Data-Centric Approach For Blood Vessel Segmentation

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Introduction

- Vasculature Common Coordinate Framework (VCCF)
- Manual label annotation is difficult!
- Current ML approaches do not generalize well (scan quality, variability in human anatomy)
- We propose a data processing pipeline that demonstrates strong generalization to unseen test data
- All visuals are original unless indicated otherwise

Data

- Hierarchical Phase-Contrast Tomography (HiP-CT)
- Kidney 1 - **50 um/voxel**, densely segmented, 2278 slices
- Kidney 3 - **50.16 um/voxel**, densely segmented, 501 slices

Train

- Kidney 2 - **50 um/voxel**, sparsely segmented, 2217 slices

Validation

- Kidney 5 - **25.14 -> 50.28 um/voxel**, approx. 1000 slices
- Kidney 6 - **15.77 -> 63.08 um/voxel**, approx. 500 slices

Test

Visualization

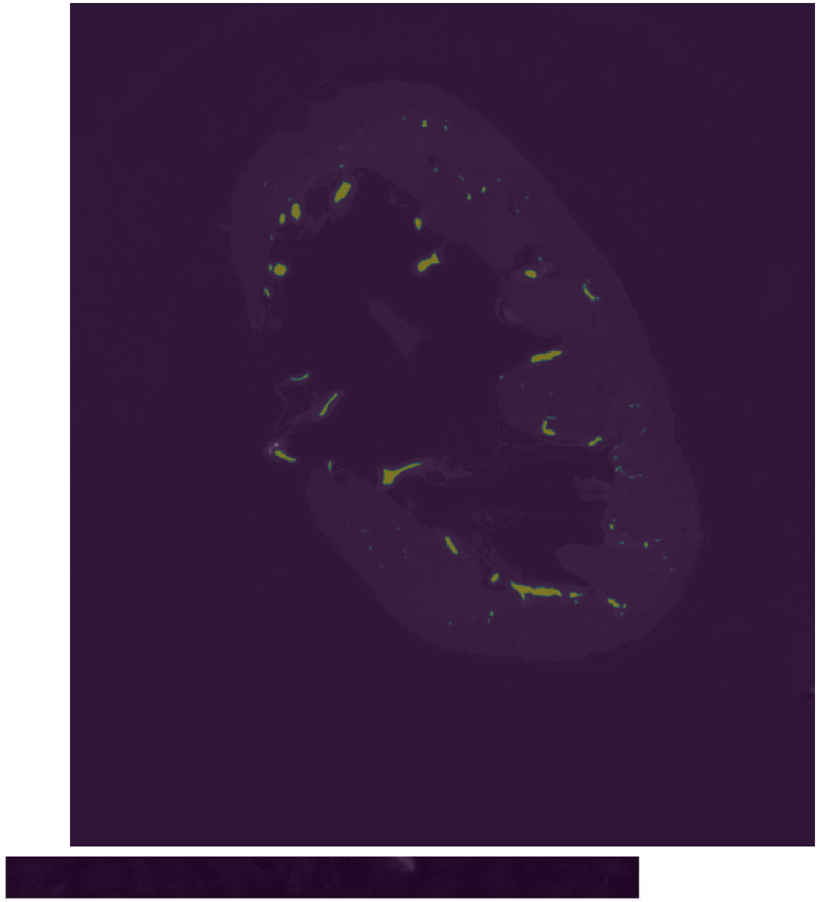
Kidney 3 – (1706, 1510)

[1]

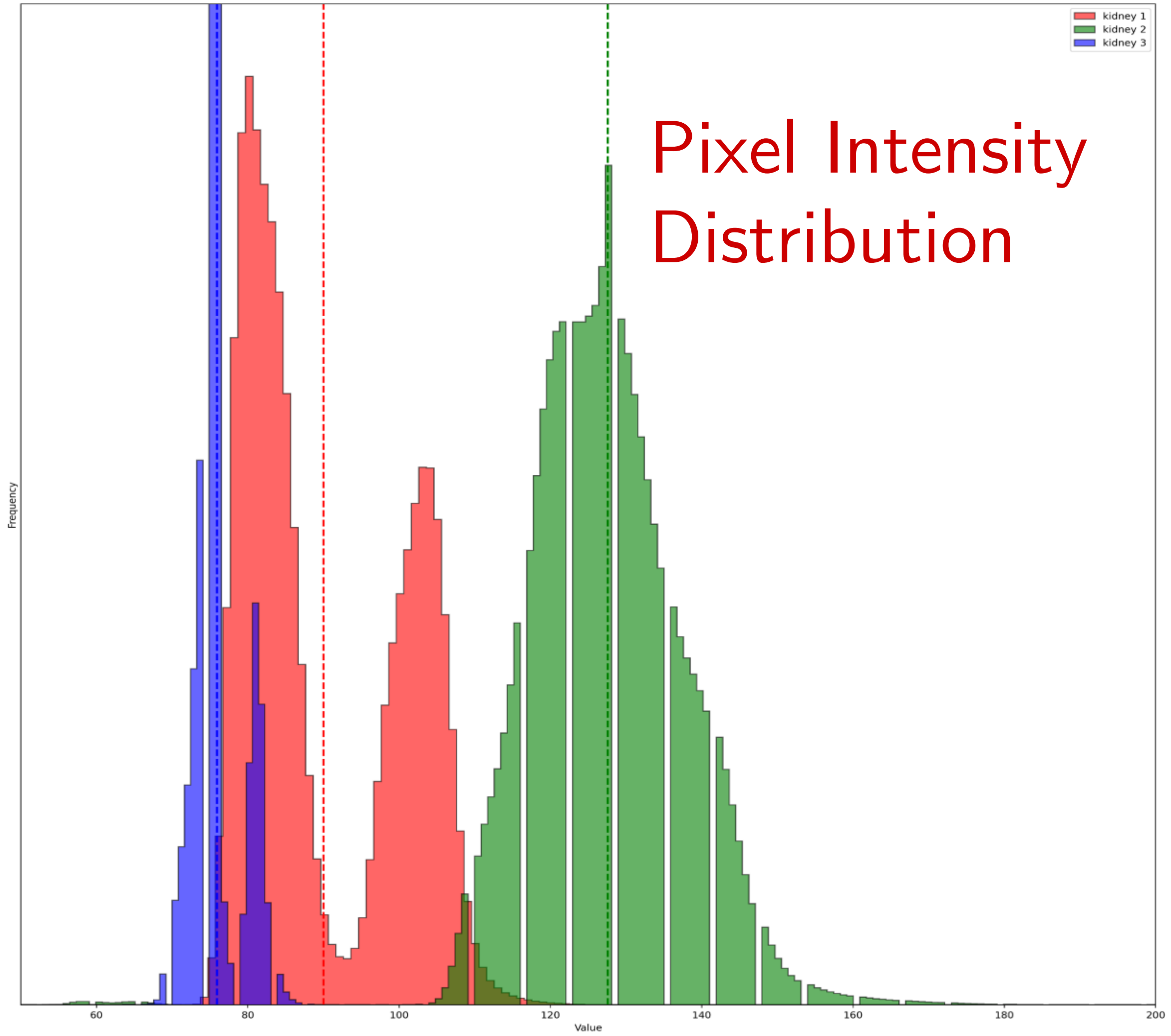
Image

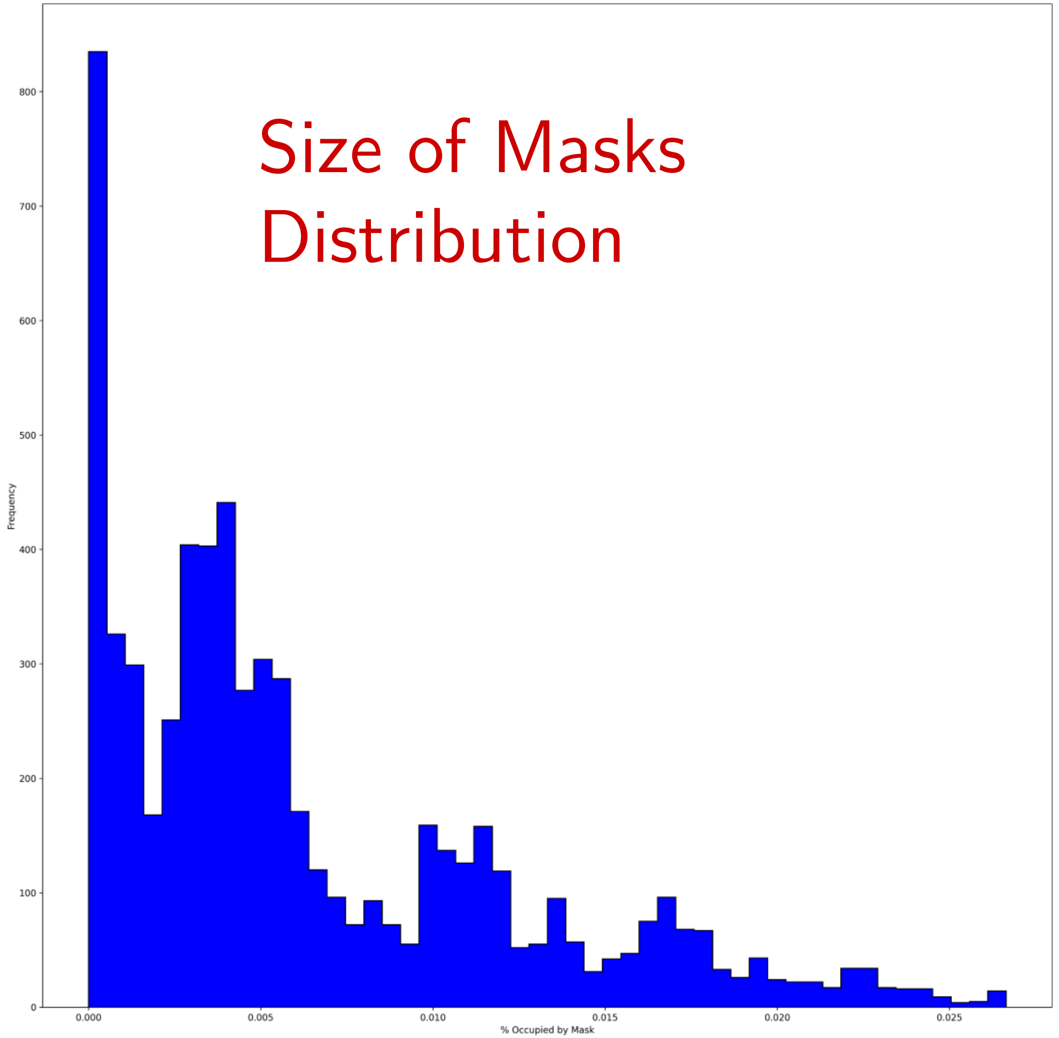
Label

Stacked



Exploratory Data Analysis

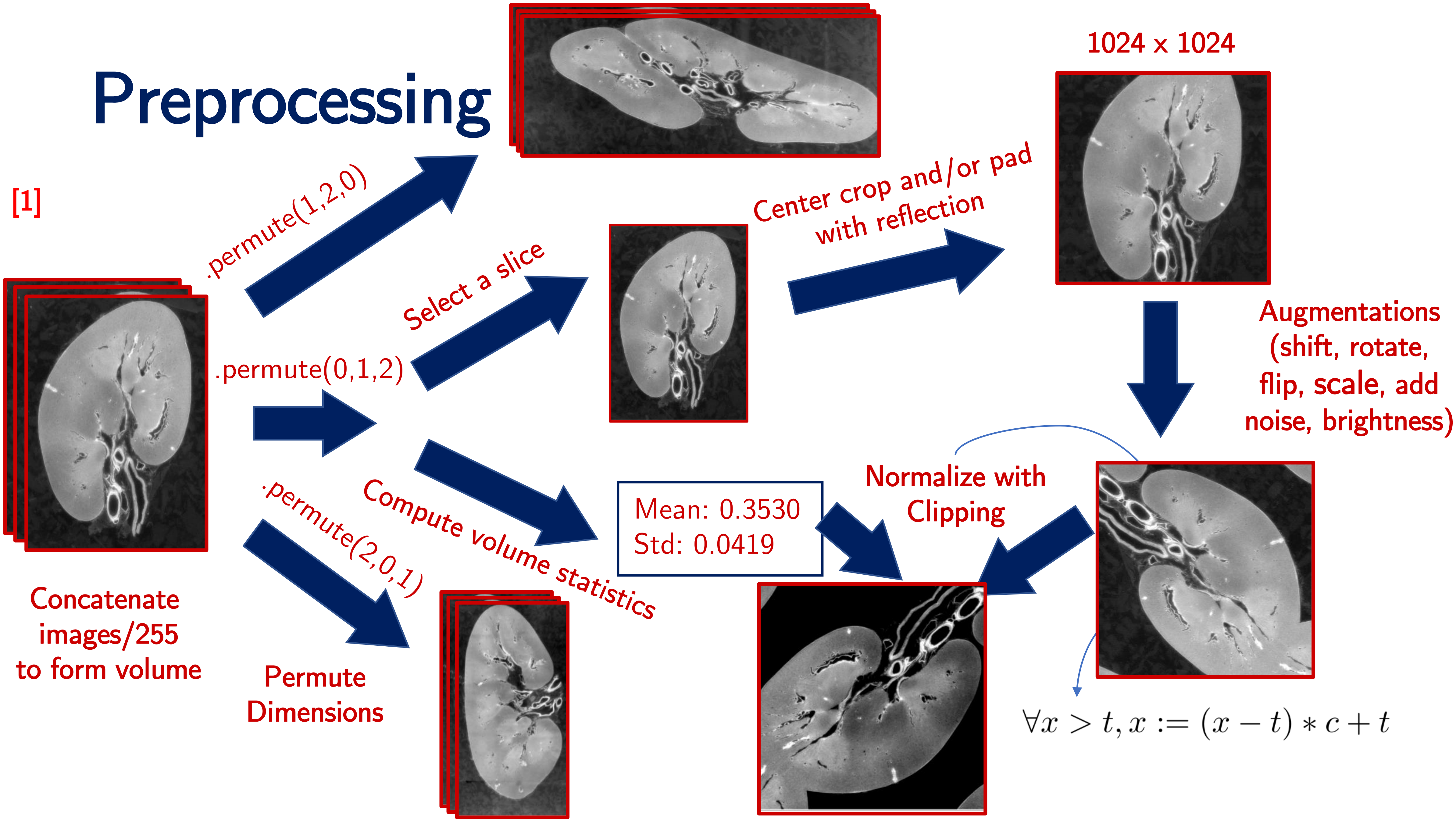




Key Takeaways

- Many fluctuations within each kidney (background noise, intensity)
- Kidneys are of different distribution (different resolution, scanning method)
- Very imbalanced dataset, hard to detect small vessels

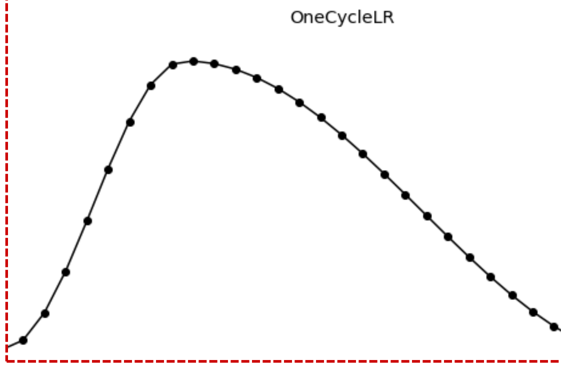
Preprocessing



Architecture

- Model: **Unet** with **SE-ResNeXt_32x4d** encoder
- Loss: **Dice Loss**
- Optimizer: **AdamW**
- LR Scheduler: **OneCycleLR** with max LR = 8e-5
- Epochs: 40

$$\text{Dice Loss} = 1 - \frac{2 \cdot y_{true} \cap y_{pred}}{y_{true} \cup y_{pred}} = \frac{2TP}{2TP+FN+FP}$$



[8]

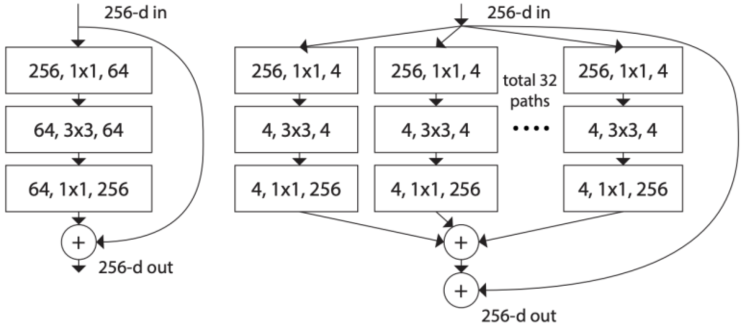
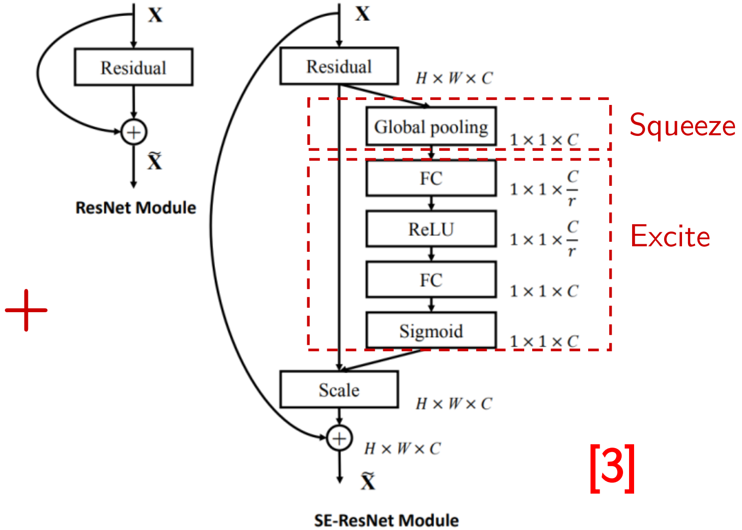


Figure 1. **Left**: A block of ResNet [14]. **Right**: A block of ResNeXt with cardinality = 32, with roughly the same complexity. A layer is shown as (# in channels, filter size, # out channels).

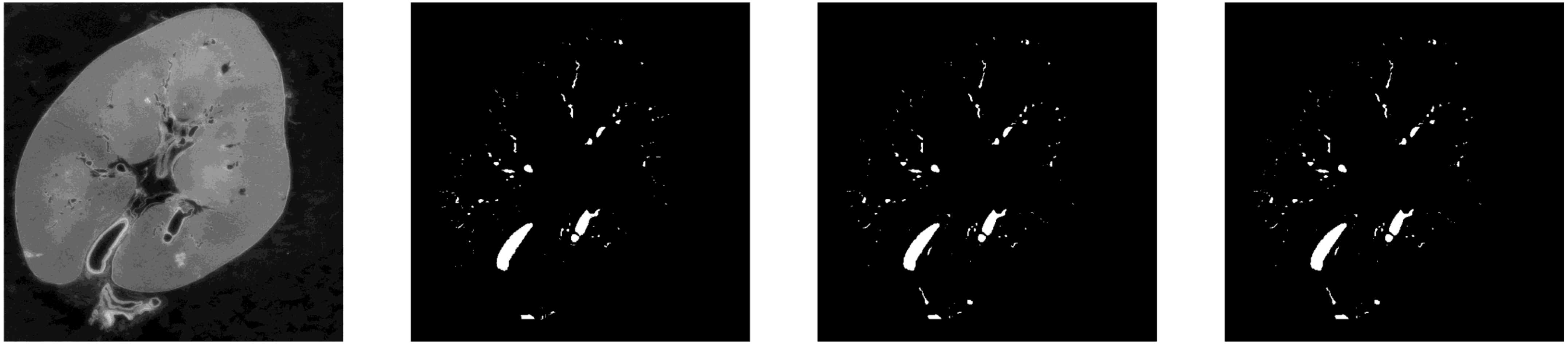
[4]



Inference/Postprocessing

- Test Time Augmentation (4 Rot, 2 Flip)
- Algorithmically determined 3D connected components to remove disconnected vessel predictions
- Then apply 3D flood fill to fix sparse predictions

Image Truth Prediction Postprocessed



Results

- Due to limited resources, we were not able to complete a full ablation study
- Strong augmentation and normalization were critical components in our pipeline, postprocessing provided small improvements
- After incorporating our pipeline, we got a final surface dice metric of 0.6017 on the test set

Citations

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5. Sudre, C. H., Li, W., Vercauteren, T., Ourselin, S., & Jorge Cardoso, M. (2017). Generalised Dice Overlap as a Deep Learning Loss Function for Highly Unbalanced Segmentations
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