Computational Approaches for Linking Comparative Genomics to Biochemistry and Evolution

Standard bioinformatics pipelines for comparative genomic data analysis typically include steps like multiple sequence alignment, phylogenetic tree reconstruction, calculation of the ratio of rates of nonsynonymous to synonymous nucleotide substitution (dN/dS), and gene tree-species tree reconciliation. Models for amino acid substitution used in these processes assume that each site evolves independently according to average properties in the absence of a protein structural or functional context. Models for duplicate gene retention assume that the process is evolutionarily neutral and do not consider functional or mechanistic underpinnings. A model for duplicate gene retention that would allow for mechanistic differentiation between nonfunctionalization, neofunctionalization, subfunctionalization, and dosage balance based upon differences in expected time-dependent retention profiles is presented. Two characterizations of amino acid substitution are also presented. One approach extends a population genetic model to inter-specific genomic data and a second approach evaluates the effects of selection for protein folding and protein-protein interaction on sequence evolution. These approaches reflect an in progress strategy for increasing biochemical and evolutionary realism in bioinformatics.

David’s research interests are in understanding the mechanism of the evolution of new functionality in genomes and how this correlates with the phenotypic divergence of species.

Detecting and collating important genomic events involves methods development, both at the DNA and protein sequence levels using model-based approaches, at protein structural levels, and at systems network levels. David’s research group is modelling the evolution of proteins to see how well their models explain observed genomic data.

To read more on David’s research, visit http://www.wyomingbioinformatics.org/LiberlesGroup/

When: Monday 7th, May, 2012
Where: Benham Lecture Theatre
Time: 4pm for 4:10 start - 5pm.

All Welcome