fred, Susan, Tim, David, Maria
**Regrets**: Charlotte

- Welcome and introduction of new attendees
- Hacktoberfest (https://hacktoberfest.com/)
    - What can we do to encourage contributions to Bioconductor packages? Encourage developers to add their repositories, add/tag issues. "Office hours"/hackathon sessions where people could come with questions?
    - Carpentries lessons have some open issues that could be suitable.
    - Can maybe use https://github.com/r-devel/r-dev-day as inspiration?
    - Create a Zulip channel? We have one #hacktoberfest
    - Reach out/coordinate with CAB?
    - https://www.educative.io/blog/everything-to-know-hacktoberfest
- BiocHowTo - where to go from here? Publicize, solicit new contributions, …
- Discussion on using generative AI (chatGPT, **Claude**, copilot) in writing code for bioinformatics (and more). [Dr. Holmes quantified Claude as like "four graduate students" (!)]

- Comments from the training BoF at GBCC2025:
    - would be useful to have some more detailed information about the Carpentries modules on the training website
    - it's hard to find the list of Carpentries workshops from the training landing page - could this be restructured? *Update from Maria: Can now be found on Workshops page: https://training.bioconductor.org/workshops/index.html*
    - is it possible to include some form of self-assessment in the modules for online learning?
    - Nathan Sheffield may be interested in contributing an epigenetics lesson
    - https://github.com/Bioconductor/workshop-template (for making a workshop landing page/website)
- Ethiopia workshop
    - 25th to 29th August 2025, BETin, Addis Ababa https://www.betin.gov.et/
- Physalia collaboration: new instructors/courses?
- Discussion about eventual Microbiome material - there's an unmet need for a metagenomics wrapper package and associated teaching material. Request from the Kenya workshop feedback. Possible contacts/developer/instructor: Izabela, Leo, Laura Symul, Susan and Fred #microbiome_metagenome channel on Zulip.
- If there is time: certificates for those that ministered bioconductor workshops

# 2025-06-09, 3-4 pm CEST

**Attending**: Charlotte, Hamdi, David, Vasileios, Maria, Jenny, Robert, Amal, Laurent, Hedia, Fred
**Regrets**: Fabricio

- Welcome
    - New member, Vasileios Lenis, Uni Birmingham. Will be instructor at EuroBioC in Barcelona, Sep 15-16. Planning to teach bulk & single-cell RNA-seq at their uni.
- Restructured minutes into tabs, reordered (recent ones) in reverse chronological order.
- Update on the Bioconductor/Physalia discussions and selection of the official Bioconductor instructors. Blog post planned.
    - How do we define Bioc certified trainers? Carpentries certification + case-by-case. Use recommended not certified.
- BiocHowTo poster for GBCC/EuroBioC: https://docs.google.com/presentation/d/1q0F_wL5Rs3VpQrr7tz2Dm2Si2VDsyH30eMCA4JXwqx4/edit?usp=sharing
- bioc-rnaseq review at Carpentries Lab has started (https://github.com/carpentries-lab/reviews/issues/29)
    - issue with installing packages from r-universe - see https://github.com/carpentries/sandpaper/issues/655. Do we switch to another package than msigdbr?
- AOB

## 2025-05-12, 3-4 pm CEST

**Attending**: Charlotte, Laurent, Fred, Maria, Robert, Jenny
**Regrets**: Fabricio (supervising exams)

- Welcome
- Updates
    - Conference submissions
        - GBCC: Maria on the Bioconductor Africa initiative, poster about the BiocHowTo collection
        - EuroBioC: Maria on the Bioconductor Africa initiative, poster about the BiocHowTo collection
    - The paper is published: https://journals.plos.org/ploscompbiol/article?id=10.1371/journal.pcbi.1012925
- Split notes in a second document? With newest meeting on the top?
- Bioc HowTos
    - PR in progress - waiting for GSVA binaries to be available for macOS arm
    - How specific should the HowTos be? If they're too specific (or too specifically named), it will not be clear that what's presented could be generalized to similar situations (and we would need lots of very similar HowTos), if they're too generic it may also be difficult for people to find the appropriate one.
    - Do we need more extensive guidelines on length, choice of a good title, naming convention? Find a good balance - informative, but not discouraging people from contributing.
    - Might be helpful to make the question that is addressed, and the motivation, explicit in the beginning of the HowTos.
    - Two of the current HowTos conflict somewhat in what they call a "gene model" (TxDb vs GRanges) - do we need conventions here? Should there be a separate HowTo on how to convert between different representations?
    - How to submit a *BiocHowTo* HowTo?
    - Glossary?
    - Collect feedback during conferences - what HowTos would people want to see? Suggestion box.
    - Reward BiocHowTo submissions

## 2025-04-14, 3-4 pm CEST

**Attending**: Laurent Gatto, Marie Hidjo, Fabricio Almeida-Silva, Charlotte Soneson, Fred, Izabela Mamede, Robert Castelo, Susan Holmes, Tim Triche, ChiomaO, Sayumi York, David Shih, Jenny Drnevich, Tobi
**Regrets**: Maria (ISCB-Africa)

- Welcome
- Updates
    - Brazil workshop summary, March 21 (Izabela)
    - Kenya workshop summary, March 24-28 (Laurent/Fabricio). Main take home messages: (1) plan for flexibility, additional rooms; (2) adapt data/examples (and instructor's experience) to the audience. Do we need material for non-model organisms?
    - Paper - submitted final proofs to PLOS CompBio
    - GBCC2025 submission: Jenny: workshop on how to (re-)use bioc-teaching material; Maria: Bioconductor Africa initiative.
- Certificates for instructors teaching Bioc Carpentry workshops (Izabela). Maria has a template.
- Physalia courses
- BiocHowTo - https://github.com/Bioconductor/BiocHowTo - poster at GBCC2025/EuroBioC?
- Bioconductor hackathons
- Bioc-intro incubator review.

## 2025-03-10, 3-4 pm CET

**Attending**: Jenny, Tobi, Fred, Javi, Susan, Fabricio, Tim
**Regrets**: Laurent, Charlotte, Maria

- Welcome
- Updates
    - The paper is accepted for publication in PLOS Computational Biology!
        - Update Arxiv - Robert
        - Moving forward with using LLMs in teaching?
        - The Carpentries are coming out against using LLMs in their workshops - conflict with BioC?
    - The review has started for the bioc-intro submission to the Carpentries Lab
- BiocHowTo
    - Transferred to the Bioconductor GitHub organisation
    - Instructions have been updated/amended based on the discussion in the last meeting
    - Publicize widely yet? One How-To per day?
    - Ask package developers to submit How-Tos?
- Home page of training.bioconductor.org
    - Should we refresh the content? Some sections, like Maintenance, might be too detailed for a home page.
    - Add link to BiocHow Tos
- Bioc Carpentry workshop website template
    - Can we create a lighter template? The current template (based on the Carpentries workshop template) requires Lori to create a new repo in the

    Bioconductor Github organization for each pre-conference workshop eg https://bioconductor.github.io/2024-09-02-RNASeq-EuroBioc/ (and I'll have to ask for another two soon for EuroBioC2025). We only use it for one page to advertise the workshop. Could we have a template that is a page from training.bioconductor.org instead?
- Submit for a talk/poster or a 1.5 hr training session for GBCC2025 based on anything in our paper? Paper abstract submission deadline is April 1st.
    - Jenny filled out the the training survey (https://forms.gle/i34Ag8SHMtBAmpPh7) and indicated I would be interested in leading a workshop on "How to re-use the Bioconductor Carpentry workshop materials for local workshops, including how to have it hosted on Bioconductor Workshop Galaxy"
    - Any of the new Instructor cohort attending GBCC2025?
    - Also do talk on paper?
    - Discuss on slack as submission deadline is April 1st.

## 2025-02-10, 3-4 pm CET

**Attending**: Laurent, Pedro, Javi, Andrew, David, Tobi, Jenny, Charlotte, Maria
**Regrets**:

- Welcome
- Updates
    - paper - revision submitted
    - Nairobi course 24 - 28 March 2025. Currently 100+ applicants, for ~25 places.
    - GBCC2025 training sessions (10 sessions x 1.5h)
    - EuroBioc Pre-conference workshops: bulk and single-cell transcriptomics. Will be call for Bioc Carpentries-certified instructors interested to teach.
    - 1 day versions of Bioc Carpentries RNA-seq workshop being created by Pedro (JSM, August), Izabela (Brazil, March). Connect them.
- BiocHowTo (initialized at https://github.com/csoneson/BiocHowTo)
    - contributions welcome
    - HowTos from https://bioconductor.org/packages/release/bioc/vignettes/GenomicRanges/inst/doc/GenomicRangesHOWTOs.pdf can be moved over
    - Languages - translations of existing HowTos?
    - Review - criteria?
        - Submissions will be reviewed by the training committee
        - Should be short
        - Should use Bioconductor packages

## 2025-01-13, 3-4 pm CET

**Attending**: Jenny, David, Charlotte, Laurent, Javi, Pedro, Tim, Hedia
**Regrets**: Maria (TeSS workshop), Robert, Fred

- Welcome
- Updates:
  - paper: working on revision, to be resubmitted shortly
  - Workshop August 2025, Nashville TN at Joint Statistical Meetings (JSM) - bioc-rnaseq. Accepted. (Pedro Baldoni)
- Website structure and community-developed tutorials
  - Ask for HOWTO community contributions: either suggest one, and/or propose a solution. Do we want a submission form? Or a *Bioconductor-howto Github repository*, with issues for suggestions/discussions and reproducible/executable PR for submissions? Test the code with GH actions? Useful to also point people to the right packages. Will need to document where/how to find easily accessible data.
    For next time, Charlotte will prepare a prototype repo, and everybody to test it by submitting short howtos.
  - Find a python user that could help with a ‘Learning Bioconductor as a python user’ tutorial.

2024

# 2024-12-09, 3-4 pm CET

**Attending**: Jenny, Harvinder, Hamdi, Charlotte, Robert, Fred, Laurent, Rema
**Regrets**: Maria

- Welcome
- Updates:
    - paper: received positive reviews, currently discussing revision
    - `Bioc-scrnaseq:` (renamed OSCA module) is now included in the carpentries incubator https://github.com/carpentries-incubator/bioc-scrnaseq and on https://training.bioconductor.org homepage
- Rearrangement/update/restructuring of https://bioconductor.org/help/course-materials/
    - What goes here, vs on https://training.bioconductor.org/?
- Other topics, or future goals/tasks for the committee
- Website
    - What to put in the "Learn" tab - structure based on the paper?
    - Improved search (e.g. of documentation) - Vince's EOSS project - ontoProc, EDAM
    - Training committee could serve as recommender of training material.
    - Emphasize pedagogical quality of what is written
- Call for community-developed tutorials
    - Express clearly what we are looking for (both format-wise and content-wise)
    - Authors should get something in return - documents will be highlighted/featured prominently on the webpage.
    - We should come up with a set of questions, can also write an example
    - Should address short, focused questions
    - Introduction, list of packages, solution, list of future reading, links to packages
    - Examples: How to cluster scRNA-seq data, how to annotate clusters, how to map protein identifiers to gene identifiers
    - Could also be more of a "guide to…", to help users orient themselves in the package ecosystem
    - Perhaps like https://bioconductor.org/packages/release/bioc/vignettes/GenomicRanges/inst/doc/GenomicRangesHOWTOs.pdf?
    - Example from Sean Davis: https://ibis-project.org/tutorials/ibis-for-pandas-users

# 2024-11-11, 3-4 pm CEST

**Attending**: Jenny, Susan, Robert, Izabela, Hamdi, Charlotte, Andrew, Tim
**Regrets**: Maria, Laurent

- Welcome
- Updates:
    - paper: Initial submission was assigned to the wrong track, lots of back-and-forth to get it re-routed, hopefully now it should be fixed.
- Jenny (from slack): What should be the "recommended" way to use/modify our Carpentries lessons? For example, here at Illinois we are planning on an Intro to R workshop and we want to use some of the BioC materials but we don't have time to do all. We also need to add in some location-specific things and would like to have it all in one nice github.io. There is forking the current repo, but as we don't ever intend to push any changes back I don't think this is best option. Other repos I've seen are set up a template that can be copied but I don't know if that is possible with this.
    - Add a section to training.bioconductor.org describing/exemplifying how the material can be used.
    - https://github.com/Bioconductor/workshop-template
- The Carpentry OSCA/scRNA-Seq module is coming along nicely and Andrew has proposed it to the Carpentries-incubator but hasn't heard back yet from Toby. Also want to discuss what to call it (consistent with other modules?) and possibly adding it to the manuscript before publication.

## 2024-10-14, 3-4 pm CEST

**Attending**: Susan, Amal, Izabela, Laurent, Dania, Charlotte, Javi, Debprasad, Toby, Robert, Hedia, Candace, Jenny, Maria, Rema
**Regrets**:

- Welcome
- Updates
    - Paper status (Charlotte) - submitted to PLOS Computational Biology on October 1 (currently "With Editor"), preprint is up on arXiv: https://arxiv.org/abs/2410.01351
    - Bioconductor Africa Courses 2025 - Instructor Expression of Interest, open until Oct 21, 2024 (Maria)
    - Bioconductor Carpentry – Name clarification (Maria)
    - A recent preprint with quick tips for writing Bioconductor packages might also be of interest to this community: https://doi.org/10.31219/osf.io/wxjky
- Workshops proposed or being planned
  *Let us know if support is needed (promotion, advice, etc.)*
    - October 2024, Tunis - Bioc-intro (Hédia Tnani, Amal Boukteb)
    - March/April 2025, Nairobi, Kenya – Bioconductor course
    - June 2025. GBCC 2025. Joint conference with Galaxy. Won't have time to run 2 day workshops. Workshops to be decided. Jenny leading for Bioc.
    - Summer 2025, Brazil – Bioc-rnaseq for undergraduates, part of an annual bioinformatics course (Izabela Mamede). Local course. In portuguese.
    - August 2025, Belém do Pará, Brazil – Bioc-rnaseq at the Brazilian Genetics Society event, open to a wider audience (Izabela Mamede)

        - Would like someone from Bioconductor to come help teach. In English. Proposal by start of next month. Accommodation covered, need funds to cover travel. Could have a round table about Bioconductor on packages, teaching. Hasn't been a Bioconductor course since 2017. Maria, Izabela, Laurent, Charlotte will discuss in Slack, talk with Vince, CAB could we get funds for the travel. Connect with Benilton who taught the Bioconductor course in 2017.
    - August 2025, Nashville TN at Joint Statistical Meetings (JSM) - bioc-rnaseq. Upon acceptance by the conference organisers. Results will be released in Dec/2024. (Pedro Baldoni)
        - How much do JSM charge for ?
        - If like ASA, Susan says may be possible to negotiate fees eg to enable students from underserved regions to attend
    - September 15-16 2025. EuroBioC 2025 (Robert Castelo)
    - Late 2025, West Africa – Bioconductor course
- Teaching Bioconductor objects to biologists (Dania Machlab) - SciLifeLab
- Bio-swirl proposal (https://swirlstats.com/) – looking for letters of support from developers and educators who'd like to be reviewers of the material (Candace Savonen)
- New training site: https://training.bioconductor.org (Maria)
    - Suggestions for additions/feedback
        - Use GitHub handles for instructors, similar to Carpentries
        - See if page template exists (or add in components) to make it look more like bioconductor.org
- *Add any other items*
    - *bioc-scrnaseq(?) – Oct 10th sprint https://github.com/ccb-hms/osca-workbench/issues/60*

## 2024-09-09, 3-4 pm CEST

**Attending**: Charlotte, Jenny, Laurent, Andrew, Fabricio, Harvinder, Fred, Ludwig, Jacques, Javi, Susan, Rema, Robert
**Regrets**: Maria (on leave)

- Report from EuroBioC BoF session
- Report from pre-EuroBioC Carpentries workshops
    - RNA-seq - may be useful to ask more questions to the applicants in the application form, to gauge the background level/decide how to shape the workshop
    - create a teaching guide for the functional analysis episode
    - What is the process/expectations for updating material once it is in the Carpentries Lab? If we want to make larger changes, is that better done before the inclusion in the Carpentries Lab?
- Follow-up discussion of the scRNA-seq Carpentries lesson (see meeting notes from 2024-05-13)

    - Small exercises now included within materials
    - Next steps towards inclusion in Carpentries and Bioc education page
        - Instructions here: https://github.com/carpentries-incubator
    - https://github.com/ccb-hms/osca-workbench
    - https://ccb-hms.github.io/osca-workbench/
    - Feedback welcome, via issues in the GitHub repo
- Paper status

## 2024-08-19, 3-4 pm CEST

**Attending**: Jenny, Fred, Fabricio, David, Amal, Charlotte, Susan, Laura, Marie, Laurent, Maria, Rema
**Regrets**:

- Presentation of the fr-translation (sub-)working group.
    - New Bioconductor channel #translation-fr
    - Is there an RStudio version in French? See https://github.com/rstudio/rstudio/issues/12717
        - Yes, one can choose their language in global options > general > advanced. (Laura just switched to trying it out).
- Bioconductor workshops in Africa
    - CZI-funded
    - Planning started
    - First one proposed for Nairobi, Kenya, March/April 2025
    - 1 week: bioc-intro, bioc-rnaseq, BYO data. With French translated Bioc Carpentries material available.
    - African + international instructors
    - Will be EOI for Bioc Carpentries instructors
- Bioconductor Carpentries workshop in North Africa,
    - Tunisia in October.
    - Amal planning, will get in touch with Maria.
- Report from pre-BioC2024 Carpentries workshop
- Paper is shaping up - aim to submit by end of September

## 2024-07-08, 3-4 pm CEST

**Attending**: Charlotte, Robert, Javi, Maria, Susan, George, Laurent, Jenny
**Regrets**:

**Agenda**:
- Do Carpentries lessons get a DOI (I could not find one)?
    - Should citation info be added to the lessons eg here: https://github.com/carpentries-incubator/bioc-intro/blob/main/CITATION
- Progress on paper

- Pre-conference workshops
- CZI EOSS 6 grant for Bioconductor training, workshops in Africa. Planning begun, will provide updates at these meetings
    - Coordinate with Susan, Laura Symul (teaching through Gates foundation)
- Next meeting on August 19, 3-4pm CEST (instead of August 12)
- Future plans for the committee
    - submission of lessons to Carpentries Lab (bioc-intro, bio-rnaseq) - then submit papers to JOSE
    - new lessons? Single-cell RNA-seq, microbiome
    - BOF at EuroBioc to advertise and discuss current projects (translation, African workshops, microbiome less..)?

## 2024-06-10, 3-4 pm CEST

**Attending**: Laurent, Jenny, Fred, Javi, Tim, Fabricio
**Regrets**: Charlotte (at a conference, may jump in and out), Maria (at CZI meeting)

**Agenda**:

- Follow-up discussion of the scRNA-seq Carpentries lesson (see previous meeting notes).
    - Ludwig not present, and no news on slack.
- Updates on the teaching paper: material is there, needs streamlining, put 3 different sections together. Next two sessions clash with US holidays. Discussion on slack to change these days.
- Registration for RNA-Seq course at Bioc2024. Planning to have bioc-intro, bioc-rnaseq and bioc-project at EuroBioc2024.
- PR to update links to rendered material on http://new.bioconductor.org/help/education-training/ sent.
- How much time was invested in preparing these lessons? How long until the material needs updated?

## 2024-05-13, 3-4 pm CEST

**Attending**: Laurent, Maria, Arnab, Jenny, Kozo, Javi, Robert, Chris, Ludwig, Anthony, Fred, Maria, Toby.
**Regrets**: Charlotte, Fabricio.

**Agenda**:

- The bioc-rnaseq lesson has not received pull requests with automatic package updates for the past two months (the other two lessons have). Where is the right place to raise an issue about this? Toby will check. Problem seems to be with ggtree package

- Paper draft is progressing with slides of figs/tables. Writing sessions every 2 weeks on Wednesday (same time). Next one is May 22. More contributors welcome. Aim to have a first complete draft by June, and submission by end of summer to PLoS Comp Bio.
- Pre-conference workshops update.
    - Bioc Instructors identified. Need to advertise. https://bioconductor.github.io/2024-07-22-BiocRnaseq-Bioc2024/
    - EuroBioc, Olly enquired with Oxford doctoral school.
- Carpentries Year 2 membership and instructor training update.
- Ludwig will present his plans for a scRNA-seq Carpentries lesson
    - Davide, Marcel, Dario, Chris, Anthony and Ludwig to contribute a lesson on scRNA-Seq. Based on the OSCA book, that is too long/complex for a lesson. ISMB condenses to something more applicable to a 1 - 2 day lessons.
    - Objectives (from ISMB): How to access publicly available data, such as those from the Human Cell Atlas. How to perform data exploration, normalization, and dimensionality reduction. How to identify cell types/states and marker genes. How to correct for batch effects and integrate multiple samples.How to perform differential expression and differential abundance analysis between conditions. How to work with large out-of-memory datasets.
    - Vignettes: Intro to SCE, EDA, cell type annotation, multi-sample analyses, working with large data, accessing data from the HCA.
    - Workbench format: https://github.com/ccb-hms/osca-workbench
    - Questions: How to get into the Carpentries incubator? Add to the Bioconductor teaching page? Community maintenance? Anyone could add their material, and they maintain it solo? How could we add Carpentries guidelines/best practice into the lesson? More exercises?
    - Ludwig to follow-up on slack.
- Kozo will present automatic PRE-TRANSLATION in bioconductor.crowdin.com.
- Kozo will present a plan for regular translation meetings for manual correction (of the PRE-TRANSLATION) leveraging the Carpentries Community Sessions. (youtube video https://www.youtube.com/watch?v=XXcXIx8mAF4)
    - Maintenance of translations when lessons get updated. Versions of translations, following the changes/commits to the original lesson?
    - Translation teams: Robert and Javi for Spanish, Laurent et al. for French.
    - Translation workflow needs to be documented.
    - Translation version control needs to be documented.
    - Crowdin-GitHub sync needs to be documented.

## 2024-04-08, 3-4 pm CEST

**Attending**: Charlotte, Laurent, Jenny, Fred, David, Javi, Almut, Susan, Fabricio, Robert, Toby, Maria
**Regrets**: Dania

**Agenda**:

- Lessons (bioc-intro and bioc-rnaseq) were submitted to Carpentries Lab. Editor/reviewers are being selected at the moment.
- Pre-conference workshops. EuroBioc: Good number of teachers ready to join, with possibility to invite trainees. Bioc: RNA-Seq will probably be run with Jenny and Tim Triche + helpers.
- From last meeting: Maria was asked to talk about Bioc teaching at ELIXIR UK training working group meeting next week - feedback?
    - There might be interest to offer to run workshops at other conferences. We could set up a form for expressions of interest.
- We are invited to report on the teaching committee activities to the CAB this Thursday (April 11) at 12 noon CEST. Suggested discussion points:
    - Carpentries instructor training status
    - Mention the paper plans (both overview and lessons)
    - Summarize organized workshops
    - Offer genomics on-line course via InStats? Or elsewhere?
- Paper draft
    - Section assignments
    - A section on “Ethics of teaching people to use tools they don’t understand”, proposed by Susan. Important to highlight risks of the tools/methods we teach, when some approaches are applicable, when not.
    - Writing sessions - Tue 16 April, 15:00 - 17:00 (using the usual Jitsi link)

## 2024-03-11, 3-4 pm CET

**Attending**: Charlotte, Wes, Fred, Dania, Javi, Susan, Fabricio, Maria, Laurent, Marcel, Robert
**Regrets**:

**Agenda**:

- Update on instructor training selection
    - applicants selected (4 last year, 11 now)
- Maria was asked to talk about Bioc teaching at ELIXIR UK training working group meeting next week
- Paper draft
- JOSE paper(s) for existing lessons

Feedback from Toby regarding lesson and paper submissions : I encourage you to submit the lesson to the Lab now. Your plan is good, to hold off on JOSE submission until the -project and -rnaseq lessons are ready. Lorena at JOSE warned me in the past that they will find it easier to accept submissions bundled together like that.

## 2024-02-12, 3-4 pm CET

**Attending**: Laurent, Wes, Charlotte, Fred, Javi, Ouso, Toby, Maria, Fabricio, Jenny

**Regrets**: Susan, Robert

**Agenda**:
- From Toby - should we change the bioc-rnaseq and bioc-project lessons from pre-alpha stage (to alpha or beta)?
    - bioc-rnaseq -> beta (Charlotte change the config file)
    - bioc-project -> alpha (reach out to Kevin)
    - change in config file
- Pre-conference (BioC, EuroBioC) workshops
    - Grand Rapids, Michigan - July 22-23
    - Oxford, UK - September 2-3
- Updates on instructor application
- Submission of bioc-intro to Carpentries Lab / JOSE
- bioc-project refactoring ideas
    - synchronize somehow between bioc-intro and bioc-project?
    - extend bioc-intro with more Bioconductor-related material? Start with an overview of the SE, motivation? May need to remove something else.
    - tidySummarizedExperiment? May lose some of the 'general R'.
    - remove the 'tidy data' episode in favor of more liaison with Bioconductor in bioc-intro?
    - TODO: rename last section to include Bioconductor in the title.
    - Suggestion: rename ‘r-intro’ and create a new ‘bioc-intro’.
    - Suggestion: spend more time on SE (at least 4 hours), reducing tidyverse, pivot and ggplot2. Although visualisation is an important incentive.
    - TODO: clarify what is teachable material, and what is for info.
- Paper about teaching efforts - coordination with CAB / core

## 2024-01-08, 3-4 pm CET

**Attending**: Laurent, Charlotte, Fred, Javi, Jenny, Fabricio, Robert, Wes
**Regrets**: Susan

**Agenda**:
- Ludwig will present his plans for a scRNA-Seq course, based on the OCSA tutorial at ISMB.
- Application open for next cohort of instructors. Form here. Several applicants interested in helping teach the pre-conference workshops, as well as virtual workshops.
- From Nov meeting: Should we move (submit) from the incubator to the Carpentries’ lab (including a paper to JOSE)? Do we want (at some point) a ‘Bioconductor-carpenty’? Bioc-intro only? (See November notes) Others?
    - There’s a consensus to submit bioc-intro to Carpentries’ lab. Email sent to Toby, as review is currently by invitation only.
    - We can always submit several lessons as a curriculum to JOSE afterwards.

- Bioc-project refactoring ideas: try to make it more teachable material - along the lines of an intro for developer
  - deprecated()/defunct()
  - Chapter on help resources for users (help pages, vignettes, forum, …) and developers (devel guide)
  - get Maria’s input with regard to what already exists on the webpage
  - Liaise with other instructors and BiocClasses working group pour S4 classes section
  - organise a hackathon
  - make sure Kevin can participate
- From Oct meeting: Paper - specific meeting
  - Liaise with Maria with regard to CAB initiative
  - Liaise with Vince and Alex regarding workshop infrastructure (see also *Orchestrating a community-developed computational workshop and accompanying training materials*)
- Kozo organized a Carpentries community session in December, on lesson translation using Crowdin. https://hackmd.io/@joelnitta/SkCSC6ZNT

2023

# 2023-01-16, 3-4 pm CET

**Attending**: Charlotte, Zuguang, Robert, Fabricio, David, Maria, Toby, Laurent
**Regrets**: Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

- These meetings were added to the Bioconductor Event calendar: https://github.com/BioconductorBoards/CABWorkingGroups/issues/50#issuecomment-1368723214
- Can non-certified Carpentries instructors teach e.g. bioc-intro to help the lessons move out of incubator (question from TAB/Kasper)
    - Toby: it depends on where you want the lesson to go - if it is intended for The Carpentries Lab (i.e. it will remain a community lesson) then it is fine to test it out with non-certified Instructors. If you hope it will become official e.g. a new Data Carpentry lesson, then the Instructors would need to be certified. If they are not certified, then I recommend you give them a heads-up on how the lesson is intended to be taught i.e. by live coding/demonstration.
    - Maria: Carpentries Lab as it's to move it out of beta
    - Test and then submit to Carpentries for peer review (at https://github.com/carpentries-lab/reviews)
    - Harvard group planning to teach bioc-intro in March. Toby says would be great if they could fill out the form (see bottom of https://carpentries-incubator.org/)
- Make a plan for the development/finalization of bioc-rnaseq and bioc-project
    - To what level can we teach fastq -> counts? See github issue (sorry Jenny can't be here today, although this should be a continuing discussion)
        - Organize a hackathon for the bioc-rnaseq
        - Carpentries offline effort, to offer Raspberry Pies and/or Arch linux on flash drives. See https://carpentries.org/blog/2022/07/carpentries-offline/ and http://carpentriesoffline.org/
- Checkout process follow-up for trained instructors
- Blog post to update on current instructor selection (Maria)
- Framework for running Bioconductor Carpentries workshops (template for workshop registration/schedule with Bioc logo, feedback form, website/page that lists upcoming workshops with registration dates e.g. something like this)
    - See slack thread on laptop vs. Orchestra vs. AMS
    - Add page/doc to Bioconductor teaching page that lists what workshops are upcoming until we have a better solution
    - Fork Carpentries repo for workshop schedule and make a Bioconductor template that instructors can use (who could do this?)
    - Feedback survey template is linked to from this page in the handbook https://docs.carpentries.org/topic_folders/lesson_development/lesson_pilots.h

        tml#collecting-feedback-on-the-lesson - I am linking the full handbook page because it also contains a bunch of other templates etc that you might find useful.
    - Laurent to start a simple list with we have so far, while we get a better form up and running: https://github.com/Bioconductor/bioconductor-teaching/issues/20
    -
- Events/outreach
    - Paper/blog post. Draft. Possible venues: F1000, PLoS CompBio (this just came out there)
    - Bioc session at ELIXIR All Hands meeting (June)
    - Interest in virtual Carpentries Bioconductor workshops for Tunis R User Group, ISCB North Africa (Hédia)

## 2023-02-13, 3-4 pm CET

**Attending**: Laurent, Jenny, Charlotte, Almut, Fred, Robert, Maria, Pageneck, Marie
**Regrets**:

- A European approach to micro-credentials: anyone heard of these (via Aedin on slack)? Are Carpentries micro-credited? Is this something we should pursue? It might be useful for future funding.
    - https://credly.com as one US possibility
    - Maria will follow up, as she is discussing micro-credentials with her university.
- Discussion about citing the lessons: https://github.com/carpentries-incubator/bioc-project/discussions/36#discussioncomment-4881216
    - Define releases for our lessons at get DOI via zenodo
    - Laurent to do that for bioc-intro.
- Hackathon for bioc-rnaseq lesson development
    - Charlotte, Laurent, Maria, Fabricio, Almut, Fred, Jenny, Toby & invite instructor trainees
    - Transition to workbench before the hackathon
    - Planning meeting Feb 27, 3-5pm CET
    - Maria to let people know on Bioc Slack #education-and-training and #carpentries
- Elixir All Hands meeting June, Bioconductor workshop abstract selected "Opportunities for Bioconductor and ELIXIR communities to co-develop training infrastructures"
- Bioconductor Carpentries blog post update on year 1 (draft in Maria's fork of biocblog here)
- Bioc-project pull request - added section on install.packages?

    - When/who merges? Should we discuss PRs before merging them? See also https://docs.carpentries.org/topic_folders/lesson_development/cac-consult-rubric.html (provided by Toby)
- Submission to BioC2023?

## 2023-03-13, 3-4 pm CET

**Attending**: Zuguang Gu, Susan, Fred, Almut, Charlotte, Maria, Fabricio, Laurent, Robert, David Shih, Marcel
**Regrets**: Jenny

- Prepare a contributions/PR merge guide, responsibilities of maintainers and the education committee, creation of a Bioc Curriculum Advisory Committee (see for example https://docs.carpentries.org/topic_folders/lesson_development/cac-consult-rubric.html)
    - Prepare document listing design decisions of the lessons.
- BioC2023 and EuroBioc2023 submissions
    - BioC2023 workshop: Jul 31-Aug 1, bioc-rnaseq, possible teachers Jenny, Chia Sin..
    - EuroBioC2023 workshop: Sep 18-19, bioc-rnaseq and bioc-intro?, possible teachers Fabricio, Leo, Almut, Olly..
    - Both conferences Birds-of-a-feather (abstract draft here, comments/edits welcome **by Thursday March 16**)
- Mention
    - Code handout request
    - bioc-workshop-template for Bioconductor workshops
        - Draft viewable here, comments/edits welcome
    - Visualisation of all Bioc Carpentries instructors and workshops (to have a list and for future blog article). Please let us know when certified and of any planned workshops.
    - Bioc participation in GTN Smorgasbord, **everyone welcome, please let us know if you'd like to help** e.g. answer questions in Slack
    - Elixir Training Platform meeting in Rome last week & All Hands meeting in June, may collaborate with them for Bioc
        - Training material and events aggregation (TeSS)
        - Training metrics database
        - Learning paths development
        - Single cell community training
- bioc-rnaseq lesson update
- **Recording a lesson**: this would be very valuable for regions that are difficult to access. Difficulty to coherently record an in-person carpentry lesson and make it a useful resource. We could try to plan this during one of the coming (Euro)Bioc conferences.

  For EuroBioc2023: once we have decided what lesson to teach, who teaches it and who can join to help, who would be interested in joining a team to record the lessons and produce an on-line version?
- Next meeting is on Easter Monday (April 10) - do we move it? -> 3 April

## 2023-04-03, 3-4 pm CEST

**Attending**: Jenny, Laurent, Toby, Charlotte, Almut, Fred, Maria, Susan, David, Zuguang, Givanna, Jaclyn, Robert
**Regrets**:

- Discuss/show the Bioconductor teaching material design and maintenance.
    - Add to bioconductor.org teaching page
    - Clarify relation/difference between maintainer and instructors
    - Clearly indicate maintainer to GitHub repos
    - Make sure the right people have admin access to lesson repositories - make sure that everyone creates a new fork of the repositories (using the workbench)
        - bioc-rnaseq: Jenny
        - bioc-project: Kevin
- bioc-rnaseq:
    - questions/keypoints added to episodes in https://github.com/carpentries-incubator/bioc-rnaseq
    - suggestion to have episodes "7a/7b", for DE analysis with DESeq2 and edgeR, respectively.
    - Aim to have a modular structure eventually - for now, start with one.
    - Start from gene counts or Salmon output? -> Gene counts.
    - Failing GH Actions - looks like the same problem with renv that we have run into in other R Markdown-based lessons. See https://github.com/role-model/multidim-biodiv-data/issues/25#issuecomment-1477898715 for some guidance on how to fix it

- Smorgasbord online training week May 22-26 update
    - Bioc tutorials participating are being added to Smorgasbord website (listed at bottom of page here https://gallantries.github.io/video-library/library, fixing speakers etc here https://github.com/gallantries/video-library/pull/74)

## 2023-05-08, 3-4 pm CEST

**Attending**: Charlotte, David, Rema, Susan, Laurent, Jenny, Almut, Maria, Toby, Robert, Zedias, Wes, Samwel

**Regrets**: Fred

- Smorgasbord May 22-26
    - Please let your networks know about the event
    - How do we know what to expect (e.g. how many people)?
    - Learners work through the tutorial using Galaxy setup
    - Don't know how many questions there will be - may be technical, or more directly about the topic. Learners may be coming from the Galaxy side - less familiar with command-line use?
    - Workshop infrastructure is being finalized
    - Virtual machines set up for the week - available afterwards? Not sure how much resources are available for continuous access afterwards. The idea is that it is for learning/temporary (not where you should be running your analysis afterwards).
    - 12-14 workshops currently. Good number to start with, but if someone else wants to present a workshop that is also possible.
- BioC2023 Carpentries RNA-seq workshop
    - Which framework to use (DESeq2 or edgeR/limma)? In any case, first step will be to convert the SummarizedExperiment to another type of object
- EuroBioC2023 Carpentries Intro and RNA-seq workshops
    - Bioc-intro workshop repo: https://github.com/lgatto/2023-09-18-BiocIntro-EuroBioc (will be transferred to Bioconductor later)
    - Organise list of potential instructors helpers of both workshops
    - Fees +/- 50 euros
- bioc-rnaseq lesson
    - Sprints on Wed 10 and Fri 12 at 3 pm (CEST) on https://meet.jit.si/BioconductorTeaching
- Lesson artefacts/handouts:
    - Either Rmd/R scripts from a different action (Charlotte can provide an example)
    - Html files could be downloaded from github gh-pages branch
    - See datacarpentry.org/R-ecology-lesson/ ‘Download handouts’ button (and make_code_handout.R (line 7) script)

# 2023-06-12, 3-4 pm CEST

**Attending**: Laurent, Charlotte, David, Zuguang, Almut, Toby, Fabricio, Fred, Maria, Jenny (from :30)
**Regrets**: Jenny (can get on ~20 min late)

- Smorgasbord Bioc report (Maria)
    - writing a blog post
    - 13 Bioc tutorials

        - Do we know how much time participants spent in each workshop? Ask Alex. Do we need "shorter versions"/subsets of these workshops?
- Elixir All Hands Bioc workshop report (Maria)
    - Maria, Aedin, Leo, Laurent presented workshop on training; identify collaborations with ELIXIR.
    - Successful workshop
    - Meet with the ELIXIR TeSS (aggregation site for training material) group. Need to add Bioschemas information for Bioc material to be automatically included.
        - Toby: re: TeSS metadata - The Carpentries' new lesson Infrastructure includes the basic info needed to conform to the BioSchemas TrainingMaterial specification in lesson websites. We are planning to expand beyond the basics to include all of the fields described in the specification (plus an additional, optional, 'reviewers' field) soon.
        - See lines 501-516 of view-source:https://carpentries-incubator.github.io/bioc-intro/ for example
    - TeSS working group (will be added here this week - https://workinggroups.bioconductor.org/currently-active-working-groups-committees.html), let Maria know if you'd like to join
- Bioconductor website redesign - survey to be circulated tomorrow
- ComplexHeatmap workshop series (Zuguang)
    - From beginner to more advanced
    - Advice on length, number of installments
    - Webinar or hands-on -> webinar, no interactive session
    - Can use Bioc workshop template to provide lesson content, make website etc
    - Suggest to follow the Carpentries development guide, start with personas, prerequisites, learning goals
        - https://cdh.carpentries.org/ and https://carpentries.github.io/lesson-development-training/
- BioC2023 Carpentries RNA-seq workshop update (Jenny)
    - Reorganized the content based on previous meetings
    - Schedule another lesson sprint to work on the material in the near future
- There is a high demand for on-line training, especially in low-income countries (see email from Hedia to Maria). It would be good to discuss the possibility to organise remote workshops (intro and RNA-Seq), and coordinate with the new instructors to see who would be interested in teaching. This could also be a really good action with respect to the CZI who funds the instructor trainings and could possibly lead to a supplement. Infrastructure: https://workshop.bioconductor.org/
    - Think about what we need: instructors, material, a way to interact (slack or similar?), video call platform (breakout rooms?)
    - How many attendees -> how many instructors required? If more than 20-30 attendees, may be better to do asynchronously and for instructors to be available for questions.

    - One-off request, or aim to more regularly host online events separate from the conferences? Use as an opportunity to think about the problem, test solutions, build a setup for the future.
    - Opportunity for Carpentries instructors who may not be able to travel to teach online.
- EuroBioc Carpentries workshops: fees 100 euros (payment to Simone - to check); 15 places reserved from UGhent/VIB
- Next steps for bioc-intro?
    - submit to Carpentries Lab (not 'official' Carpentries lessons, but have passed peer review)
    - open review -> material can be automatically sent to JOSE after review, for publication.
    - Ongoing JOSE review of Metagenomics curriculum: https://github.com/openjournals/jose-reviews/issues/209 & completed Carpentires Lab review of the same: https://github.com/carpentries-lab/reviews/issues/11
    - alternative (not mutually exclusive): get the whole curriculum ready and add to e.g. Data Carpentry (email Data Carpentry steering committee to request a new curriculum to be added - dc-governors@lists.carpentries.org)
    - sufficiently different from ecology intro to R lesson?
    - can make a change in the config file of bioc-intro - from beta to stable. Then wait until the other lessons are more mature and submit as a curriculum.
    - summary of the feedback - currently in email to Laurent, will copy into GitHub issue
        - Toby: you will find a link to a template post-workshop feedback survey for Incubator lessons on this handbook page https://docs.carpentries.org/topic_folders/lesson_development/lesson_pilots.html#collecting-feedback-on-the-lesson - if it would be helpful, you could use this to prepare a ‘bioc-intro pilot workshop feedback survey’ to share with anyone that you know will be teaching the lesson.
- Note from Toby: I have started a (planned) break from The Carpentries core team, which will last until 11th September 2023. I plan to continue attending these meetings and will still be active in the community, on Slack, GitHub, etc. However, you will not be able to contact me on my normal tobyhodges@carpentries.org email address - please get in touch at tbyhdgs@gmail.com if you need to send me an email. Queries that need an official response should be sent to curriculum@carpentries.org or ebecker@carpentries.org (Erin Becker, Associate Director and acting Curriculum Team Lead).

# 2023-07-10, 3-4 pm CEST

**Attending**: Charlotte, Jenny, Givanna, Fred, Zuguang, Almut, Robert, Maria, Marcel
**Regrets**: Laurent

- Communication channels: Givanna suggests having a slack channel to coordinate/discuss the workshop organisation. Any interest? Note that we will also have the workshop repos.
    - Maria to make two private slack channels (one for BioC2023, one for EuroBioC2023)
    - Maria: Done. Named carpentries-workshops-bioc2023 and carpentries-workshops-eurobioc2023
- EuroBioc workshops: need to set up the workshop pages. Here's the bioc-intro one (waiting for the course location to finalise it). Please let me know here or on Github of any changes before I migrate the repo to the Bioconductor Github organisation. Note that I have made several changes to the config and _includes files that I haven't ported to the Bioc workshop template yet. Once the bioc-intro workshop page is good, I am happy to work on the bioc-rnaseq, unless somebody else wants to get started.
    - Set up registration and announce
- Update on bioc-rnaseq lesson/BioC2023 workshop
    - Lessons 1 and 2 : done
    - Lessons 3 and 4 : Jenny
    - Lesson 5 DE: Almut
    - Lesson 6 Gene set: Zuguang
    - Lesson 7: Next steps : Charlotte do outline
    - Lesson 8: Extra design matrices: Charlotte add some text
    - Authors: put for now on https://github.com/carpentries-incubator/bioc-rnaseq/blob/main/index.md
        - Explicitly list maintainers
        - Link to https://github.com/carpentries-incubator/bioc-rnaseq/graphs/contributors
    - LInks to instructions on how to contribute:
        - https://docs.google.com/document/d/12hUqVo2MhgYH9IT8ShJKSZgeMLzjeUh2EKdxM_siWwM/edit
        - Fred's screen shots (Jenny is adding text to notes at bottom): https://docs.google.com/presentation/d/1UIGhICQZsmDfFhc6kEbC_z87CJEPY89nww9eUKt-qYc/edit#slide=id.g2433b202126_0_80

    - 24 people have applied; 6 said they're attending BioC virtually so unlikely to attend.
    - Deadline to have materials done: **Wed July 19th.**
    - Meet again Wed July 19th at the usual time and jitsi link
    - Get backup on https://workshop.bioconductor.org/

# 2023-08-14, 3-4 pm CEST

**Attending**: Charlotte, David, Wes, Susan, Jenny, Maria, Sehyun, Fabricio, Givanna
**Regrets**: Laurent, Fred

- Poster for EuroBioC2023 (draft)
- bioc-rnaseq workshop BioC2023
    - Episode timings
- workshops EuroBioC2023
    - currently one applicant for bioc-intro, two for bioc-rnaseq
    - payment page has been set up
    - meeting to plan EuroBioC RNA-seq workshop in more detail: Mon, Aug 21, 3pm CEST
    - Will ask intern, Anna Powell, to create flyer for circulation similar to BioC2023
- Translation of bioc material
    - Interest from Bioc Carpentries instructor trainees and others in Bioc in teaching/translating Bioc material into Spanish (Javier), Portuguese (Rodrigo) and French (Hedia)
    - Do they need separate repos e.g. 1 per module per language? Should we use DeepL as a first pass then use human feedback?
    - Carpentries Bioconductor translation session (led by Kozo Nishida) Sep 13- https://pad.carpentries.org/community-sessions-2023#L230

## 2023-08-21, 3-4 pm CEST (bioc-rnaseq, EuroBioC2023)

**Attending**: Charlotte, Jenny, Fabricio, Almut, Marcel, Maria, Susan

Planning document: bioc-rnaseq, EuroBioC2023

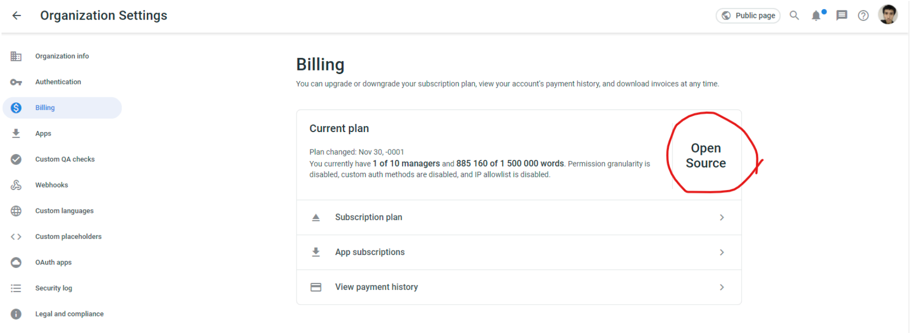
## 2023-09-11, 3-4 pm CEST

**Attending**: Laurent, Charlotte, Jenny, Fred, Marcel, Givanna
**Regrets**: Maria

- EuroBioC workshops
- Poster for EuroBioC2023 (draft)
- Hacktoberfest
- Translation progress from Kozo:
    - successfully set up is the integration of Crowdin, GitHub, and DeepL. So first is automated translation with DeepL then human curation to refine through GitHub/Crowdin.
      https://bioconductor.crowdin.com/bioc-intro
      https://github.com/bioconductor-translations/bioc-intro-translation

- proposing one [Carpentries Community Session]() on Bioconductor translation at a time that is: the early morning of 28th in Japan / the late night of the 27th in Europe / the evening of the 27th in U.S. Add your name here if you're interested to attend: Kozo, Maria,....
- start with bioc-intro translation as proof of principle
    - how many languages? Spanish, Portuguese, French, Arabic, Chinese, Japanese to cover most of the world. Limit on number of languages by Crowdin (**Question for Kozo - how many allowed?**)
        - 546811 / 68029 = 8 more languages can be added to the list of languages to be translated.
    -

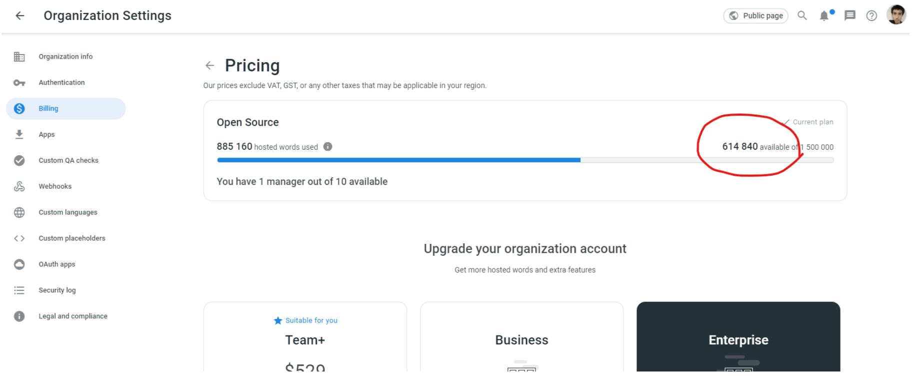
    The bioconductor.crowdin.com Organization Settings



You can upgrade or downgrade your subscription plan, view your account's payment history, and download invoices at any time.

Plan changed: Nov 30, -0001
You currently have **1 of 10 managers** and **885 160 of 1 500 000 words**. Permission granularity is disabled, custom auth methods are disabled, and IP allowlist is disabled.

    -



Our prices exclude VAT, GST, or any other taxes that may be applicable in your region.

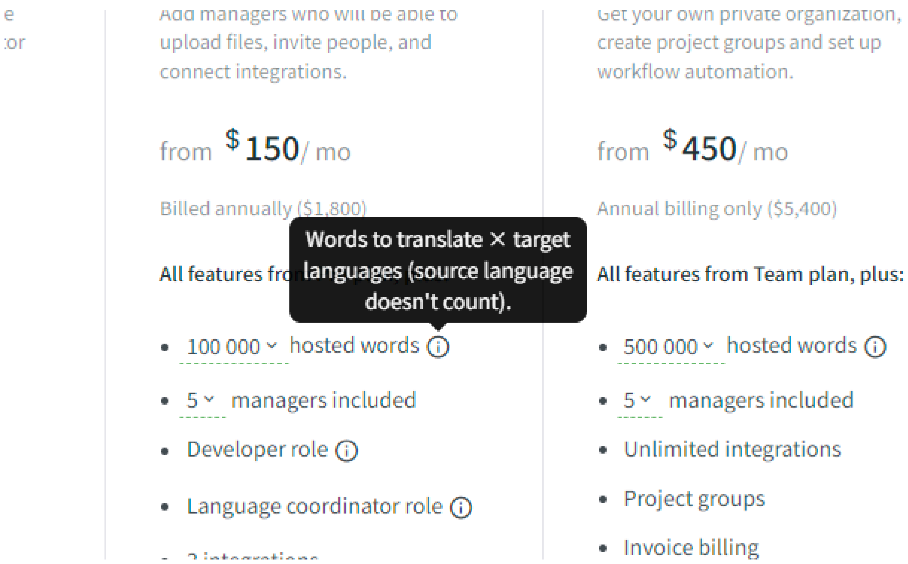
885 160 hosted words used

614 840 available of 1 500 000

You have 1 manager out of 10 available

Get more hosted words and extra features

    -
    -



e
:or

Add managers who will be able to upload files, invite people, and connect integrations.

from $150/ mo

Billed annually ($1,800)

All features fro

Words to translate × target languages (source language doesn't count).

- 100 000 hosted words
- 5 managers included
- Developer role
- Language coordinator role
- 2 integrations

Get your own private organization, create project groups and set up workflow automation.

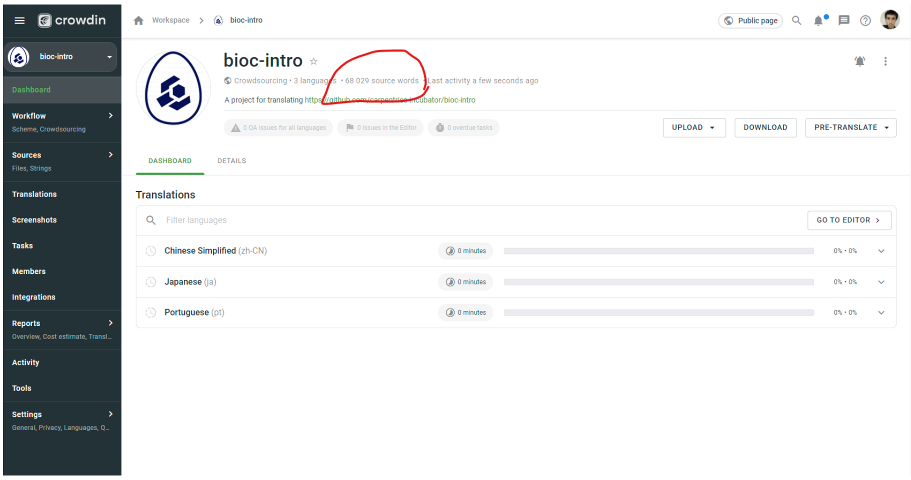
from $450/ mo

Annual billing only ($5,400)

All features from Team plan, plus:

- 500 000 hosted words
- 5 managers included
- Unlimited integrations
- Project groups
- Invoice billing

-
-



bioc-intro

Crowdsourcing • 3 languages • 68 029 source words • Last activity a few seconds ago

A project for translating https://github.com/carpentries-incubator/bioc-intro

0 QA issues for all languages · 0 issues in the Editor · 0 overdue tasks

Translations

| | | |
|---|---|---|
| Chinese Simplified (zh-CN) | 0 minutes | 0% • 0% |
| Japanese (ja) | 0 minutes | 0% • 0% |
| Portuguese (pt) | 0 minutes | 0% • 0% |

-
-
- choose language(s) that has a native speaker(s) to lead translation. **Do we have volunteers?**

# 2023-10-09, 3-4 pm CEST

**Attending**: Charlotte, Laurent, Federica, Zuguang, Jenny, Almut, Robert, Toby, Fred
**Regrets**: Maria

- Recap of EuroBioC workshops
    - bioc-rnaseq comments
        - 20-25 participants
        - feedback requested after each half day (sticky notes) - overall positive, learners appreciated the challenges where they discussed with each other.
        - timings updated based on BioC2023/EuroBioC2023 experiences

        - a bunch of new issues have been added (https://github.com/carpentries-incubator/bioc-rnaseq/issues) - help welcome
        - need code handouts
        - should we define a ggplot theme in the beginning of each episode, to reduce the amount of repetitive typing in plotting sections?
        - should we add some form of 'workflow diagram', explaining what type of data is used for what analysis aspect (counts vs normalized/transformed data)
        - should we add volcano plots? EnhancedVolcano?
    - bioc-intro comments: good feedback on sticky notes; activities for instructors - see notes below.
- Bioc Asia workshop (RNA-seq): Oct 15 (Sun), 09:30-17:30
- Hacktoberfest
    - Google doc here - can add any repos accepting contributions (Kozo has added his Bioc YouTube TimeStamps one), see discussion in #hacktoberfest channel.
- Several people have expressed interest in hosting a workshop - (how) do we organize this on our side? Do we want to provide a set of guidelines/expectations?
- Additional Carpentries-style lessons? Intermediate general R course: apply, writing functions, writing packages, … ?
- Other activities? Should we reactivate the idea of restructuring the teaching material on the Bioconductor website?

**Notes**

Supporting our instructor community:
- Difficult with a global community; much easier for local community
- Systematic debriefing after a workshop; locally, at the workshop and on-line; could have specific on-line meetings with this.
- Specific instructor discussions during conferences
- Related to what's next for this group. We have 20+ instructors so far, plus the next batch coming.
- Observing is very useful. Could pair-up new instructors with more experienced ones.
- We could systematise the organisation of workshops to also offer opportunities and pair up instructors.
- Ask newly-trained instructors to take the lead on some activities.
- Carpentries lesson development training programme: will be announced in 1 week, paid (as instructor training), Bioconductor could budget for some people to join.

Carpentries workshops (https://carpentries.org/workshop_faq/):
- Workshop request form on Amy.
- Request reviewed
- Event object created, to invite instructors to join, then selected until enough instructors involved

- Once instructors have been selected, organisation is handed out to instructors and hosts.
- Register interest through google group or (better) as a Github issue. Info needed: what workshop, where, when, …
- We could publicise this at the top of our workshop pages.
- TODO: add a couple of sentences on our training page on bioconductor.org

Other activities:

- Paper - specific meeting
    - Scope: short about meeting/course
    - Elixir has also some short papers
    - Journal of open source education for a specific lesson
    - Overview of our committee and education efforts with Bioconductor
- Organise teaching material available on the webpage, annotated with labels
- Learning paths
- Elixir, TESS collections, micro-credits

## 2023-11-13, 3-4 pm CET

**Attending**: Laurent, Almut, Fred, David, Jenny
**Regrets**: Charlotte, Robert, Maria

**Agenda**:

- Report from BioC Asia RNA-seq workshop?

**Notes:**

- Teaching committee not present/found under ‘Learn’ tab on new.bioconductor.org
- Fred used the intro material (internal workshops)
    - Carnegie internal Oct 3/4 2022, Oct 12/13 2023
    - JHU/Carnegie/Weill Cornell workshop Dec 5/6 2022, Oct 30/31 2023
- How to keep track of workshops that use our material? Ask what Maria would find most useful.
- Bioc Asia: rna-seq compressed in one day (dropped last 2 modules), good feedback.
- Should we rename ‘Next steps’ with something like ‘Working with Bioconductor’, especially when the intro course is considered as an intro for the domain specific courses (RNA-Seq, single cell, proteomics, …).
- Efforts to start a single-cell course starting from OCSA tutorial at ISMB. Contact is Ludwig Geistlinger.
- Learning pathway: to what extent should intro/rna-seq be pre-requisites for other courses (for example scRNA-Seq)? Or should we add ‘a little bit’ of these in the more advanced courses? There is a lot of implicit knowledge about RNA-Seq that isn’t mentioned/expected for scRNA-Seq for example. See also https://dmgatti.github.io/SingleCellRNAseq/ and https://github.com/carpentries-incubator/proposals/issues/178

- Should we move (submit) from the incubator to the Carpentries' lab (including a paper to JOSE)? Do we want (at some point) a 'Bioconductor-carpenty'? Bioc-intro only? Others?
    - Review via github issue, using issue template/webform: basic info about the lesson, URL, authors, assertions about CoC, beta-tested, …
    - Toby will take it on as editor, first set of checks on formatting, accessibility, … with PR to get it to review stage
    - Community review, comments/discussions in github issue
    - Upon acceptance, a JOSE paper can be prepared and submitted (with link to GH review issue).

## 2023-12-11, 3-4 pm CET

**Attending**: Laurent, Jenny, Maria, Charlotte, Fred, Federica, Javier, David
**Regrets**: Susan, Robert

**Agenda**:

- Ludwig will present his plans for a scRNA-Seq course, based on the OCSA tutorial at ISMB (postponed).
- Vince was contacted by Instats (https://instats.org/) about a partnership. An "academic organization devoted to providing research methods training through livestreamed and on-demand workshops." They "share all revenue equitably -- 50% for individual partners and 80% for our institutional partners, and we would consider Bioconductor an institutional partner." Also "happy to allow all of your institution's students and researchers free access to your workshop content both in the live and on-demand spaces". UCLouvain seems to be a partner.
    - Laurent - can we get a bit more information from your colleague, e.g. concerning whether we would also be able to make the material available freely/outside of the platform?
    - May be helpful in terms of certification, maintenance
    - Maria would be happy to join a meeting with them if it's happening
- Pre-conference workshops 2024 - which workshops, who might be interested in teaching?
    - BioC2024, Grand Rapids, Michigan, July 24-26 (workshops would be Jul 22-23). Jenny will be there
    - EuroBioC2024, Oxford, UK, September 4-6 (workshops would be Sep 2-3)
    - BioC Asia 2024 - ?
- Bioconductor Carpentries next cohort of instructors, will be advertising this week. Form here. (Add question are they interested to teach at workshops above)
- Bioconductor Carpentries blog post to summarise 2023 activities - BioC2023, EuroBioC2023, BioC Asia workshops and any other workshops by new instructors (Maria)
- Training material for Bioc, including people running workshops with Bioc Carpentries material. To discuss next year, should they go on

https://www.bioconductor.org/help/course-materials/. For the moment, add them here: https://mblue9.github.io/bioconductor-carpentries/workshops.html (Maria will update from EuroBioC teaching poster. Fred send Maria his workshops)

- Let Carpentries know about the workshops we have taught? (https://carpentries.github.io/instructor-training/15-carpentries.html#reporting-a-mix-and-match-workshop) BUT: “At this time we are not seeking registration for lessons taught from The Carpentries Incubator or Carpentries Labs.”
- Maria - attempt to update the time for these meetings in the Bioc event calendar (https://github.com/BioconductorBoards/CABWorkingGroups/issues/50#issuecomment-1807176396)
- Interest in providing remote workshops? Maria will reach out to people who have shown interest in having remote teaching. Jenny, Fred, Federica would be willing to contribute (if time/planning allows)
- bioc-project lesson may be good for a pre-conference workshop

2022

# 2022-01-10, 2-3pm CET

**Attending**: Laurent, Jenny, Charlotte, Robert, Toby

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Application form for workshop in March. Draft to finalize during the meeting: https://docs.google.com/forms/d/15rkn8Z1JZnqf7Oy8EHFZOgaC8p6aCvu0G7R3qXD-mLU/edit?usp=sharing
    - We should set up a workshop website based on https://github.com/carpentries/workshop-template - see https://github.com/lgatto/2022-03-14-BiocIntro-Heidelberg, but should probably be transferred to github.com/Bioconductor once done.
    - During the pilot, you might want to keep notes about issues that come up/improvements that could be made to the lesson based on the experience. I created this template back in Dec 2021, which might be helpful? https://codimd.carpentries.org/lesson-pilot-observation-notes-template <- Assign someone to do this
    - Names instructors/helpers: Charlotte, Laurent, Kevin, Marco.
    - Aim for 20 participants, but no need to advertise exact number, as restrictions might change this anyway.
    - We decided that we only plan to run the workshop as part of the in-person conference. If the in-person part of the conference was to be scrapped, we would also cancel the workshop
- Bioc-intro data download - ok to remove `!file.exists("data/rnaseq.csv")` to always download the data. YES
- Bioc-intro: Add timings for intro lessons;~~ fix other issues~~.

# 2022-02-14, 2-3pm CET

**Attending**: Laurent, Charlotte, Estefi, Toby, Kevin, Jenny, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Update on Carpentries membership; volunteers to become instructors; announcements; expectations for new instructors. Membership start date.
- Education working group added to http://workinggroups.bioconductor.org/. Please mention or add any missing members.
- Intro workshop postponed to September 12-13 in Heidelberg (preceding EuroBioC)
- Remote intro workshop by Saskia (see email) towards the end of April; also Jenny (March 23 - April 1; 8 hrs total).
- Question from Galaxy about joint trainings

    - Next big Galaxy training is in March: https://gallantries.github.io/posts/2021/12/14/smorgasbord2-tapas/. Possible ways to contribute:
        - They have R courses/transcriptomics tutorials (GUI or GUI mixed with coding/plotting in RStudio) - not all is done strictly via the Galaxy UI.
        - The easiest way to contribute would be to hang out in a chat and answer questions of the learners - lots of non-Galaxy-specific questions.
        - Could also develop a specific Bioconductor tutorial and record a video for the Galaxy Training Network.
    - Should we include a section on running Bioc tools as Galaxy tools in the bioc-project course?
- Ideas for presentation/s at Bioc2022 (and EuroBioc2022)?
    - Long or short workshop on “How to run your own workshop” using our teaching materials

**Notes/TODO:**

- Select people who have the opportunity/goal to organize workshops, teach the material
- Instructor training - foster feeling of community (even if remote, book (up to) 15 slots to the same remote training event, in conjunction with a conference (EuroBioC2022, BioC2023), participants can come together in the same place)
- Advertise committee a bit more - list instructors
- Branding - official Bioconductor workshop (with at least one of the trained instructors).
- Set up a page on bioconductor.org (or the working group page) - brief description of what we've done so far (Charlotte TODO), list current members, we'll become members of Carpentries, have opportunities to train instructors, invite people to register interest/availability around EuroBioC2022/BioC2023.
- Finalise intro lesson and submit lesson
- Toby will start organising Carpentries instructor meet-ups (one evening, in a bar, typically) in Heidelberg again, and we could co-organise this with the EuroBioc conference.
- Next meeting 28 Feb to discuss activities at next Bioc/EuroBioc conferences.

## 2022-03-01, 2-3pm CET

**Attending**: Charlotte, Kevin, Robert, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Workshop planning: who can be physically present? What contents?
- Seattle: Carpentries demo workshop?

## 2022-03-14, 2-3pm CET

**Attending**: Laurent, Charlotte, Marco, Toby, Kevin, Estefi

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:
- Carpentries membership intended to start from August 1
- Plans for/thoughts about https://docs.google.com/document/d/1_TiMqRB3w79-SMjxfsgFs0ilAtzcS74qAwlpnju5VP8/edit?usp=sharing
- Submit (one of) these lesson projects as a proposal for Biohackathon Europe 2022? (added by Toby)

**Notes:**
- How to recruit candidates for the upcoming instructor training?
- Confirm with Erin Becker if we could organise a centralised training - done.
- Start making a google form for applications
- Jenny submitted an abstract for a demo for Bioc2022. Jenny plans to be there in person. Others will likely attend remotely.
- Biohackathon Europe 2022 in Paris, November - project proposals, training is one of the relevant domaines/topics. Project proposal deadline 8 April 2022.
- Kozo started a BioC blog (https://github.com/Bioconductor/biocblog) where this group could publish a post (or more).
- What other events would we like to promote to engage with more people, beyond what we have done so far in these meetings and conferences (education-related discussion table)? How do we want to frame this committee and its actions in the future? Possibly organise a developer-forum like activity/discussion to gather ideas from the wider community. Discuss with Mike (developer-forum organiser). What do we need from a community point of views, what is missing, what should we organise?
    - Two things: (1) what people would like to do as part of the committee and (2) the more general question of what is missing/what the community want - important to keep these separate to manage expectations (people that suggest can but don't have to implement them), at the risk of getting many suggestions without being able to implement everything.
    - Monthly Carpentry instructor meetings to share experience - what has worked, … our trainers should participate.
    - Our initial aims are described in the paper/blog, but we don't have anything for the future - we should have a mission statement paragraph, to define our long term ambitions. The wider consultation will help to define this for ourselves.
    - Liaise possibly with other communities such as Galaxy, …
    - Organise this input gathering over a slightly larger period (1 weeks for example) with multiple live events for different time zones, a letter box, idea

generation, slack, … We can then digest all these, publicise them, possibly implement some, … and use these to define our future strategies.
    - Suggestion: June?

## 2022-04-11, 2-3pm CEST

**Attending**:

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Planning of the education week, tentatively planned for 7 - 10 June
- Future instructor trainings: it looks like in-person instructor training isn't on the Carpentries agenda. I would thus suggest
  - we organise an instructor/helpers lunch/dinner/get-together at the conferences
  - if there was a training close enough to a conference, to reserve seats and tag it to the conference
  - generally coordinate our instructor trainings so that people get to know each other even before the training
- Draft of application form for instructor training: https://docs.google.com/forms/d/1Hsx8w1lutaVhkZT3WZ2oqVE8NJcOwFBvrAlXiY6h5o0/edit?usp=sharing

**Notes**:

- Education week
  - Laurent talked to Mike about organizing a "developer forum" or two during that week.
  - A couple of events to get people's input on what should our priorities/next steps be for the education activities in the community. May also get new people to join and get engaged.
  - Advertise what we do, workshop in September, instructor training opportunities.
  - 10-15 min presentation, possibility to ask questions, form for people to submit ideas.
  - How to collect ideas?
    - Jamboard
    - GitHub issues
    - Support site
    - sli.do
    - wooclap - can have multiple categories (but 100 character limit?)
    - google doc (or add link to google doc in e.g. wooclap)
    - google form
  - June 7: 8:00 CEST - 16:00 Melbourne
  - June 8: 14:00 CEST

        - June 9: 18:00 CEST - 9:00 Pacific, 12:00 East Coast

- Action items for next time: finalize application form, plan outreach/advertisements for the education week.

## 2022-05-09, 2-3pm CEST

**Attending**: Laurent, Toby, Charlotte, Susan, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Planning of the education week, tentatively planned for 7 - 10 June
- Draft of application form for instructor training: https://docs.google.com/forms/d/1Hsx8w1IutaVhkZT3WZ2oqVE8NJcOwFBvrAlXiY6h5o0/edit?usp=sharing
    - Suggest to change “Preferred pronouns” to “What are your pronouns?” as recommended e.g. in https://www.morgan-klaus.com/gender-guidelines.html#Preferred-Pronouns
- Beginner’s course before EuroBioc 2022 - advertisement, registrations. Form: https://forms.gle/B6p9VSWDWaxHxMV69

**Notes:**

- How to collect ideas during the education week? Wooclap, to allow participants to add suggestions and up/down vote. Issue is the 100 character limit. Get past that with a link to a google doc.
- Prepare some questions to follow up with the 10-minute presentation. Concrete questions to get feedback, such as:
    - Start with a poll to get a feeling why people are here: trainers or learners?
    - Learners: What type of Bioconductor teaching material are you familiar with? Vignettes, workflows, videos, OSCA book, … ?
    - Learners: What are your biggest needs in terms of training and education? Installation, download, statistics, data structures, …
    - Educators: what are the most common missing (unexpected) prerequisites of your learners when running a workshop.
    - Community: What kind of events/gatherings would be useful to organise? How to best engage with the community at large?
    - Community: would having material and/or courses in different languages useful? Is English a hurdle that stops you from reaching your learning outcomes?
    - Instructors: challenges in maintaining CI and/or large documents such as the OSCA book. Do we need a working group to maintain the OSCA book, vignettes and other longer teaching resources? Facilitate the setting up of other similar efforts. Susan and Wolfgang have similar issues with the MSMB book. This working group could also discuss what constitutes a Bioconductor teaching resource, and which ones to commit to and maintain.
- Learning workflows - how to get started or advance in your learning path?

- Education week advertisement: how (usual channels and Carpentries channels via Toby) and when?
- Education week: developer forum or zoom link? Check with Erika if we can use the Bioconductor zoom account (used for the Bioc conference).
- Charlotte and Laurent are available for the 3 calls. Others?
- Prepare the slides. Links: EuroBioC2020, BioC2021
- Do we need a public drive/dir for our documents? Currently only this (long) document with links.

- EuroBioc course
    - 20 participants
    - Open registration when conference registration opens.

- Next meeting moved from 13 to 27 june to discuss the outcomes of the education week. Another meeting to discuss the workshop at Bioc 2022 (https://docs.google.com/document/d/1n4kpd5QZbvFT8sMSg3TZDuyJUo_QJHN5yhWwIeKHnEg/edit?usp=sharing) will also be organised either on 11 July, or Jenny will announce it on the mailing list.

Education week announcement:

- Interested in education, teaching material and Bioc, have ideas and/or time, join us here/when.
- Open to everybody, trainers and learning.
- Clarify that the 3 calls are the same, just for 3 time zones.
- Prepare wooclap
- Online channel: zoom?

The Bioconductor teaching committee invites anyone interested in Bioconductor and education, learners and educators, to join us for the Bioconductor education week on June 7 (8 - 9 am CEST), 8 (2 - 3 pm CEST) and/or 9 (6 - 7 pm CEST) to discuss your needs and ideas in terms of education. We are looking for your ideas, suggestions and time (if available) to define and discuss our future efforts. What community resources have worked for you? What is missing? What is the best learning resource/experience that you found recently, and that we should add? What was the hardest thing you had to learn to do in Bioconductor?

## 2022-06-27, 2-3pm CEST

**Attending**: Charlotte, Jenny, Laurent, Robert, Toby, Vince

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Carpentries membership agreement is signed. We asked for it to start on August 1.
- Plan Bioc teaching week

    - Draft slides: https://docs.google.com/presentation/d/1oBLrC16nsU7IgpSfGXf65rhKdwcERA2XTwS4flsejr8/edit?usp=sharing
    - Suggestion: Tue 6 Sept at 8 am, Wed 7 Sept at 2pm, Thu 8 Sept at 6 pm (all time EU time).
    - Check with Erica about virtual platform
- Draft of application form for instructor training: https://docs.google.com/forms/d/1Hsx8w1IutaVhkZT3WZ2oqVE8NJcOwFBvrAIXiY6h5o0/edit?usp=sharing
    - Upcoming instructor training events: https://carpentries.github.io/instructor-training/training_calendar/index.html (we have received a code that people should use when signing up)
    - Template email from the Carpentries to recruit candidates: https://docs.carpentries.org/topic_folders/instructor_training/members_join.html#trainee-recruitment-email-from-member-contact
    - Suggestion: write a blog post at https://bioconductor.github.io/biocblog/ to announce membership and instructor course (suggest to do the course in 1st half of membership year), then post on support site, twitter, … remind those that registered 2 years ago by email
    - Application form:
        - pronouns - if someone does want to select "Other", they probably want to tell you what those are: in the settings for that question, you should be able to tell it to include an "Other" field that will allow the respondent to write a comment when selecting that option.
        - Include a field to ask about research focus
- Beginner’s course before EuroBioC 2022 - advertisement, registrations. Form: https://forms.gle/B6p9VSWDWaxHxMV69
    - Need to coordinate with Simone/conference committee regarding venue capacity
    - Currently 3 applications (all have also submitted an abstract for the conference)
- Demo at BioC 2022 - will be discussed at July 11 meeting. https://docs.google.com/document/d/1n4kpd5QZbvFT8sMSg3TZDuyJUo_QJHN5yhWwIeKHnEg/edit?usp=sharing
- Vince presenting: https://vjcitn.github.io/YESCDS/, https://yes4cure.bioconductor.org/, Educational hub for enhancing diversity in teaching genomics.

1) Create a network of computational genomics and data science educators at institutions serving underrepresented populations.  We plan to engage faculty at ... to identify barriers and opportunities in the use of cloud computing to democratize access to modern computing methods and to genomic data in contexts that are appropriate to undergraduates, graduate students, and to faculty members who wish to expand research capabilities of their institutions in computational genomics and data science.

2) Develop and maintain an authoring platform for educational materials related to hands-on learning in genomic data science.  The specific technology that already exists combines Galaxy, Rmarkdown, docker, and kubernetes.  Instructors

only need to be willing to use a high-level language like R or python to express the needed computations, and markdown for Rstudio or Jupyter, to compose workshops that will be deployable in hosted cloud platforms or on any docker- or singularity-enabled environment. Genomic data science components (annotation, exemplary experiments, algorithms) are all available via Bioconductor.

3) Build dynamic curriculum components to introduce and mature understanding of key concepts of genomic data science at various points in science education. An example of an entry-level treatment of data science for cancer research is at https://vjcitn.github.io/YESCDS/ -- the "Articles" tab at the top gives a dropdown on subjects covered. This material will be deployed in a Galaxy instance; https://yes4cure.bioconductor.org/ is an example currently under development.

4) Establish governance and sustainability for the materials and tools developed in the first two aims. This will involve defining criteria for inclusion and revision of materials, defining educational performance metrics, and assessing inclusiveness and user effectiveness for both authors and students who use the system.

## 2022-07-11, 2-3pm CEST

**Attending**: Charlotte, Jenny, Laurent, Susan, Toby, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Blog post about the Carpentries membership - ready to go?
- Application for Carpentries course in Heidelberg - applicants to be informed on July 15
    - Advertise more broadly, don't require conference attendance - reach out to local networks in Heidelberg and surrounding. Advertise workshop on support site, twitter, … BioIT in Heidelberg, advertise among EuroBioc organisers tomorrow.
    - Inform the people who have applied about the situation.
- BioC2022 demo
    - https://bioconductor.org/help/education-training/ is not linked anywhere from https://bioconductor.org/help/? Or anywhere else on the website?
- The Carpentries are hiring a director of technology: https://carpentries.org/blog/2022/07/director-of-technology/ - share announcement in networks
- Workbench - reach out to @zkamvar in an issue on your GitHub repository to ask for help making the transition.
- For the past few years The Carpentries have been working on a project to redesign the infrastructure supporting the lesson website. Current lessons build on a combination of Jekyll (static site generator behind GH pages), R, python, bash scripts. Workbench - new infrastructure to replace lesson template for all official lessons, and any lessons in the incubator that want to. Accessibility as the central

principle. Automated checks and tests, to flag inaccessible links etc. Accessibility also in terms of how easy it is to get involved in contributing to a lesson. With workbench the R Markdown gets turned directly into the lesson. The whole infrastructure runs on R, works best with R Markdown source files. Currently beta testing. May be a good time to consider switching over. Many things are easier to do. There is a script that can help you do the transition automatically - open an issue in your lesson repository and tag @zkamvar to get the process going.

  - Example: https://fishtree-attempt.github.io/R-ecology-lesson/04-visualization-ggplot2.html
  - https://carpentries.github.io/workbench/
  - Aim to switch the bioc lessons after the September workshop

## 2022-08-08, 2-3pm CEST

**Attending**: Susan, Toby, Kevin, Laurent, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Teaching week (September 6-8)
  - Tue 6 Sept at 8 am CEST, Wed 7 Sept at 2pm CEST, Thu 8 Sept at 6 pm CEST
  - Announcement
    - Bioc slack
    - Twitter
    - support site
    - Add to the Bioconductor event calendar (submit issue; draft: https://docs.google.com/document/d/1wBo76bSv2BWUARqoWjxwOKtGkG-XVmMW3dYPi1-HjIs/edit?usp=sharing )
    - Was advertised at Bioc2022
  - Slides
  - Probably need to mention somewhere that we expect people to follow the Code of Conduct
  - Set up Wooclap
  - Virtual platform
    - We can use the Bioconductor Zoom license - Charlotte has reached out to Erica and she will set up the sessions.
- BioC2022 demo debrief/summary
  - Notable interest, applications for instructor training
  - Questions: whether training is open to all or only package developers; what is needed to be part of the Bioc community; teaching experience?
  - Slides: https://docs.google.com/presentation/d/1vj-sIcYAbU9doEguPcOv3Ictdkze1KVcsprx3foRmTA/edit?usp=sharing

    - TO DO:
        - Provide our material as template (or give instructions on what to do) and allow others to modify it.
        - Translating course, accessibility (cf Quarto for screen readers).
- Plan for Heidelberg course 12-13 September
    - Simone asked about the room, we concluded it would be better with a smaller room with desks than a larger room without proper desks.
    - Who will be there?
        - Charlotte, Laurent
        - Toby could join
    - Who does what?
    - What still needs to be addressed in the training material?
        - Timing
    - Send acceptance email to applicants, make sure that the content is clear, ask them to confirm that they will be there in person.
- Carpentries membership council, August 23, 4pm Central European time. Who wants to attend?
- Currently six applications for instructor training - should start selecting so that they can sign up for a suitable training instance.
- Organising remote workshops:
    - Remote allows to flip parts of the courses, define async parts of the course
    - Add videos (that could be re-used in different contexts) to lessons, or sections. Students to watch the videos before the lesson and prepare 5 questions. Diversity of media can be very useful.
    - Also consider recording workshops.

## 2022-09-19, 2-3pm CEST

**Attending**: Charlotte, Laurent, Lisa, Fred, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Follow-up on teaching week. Notes here (I tried to make some form of summary in the end).
- Follow-up on Carpentries course in Heidelberg:
  - Good, but would need more time to go through all the material (we skipped the chapter on joins).
  - SE was also very confusing, just very different from the rest of the material, and it was difficult for participants to conceptualise why/when this would be useful. Especially as the long format, as they were given, already contains all data. Maybe we could provide the 3 independent tables (matrix, col and row data) and they build the SE, which corresponds to reality. A summary exercise could then be to extract some counts for some features/sample from the SE and long table, and confirm they are identical.

  - A demo on tidySE was probably adding to the confusion - we should limit ourselves to a link/mention to tidySE.
  - Clarify focus on R and/vs Bioconductor. It isn't really an intro to Bioc and genomics data.
  - TODO: Mention Bioc in "intro to R" (e.g. BiocManager::install), clarify differences between tidyverse, base R and Bioconductor.
  - We should make sure we fit everything in 2 days, not aim for a 3rd day.
- CCB seminar (September 26)
- Selection of Carpentries instructor training participants
- How to move bioc-intro out of incubator?
  - The next step is to invite others to teach the lesson and provide more feedback (a "beta" pilot is a workshop taught by people who have not been heavily involved in the development of a lesson to that point). After the lesson has been tested like this in at least one of those beta pilots, it will be eligible for open peer review in The Carpentries Lab. Once accepted, the repository would be transferred into https://github.com/carpentries-lab/ and we will leave a placeholder repository in the Incubator to redirect visitors to a lesson's new location under https://carpentries-lab.org/.
- Can we get access to the post survey feedback?
  - Laurent contacted Toby
- Add teaching calls to Bioc event calendar?
- Planning ahead, from Aedin: The SFI center for research training in Galway (Ireland) is asking if I can give training in Bioconductor on December 5th/6th. Would that work if you want to give a course?
- Suggestion to move call by 1 hour at 3 pm CEST. Fred to send an email on google group.

## 2022-10-10, 3-4 pm CEST

**Attending**: Charlotte, Almut, Toby, Fred, Jenny, Maria

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Follow-up on teaching week (notes here) and define our next goals.
- Summary of Charlotte and Laurent's CCB talk
  - What is an 'intermediate' Bioconductor user? Help users/developers place themselves to find the appropriate training material. Maybe someone who is in the process of doing their first analysis/writing their first package. Is it simplistic to suggest that intermediate users are the people in the middle, i.e. they know the stuff in the beginners' resources, but do not yet know how to find whatever they need to know?
  - Get people to be able to actually analyze their own data

        - https://competency.ebi.ac.uk/framework/iscb/3.0
        - Can we add exercises to the books, to make them more into teaching material?
- Selection of Carpentries instructor training participants
    - 10 offered places, 6 so far have told us they've registered for Carpentries Instructor training in December
    - Can we find out from Carpentries how many people have signed up with our member code? Toby says contact membership@carpentries.org. TODO: Maria will contact.
    - Revising our application form to add qus about diversity and languages, then will circulate
    - Note that the teaching demo for the checkout has to be on an official lesson (can check with trainer whether a lesson from the incubator will be ok, but no guarantee).
- Hacktoberfest for Bioc modules (Kevin's comment in Slack here)
    - Add hacktoberfest as a topic to the lesson repos TODO: People with access (Charlotte, Laurent?)
    - TODO: Everyone - If know anything for bioc repos that would be good for this please create issues
    - TODO: Maria advertise on Twitter
    - To participate:
        - Register before October 31 https://hacktoberfest.com/auth/
        - Have 4 pull/merge requests accepted between October 1 and October 31 (on any repo participating in Hacktoberfest)
        - The first 40,000 participants (maintainers and contributors) who complete Hacktoberfest can elect to receive one of two prizes: a tree planted in their name, or the Hacktoberfest 2022 t-shirt
- Plans for a short paper (or blog post?) about the teaching committee's activities
    - Do a survey of the needs of the community? Could combine with survey for the website needs. The results could go in the paper, with a discussion of what's there and what can be done.
- Carpentries lessons
    - Workbench transition
        - Toby recommends going ahead with transitioning
            - Examples of template here https://fishtree-attempt.github.io/R-ecology-lesson/index.html
            - https://preview.carpentries.org/r-socialsci/ (old version https://datacarpentry.org/r-socialsci/)

        - Future plans are to use Quarto (probably next year) but advise transitioning now and not waiting til that
            - https://github.com/carpentries/sandpaper/issues/161
        - https://carpentries.github.io/workbench/transition-guide.html
        - To initiate transition, Toby recommends tagging @zkamvar in an issue on each of your lesson repositories, requesting that the lesson be transitioned to the workbench. You may need to wait a short while for

        him to be able to do that - he is currently very busy planning the Workbench Beta Phase - but I hope he will be able to make it work for you. Otherwise/if you do not want to wait, you can study https://carpentries.github.io/workbench/transition-guide.html and try to reformat the content/reorganise the files and folder on your own.
    - Access to post-survey feedback from Heidelberg course
        - Toby asked for the workshop URL to find out
        - View your responses at https://workshop-reports.carpentries.org/?slug=2022-09-12-BiocIntro-Heidelberg&key=c2a36928b40073714b5f9af58177fcd981c501f0 BUT the central pre- and post-workshop assessments are designed for official lessons and take time from the Workshop Administration Team to process, so please create your own feedback surveys (see https://docs.carpentries.org/topic_folders/lesson_development/lesson_pilots.html#collecting-feedback-on-the-lesson) and  follow the instructions for Incubator lesson pilots in https://carpentries.github.io/workshop-template/customization/#configuration-file-_configyml for your next pilot(s).

## 2022-11-14, 3-4 pm CET

**Attending**: Laurent, Charlotte, Fred, Robert, Jenny, Jaclyn, Kevin, Leo, Maria
**Regrets**: Susan, Toby, Almut

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda**:

- Carpentries revised application update
- Hacktoberfest Bioc Carpentries update
- Bioc Carpentries transition to workbench update
- BioC2023 Carpentries workshop(s)
- Education requirements for website redesign
- Plans for a short paper (or blog post?) about the teaching committee's activities
    - Suggestion from Aedin: ISMB Education session (paper deadline Jan 19, conference July 23-27), on Yes4Cure, Orchestra, Carpentries, Teaching committee, translation events, …

- Maria with CAB, Laurent & Charlotte revised the Bioc instructor course applications, with more diverse new applications. New applications probably for year 2. CCB is also working on becoming a Carpentries member.
- Any news regarding the migration to the workbench? Each maintainer has tagged @zkamvar in issues. He has replied, adding the repos to

https://github.com/carpentries/lesson-tranisition. Toby, do you know what the status or timing are?
- Hacktober fest: meet-up organised by Kevin, with decent turnout (5- 10 people). One person contributed a great PR to bioc-project. Would help if we, as maintainers, created some issues to ask for specific help (example typos). https://hacktoberfest.com/events/ Planning for next year?
- Workshop at Bioc2023 workshop (conf is 2nd - 4th August) on 31st and 1st July? Plan to teach the RNA-Seq course. Instructors: Jenny will be there, also favour newly trained instructors to teach, help, provide feedback. Last years, we had talks/discussions - plans for 2023?
- There will also be a workshop at EuroBioc2023 in Ghent in September, which will be useful to provide some practice sur newly trained European trainers.
- Discussion channel with/for trainees/trainers? Let's add all trainers/trainees to the bioc-teaching google group. Do we need another private one for all trainers/trainees?
- Paper/blog post: where? F1000, PLoS Comp Bio education section, ISMB education session (700 USD), ISMB tutorial sessions, … Could also submit lessons to Journal of Open Source Education. See short paper plan we have for now. **Paper session after our next bioc-teaching meeting**: homework is to read draft and think about structure, and/or make contributions (with track change) by then.

For next meeting:
- Education requirements for website redesign - to be discussed next time, Maria will keep us posted.

## 2022-12-12, 3-4 pm CET

**Attending**: Jenny, Charlotte, Almut, Laurent, Robert, Maria
**Regrets**: Fred

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

- TODO: Update based on previous meeting notes
    - Laurent made Maria co-owner of Google group, TODO: Maria add trainees so they can get teaching meeting notifications. - DONE
    - Decided we will create public #carpentries channel in Bioconductor Slack so can more easily communicate with Bioc Carpentries instructor trainers and trainees and so they can get to know each other. Created here https://community-bioc.slack.com/archives/C04FH035XK2 TODO: Maria add trainees - DONE
- Do we have any specific needs for the website? Some good points were raised during the teaching week - finding relevant help, especially for newcomers, was a major issue that came up several times.
- Possibility to teach at workshops in Gent on 18-19 September 2023 as part of EuroBioc.

- Frederick Tan feedback on bioc-intro remote/in-person workshops.
- Appetite to align the length of bioc-intro episodes closer to how workshops run (i.e. day1-morning session topic, day1-afternoon session topic, etc. akin to unix/python/git/python at http://mahdisadjadi.com/2016-08-22-johnshopkins)?
- Interest in developing a new bioc-scrnaseq based on OSCA (and general thoughts on how additional Bioconductor Carpentries content will be organized)?
- Bioc instructor check-out:
    - Ask for PRs to our lessons. Carpentries checkout info says community developed lessons in incubator (i.e. the 3 bioc lessons) are eligible.
    - Take part in at least one of our monthly bioc-teaching discussion.
      TODO: Maria to send this info to trainees - DONE

2021

# 2021-01-11, 2-3pm CET

**Attending**: Charlotte, Laurent, Toby, Federico, Kevin, Robert, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**
- Update on action items from last meeting
    - Laurent to prepare a light frame with high-level flow to be filled in by contributed exercises. (see https://github.com/Bioconductor/bioconductor-teaching/blob/master/overview.md)
    - Kevin to prepare the data set as csv files and upload to a public place (figshare)
- Carpentries lesson development study groups (application deadline Jan 13): https://carpentries.org/blog/2020/12/lesson-development-study-groups/ (see also study group page https://carpentries-incubator.github.io/study-groups/)

**Meeting notes:**
- Several people got in touch to create specialised lessons. The current plan is still to postpone the creation of new lessons until we have a clear plan for fundamental lessons, gain experience on what and how to do things. Make sure we have the intro/fundamentals in place.
- In particular, there is broad interest in a lesson on single cell analyses, notable from the Carpentries.
- https://github.com/Bioconductor/bioconductor-teaching/blob/master/overview.md: possible topics for the intro course. "DC" - topic taken from the Data Carpentry ecology lesson.
- Data organization with spreadsheets - good to have, probably can be a bit shorter than the ecology one. Once they understand spreadsheets, it's easier to understand the dplyr stuff. Largely drop sections about dates. **This section could also be used to introduce some concepts related to experimental design.**
- Starting with R - close to what DC ecology provides. Introduce vectors, subsetting, logical operators.
- Starting with data - intro to data frames. Part about factors can be simplified (since it doesn't automatically come up when reading csv file anymore).
- Manipulating and analyzing data with dplyr - use the single-cell data instead of what's used in DC ecolory.
- Joining tables (not currently included in DC) - protein info data.
- Reproducible research. Rmd documents (up until here, use R scripts)
- Bioinformatics - expose learners to Bioconductor. Some wider context, Bioc project. Notions on experimental design (fundamental to following lessons, relate to colData). Conclude with the SummarizedExperiment class.

- Optional chapter on additional programming concepts - useful as a preparation for the next level of lessons. Could be more of a demonstration.
- Use Rmd throughout - introduce in the very beginning? Encourage learners to take notes as they go along, together with code chunks. Sometimes people use Rmd when they really want an R script (an Rmd file with a single long code chunk). Scripts still relevant for execution in workflows.
- There were opinions for both script vs Rmd during the instructor course. Toby suggests that the best from a teaching point of view is to keep a single platform during a course, but the risk is that learners could believe that is the only option.
- Carpentries currently teach python in Jupyter (for consistency and simplicity), but make sure to mention in the beginning, middle and end that python != Jupyter. Make sure to build that time into the workshop.
- Possible complications linked to working directories (Rmd file - not necessarily the same working directory). RStudio projects helps to not use setwd().
- General project management - absolute/relative paths, … can spend a lot of time on it, but we probably don't have that time.
- Even with RStudio projects, we still have to deal with data organization (we don't put all the files into the main directory).
- Learn to recognize when you're lost (in the file system) - strongly encourage to follow the instructions precisely to avoid getting lost.
- Practice how to build a data frame representing a specific experimental design (i.e., just to create the data.frame in itself). Make sure order matches, add another column, …

- Carpentries lesson development study groups: aim to bring together people who are planning to build new lessons.
- Reading tasks for each week
- Weekly meetings to discuss reading material and how it applies to the material that is being developed
- Small homework tasks designed to get participants to apply the techniques to the lessons that are being developed
- 10 weeks, 9 sessions (to allow time to try to teach some of the material)
- Starts on Feb 8 - will hopefully be more rounds in the future
- Estimated 3-4 hours per week
- Up to 3 (or 4) participants per lesson

## 2021-02-08, 2-3pm CET

**Attending**: Kevin, Jenny, Robert, Charlotte, Toby, Laurent

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- What data do we need, and how to distribute it? At the previous meeting, we discussed that it would be useful to have a single csv (tsv) file with the data for the lessons about data.frames, dplyr and ggplot2. That file could be hosted on figshare, and learners would download it manually and copy/save it to their project's data folder. We will need other data/files, such as a SummarizedExperiment, a coldata file to create a SummarizedExperiment by hand, and a couple of smaller data.frames for the section about joins? These could be put into a small data package. To be further discussed.
- Mention RNA-Seq lesson development as part of the Carpentries lesson developed by Elnaz AmanzadehJajin and Batool Almarzouq (Batool's preliminary notes here).
- **Did we choose the right dataset for the intro lesson?** Would a bulk RNA-Seq experiment not be a good choice, so that that same data could be used for the RNA-Seq lesson. This would be particularly useful when both intro and RNA-Seq lessons are taught back to back.
    - Possible bulk experimental data set: Blackmore et al. 2017 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5544260/
    - https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE96870
    - 45 Mouse samples: cerebellum and spinal cord tissues (paired by mouse), males and females,  day 0, 4 and 8 after influenza infection. Mostly 4 reps per tissueXsexXday group. Jenny analyzed these data initially and can find 30-40 genes with expression patterns useful for the various visualizations.

Meeting notes

- Update from last Friday's discussion with Elnaz and Batool
- Jenny's data (see above).
- **Data TODO**: Laurent: assess the sc and bulk data sets in light of WSBIM1207 course redesign. Charlotte and Jenny: assess that GSE96870 is a good fit for DESeq2 course.
- GitHub repository and data folder - for instructors to explore various data sets
    - https://github.com/Bioconductor/bioconductor-teaching/

## 2021-03-08, 2-3pm CET

**Attending**: Charlotte, Lukas, Toby, Laurent, Robert, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Discussion on the data set selection for the lessons.

Meeting notes:

- Carpentry lesson development group: Elnaz and Batool are developing a scRNA-seq lesson, with Bioconductor tools.

- We are going to summarise each meeting in a short 1-2 sentence executive summary to report back to the CAB.
- Bulk data set discussed previously may be too small to properly motivate using R for analysis
- Long format - works for everything up until scatter plot of gene A vs gene B; would need to introduce pivoting
- Need data set which is "colData + some gene columns".
- BachMammaryData (from scRNAseq package) has ~25,000 cells. Developmental time course (4 stages)
- Acknowledge difference between "traditional" data (samples x variables) and molecular data (variables x samples)
- There are packages in Bioconductor that can make plots directly from SE/SCE objects etc (scater, dittoSeq, …)
- scater::ggcells can be used to plot SCE data using ggplot: ggcells(example_sce, aes(x=PCA.1, y=PCA.2, color=Gene_0001)) + geom_point(). See ?scater::ggcells for details.
- Once we have agreed on a dataset, Laurent will present the updated WSBIM1207 course and, if considered acceptable, move it to the Carpentries template for collaborative development.
- Now is probably a good time to start planning the other lessons. The audience is probably similar to what we have for the intro course, with attendance of that intro course (or any similar course) a prerequisite. No need to master SE, some familiarity would be an advantage. Make sure to align the workshops
- Charlotte to start a new document for other lesson development.
- RNA-Seq lesson could start with an exploration and discussion of the experimental design, and then only move on with the analysis. Include tips and best practice on how to design an experiment, and what not to do.
- Using DESeq2 for the RNA sequencing lesson, as it uses SE by default and slightly easier to teach. Could be good to mention edgeR at the end, and briefly discuss differences. Carpentries lesson template allows to have extra material/page to describe alternatives to the core material.
- Do we also do gene set enrichment and over-representation? How much linear modelling do we need/want to cover. See *A guide to creating design matrices for gene expression experiments*.

**Executive summary: Progress in the intro plans, pending final decision on data (see here) and starting development of next lessons.**

## 2021-03-12, 4-4:30pm CET

**Attending**:

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Plan submission for BioC2021
- Suggestions:
  - short talk
  - joint lesson development session (contribute to existing lessons, start planning new ones, form working groups, …)
  - birds-of-a-feather session to gather feedback
  - workshop
- From Toby: If you decide to run such a development session, you may find these recommendations for organising/running a lesson development sprint useful, and any feedback you can provide would be appreciated! https://github.com/tobyhodges/lesson-sprint-recommendations
- Link to abstracts

## 2021-04-12, **5-6pm** CEST

**Attending**:

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Abstracts for short talk and long workshop (lesson development session) submitted to BioC2021 - notifications should come later this week
- Quick update on new single-cell data set for intro lesson
- Quick update on progress for Bioc project and RNA-seq lesson preparation
- 8 April 2021: Kevin Rue-Albrecht replaces Saskia Freytag on the Bioconductor CAB Education committee (with Laurent Gatto and Charlotte Soneson).
- Presentation/discussion from the BiocSwirl team (https://github.com/biocswirl-dev-team/BiocSwirl)

**Notes:**

- Bioc submission - expecting answer this week
- Kevin is now the contact person with CAB. Kevin could also coordinate with the Carpentries if needed.
- Work in progress:
  - scRNA-seq data for the intro lesson; Laurent to start writing the lesson. Continue discussion on google group and/ior github repo.
  - Charlotte started the development for the rna-seq and bioc project lessons. Continue discussion next meeting.

**BiocSwirl presentation**

- Participants: Lisa Cao (Simon Fraser University, BiocSwirl founder and technical lead), Julia Philipp (University of California Santa Cruz, BiocSwirl developer), Matt Moss, Almas K
- Presentation
- Diverse BiocSwirl Development team

- BiocSwirl = Bioconductor + Swirl
- Swirl = R console-based learning environment
- Interactive courses on Bioconductor analysis workflows
- Can be completely entirely in R/RStudio - focus on local machines
- Material to bridge code and biological significance
- Using standardized datasets, sometimes trimmed to fit users' environments
- Metafunctions to verify working environment
- Self paces, self contained, and support modularity
- Material presented in digestible chunks
- Active positive and constructive feedback
- Completely free
- BiocSwirl: Interactive, asynchronous, feedback
- Target audience: grad students and adult learners, often code-phobic
- BiocSwirl 5 minutes demo
- Lessons format breakdown: learn (material presented in digestible chunks) - practice (direct application of knowledge: testing (multiple choice, short answers, code chunks) + active feedback) - apply (interpretation of results)
- **Current course offerings**, more under development: intro to R for life scientists; intro de biostatistics; bioinformatics workflows: sc-RNA-seq workflow, RNA-seq workflow, ChIP-seq workflow; software devel and generating research reports
- **Culture and philosophy**: open and free, community frun; accessible to anyone with a computer; foster a positive learning environment; down to earth and accessible.
- **Challenges and setbacks:** normalising the 'practice' step, rather than skipping; lack of manpower and resources; funding; knowledge gaps.
- **Classroom applications**: workshops (wich CSHL DIAS), undergrad course (currently used at instructor's discretion)
- **Future directions**: more courses, submit package to Bioc; MS under preparation; facilitate adoption and user feedback via workshops; containerised courses about pre-processing; continuation of BiocTerm Development and CI/CD pipeline.
- On twitter @bioctools, on github biocwirl, biocswirl-dev-team org
- See also swirlstats.com

- BiocSwirl workshops so far: 4 hours, self paces, instructors there to help with errors and explanations. Periodical checks with about 15 - 20 minutes work chunks.
- During exercises: how do you deal with actual errors (learner has no idea how to start)? Try to prevent such situations by providing the learners with all the information they need in the text.

- Ideas for collaborations: develop asynchronous lessons of our Bioc-teaching curriculum via BiocSwirl. This would be a great way to allow learners to check/address prerequisites.
- We should have a closer look to the BiocSwirl material, which might already address some of our needs.
- We could also share the same datasets that are used in our and BiocSwirl lessons. This would be a nice bridge between the two communities.

**Executive summary: Progress: (1) Bioc2021 abstracts submitted; (2) continuation of lesson development (data for intro lesson and planning for RNA-seq and Bioc project). BiocSwirl presentation and opportunities to collaborate on an asynchronous Bioc lesson.**

## 2021-05-10, 2-3pm CEST

**Attending**: Laurent, Kevin, Charlotte, Robert, Toby, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- BioC2021 abstracts accepted:
  - short talk (Aug 5, 5pm pacific time)
  - long workshop/joint material development session (Aug 5, 7am pacific time)
- Bioc project and RNA-seq lesson preparation

**Notes**

- Workshop is on Thu at 4pm CEST.
- Bioc2021 talk is on Fri at 2:00am CEST!
- We decided to keep the talk/workshop as they are set and have a Teaching booth for those that want to see the talk and ask questions outside of the slots.
- Workshop organisation: https://github.com/jdrnevich/BuildACarpentriesWorkshop
- Where will we be at the time of the workshop? What are we looking for: (1) specific contributions or (2) for new groups on other specific topics or build on existing material?
- Good target would be for people to go through the intro session, catch errors, and suggest improvements.
- **TODO:** Prepare a list of well defined learning objectives and ask for exercise contributions, for example. This requires an intro on objectives and exercise design. Having a list of expected contributions will avoid having people to randomly write sections.
- We will have an intro on how we design our lessons.
- We should aim for a scaffold for the intro and RNA-seq lessons for the workshop.
- **Discussing the RNA-Seq lesson**. TODO: add suggestion reading for the pre-reqs, for example (https://www.nature.com/collections/qghhqm/pointsofsignificance, https://carpentries-incubator.github.io/statistical-inference-for-biology/, Aedin's PCA primer)
- Set deadlines and more meetings before the conference: **25 May at 3pm (CEST)**. Have something up on github by then.

**Executive summary: planning the Bioc2021 conference (short talk and workshop) and RNA-seq lesson fleshout.**

## 2021-05-25, 2-3pm CEST

**Attending**:

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- RNA-seq lesson is being developed at https://github.com/carpentries-incubator/bioc-rnaseq (rendering at https://carpentries-incubator.github.io/bioc-rnaseq/)

**Notes**:

- How to deal with raw data for the RNA-seq lesson? Include quantification code in an episode (which is not necessarily covered in the actual workshop)? Do we do the quantification inside R (which is not necessarily how we would do it in practice), or add e.g. shell code?
- How to enable dependencies between Rmds in the repository (e.g., if data is saved from one and used in another)? The GHA workflow seems to compile them in random order.
- Discuss setup of repository for BioC2021 workshop.

Agenda item for next meeting (from Toby): include Bioconductor lesson(s) in an Incubator Lesson Spotlight feature on The Carpentries blog/newsletter? This could be a good way to attract new contributors to help develop the RNA-Seq lesson, or any of the others. We try to publish them monthly, and could schedule this to be published whenever you think would be most beneficial for the ongoing development of the lesson.
More information about the series.
The most recent post in the series, as an example.

## 2021-06-14, 2-3pm CEST

**Attending**: Charlotte, Kevin, Toby, Laurent, Jenny, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Agenda item for next meeting (from Toby): include Bioconductor lesson(s) in an Incubator Lesson Spotlight feature on The Carpentries blog/newsletter? This could be a good way to attract new contributors to help develop the RNA-Seq lesson, or any of the others. We try to publish them monthly, and could schedule this to be published whenever you think would be most beneficial for the ongoing development of the lesson. More information about the series. The most recent post in the series, as an example.

- Lessons are now autocompiled/deployed upon push to the **main** branch in the repositories:
    - https://carpentries-incubator.github.io/bioc-rnaseq/
    - https://carpentries-incubator.github.io/bioc-project/
    - https://carpentries-incubator.github.io/bioc-intro/

**Notes**

- Toby presenting the Incubator Lesson Spotlight feature on The Carpentries blog/newsletter. For lessons at the very beginning or later in their development. **This is something we want to do, aiming for a blog post beginning of July**. Toby will initiate this as a google doc.
- The three lessons now build automatically upon push. Files in _episodes_rmd/*Rmd simply need to be updated.
- How to deal with pre-processing outside of R? Either simply download the data, or re-process it as an independent episode. Charlotte's classes use salmon, and that output is read directly into R as a SummarizedExperiment. This second approach offers better traceability, as opposed to downloading from GEO and explaining what was done. The pre-processing would be added as an extra episode. The idea is not for the learners to run the pre-processing.
- Providing the SummarizedExperiment is probably too advanced, as it's unlikely that this is what they would get from a standard pipeline. Count matrix and sample annotation would be a better start.
- We should discuss *Different ways to import RNA-seq data* in the extra.
- Note that the data we use (feature counts matrix or salmon for instance) will affect the results. This is possibly not among the main points of the lesson. How opinionated do we want to be - salmon specific or more general?
- Also stress out that the particular software/decision isn't the most important point. Toby also notes that the goal of these lessons is to teach skills rather than tools. What are the important concepts they need to understand? And allow students to apply these on their own data.
- Using csv files as a starting data would also lead on from the intro lesson, and would allow to define a prerequisite more precisely.
- However, starting from a count matrix isn't the standard way of getting data, unless one uses featurecounts.
- We can't quite decide what the best starting point is. That doesn't stop us from making progress. We should pick one and continue with the lesson development. Indeed, we are not aiming at releasing a single/best way to analyse data.
- It is also important to teach how to retrieve annotations for the genes/transcripts, including issues with id mapping. This is even more important if we start from a count matrix. We also need to stress out the reference files that were used for the alignment and counting.

**Action items**

- Next meeting Mon 28 June at 5pm (Berlin time)
- During our next meeting, we will discuss the progress of various lessons and the short talk at Bioc2021.

**Executive summary: Lessons now all have a website. Preparation for the workshop to invite community contributions. Decided to publish a blog post in the Carpentries lesson incubator newsletter.**

## 2021-06-28, 5-6pm CEST

**Attending**: Jenny, Robert, Kevin, Charlotte, Laurent

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Draft slides for BioC2021 short talk. Who presents?
- More detailed plan for BioC2021 workshop
  - recording? Perhaps not terribly useful to upload to YouTube afterwards
  - People can split up into subgroups on tables
  - Contribute via issues or PRs - ask people in advance to create a GitHub account
  - slack channels for communication
  - create one table per lesson (at least to start with) - also need to define initial table moderators/leaders
    - bioc-intro - Laurent
    - bioc-rnaseq - Charlotte
    - bioc-project - Kevin
- Plan for adding more details to the lessons before BioC2021
  - https://github.com/carpentries-incubator/bioc-intro
    - chapters 1-3 ready
    - dataset tested, works nicely
    - working on chapter 4->
  - https://github.com/carpentries-incubator/bioc-rnaseq
  - https://github.com/carpentries-incubator/bioc-project
- CAB 2020 review, slide for Education Committee: https://docs.google.com/presentation/d/16bIqufKgA60cFbJ4oAuvCyJiwJoqkjbt1m3fnziNBA8/edit#slide=id.gce0628b703_0_375

Action items:

- Contribution guide for the BioC2021 workshop repo - **Jenny** (add a link to code of conduct, mention that all contributions are recorded and acknowledged, add details on how to build locally)
- Export csv files for RNA-seq data - **Charlotte**
- Gene set analysis episode (Fisher exact test, clusterProfiler?) - **Robert**
- Importing and annotating data/RNA-seq episode - **Charlotte**
- Add material to the bioc-project lesson - **Kevin**
- Next meeting: 26 July 2021

**Executive summary: preparation of the Bioc2021 workshop and presentation.**

# 2021-07-12, 2-3pm CEST

**Attending**: Charlotte, Toby, Kevin, Robert, Jenny

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Update on Action items from last time:
    - Contribution guide for the BioC2021 workshop repo - **Jenny** (add a link to code of conduct, mention that all contributions are recorded and acknowledged, add details on how to build locally)
    - Export csv files for RNA-seq data - **Charlotte. Done**
    - Gene set analysis episode (Fisher exact test, clusterProfiler?) - **Robert**
    - Importing and annotating data/RNA-seq episode - **Charlotte. Scaffold in place**
    - Add material to the bioc-project lesson - **Kevin**

- Include information about chromosomal location (chromosome + position) in the rowdata (when exporting from the bioconductor-teaching repository), i.e., add the rowRanges part to the SE object.
- Add exercise placeholders in episodes

# 2021-07-26, 2-3pm CEST

**Attending**: Charlotte, Laurent, Kevin, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Status update on lessons
    - bioc-intro: missing part: missing values
    - bioc-rnaseq: SE has rowRanges, gene set analysis (female vs male, time contrast GO analysis)
    - bioc-project: S4 classes
- Recording for BioC2021 talk (Charlotte)
- BioC2021 workshop material
    - contribution guide: code of conduct, mention that all contributions are recorded and acknowledged, add details on how to build locally
    - add link to Toby's slides

## 2021-08-09, 2-3pm CEST

**Attending**: Laurent, Toby, Kevin, Charlotte, Marco, Jenny.

**Join the meeting**: [https://meet.jit.si/BioconductorTeaching](https://meet.jit.si/BioconductorTeaching)

**Agenda:**

- Debrief after conference workshop
- A (possibly optional) lesson on tidy functions for SEs (suggested by Hugo Tavares)

**Notes:**

- New member Marco Chiapello, offered help with bioc-intro
- bioc-rnaseq: discussions about the structure. People from Gent/Lieven Clement's group were planning to develop an RNA-seq lesson, interested in helping out. There is also interest in using the material. Susan was interested in seeing how we planned to cover all the material in 1 or 2 days. Christophe asked about interactive visualisation (iSEE, Genetonics).
- bioc-project: Hugo Tavares joined the project table. Not too technical with S4 classes, for instance no need to get into how classes are made and slots; focus on examples/illustrations with concepts. Important to explain why we need classes, and demonstrate the diversity of available classes/applications. Classes (more generally) are a way to label things to inform on what can be done with them/how to use them.
- From bioc-project table discussion, it became clear it was important to highlight that contributions aren't limited to material or teaching. This also came up during the Meet the TAB session. Toby has started to update the contribution guide page. There's an opportunity to gather wider feedback and contributions. Also need to clarify how we decide what will make it into the lesson - explain that issues and comments are welcome, but that decisions will be made during these calls, and if people want to join the decision making about what is included, they should also join the calls. It is important to make decisions, rather than discussing what to do and how to do it.
- Also need to establish governance and document decision making for this project/lessons (and incubator in general, cf Toby)
- bioc-intro: Marco joining the team. Some technical issues.
- Some technical issues - commit rmd files to main, and then md files are added to gh-pages that deploys the web page. No md files in main branch; gh-pages branch has (or can have) md and rmd files. NB: when deleting an rmd, md must also be deleted manually in the gh-pages branch. Would be good to have a patch that commits deletes. Would be nice to work on a patch on this.
- Toby shares [https://documentation.divio.com/](https://documentation.divio.com/) suggesting to document things as 4 parts: tutorials, how-to guides, technical reference and explanation.
- Didn't get the 'collaboration fest' during the conference - is there value to try again, possibly in a more coordinated/organised way? Many participants in the conference were more interested in learning about and discussing the teaching initiative, less to work on specific tasks. Important to create well defined atomic tasks, and tag them

as ‘help wanted’ to encourage spontaneous contributions via the Help Wanted Issues page on The Carpentries website.
- Read about the new lesson infrastructure (entering beta testing soon) in this blog post: https://carpentries.org/blog/2021/07/infrastructure-testing/

## 2021-09-13, 2-3pm CEST

**Attending**: Laurent, Charlotte, Kevin, Christophe, Marco, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**
- A (possibly optional) lesson on tidy functions for SEs (suggested by Hugo Tavares)
- BioC2021 committee suggests that it would be good to have a core set of Bioconductor workshops to offer at every BioC/at other occasions, by various people - have a look at the "100 level" workshops from previous conferences, which ones would fit well in the Carpentries style? How should this be organized? There is money available to pay for someone to help put things together.
- CZI EOSS grant "Bioconductor: High Quality Training and Support for a Worldwide Community" (submitted by Aedin) was funded. Website development, training platform, Carpentries membership, community manager.

**Notes:**
- Bioc-intro: added additional variables with missing values to the SummarizedExperiment object.
- Bioc-project: Kevin has a presentation on that topic, demo of Bioc using Biostrings, S4 class system, help pages and vignettes, installing and updating packages, BSgenome in conjunction with Biostrings, GenomicRanges (by hand) and rtracklayer from gtf, Bioconductor’s DataFrame class, annotation packages and biomaRt, SummarizedExperiment by hand and from txmeta.
- RNA-seq: outline is done, need to add exercises and general text.
- **Plans for the future**, including making the best with available resources. (1) Bioc conference wrap-up: would be good to have the core courses to deliver during conferences. Could we turn some workshops (for example ‘What is Bioconductor’) into Carpentries lessons? Are there any workshops that don’t fit and could be reshaped into a workflow. Conference money is available for this. (2) Aedin’s CZI EOSS grant is funded. See above for details.
- **TODO**: liaise with Aedin’s as to when CZI EOSS starts, when to start the process to become members of the Carpentries board, when to plan instructor lessons, ...
- Community manager job description is being written. We might want to stress out the needs for our education committee. **TODO**: liaise with Aedin/CAB to make sure that the needs and inputs from the training committee are addressed.
- New trainers: **what are we expecting from them**? Specific contributions to Bioconductor? New lessons (even though we want to avoid fragmentation)? We need

to think about what we want from instructors to make sure we can advertise these opportunities. We could ask new trainers to choose among the workshops that already exist if they want to create new lessons or workflows. We could also ask them if they would **consider/commit running workshops** at the next Bioc/Euro/Asia conferences. **TODO**: brainstorm about this, before opening a call for new instructors.

- Bioc has already: vignettes, workflows, workshops, our Carpentries lessons, … we need to think about what people want from these lessons. **TODO for next time, list and define all types of teaching material we have**. For example: Carpentries lesson are developed collaboratively, maintained over time, taught several times by different **trained** people, focus on mature material (as opposed to workshops, that are focused on new material/packages, developed by one person/maintainer, and likely to change).
- Through our lesson development, we also harmonise the different materials/lessons. This could lead to an online collection/book about Bioconductor. (As opposed to a more organic growth of the other material, that are more of a one-shot).
- We should also think of a **life cycle for our lessons**.
- Translations - ask for contributions.
- Do we have plans to organise other events/hackathons? We probably need a better idea of what we want. Note, airmeet still available.
- Any plans as to when we want to run our first workshops? **Should we aim for EuroBioc in March?** Intro and/or others? Maybe only an intro course with all instructors, to share the teaching load, share experience, … **TODO** To be discussed with the EuroBioc conference committee. Such a workshop would be a great to introduce people to Bioconductor before the conference.
- A topic that came up several times: have guidelines for workshop authors.

## 2021-10-11, 2-3pm CEST

**Attending**: Laurent, Charlotte, Kevin, Jenny, Robert
Note: Kevin only available for the first 30 min

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- ~~Running an intro course at EuroBioc2021 |> 2022: discuss logistics, how many students would we include, in-person and/or hybrid (?), interest to teach/help. Decisions to be transmitted to Simone Bell and EuroBioc conference organising committee.~~
- ~~Updates on bioc-intro advancement.~~
- Bioc-project on hold for another week (Kevin teaching). Contents will be based on a lesson that Kevin wrote from the University of Oxford (will be taught Wednesday after this meeting -> 1_r_bioconductor.pdf ).

TODOs from last time, for reference:

- TODO: liaise with Aedin's as to when CZI EOSS starts, when to start the process to become members of the Carpentries board, when to plan instructor lessons, … (*progressing*)
- Community manager job description is being written. We might want to stress out the needs for our education committee. TODO: liaise with Aedin/CAB to make sure that the needs and inputs from the training committee are addressed. (*progressing*)
- **DONE for next time, list and define all types of teaching material we have**.
- We could ask new trainers to choose among the workshops that already exist if they want to create new lessons or workflows. We could also ask them if they would **consider/commit running workshops** at the next Bioc/Euro/Asia conferences. TODO: brainstorm about this, before opening a call for new instructors.
- **Should we aim for EuroBioc in March?** Intro and/or others? Maybe only an intro course with all instructors, to share the teaching load, share experience, … TODO To be discussed with the EuroBioc conference committee. **YES**

Attempt to define the different types of educational material provided within Bioconductor:

- *Help pages*: provide detailed instructions for calling a specific function.
- *Vignettes*: provide an overview of the functionality of a Bioconductor package and how the functions from the package (and possibly other packages) can be used to perform some type of analysis.
- *Workflows*: provide more comprehensive, end-to-end descriptions of how to analyze a specific type of data or perform a certain type of analysis. Workflows often involve several Bioconductor packages and show how they work together to achieve the stated goal.
- F1000 Research Bioconductor Channel (publications for workflows and additional topics) - https://f1000research.com/channels/bioconductor
- *Books*: provide extensive coverage of entire research fields, and often consists of both theoretical expositions and worked-through examples.
- *Carpentries lessons*: educational material aimed at in-person or virtual training, structured according to the Carpentries guiding principles. Rather than providing end-to-end analysis workflows, these lessons aim to teach concepts, and give the learners plenty of opportunity to practice these.
- *Workshops (Orchestra)*:

**Notes:**

- EuroBioC 2021 |> 2022: organize an in-person workshop on Mon-Tue (March 14-15 2022, Heidelberg). Aim for 20-25 learners. 2-3 instructors, 3 helpers.
- Course announcement: first via conference channels, then outside.
- bioc-intro updates: first draft ready (on http://bit.ly/WSBIM1207). Uses the new data (including variables with missing data). Todo: change format to carpentries format, trim down material, port to carpentries-incubator/bioc-intro (Laurent, Christophe, Marco). Once it's there, work on it together.
- (Action item: **Kevin**) Consider telling about conflicts across packages in bioc notes. (possibly add this to bioc lesson https://swc-uiuc.github.io/r-genomics/06-extras.html)

- Existing material (see above): can we identify links or a hierarchy between these types of material? How can newcomers or more experienced users (R but not Bioconductor for example) get started? What type of document is most appropriate? A high level **meta-documentation** for new/experienced users could be a valuable resource.

## 2021-11-08, 2-3pm CEST

**Attending**: Laurent, Charlotte, Kevin, Jenny, Chris, Marco

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Notes:**
- Room fitting 25 people has been booked on Mon/Tue before the EuroBioc2021>2022 conference.
- Action item (Charlotte): check with Simone if there's a possibility to reserve a larger room to make sure that we will be able to fit 20 participants + instructors regardless of restrictions in place at the time.
- Discussion about the possibility of running another more advanced course.

## 2021-12-13, 2-3pm CEST

**Attending**: Charlotte, Marco, Jenny, Laurent, Toby, Kevin, Estefi

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**
- Carpentries workshop in March: set up Google Form for applications.
- First draft for bioc-intro lesson: https://carpentries-incubator.github.io/bioc-intro/.
- Organization of training courses in Spanish, Latin America (Estefania).
- Carpentries membership (pricing update for 2022).
- Community manager job description.

**Notes:**
- Interest in: (1) ~~translating our courses in other languages~~ (Spanish) and/or (2) teaching workshops in other languages.
- Translation: good if it's coordinated, risk of becoming out of sync. Need maintainers for translations.
- Carpentries is actively looking for funding to formalise and coordinate translations. Includes: infrastructure, release cycles, how to improve any lesson/translation and how to synchronise all these.
- bioc-intro lesson: https://carpentries-incubator.github.io/bioc-intro/. Episodes 1-3 mostly similar to the Carpentries ecology lesson, more substantial differences in episodes 4-6 (mostly related to the different dataset that is used). New episode on

joining tables (could be moved to the dplyr section). Laurent has run the same material in a 2-day workshop already. Final section on SummarizedExperiment - more of a demo, mentally prepare people for the next step/lesson.
- Moving forward: go through material on GitHub, make suggestions/PRs. More substantial changes/additional exercises - open an issue.
- Setup: From the Carpentries guidelines, ideally, users should be able to run things locally. But also don't leave anyone behind and make it accessible. Backup in case something breaks (Orchestra?). Send instructions in advance.
- Application for workshop - finalise application for next call 10 Jan 2022. Put a link to the workshop application form in conference registration. Mention that registration to the conference is mandatory to participate in the workshop.
- Membership to Carpentries: still waiting for funds. Job description of the community manager is being written. Kevin to liaise with Aedin to follow up.
- Charlotte to put together a google form for application to the workshop in March.

2020

# 2020-07-06, 5-6pm CEST

**Attending:** Laurent Gatto, Charlotte Soneson, Nitesh Turaga, Robert Castelo, Kayla Interdonato, Toby Hodges, François Michonneau, Ludwig Geistlinger, Marcel Ramos

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

- Material for in-person and/or remote teaching?
- Plan for a Bioconductor curriculum (see comments and suggestions above)
    - What kind of pre-requisites?
        - R / Tidyverse / carpentries ?
        - What kind of basics will we require from them?

Meeting Notes:

1. Material for in-person and/or remote teaching?
    - (FM) - Convert in-person classes to online/remote format (recommendations: https://carpentries.org/online-workshop-recommendations/) Follow along in RStudio cloud. Pre-installed software infrastructure is needed on the cloud to use software after the workshop (remote).
    - (NT) Bioconductor has Bioc docker images readily available.
    - (LG) Remote workshops were 2 days?
        - Other setups - 4 days instead of 2 days. Not enough feedback right now. (FM)
    - (TH) - Gathering experiences teaching online
        - Most successful has been using Data Carpentry lesson material, but not run in carpentry style.
        - Material adapted reasonably well from DC to remote settings. (Good news)
        - The teaching style/infrastructure is more the issue and not the lesson material.
    - (CS) - How many helpers? (compared to carpentries)
        - (TH) - More helpers are needed!!! It affects how much you can scale.
        - (FM) - New role called (Supporting Instructor)
            - Online format -- 2 main instructors and 2 supporting instructors
2. Round table -- preference online vs in-person vs both?

- (LG) Inverted material (flipped classes) --
    - (CS / LG) pre-requisites need to be made clear.
    - (NT) - Pre-course surveys?
        - LG - isn't this more work?
        - FM - Very quantitative, automate the delivery of results of the survey. Similar questions after the workshop. It is VERY hard to design

        - classes that require heavy pre-requisites because people don't know how to self-access correctly.
    - (NT) - have an extra day (or few hours) just introducing R?
        - (RC) - People interested in Bioconductor are MD, Biologists, etc..they don't know how to import things into R. It might be important for the success of the Bioconductor course later on to have an extra day involving just teaching R.
    - (CS) - Pre-course survey for CSAMA have anything else?
    - (KI) - Online better introduces Bioconductor better to the community. **Bioconductor strives to have a community around the project**.
        - NT - reaches a wider demographic. Affordability?
    - (NT) - Maybe material doesn't need to change much. First, prepare material which lends itself both ways.
        - TH - Just preparation needs to change to teach.

3. What kind of material should we develop?

- CS - Allow people to do things they did not know before? Overcome the initial fear.
    - What is Bioconductor? Why is it different from just running R?
    - **Teach basic structures** - how to search website, vignettes
    - DNAStringSet, SummarizedExperiments.
    - Why do we need specialized classes for specific types of data? Why not use "basic" R structures?
    - Demonstrate that there is a smooth bridge between Bioconductor and the tidyverse (Tidy bioconductor) (dplyr/ggplot2 is what they will have learned in the introductory carpentries courses)
- TH - Helpful to think about "what" people will be coming to the course for ?
    - Don't worry about advertising that "Bioconductor is useful".
    - "Learn to do powerful things with Biological data in R" -- maybe advertising like this is more useful to get into introducing Bioconductor.
- RC - Maybe attempt to develop courses with specific analysis goals?
    - Proteomics
    - RNA seq
    - Single cell
    - …..
    - Maybe this is the way to go at the risk of not getting to a specific audience.
- CS - what level are we developing material
    - FM - develop a lesson first. Data Carpentry - Bioconductor lesson
        - Day 1: R (DC-R lesson)
        - Day 2: R → Bioconductor (Aaaha moment)
    - FM - Other format, 2-4 lessons of Bioconductor and 2 full days of Bioconductor.
        - Focus on ONE curriculum and make it robust. Do not diffuse the energy on multiple things.
        - Goal should be to get people from the carpentry community to contribute with their expertise (proteomics, single cell etc).

        - We need a large community of maintainers to take these lessons.
    - TH - https://cdh.carpentries.org/the-lesson-life-cycle.html
        - I remember talking to someone at CarpentryConnect last summer, who wanted to develop an "R for RNA-Seq Analysis" lesson. potential overlap in interests here? please drop me an email if you'd like me to connect you with them.
    - Modularity will likely be important - helpful if it's possible to combine episodes/modules into different workshops.

- Start with 1 good lesson before spreading efforts too much. Also good to recruit new members.

**Questions for next time**

1. How can we measure success? What do we aim for and how to check this?
2. How to certify new people to help us teach, and to grow the community? Is there Interest in a *train the trainers* course?
3. How can we leverage the current momentum to start building something tangible? **Start a GitHub repository**?
4. How can we benefit from teaching material that we already have (developed for other courses)?

## 2020-08-17, 1-2pm CEST

Attending: Laurent Gatto, Charlotte Soneson, Peter Hickey, Nitesh Turaga, Mike Smith, Kevin Rue-Albrecht, Jenny Drnevich

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

Meeting notes:

- Summary from last meeting. Questions from last time. Where to take it from here?
- From the TAB: interest to have an instructor trainer in the group, to be able to train new Bioc instructors. Growing the Bioc instructors community.
- Jenny mentioned there will be a train-the-trainers course in fall. See https://carpentries.org/trainers/
- Re-use some existing material. Bioconductor website lists the material from previous courses. It should be fine to re-use any of these materials. Need for a common theme throughout the lessons.
- Start with a lesson composed of short and coherent modules. Should be possible to choose from these modules, without having to teach all of them. Not aim for a full curriculum.

- Question: how will our material fit in current DC courses? Jenny suggests with basic R, fitting with the data carpentry type of courses (rather than software carpentry). Important to start from the beginning.
- Bioconductor basics would already be steep. Need basic R pre-reqs.
- Idea: take (e.g.) the ecology curriculum, and adapt instead to Bioconductor needs/structure. Underline important Bioconductor-specific aspects from the start. **Challenge**: find an interesting data set to replace the one used in the ecology curriculum. https://uclouvain-cbio.github.io/WSBIM1207/
- Note: genomics curriculum starts from the command line, before R analysis. It focuses on pre-processing. Not what we need.
- We should first focus on our needs, not necessarily adding to Carpentries, which is pretty difficult. There is a Carpentries incubator. (https://github.com/carpentries-incubator/proposals#readme)
- What Bioconductor specific material do we need? Intro material such as WSBIM1207 chapter 8 for example. Plus RNASeq, proteomics, … specific modules.
- **TODO** Create new repos for our new material. With bookdown rendering. **Suggestion**: repositories under Bioconductor organisation. Meta-repo for management and discussions (bioconductor-teaching, **Nitesh ~~to create~~ DONE**), then individual repos for modules?
- **Modules examples**: DC for medical sciences; introduction to the Bioconductor project (see, also managing, conflict between packages, ), RNAseq data analysis.
- Start from the Carpentries template if we want to contribute back (see Carpentries incubator for details).
- **Bioconductor intro material**:
    - Jenny's
        - Bioc teaching material: https://wiki.illinois.edu/wiki/pages/viewpage.action?pageId=721093952
        - Extra DC module on package conflicts. https://swc-uiuc.github.io/r-genomics/06-extras.html
    -
    - Charlotte (et al)'s teaching material: https://ivanek.github.io/analysisOfGenomicsDataWithR/02_IntroToBioc_html.html
    - Chap 8 WSBIM1207

- Plan meeting for next month.

## 2020-09-14, 2-3pm CEST

**Attending**: Charlotte, Toby, Jenny, Kayla, Laurent, Francois, Robert, Nitesh

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Updates on the initial repository (https://github.com/Bioconductor/bioconductor-teaching) setup and creation of module-specific repositories.
- Request for input for the 3 initial modules: (1) General data science intro, (2) The Bioconductor project, (3) Analysis and interpretation of bulk RNA-Sequencing data.
- **Suggestion**: 1 or two lessons leads that have write access and contributions by pull requests (including the lesson leads); this makes it easier for everybody to review/discuss contributions and stay informed.
- Discussion on workshop organization for BioC2021 (August 4-6 2021)
    - The BioC2021 organization committee had its first planning meeting last week, and there was a suggestion that the teaching group could take the lead on the workshop organization/planning for BioC2021
    - Suggestion to go back to a more 'education' focus, with more introductory material, and possibly run the workshops separately from the conference (e.g. the days just before)
    - Can we 'test drive' some of the workshops during the year?

**Call notes:**

- meta-repository set up
- 3 initial modules:
    - data science intro, but with Bioc focus
        - vignettes
        - change data set
    - Bioc project
        - workflows
        - vignettes
        - landing page
        - installation
        - workflows
        - could be combined with other modules
    - bulk RNA-seq analysis
- **TODO**: create new repositories (one per module). Everyone provides contributions via pull requests.
- What would we need to do in order to be able to contribute this back to the Carpentries afterwards? Open repositories in the Carpentries incubator directly? There's a template repository. Access to support, community would be easier.
    - Requirements from the Carpentries side: Code of conduct, license (CC0, CC-BY), use their lesson templates, no lesson on exactly the same topic existing/under development
    - Goal of the community lessons are to get included in the Carpentries official curriculum or as more specific lessons in the Carpentries lab. Latter would be a good fit for the Bioconductor lesson.
    - Intention to have an open peer review for lessons that get into the Carpentries lab and get published as an educational paper.

    - **TODO**: Toby to create repositories under the Carpentries incubator. Naming convention: start names with **bioc**. Create a team with people developing a set of lessons.
        - open 3 issues at https://github.com/carpentries-incubator/proposals/issues - include title of lesson and list of names/GitHub usernames of those who will be collaborating on the lesson(s) material. The one who opens the issue will become the administrator of the repository, other people who are named will become maintainers.
            - data science: Laurent, Robert (rcastelo)
            - Intro to Bioc: Laurent, Jenny (jdrnevich), Kayla (Kayla-Morrell)
            - RNA-seq: Charlotte , Jenny (jdrnevich)
            -

- **Feedback from the Bioc2021 call**: still largely virtual meeting in August 2021, with watch parties or small get-together. In 2020, different workshop formats, little interaction, mostly demo of packages, too fast.

**Idea**: gear the next set of workshops towards education, more intro material (possibly to be run before conference). Workshops to be taught and tested throughout the year. As the education group, would we want to take this on? Think about how to deliver these workshops in a more efficient, coherent way?

    - Yes, part of our work anyway.
    - 1 hours isn't enough. We could guide on the format and duration. Up to 3 hours if that's what we think is needed.
    - Jenny is testing 2 formats: bits by bits and people work on their own vs live, as in person. See also **https://static.carpentries.org/online-workshop-recommendations**
    - Cloud infrastructure is still available, will probably be. Could also have on complete lesson available for recurrent workshops.
    - Cloud vs using one's own computers. Would also fit other efforts, like using cloud computing (Vince)
    - Live coding (see also this paper). How to keep this interactivity for larger data. Maybe externalise some parts to other workshop, or supplementary information of the course. Focus on parts of the lessons to give learners enough time.
    - Manage expectations. Define prerequisites for/between different lessons.
    - Provide teachers/presenters with material **on how to set it up**. Don't be too ambitious. Describe pre-requisites, existing resources, intro material, … so that the workshop developers can **focus on their core material**.
    - Prepare tips/howto build a workshop document/guide in the main repo: https://github.com/Bioconductor/bioconductor-teaching/blob/master/workshop-guide.md

- Keep **2nd Monday of month at 2pm** (EU time) for next meetings.

# 2020-10-12, 2-3pm CEST

**Attending**: Laurent, Charlotte, Toby, Nitesh, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Toby: Tips for formulating learning objectives/end goals for lessons
- Group exercise: Formulate high-level objectives for the first three Bioc modules - repositories: bioc-intro, bioc-project, bioc-rnaseq
- Shall we aim to offer a workshop already at EuroBioc2020 (December 14-18)?

How to formulate learning objectives: Link to the slides:
https://docs.google.com/presentation/d/1O-FJL72weYgyzmiWc5LnS6AuK4nMlw0ZfxsiMm_2dPI/edit?usp=sharing

## Defining Target Audience

Example Persona
Mehrdad Mapping is a graduate student studying bark beetle infestations in the Canadian taiga.

He has never taken a programming course, but used SAS in an undergraduate statistics course.

For the last three years, Mehrdad has spent six weeks every autumn counting beetle bores in pine trees in the Yukon and Alaska. He now has a spreadsheet with 5,000 entries, each recording the location and time of a measurement, the number of bores found, and the values of environmental variables. He also has two hundred text files containing 7,000 measurements that his supervisor made in the same regions in the 1970s and 1980s. His task now is to clean up and analyze both sets of measurements so that he can start to correlate changes in bark beetle distribution with changes in climate.

In high school, Mehrdad was diagnosed with Attention Deficit Disorder, which he learned to manage.

Software Carpentry will teach Mehrdad how to standardize, merge, and set up basic analyses for these data sets, and how to produce the figures and tables he needs for his papers with just a few lines of code. In addition, it will show him how to use web services to generate and share maps of these data with colleagues.

Minimal questions for **bioc-intro course**:

- (Laurent)
- Who are they? Bachelor student (year 2 or 3) in biomedical sciences. No experience in programming or data analysis as part of their curriculum. Some students also struggle with Excel and/or concepts such as file/directory, relative/absolute path. Some haven't much experience using Excel either.
- What is the problem they face? At a later stage during their curriculum, they will have to *analyse all sorts of data* but will never have been taught how to do it or what tools to use.
- How will your lesson help them address that problem? The bioc-intro lesson should provide them with enough R knowledge to perform simple data manipulation and visualisation to be able to analyse data in a tabular format. In addition, they should also be introduced to the fact that some data won't fit in a single tabular data, and that omics data typically doesn't, and that the Bioconductor project offers dedicated tools for such data, as get introduced to basic/important Bioc objects (needed for next courses). They should also be familiar with the concept of package and their installation.

- (Nitesh)
- who are they? - Students from different backgrounds, Bachelors, Masters, MD, PhD but are looking to gain experience in high throughput genomics analysis with Bioconductor. They are looking to do the analysis themselves and need a place to start. They have domain knowledge in genomics.
- what is the problem they face? - Data is complex and they have no structured way of analyzing their data. They don't know what technology or how to use i.e Galaxy, R/Bioconductor, something else….or don't know what is available.
- how will your lesson help them address that problem? - Help teach them basics, importing data, analyzing data using Bioconductor packages and data structures, writing results in a coherent reusable manner. (Maybe even "tidy")

- (Robert)
- who are they? Researchers generating molecular data without prior computational experience.
- what is the problem they face? How to read molecular data into R, how to explore that data.
- how will your lesson help them address that problem? They'll be able to import their molecular data into R, store it into the appropriate Bioconductor data container and explore it with the methods associated with that data container.

- (Charlotte)
- who are they? PhD student in biology, who has generated some omics data, but never done any analysis on their own. Gets processed data back from the facility.
- what is the problem they face? They can't explore the results on their own, and are 'stuck' with what is provided.
- how will your lesson help them address that problem? Get over the initial hurdle of importing and exploring data in R (specifically data stored in 'omics-specific'

containers), understanding how to write simple scripts for exploration and plotting of specific aspects of their data.

- (Jenny)
- who are they? Users of the U of I biotechnology facility (mostly graduate students and post-docs, but a few undergrads and faculty members) who have generated -omics data. They come from a wide range of departments (e.g., Biology, Chemistry, Engineering, Statistics, Computer Science, Agriculture, etc.) so background knowledge varies a lot and they work on a wide range of organisms, often non-model.
- what is the problem they face? They need to learn how to handle, process and analyze their -omics data.
- how will your lesson help them address that problem? Show them how to install R and packages, introduce basic R syntax and data structures, teach them how to read and modify code so they can follow and adapt package vignettes.

See more examples of personas here:
https://carpentries-incubator.github.io/building-websites-with-jekyll-and-github-or-gitlab/index.html (there are also learning objectives on the landing page of this lesson)
https://software-carpentry.org/audience/

Expanded set of questions
- What is the expected educational level of your audience?
- What type of exposure do your audience members have to the technologies you plan to teach?
- What types of tools do they already use?
- What are the pain points they are currently experiencing?
- What types of data does your target audience work with? What are the commonalities in the datasets your target audience will encounter?

## Objectives and reverse design

Define the end goal of your lessons.
Make a list of 5-7 skills you will need to teach to get your learners there.

1. **Define an objective: a specific, practical skill your learner will have when they leave your lesson:**
2. **What skills/concept understanding do they need to have gained to be able to achieve this? (functions, syntax elements, concepts, etc)**

(Nitesh)
Objective: Load data from a CSV (excel) file and manipulate it using tidyverse vocabulary in R so that it arranged in a genes as rows and columns as values.

Skill: tidyR, dplyr, dyplr verbs, basic R

```
dat <- read_csv(“mydata.csv”)
dat_1 <- dat %>% select(Gene, Val, metadata) %>% arrange(desc(Val)) %>% pivot_long(...)
```

(Charlotte)
**Objective**: Load an expression matrix and sample metadata, select a gene and plot the expression level in different groups.
**Skills**: Read csv file, understand tabular data structure (matrix, data.frame), subset tabular data, merge data from different tables (to combine expression data with sample metadata), ggplot syntax

(Laurent)
**Objective:** Visualis the expression of a set of genes in different sample (or group of sample).

```
        expression_table %>%
        rowname_to_column(gene) %>%
        pivot_longer(names_to = “sample”, values_to = “expression”, starts_with(“sample”))
        %>%
        ggplot(aes(x = sample, y = expression)) +
        geom_point() +
        facet_wrap(~ gene)
```

**Skills needed:** get data into R as a data.frame/tibble, understand concept of wide/long tidy data, including familiarity with dplyr, and knowledge of ggplot2 syntax.

(Robert)

```
## Import molecular and phenotype data into a Bioconductor data container
library(SummarizedExperiment)
row_data <- read.csv(“expression_data.csv”)
col_data <- read.csv(“phenotype_data.csv”)
se <- SummarizedExperiment(assay=row_data, colData=col_data)
seqdepth <- barplot(colSums(assays(se)$counts))
```

(Jenny)
**Objective:** Read in a .gtf or .gff file and assess what feature type and attribute name they should use for alignment and counting.
**Skills needed:** knowledge of the structure of a gff file, how to read one in using rtracklayer, understanding of the structure and accessors of an S4 GRanges object, basic R skills like subsetting via brackets and $, table() and names()

```
library(rtracklayer)
```

```
gff0 <- import("GCF_000146045.2_R64_genomic.gff.gz")
methods(class=GRanges)
table(gff0$type)
gff_exon <- gff0[gff0$type == "exon"]
mcols(gff.exon)
names(mcols(gff.exon))
```

## 2020-10-15, 5-6pm CEST

**Attending**: Laurent, Nitesh, Charlotte, Jenny, Robert.

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:** Follow-up on work done during the last meeting (2020-10-12).

- First Bioc intro course should take people from no prerequisites. End point would be to create and understand a SummarizedExperiment. **TODO: compile the above objectives into one document in the bioconductor-teaching repo.** Jenny's objectives are probably a bit too advanced for the intro course.
- Also - what is crucial in learning Bioconductor.
- Structured vs unstructured data.
- Interest is developing some fully autonomous asynchronous lessons (edX, coursera). Could be useful to get people to meet prerequisites on their own before a kuve workshop. (swirl, learnR, exam).
- Note about the bioc-project lesson: a meta resource about the Bioconductor project. Educational version of the website.
- Do we expect the participants to have data or not? Undergrads probably not. PhD students, possibly yes. These two learners will approach the workshop with a different timing in mind: spend some time to learn something, or learn something to apply it as soon as possible.
- **TODO** Intro course: decide on a central data type to analyse. Could we use **reverse instructional design to design/define the central data set to be used throughout the course**. Data that can be used for certain data manipulations (dplyr, ...) and visualisation (ggplot2, ...). Ideally a real data set, but might be artificial to make sure it fits all the needs.

## 2020-11-09, 2-3pm CET

**Attending**: Laurent Gatto, Charlotte Soneson, Paul Harrison, Pariksheet Nanda, Lukas Weber, Toby Hodges, Jenny Drnevich, Kevin Rue-Albrecht, Kozo Nishida, Robert Castelo.

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- Shall we aim to offer a workshop (might be too early for intro workshop) or short talk (or discussion format?) about the past 6 months to publicize the effort already at EuroBioc2020 (December 14-18)?
    - **TODO**: Charlotte to start composing a short abstract for a short talk. Link
- Laurent has moved our work on target audience and objectives to the bioconductor-teaching repository. Still want to expand on the conclusions of our discussions.

- What do we need from a data set that can be used throughout the 'intro' module? Can we find such a data set, or generate a synthetic one? Recommended that the data is provided under a CC0 license. Further guidance from the Carpentries: https://cdh.carpentries.org/designing-challenges.html#picking-a-dataset
    - Tobi: Main thing to look out for is dataset published with a permission license to avoid trouble with sharing or modifying license; recommended is CC0 license to remove complications. Often easier to find a dataset first and then write a story to match it.
    - Laurent: My ideal dataset would be what we have in the data carpentry ecology lesson: different species from taxonomic groups sampled from different patches. Capture / recapture experiment going on since the 1970s. Can do everything with that dataset. But ecology, whereas we would want something about biomedical data science:e.g. 10-40 genes about a similar number of patients. Would be good to have variables about diseases, sub-types of diseases, gender. Also category of data acquired from different technologies. Should be able to produce box- and density-plots for expression for different patients. Count data gene intensities, similar to the ecology dataset, to apply log-transformation. Color scatterplots. Data over time: geom_line shows the power of tidyverse and ggplot2. Also show and explain faceting.
    - Charlotte: I was even thinking a small single cell data (so not 10k cells). Categories, combine, pre-classification of cells with QC tables. Development time things. Ecology has a lot about dates, which we don't do a lot in genomic data: we have time, but not dates. They spend a lot of time talking about dates. Barplots and frequencies of different types. In the end take data frames and compile a summarizedExperiment()
    - Lukas: could demo heatmaps though they are more complex. But very useful for people. I like the idea of single-cell datasets.
    - Jenny: Question about licensing. Any datasets publicly available in GEO, or the European equivalent repository, etc?
    - Toby: Check that the public data can be republished in a modified form: terms like that do exist on datasets.
    - Kevin: Everything on GEO should be completely reusable? I've never seen reuse or teaching limitations.

- Laurent: We assume, but that's not always the case. For proteomics dataset in PRIDE they didn't have a specific license: it was unclear. Same for Uniprot: was not explicitly under CC0.
- Kevin: I didn't know which license to pick. If you don't provide a license.
- Pariksheet: same data can be licensed multiple times. We could always reach out to the copyright holder, independently of the repository it is currently available from.
- Toby: GEO - unless otherwise stated, … need to check any additional terms. Also provide guidance to cite the data. https://www.ncbi.nlm.nih.gov/geo/info/disclaimer.html
- Kevin (https://www.nature.com/articles/s41467-018-07329-0 and http://kevinrue.github.io/DCsc-website and https://github.com/kevinrue/DC_sc ): Co-authors are quite keen on being cited and their data being reused. On Laurent's point about multi-group comparison, even as little as 3 time points can be a time series. Going back to what Tobi was saying, I've included bad cells excluded during QC. For packaging the dataset we could remove those.
- Jenny: In single-cell dataset from last year can be quite different from fresh, new data. In RNA-seq workshop would be good to have a modern dataset.
- Kevin: Even for single-cell data, would be nice to have enough information to almost process as bulk RNA-seq.
- Robert: Some pattern or biological insight should be revealed by basic boxplots and scatterplots. There may be such datasets in biomedical human data, but might be easier for knock-out data from model organisms. Might be possible from human data depending on the situation. For introductory material it's nice to have pristine datasets where assumptions apply. Great to show biological or batch effects.
- Laurent: We assume all participants have some knowledge of biology. Even if they don't know all the technologies, they know what cells are, what expression is, etc.
- Laurent: We can think of 3-4 plot types we would like to see and evaluate the dataset by being able to reproduce them.
- Tobi: Having the final goals as the plots is quite sensible because that's what the learners are producing. Also worth thinking of the added value of Bioconductor in all of this. What would you like to teach them about using Bioconductor between loading the data and making the plots? Having the plots there are what incentivizes them to learn anything in the first place.
- Laurent: Not sure how important the in-between steps are for bioconductor. What makes learners come to the next session is getting past the data cleaning and identifying clusters and gene expression: those would be different tools not in this course but lead them to the next course for that data analysis. We should show them the next step.
- Laurent: We could mention "objects" being the central point of answering questions for making clusters, etc. That would be a nice place to stop.
- Robert: Thinking of what Tobi said of identifying the Bioconductor part: could grab things from 2 different objects, ensure the columns are in the same order and that Bioconductor **guarantees integrity** of the data.

    - Important to finish with the message that we want to combine the different parts of the data and metadata, that we want to shape the data into these containers. If possible, highlight the risks of not using classes. What would we miss by not moving to Bioc data structures
    - Jenny: So is the idea to mainly make the plots in the introductory workshop and not do the statistics long with it?
    - Laurent: Right, we don't want to assume familiarity with some of the statistics and underlying concepts: we won't talk about p-values, hypothesis testing.
    - Kevin: So we mainly want to teach visualizing raw data.
    - Robert: Data visualization to some extent is statistics.  Can intuitively visualize uncertainty from data scatter.
    - Jenny: I agree the data visualization is really important to see.  Bume plots: MA plot on one side showing significant genes,  can mouse over to see normalized data showing exact fold change difference, but variation among the groups.  Might be more of an RNA-seq workshop plot.
    - Lukas: Would be great for the same dataset to work in downstream workshops.
    - **Paul: Might be worth thinking about how many concepts are needed before SummarizedExperiment makes sense.**
      (To get past beginner stumbling points: vectors, vector operations, data frames, matrices, data frame/matrix distinction, indexing and logical vectors, S4 classes, finding help on classes, accessor functions, type conversions and wrangling needed to work with ggplot2)
    - 
- Example plots:
    - Boxplot of gene expressions
    - Density plots of gene expression
    - Scatter plot gene 1 vs gene 2, showing samples/cells, coloured based on their annotation.
    - Lines showing expression of genes over time.
    - Lines showing expression of genes over time for different variables.
    - Faceting is very important.
    - Plots being added to: https://docs.google.com/document/d/1Pe0EKQAGkT2-FpYdNAxbgYkaW-LhU3YFHVIpM3exVJo/edit?usp=sharing
    - Repository: https://github.com/kevinrue/bioc-teaching-intro

## 2020-12-07, 2-3pm CET

**Attending**: Toby, Kayla, Lukas, Laurent, Paul, Kevin, Charlotte, Jenny, Robert

**Join the meeting**: https://meet.jit.si/BioconductorTeaching

**Agenda:**

- The Carpentries 2021 Instructor Training schedule: https://carpentries.github.io/instructor-training/training_calendar/index.html
- We have a sticker (credits to Johannes Rainer)
- Draft slides for EuroBioc2020 (feel free to add comments)
- Toby leading an **Exercise design** session.
    - Slides here: Designing-Exercises
- What about additional more advanced lessons? Now or wait to gain experience with first lessons first?
- In the long run, should we welcome many contributions and/or should we aim for a set of “official”/reviewed lessons?
- Need/interest to train more people.
- Paul’s comment from last meeting: Might be worth thinking about how many concepts are needed before SummarizedExperiment makes sense. We need to think about what makes SummarizedExperiment so useful and important. Are we able to convey this to non-Bioc users.
- **TODOs** from last time: EuroBioc2020 abstract submission and agreement on bioc-intro dataset.

**Meeting notes:**

- We have a sticker and initial draft for EuroBioc slides (8 minutes at 5pm on Thu, to introduce the **official** teaching committee under CAB).
- Dataset: Kevin to display the figures described last time.
    - Bioc-teaching plots - proposal GSE111546
    - Users should be provided with csv files and work from them. Kevin will also push this data to ExperimentHub for the more advanced lessons.

- Toby, Exercise design. Slides here: Designing-Exercises. See further reading in the slides for details: Teaching Tech Together (Greg Wilson), Carpentries Curriculum Development Handbook, Carpentries Instructor Training Curriculum. So far, we have defined learning objectives and target audience. How to assess whether the teaching has been effective.
- Formative assessment: use exercises to assess this (especially for self-paced teaching!), used while learning (as opposed to summative/final assessment). There’s still time to adjust the approach, based on the misconceptions learners have. **Aim for ~1 exercise per (specific) learning objective**.
- Example: If your learning object is “describe essential job input parameters in a YAML file”, as suitable exercise would be a “fill in the blanks” assessment.
- Designing exercises: incorrect answers should have a **diagnostic power**, to assess what hasn’t been understood (rather than only identify that the answer was incorrect). Then address the misconception in a targeted way. Aim for at least one every ~15 minutes to avoid information/cognitive overload. Application of new material allows transfer from short term memory to long term memory.

- Potentially suitable exercise formats for novice learners, well suited for individual learning (see Teaching Tech Together reference for a whole chapter): 1. multiple choice questions, 2. code and run, 3. fill in the blanks, 4. minimal fix, 5. theme and variations, 6. labeling a diagram.
    - More detail and more exercise formats here: http://teachtogether.tech/en/index.html#s:exercises
- **MCQ**: each incorrect answer should be a **plausible distractor**. Avoid obviously (useless) wrong answers. Each plausible distractor aims at increasing diagnostic power and then address misconception accordingly.
- Check proportion of correct/incorrect answers, to assess if most learners understood the new concept. Most difficult thing about MCQ is figuring out these plausible distractors.
- **Code & Run**: give the learners a task (write some code to get an expected answer) and let them figure it out. Be aware that it is very easy to make these exercises too difficult for novices. Risk of blank page problem.
- **Fill in the blanks**: middle ground between code and run and providing finished code. Much less intimidating for novices. The blanks are focused on the specific topic. The part of the code that isn't specific to what is being assessed. Avoids blank page problems.
- **Minimal fix**: helps learners to develop debugging skills. Careful that this is a **minimal** fix - single/small fix. Also avoids blank page problems. Relevant to real life.
- **Theme and variation**: adapting existing code for a new purpose is a key skill. Ability to re-use somebody else's code and adapt it for their own task - real life skill!
- **Parson's problem**: provide written code with correct lines but in different order, ask learners to put them back in the right order.
- **Labeling a diagram**: provide label and figure (or only figure). Possibly better suited to a physical classroom. Helps learners to create their mental model of the topic/problem. Interrogates their understanding of that model and key concepts.
- How to figure out misconceptions with a code and run exercise? Difficult to identify the misconceptions, especially when learners don't ask for help early. Other formats are better suited for that.
- Importance of type of exercise to promote **engagement**! Especially with remote teaching. Polls in zoom are a good fit for MCQ.
- **Lesson infrastructure**: exercises in block quotes in Rmd files with `results = “hide”` and `{: .solution }` and `{: .challenge }` for css styling. Naming files: `nn-epsiode-name.Rmd` and add appropriate header.
    - More info on The Carpentries Lesson Example (the info about Rmd episodes is not very complete here, but Toby is working this week on some Pull Requests to address this!)
- Teaser: **lesson development study group** starting in Feb. See Carpentries Blog for more information.
- **Next steps**: Laurent to prepare a light frame with high-level flow to be filled in by contributed exercises.
- **Next steps (2)**: Kevin to prepare the data set as csv files and upload to a public place (figshare)

# Background

# Notes from Feb TAB:

- Question of whether to support attendance at Carpentry instructor training (https://carpentries.github.io/instructor-training/) and to develop a Bioconductor course. (https://datacarpentry.org/lessons/#workshop-materials-under-development-or-consideratio)
- May instructor training page: https://mkuzak.github.io/2020-05-19-TtT-online-elixir
- Working group, led by Laurent. With Charlotte. Opportunities for training; scope of training material; benefits to project.

# Goal 1: Training instructors

**Get members of the Bioconductor community to become certified (Data) Carpentr(y)ies instructors**. Options are to (1) get some people to participate in remote instructor courses (either pre-approved or open training application), (2) send them to in-person trainings or (3) if there are enough candidates, organise an instructor course (see also Becoming a Member Organisation, that include instructor trainings - note that we might have some ties with members organisations - Hutch is a gold member; EMBL/Elixir might have some other ties).

Information from:
Allegra Via, PhD
IBPM-CNR | ELIXIR-IIB Training Coordinator
allegra.via@gmail.com | allegra.via@cnr.it
Skype: allegra.via | +393291535017
https://allegravia.github.io/website/

> We (ELIXIR-Carpentries WG) will deliver a **Carpentry Instructor training online on 19-20 May**, in the framework of the ELIXIR-Carpentries agreement: it would be a great occasion for some members of the Bioconductor community to become Carpentries certified instructors.
> The training should be advertised in the coming weeks and I will include your contact in the mailing list (though TrCs will be informed and will be asked to advertise the workshop within their nodes).

Elixir/Carpentries agreement: https://elixir-europe.org/news/elixir-carpentries-agreement, https://f1000research.com/articles/6-1040/v1

**TODO**:
- Identify candidates to become trainers - done

- Any restrictions to participate (Laurent to ask Allegra) - no
- Cost (Laurent to ask Allegra) - none

**Possible candidates:**

- Stephanie Hicks (Hicks lab) (registered)
- Charlotte Soneson (FMI) (**will be participating**)
- Marcel Ramos (Waldron lab) (**will be participating**)
- Nitesh Turaga (Bioc core) (**will be participating**)
- Kayla Interdonato (Morrell) (Bioc core) (**will be participating**)
- Ludwig Geistlinger (Waldron lab) (registered)
- Robert Castelo (UPF) (**will be participating**)
- Saskia Freytag (HPI) (registered)
- Aedin Culhane (registered)
- Susan Holmes (registered)

Comment from an instructor: *I'd say go ahead and in the 'role in ELIXIR', in registration form, write 'bioconductor community', based on the availability we will be selecting participants to spread evenly across ELIXIR nodes while reviewing,*

**Also interested?** Add your name, email address, and any specific efforts you would like to contribute to below

- Jenny Drnevich drnevich@illinois.edu
- Peter Hickey (hickey@wehi.edu.au). I've done Software Carpentry training and have taught Bioconductor (bulk RNA-seq, scRNA-seq) and developed teaching material (scRNA-seq).
- Kevin Rue-Albrecht, kevin.rue-albrecht@imm.ox.ac.uk (University of Oxford, UK) - Interested in becoming a certified Carpentries trainer and develop short courses for genomics workflows (i.e., bite size workshops with specific analysis goals).
- Pariksheet Nanda pariksheet.nanda@uconn.edu I'm certified and have been teaching with the Carpentries for a few years (https://omsai.gitlab.io/teaching/). Martin Morgan also organized a Bioconductor specific training for us at the Jackson Laboratory which was very useful. Here are Martin's training materials: https://github.com/Bioconductor/BiocTrainer and our notes from the training: https://docs.google.com/document/d/12FSFXpXZAN43CM5iiYiVJlQPG_myBBMHXy0iWsBU5uI/edit
- Susan Holmes. (Interested in training for postdoctoral fellows, continuing work I have done over 10 years for PhD students and postdocs, but would like to specialize in biomedical trainees).

# Goal 2: Bioconductor carpentry lessons

Using the Carpentries model and pedagogy, collaboratively develop and maintain a **Bioconductor curriculum**. We collectively already have a lot of teaching material. It will probably mostly be a matter of reorganising and harmonising it.

- Typical DC curriculum has: OpenRefine, RStudio/R intro, tidyverse and ggplot basics (or equivalent with python), data management with SQL.
- Should a Bioconductor curriculum be accessible to complete beginners (i.e. intro to R, RStudio, ...) like a typical DC curriculum, and then extend into Bioconductor technologies, or assume the former as prerequisites?
- An alternative would be to develop a set of Bioconductor lectures and aim to add these to the Genomics curriculum (https://datacarpentry.org/lessons/#genomics-workshop). There is already an introduction to data analysis with R being developed for that curriculum.
- A Data Carpentry workshop must contain a Data Carpentry lesson on data organization, plus three Data Carpentry modules from the same domain.
- Define some topics of interest for a Bioc curriculum
- Identify existing material to start with

Related carpentries material:

- https://datacarpentry.org/genomics-workshop/
- https://datacarpentry.org/genomics-r-intro/
- https://elixir-belgium.github.io/2019-05-13-Ghent/
- https://datacarpentry.org/semester-biology/nav/getting-started/
- This one uses the Bioc workshops: https://smcclatchy.github.io/2018-10-12-bioconductor-bh/
- https://tmogrady.github.io/bioconductor-2018-01-29-maxplanck/index.html
- https://swc-uiuc.github.io/2020-02-06-dc-illinois/
- **Curriculum Development Handbook**

## Working group participants

We will schedule a call at the end of May or in June to share our thoughts and ideas about developing a Bioconductor Carpentry curriculum. Please add your details (name, affiliation and country of residence) to be included in the group. The outcome of these discussions will also be shared on the education-and-training slack channel.

- Laurent Gatto (UCLouvain, Belgium; TAB)
- Ludwig Geistlinger (Waldron lab, City University of New York, USA)
- Marcel Ramos (Waldron lab, CUNY SPH, Bioc core, New York, USA)
- Jenny Drnevich (Carver Biotechnology Center, University of Illinois, USA)
- Charlotte Soneson (FMI, Basel, Switzerland; TAB)
- Robert Castelo (UPF, Barcelona, Spain)

- Kayla Interdonato (Morrell) (Bioc core, Buffalo, NY)
- Nitesh Turaga (Bioc core, Buffalo, NY)
- Erin Becker (The Carpentries, California, USA)
- François Michonneau (The Carpentries, France)
- Mike Smith (European Molecular Biology Laboratory, DE)
- Peter Hickey (Walter and Eliza Hall Institute of Medical Research, Australia).
- Marco Chiapello (Italian National Research Council, Italy)
- Vince Carey (Harvard Medical School, USA)
- Kevin Rue-Albrecht (University of Oxford, UK)
- Nadine Bestard Cuche (University of Edinburgh, UK)
- Pariksheet Nanda (University of Connecticut, CT)
- Susan Holmes (Stanford University, USA and Tecnico, Lisboa, PT)
- Tim Triche (VAI, USA)

**Discussion group**: bioconductor-teaching

## Goal 3: Bioconductor teaching team

Have a group of **Bioconductor instructors** (ideally, but not necessarily all Carpentry-certifier) that can deliver Bioconductor Carpentry workshops at Bioc-related events. **Share these same material under CC-BY for wider use** (i.e. non-official Bioconductor Carpentry workshops taught by others).

# Meetings and discussions

- **Join the meeting**: https://meet.jit.si/BioconductorTeaching
- To join by phone instead, tap this: +1.512.647.1431,,2105280635#
- Looking for a different dial-in number? See meeting dial-in numbers: https://meet.jit.si/static/dialInInfo.html?room=BioconductorTeaching
- If also dialing-in through a room phone, join without connecting to audio: https://meet.jit.si/BioconductorTeaching#config.startSilent=true