

Unsupervised clustering of tubules in kidney biopsy images

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Background: Chronic kidney disease (CKD) affects about 10% of people globally and can lead to kidney failure, potentially necessitating replacement therapy. Pathologists diagnose CKD by identifying lesions in kidney tissue and assessing structural changes relative to normal kidney morphologies. Specifically in digital nephropathology, whole-slide images (WSIs) of kidney biopsies enable machine learning to support diagnostic and prognostic assessments. Detecting abnormalities in tubules is essential for accurate diagnosis, yet tubular lesions are less studied than other kidney structures. To close this gap, this project aims to develop a beneficial clustering strategy for labelling tubular lesions. This will help lay the groundwork for an AI tool to assist pathologists with tubular-lesion labelling and review.

Method: The dataset consists of 809 labelled tubular annotations classified as normal, chronically damaged, acutely damaged, or atrophic. Tubules classified as normal are considered healthy, whereas all remaining categories are regarded as lesioned. First, tubules are extracted from WSIs using three distinct approaches. This produces three datasets: (1) scaled patches, (2) masked and scaled patches, and (3) masked and centred patches, retaining the relative tubule size. Next, the datasets are analysed using different clustering strategies. The dataset type that works best is undetermined, so a key objective is to compare their performances. Finally, the clustering outcomes will be evaluated to determine whether they correspond to pathological classification.

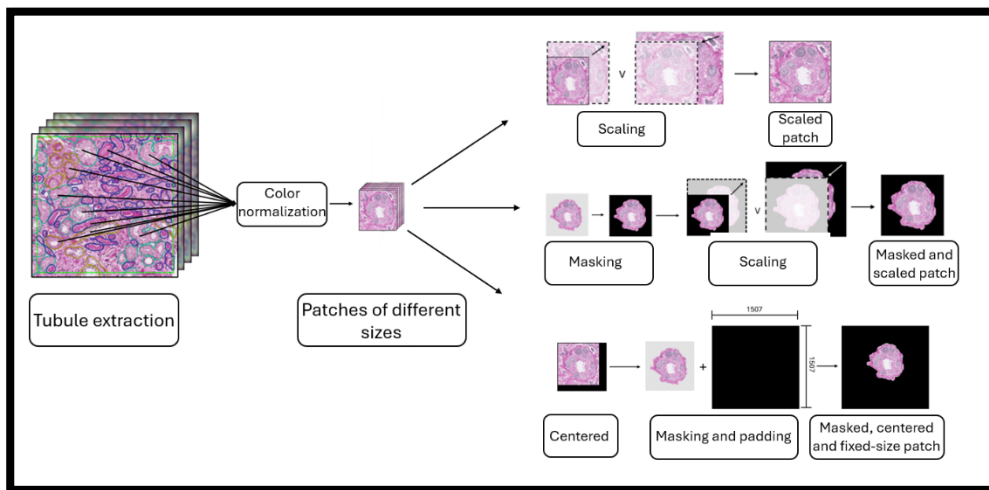


Figure 1: The three different extraction approaches.

Preliminary Results: Figure 2 shows the results of Leiden clustering on the non-masked dataset. These results indicate that the clustering can distinguish atrophic tubules from other classes and is also capable of separating normal tubules from lesioned tubules. Additional subgroup structures also appear to emerge.

Since the clustering appears to distinguish between atrophic and normal tubules, we constructed a dataset containing only these two tubule types. Figure 3 presents the results of Leiden clustering on the masked tubular dataset, including only atrophic and normal tubules. The clustering clearly separates atrophic from normal tubules, and additional subgroup structures are observed, suggesting potential subclasses within the normal tubules.

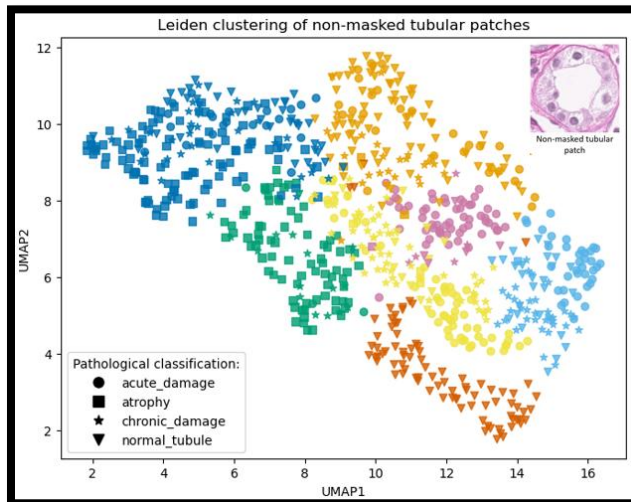


Figure 2: Leiden results clustering on non-masked dataset

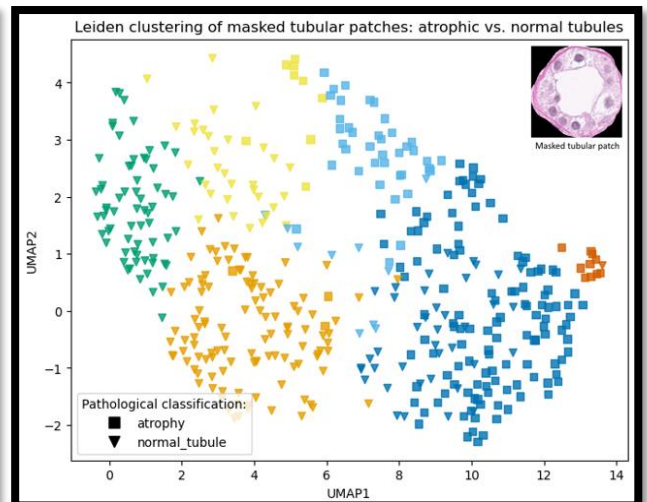


Figure 3: Leiden clustering results for masked tubular datasets including only atrophic and normal tubules.

So far, the Leiden clustering strategy appears to provide the most effective clustering results, and UMAP seems to be the best dimensional reduction for visualization. The different datasets yield varying cluster structures, but overall, their performance seems comparable. Additional clustering strategies and alternative models remain to be explored. Overall, these preliminary results indicate that the clustering can distinguish atrophic and normal tubules from other types, which is both promising and interesting.