New course description
BMB 497 Functional Genomics, Spring 2012 **3.0 credits**

What is it in your DNA that makes you different from chimpanzees, mice or flies? What sequences in your DNA make it more or less likely that you will develop diabetes or cancer?

These are questions of widespread interest, answers to which could play a major role in personalized medicine and in our understanding of our place in the biosphere. Modern genomic analysis is bringing great insights to their pursuit, with occasionally some very exciting answers. One hallmark of contemporary genomic research is that data are released rapidly along with tools for browsing and analyzing it. Thus not only can you learn the major results by reading papers, but you can examine the underlying data and do your own analyses. Discovery is not longer the exclusive domain of the data producers – you can join in!

The goal of this course is to introduce students to some of the ongoing research aimed at identifying functional regions in genomes and to encourage them to use web-based bioinformatics tools for exploring the databases of genomic and epigenetic data. Students will be expected to develop creative projects that address issues in functional genomics of high interest to them. The objective of each project will be determined mainly by the student's interest; it can be research or educational. The medium used to convey the results of the student's work will be chosen by the student in consultation with the instructor. Employing traditional media such as term papers or oral presentations is fine, and creative and effective use of novel media (video, music, dance, etc.) is encouraged.

Topics that are planned include:

1. Finding protein-coding genes within genomes: How many are there? How are they distributed along chromosomes? How do you find out what function they have?

2. Finding genes that do not code for proteins: How much of the genome is transcribed? Do they produce stable noncoding RNAs? What roles do they play in the cell (regulatory and enzymatic)?

3. Finding evolutionary signatures of function: Do protein-coding genes account for all or most of the functional sequences? How can you use genome comparisons between species to estimate the amount of functional sequence – and to identify it? This non-coding DNA inferred to be functional can be considered "dark matter" of the genome.

4. Finding non-genic functional sequences: How can we illuminate the dark matter? How do you use high throughput genomics to find DNA sequences likely to be involved in gene regulation? This section will emphasize genomic approaches to mapping epigenetic features associated with gene regulation, such as histone modifications, DNase hypersensitive sites, and transcription factor occupancy. Again students will be encouraged to examine and analyze these data according to their interests.

5. Finding function by phenotype: Genetic association studies are currently identifying with high precision and statistical support loci that contribute to complex traits, such as disease susceptibility. How can you find these results easily? How can you use the data and insights from the earlier topics to develop testable hypotheses about how variation among humans at these loci lead to increased susceptibility to disease?