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GSV/mGSV: Web-based genome synteny visualization tools for customized data

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Web-based synteny visualization tools are important for sharing data and revealing patterns of complicated genome conservation and rearrangements. Such tools should allow biologists to upload genomic data for their own analysis. This requirement is critical because individual biologists are generating large amounts of genomic sequences that quickly overwhelm any centralized web resources to collect and display all those data. We have developed a web-based synteny viewer package, GSV/mGSV, which was designed to satisfy the above requirement. GSV (http://cas-bioinfo.cas.unt.edu/gsv/) allows pair-wise genomic comparison, while mGSV (http://cas-bioinfo.cas.unt.edu/mgsv/) extends the comparison to multiple pairs of genomes. Users can upload their own genomic data files for visualization. Multiple genomes can be presented in a single integrated view with an enhanced user interface. Users can navigate through all the selected genomes in either pairwise or multiple viewing mode to examine conserved genomic regions as well as the accompanying genome annotations. Besides serving users who manually interact with the web server, Web Services were also provided for machine-to-machine communication to accept data sent by other remote resources. The entire GSV/mGSV package can also be downloaded for easy local installation.

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