

Laboratory Worksheet, Monday, Oct. 3.

I. Familiarity With Web Resources. Go to the NCBI. I want you to download Cn3D, a structure viewer available free from the NCBI. To do this, look up PDB number 1U19 in the structure section of NCBI. This will be a crystal structure of bovine rhodopsin, one of the proteins we had considered earlier. If you have your laptop, you can download Cn3D 4.1 from the records page you will get with the answer to your query. For now let us just look at the structure which is presented. I will show you a few of the adjustable features. For now, answer the following simple questions from the pictures. How many trans-membrane helices does bovine rhodopsin have? What portion of bovine rhodopsin are you looking at? (I.e., is it a monomer or a multimer of some degree?) For a non-membrane protein which is old and well-studied, look up either a cytochrome-c or myoglobin. We will look at cytochrome-c again next week as an exercise when we get p-values available for alignment!

II. Background to an Exercise. There are simple but illustrative calculations behind a paper of Karlin and Mrázek on predicting highly expressed genes. The paper is available from the 548 resource directory, where it is listed under KMjbac.pdf. You should begin having a look at this paper, especially the first two or three pages.

You were supposed to look at this paper and begin outlining what it would take to program the calculations in this paper. We will go over the introduction to the paper and these outlines today.

III. Perl. We will begin the tutorial this afternoon. You don't have to stay around for this if you already know Perl, or if you will use another language to do your projects. You will have to state which language. The presentation will be more just helping people work through the tutorial. NOTE: if you use another language, we cannot guarantee that your papers will be corrected substantially, i.e., there will only be one test for the work: does it run or not!