

Traditional single gene phylogenetics can establish evolutionary relationship among closely related organisms, relatively easily. However, they suffer from several drawbacks. Large scale, whole genome phylogenomics can provide much more insights about the evolutionary relationship and are preferred due to availability of whole genome sequences for large number of organisms. These large scale analyses requires huge amounts of computational power as well as UNIX skills to manipulate data.

This workshop will provide a workflow for such large scale phylogenomic analyses on High Performance Computing nodes. We will provide a logical workflow, starting from downloading the whole genomes, identifying the orthologs, multiple sequence alignments, trimming and merging alignments, and constructing Maximum Likelihood Bayesian phylogenetic tree.

This workshop requires users to be familiar with UNIX. The intended audience for this workshop is faculty, staff and students who are already familiar with the theory and concepts of phylogenetics but want to use the computational resources of Bioinformatics Core and RCAC servers for their analyses.

Some references and suggested reading:

Delsuc F, Brinkmann H, and Philippe H. 2005. Phylogenomics and the reconstruction of the tree of life. *Nat Rev Genet* 6:361-375

Fischer S, Brunk BP, Chen F, Gao X, Harb OS, Iodice JB, Shanmugam D, Roos DS, and Stoeckert CJ, Jr. 2011. Using OrthoMCL to assign proteins to OrthoMCL-DB groups or to cluster proteomes into new ortholog groups. *Curr Protoc Bioinformatics* Chapter 6:Unit 6 12 11-19.

## Bioinformatics Core Phylogenomics Workshop

**(Registration required)**

**Friday, November 8, 2013**

**9:00 AM to 3:00 PM**

**Nelson (Phillip E.) Hall of Food Science  
 (NLSN) 1195**

### Purdue University

**Contact for details: [bioinformatics@purdue.edu](mailto:bioinformatics@purdue.edu)**

Please register by 5 PM on Wednesday, Nov 6, 2013 by sending an email to [bioinformatics@purdue.edu](mailto:bioinformatics@purdue.edu) with the following information:

Name and email (only @purdue.edu will be accepted):

Advisor's Name:

Familiarity with UNIX: Basic/Intermediate/Advanced



