**Directory Structure:**

* /home/exacloud/gscratch/BayouthLab/

*This is the general shared Lab directory. The directory has a storage limit of 1 TB and is intended for storing datasets currently being processed. All authorized users can access it. The ProcessedResults, JacsToProcessForLERN, and DataToProcess directories should be cleared out once data has been processed and stored on another machine.*

*The src and ScriptsToProcessIPF folders contain all programs and scripts used by the group - do not delete or move anything from these without asking the owner of the script.*

* + anaconda3/

*This is the location that anaconda installation is stored in addition to the environments necessary for the lung segmentation code to work. Do not edit.*

* + DataToProcess/

*This is where the 4DCT scans of the subjects needing to be processed are stored*

* + - DICOM
      * SUBJECTS/
        + SCANS/

sorted (where sorted DICOMs are uploaded for new subjects)

* + - SUBJECTS/
      * SCANS/
        + SUBJECT\_SCAN\_PHASE.nii.gz *(1 scan for all 10 phases of the 4DCT)*
  + JacsToProcessForLERN/

*This is where the Jacobians of the individual phases for subjects are stored so they can be offloaded for R processing to create the LERN*

* + - SUBJECTS/
      * SCANS/
        + PHASE\_to\_0EX/ *(1 directory for all 10 phases of the 4DCT registered back to 0EX)*

Jac\_2\_2\_2\_4\_4\_4.nii.gz

* + ProcessedResults
    - SUBJECTS/
      * SCANS/ *(1 directory for each of the scans processed)*
        + Avoidance *stores the avoidance contours for any subject randomized to the experimental arm*

DICOM *stores the DICOM converted avoidance contours*

* + - * + lung

preseg

*stores the preseg masks (masks without vessels and tumor included)*

SUBJECT\_SCAN\_PHASE.mask.nii.gz *(1 mask for all 10 phases of the 4DCT)*

ParamImage3Dto4D.txt

alpha

*stores the filled masks*

SUBJECT\_SCAN\_PHASE.mask.nii.gz *(1 mask for all 10 phases of the 4DCT)*

* + - * RegistrationWithVessel

*Stores the registrations and transformation matrices between scans*

* + - * + SCANM\_PHASEM\_to\_SCANF\_PHASEF

*Different folders for each scan/phase combination where ScanM\_PhaseM is registered to ScanF\_PhaseF*

* + - * RegistrationWithVessel\_Low\_Epsilon\_005
        + SCAN\_PHASE\_to\_SCAN\_0EX

*Stores the Jacobians between every phase and the reference phase for the scan currently being processed*

* + - * LERN

Place the LER4D scan is placed and where the warped scans are stored

* + - * + SUBJECT\_LER4D\_of\_SCAN.nii.gz

This is the scan the R script creates. It should be uploaded here after processing

* + - * + SUBJECT\_LER4D\_of\_SCAN\_rigid.nii.gz
        + SUBJECT\_LERN\_SCAN\_warped\_to\_REFSCAN\_0EX.nii.gz
  + ScriptsToProcessIPF

*Stores all the scripts needed to coordinate all image processing*

* + src

*Stores all the source and compiled codes needed to process images*