

Software and tools for analyzing Mauve alignments

This is a listing of software written by third-parties which either uses Mauve directly or can be used to analyze Mauve genome alignment output. If you would like to add a project to this list, please contact Aaron Darling <darling@cs.wisc.edu> with the project name, a brief description of the software, and how Mauve is used.

ClonalFrame - <http://www2.warwick.ac.uk/fac/sci/statistics/staff/research/didelot/clonalframe/>

ClonalFrame implements a statistical model for inferring bacterial microevolution. ClonalFrame can infer the genealogy of closely related bacteria and identify regions likely to have undergone homologous recombination.

GenoPlast- <http://www2.warwick.ac.uk/fac/sci/statistics/staff/research/didelot/genoplast/>

Given a Progressive Mauve genome alignment and a reference phylogeny, GenoPlast can infer where on the phylogeny fragments of the chromosome were gained and lost. GenoPlast uses a Bayesian model, also inferring lineage specific changes in the overall rates of gain or loss.

Barphlye- <http://bioinformatics.org.au/barphlye>

Barphlye is an extension of the BADGER software to designed to quantify patterns in ancestral chromosome structures during the course of genome rearrangement. Given a Mauve alignment on a set of rearranged genomes, BADGER and Barphlye can infer the phylogenetic tree relating those organisms and simultaneously estimate the inversion events occurring on each branch of the tree.

MochiView - <http://johnsonlab.ucsf.edu/sj/mochiview-start/>

MochiView is a genome browser that integrates genome sequence annotation view with sequence motif visualization and analysis.

SPRING genome rearrangement server - <http://algorithm.cs.nthu.edu.tw/tools/SPRING/>

SPRING is a tool to infer the history of genome rearrangements using block interchange and reversal as mutation operations. SPRING uses Mauve to identify locally collinear blocks in the input genomes.

ROBIN genome rearrangement server - <http://genome.life.nctu.edu.tw/ROBIN/>

ROBIN is a tool, similar to SPRING, which allows inference of genome rearrangement history using block interchange as the mutation operation.

Geneious sequence analysis toolkit - <http://www.geneious.com/>

Geneious is a slick piece of software for sequence analysis, including features such as sequence alignment, database queries, collaboration, and phylogenetic inference.

tRNAcc - <http://www.le.ac.uk/ii/staff/kr46/tRNAcc/index.htm>

A tool for identifying genomic islands (novel gene content) associated with tRNA genes

MobilomeFINDER - <http://mml.sjtu.edu.cn/MobilomeFINDER/>

A web-based tool for identifying genomic islands and other mobile DNA

ASAP - <http://asap.ahabs.wisc.edu/asap/logon.php>

A community-oriented genome annotation database for bacteria and other organisms