Deep Learning-Based Diagnostic Evaluation of Cholangiocarcinoma in Bile Duct Cytology Whole Slide Images

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ABSTRACT

- Deep learning algorithm to accurately predict the malignancy of bile duct cell clusters
- Multi-class classification model leveraging cellular architecture was used to differentiate clusters as atypical or benign
- Utilized pre-trained AlexNet Model and ResNet model.
- Reduces the need for manual diagnosis and extensive labor with aims to improve early diagnosis and patient outcomes

INTRODUCTION

- Bile duct cancer (**Cholangiocarcinoma**) is an extremely rare cancer affecting only approximately 8,000 people annually in the U.S.
- Particularly challenging to identify due to its internal location, often remaining asymptomatic until it reaches an advanced stage
- Techniques like ERCP and EUS are commonly used but are expensive, with costs ranging from $4,000 to $11,000 per test.
- Over 35% of cases are initially misdiagnosed as other types of cancer (ASCO Post Staff, 2021).

Goal

- Enhance identification and classification of cell types (atypical or benign) within bile duct tissue.
- Train a CNN to identify clusters of atypical and benign clusters

METHODS

Dataset

- 300 whole slide images provided by Dartmouth Hitchcock Medical Center
  - Visual images of individual cells and cell clusters

Connected Component Analysis (CCA)

- Using Jupyter notebook, all WSI's had white background filtered and clusters extracted

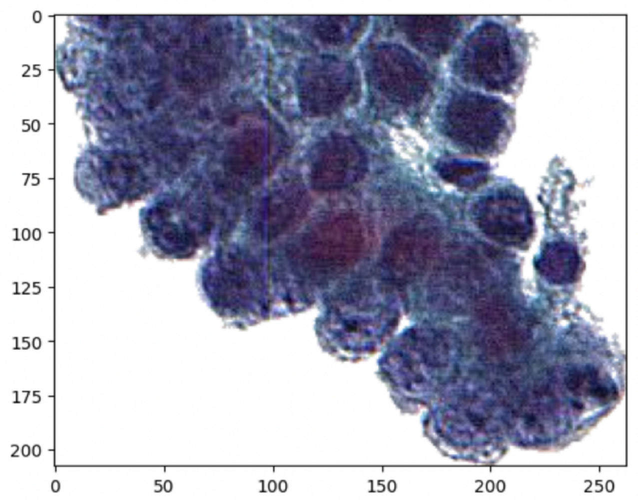


Figure 1. A WSI after being processed through Connected Component Analysis

Methods

SAM Annotations

- Tool for semantic segmentation of cells from cluster images
- ~30 WSI's of each cluster type were annotated: atypical cells, benign cells, SUSPos areas, and white blood cells

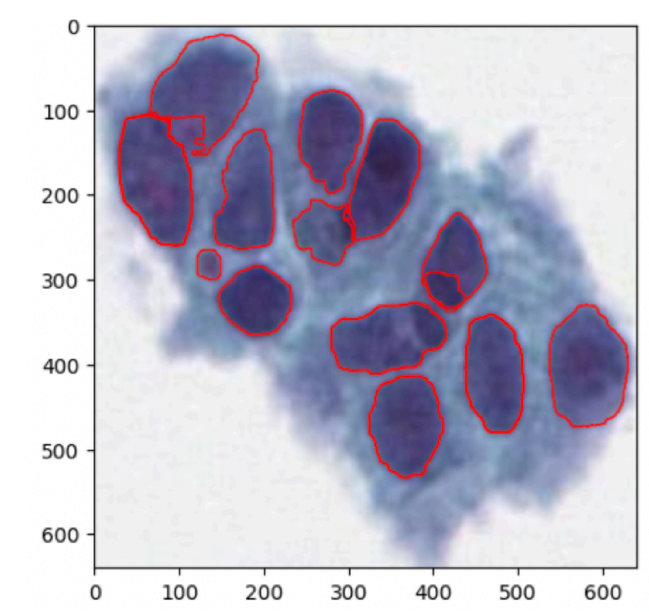


Figure 2. Cell cluster with masks around individual cells.

YOLO Object Detection

- Applied YOLO object detection framework to identify and classify various cell types within images
- Trained with 20 images
- Validated with 10 images
- Confidence threshold was lowered from 0.95 to 0.7 to avoid overlooking any overlaps

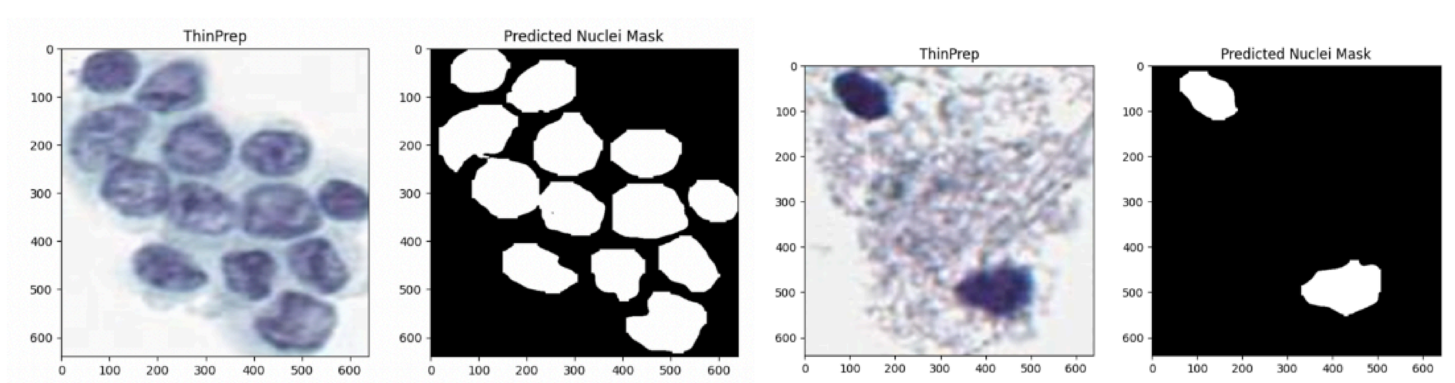


Figure 3. YOLO accurately masking the cells.

Convolutional Neural Network (CNN) First Model:

- Based on AlexNet and was employed for the binary classification of cell images into atypical and benign categories
- Images resized to 224x224 pixels and normalized using standard mean and standard deviation values to facilitate effective training
- CellDataset class created to handle data loading and preprocessing, while the dataset was split into training and testing subsets to evaluate the model's performance
- Includes a set of fully connected layers with dropout layers to mitigate overfitting
- Training performed using the Adam optimizer and binary cross-entropy with logits loss function

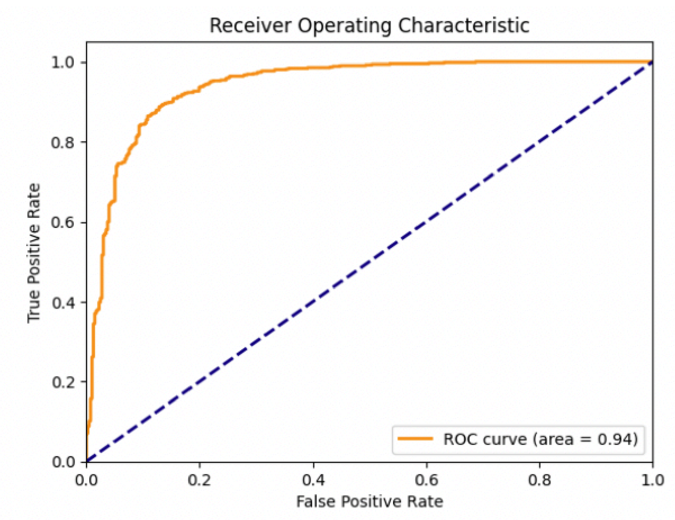
Convolutional Neural Network (CNN) Second Model:

- ResNet-50 was applied with transfer learning to classify cellular clusters.
- Stratified five-fold cross-validation was used to ensure robustness and mitigate overfitting, with performance evaluated across folds to assess generalizability.

RESULTS

ROC Curve

- Demonstrates high level of discriminative ability with an area under the curve (AUC) of 0.94 suggesting the model effectively distinguishes between atypical and benign cell images



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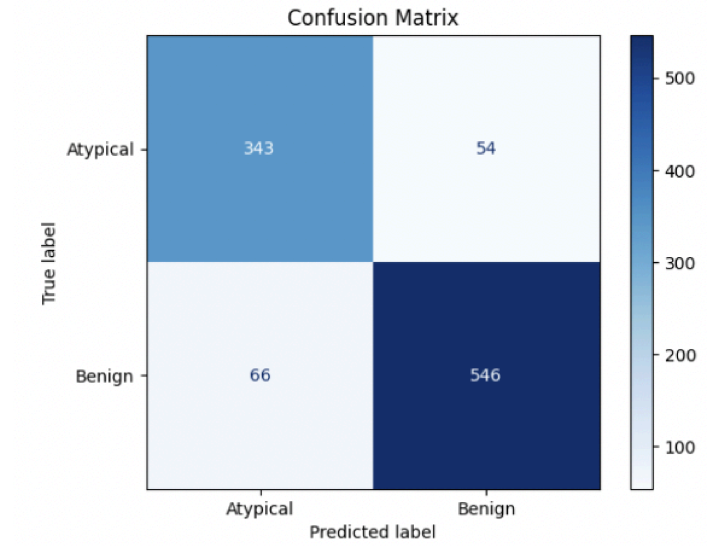
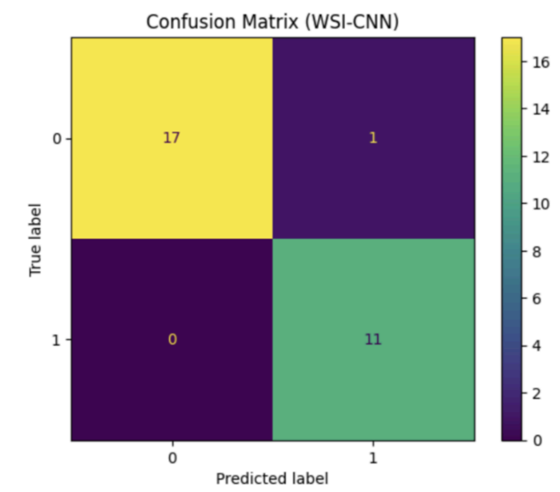


Confusion Matrix

- Reveals accuracy of 88% on the test dataset
- High accuracy indicates the model's effectiveness in correctly classifying the majority of cell images into their respective categories

Confusion Matrix - ResNet

- Reveals accuracy of 96% on the test dataset
- Full-slide context improved classification accuracy
- High sensitivity and specificity across categories



CONCLUSION

Potential for Clinical Impact

- Study demonstrates potential of integrating WSI's with deep learning techniques to enhance early detection and classification of bile duct cancer

Limitations

- Data was provided only from one center leading to underlying bias
- Presence of significant false positives and false negatives highlights potential risks in clinical settings

Future Directions

- Train a model to identify malignent cells
- Use additional testing sets to verify our model's accuracy rate

REFERENCES

References Link:
https://docs.google.com/document/d/1TYUzN0DfHAQ1mhjpJRLdbc3XAZfpoRC9utN7BOtBu0A/edit?usp=sharing

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