Introduction to Bioinformatics for Metagenomic Microbiome Analysis

Instructor: Dr. Benjamin Tully, C-DEBI Bioinformatic Specialist

Where? The University of Southern California
When? June 21-22, 2018
Why? Detailed insight into the microbiome of a system can shape our understanding of it, but the learning curve for incorporating computationally intensive tools can be very high!
Cost? NOTHING! All expenses are covered courtesy of the NSF STCs C-DEBI, EBICS, and BEACON

TOPICS

- Unix command line
- Illumina sequence quality control
- Metagenomic experimental design
- Sequence Assembly
- Metagenomic binning
- Functional Annotation
- Phylogenetic analysis

Requires laptop with 40GB of hard drive space
15 participants maximum
All levels welcome

To apply: Email tully.bj@gmail.com by May 28th - be sure to include your home institution, your home STC, and what you hope to get out of the workshop