Github repository: <https://github.com/nnoll/tissueAnalysisSuite>

Paper: <https://journals.aps.org/prx/pdf/10.1103/PhysRevX.10.011072>

Main function: inverse\_pipepline

Reads images output from Ilastik, segments the images using the function seg.memWS to return a label matrix for each image (zeros on cell boundaries, integer value for each cell). We create these matrices (though don’t save them) in extractCellData.m – so can interface with the code this way.

seg.generate\_structs – reads the label matrices and creates a data structure from the label matrices, including data on cells, vertices, neighbours. This runs an internal function create\_Cdat\_Vdat\_initial (which runs a few other internal functions) to generate the structure.

Next step is removing bad cells from segmentation and re-running structure function, which we can skip.

Preparing for inverse calculation:

* Flagging 3-fold vertices
* Adding bonds data to the struct