



Initiative for Bioinformatics & Evolutionary Studies

Fall 2009 Seminar Series (BCB 501)

What to do with “next generation” sequencer data

The Initiative for Bioinformatics and Evolutionary Studies (IBEST) presents an interdisciplinary seminar series on the challenges of using 'next generation' DNA sequencing technology to address a broad range of biological questions. Sequencers such as the IBEST Roche 454/FLX can sequence a genome a day, or take a complete inventory of species in a micro habitat. But what does one do with such mountains of data? We will hear practical advice from practitioners who have dealt with that problem “on the ground”.

The talks are intended for students and scientists from a broad range of backgrounds, and are open to the academic public.

Where: TLC 044

Time: 12.30-1.20, Friday afternoons

Open: Open to university and general public

Credit: 1 cr (P/F) as BCB 501, Students will be required to prepare written evaluations of speakers and occasionally to read an assigned paper in preparation for the seminar. Additional classes may be required.

Coordinators: James A. Foster and Larry J. Forney, Professors of Biological Sciences and BCB

Funded by NIH NCRR P20RR16448 and IBEST

Date	Who	Topic (titles TBA)
28 Aug	Suresh Iyer, Bioinformatics Scientist, IBEST, U. Idaho	Intro to 454/FLX services at UI
4 Sept	James A. Foster, Prof., Biological Sciences, IBEST, U. Idaho	The data flood: we need a bigger boat
11 Sept	Jason Stajich, Asst. Prof., Plant Pathology and Microbiology, UC Riverside	Comparing genomes
25 Sept	Victor Kunin, Project Scientist, DOE Joint Genome Institute	Next generation bioinformatics
9 Oct	Pawel Gajer, Research scientist, Institute for Genome Sciences, UMD	Next generation statistics
23 Oct	David Rasko, Asst. Prof, Microbiology & Immunology, UMD	Comparative bacterial genomics
6 Nov	Matt Settles, Bioinformatics Scientist, IBEST, U Idaho	Analyzing expression data
20 Nov	John Bunge, Assoc. Prof., Statistical Sciences, Cornell U.	Assessing microbial diversity
4 Dec	Alan Lemmon, Asst. Prof., Florida State U.	Transcriptome analysis of 454 data