APh161: Physical Biology of the Cell
Homework 2
Due Date: Thursday, January 19, 2005

"An ounce of application is worth a ton of abstraction." – Booker T. Washington

1. More on the Size of Things

(a) Estimate the number of protein units that make up a viral capsid for influenza virus. In addition, estimate the number of lipid molecules associated with one of these viruses. The lipid molecules surround the protein coat in lipid bilayer form. Make sure you show a picture of the virus and give a rough description of what the structure is like - where is the nucleic acid, what is the shape, etc..

(b) Give a little story about the life style of *Dictyostelium* when it is starved and try to estimate the number of cells associated with the fruiting body. You will find it useful to look at the little article by Bonner that is on the website in association with HW2. The bottom line is that a) I want you to explain a bit about what happens when these cells are starved and then b) make a sensible estimate of the number of cells associated with the collective they form.

(c) Use the video entitled "15.1-cell_compartments.mov" from *Essential Cell Biology* to estimate the size of the vesicles associated with the Golgi and their density (i.e. how many of them are there per cubic micron). Later on we will use these numbers to try and get a sense of the energy cost associated with vesicle budding.

2. A Feeling for the Numbers: The Rates of Things

In the previous homework, we worked hard to get a sense for the physical sizes of various biological entities. Another interesting angle on all of this is to try and get a feel for the *rates* at which things happen. Following in the tradition of the previous problems, here you will try to make some estimates of the rates of some processes. Much of what you will do in this problem I

have already done partially in class - your job is to make it your own now.

(a) Consider the division of an *E. coli* cell. Think of such a cell during rapid growth phase where the cell is dividing roughly once every 20 minutes. Make estimates of the number of water molecules being taken on board per second during this phase, the number of lipid molecules that are being added onto the surface membranes, the number of proteins being synthesized per second and how many ribosomes are needed to do so.

(b) In this case, think about the motility of the bacterium *Listeria monocytogenes* and a typical eukaryotic cell. In the case of *Listeria*, the motion of the bacterium is mediated by the formation of actin comet tails which depend in turn upon the linear polymerization of actin filaments. The formation of the actin comet results in a speed for the bacterium of something around 0.1 μm/sec. In the eukaryotic setting, the cell extends arms called filopodia which permit it to crawl, again by virtue of actin polymerization. For *Listeria*, use the measured rate of motion of the bacterium to *estimate* the rate of actin polymerization both in microns/sec and monomers/sec. Make sure you draw a picture of the process and explain your rationale. Now, take that estimate for the rate of actin polymerization and estimate the rate at which a filopodium extends on a eukaryotic cell. Anything you can do to compare these estimates with measurements would be useful - one excellent source is **Cell Movements** by Dennis Bray.

(c) Look at fig. 6-9 of *Essential Cell Biology* and assuming that this is a representative sample of the replication process, estimate the number of DNA polymerase molecules in a eukaryotic cell like this one from the fly. Note that the fly DNA is about 1.8×10^9 nucleotide pairs in size. Estimate the fraction of the total fly DNA shown in the micrograph. There are eight forks in the micrograph, numbered 1-8. Estimate the lengths of the DNA strands between replication forks 4 and 5 where we count the forks from left to right. If a replication fork moves at a speed of 100 nucleotides/s, how long will it take for forks 4 and 5 to collide. Also, given the mean spacing of the bubbles, estimate how long it will take to replicate the entire fly genome.

3. Biological Sequences

One of the important classes of data that have catapulted biology forward is biological sequence information. In particular, the sequences of genomes (i.e. the string of letters A, T, G, C) and the sequences of proteins (i.e. the linear arrangement of amino acids that make the protein) have made it possible to reason about the evolutionary and functional relationships of molecules from different organisms. In this problem, you will do a combination of estimates and computer exercises.

(a) Make an estimate of the total number of bacteriophage that have existed on Earth since the beginning of life. Don't worry, no one really knows, but even if you are good to within a factor of 10^6 it will still be useful. Now, given that the length of the lambda phage genome is roughly 50kbp, estimate how many different possible sequences we could make out of a genome that is 50kbp long. Finally, estimate the fraction of all possible genomes that all of the bacteriophage that have ever existed could explore if every one of those phage had a completely new sequence (a silly idea, but let's run with it for a moment)? Compare this to the total number of possible phage sequences with a length of 50kbp.

(b) A friend of mine and I were chatting about mechanisms of evolution. He told me that he had estimated the total number of cell divisions in the history of life. I haven't tried this yet, but let's have a go at it. Try to estimate the total number of cell divisions. Above all, be clear about what assumptions you have made in order to make such an estimate. Note that the reason for thinking about this is that these cell divisions are the raw material of evolution and we want to get a sense of the numbers.

(c) Please go through the bioinformatics tutorial on the HW2 part of the course website. Make sure to carry out all of the operations expected of you there.