Systems Biology course project III (due June 2nd, midnight)

Simulation and analysis of brownian motion and chemotaxis, consistent of 4 parts

**1**. Simulate simple 2D brownian motion of E coli,

**2**. Simulate 2D brownian motion of E coli with constant chemoattractant (A) gradient along x-direction,

1. hypothesize your own chemotaxis actions (chemotaxis force(drift force) f=f(A, ∂A/∂x)
2. compare the "mean displacement" and "mean displacement-square" overtime between "simple brownian motion" with "brownian motion with chemotaxis in x-direction" for 10000 cells

**3**. image processing and tracking of all the cells in the given E coli movie (1.6GB video files) using u-track 2.0 （ <http://www.utsouthwestern.edu/labs/danuser/software/#utrack_anc> ）; and perform data analysis. (If you can use other commercial or freeware, you are more than welcome to try).

1. for the video: 1 pixel=0.65m, 1 frame=0.1 second

**4**. simulate 1000 cells with brownian motion and chemotaxis, while the chemoattrant (not mandatory, additional points)

1. is secreted by each e coli,
2. diffuse with constant diffusion coefficient D, simulate individual molecules
3. degrades with rate constant , simulate individual molecules
4. hypothesize your own chemotaxis actions (chemotaxis force(drift force)

final report: everyone wrote their own, with biological background, hypotheses for simulation and data analysis, comparing your simulation with experiments based on data analysis of both, and discuss it, you can chose to write about the last part(no.4) or not. It doesn't need to be very long.