# Glomerulus Segmentation in Kidney Biopsies Computer Vision Project, Group 9

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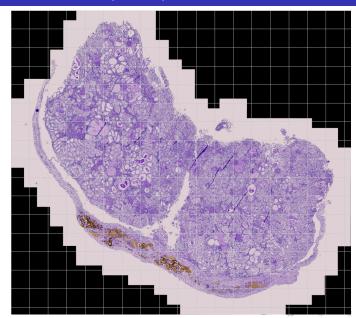
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## Problem Statement

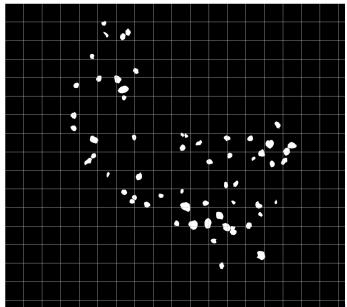
**General:** Accurate segmentation of glomeruli in kidney biopsy images is crucial for diagnosing chronic kidney diseases.

**Precise Tasks:** Segment glomeruli at patch-level and whole-slide level in kidney tissue images as part of the MICCAI 2024 KPIs Challenge.

# WSI Example: $train \56Nx \12_116$



# WSI Mask Example: train\56Nx\12\_116



## VariableUNet Model

- Standard UNet architecture with 8 double convolution layers split into encoder and decoder layers with skip connections between them.
- Dilated convolutions in the bottleneck (with dilation rates 1, 2, 4 on  $\frac{1}{3}$  of the channels each) for multi-scale feature extraction.<sup>1</sup>
- Channel quantities scale with variable patch size.

# **Experimental Design**

- Trained on official KPIs dataset (train/val/test splits).
- Combined binary cross entropy (BCE) and Dice loss to address class imbalance.
- Hyperparameter tuning: BCE/Dice ratio, Dice smooth, positive class weighting for BCE, learning rate for Adam optimizer.
- Experiments with different patch sizes (256<sup>2</sup> and 2048<sup>2</sup> pixels) and data subsets.
- Evaluated using accuracy, precision, recall, and  $F_1$ -score.
- Qualitative assessment via visual inspection.

# Metrics of our best performing Models

| Patch size | Split      | Accuracy | Precision | Recall | F <sub>1</sub> -score |
|------------|------------|----------|-----------|--------|-----------------------|
| 256        | Validation | 0.9781   | 0.7479    | 0.7660 | 0.7569                |
|            | Test       | 0.9757   | 0.7537    | 0.7133 | 0.7330                |
| 2048       | Validation | 0.9705   | 0.9299    | 0.3662 | 0.5255                |
|            | Test       | 0.9643   | 0.9159    | 0.2616 | 0.4070                |

## Hyperparameters:

- BCEDiceLoss Ratio = 0.8
- BCE Positive Weight = 25
- Dice Smooth =  $10^{-6}$
- Learning Rate =  $10^{-4}$

# **WSI** Segmentation

## Implemented patching pipeline with the following hyperparameters:

- Patch size
- Patch overlap (stride)
- Trivial patch threshold for positive pixels

### Possible next steps:

- Implementation of a stitching pipeline to combine patch predictions into a full WSI mask.
- Train VariableUNet using the complete patching and stitching pipeline.

## Discussion

#### What worked:

- BCE + Dice loss crucial for recall and  $F_1$ -score.
- Hyperparameter tuning improved glom detection.
- WSIs can be patched for patch-level segmentation.

#### **Limitations:**

- Instability in training, especially with full-size patches.
- Our configurations, trained on small patches, did not generalize well to larger patches.
- No empirical validation on WSI segmentation due to time constraints.

## Discussion

### In retrospect:

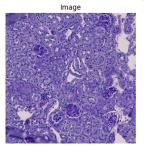
- Greater emphasis on pre- and post-processing (downsampling patches and upsampling predictions).
- More in-depth data exploration regarding samples of different diseases.

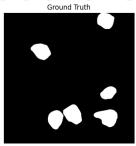
#### Future work:

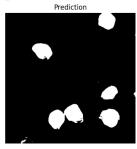
- Exploring different model architectures and methods.
- Search for more robust hyperparameters and domain adaptation.
- Continued work on WSI segmentation pipeline.

# Example Model Prediction

Model: ps2048\_po0\_ep20\_bs16\_lr0p0001\_bceW0p8\_ds1e-06\_posW25.pth







# Backup

## **UNet Architecture**

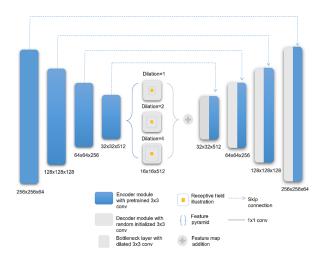
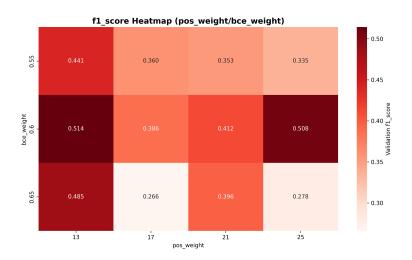


Figure: Source: Li et al. (2021), Figure 3 (edited)

## Double Convolution in our Code Base

```
1 class DoubleConv(nn.Module):
     def __init__(self, in_channels, out_channels):
          super().__init__()
          self.double_conv = nn.Sequential(
              nn.Conv2d(in_channels, out_channels, 3,
                 padding=1),
              nn.BatchNorm2d(out_channels),
              nn.ReLU(inplace=True),
              nn.Conv2d(out_channels, out_channels, 3,
                 padding=1),
              nn.BatchNorm2d(out_channels),
              nn.ReLU(inplace=True),
     def forward(self, x):
13
          return self.double_conv(x)
14
```

# $F_1$ -Score Heat Map from Experiment 2



# Recall Heat Map from Experiment 2



# FlipFlop Graph from Experiment 3

