

Comparative Genomics: Synteny and genome rearrangements

Comparative analysis of closely related genomes is expected to yield significant insight into the processes of evolution, development, and regulation. The primary focus of this talk is on computational analysis of genome synteny (analysis of relative gene-order conservation), chromosomal dynamics, and genome rearrangement between various species. The genomes of twelve fruit fly species (genus *Drosophila*) were used in this study.

We have developed a computational pipeline to process draft genome assemblies to infer cross-species synteny and algorithms to infer evolutionary rearrangement event counts and ancestral synteny blocks with the ability to handle a large set of species with high "gene counts". We have also analyzed chromosomal rearrangements due to large-scale events such as multi-gene inversions, and fine-scale events such as single-gene relocation. This talk will cover various methods used in these analyses and the primary results of our investigation.