

WORKSHOP

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“Comparative Genomics using CoGe”

CoGe is a web-based software system designed to allow researchers an easier alternative for finding and comparing genomes and genomic regions of interest within and across all domains of life. Using CoGe, many patterns in the evolution of genomes may be characterized including synteny, whole genome duplication events, fractionation, gene deletion events, local gene duplications, inversions, translocations, mis-annotations, and conserved noncoding sequence. In addition, CoGe can help researchers better understand the evolutionary relationships among homologous genes (orthologs, paralogs, out-paralogs, horizontal gene transfer events) for which whole genome sequence is available. This informal workshop will provide an overview of the types of research questions CoGe can help answer, how its interconnected tools provide an open-ended analysis pipeline allowing researchers to explore their own questions and hypotheses, and focus on using CoGe "live" to identify and characterize various patterns in the evolution of genomes. Limitations in CoGe will also be addressed. Currently storing genomes from over 5,500 organisms, CoGe forges a powerful new tool for many biologists by allowing researchers anywhere in the world to rapidly identify genes and genomic regions of interest, analyze them with a variety of tools, and visualize their evolution. CoGe is publicly available at: <http://synteny.cnr.berkeley.edu/CoGe>

***** BRING YOUR OWN LAPTOP *****

Date:	Tuesday, June 30
Time:	2:00 p.m. - 5:00 p.m.
Location:	Gerdin Business Building, Room 0129

Presented by the L. H. Baker Center for Bioinformatics and Biological Statistics and
the Computational and Systems Biology Summer Institute
<http://www.bioinformatics.iastate.edu/seminars/index.html>