Chado - Getting Started

From GMOD (Redirected from Chado)

Chado is a relational database schema that underlies many GMOD installations. It is capable of representing many of the general classes of data frequently encountered in modern biology such as sequence, sequence comparisons, phenotypes, genotypes, ontologies, publications, and phylogeny. It has been designed to handle complex representations of biological knowledge and should be considered one of the most sophisticated relational schemas currently available in molecular biology. The price of this capability is that the new user must spend some time becoming familiar with its fundamentals.

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Status

Mature release
Active
development
Active support

Resources

Introduction
Manual
Tutorial
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Mailing List
(https://lists.sour
schema)
Tagged
2008 Survey
(http://gmod.org/

Documentation

- Introduction to Chado
- Chado paper in Bioinformatics (http://bioinformatics.oxfordjournals.org/cgi/content/abstract/23/13/i337?ijkey=QYeUct9uLSzefgk&keytype=ref)
- Chado Tutorial
- Chado Manual
- FAQ for Chado
- Chado Tables
- Chado Best Practices
- Sample Chado SQL
- PostgreSQL Performance Tips

Modules

Chado is a modular schema, designed in such a way as to allow the addition of new modules for new data types. The existing modules are:

- Audit for database audit trails
- Companalysis for data from computational analysis
- Contact for people, groups, and organizations
- Controlled Vocabulary (cv) for controlled vocabularies and ontologies
- Expression for summaries of RNA and protein expresssion
- General for identifiers
- Genetic for genetic data and genotypes
- Library for descriptions of molecular libraries
- Mage for microarray data
- Map for maps without sequence
- Natural Diversity (ND) for multiple experiments, such as phenotyping and genotyping
- Organism for taxonomic data
- Phenotype for phenotypic data
- Phylogeny for organisms and phylogenetic trees
- Publication (pub) for publications and references
- Sequence for sequences and sequence features
- Stock for specimens and biological collections
- WWW -

Installation

First you will need database software, or Relational Database Management System (RDBMS). The recommended RDBMS for Chado currently is Postgres (http://www.postgresql.org/). Postgres is free software, usually used on a Unix operating system such as Linux or Mac OS X. You can also install Postgres, and Chado, on Windows but most Chado installations are found on some version of Unix - you'll probably get the best support by choosing Unix. (See Databases and GMOD for more discussion.) Once you've installed your RDBMS you can install Chado.

Download a Stable Release of Chado

See Downloads

Chado From SVN

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You can get the most up-to-date, not even released yet, version of Chado from Subversion. To get a copy of the latest Chado source, enter this at the command line:

| |svn co https://svn.code.sf.net/p/gmod/svn/schema/trunk

Once the package has been downloaded cd to the trunk/chado directory.

Follow the instructions in the INSTALL.Chado file, including the installation of the prerequisites. Or read INSTALL.Chado (http://qmod.svn.sourceforge.net/viewc/gmod/schema/trunk/chado/INSTALL.Chado) online.

Loading Data

After completing these steps, you can load your chado schema with data in a number of ways:

- Load RefSeq into Chado HOWTO
- Load GFF into Chado HOWTO
- Using XORT

You can also use the application Apollo to curate data in Chado.

Mailing Lists

	Mailing List Link	Description	Archive(s)
Chado	gmod-schema (https://lists.sourceforge.net/lists/listinfo/gmod- schema)		Gmane (http://dir.gmane.org/gmane.science.biology.gmod.schema), Nabble (2010/05+) (http://gmod.827538.n3.nabble.com/Chadof815597.html), Sourceforge (http://sourceforge.net/mailarchive/forum.php?forum_name=gmodschema)
	gmod-schema-cmts (https://lists.sourceforge.net/lists/listinfo/gmod- schema-cmts)	Chado code updates.	Sourceforge (http://sourceforge.net/mailarchive/forum.php? forum_name=gmod-schema-cmts)

Pronunciation

Chado is usually pronounced like this.

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