

GBS 787 - Special Topics (Computational Genomics) – CRN 43201

Purpose:

The purpose of this course is to provide an introduction to main problems in Computational Genomics. Specifically, the participants are exposed to practical use of standard web available resources and tools for the analysis and comparison of genome sequences. A successful participation includes the development of a project that will result in the implementation of computational tools and/or pipelines for large-scale studies in Computational Genomics. 2.00 Credit hours

Instructor: Malay Basu, PhD

Levels: Graduate

Schedule Types: Lecture and Hands-on lab

Type: Class

Time: 10:00 a.m. – 1:00 p.m.

Days: Mondays, Tuesdays, Thursdays and Fridays

Where: TBA

Date Range: March 7, through April 7, 2014

Graduate Biomedical Sciences (GBS 787) Program and Pathology (PAT 728)

Course Attributes:

Tuition Joint Health Science

Rationale and history:

More efficient high-throughput sequencing techniques are exponentially expanding the knowledge about genomic sequences. Computational analyses of such massive genomic data are fundamental aspects of new biological discovery. The course will summarize recent findings in the field of computational biology and genome analysis focusing on the rationale behind the implementation of the methods that enabled the most significant breakthroughs. In the “Big Data” era a solid training in the computational analysis of experimental molecular biology data will be key for the delivering of high quality research in biomedical sciences.

Organization:

This course is organized as a hands-on training for graduate students, faculty and computational staff. A limited number of slots are made available for Pathology residents, fellows and graduate students with research interests in understanding and analysis of genomic data.

In the first part of the course an introduction about the computational skills required to perform basic tasks of sequence analysis will be provided. The course will mainly focus on the study of genomic sequence data. The attention will be focused on the algorithms for the prediction of the sequence data handling, similarity search, variation detection, with special emphasis on comparative genomics using Next-generation sequence data. Further details and information about the course and the lectures will be made available at <http://cmb.path.uab.edu/training>.

Evaluation:

Evaluation is based on class participation and project development. The attendees are required to orally present their implemented projects at the end of the course.

Additional Information:

- Cap class at 15 students
- Lecture Course
- Interview with course master before accepted in class
- Grading: letter grade
- Cross link PATH course with GBS and open to all 8 themes.
- Must drop class within first week