



Genome Synteny Viewer

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Background

- ▶ What is Synteny?
 - ▶ Refers to a set of genomic features (e.g., genes or other genomic markers) that are conserved in the same relative order in two species (or two chromosomes in the same species).
- ▶ Why are we interested in Syntenic regions?
 - ▶ To decipher the genome evolutionary history
 - ▶ To identify functionally conserved genomic elements.
- ▶ Tools to detect synteny. e.g., BLAST
- ▶ Visualization of Syntenic regions.
 - ▶ Biologists can eyeball the image to analyze patterns of complicated genome rearrangements



Synteny Visualization Tools

- ▶ Currently available web-based synteny visualization tools
 - ▶ Ensembl SyntenyView (Flicek, *et al.*, 2011)
 - ▶ NCBI's MapView (Wolfsberg, 2010)
 - ▶ SynBrowser (Pan, *et al.*, 2005)
 - ▶ Cinteny (Sinha and Meller, 2007)
 - ▶ Gbrowse_syn (McKay *et al.*, 2010)
 - ▶ CoGe* (Lyons *et al.*, 2008)
- ▶ Limitation
 - ▶ Visualize synteny of pre-selected genomes provided by the web services.
 - ▶ Biologists do not have the option to upload their own data and visualize synteny. (CoGe requires sequence input).



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Software

Highly accessed

Open access

GSV: a web-based genome synteny viewer for customized data

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