A graphical package for the visualization of genomic analysis and comparisons of one or more genomic segments

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Abstract

The generation of complete genomes and large regions of genomic sequence has resulted in the need for tools which can display information on a genomic scale as opposed to a gene-by-gene basis. Viewing the entire genome of an organism with various data attached to individual genes can be useful for understanding the organization and function of the genome as well as the evolution of two or more genomes. This information is not readily obtainable from studies of individual genes or small regions. Therefore, systems which can provide a flexible method for displaying large amounts as well as different kinds of data on a complete genome will allow analyses which have been previously difficult to accomplish.

To assist in our analysis, we have constructed a series of Perl/Tk programs and modules which allow us to display many types of information simultaneously. These modules display a wide variety of data and comparative data on a single genomic backbone in either circular or linear form. We have used this system to display the genomes of Methanobacterium thermoautotrophicum, Clostridium acetylbutylicum, and Helicobacter pylori as well as the comparison of the genomes of two distinct strains of H. pylori.

The display platform is a Unix system using X-windows. The code takes data from a tab-delimited file. It can zoom in and out on the display and scale the display to fill the window. Additionally the display can be printed or saved as a postscript file. This code can be easily customized by modifying the input and display routines.

References

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