

Image Domain Transfer for Liver Analysis in Histology

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1 Introduction

The master's thesis aims to address the limitations imposed by liver tissue samples by exploring computer vision and deep learning methods of *image domain transfer* (**IDT**). The goal is to transform the domain of large microscopic porcine liver images obtained from native samples into a different domain that represents decellularized liver tissue. Specifically, the focus is on two distinct visual characteristics observed in these domains: the color variations and the structural differences, both in large global shapes and microstructures that only show in high resolution.

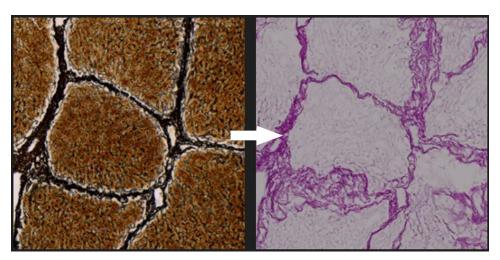


Figure 1: Image domain transfer from native to decellularized tissue sample

By erasing this domain gap, as illustrated in Figure 1, we can overcome some of the constraints of liver tissue analysis and unlock new possibilities for comprehensive image-based studies, for example, using proven analysis tools from the *scaffan* library (Moulisová et al. (2020)) in the desired domain and comparing the results of given selected metric with comparable data. This allows for a further higher quality evaluation of the sample.

2 CycleGAN for unpaired training data

CycleGAN is a GAN framework focused on solving problems in unpaired IDT, particularly when paired training data is not available. Introduced by Zhu et al. (2017), it utilizes the idea of using 2 pairs of GAN networks that transfer images back and forth between domains. It uses **cycle consistency** to ensure that the learned transformations maintain the key attributes of the original images.

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The custom dataset (nicknamed *liverGAN*) was created from a selection of porcine liver tissue samples provided by the LFP UK Biomedical Center. Separate high-resolution (e.g. 85000x55000) .czi files needed to be loaded and read using the *scaffan* library (Moulisová et al. (2020)) and then split into overlapping smaller pieces (tiles) in 1000x1000 resolution, and hand-filter them for corrupt data. The final number of these images is 13 057.

3 Results

Evaluation of performance in IDT tasks is complicated. In this thesis, the Fréchet inception distance (FID) metric is used. The cumulative FID score below 170 was achieved by implementing CycleGAN¹, compared to 615, the baseline FID of the dataset.

FID scores generally correlate well with human judgment, making it a reliable metric for quality assessment in image generation tasks. However, while FID is a useful quantitative measure, it does not capture all aspects of image quality, such as semantic correctness or small details. Therefore, we asked histologists to evaluate the generated data and compare the models with a relevant success rate. There will also be a test using the *scaffan* metrics on generated data. Furthermore, it is possible to split a whole-slide image into tiles, transform them, and then merge it back (example shown in Fig. 2).



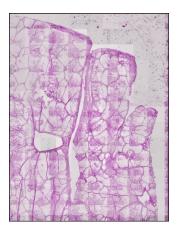


Figure 2: Splitted and merged whole-slide image sampleg

Acknowledgement

Computational resources were provided by the e-INFRA CZ project (ID:90254), supported by the Ministry of Education, Youth and Sports of the Czech Republic.

References

Zhu, J.Y., Park, T., Isola, P. and Efros, A.A., 2017. Unpaired image-to-image translation using cycle-consistent adversarial networks. In *Proceedings of the IEEE international conference on computer vision* (pp. 2223-2232).

Moulisová, V., Jiřík, M., Schindler, C., Červenková, L., Pálek, R., Rosendorf, J., Arlt, J., Bolek, L., Šůsová, S., Nietzsche, S. and Liška, V., 2020. Novel morphological multi-scale evaluation system for quality assessment of decellularized liver scaffolds. *Journal of Tissue Engineering*, 11, p.2041731420921121.

¹Source code and examples can be found at https://github.com/VaJavorek/livergan