

SEMINAR

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CoGe: Making comparative genomics easier

The biological research community has entered the genomics age. Although there are many freely available online software solutions for obtaining, comparing, and visualizing genomic data, these resources suffer four major limitations. First is the disparate nature of obtaining data where researchers often have to navigate to multiple websites because each genomics platform provides access to a limited subset of all publicly available genomic information, and in many cases, only to a single genome, all of which change as genomic data is periodically updated. Second, sequence analysis tools differ widely in their ability to detect particular patterns of sequence similarity, are likewise dispersed across multiple websites, and in some cases are only available for online use against a limited number of genomes. This requires researchers to not only navigate to multiple locales to analyze their sequence data, but sometimes reformat their data in order for it to be properly used by an algorithm. Third, and often neglected, is the ability to easily visualize sequence data and their comparisons in order to glean patterns of change. Fourth is the ability to iteratively refine an analysis in order to expand the amount of genomic sequence analyzed, hone in on a particular region of interest, or change sequence comparison algorithms in order to detect different patterns of sequence similarity. Importantly, interlinking these four steps has not been accomplished to make this process efficient.

CoGe represents a web-based software system that addresses all of these limitations facing comparative genomics. 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. CoGe currently stores genomes from over 5,500 organisms. CoGe's ability to allow researchers anywhere in the world to rapidly identify genes and genomic regions of interest and visualize their evolution forges a powerful new tool for any biologist.

CoGe is publicly available at: <http://synteny.cnr.berkeley.edu/CoGe>

Date: Tuesday, June 30

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Location: Gilman Hall, Room 1352

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