This is a file explaining the meaning of each parameter in the parameter files.

You can change the parameter files directly when you run the simulation. You can also control whichever the parameter you want to do some analysis.

Parameters:

nx , ny: This two parameters are the size of the rectangle we use to generate the initial ellipse shape tissue. We can choose to cut an ellipse tissue from the rectangle tissue. You can change it to make the initial ellipse larger or smaller. But you also need to change the parameter “rx” to do change the size of the ellipse.

pos\_noise: noise of the tissue, the larger the parameter, the larger the randomness of the cell positions in the generated rectangular tissue above.

rx: the minor axis of the initial ellipse tissue. Change this number would influence the size of the initial tissue, but you may also need to change the nx and ny to make sure that the rectangle is large enough to generate the ellipse you want. For the eye disc, this was taken from Fried et al 2016 “A Model of the Spatio-temporal Dynamics of Drosophila Eye Disc Development”.

MF\_low, MF\_high: The density range of the Hedgehog(Hh) in the Morphogenetic Furrow(MF) cells. In other words, the cells consisting the MF are defined as the ones that have a density of Hh (or the effective morphogen) between MF\_low and MF\_high. Changing these two numbers would influence the behavior and width of the MF.

boundary\_flux: At the early stages of the eye disc simulation, Hh seeps in from the boundary. This parameter controls the rate of the Hh diffusion into the tissue.

t\_mech: simulation time scale. This parameter represents the transition between the simulation time and real time. The smaller the parameter, the more frequent the structural updates per unit real time.

t\_f: the simulation end time. Simulation will automatically stop after time t\_f.

t\_proliferation: Proliferation time for the tissue before the MF occurs. We set it to be 0 since we already use the correct size of the initial tissue before the MF occurs. This is non zero in the uniform growth case since we only model proliferation.

t\_plot: plot time interval, 50 means that we plot the tissue and the relative data every 50 simulation frames.

y\_diff: diffusion constant, define diffusivity Hh, which is our single effective morphogen in the eye disc simulation.

y\_dec: decaying constant, define the speed of decay of Hh.

h\_auto: threshold of the Hh concentration for the cell to become source cell of Hh itslef. In other words, if the Hh density inside a cell is larger than h\_auto, it starts to produce Hh.

growth\_control\_by: z\_concentration, Unused for the publication but this can specify which morphogen one wants to use to regulate cellular growth. In the manuscript, we do not use a morphogen/chemical dependent growth.

int\_cell\_cycle, amin, amax, gamma\_G, gamma\_S: Initialization of cell cycle, area range and other factors control the division rate. All these 5 parameters are using in the function cell\_GS, in which cell division are controlled by cell cycle. This is not used for the manuscript, but offers an alternative way to model the cell cycle with higher resolution.

boundary\_tension: boundary tension for the tissue. The default value is 0.12, which means the edge tension in the bulk of the tissue is 0.12. Here the boundary\_tension gives the edge tension on the boundary of the tissue. Usually, this tension is larger than the tension in the bulk of the tissue since we want to keep the shape of the tissue. The tissue boundary is more regular under larger boundary tension.

proliferation\_type: area or uniform. Area means the division of the cells would be influenced by the area of the cell, and a cell has a larger chance to divide when its area is larger. This is division rules are stored in division\_functions\_aegerter.py and are taken from Aegrtel et al 2010 “Exploring the effects of mechanical feedback on epithelial topology”.

proliferation\_time\_dependent: exponential, area or no. This parameter controls the time dependence of the proliferation rate. For the eye disc , both exponential and area dependent growth have been shown to fit the experimental data very well. For uniform growth the choice is no.

proliferation\_magnitude: If the proliferation is not time related, then this parameter defines the speed of proliferation.

conversion\_t\_magnitude: the conversion factor between simulation time and real time. If one changes t\_mech (controlling the number of updates per unit real time) , conversion\_t\_magnitude is rescaled such that the real time conversion remain consistent.

long\_axis\_div: whether the cell division happens according to the shape of cells or not, if yes, the cell is firstly embedded by an ellipse, then divides along the minor axis of the ellipse.

number\_of\_slice, number\_of\_slice\_pa: Analysis related parameters. The first parameter is the number of equal slices we cut along the y direction from the Anterior end to the position of the MF. The second parameter is the number of equal slices we cut along the y direction from the Anterior end to the Posterior end. This did not end up being used in the manuscript but is useful to probe the spatial dependence of mitosis.

Repeats: Parameter used for plotting when repeating the same simulation multiple times.

random\_init\_cycle: whether the initial cell cycle(volume) of the cell is random or not.

cycle\_magnitude: if the random\_init\_cycle parameter is no, this parameter defines the initial cell cycle of the cells. (so it only works when random\_init\_cycle = no)

mechanosensing\_magnitude: the feedback of the difference between the target cell area and the average cell area on cell cycle. (only works when proliferation\_type = area)

inactivate\_posterior : This is significant for the eye disc simulations. If yes, the vertex positions of posterior cells are fixed after the MF has passed with a time lag specified in the next parameter.

hours\_to\_inactivate : This is significant for the eye disc simulations. If inactivate\_posterior = yes, this parameter defines the time lag after the MF passes that cells become inactive.

viscocity\_solver: if Yes, the tissue is solved using viscosity solver. Note that in the manuscript the main results are obtained using the quasistatic solver.

viscocity\_solver\_iterations: The number of steps on one mechanical structure update when using the viscosity solver.

viscocity\_factor: This factor is inversely related to the viscosity. The higher it is, the lower the viscosity. It is only relevant when using the viscosity solver.

Parameters below are going to be included in future releases or upon request, generated according to peer review comments:

rlarea\_controlled\_type: change a term in energy function according to relative cell area (cell area compared to average cell area), if the cell is larger than average cell area, then it’s contractility/tension/preferred\_area would be larger and vice versa. default:0 contractility:1 tension:2 prefered\_area:3

rlarea\_response: a parameter that changes the amount of change of certain factor if the cell area is larger or smaller than average area. Only works for rlarea\_controlled\_type is not equal to 0 (works for 1,2,3). For example, if this factor is 0.1, and rlarea\_controlled\_type = 1, which is contractility, then the contractility will become smaller/larger by a factor of 0.1 if the cell area is smaller/larger then average cell area.

pressure\_switch: default: OFF. If it is ON, then in each simulation the code would calculate the pressure for each cell.

default\_tension: default value:0.12, which means that the bulk tension in the simulation is 0.12, otherwise the bulk tension in the simulation would be the value set here minus 0.88.

t1\_threshold: a parameter represents the threshold length for t1 transition. If an edge is shorter than this parameter, than t1 transition can happen.