

# Automatic segmentation of glomerular substructures by deep learning

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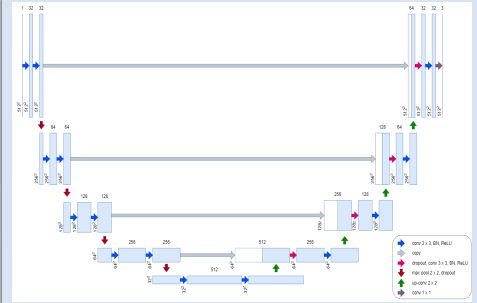
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## Introduction

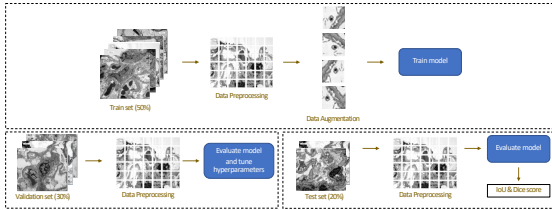
Electron microscopy (EM) complements light microscopy (LM) evaluation of the kidney biopsy. Foot process effacement, as assessed by EM, helps in diagnosing podocytopathies. However, human interpretation of EM images is time-intensive and often subjective. In this pilot, we investigate how deep learning techniques can help in segmentation of the glomerular basement membrane (GBM) and podocytes in EM images, in order to contribute to reliable and fast assessment of foot process effacement.

## Methods

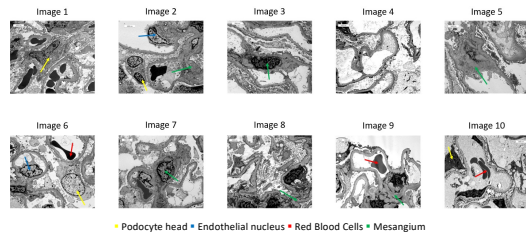
Glomerular basement membranes (GBM) and podocytes of 10 patients, 5 with podocyte disease (minimal change nephropathy) and 5 without glomerular changes, were annotated manually and using a thresholding technique, respectively, in order to provide ground truth. After data preprocessing, including cropping and tiling, a modified U-net model was trained ('baseline model'). The baseline model was compared to a fine-tuned contrastive learning model. The U-Net encoder of the fine-tuned model was pre-trained on 100 additional unlabeled images (SimCLR framework, 'fine-tuned model'). Segmentation performance was measured by IoU score. Models were evaluated on whole images and on diagnostically relevant ROIs (where the regions for diagnostic relevance were indicated by an experienced renal pathologist). Analysis with and without class weights (to correct for overrepresented areas in the images) was performed.



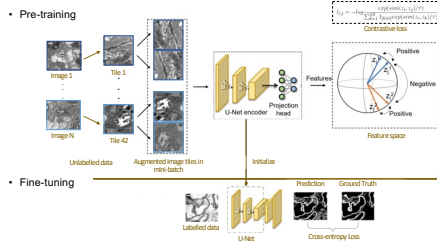
### Baseline model training and evaluation (5-fold cross-validation)



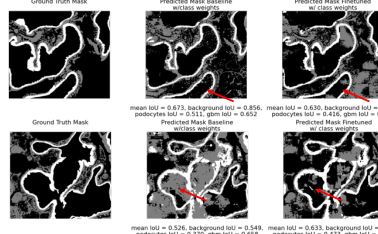
### Key image features affecting performance



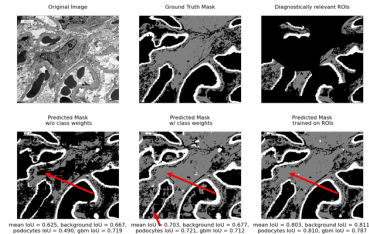
### Self-supervised learning (fine-tuned model)



### Baseline vs. fine-tuned model



### Training on ROIs improves performance



## Results

	Mean IoU (%)	Background IoU (%)	Podocytes IoU (%)	GBM IoU (%)
Evaluated on whole image				
Baseline Model w/o class weights	56.13±5.6	72.59±8.0	43.67±10.3	52.09±13.9
w/ class weights	56.03±8.7	63.74±11.5	45.44±10.6	<b>58.93±14.5</b>
trained on ROIs	55.95±10.8	68.42±10.9	<b>46.03±13.8</b>	53.36±13.6
Evaluated on ROIs				
Baseline Model w/o class weights	66.57±4.5	78.07±5.8	58.03±12.0	63.63±11.9
w/ class weights	<b>68.18±6.3</b>	74.34±6.6	59.10±11.8	<b>71.13±8.9</b>
trained on ROIs	67.30±9.2	<b>78.52±6.7</b>	<b>59.72±15.6</b>	63.68±11.4
Evaluated on whole image				
Finetuned Model w/o class weights	57.22±6.6	<b>75.35±8.4</b>	45.31±10.5	50.94±9.6
w/ class weights	<b>58.71±7.0</b>	69.87±7.0	<b>49.16±10.0</b>	<b>57.12±13.3</b>
Evaluated on ROIs				
Finetuned Model w/o class weights	65.64±7.3	<b>78.13±7.8</b>	56.76±13.1	61.99±9.1
w/ class weights	<b>68.42±5.6</b>	76.85±5.2	<b>60.89±11.8</b>	<b>67.47±9.3</b>

In this table the mean cross validation IoU scores are illustrated for all tested models.

Segmentation of the **glomerular basement membrane (GBM)** was best achieved by the baseline model and resulted in an IoU score of  $0.711 \pm 0.089$  compared to a IoU score of  $0.675 \pm 0.093$  in the fine-tuned model.

Segmentation of the **podocytes** was most successful in the fine-tuned model, with a IoU score of  $0.609 \pm 0.118$  compared to a IoU score of  $0.591 \pm 0.118$  in the baseline model.

When we evaluate the models on **ROIs** compared whole image evaluation, we can see a great increase. These higher scores confirm that the models can classify correctly the pixels of these regions.

Overall, segmentation performance of all models was better for GBM than for podocytes.

## Conclusion

This study pioneers in segmenting glomerular substructures on EM images by means of a modified U-net architecture. The next step is training and validation in larger datasets. Data annotation remains a challenge. Inclusion of more images and labelling of additional substructures (mesangium, endothelium) is expected to greatly improve the performance of the model.