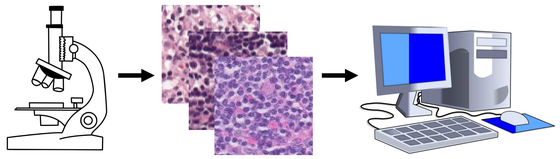
Designing a Machine Learning Architecture for Cancer Detection in Histological Images to Address Inter-Hospital Variation

Peter Hsu[1], Kianoush Falahkheirkhah[2], Rohit Bhargava[1]
[1]Department of Bioengineering, College of Engineering, University of Illinois Urbana-Champaign
[2]Department of Chemical and Biomolecular Engineering, College of Engineering, University of Illinois Urbana-Champaign
pwhsu2@illinois.edu

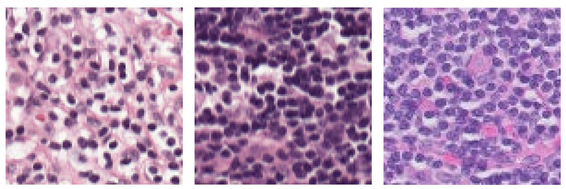
Introduction

Breast cancer that has spread to other parts of the human body can be detected by looking at a patient's cells under a microscope. The images taken, called histological images, can be efficiently analyzed using machine learning.



Histological images taken from various hospitals may look very different in their color intensity, image quality, and other factors. Machine learning models may make inaccurate predictions due to these differences.

Variation among Hospitals in Stain Color Intensity



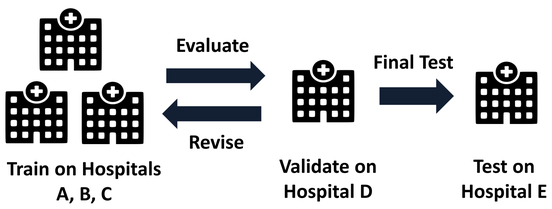
Hospital A | Hospital B | Hospital C

Machine learning models can speed up the diagnosis process for patients, lessen the workload for histopathologists who manually examine these images, and provide a more objective diagnosis.

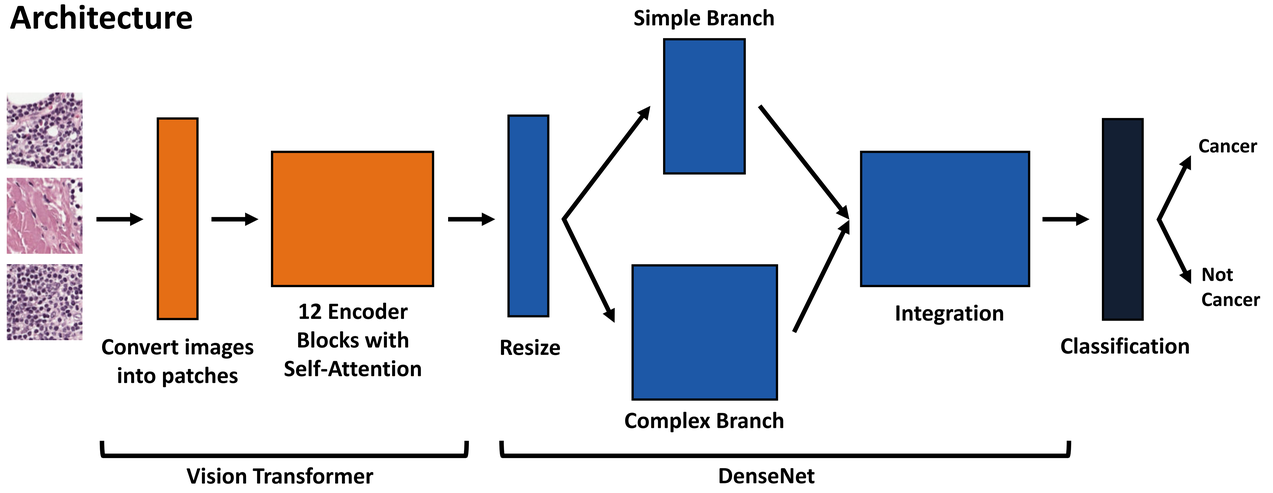
However, this domain shift problem prevents such models from being used in hospitals.

Methods

We used a dataset consisting of histological images from human lymph nodes [1]. The images were labeled by their presence or absence of metastatic breast cancer.

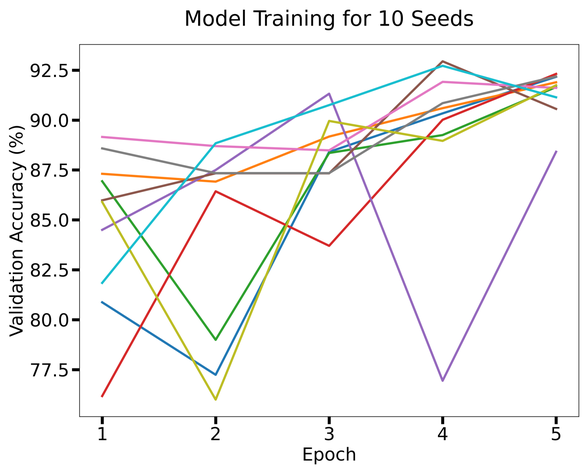


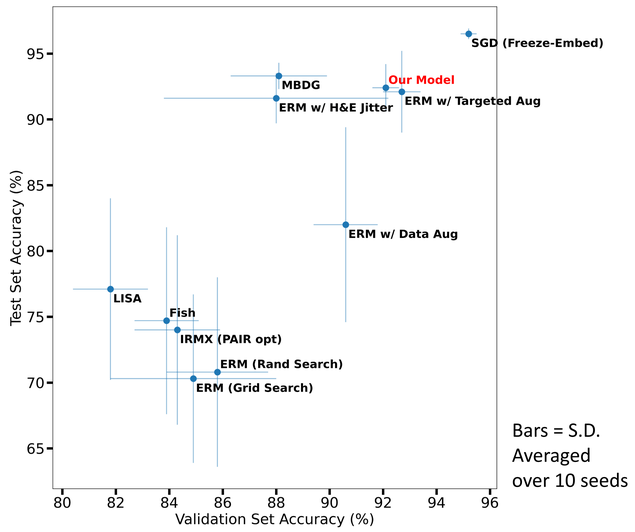
Architecture



Results

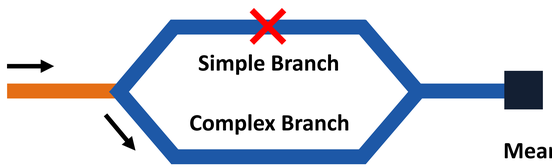
Mean Validation Accuracy (S.D.): **92.1%** (0.5)
Mean Test Accuracy (S.D.): **92.4%** (1.8)





Ablations

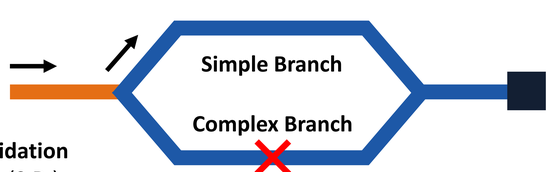
Does the simple branch add unnecessary parameters, hurting performance?



91.90% (0.26) → **90.82%** (0.61)
P = 0.96 n = 3 seeds

Mean Validation Accuracy (S.D.)

Does the complex branch enable high performance?



91.90% (0.26) → **90.75%** (0.96)
P = 0.08 n = 3 seeds

Discussion

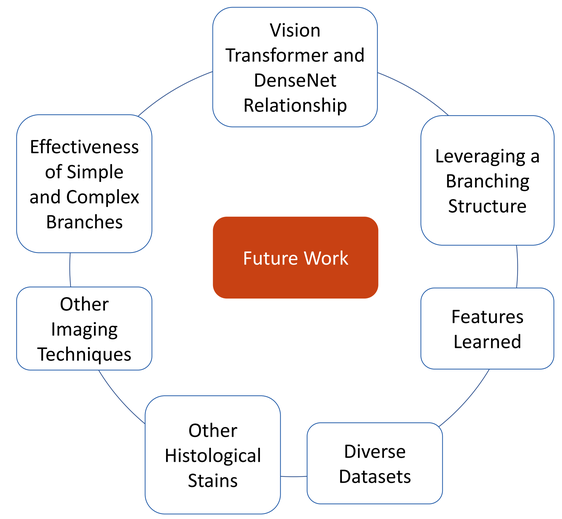
Novel machine learning architectures can be designed to address inter-hospital variation in histological images.

Ideally, a model architecture that is resistant to domain shift can be broadly applied to different types of cancer, staining techniques, and hospitals across the world.

Ongoing Challenges

Identify broadly-applicable solutions + **Verify applicability without external datasets** + **Ensure practicality for histopathologists**

Future work will be needed to improve our understanding of how these models function and refine the process of searching for new model structures.



Acknowledgements

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References

[1] P. W. Koh *et al.*, "WILDS: A benchmark of in-the-wild distribution shifts." arXiv, Jul. 16, 2021 [Online]. Available: http://arxiv.org/abs/2012.07421.

[2] V. Kindratenko *et al.*, "HAL: Computer system for scalable deep learning," in *Practice and Experience in Advanced Research Computing*, Portland OR USA, Jul. 2020, pp. 41–48, doi: 10.1145/3311790.3396649 [Online]. Available: https://dl.acm.org/doi/10.1145/3311790.3396649.