Automated Image Alignment for Multimodal Biological Imaging

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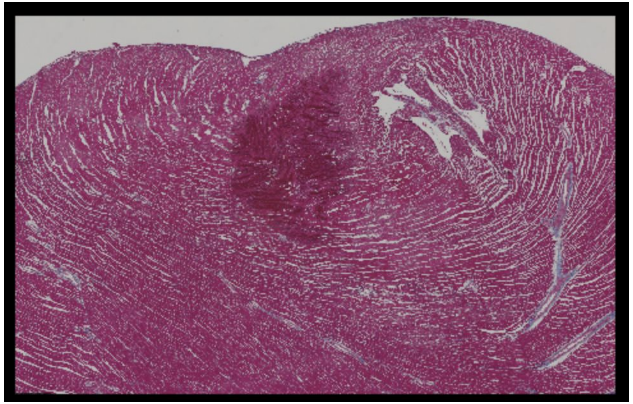
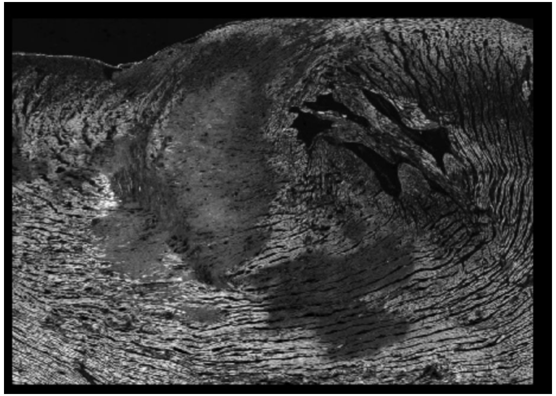
Background

- Histology images provide information about the cells, collagen content, and other tissue properties
  - Polarized collagen images provide context for the structural properties of the tissue
  - Location of the cells on the brightfield images



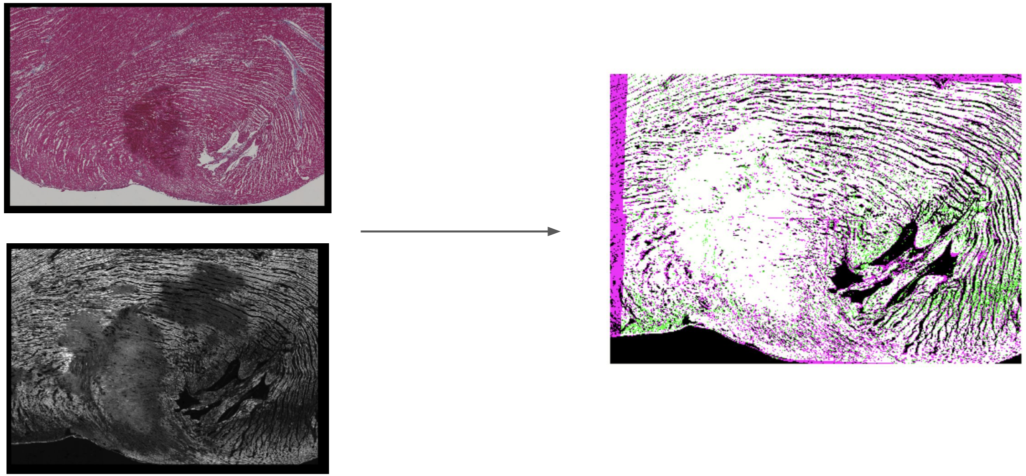
Brightfield H&E



Polscope H&E

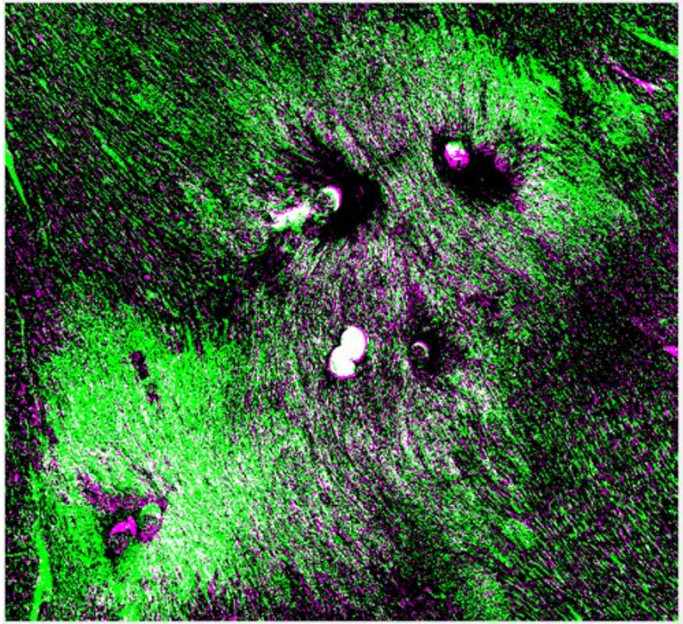
Project Goals

- Compare histological samples with images taken using different imaging modalities and on different scales
- Develop workflow to import and edit the images before alignment, then print out the final corresponding images



Challenges

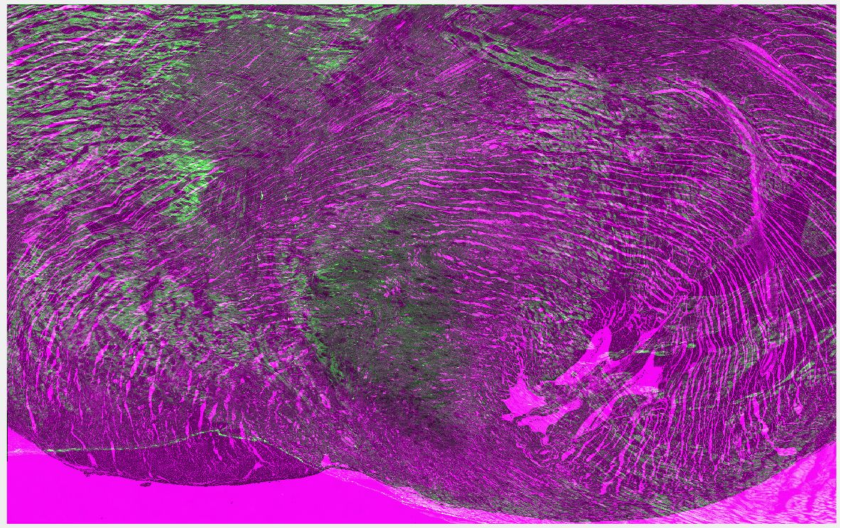
- Need to register images from different modalities even though they contain different information
- There is global, translation, rotation and scaling
- Regional variation in translation, rotation, shear → Global homography won't match up across whole sample
- Very large images
- Images are taken at different scales



Global Homography Leads to Poor Local Matching

Current Methods

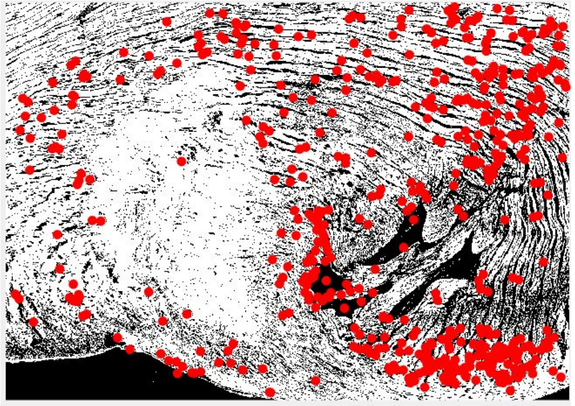
- MATLAB
  - Automatic Registration
  - Control Point Registration
  - Is extremely slow due to large image size
- ImageJ
  - Was only able to handle images from the same sample and modalities at different scales
- These methods struggled with the high variation between samples and the sample size

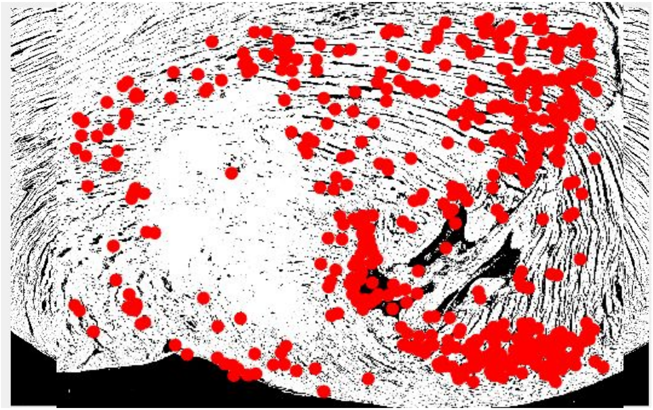


MATLAB Image Automatic Image Registration

Our Approach

- Import, resize, and threshold the images so interesting landmarks are clear
- Used automated SIFT algorithm to match landmarks in the images
- Crop images to align area of interest
- Compute homography matrices to map sections of one image to the other
- Display the result





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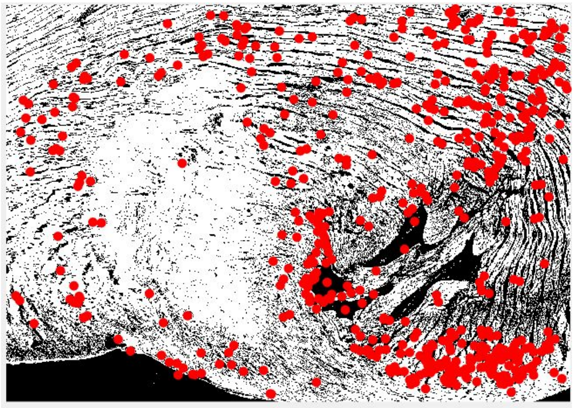

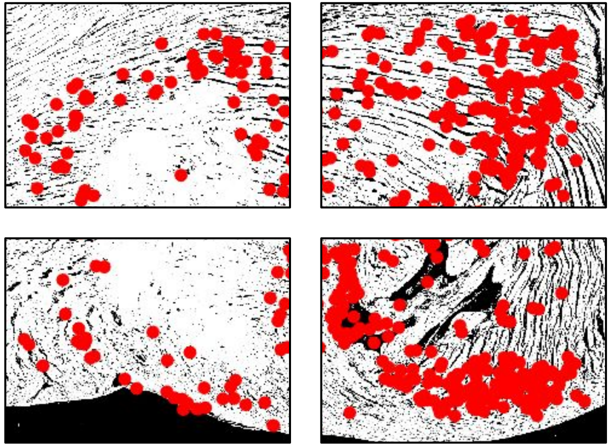

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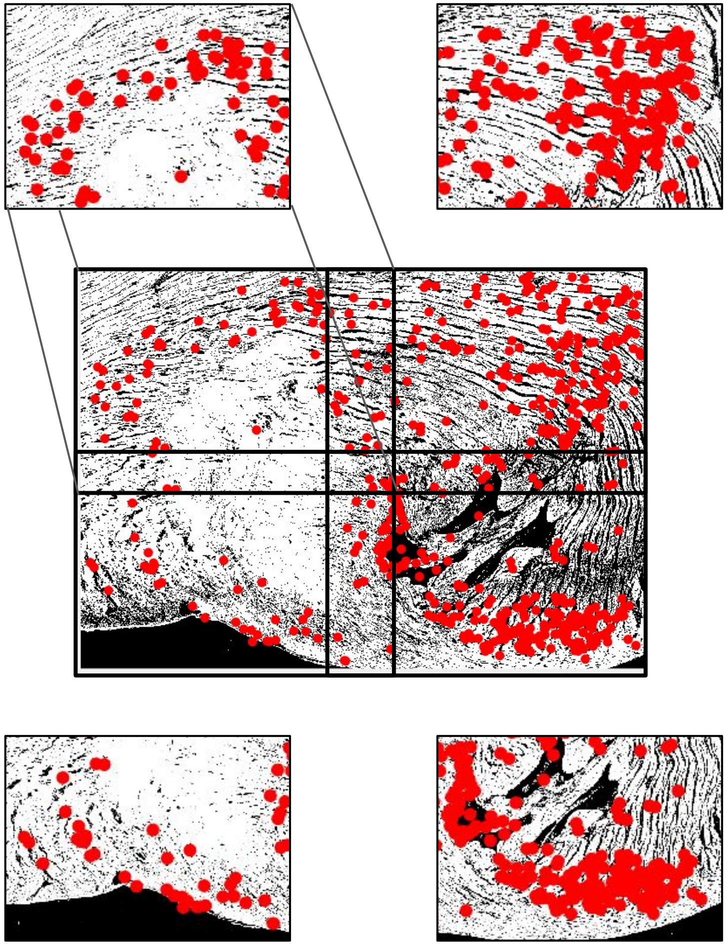
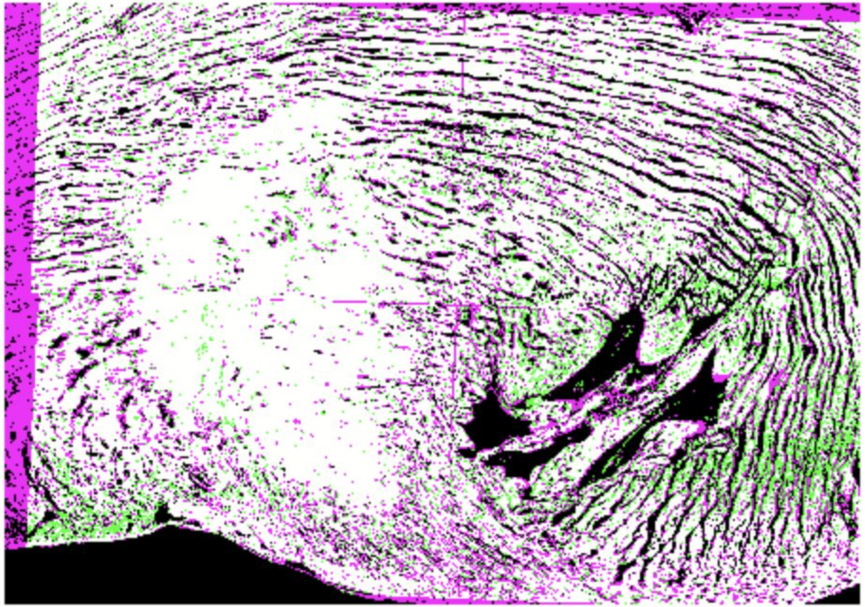
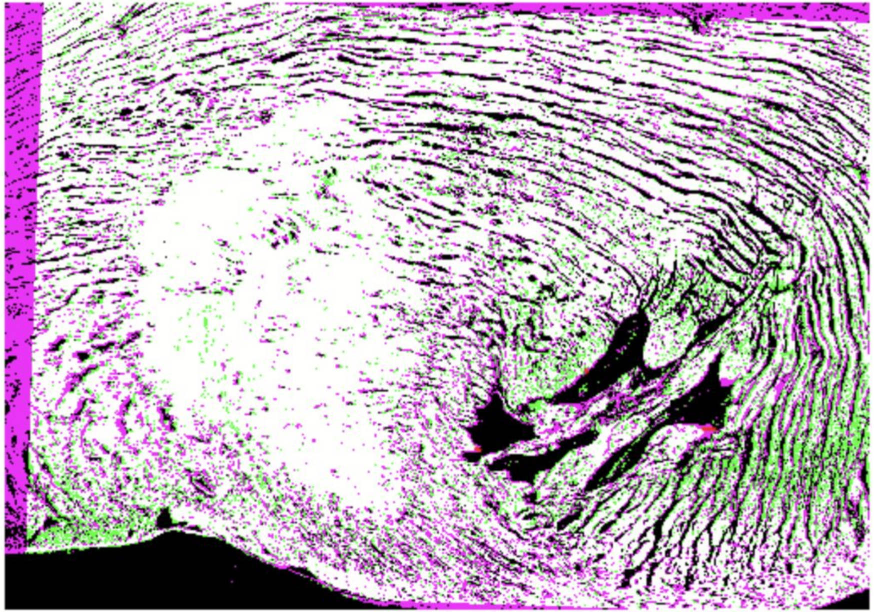


Results

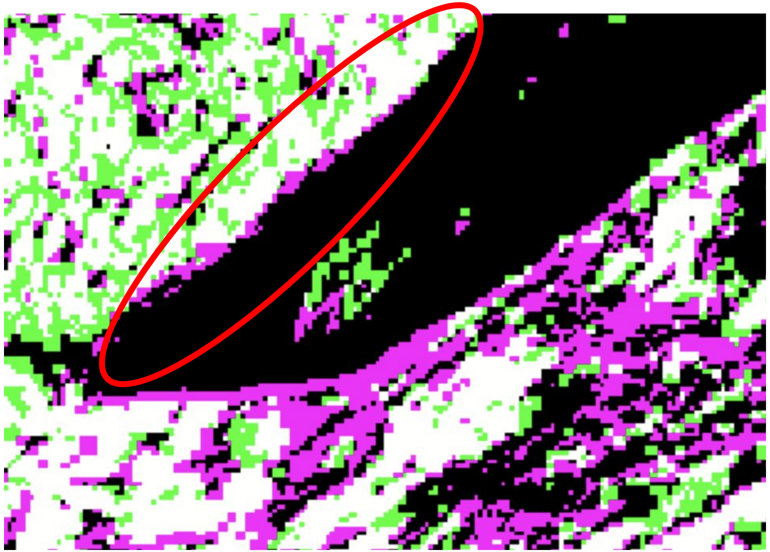
- Comparison of registration with patches (left) and with no patches (right)



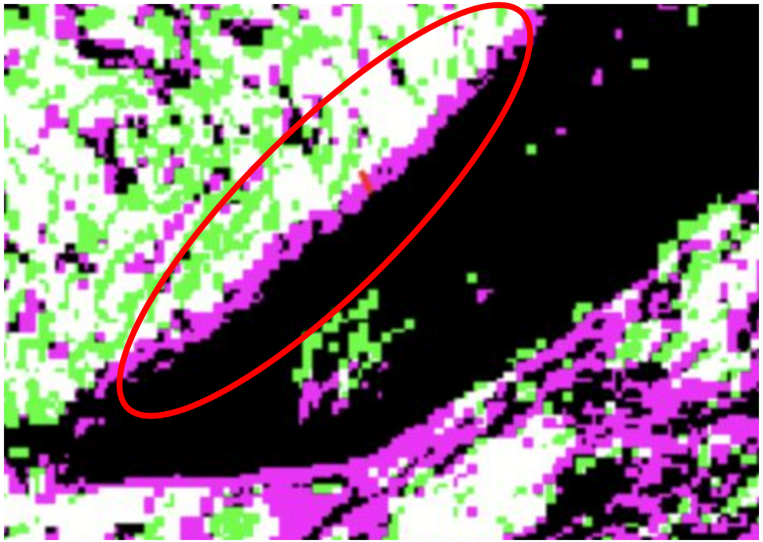


Results

Patches

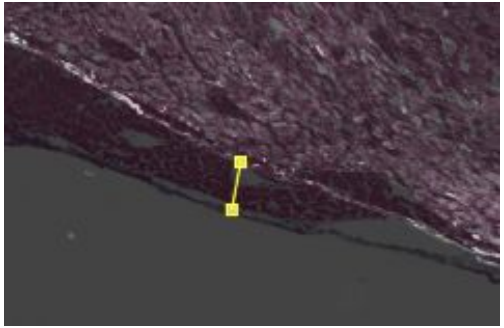


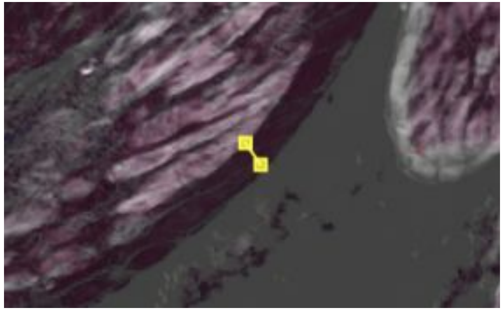
No Patches

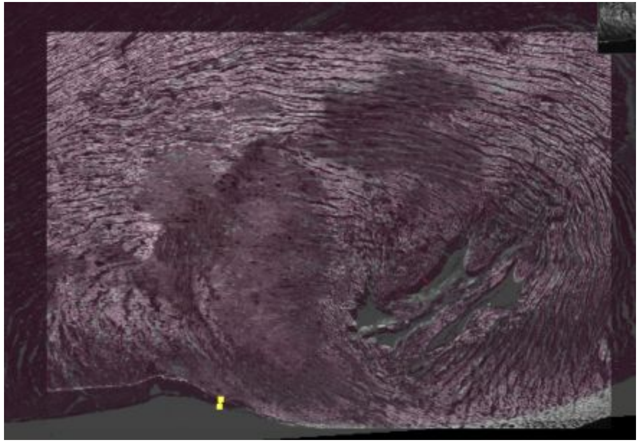


Comparison with Manual Registration

- Performed manual affine transform based on selected points in the image
- Accuracy is heavily dependent on the number of points
- Generally, affine accuracy was within 10s - 100s of pixels, while our algorithm was within 10s of pixels more globally
- Affine transform has more distortion away from selected points

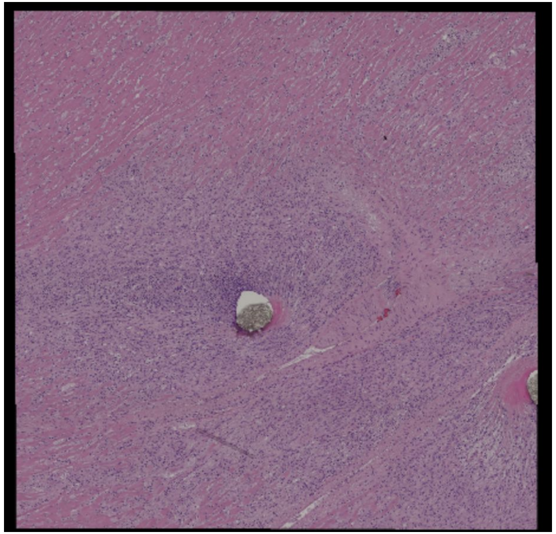






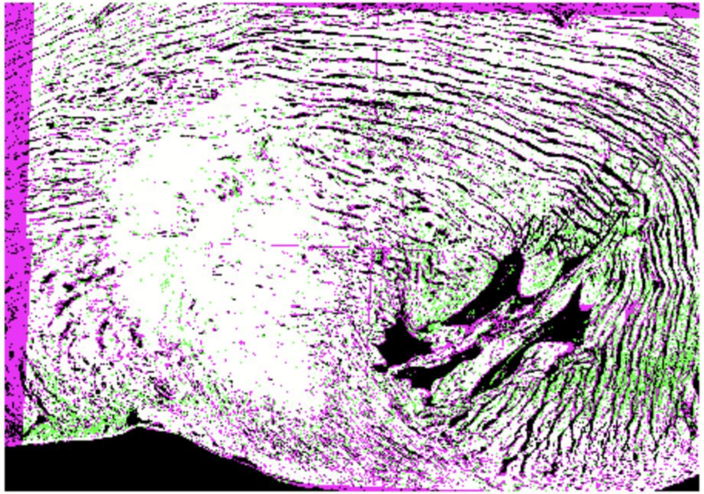
Limitations

- Works well when the tissue has well defined features that appear in both images, but not as well when the information contrasts (light in one, dark in other)
- Also works better when there are features in all four corners of the image



Takeaways

- Enables matching images with different information, scales, and warpings
- Runtime is dependent on number of patches and number of iterations, generally we ran in under 2-3 minutes, which is significant improvement over manual or MATLAB implementation

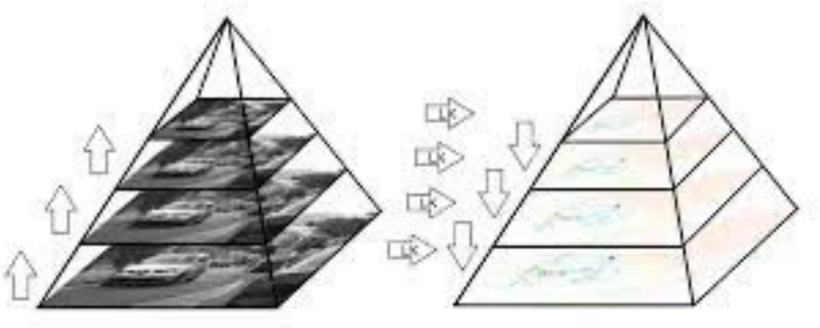


Future Work

- Homographies can be rescaled to apply to the original image enabling faster processing
- Compute homographies at iteratively finer scales to produce better local alignment

$$\begin{bmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & h_{33} \end{bmatrix} .* \begin{bmatrix} \frac{s_2}{s_1} & \frac{s_2}{s_1} & s_2 \\ \frac{s_2}{s_1} & \frac{s_2}{s_1} & s_2 \\ \frac{1}{s_1} & \frac{1}{s_1} & 1 \end{bmatrix}$$

Rescaling Homography Matrix



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Thank you! Any questions?