G proteins
1. Use the given sequences for GNAT 1, 2 and 3 and GNAI 1, 2, and 3 to make a phylogeny. The outgroup is the Arabidopsis GNAT sequence. What does this phylogeny tell you about the evolution of the alpha subunits of these G proteins? Within any given G protein, are the sequences related as you expect? What series of gene duplications would explain this tree?

2. Make a bootstrap distance tree for the alpha subunit of the G proteins in problem 1:
   a. Use clustalw-multialign to align the sequences.
   b. Send the results to protdist
   c. On the input Protdist page, scroll down to the Bootstrap options box. Click the “Perform a bootstrap before analysis” box and enter a “Random number seed” in the input box. Leave the number of replicates at 100. RUN.
   d. A new window will open. It may take a while for this to run – you can “Update job status” from time to time to see if it has finished. (You may get some emails with regards your job status – note this took 15 minutes when I did it).
   e. Send the results to neighbor to make the bootstrap tree. Go down to Bootstrap options. Select “Analyze multiple data sets” Tell it how many data sets (the number of replicates from above = 100) and the random number seed. (I don’t know if this has to be the same number as before. Click “Compute a consensus tree” and tell it to RUN.
   f. Save the consensus output tree and view it in FigTree. Remember to reroot it with Arabidopsis as the outgroup. What deep node has low bootstrap support? Extra credit: Look at the consense.outfile and see what other groupings occur at this node, a large fraction of the time.

3. For the GNAT genes, what is the function of each of these genes? What cell types do they function in? (Use OMIM if necessary). What is known about the GNAI genes?

4. Use the Human map viewer, to find one of the genes. (Enter its official name (e.g. GNAT1) in the “Search for” box. The map viewer is located at:
   a. Why are there so many hits for just one gene?
   b. Click on the chromosome number to see the expanded view of the chromosome. Scroll all the way to the right to find the gene names and a bunch of links. What are all the links beside the gene name? (OMIM, HGNC, sv etc)?
   c. Find the chromosomal location of each of the six genes from question 1. Note the chromosome #, arm and approximate location for each gene (perhaps in thousands of bp). For example GNAI2 is located at 3p21 at 50.5 M bases. What does this tell you about how these genes arose?