



CISGen Web-based Visualization Tools for the Mouse Genome

Department of Computer Science

University of North Carolina at Chapel Hill

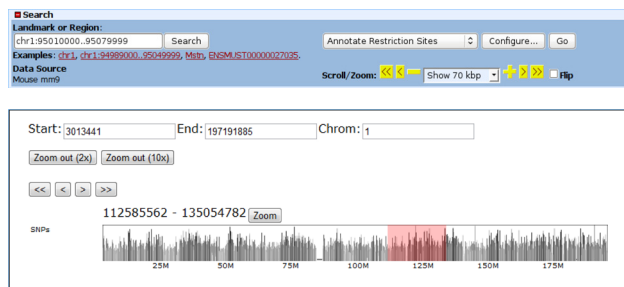
March 2012

Overview

CISGen browser (gbrowse.csbio.unc.edu) is a genome viewer built for integrating, annotating, and visualizing mouse genomes of the Collaborative Cross population used in the CISGen experiments. The CISGen browser is built using Gbrowse 2.0. Its current version integrates annotations from known genes, SNPs, phenome database, CpG islands, and links to the complementary Mouse Subspecies and Phylogeny Browser.

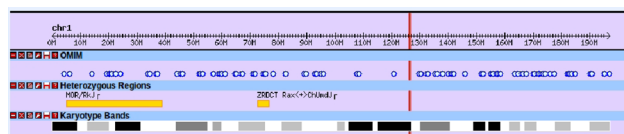
The Mouse Subspecies and Phylogeny Browser (msub.csbio.unc.edu) is an interactive web-based tool for visualization and analysis of mouse genomes simultaneously. Along with generic genome annotations including SNPs and genes, individual mouse data are displayed for a customizable subset of 100 classical lab strains, 62 wild-derived lab strains, and 32 wild mouse strains.

Navigation

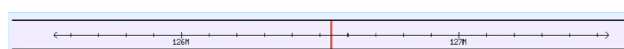


Both tools include controls to navigate through and view the entire mouse genome. Controls include the ability to pick a particular region within the genome by chromosome and position as well as to pan left and right, and to zoom in and out.

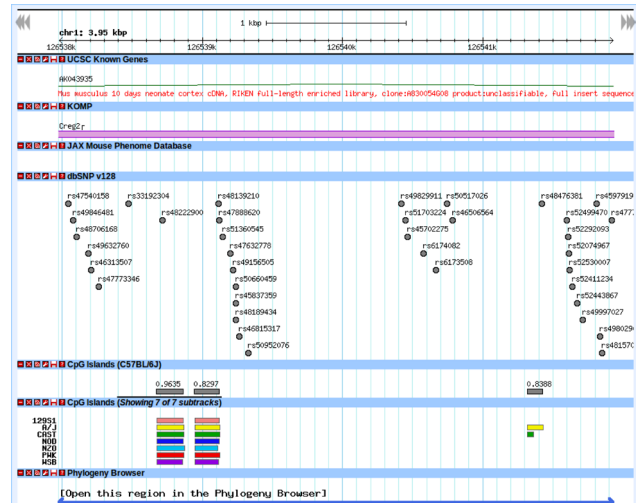
Data



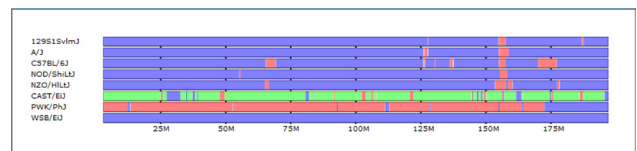
The overview part shows a bird's eye of the whole genome, including karyotype bands, heterozygous regions on inbred strains, and OMIM in a genome-wide scale.



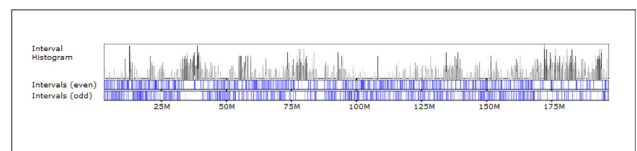
The region view part shows a smaller region in the overview.



The details view part contains full information on a the selected area (less than 5Mb). Tracks include: UCSC known genes, Knock Out Mouse Project, Jax Mouse Phenome Database, dbSNP v.128, and CpG Islands of Collaborative Cross strains.



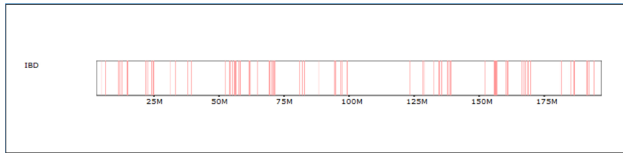
Assignment of subspecific origin across the genome. Origin is assigned as domesticus (blue), musculus (red), or castaneus (green). (Yang et al. Subspecific origin and haplotype diversity in the laboratory mouse. Under review.)



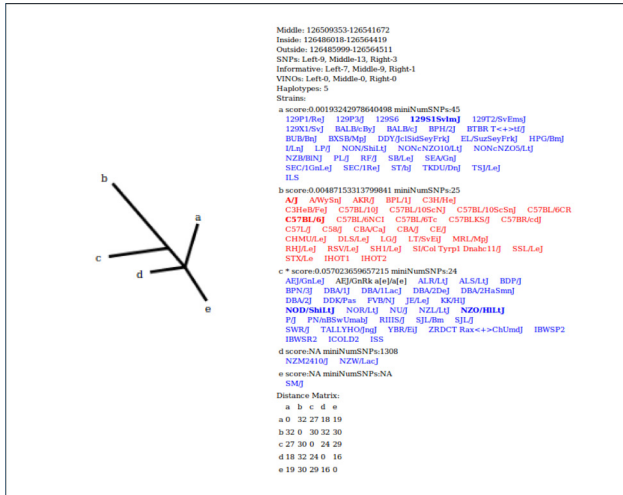
Overlapping maximal-k perfect phylogeny intervals. (Wang et al. Genome-wide compatible SNP intervals and their properties. ACM International Conference on Bioinformatics and Computational Biology. 2010.)



Strains are colored based on haplotype similarity. Color is assigned to minimize total color transitions.



Regions of identity by descent among all selected strains.



Phylogeny trees computed using neighbor-joining based on sequence identity over max-k intervals. Strains are colored according to subspecific origin to show the relationship between phylogeny and subspecies.

Current Project Members

Leonard McMillan, faculty member

Wei Wang, faculty member

Shunping Huang, graduate research assistant

Jeremy Wang, graduate research assistant

Isa Kemal Pakatchi, graduate research assistant

Research Sponsors

Center for Integrated Systems Genomics (CISGen)

1-P50-MH090338-01

NSF IIS 0534580: “Visualizing and Exploring High-dimensional Data”

NSF IIS 0448392: “CAREER: Mining Salient Localized Patterns in Complex Data”

For More Information

Wei Wang

Professor

919-962-1744

weiwang@cs.unc.edu