HATs: Hierarchical Adaptive Taxonomy Segmentation for Panoramic Pathology Image Analysis

Supplementary Materials

1 Data Introduction

Our model leverages a 15-class, partially labeled dataset spanning various biological scales, from regions to cells. We sourced the human kidney dataset from three distinct resources:

1.1 Regions

Whole slide images of wedge kidney sections stained with periodic acid-Schiff (PAS, n=138) were obtained from non-cancerous regions of nephrectomy samples. The samples were categorized into several groups based on clinical data, including normal adults (n=27), patients with hypertension (HTN, n=31), patients with diabetes (DM, n=4), patients with both hypertension and diabetes (n=14), normal aging individuals (age>65y, n=10), individuals with aging and hypertension (n=36), and individuals with aging, hypertension, and diabetes (n=16). These tissues were scanned at 20× magnification and manually annotated in QuPath [1], delineating medulla, inner cortex, middle cortex, and outer cortex contours. The WSIs were downsampled to 5× magnification and segmented into 1024×1024 pixel patches. Corresponding binary masks were derived from the contours.

1.2 Functional Units

NEPTUNE The distal tubular, proximal tubular, glomerular capsule, glomerular tufts, arteries, and peritubular capillaries are from the NEPTUNE study [2] with 459 WSIs, encompassing 125 patients with minimal change disease, we extracted 1,751 Regions of Interest (ROIs). These ROIs were manually segmented to identify four kinds of morphology objects with normal structure and methodology outlined in [5]. Each image, at a resolution of 3000×3000 pixels (40× magnification, 0.25 μm per pixel), represented one of four tissue types stained with Hematoxylin and Eosin Stain(H&E), PAS, Silver Stain (SIL), and Trichrome Stain (TRI). We treated these four staining methods as color augmentations and resized the images to 256×256 pixels, maintaining the original data splits from [5].

HuBMAP Complementing the NEPTUNE dataset, we also incorporated data from HuBMAP. This dataset is comprised of 5 PAS-stained WSIs from varied donors, chosen based on criteria such as image quality (minimal artifacts or blurring), demographic diversity (considering age, sex, BMI), and encompassing different kidney regions (cortical, medullary, papillary). Expert segmentation was performed on the WSIs using

QuPath by a lead anatomist, assisted by four other trained anatomists. They identified three types of microvascular structures: arterial/arteriole, peritubular capillary/vasa recta, vein/venule. These were later grouped under a single category termed "microvasculature" [4]. The WSIs were then transformed into patches of dimensions 512×512 at a 20× magnification.

1.3 Cells

We employed 17 WSIs of normal adult cases from the aforementioned nephrectomy dataset. These pathology images were scanned at 20× magnification and cropped into 512×512 pixel segments to facilitate cell labeling, following the annotation process described in [3].

References

1. Bankhead, P., Loughrey, M.B., Fernández, J.A., Dombrowski, Y., McArt, D.G., Dunne, P.D., McQuaid, S., Gray, R.T., Murray, L.J., Coleman, H.G., et al.: Qupath: Open source software for digital pathology image analysis. Scientific reports **7**(1), 1–7 (2017)
2. Barisoni, L., Nast, C.C., Jennette, J.C., Hodgin, J.B., Herzenberg, A.M., Lemley, K.V., Conway, C.M., Kopp, J.B., Kretzler, M., Lienczewski, C., et al.: Digital pathology evaluation in the multicenter nephrotic syndrome study network (neptune). Clinical Journal of the American Society of Nephrology **8**(8), 1449–1459 (2013)
3. Deng, R., Li, Y., Li, P., Wang, J., Remedios, L.W., Agzamkhodjaev, S., Asad, Z., Liu, Q., Cui, C., Wang, Y., et al.: Democratizing pathological image segmentation with lay annotators via molecular-empowered learning. In: International Conference on Medical Image Computing and Computer-Assisted Intervention. pp. 497–507. Springer (2023)
4. Howard, A., HCL-Jevster, Gustilo, K., Borner, K., Ryan, H., Jain, Y.: Hubmap - hacking the human vasculature (2023), `https://kaggle.com/competitions/hubmap-hacking-the-human-vasculature`
5. Jayapandian, C.P., Chen, Y., Janowczyk, A.R., Palmer, M.B., Cassol, C.A., Sekulic, M., Hodgin, J.B., Zee, J., Hewitt, S.M., O'Toole, J., et al.: Development and evaluation of deep learning–based segmentation of histologic structures in the kidney cortex with multiple histologic stains. Kidney international **99**(1), 86–101 (2021)