The “Patterns” simulation package includes model and config files created by Alexis Pietak and

with some results presented in:

Pietak and Levin. Bioelectrical control of positional information in development

and regeneration: A review of conceptual and computational advances. Progress in Biophysics and

Molecular Biology. 2018. 137:52-68.

Please cite and discuss the above article if you have used/adapted these model/config files in your work. The model in all “Patterns” config files is the same (only the size of the model is changing) and is the same model presented in Fig 4 of the above-mentioned publication, with mathematics presented in the Appendix.

To obtain different patterns, there are only a small number of "master" variables that alter pattern,

importantly, many of these are in the extra\_configs/worm\_3.yaml file included with this simulation

package. Different parameters that are worthy of being altered are marked by a '@' symbol, with

a useful range given.

To use these simulations, at the command line switch to the directory where you have placed this folder with the ‘yaml’ config files and run the following steps:

1. Make the computational mesh:

> betse seed ellipse\_small.yaml

2. Perform the initialization:

> betse init ellipse\_small.yaml

3. Plot the initialization (optional):

> betse plot init ellipse\_small.yaml

4. Perform the simulation, which adds Nicotine from the global boundaries:

> betse sim ellipse\_small.yaml

5. Plot the simulation (optional):

> betse plot sim ellipse\_small.yaml

Repeat the above with the different config files.

ellipse\_small.yaml runs the gating-electrodiffusion model on a relatively small number of cells

ellipse\_medium.yaml runs the gating-electrodiffusion model on a relatively small number of cells

ellipse\_large.yaml runs the gating-electrodiffusion model on a relatively small number of cells