

## Integrating Genomic Visualization

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Navigating genomic information for a single organism is challenging, let alone doing so for the many hundreds of genomes currently available. The datasets are huge, containing the sequence as well as all associated annotations. The graphical display of genomic information depends on the logical organization of these data and the speed at which this data can be accessed. Additionally, an interface for visualizing genomic data should be easy to understand. Many current visualization tools render static snapshots of a genome landscape requiring the user to reorient the viewer and render another snapshot when they are navigating the data (e.g. Ensembl). We have developed a novel system to store, navigate and visualize genomic information using technology found in modern web-based display systems that presents the user with a "fluid" interface for navigating genomic information.

To store the data, we developed the CoGe genome database, a MySQL database with a PERL interface. This database includes several genomes and their associated genomic annotation from a variety of data sources. The CoGe visualization package was developed as a stand-alone PERL system for graphically representing genomic data. This system is highly customizable and has been extended to retrieve data from the CoGe genome database. To assist in navigating the graphically displayed information for a genomic region, we developed Tiler - a Javascript system for rendering genome data with a GoogleMap-like interface. Tiler allows users to dynamically drag genome image tiles using their mouse. Together, these tools offer a new and unique view of a genome that we believe benefits genomic science.