Genomics and Bioinformatics Final project

Pick one of the topics below and write a paper of approximately eight pages in length (double spaced). Carefully cite your references at the end of the paper (not included in the 8 pages). Please submit an electronic version of your project on the Classes2 server (http://classes2.yale.edu) on or before the due date listed below. No hard copy needs to be turned in. Your project will be put on our public website after grading (http://www.gersteinlab.org/courses/452/).

Topics:
1)   Synteny mapping seeks an alignment of entire chromosomes or genomes across species. Write a research proposal focused on the problems of creating these maps. What differentiates the creation of syntenic alignments from other sequence alignment algorithms, such as Needleman-Wunsch or FASTA? What technique would you use to create a synteny map between two species?

2)   As covered in class, structural alignments are less straightforward than sequence alignments. Write a research proposal dealing with aligning the structures of two macromolecules. Assuming that both structures are known, what issues arise in creating the alignment? Is it possible to produce a verifiably "best" alignment? What technique would you use to align two macromolecules? Why did you choose this method over the others?

3)   If you have another topic that you would like to write about or if you would like to write a program in lieu of a paper, please talk with Mark Gerstein and the TA's before Wednesday, Dec. 6. Programs may be based on the topics above or other areas of bioinformatics. If writing a program, please submit source code and a brief (approximately one page) write-up explaining: the task your program is used for, the algorithm you implemented, and instructions for compiling and using the program.

Due Date:
All projects must be submitted by noon on Wednesday, Dec. 13.