

Mimosa

Miniature  
Model  
Organism  
Sequence  
Aligner

Leto

# Mimosa

Miniature Model Organism Sequence Aligner

Jonathan "Duke" Leto  
Sol Genomics Network  
<http://solgenomics.net>

# What is Mimosa?

- Next Generation of the SGN BLAST Tool
- Why does everyone reinvent the web alignment wheel?
- Why are they all square-ish ?

# Design Goals

- Pluggable
- User-Friendly
- Interoperable
- Easy To Deploy

# Pluggability

- Supports any database that DBI knows about
  - SQLite
  - PostgreSQL
  - MySQL
  - ...
- Can run standalone or through webserver

# User-Friendly

- Tooltipped context-sensitive help
- Support different workflows for different user types
- Download all results in various formats
- Ability to save user preferences
  - Preferred Organism
  - Default e-value/substitution matrix/etc

## Easy To Deploy

- What, you don't want to install 5000 CPAN modules?
- Packages will be available for Debian/Ubuntu/etc
- Goal: Download 1 file, Run 1 command to install

# Interoperable

- Work with current GMOD software
- Web API to integrate with other web services
- Possibly an InterMine Plugin?

## Screenshot

Mimosa - Miniature Model Organism Sequence Aligner

Organism

Sequence Set  [Edit Sequence Sets](#)

Program

Query sequence

Advanced Options

Powered by [BioPerl](#), [jQuery](#) and many [CPAN](#) modules



# Killer Features

- Web-based Sequence Set Administration
- Sequence Set Filtering by Organism
- Automated Sequence Set Updates (from NCBI/etc)
- What else?

# What is under the hood?

- Moose
- BioPerl
- Bio::Chado::Schema
- Mason
- jQuery

## Resources

- <http://github.com/GMOD/mimosa>
- <http://solgenomics.net>
- #gmod on irc.freenode.net

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