**Registration Pipeline**

1. **Set Landmarks in MRI sequences.**

Pre-select MRI sequences of interest. Selected Sequences: T1 nativ, T1 KM, T2, Diff.

Landmarks overview:

|  |  |
| --- | --- |
| **Liver metastasis dataset** | **Brain metastasis dataset** |
| Most apical liver poin | Right eye, most apical point |
| Rightmost point of the spleen | Left eye, most apial point |
| Most apical point of the right kidney | Third ventricle, most caudal point |
| Exit of the A. renalis dextra from the Aorta | Right lateral ventricle, most apical point |
| Gall blader | Left lateral ventricle, most apical point |
| Liver, most caudal point | Right eye, most caudal point |
| Most prominent point of V. portae | Left eye, most caudal point |

1. **Registration**

* Select one of the sequences as the reference one. All of the other sequences of interest are registered to the reference sequence.

*We’ve registered T1 KM, T2 and Diff sequences to T1 nativ.*

* Save the resulting sequence (right click, export DICOM files (Select “All images”))
* Exit to the overview and export the DICOM files again, saving them into a separate folder

1. **ROIs**

* Save the Landmark ROIs of the reference sequence (ROI -> save all ROIs of this Series).
* Delete all ROIs of the reference sequence. (ROI -> delete all ROIs of this Series)

1. **Tumor ROIs**

* Localize the Tumor and select in using the polygon selection tool.
* ROIs don’t have to be selected in each slice, but be sure to draw a polygon every 2-4 slices.
* Rename the ROIs (ROI -> ROI Rename -> All ROIs in this series)
* Generate ROIs in the missing slices. (ROI -> ROI Volume -> Generate missing ROIs).
* Save the tumor ROIs (ROI -> save all ROIs of this Series).
* Load ROI to the registered series.
* Save a XML-ROI file. (PlugIns-> ROI Tools -> Export ROIs -> Select XML file)

This ROIs can now be loaded to any of the registered series.

1. **Matlab**

The pipeline enables a semi-automatic extraction of a vector of features from a list of MRI data with preselected volumetric ROI (3D) for further analysis.

Preprocess:

* MRI sequences should be manually annotated. Tumor should be selected as a ROI. Sequences should be registered.
* The table containing the description of which patients were annotated.
* All the necessary parameters can be adjusted in radio\_data\_analysis\_main.m.

Input:

* List of folders containing MRI sequences
* A table containing all of the annotated patients
* A table specifying, which patients should be analyzed (just extract the lines from the main table).

Output:

* all\_mir variable contains a 4 dim matrix. Height x length x depth x number of registrations done. ROIdata contains the parsed XML ROI data.
* ROI\_features\_all contains the features of the ROI for each of the sequences used (in case there are more than one registrations done)
* A list of features of the tumor ROI (3D) for each of the patients.
* 3D Tumor visualization