Genome Synteny Viewer

Qunfeng Dong
Department of Biological Sciences
Department of Computer Science & Engineering
Founded in 1890

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Campus
  1167 acres in Denton, Texas
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UNT offers 97 bachelor’s, 88 master’s and 40 doctoral degree programs.
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).
Software

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

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Live Demo

- GSV
  - http://cas-bioinfo.cas.unt.edu/gsv

- mGSV
  - http://cas-bioinfo.cas.unt.edu/mgsv
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