Final Week Project and Report (2017)

In the final week of COSMOS, we would like you to do a short project and write a report on the Computational Biophysics part. In the report you need to first state and answer the following two questions:

[1.] <u>Programming</u>: In this cluster, you have written programs in both C and python. Which language do you prefer to program in based on your experience to date (C, python, no preference)? Why do you make that choice? How do C and python compare to each other or to another language you may know?

[2.] <u>Biophysics</u>: Explain, in what sense, is the following statement true: 'Everything that animals do, atoms do.'

Complete a miniproject, which could be one of the following, or some other problem of your choice. Talk to one of us if you want to do something different.

- A. Study quantitatively the Gambler's ruin problem.
 - (i) For p=0.5, show that probability of Gambler 1 winning is M1/(M1+M2). Make a suitable plot to illustrate your result
 - (ii) For p=0.5, show that average number of steps to ruin is M1*M2. Make a suitable plot to illustrate your result.
 - (iii) Make a histogram for the number of steps till ruin for a few different values of M1 and M2.
 - (iv) Study the Gambler's ruin problem for p different from 0.5, with M1=M2=M.
 Make a plot of winning probability for Gambler 1 or 2 as a function of p for several different values of M. Allow p to range from 0 to 1. Make the same plot for fixed p as a function of M. Can you guess the dependence on M for large M?
- B. Study the distribution of one and two (and possibly three) dimensional random walks as a function of number of steps:
 - (i) What is the mean and standard deviation of the position of the walker after N steps? Make a plot versus N for different dimensions.
 - (ii) Make a plot of many walks in two or three dimension. Does the resulting shape resemble something?
 - (iii) Make a histogram of the distance traveled after N steps. Show the histogram for several N (say 10, 50, 100, 500, 1000) in one plot.
- C. Study and plot target-finding inside 2D or 3D cells. Analyze how average number of steps to target changes based on varying a single parameter and leaving all other choices the same. For example, you might select a specific shape and size(volume) for the boundary and target and then vary the distance from the start of the random walk to the target. Then graph the average number of steps vs distance from target and draw conclusion. Other single parameters you may consider studying are:
 - (i) size of cell (same shape , different volume),
 - (ii) shape of cell(different shapes, same volume)

- (iii) shape of target,
- (iv) size of target,
- (v) rule used for random walk moves (grid vs angle)) *etc.*.

Remember to vary only one parameter at a time in a study; otherwise, it will be difficult to draw meaningful conclusions.

• D. Random walks on a circular DNA (Finding origin of replication).

Generate a (circular) list of 4,000-10,000 of random DNA base pairs ('A','T','G','C'). Insert a new "primer" string of DNA: 'AAAAAAAAA' into the list above at a random location. This will repesent the origin of replication or the point at which DNA cloning will start. Investigate the best strategy (minimum nmber of steps) for the DNA polymerase to find the origin of replication in the larger DNA string. Possible strategies include (a) single step walks starting from random location or (b) walks with steps of arbitrary length (randomly jumping around list)or (c) some combination of a and b (your choice). Be careful with indexes so you don't overrun the start or end of the DNA string.

Present a brief writeup on your project, with suitable figures and conclusions. Attach your program to the project report and explain key lines of the code. Use graphs to make your report and conclusion visually compelling.