CIS 454 (Undergraduates)

Use the Web or conference proceedings or journals to find information about a current bioinformatics project. It could be an academic project, or a project at a government or industry research lab. Write a 5 to 10 page paper that addresses issues such as

- the goals of the project
- the state of the project (e.g. is it completely finished, in its early stages, ...)
- why did the members of the group decide to use a computational approach, i.e. what benefits do they expect from using computational methods instead of purely theoretical or experimental methods?

Most importantly, explain how the project relates to topics we've discussed in class this term, e.g.

- how are they using databases?
- are they using scripts to automate large scale analyses?
- what bioinformatics methods are they using? BLAST? phylogenetic inference? structural or functional predictions?
- are they developing any new techniques? why?

The above list is not complete -- feel free to bring in other topics presented in lectures. It is probably not possible to get information on all these topics, but be sure to try to address two or three of these issues at least.

CIS 554 (Graduate Students)

The writing assignment for graduate students is more research-oriented. Pick a topic area, read two or three research papers related to your topic, and write a 10 page paper that

- introduces the subject area
- explains some of the important problems in this area
- describes briefly how each paper you read proposes a solution to one or more of the problems

Here are some suggestions for topics. If you want to write on a topic that is not listed here, send me e-mail with a list of papers you want to read.
Databases for Bioinformatics

Summarize issues in representing and retrieving biological information. Describe some current approaches, e.g. issues with using relational databases or reasons why others prefer object databases, and report on one or more projects that are exploring new databases or organizations.

Genome Assembly

A hot topic in bioinformatics is sequence assembly, especially for the “next generation” sequencing technology that works with very short reads. What are the new systems introduced in the last couple years? What challenges do they pose for sequence assembly algorithms?

Visualization

What sorts of new data visualization techniques are being developed for bioinformatics? For what types of information are they suitable? Do methods developed for physics, engineering, or other areas apply here?

Application Area

Give a brief introduction to a research area where computational methods are being used, a description of the methods, and a survey of some important applications. What seem to be the important unsolved problems in this area?