The goal of the GMOD project is to create a suite of applications that interoperate, sharing data between them. That goal has been partially realized by the latest release of the GMOD project, in which several applications share genome feature data via a standard database schema called Chado. Chado is a modular schema designed by developers at FlyBase to contain all of the data a model organism database would need. Applications that currently are ‘Chado aware’ are Apollo for feature editing, CMap for comparative map displays, the Generic Genome Browser (GBrowse) for browsing genome features, Turnkey for customized views of data in the database and BioMart (via a GFF3 to BioMart conversion script).

Chado is a modular, generic genomics schema. It is intended to model all data that might be required of a model organism database. Current modules include ones for sequence features, expression data, genotypes, phenotypes and maps. (Chris Mungall, David Emmert, Scott Cain, Allen Day)

GBrowse is a web-based genome feature browser. It can use several data sources for displaying features; here it is using a Chado adaptor that allows it to show the contents of the database ‘live’—that is, as edits are done on the database, they are reflected in GBrowse. (Lincoln Stein, Scott Cain and Ben Faga)

CMap is a comparative map viewer. Here it is being used to show synteny between two related yeast species. (Ben Faga and Ken Clark)

Textpresso is a literature search tool; in this case, it is being hosted at SGD and linked via URL (SGD developers and Eimear Kenny)

Here six GMOD tools are used to create an example comparative genome model organism database. Data obtained from the Saccharomyces Genome Database (SGD) was used to populate a Chado schema to power several views of the data. These applications are hosted at http://gmod.cshl.edu/