Segmentation analyses to identify and quantify cells in 3D image stacks

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Abstract

Image analysis techniques have progressed quickly in the past decade, driven largely by the expanding field of robotics. These techniques have strong applications for biomedical images. Imagery for this work has been collected using time-lapse con-focal laser microscopy. We plan to develop a method to efficiently and accurately compute properties such as movement speed, total movement over a given period, number of cells of interest in the image, and other metrics to support researcher needs. Manual segmentation and analysis for this type of imaging are tedious and time-consuming tasks. Due to the repetitive nature of this work, the data is subject to human bias or error. However, repetitive processing and analysis make these tasks optimal candidates for automated pipelines. With this approach, the efficiency and repeatability of analysis will be consistent and maintain a reasonable margin of error. This is due to a computer's non-bias functionality of including or excluding numerical color values(pixels) in digital images. Applications of these automated pipelines will facilitate experimental screening for phenotypes that result in changes to cell numbers, cell behavior, etc., in animals carrying mutant alleles in genes of interest.