1) Final project progress
Please write an outline of the calculations or simulations you will do for your final project. You can approach this as an exercise in writing a problem set: break your project into discrete pieces and frame the question for each in a form that can be answered by a calculation or simulation.

2) Action potential propagation

In the last homework you developed a simple conductance-based neuron model:

$$C\frac{dV}{dt} + g_{Na}m_\infty(V)(V - E_{Na}) + g_K n(V, t)(V - E_K) = I$$
$$\frac{dn}{dt} = \frac{n_\infty(V) - n}{\tau(V)}$$

In this problem you will extend the model to include conduction between cells. In the heart, cardiomyocytes couple to each other through electrical gap junctions (connexins). A current will flow between neighboring cells whose membrane voltages differ. The voltage equation then becomes:

$$C\frac{dV}{dt} + g_{Na}m_\infty(V)(V - E_{Na}) + g_K n(V, t)(V - E_K) = I + g_{cxn}l^2\nabla^2 V$$

where g_{cxn} is the conductance of the connexin channels, and l is the length scale of an individual cell. In discrete space in 1 dimension, i.e. where we treat each cell as a unit, the equation becomes:

$$C\frac{dV_i}{dt} + g_{Na}m_\infty(V_i)(V_i - E_{Na}) + g_K n_i(V_i, t)(V_i - E_K) = I_i + g_{cxn}(V_{i+1} + V_{i-1} - 2V_i)$$

Here i is the index of the cell. At the left edge, the Laplacian becomes just $V_2 - V_1$ and at the right edge, the Laplacian becomes $V_{end-1} - V_{end}$.

A) Adjust your HHmodel equation so that it can take a vector for V and for n, and add a gap junction term which couples the current from each cell to its neighbors, as above. Let there be an external current I_{inj} injected into cell 1.
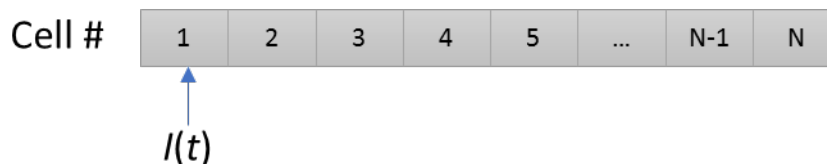
Let's add a gCxn term to the set of parameters. The function header then becomes:

```
Function [dvdt, dndt] = HHmodel(V, n, params);
% V is the membrane voltage
% n is the gating variable on a Kv channel
% params is a vector containing:
```

```
% [membrane capacitance (F), gNa (S), ENa (V), VNaHalf (V),
% qNa (dimensionless), gK (S), EK (V), VKHalf (V),
% qK (dimensionless), tau(V = VKHalf), gCxn (S), I (Amps)]
```

B) Adjust your HHwrapper equation to accept a time-dependent current. The easiest way to do this is to change it as below. Here iTimes are a set of times where the current is specified, and iVals are the corresponding values. The first and last values of iTimes should be the start and stop times of the interval used in ode45. The wrapper uses linear interpolation ('interp1') to infer the injected current at other times.

```
function out = HHwrapper(t, y, params, iTimes, iVals);
% function out = HHwrapper(t, y, params, iTimes, iVals);
%
% wrapper function for HHmodel that concatenates the outputs into a single
% vector.  Useful for evaluating with ode solvers.
%
% params is a vector containing:
% [membrane capacitance (F), gNa (S), ENa (V), VNaHalf (V),
% qNa (dimensionless), gK (S), EK (V), VKHalf (V),
% qK (dimensionless), tau(V = VKHalf), gCxn (S)]
%
% NOTE: params does not contain Iinj--this parameter is extracted from the
% time-dependent current
%
% y is a vector whose elements 1:nCells are the voltages in each cell, and
% whose elements (nCells+1):end are the n variables in each cell.

nCells = length(y)/2;

V = y(1:nCells);
n = y((nCells+1):end);
iInj = interp1(iTimes, iVals, t);
params = [params, iInj];

[dvdt, dndt] = HHmodel(V, n, params);
out = [dvdt; dndt];
```
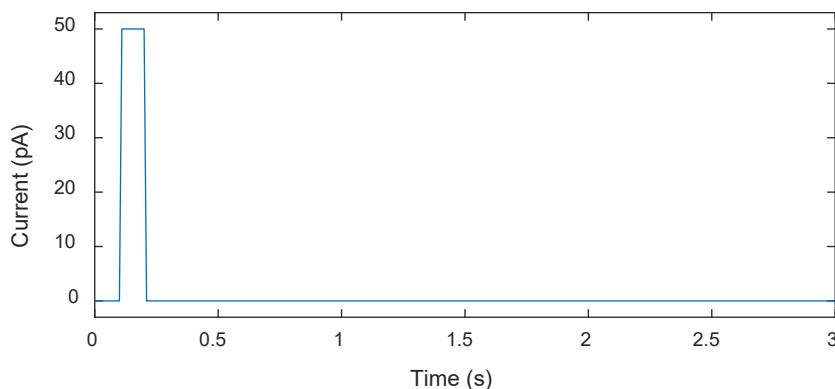
C) Test your system with a current pulse of magnitude 50 pA from 0.1 to 0.2 s, i.e.:

Consider a chain of 50 cells. A good starting value for the connexin conductance is g_{cxn} = 2.1 nS. Use the function ode45 to solve for V(x,t) and n(x,t) on t in [0, 3 seconds] using the parameters from last week. See if you find parameters that lead to a propagating wave.

Here is an example solution, where the injected current is shown in black:
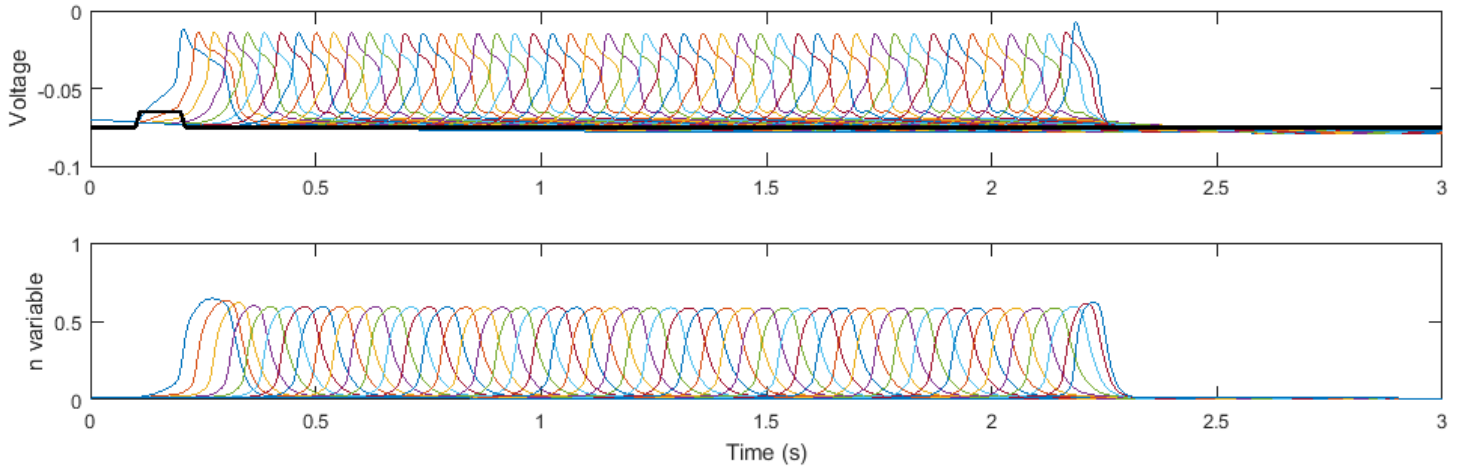
3) Radius of gyration of a polymer
In class we calculated the root-mean-square *end-to-end* distance for a freely jointed chain polymer. Calculate the root-mean-square distance of one of the ends from the *center of mass* (assume a 3-D FJC with N steps of length b), i.e. $\langle(\mathbf{r}_{end} - \mathbf{r}_{cm})^2\rangle^{1/2}$, where the average is over all conformations of the polymer.
Just fyi, the root-mean-square distance of any point on the polymer from the center of mass is called the radius of gyration, i.e. $r_g = \left[\frac{1}{N}\sum_{i=1}^{N}\langle(\mathbf{r}_i - \mathbf{r}_{cm})^2\rangle\right]^{1/2}$.

4) Phillips problem 8.10 or 8.11 (depending on you version).
DNA subjected to a stretching force exceeding 60 pN undergoes a structural transition from the usual B form to the so-called S form ("S" for stretch). Here we examine a simple model of this transition based on the freely joined chain (FJC) model of DNA and compare it with experimental data.
   a) Consider the FJC model in one dimension. Each link of the polymer points in the +x or the -x direction. There is a force f in the +x direction applied at one of the ends. To account for the B to S transition we assume that thinks are of length b (B state) or a (S state), with a > b. Furthermore, there is an energy penalty ε of transforming the link from a B state to an S state. (This is the energy, presumably, for unstacking the base pairs.) Write down the expressions for the total energy and the Boltzmann factor for each of the four states of a single link.
   b) Compute the average end-to-end distance for one link. The average end-to-end distance for a chain of N links is N times as large.
   c) Plot the average end-to-end distance normalized by Nb (that is, the relative extension) as a function of force using the numbers appropriate for DNA: b = 100 nm, a = 190 nm. To estimate ε take the *energy per base pair* for transforming B-DNA to S-DNA to be 5 k_BT (the length of one base pair is approximately 1/3 nm for B DNA). How does your plot compare to the data posted on the website?

5) Persistence lengths
This problem will require you to do some research on the Internet or in a library. Give the bending moduli and room temperature persistence lengths of some common materials (you should only have to look up one property; calculate the other).
Double stranded DNA
Actin filament
Microtubule
Pencil
For the pencil, use a Young's modulus for wood of 13 GPa, and a radius of 3 mm. The bending modulus of a solid rod is given by $\kappa = E_m I$, where E_m is the Young's modulus and I is the moment area of inertia, given by $I = \frac{\pi r^4}{4}$ for a solid cylindrical rod.