AUTOMATIC NUCLEI DETECTION AND DATAFLOW IN BISQUIK SYSTEM

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Identification of cell nuclei is a fundamental operation,and nuclei centroids are used in a wide gamut of biological and medical analysis. Many methods exist for semi-automated and automated counting but usually require extensive parameter tuning to make tthem work for specific applications. While one can still do manual counting in 2-D, this is a practically impossible task with 3-D images. Furthermore, the scale difference between X-Y and Z dimensions might cause manual counting to be subjective and highly inconsistent, thus it's important to build robust and reliable automatic nuclei detector. We describe here a robust approach to 2-D and 3-D nuclei detection/counting that has been extensively tested on a large collection of retinal images. The nuclei are modeled as circular objects (although they are mostly ellipsoids) to achieve rotation invariance. The parameters needed, such as the filter dimensions, are extracted from the meta-data. One of the main challenges here is the extension to 3-D since the sampling resolution is significantly different in the Z-direction compared to the XY-plane. Also, the Z-series data is usually quite large, and hence requires a computationally efficient implementation. Our method is tightly integrated into the UCSB BISQUIK database system. The result of automatic detection can be validated by the total count and by the position of detected nuclei compared to the known ground truth (GT) data. Validation using centroid counts is implemented in the Bisquik. Because manual counting is time-consuming and GT can only be acquired for small numbers of images, the leave-one-out cross-validation method is employed. We would be able to demonstrate at the workshop the working prototype of this system.

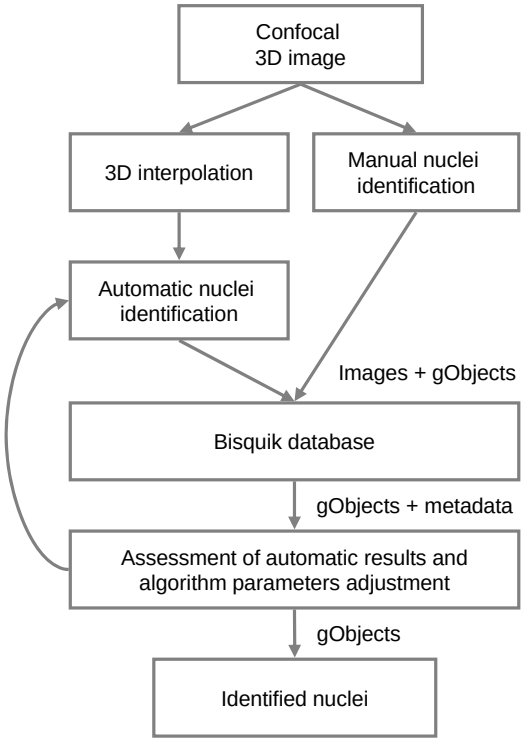

Fig. 1. The nuclei detection workflow in Bisquik system.

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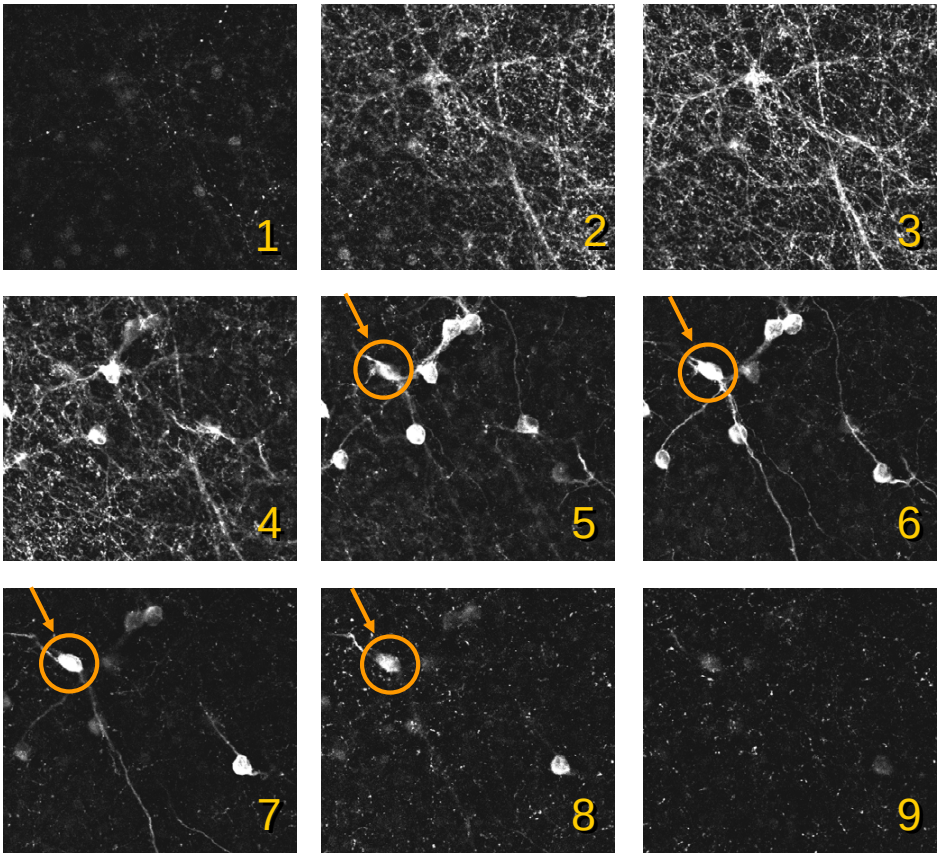

Fig. 2. Original planes of the fluorescent confocal image of whole mount retina. One particular cell is outlined in order to highlight it's location and shape in different planes. We are interested in detecting the centroid of the cell's nuclei, which in this case probably lies somewhere between planes 6 and 7. In order to to compensate for scale difference between Z and X/Y axis and perform fast and accurate template matching intermediate planes are interpolated. Authors would like to thank Benjamin E. Reese from Neuroscience Research Institute, UCSB, for kindly providing this image set.