Computational Molecular Biology and Genomics 02-711/03-711/15-856
**Assignment** 3: Metagenomics Due November 15th

Articles:

- *Metagenomics for studying unculturable microorganisms: cutting the Gordian knot.* Schloss PD, Handelsman J. Genome Biol. 2005;6(8):229
- *Get the most out of your metagenome: computational analysis of environmental sequence data.* Raes J, Foerstner KU, Bork P. Curr Opin Microbiol. 2007 Oct;10(5):490-8.

Read these commentaries and briefly answer the following questions ***in your own words***:

1. Studies of cultured organisms in the laboratory focus on complete characterization of the sequence and functional repertoire of a single species. Metagenomics, in contrast, provides partial information about many species. What information can be obtained from metagenomic analysis that cannot be obtained from laboratory studies? What information can be obtained from studies of cultured microorganisms that would be hard to obtain from metagenomic analysis?

2. How does the microbial diversity of the sample influence the analysis of metagenomic sequence data. What are two methods used to assess species composition of a sample?

3. What are the dangers of analyzing metagenomic data using database comparison?

4. An early metagenomic study of waste water from an iron mine sampled proteins, as well DNA, from the acidic drainage water. What was the advantage of using a combined analysis of protein and DNA samples?

5. What is comparative metagenomics? What is the benefit of the comparative approach?

6. How can differences in effective genome size influence functional analysis of metagenomic data?

*7.* Why, according to Raes *et al.* , is a metagenomics data analysis standard is needed?