

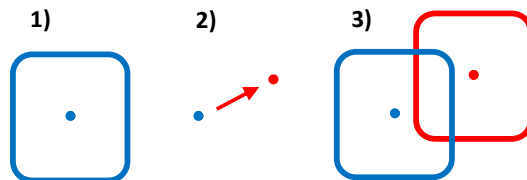
tissueRipper

- 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 tiffle 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.

