

Comparative Genomics Software Packages at GMOD



Scott Cain¹, David Clements² and the GMOD Consortium

¹Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724 USA ²National Evolutionary Synthesis Center, 2024 W. Main Street, Suite A200, Durham, NC 27705-4667 USA

The study of comparative genomics has been increasing recently due to the explosion of inexpensive genome sequences, and the visualization software packages at the Generic Model Organism Database (GMOD) project reflects that interest in comparative genomics. There are at least six software packages for visualizing synteny at GMOD. Here we present each of those packages, along with suggestions for use cases as well as caveats for their use. Software packages presented here include Apollo, CMap, gbrowse-syn, SynBrowse, SynView, and Sybil. All of these packages are free and open source. The GMOD project is supported by grants from the National Institutes of Health and the USDA Agricultural Research Service.

Application	Number of Genomes	Platform	Database	Other software required	Comments	Screenshot
Apollo ^{1,2}	2 to 3	Java/ Desktop	Chado or XML files	None	Apollo is a desktop application for editing genome features. As part of its suite of tools it can show synteny to facilitate feature editing and so can be used as a synteny browser.	Pietrical
CMap ³	Unlimited*	Web	CMap Database	Standard CPAN Modules	CMap is a comparative map viewer that can display a variety of maps including sequence, genetic and physical, and so can display the comparison between syntenic genomes. CMap can also generate chromosome comparison dot plots.	S. biscolor Surveys School Otherwoseries 9 1-74.423.111 bp
gbrowse_syn ⁴	2 to 5 with more in an upcoming release	Web	GBrowse Compatible plus an Alignment Database***	GBrowse 1.69	Each organism's data are stored in its own GBrowse compatible database and gbrowse_syn uses an alignment database to draw synteny data. Any genome can be used as the reference and each GBrowse database stands on its own as a standard GBrowse instance	C. rename: (reverse) Supercontig!7 Supercont
Sybil ^{5,6}	Unlimited**	Web	Chado	Standard CPAN Modules	Chado was designed from its inception to allow data for multiple organisms, so no special modification to the schema is required. In addition to synteny views, Sybil also provides a "whole genome comparison" view. Steptococcus perazonas OF Steptococcus perazonas (COC 1973-16) Steptococcus peraz	Prophenocous parameters (DOISS 24 month) 780 mont (DOISS 24 month) 780 month) 780 mont (DOISS 24 month) 780 mont (DOISS 24 month) 780 month)
SynBrowse ⁷	Unlimited**	Web	GBrowse Compatible	At least GBrowse 1.68, 1.69 may work	All data are stored in one GBrowse database, though it is possible to switch reference genomes for comparison.	The state of the s
SynView ^{8,9}	Unlimited**	Web	GBrowse Compatible	Any recent version of GBrowse	All data is stored in one GBrowse database, with a single reference organism and other organisms' dat included in ninth column of the reference organism GFF file. It is not possible to switch reference organisms. Synteny data is drawn with custom per code in the GBrowse configuration file.	Pktorivisi Pfalciparum synteny PKS chvi 3 Pktorivisi Pfalciparum synteny PKS chvi 3 20k 22k 23k 24k 25k 26k 27k 29k 30k 31k 32k 33k 33k 33k 33k 36k 37k 38 39k 40k 44k 43k Pktorivisi Pfalciparum syntenic genes PKH 130030 PKH 130050 PKH 130050 PKH 130060

^{*}Limited only by horizontal screen real estate, unlimited with side scrolling.

¹Using Apollo to browse and edit genome annotations. Misra S, Harris N., Curr Protoc Bioinformatics. 2006 Jan; Chapter 9: Unit 9.5. ²Download: http://apollo.berkeleybop.org/current/install.html.

³CMap work by Ben Faga; download at http://gmod.org/wiki/Downloads.

⁴gbrowse_syn work by Sheldon McKay; distributed with GBrowse, download at http://gmod.org/wiki/Downloads.

⁵Sybil: methods and software for multiple genome comparison and visualization. Crabtree J, Angiuoli SV, Wortman JR, White OR. Methods Mol Biol. 2007;408:93-108. ⁶Download: http://sybil.sourceforge.net/downloads.html. ⁷Download: http://www.synbrowse.org/.

8SynView: a GBrowse-compatible approach to visualizing comparative genome data. Wang H, Su Y, Mackey AJ, Kraemer ET, Kissinger JC. Bioinformatics. 2006 Sep 15;22(18):2308-9. Epub 2006 Jul 14. ⁹Distributed with GBrowse, download at http://gmod.org/wiki/Downloads.

^{**}Limited only by vertical screen real estate, unlimited with vertical scrolling.

^{***}Requires an alignment database to store synteny data and one GBrowse database for each genome; additionally, each GBrowse database may be from a different schema (i.e., one SeqFeature::Store and one Chado database).