Histology Whole Cell Slice Fine Tuned Classification and Variational Autoencoder for Histology Reconstruction

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Extra-placental Membrane (EPM) Results:

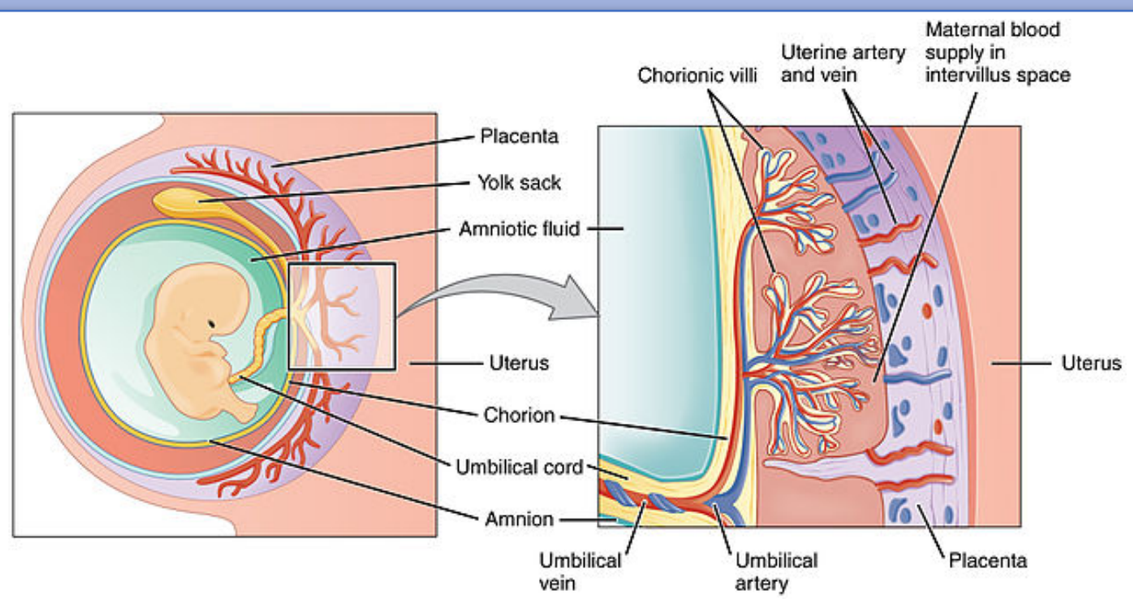
- Fine tuned accuracy comparable to the classification task over the villous parenchyma
- Robust to changes in slide presentation
- Accommodates two new cell types local specifically to the EPM
- Sensitive to equipment used by lab for slicing

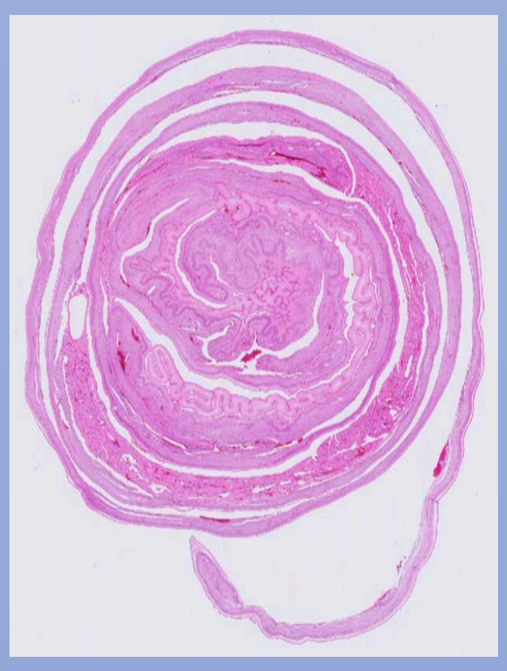
Reconstruction Results:

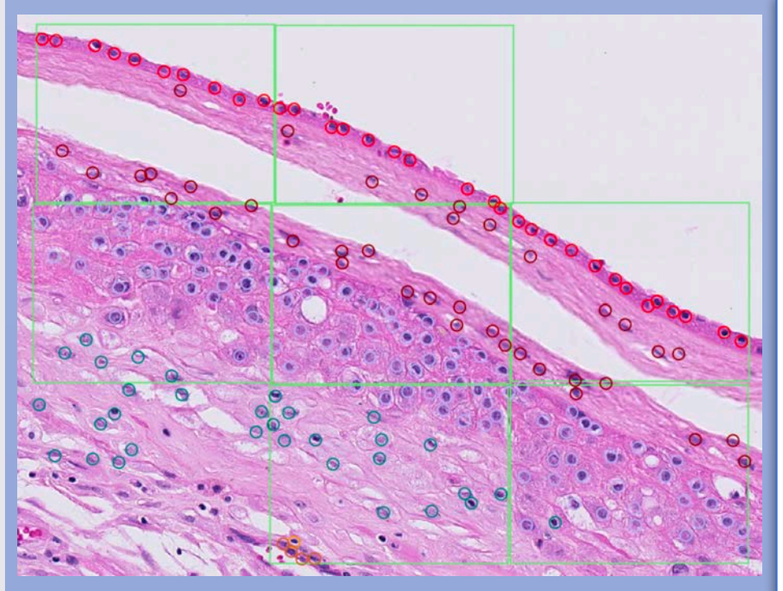
- Extend original classification task to a dual reconstruction loss task without a significant loss of accuracy
- New model can recover basic cell and staining characteristics from its initially learned embedding function
- Affine transformations and KL-divergence normalisation ignored (with the current architecture)

Background:

Pathology assessment is essential for managing maternal and newborn health, but the variability of the placenta presents challenges for histology analysis. Tools exist to assist in the quantification of this variability across tissue slices [1]. Our work hones into these pre-existing tools, and seeks to make them robust to changeability in preparation and presentation. It additionally works towards cell encodings that are more representative of fundamental characteristics of cell morphology.





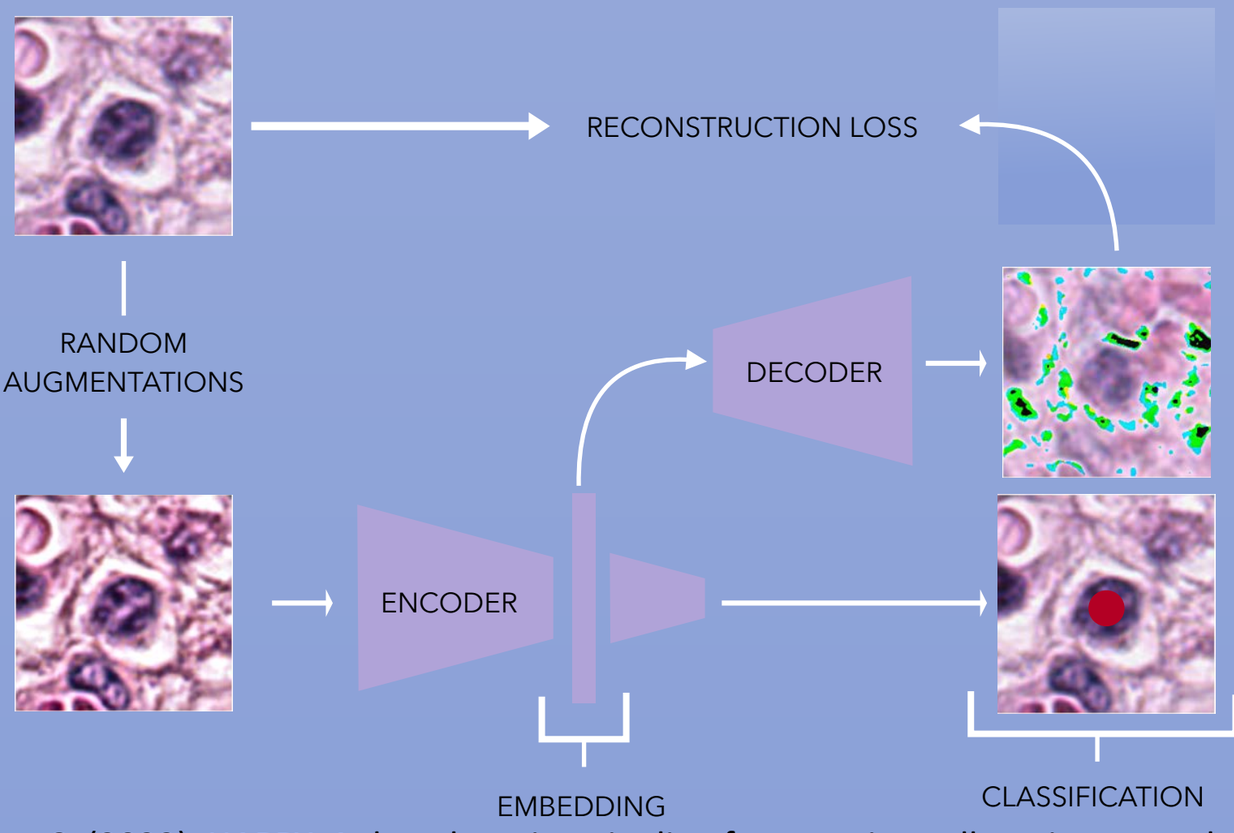


Fine Tuning:

Fetal membrane tissue rolled into a spiral was a new form of delivery unseen by the model during training. As well as this, EPM included two new types of cells, “Epithelial Cell” in the Trophoblastic lining and “Maternal Decidua” [2]. These are displayed as the red and green highlighted circles on the left, respectively. Transferring the models capabilities to this new scenario required fine tuning the model with thousands of hand annotated data points.

Variational Autoencoder:

We sought to extend the original histology pipeline [1] in order to enrich the embeddings for downstream tasks. By introducing a reconstruction loss for the model to optimise on, we train the model to learn aspects of cell morphology. To include this into the pipeline, we inference the classification model, hook an embedded representation, and pass that to the decoder. We then performed a MSE loss to compare the quality of the reconstruction. A sparse diagram of the pipeline can be seen on the right.



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[1] Vanea, C., Džigurski, J., Rukins, V., Dodi, O., Siigur, S., Salumäe, L., ... & Nellåker, C. (2022). HAPPY: A deep learning pipeline for mapping cell-to-tissue graphs across placenta histology whole slide images. *bioRxiv*, 2022-11.
[2] Ernst, L.M., Carreon, C.K. (2019). Placenta. In: Ernst, L., Ruchelli, E., Carreon, C., Huff, D. (eds) Color Atlas of Human Fetal and Neonatal Histology. Springer, Cham. https://doi.org/10.1007/978-3-030-11425-1_36

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