tissueRipper

is an algorithm that transforms 3D single-cell segmentations of confocal fluorescence microscopy data in a very particular way for the purpose of visualization.

is really just shifting the segmented cells apart such that cell size and shape as well as overall tissue architecture are preserved but all cells can be seen individually.

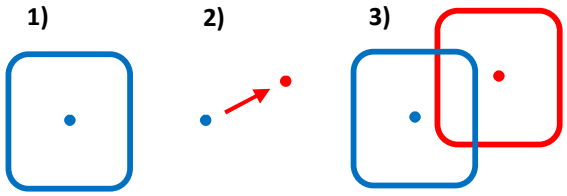
is written in Python 2.7 and requires the packages NumPy and SciPy (and optionally scikit-image and tifffile for import from and export to tif files).

is not a useful intermediate step in a quantitative analysis pipeline: it is well suited for showing off the power of 3D single-cell segmentation, but it does not itself improve segmentations or help with the analysis of segmented data.

Principle

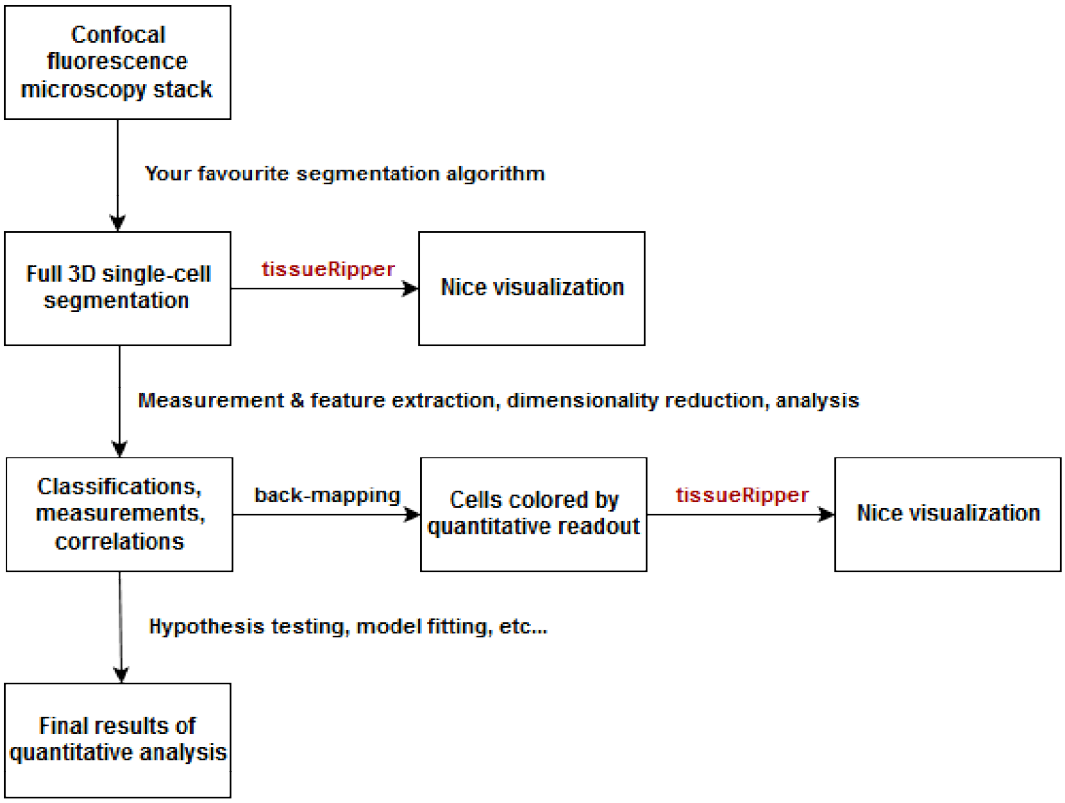
The tissueRipper algorithm functions as follows:

1) Extract the centroid positions of each segmented cell.
2) Calculate the distance each centroid would have to be translocated in order to expand the entire tissue by a (user-specified) factor.
3) For each cell, translocate its pixels by the distance calculated in step 2.



Usage in Context

How tissueRipper could be used in the context of segmentation and quantitative analysis of a tissue at the single-cell level, starting from 3D confocal fluorescence microscopy data.



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