

Project week page: https://projectweek.na-mic.org/PW35_2021_Virtual/Projects/mpReview/

Discord channel for the project week: <https://discord.gg/5TC5H2g63e>

Agenda of the Project Week: https://projectweek.na-mic.org/PW35_2021_Virtual/

Dora: Chicago have a private version with features added based on Aytek's needs

Masoom:

- Applications:
 - Large prostate dataset
 - Large breast dataset
 - Renal cell carcinoma
- Used manual naming conventions, mistakes still are being made
- Hard to find any other publicly available tools to support 3d annotation of data with the flexibility needed
- Commercial solutions are very expensive
- Timeline - September
- Timeline is important - can we stage the development? Start with something that can be made to work quickly, and have longer-term development plan?

For the project week:

- Understand what is broken in current version of Slicer
- Make sure we can make the extension work at Masoom's lab?
- Understand longer term how we can leverage AI annotations

What are the alternatives?

- MONAI can help with annotations - is being integrated with Slicer
- Masoom looked into MITK, and found Slicer much faster and stable than MITK
- OHIF is slow

Related demo from Dora: <https://learn-radiology.rcc.uchicago.edu/takecourse/>

Next steps (by 06/28/2021):

- Revisit documentation (Andrey and Dora)
 - Andrey to document the specific version that works
 - Source code (will add docs here) <https://github.com/SlicerProstate/mpReview>
 - Defunct/empty documentation page in wiki <https://www.slicer.org/wiki/Documentation/Nightly/Extensions/mpReview>
 - mpProcessing - improve documentation
- Define multi-site test dataset (BWH, Chicago, Nijmegen) (Andrey and Dora)
- Masoom and Batu will work to set it up at his lab (Masoom and Batu)
- Test with the latest version of Slicer (Andrey and Dora)
- Document extra features implemented at Chicago (Dora)
 - Maybe also give a demo of the internal Chicago version ?
- Test extension with the current version of Slicer (Dora will start with this)

- Check out Slicer PI-RADS module (work in progress from few years ago)
<https://github.com/SlicerProstate/SlicerPIRADS>

GitHub IDs:

- Batuhan-gundogdu
- Haidermri
- LalehSeyyed
- DoraSzasz

Comments from Masoom

Hi Andrey and Dora

I've had a chance to play with the mpreview tool

It is going to be difficult for us to use the tool in its current form as there are a few too many steps for pre-processing outside of slicer and annotation tools are too limited.

If there is interest in rebuilding the tool I put together a draft list of requirements or features. At the top of the list is the ability to store some sort of template for a particular annotation use case. For example a list of segmentation's and their hierarchy that you can save and load would be a good start. If that can happen before Sept that works

Current Workflow - (outside of mpReview ?)

- load dicom data (faster)

Painful to install prerequisites and do preprocessing - this can be simplified by installing all dependencies automatically? **(priority 2)**

Is DICOM Browser fast enough to load data directly from DICOM?

- map series to specified series names in template

In practice can have multiple series that match the same type, need to be able to quickly map specific series to what should be loaded by hanging protocol

Can assignment of the series be done based on the user selection from the Slicer UI? **(priority 3)**

- Load series into desired display layout for annotation (for prostate load all axials, customize the layout for the application)

- Perform series coreg (optional) (no perfect solution, in practice not always helpful)

Could apply oversampling

- Load a segmentation naming template (priority 1)

No user-level functionality to define templates, no documentation how they could be defined

- Perform segmentation (whole gland, PZ, TZ, up to 4 tumors for prostate; for liver - whole liver + up to 2 tumors, metastatic disease; RECIST - 2 lesions per organ)
- Save segmentations and segmentation labelmaps
- save coreg volumes

Template data

- List of series and name of home series
- **segmentation names and hierarchy THIS ONE IS ENOUGH TO GET STARTED**
- display layout - which series go in which windows

Dicom folder load can be done through existing slicer dicom tool but need extra tool to map each series to the specified series list in template

Masoom Haider

06/28/2021 - Day 1

- <https://www.radiantviewer.com/> - currently used to separate the files into different series (MAPPING)
- UChicago Test data - [Example1](#)

Implementation plan:

- 1) Andrey to look at pre-processing, how to make it easier using Slicer UI
- 2) LUT is already configurable, waiting for feedback from Masoom
- 3) Dora will look into series tagging:
 - a) User chooses the directory setting
 - b) List of studies is loaded
 - c) User selects a study
 - d) List of series is populated: for each series
 - i) do string regex for SeriesDescription to guess the type of series (T2AX, DWI, ADC, DCE, Subtract?)
 - ii) In the series list, add another column that will show the type of series, or leave that selection blank
 - iii) Allow user to choose series type from the dropdown when it is not populated, or override when not guessed correctly automatically

- iv) Save the series type to a JSON file under the series folder (what I did in the past was to create Canonical folder, which is sibling to Reconstructions and Segmentations, and save that JSON file - one per series - with the series tagging result)

Data directory:

.../sample_data/prostate_repeatability_mpReview

▸ Studies

Series

- ☒ 6:T2 Weighted Axial
- ☐ 9:DWI
- ☒ 100:DCE Subtraction
- ☒ 901:Apparent Diffusion Coefficient

Series type

T2 Axial
DWI
DCE
ADC

**Configurable
Dropdown
list**

▸ Data Probe

v)