Turnkey is...

- A website auto-generator

**SQL:**

Create table foo...
GMODWeb is...

- GMODWeb = Turnkey + Chado + Integration w/ other projects (GBrowse, Amigo, etc)

SQL:
Create table foo...

Chado

GMODWeb
Active Code Generation

SQL Schema

Create table foo...

SQL::Translator

Directed Graph

XML Layout & Templates

Mapping Layer

Data Objects
Strengths & Weaknesses

● Strengths
  • Good prototyping tool
  • Great tool for active code generation
  • Quickly build up-to-date webapps integrated with other GMOD tools

● Weaknesses
  • Perl dependencies are ridiculous and the source of all pain
  • Early design decision to use custom Perl rendering engine limits performance and appeal to users
Status

- Turnkey 1.4 is available and addresses some bugs since the release of the paper
- **GMODWeb**: a web framework for the Generic Model Organism Database. Genome Biol. 2008; 9(6).
- Try the virtual machines at: [http://gmod.org/wiki/VMWare_HOWTO](http://gmod.org/wiki/VMWare_HOWTO)
- Working on Updated RPMs
- [http://turnkey.sf.net](http://turnkey.sf.net)
http://Biopackages.net

What's available?

Biopackages.net currently provides packages as RPMs for Fedora Core Linux, CentOS Linux, and Apple Darwin (OS X). Packages can be browsed and downloaded directly for both stable and testing repositories. These are also available by using yum. See Configuration for details on how to set up yum to be Biopackages-aware. Notable packages available include Bioperl, Bioconductor, The Generic Genome Browser, Chado, Turnkey, GMODWeb, Textpresso, BLAT, EMBOSS, and Hmmer.

Configuration

Biopackages.net hosts a yum repository for distribution of Linux packages. To configure yum to be aware of the Biopackages.net repository, install one of the following configuration RPMs:

- Fedora Core 2
- Fedora Core 5
- CentOS 4

Some of our packages depend on other packages that are maintained by RPMForge, so please also install the respective RPMForge configuration RPM:
Biopackages.net is...

- A repository of software compiled for CentOS (mostly CentOS4) and Fedora
- Packages like chado-hg18, gbrowse, textpresso, bioconductor, bioperl, etc.
- “yum install chado”
Biopackages

Dependency resolution is a huge part of the work
Biopackages
Build Farm

Goal is to build as much in an automated way as possible

Build Host Platforms:
{FC2,FC5,CentOS} * {i386,x86_64,noarch}
Status

• Previously focused on CentOS4 RPM packages for the Nelson Lab
• Transitioning now to CentOS5
• Currently packaging Chado DBs using the 1.0 schema:
  • Base DB with ontologies
  • Human hg18 DB
  • Possibly others (mm9, rn4, panTro2, rheMac2...)
• DAS/2 reference server
• Dependencies
Virtual Machines

- On paper RPMs solve many problems
- However, machines can be tainted by other repositories, source-based installs, other customizations
- Virtual machines can be used to:
  - A mechanism to quickly try the GMOD catalog of tools
  - A mechanism to distribute clean testing and development environments
Status

- Idea is to have a virtual machine with all the Biopackages-provided tools pre-installed
- Currently based on CentOS4
- Have a prototype CentOS4 machine with Chado 1.0 schema, recent BioPerl, and Turnkey/GMODWeb 1.4
- Working with Dave Clements on RPMs to create an updated CentOS5 VM
Status

- http://gmod.org/wiki/VMWare_HOWTO
Contact Me…

- **Turnkey/GMODWeb**: looking to expand Java producer to eliminate Perl dependency problem
- **Biopackages**: looking for RPM developers (or deb package builders for Ubuntu)
- **Virtual Machines**: looking to create CentOS5 machines
  - Pre-configured GMOD demo/dev kit
  - Pre-configured Biopackages dev kit
- **Anyone using GMOD tools for Next Gen Sequencing??**
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