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Mauve: Multiple Genome Alignment**Abstract**

Mauve is a system under development to efficiently compare the DNA sequence of several genomes simultaneously. Comparison of whole genome sequences presents a challenge not posed by comparisons of shorter sequences. Recombination causes frequent genome rearrangements that require new methods of identification and special handling that are not necessary when aligning short collinear sequences. Horizontal transfer introduces new sequences into bacterial chromosomes and deletions remove segments of the genome. Consequently, each genome is a mosaic of unique lineage specific segments, regions shared with a subset of other genomes and segments conserved among all the genomes under consideration. Further, the linear order of these segments will be shuffled among genomes. Mauve identifies large-scale rearrangements and discovers common elements in subsets of the aligned sequences.

Mauve constructs multiple genome alignments by locating exactly matching subsequences and grouping them into collinear regions called locally collinear blocks (LCBs). The exactly matching subsequences are used as anchors for further refinement of the alignment. The resulting alignment provides a basis for research into comparative genomics and the study of evolutionary dynamics on a new scale.

Tuesday, December 3rd
4:00 p.m.

Room 1111
Biotechnology Center/Genetics
425 Henry Mall