Pulmonary Vessel Segmentation Notes

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1   Lung Extraction Pipeline

- Threshold the CT image at -2000 to get a *cylinder* mask. The -2000 value may change across patients?

```
fslmaths /scratch/datasets/PE/PE000919.nii.gz -add 2000 -thr 0 -bin
PE919/round_mask.nii.gz
```

- First run GMM with 3 components: lung, tissue, and bones. Initial mean set to -800, 0, 1000, and initial standard deviation of GMM set to 100 for all components. In some cases, we need to run GMM with 2 components.

```
gmm --input RV01.nii.gz --seg seg.nii.gz --mask round_mask.nii.gz --ncomp 3
--mean -800 0 100 --sigma 100 100 100 --prop 0.33 0.33 0.33 --maxit 30
```

- Convert the GMM label map into a component map, so the non-connected regions with same GMM labels are assigned different component labels.

```
sitkfuncs.extract_comp('RV01/gmm_seg.nii.gz', 'RV01/cc.nii.gz')
```

- Use ITK-SNAP to check the label corresponding to the left and right lung. If left and right lungs are connected, identify only one label. Otherwise, identify both labels.

- Extract the lung component and output a binary volume.

```
sitkfuncs.extract_lung('RV01/cc.nii.gz', [1], 'RV01/lung.nii.gz', 10)
```

- Optionally, fill hole in the lung mask with the fillhole filter. ITK fillhole filter has a bug, that it only fill holes in a axial slides. That is, the filter applies only on 2D slide, instead of on 3D volume. The below command call ITK filter, so it does the same thing.

```
fillhole_filter -i lung.nii.gz -o lung.nii.gz
```

2 Vessel Extraction

- Manually define seed regions.

- Estimate the density and get a density map, which will be used as the speed map of fast marching method.

```
est_density -i RV01.nii.gz -e seeds.nii.gz -m lung.nii.gz
-o density.nii.gz
```

The standard deviation parameter of the density estimation routine controls how much belief the user should give to the seed region. With a small deviation, only the voxels with intensity close to the mean intensity of the seed regions will have larger density value. With a larger standard deviation, the voxel have non-zero density value even its intensity is quite different from the mean intensity. Therefore, the standard deviation parameter can be seen as a regularization. A larger value will make the histogram of the density map more flat, and make Vessel and non-vessel voxels density more similar. accordingly, fast marching have more chance to propagate to non-vessel regions.

- Run the fast marching method:

```
fmm_upwind -p density.nii.gz -e seeds.nii.gz -m lung.nii.gz -t 500
-o fmm_out.nii.gz
```

The seed region can be manually defined as a binary mask file, where intensity value 1 means seed region. Or, it can be the manual segmentation of arteries that has been obtained before. Sometimes, when we are only interested in arteries and only give seeds within arteries, the routine will leak into the vein region and end up finding vein.

- Inverse the value of the *time of visit* map to get a heat map, where larger values represent vessels. The largest time steps should be same with the previous fmm_upwind command.

```
inverse_distmap -i fmm_out.nii.gz -m lung.nii.gz
-o vessel.nii.gz -x 500
```