

Overview

The work of Dr. Zarella and Dr. Breen in the Advanced Pathology Imaging Laboratory (APIL) at Drexel College of Medicine focuses on the intersections of computing, digital imagery, and pathology. Work in the lab explores techniques to improve pathological diagnosis of histological images stained using hematoxylin and eosin (H&E) which has been described as "the cornerstone of anatomical pathology diagnosis."¹





Examples of H&E stained histological images

Researchers at University of North Carolina produced a convolutional neural network (CNN) to obtain statistically significant predictions of the pathology of tissue samples. The findings, detailed in the paper "Image analysis with deep learning to predict breast cancer grade, ER status, histologic subtype, and intrinsic subtype,"² have implications for reducing the speed and cost of diagnosis while increasing its accuracy.

Project Description

APIL is exploring algorithms to classify pathological structures using machine learning. The research and algorithms from UNC provide a point of comparison for approaches used by APIL. The work may provide insight into the features algorithms use to make predictions. This research has several aims:

- reproduce the findings of the original programs
- save trained machine learning models
- use the models to predict the malignancy of a tumor from a new dataset

Generalization of a CNN-based Approach to Predict Breast Cancer Grade

Laurence Liss, Faculty Advisors: Dr. Mark Zarella and Dr. David Breen

Activities

The programs used in the original research are posted on GitHub³ and a fork of the project was created⁴. A clean development system was provisioned and all dependencies were installed.

Successful output of the program resulted in a trained model as well as a confusion matrix, used for visual assessment of the program's classification performance. The diagonal values of the matrix denote correct classification. We reviewed images that were falsely classified.



nodel was able to correctly classify 239 of 255 benign tumors and was able to correctly classify 447 of 489 malignant tumors. There were 16 false positives (6.27%) and 42 false negatives (8.59%).





nages categorized as malignant but labeled as benign in the dataset.



nages categorized as benign but labeled as malignant in the dataset

The program was altered to save trained models and a standalone component was developed. This new program accepts, as input, a trained model and features extracted from histological images. A full slide histological image was selected for evaluation on a previously trained model. The image was tiled into 224x224 pixel squares and each tile was passed to the program for prediction. The resulting predictions were overlaid as green (benign) and yellow (malignant) on the original image.



A full slide histological image tiled into 224 x 224 pixel squares. Each image was passed to the program and was predicted to be either benign or malignant.





The trained model was able to correctly classify 147 of 168 benign tumors and was able to correctly classify 375 of 429 malignant tumors. There were 21 false positives (12.50%) and 54 false negatives (12.59%).







When overlaid on the original slide, predictions of the trained model revealed clustered areas of benign prediction and similar areas of malignant prediction. In some cases, related areas within the same cluster of tiles showed large disparity in the prediction. The causes for these classifications requires further investigation.



Additionally, the Advanced Pathology Imaging Laboratory has a large collection of H&E stained breast cancer slides at high magnification and we would like to prepare these to be trained with the program for comparison to the original findings.

I am working to create a simple neural network to be combined with new lecture materials to allow students to observe the structure of such a program as well as the features of the model that influence its predictions.

1. The American Heritage Dictionary of Medicine (2nd ed.). (2015) Boston: Houghton Mifflin 2. Couture, H. D., Williams, L. A., Geradts, J., Nyante, S. J., Butler, E. N., Marron, J. S., . . . Niethammer, M. (2018). Image analysis with deep learning to predict breast cancer grade, ER status, histologic subtype, and intrinsic subtype. npj Breast Cancer, 4, 30. 3. GitHub ImageMIL Original Program. (2019, 07 27). Retrieved from https://github.com/hdcouture/ImageMIL 4. GitHub ImageMIL Fork. (2019, 7 27). Retrieved from https://github.com/lliss/ImageMIL



REThink@Drexel Research Experiences for Teachers Site for Machine Learning to Enhance Human-Centered Computing

This material is based upon work supported by the National Science Foundation under Grant No. CNS-1711773 Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and d not necessarily reflect the views of the National Science Foundation

Future Work

Course Materials

References

Acknowledgements

