

## Presentation 2

- Links to presentation(s) and code(s) on GitHub
  - <https://docs.google.com/presentation/d/19nkjkmNrdSh5d7TP2qkPXQKUFBikS9LrFrL17EElqhY/edit?slide=id.p#slide=id.p>
  - Spring Model Rerun:  
[https://github.com/arvindkrishna87/STAT390\\_CMIL\\_Fall2025/blob/main/Code/MIL/springMIL\\_rerun\\_22Oct\\_Luna.ipynb](https://github.com/arvindkrishna87/STAT390_CMIL_Fall2025/blob/main/Code/MIL/springMIL_rerun_22Oct_Luna.ipynb)
  - Color Conversion (in progress)  
[https://github.com/arvindkrishna87/STAT390\\_CMIL\\_Fall2025/blob/main/Code/MIL/colorbenchmark\\_22Oct\\_Luna.ipynb](https://github.com/arvindkrishna87/STAT390_CMIL_Fall2025/blob/main/Code/MIL/colorbenchmark_22Oct_Luna.ipynb)
- What did you do?
  - Coding
    - Run Hannah's model with H&E stains only (trained for ~1.5 days) with added data & correct train-test split.
    - Add a function to save checkpoints to Google Drive instead of the local path, as Hannah did: `save_checkpoint_to_drive(model, arch, optimizer, epoch, drive_folder="MyDrive/Checkpoints")`
    - Add function to load the latest checkpoint:  
`load_latest_checkpoint(checkpoint_dir, model, optimizer, device)`
    - Change the `train_model` function to train from last checkpoint:  
`train_model(model, optimizer, criterion, train_loader, val_loader, arch, epochs=5, start_epoch=0)`

- Change the model eval logic so it actually saves attention weights!  
Original code rerun model eval multiple times for getting prediction for slice, patch and case & for getting attention weights to visualize.
  - Start coding the color conversion part to benchmark with Hannah's model.
- Research
  - Research way to implement other color spaces, specially focusing on h&e. Read on paper relating to color decolonization: separating hematoxylin channel & eosin channel.
- How does it help the project?
  - Establish a baseline model evaluation (rerunning hannah's model) for later comparison
  - More sustainable code and helpful functions
- Issues faced (if any)
  - Training time is too long, making it hard to test ideas.
- Attempts to resolve issues (if any)
  - Will switch to quest, hopefully will make it faster
  - Just do 3 epoch for benchmarking instead of 5 epoch
- Issues resolved (if any)
- Next steps
  - Complete the 2 action plans mentioned above
  - Since we decided to use Option A, I can also try to tune color space independently for each stain. As mentioned, brightness would benefit H&E stain, but for IHG stains, color seems to be more important.
- References (Mention if you built up on someone else's work)

- [https://scikit-image.org/docs/0.25.x/auto\\_examples/color\\_exposure/plot\\_ihc\\_color\\_separation.html](https://scikit-image.org/docs/0.25.x/auto_examples/color_exposure/plot_ihc_color_separation.html)

## Presentation 1

- Links to presentation(s) and code(s) on GitHub
- What did you do?
  - I researched different methods of color representation and gained insights from past literature relating to histological imaging. I outlined 2 action plans: (1) transform RGB images into other well-performing color spaces, such as LAB and HSV, and benchmark with MIL model from last quarter; (2) test whether features containing brightness information are important for model training.
- How does it help the project?
  - Improving color representation could improve training data quality, leading to better classification. Brightness information is shown to be helpful in shape detection. By using a color space that decouples brightness from color, our model could potentially have better learning on the distribution of melanocytes.
  - The previous cross-stain model averaged out the RGB channels from three stains. If we found that the brightness channel alone performs well, we can use only the brightness channel for each stain, so that each stain has its own dimension, but the overall dimension is still kept low.
- Issues faced (if any)
- Attempts to resolve issues (if any)
- Issues resolved (if any)
- Next steps
  - Complete the 2 action plans mentioned above

- Since we decided to use Option A, I can also try to tune color space independently for each stain. As mentioned, brightness would benefit H&E stain, but for IHG stains, color seems to be more important.
- References (Mention if you built up on someone else's work)
  - Madusanka, N., Jayalath, P., Fernando, D., Yasakethu, L., & Lee, B.-I. (2023). Impact of H&E Stain Normalization on Deep Learning Models in Cancer Image Classification: Performance, Complexity, and Trade-Offs. *Cancers*, 15(16), 4144. <https://doi.org/10.3390/cancers15164144>
  - Bishnoi, Vidhi, and Nidhi, Goel. (2023). A Color-Based Deep-Learning Approach for Tissue Slide Lung Cancer Classification. *Biomedical Signal Processing and Control*.  
[www.sciencedirect.com/science/article/abs/pii/S1746809423005840](https://www.sciencedirect.com/science/article/abs/pii/S1746809423005840)