

Automatic Feature Characterization of Liver Tissue Section Image

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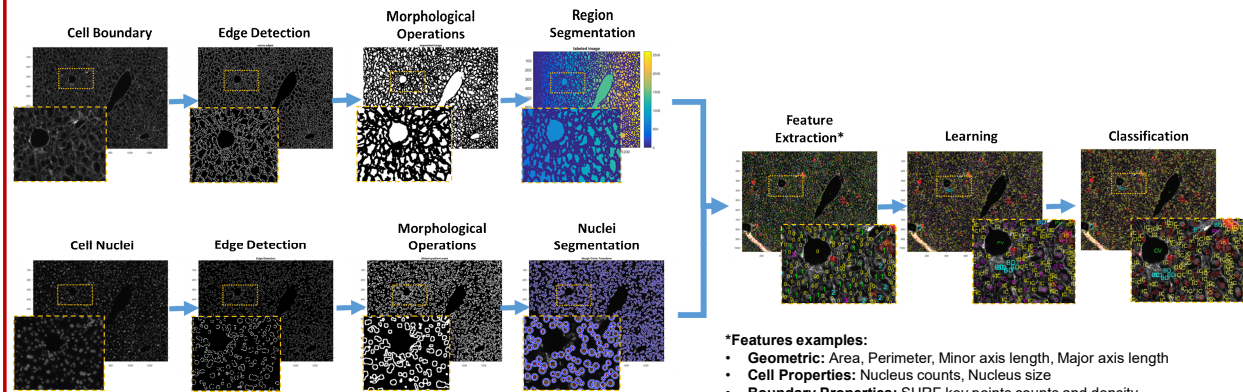


Introduction

The Nusse Lab of the Stanford Institute of Stem Cell Biology & Regenerative Medicine studies the regenerative properties of the liver. The purpose of this project is to develop MATLAB programs automating the tasks of cell counting and characterization of liver tissue section images, leveraging image processing and machine learning techniques. We aim to achieve the following goals:

- **Accurately detect cell counts irrespective to their stain at a precision of greater than 90%.**
- **Correctly classify features, such as portal vein, central vein, and bile duct, at a precision of greater than 90%.**
- **Correctly segment clustered nuclei at a precision of greater than 90%.**

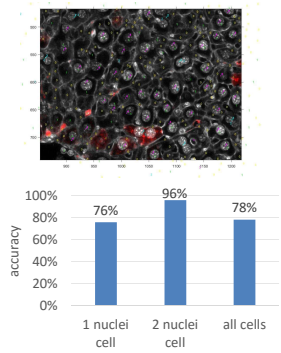
Feature Extraction Image Processing Pipeline



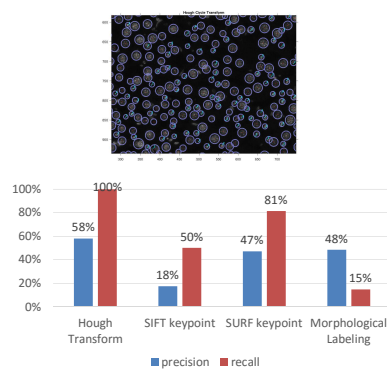
- *Features examples:
- **Geometric:** Area, Perimeter, Minor axis length, Major axis length
 - **Cell Properties:** Nucleus counts, Nucleus size
 - **Boundary Properties:** SURF key points counts and density
 - **Neighboring Regions:** Average cell area and relative distance from vessel

Experimental Results and Analysis

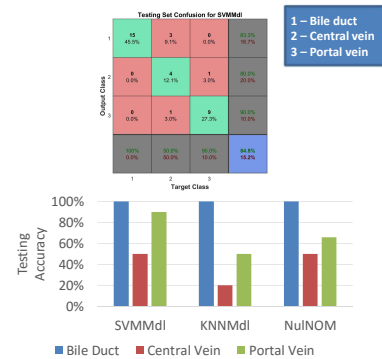
Cell Segmentation



Nuclei Segmentation



Feature Classification



Conclusion

- Successfully detected cell counts irrespective to their stain with about **80% accuracy**, using **Canny Edge Detection, Opening and Closing**
- Successfully classified notable features, including portal vein, central vein, and bile duct, with **85% precision**, using **multi-class SVM**
- Successfully segmented clustered nuclei with about **60% precision** and **100% recall**, using **Hough Transform**

Challenges

- Segmenting **ambiguous** cell boundaries
- Segmenting **non-uniform** nuclei shapes
- Extracting **relevant** features
- Feature classes **underrepresentation**

Future Work

- Improve classification accuracy
- Quantify morphological parameters
- Detect cell types and clones

References

- [1] J. Cheng and J. C. Rajapakse. Segmentation of clustered nuclei with shape markers and marking function. IEEE Transactions on Biomedical Engineering, 56(3):741–748, March 2009.
- [2] IV Grishagin. Automatic Cell Counting with ImageJ. Analytical Biochemistry, 2015.
- [3] Constantinos G. Loukas, George D. Wilson, Borivoj Vojnovic, and Alf Linney. An image analysis-based approach for automated counting of cancer cell nuclei in tissue sections. Cytometry Part A, 55A(1):30–42, 2003.
- [4] Fumio Maruhashi, Sei Murakami, and Kenji Baba. Automated monitoring of cell concentration and viability using an image analysis system. Cytotechnology, 15(1):281–289, 1994.