**FINAL PROJECT**

ZMB - Summer 2017

**Due date: 2.6.2017**

**Description:**

In this project you will implement your knowledge of network motifs to propose a transcription regulatory network that leads to correct identification of pathogenic cells in a chamber of a microfluidic channel (e.g., a lymph node).

As a starting point, you are given the example file ZMB\_NAR.cece, wherein an exogenous signal is generated within the channel and a cells of a single type detect this signal using the NAR motif.

You are free to build on this file as you like, i.e., be creative!

The following guidelines are provided to assist you, if and when you need assistance.

1. Introduce pathogenic cells. These cells should constitutively secrete a signal into the environment.
2. The topology in the ZMB\_NAR.cece simulation is a straight channel (see the file channel\_straight.svg). Use this topology as your control and create a modified topology to represent the chamber (e.g., see the provided file channel\_chamber.svg).
3. Use the provided files plotCells.m and plotshaded.m to quantify the cell responses in the straight and chamber files. Compare the responses. Your transcription network should maximize the activation difference between the straight and chamber files.

In real life, your parameters would be limited by physical reality. For the purposes of this assignment, you are allowed to use any positive values for the transcription network reaction rates.