

# GMODWeb, Biopackages, & Virtual Machines

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# Turnkey is...

- A website auto-generator

SQL:  
*Create  
table  
foo...*



Turnkey - Mozilla (Build ID: 000000000)

File Edit View Go Bookmarks Tools Window Help Debug QA

http://mammoth.wooly.org/?id=110822&class=Turnkey:Model:Featu... Search

Home My Favorites Downloads Preferences Help

Pub Feature

Interaction Fas2 (..)

Genotype

Phenotype Fas2

Cvterm CG3665

KEY:  
gene

subfeatures:

- CG3665-RA
  - start: 105726 length: 3447 mRNA
    - CG3665:1
      - start: 105727 length: 191 exon
    - CG3665:2
      - start: 105728 length: 296 exon
    - CG3665:3
      - start: 105729 length: 172 exon
    - CG3665:4
      - start: 105730 length: 164 exon
    - CG3665:5
      - start: 105731 length: 125 exon
    - CG3665:6
      - start: 105732 length: 1494 exon
    - CG3665:7
      - start: 105733 length: 184 exon

# GMODWeb is...

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

SQL:  
*Create  
table  
foo...*

Chado



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GMOD Turnkey

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name plasma membrane

definition

cv\_id 7

dbxref\_id 2682

Link

name response to ethan01 (sensu Insecta)

definition

cv\_id 9

dbxref\_id 11854

Link

name learning and/or memory

definition

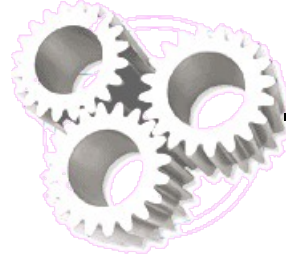
GMODWeb

# Active Code Generation

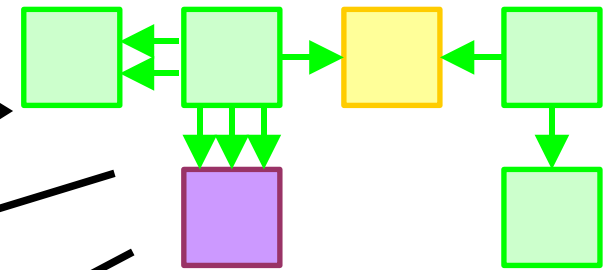
## SQL Schema

```
SQL:  
Create  
table  
foo...
```

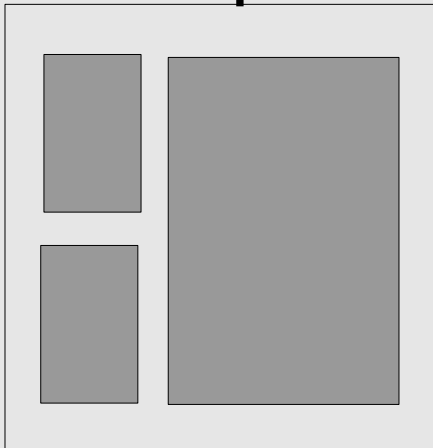
## SQL::Translator



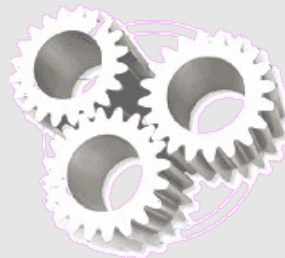
## Directed Graph



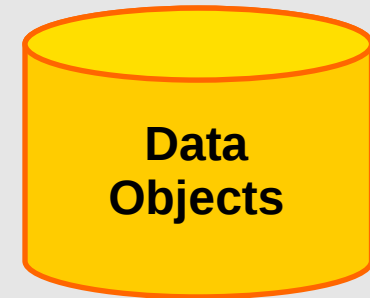
## XML Layout & Templates



## Mapping Layer



Data  
Objects



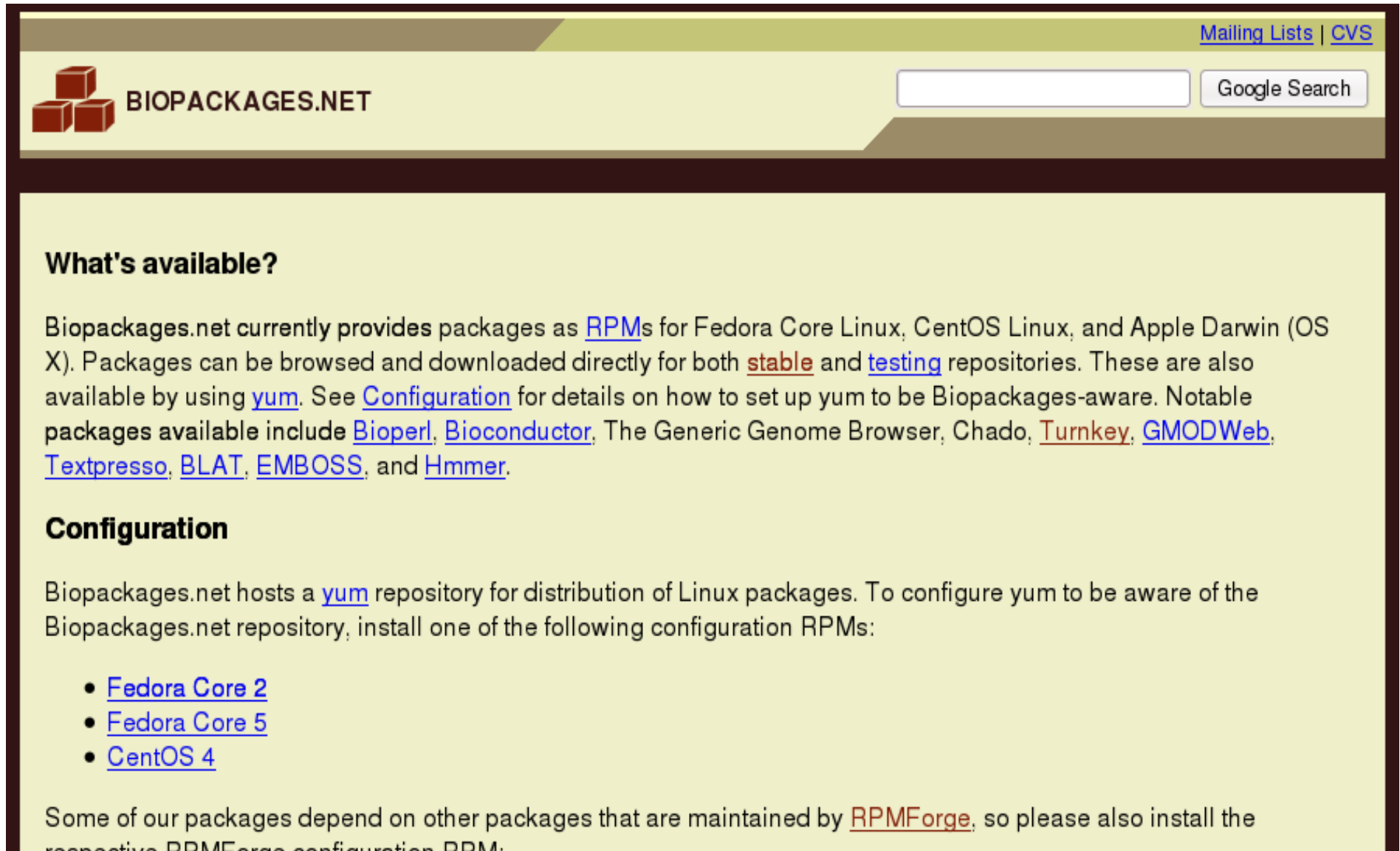
# Strengths & Weaknesses

- 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://Biopackages.net



The screenshot shows the homepage of Biopackages.net. At the top right, there are links for "Mailing Lists" and "CVS". The header features the Biopackages.net logo (three red cubes) and the text "BIOPACKAGES.NET". To the right of the logo is a search bar with a "Google Search" button. The main content area has a yellow background and contains the following sections:

## 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:

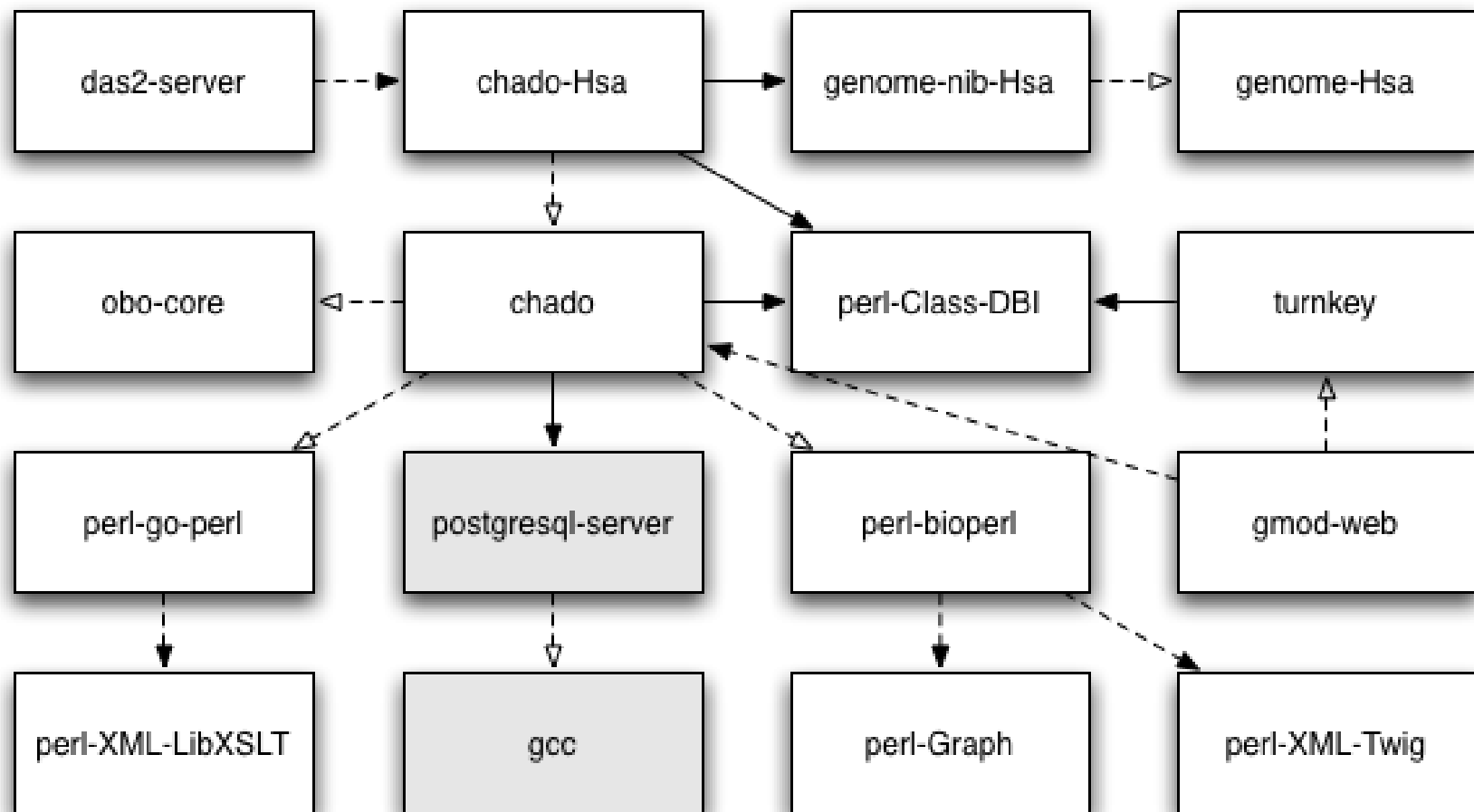
# Biopackages.net is...

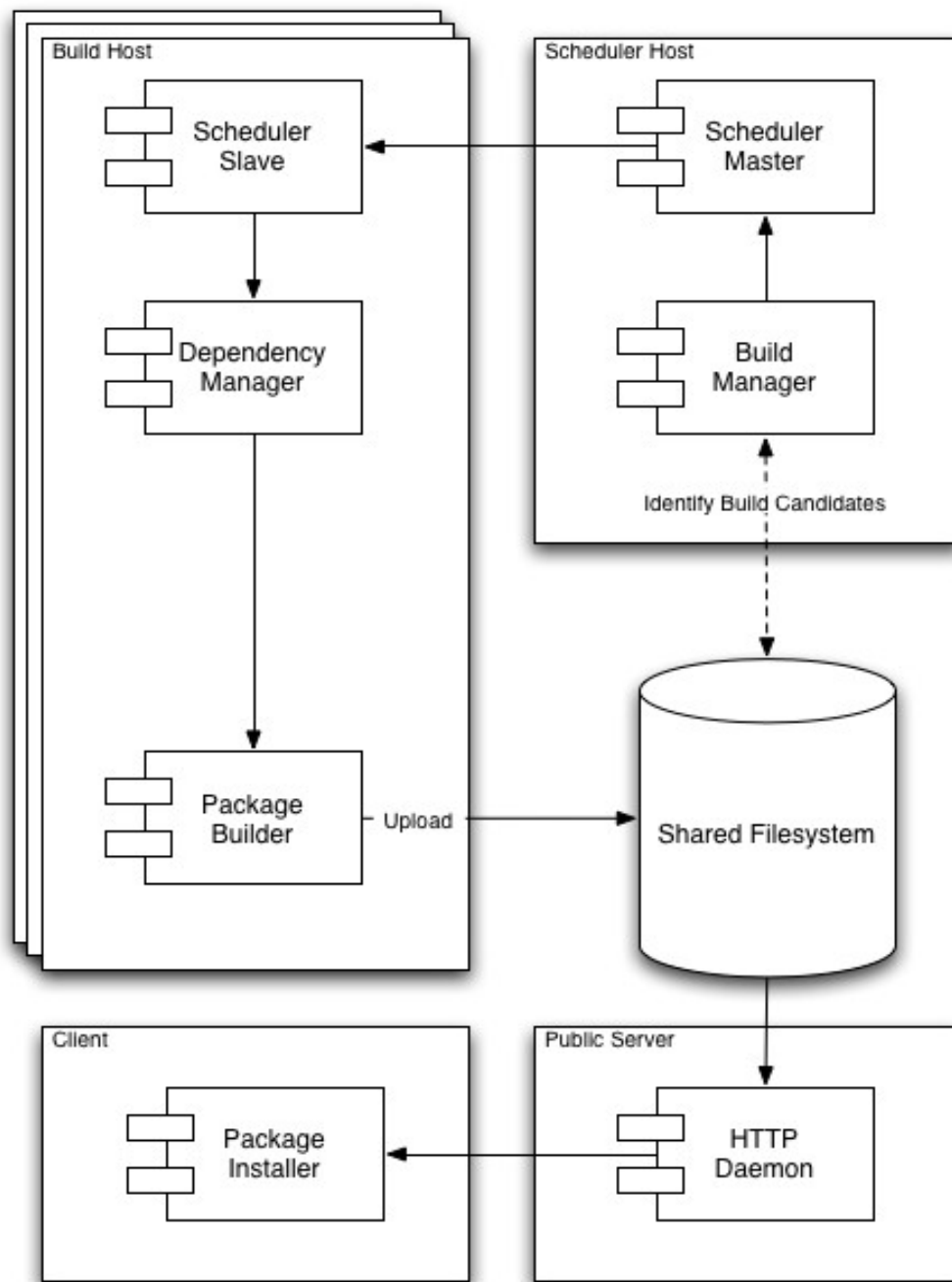
- A repository of software compiled for CentOS (mostly CentOS4) and Fedora
- Packages like chado-hg18, gbrowse, textpresso, bioconductor, bioperl, etc.
- **“yum install chado”**



# 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](http://gmod.org/wiki/VMWare_HOWTO)

The screenshot shows a VMware Workstation window titled "gmod-dev-centos-4-i386-boconnor - VMware Workstation (on lacrimal.genome.ucla.edu)". The interface includes a menu bar (File, Edit, View, VM, Team, Tabs, Help) and a toolbar with buttons for Power Off, Suspend, Powered On, Reset, Snapshot, Revert, Snapshot Manager, Quick Switch, Full Screen, Summary, Appliance, and Console. The Sidebar on the left lists various virtual machines, with "gmod-dev-centos-4-i386-boconnor" selected and marked as "Powered On".

The main window displays a Mozilla Firefox browser window. The address bar shows "http://localhost/". The page content includes:

## The GMOD Virtual Machine

This is a sample GMOD Virtual Machine that contains the following applications pre-installed:

- [GMODWeb for the Yeast Genome](#)
- [GMODWeb for the Human Genome](#)
- [GBrowse](#)
- Chado Sample Databases (Human, Yeast, & Ontologies Only)
- Textpresso
- BlastGraphic
- AmiGO

These GMOD packages can be accessed via the GMODWeb samples linked to above. GBrowse can be used through these example sites or with the sample yeast chr1 linked to above.

For more information about these tools see the [GMOD Homepage](#). Information about this virtual machine can be

# 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???**
- [briandoconnor@gmail.com](mailto:briandoconnor@gmail.com)