Melanocyte Detection in Skin Whole-Slide Histopathological Images

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1 Project Goals

Diagnosis of melanocytic lesions is one of the most challenging areas of pathology. The gold standard for diagnosis is the examination of histopathological whole slide skin biopsy images (WSI) by pathologist [Cireşan et al., 2013]. However, the WSI of one tissue sample usually composed of 2.2×10^9 pixels, which makes analyzing the entire image impossible for pathologist. As a result, manual diagnosis based on a small part of the image is often performed despite it being subjective and prone to variability. Thus, automated computational tools based on the entire slide is more desired [Cheng Lu and Mandal, 2012].

Our major aim for this project is to detect melanocytes in histopathological WSIs. Melanocytic nuclei are the most important cellular-level indicators of skin melanoma [Lu et al., 2013]. If we can find the melanocytes accurately, cellular features and architectural features can later be used for diagnosis of the melanocytic lesions. As the only former study worked on this issue, Lu et al. derived an algorithm based on the observation that melanocytes are surrounded by a pink "halo" region. They uses gradient magnitude and radial vectors to estimate the area of the halo region of given nuclei. An area ratio between the halo region and the nuclei is used to separate the melanocytes. However, based on our pathologist in contact and our observation of the data, the "halo" region is not an accurate measure of the melanocyte. The deliverables of this project would be an reliable classifier for detecting melanocytes from histopathological WSIs. We have an available nuclei detection `AdaBoost` classifier which have been tested on histopathologcal WSI dataset with successful performance. We will use this classifier to extract nuclei from images. Then, a set of pixel-based and textural features for each nuclei will be calculated. Next, we will train SVM and `AdaBoost` on features and compare the performance. Validation on learner would be performed to avoid overfitting. Moreover, we would like to discover patterns/features that are indicatives of melanocytes through feature ranking.

2 Dataset

We have access to 2 cases of whole-slide skin biopsy images (WLI), acquired by UW School of Medicine in their MPATH study (R01 CA151306). Each case has a normal stained slide and the same slide with melanocyte-specific staining. The two melenocyte specific stainings, which would be used as ground truth, are Melan-A and Sox-10. Melan-A is specific for melanocytes and stains the cytoplasm. Sox-10 is sensitive for melanocytes and stains the nuclei. This dataset contains 2 different diagnoses: moderate dysplastic nevus and the other an invasive melanoma, which should gives us a great variety of melanocytes of different characteristics. Figure 1 shows the normal staining of moderate dysplastic with size 39680×22144. Figure 2 shows a comparable views of the normal and melanocyte staining (Sox-10) side-by-side. Note that the red nuclei in Figure 2b are positive staining for melanocytes.

3 Milestones

As can be seen from the dataset section, we need to preprocess melanocyte stained slides to convert the label to binary. By Feb 23rd, we aim to accomplish the preprocessing step, extract features and train classifiers to get preliminary results on the test image. We would like to start on tuning the hyper-parameters (e.g. C, α, choice of kernel and etc. in SVM; α and number of weak classifiers in Adaboost) and show partial results as heat map. After that, one week would be spent on parameter optimization and generating result using the entire data set. The rest of the quarter would be used to prepare for poster presentation on Mar 9.

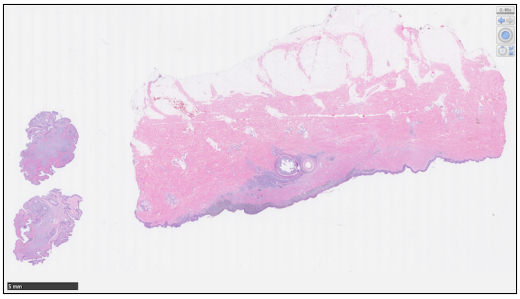
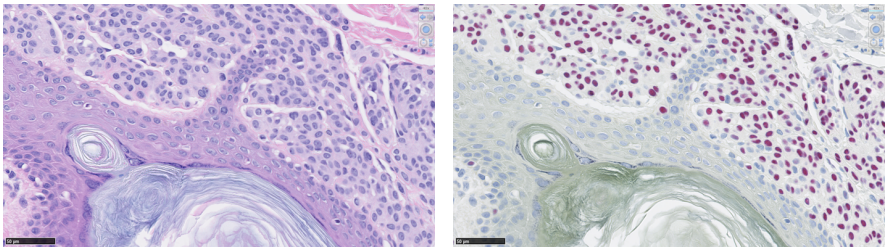


Figure 1: Case 10220: a skin biopsy image, moderate dysplastic nevus.



(a) Normal stain (b) Sox-10 staining: red for positives.

Figure 2: Comparison of normal and melanocyte staining at high power on a random area in case 10220.

References

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