Mimosa
Miniature Model Organism Sequence Aligner

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What is Mimosa?

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

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Design Goals

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

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Pluggability

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

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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

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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

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Interoperable

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

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Screenshot

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Killer Features

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

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What is under the hood?

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

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Thanks

- Boyce Thompson Institue for Plant Research
- NESCent

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Resources

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