

Special Topics Course, Spring semester 2008.

## **Comparative Genomics: Illuminating the dark matter of genomes**

BMB 497B                      Tuesday and Thursday, from 4:15pm to 5:30pm, 106 Wartik Lab  
3 credits

Course index 961342

Course web site: <http://www.bx.psu.edu/~ross/ComparGeno/>

Instructor: Ross Hardison

[rch8@psu.edu](mailto:rch8@psu.edu)

304 Wartik Lab

814-863-0113

Just as we cannot see most of the matter in the universe (it is “dark”), we currently know little or nothing about the function of most of the DNA in complex genomes. A full understanding of the functional regions of even the smallest, simplest genomes eludes us. Distinguishing functional from “neutral” DNA is a major contemporary challenge for those studying any species with a complex genome, including fungi, plants invertebrates and vertebrates. The challenge becomes more difficult as the genome size increases largely by expansion of presumably neutral DNA. In fact, we estimate that roughly only 5% of the human genome is engaged in functions common to many mammals. The major methodology for distinguishing functional from neutral DNA is to compare genome sequences among species and apply the principles of molecular evolutionary genetics to predict regions under negative (purifying) selection or positive selection (i.e. undergoing adaptive evolution). Those sequences subject to selection are deduced to be functional. In addition, new technologies are enabling high-throughput functional assays to be run genome-wide. We will also examine these approaches in concert with the comparative genomics.

This course is intended to introduce students to the goals, principles, and methods of comparative genomics, and use this information for cutting-edge exploration of functional regions of genomes. It is appropriate for upper-level undergraduates and graduate students. Students should have knowledge of molecular and cell biology and genetics, and not be reluctant to talk in class. Computer programming skills are not required, but can be used in projects.

Readings are posted on the course web site. They will consist of some survey chapters and articles on comparative genomics, plus more in-depth articles from the primary literature.

The students will be graded on class participation and two projects, which can range from summaries of current knowledge, to new research results, to new methods of presenting material.

I hope this course will also serve as a forum to explore new approaches to self- and group-learning. I am convinced that using class time only for lectures and evaluation by multiple-choice tests are not the most effective means of teaching. I expect that they will not even be supported in any course within a few years. However, I doubt that I have the most creative ideas for alternative ways to conduct classes. Thus I invite and encourage students to come up with ideas for effective interactions during the classroom time. One option for the projects is to develop creative and engaging media for learning comparative genomics. My hope is that the YouTube generation will inspire some methods that take us far beyond PowerPoint. The class size has been limited to 24 for this initial offering to facilitate the interactions.