# Key

Terminal commands that need to be run are denoted in pink

Variables are denoted in blue

# System Requirements

The following instructions assume the following:

* User has previously installed the LungSeg and LungReg codes (instructions specified in the LungSegBuild and LungRegBuild Documents)
* R version 4.1 or later
* MATLAB version 2022 or later
* HPC or HTC job scheduling system
* User has the permissions and home directory has space available to install R packages, anaconda, as well as write and store several large files (total directory space of 1 TB is sufficient)

# General Note

All instructions assume all files, scripts, and installation paths are organized following the Directory Organization specifed. If anything differs from this structure, paths to many of the scripts mentioned in the ScriptsToIPF folder will need to be modified to reflect those deviations.

# Storage Management

Storage on supercomputer systems is typically limited and running this process writes a large amount of data. Once a subject has been fully processed it’s important to transfer all subject data off the system in order to allow space for further processing of other subjects. For all file transfers, the scp command can be used. Further documentation on this can be found [HERE](https://phoenixnap.com/kb/linux-scp-command#:~:text=SCP%20(Secure%20Copy%20Protocol)%20is,the%20cp%20(copy)%20command.).

**Any REFERENCE scans should be stored on the system until all follow up scans are complete and processed. The reference scan’s scan, mask, and sorted DICOM will all be needed for processing follow up scans on the same subject. For any follow up scans being processed, use the following guidelines to manage space available.**

**First transfer the following on a local machine or lab disk**

* Nifti CT images of each phase – DataToProcess/SUBJECT/SCAN/ folder
* Masks for each phase - /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/SCAN folder
* LERN warped image - /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/LERN/SUBJECT\_LERN\_SCANB\_warped\_to\_SCANA\_0EX.nii.gz
* LERN DICOM - /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/LERN/ DICOM/SCANB/
* Deformation Matrix - /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/RegistrationWithVessel/SCANB\_0EX\_to\_SCANA\_0EX/SUBJECT\_ SCANB\_0EX\_to\_SCANA\_0EX\_displacementField.mha
* Avoidance DICOMs (if applicable) - /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/SCAN/Avoidance/DICOM/

**Items to delete – verify everything has transferred successfully BEFORE proceding**

* DataToProcess/SUBJECT/SCAN/ folder
* /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/LERN/ folder
* /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/SCAN folder
* /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/RegistrationWithVessel/SCANB\_0EX\_to\_SCANA\_0EX folder
* /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/RegistrationWithVessel\_Low\_Epsilon\_005
* /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/SCAN/Avoidance/ Folder

# Subject Instructions:

New subject scans come from the clinic in DICOM format and need to be sorted into the individual phases. However all processing is run in NIFTI format. The following instructions assume the directory structure has been set up as explained in the Directory structure document. In all directions commands are written in reference to directory’s set up in this structure beginning in a home directory designated as *$HOME\_PATH*

1. **Sort list of DICOM files into folders by phase (if needed)**

If the files from the clinic are not in folders (it is just one folder of many DICOM folders). You will need to first sort the dicoms into folders such that they can be processed in step 2. If they are already in folders you may procede to step 2.

Note: this has ONLY been developed for the GE system. Any other scanner manufacturers will need to be developed separately. Any SIEMENS scans should be pre-sorted and able to proceed to step 2.

Navigate to the scripts directory

*cd $HOME\_PATH/ScriptsToProcessIPF/*

Open a MATLAB session in terminal. Once the MATLAB interpreter opens run the following script – make sure you use single quotes like written below

SortCTToFolders(‘*$HOME\_PATH* /DataToProcess/DICOM/NAME/’, SUBJECT)

NAME is the name of the folder containing the DICOMs (usually it’s a string of numbers or in Date format)

SUBJECT is the name of the subject you are processing (example IPF001). You must enter this in single quotes.

1. **Sort the DICOM files in MATLAB**

Navigate to the scripts directory

*cd $HOME\_PATH /ScriptsToProcessIPF/*

Open a MATLAB session in terminal. Once the MATLAB interpreter opens run the following script – make sure you use single quotes like written below

parseDicomNewStructure(‘*$HOME\_PATH* /DataToProcess/DICOM/NAME’, ‘SCAN’)

NAME is the name of the folder containing the DICOMs (usually it’s a string of numbers or in Date format). You must enter the path in single quotes.

SCAN is the name of the scan you are processing (example SCAN1). You must enter this in single quotes.

1. **Convert from DICOM to NIFTI**

*cd $HOME\_PATH /ScriptsToProcessIPF/*

*sh convertAllCT.sh SUBJECT SCANTEXTFILE KERNELTEXTFILE*

SUBJECT is IPF\*\*\*

SCANTEXTFILE is a text file that contains a list of scans you want to convert. Pre-written in the ScriptsToProcessIPF folder are scan1.txt, scan12.txt, scan34.txt, scan56.txt, scan78.txt for the different combinations of time points. A custom text file can be created and used if different scans or only 1 scan is needed using these as examples.

KERNELTEXTFILE is convert\_kernels.txt. This is a text file that specifies the reconstruction kernels. The dependence on kernel has mainly been removed in this installation so you should not need to edit this file.

1. **Make Output directory for lungmasks**

mkdir -p -m777 *$HOME\_PATH/ScriptsToProcessIPF/*SUBJECT/SCAN/lung/alpha

SUBJECT is IPF\*\*\*

SCAN is the name of the scan you are processing (example SCAN1)

1. **Install anaconda if it is not already installed**

cd $HOME\_PATH

Go to the Anaconda website and download the Anaconda3-2023.03-1-Linux-x86\_64.sh file to your home directory

bash Anaconda3-2023.03-1-Linux-x86\_64.sh

Follow the prompts to complete installations. Once this completes successfully you will need to log out and log back in

1. **Install masking code – only needs to be done the first time you run it**

cd $HOME\_PATH/src/DeepLung

conda create --name deeplung python=3.9

conda activate deeplung

pip3 install .

conda deactivate

You will need to log out and log back in

1. **Create lung masks (needs to be done for all scans– reference and scan you are processing)**

conda activate deeplung

sh CreateCNNMask.sh SUBJECT SCAN

*This will create lung masks for all 10 phases of the 4DCT for the subject and scan input. If for some reason you need to do less than the 10 phases open the CreateCNNMasks.sh file and change the for loop to only include the phases you want.*

conda deactivate

1. **Run Registrations**

This step involves submitting a job to a scheduler. Depending on the job scheduler used at your institution, the syntax and requirements of the job script will vary. Instructions have been written to describe which scripts the job should run and which variables should be passed to the script.

* 1. **For ALL Scans regardless of timepoint (this will take 4-8 hours to complete)**

runAllPhaseReg.sh SUBJECT KERNEL SCAN

SUBJECT should be selected as the subject you are running

SCAN should be selected as the scan you are running.

KERNEL is the kernel the data was reconstructed with (usually B50f\_1mm or Br51f\_1mm)

* 1. **For any scans that are NOT the reference scan you will also need to calculate the deformation matrix between the scan you are running and the reference scan** 
     1. **If the scan you are running is from the same timepoint as the reference scan (example you are running SCAN2 and the reference is SCAN1) – this will take 1-3 hours to complete.**
        1. regWorkflowVessel.sh SUBJECT SCANA SCANA\_MOVE SCANA\_FIXED SCANB SCANB\_MOVING SCANB\_FIXED
     2. **If the scan you are running is a follow up scan – this will take 4-6 hours to complete**
        1. regWorkflowVessel1ScanPost.sh SUBJECT SCANA SCANA\_FIXED SCANB SCANB\_MOVING SCANB\_FIXED

SUBJECT should be selected as the subject you are running

SCANA should be selected as the frame of reference of the treatment.

SCANB is the scan you are running that needs to be registered to the reference

SCANA\_MOVING and SCANB\_MOVING are the max inspiration phases (set at 100IN)

SCANA\_FIXED and SCANB\_FIXED are the reference phases (usually we choose this to be max expiration phase which is 0EX)

1. **Create LERN Map – run the LER4D\_100.R script from the LERN subfolder**

**The first time you run this you will need to install the oro.nifti package of R**

Note: The LER4D\_100.R script uses all 10 phases of the 4DCT to create the LERN map. If you wish to use fewer phases. This can be done by editing line 52 to another number and commenting out the respective phases you do not wish to use in lines 53-62.

cd $HOME\_PATH/ScriptsToProcessIPF/LERN/

Rscript LER4D\_100.R SUBJECT SCAN

SUBJECT should be selected as the subject you are running

SCAN should be selected as the scan you are running.

1. **Warp LERN Map to reference**

This will create a file named SUBJECT\_LERN\_SCANB\_warped\_to\_ SCANA\_0EX.nii.gz in the folder /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/LERN/

cd $HOME\_PATH/ScriptsToProcessIPF/

sh WarpLERN.sh SUBJECT SCANA SCANB

**SUBJECT** is the subject you are running

**SCANA** is the reference scan you want to warp to

**SCANB** is the scan you are running

1. **Convert Jacobians to DICOM**

sh jacobiansToDICOM.sh SUBJECT SCANA SCANA\_FIX SCANB

**SUBJECT** is the subject you are running

**SCANA** is the reference scan the LERN was warped to

**SCANA\_FIX** is the reference phase (usually 0EX)

**SCANB** is the scan you are running

1. **Qualitative analysis of Jacobians in Slicer**

Transfer the warped LERN file to your home machine and open in slicer – make sure there are no horizontal streaks.

**IF THE SUBJECT IS RANDOMIZED TO THE EXPERIMENTAL ARM AND THIS IS THEIR PRE\_RT SCAN**

Note this is based on our old processes and will likely be changing as we get Eric’s code running on the cluster for his cGAN model and treatment planning scripts.

1. **Create Avoidance Maps - \*\*cannot currently run because the trained model is not on OHSU’s system.**

Open a MATLAB session in terminal. Once the MATLAB interpreter opens run

CalculateAvoidanceMapsAuto(SUBJECT, SCANA, SCANA\_FIX, SCANB) – Note you must enter variables in single quotations ex. ‘IPF002’.

**SUBJECT** is the subject you are running

**SCANA** is the reference scan the LERN was warped to

**SCANA\_FIX** is the reference phase (usually 0EX)

**SCANB** is the scan you are running

This script will create several avoidance structures named in the format SUBJECT\_DOSEGyAvoidance.nii.gz

These generated avoidance structures will be placed in /home/exacloud/gscratch/BayouthLab/ProcessedResults/SUBJECT/SCAN/Avoidance/

1. **Convert Avoidance Maps to DICOM**

sh avoidanceToDICOM.sh SUBJECT SCANA SCANB PHASE for all phases you want the DICOMs for (usually just the planning phase is needed)

**SUBJECT** is the subject you are running

**SCANA** is the reference scan the LERN was warped to

**SCANB** is the scan you are running