

# Database Integration In Website



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# Class Content



- Frameworks
- Catalyst demo
  - Web elements and programming languages



# Frameworks



Ruby On Rails

**django**



**MVC**  
**Model View Controller**



**MySQL**®



**PostgreSQL**



**SQLite**



**Perl**



**python**

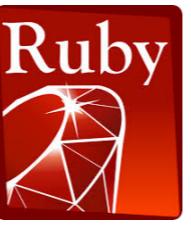


**Ruby**



# Frameworks



Framework					
Model	<b>DB</b>	<b>DB</b>	<b>DB</b>	<b>DB</b>	<b>DB</b>
View*					
Controller					

\*HTML + CSS + JS + Other



# Frameworks



**Drupal**™

<https://www.drupal.com>

Drupal is a free and open-source content-management framework written in PHP and distributed under the GNU General Public License. It is used as a back-end framework for at least 2.1% of all Web sites worldwide

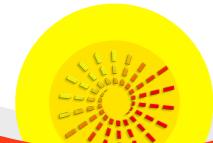


<http://tripal.info>

Tripal is a suite of Drupal modules for construction of biological, research-oriented, scientific websites. In particular, it supports genomic, genetic and breeding data.

## Major Features

- Incorporates the **GMOD Chado database schema** which serves as the data warehouse.
- Integrates with Drupal for user management, and non-biological content.
- Data loaders for commonly used file formats (FASTA, GFF3, GAF, OBO, tab-delimited, etc.).
- Sites can be customized as desired.
- Site developers can create new extension modules to share with other Tripal sites.



# Frameworks



Catalyst is the most popular  
Perl MVC framework

<http://www.catalystframework.org>

**Model**

**CHADO**  
**DBIx Class**

**View**  
**Mason**

**Controller**



**Perl**





# GMOD



[http://gmod.org/wiki/Main\\_Page](http://gmod.org/wiki/Main_Page)

The **Generic Model Organism Database** project, a collection of open source software tools for managing, visualizing, storing, and disseminating genetic and genomic data.



Galaxy: Data analysis & integration



GBrowse: Genome annotation viewer



Chado: Biological database schema



JBrowse: Super-fast genome annotation viewer



BioMart: Data mining system



WebApollo: browser-based annotation editor



MAKER: Genome annotation pipeline



GBrowse\_syn: Synteny viewer



Tripal: Chado web interface



InterMine: Data warehousing



CMap: Comparative map viewer



Pathway Tools: Metabolic, regulatory pathways



Canto: literature annotation tool



# Chado Schema

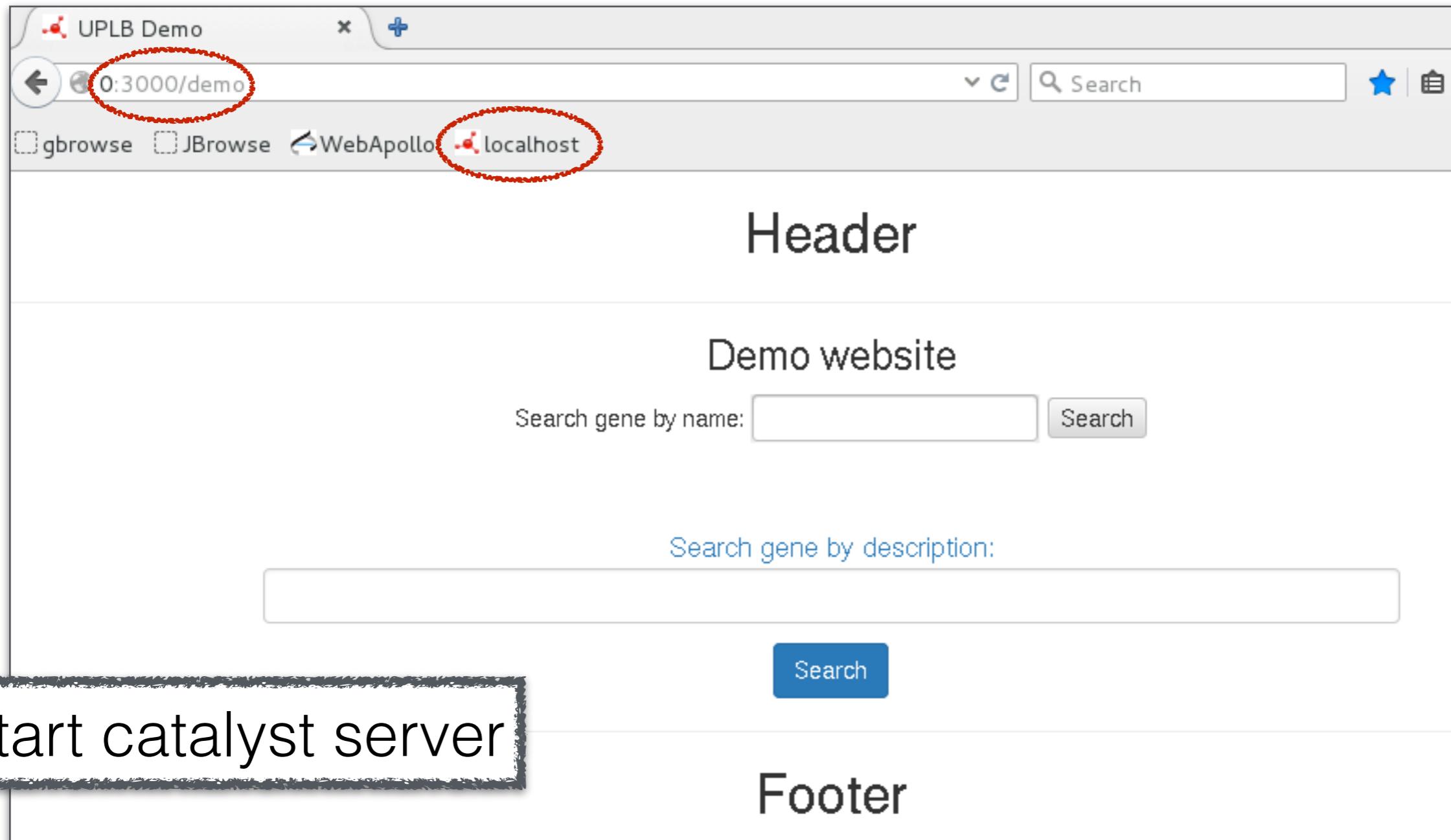


# CHADO

[http://gmod.org/wiki/Chado Tables#Table: organism](http://gmod.org/wiki/Chado_Tables#Table:_organism)



# Catalyst Demo



UPLB Demo

0:3000/demo

gbrowse JBrowse WebApollo localhost

Header

Demo website

Search gene by name:

Search gene by description:

Start catalyst server

Footer

```
bioinfo@biodebian:~/catalyst/demo$ perl script/demo_server.pl -r -d
```



- Demo website
  - Input and output
  - Header and footer
- HTML, JS, jQuery and CSS

<http://www.w3schools.com>



# Controller



- Demo catalyst controllers



# Form and AJAX



- Two types of search in demo website



# Bootstrap



- SGN example: responsive, style
- Demo output Modal and table



# HTML5 Canvas



- Canvas - TEA and VIGS example



# HTML Exercises



- Create a new html file and write basic elements:
  - Title h1, h2, h3, h4
  - Paragraph
  - Table
  - Links
  - Image



# Demo Exercises



1. Add links to gBrowse, JBrowse and WebApollo
2. Create a html table like this one:

a	b	c	d
1	2	3	4

3. Add the bootstrap class 'table' to the table

