Using Fiji / Image J to automate analysis of slide scanner generated files

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Slide-scanners are able to process thousands of slides in a near fully automated manner resulting in a large number of high quality images to be produced for a comparatively low investment of researcher time. The scans can be stored at very high resolutions which allows whole slides to be analysed in detail, rather than smaller random regions of interest (ROIs), leading to more robust scientific explorations.

The slide scanners themselves utilize proprietary file formats to store the data, which leads to challenges for researchers when attempting to analyse their data unless they also have access to the vendor specific software. While there are some freely available software alternatives for most file formats, the size of the files involved and the lack of automation in converting the image files can prove to be a bottleneck in the research workflow.

In this work we will outline methods which streamline the process of slide scanner image analysis using the open source image analysis platform FIJI[i] and detail how these large single files can be processed into a more manageable file format and size. Examples of analysis such as, but not limited to, cell counting, mean fluorescence intensity measurements of cells, the absence of staining areas and colocalisation measurements will be shown.

Overall these methods are designed to save researchers time through the automation of analysis of slide scanner files to produce more robust scientific data compared to currently accepted analytical methods utilising random ROI selection.

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[i] Schindelin, J.; Arganda-Carreras, I. & Frise, E. et al. (2012), "Fiji: an open-source platform for biological-image analysis", *Nature methods* **9(7)**: 676-682, PMID 22743772, doi:10.1038/nmeth.2019