This problem set is in a way a “final” review of everything we have done in the course. My aim is to get you to review all the different topics we have covered and to bring them together as a full toolkit for examining important and exciting biological problems.

1. Your Turn to Teach 161

RP: all answers to this problem must be submitted electronically to the TAs and me in pdf form.

Some have argued that only by quantitation will we really be able to come to terms with the complexity of living organisms, with the quantitative approach advocated in this class meant to give you a feel for how such quantitative dissection of biological problems might work. Others have argued that the approach we have taken is a mopping up operation which amounts to dotting the "i"s and crossing the "t"s already worked out by biologists. Write one paragraph defending each of these two points of view. One document you might find interesting to look at is “Bio2010” from the National Academy of Sciences.

Next, make a syllabus for the course. Start with one brief paragraph on the mission of your course. Issues that you might want to consider include: is it important to do hard calculations, or is that the province of other physics courses and our goal here is to illustrate the style of thinking? Are estimates a part of the way you will present the material (if yes, why, if no, why not?). How will you organize the material - note that in typical biology books DNA and actin would never be in the same chapter but for PBoC they are both in chap. 10 as examples of ”beam theory”. The course is only 10 weeks long. What will you cover, what will you skip and why? How will you balance the desire to cover more topics with the resulting superficiality? This is not a look up something in Wikipedia question, nor is it a request to regurgitate
what I did in the course. It is asking you how to organize a new and un-
finished topic and to present it to advanced Caltech undergrads and to grad
students at the beginning of their grad careers. What are the important
points? Give a syllabus - state what topics you will consider each week in
your lectures and why.

2. Cytoskeletal Length Control.

In class we discussed the ways in which cytoskeletal filaments are tuned.
Work out problem 15.7 from PBOC2. Then, as a new part to the problem
now that you figured out the rate at which filament monomers are lost from
the end, imitate what we did in class and work out a master equation for
this problem. Then, using the same kind of strategy described several times
in class, work out the steady-state probability distribution.

3. Turing Instability Revisited.

In this problem, you are going to work out the Turing instability for a
one-dimensional array of cells in two different ways. First, carry out the
derivations shown in eqns. 20.39-20.45 for yourself. Make sure you explain
all of the mathematical steps and what they mean and then make your own
version of the plot in Figure 20.12(B). Once you have done this, repeat the
examination of the same problem by solving problem 20.5 in PBOC2.

4. Biological Fidelity.

(a) Work out problem 21.10 in PBOC2. However, when doing part (B),
make sure you work out the entire probability distribution for finding 0 in-
correct amino acids incorporated in the protein, 1 incorrect amino acid incor-
porated in the protein, 2 incorrect amino acids incorporated in the protein,
etc. That is, I want $p(n)$, where $n$ is the number of incorrect amino acids
in the protein. Hint: Begin by writing a binomial distribution for having $n$
mistakes in a protein of length $N$. Then, using that the probability of a mis-
take is very small (i.e. $p_{\text{mistake}} = 10^{-4}$), derive the corresponding distribution.

(b) Read section 21.5.1 up until eqn. 21.62. The point of this section
is to illustrate that thermodynamic discrimination by itself is insufficient to
explain translational fidelity. Give a cogent derivation (all words included explaining your logic) of eqn. 21.61 and make your own version of figure 21.36. Make sure to explain what the figure is demonstrating and what you think it means about translational fidelity.