



# GMOD in action: the Legume Federation project

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Iowa State University  
GMOD 2016



## Goals for this talk

- Describe the Legume Federation
- Show how we are using GMOD components to achieve our aim
- Open a discussion:
  - Why form federations?
  - What are we missing that GMOD can provide?
  - What is missing in GMOD to support a federation?

The Legume Federation - <http://legumefederation.org/>



The **Legume Federation** is an NSF project to build a federation of legume databases through data standards, distributed development and comparative analysis, to support research across the legume family, and to support robust agriculture for a world that is significantly "legume-fed".

# The Legume Federation - <http://legumefederation.org/>



## Investigator institutions:



Iowa State University



National Center for Genomic Research (NCGR)



USDA-ARS



J. Craig Venter Institute (JCVI)



CyVerse

# The Legume Federation - <http://legumefederation.org/>



## Members and collaborators:



Alfalfa Genome



Cool Season Food Legume Database



Feed the Future Climate Resilient Chickpea



KnowPulse



**Legume Information System (NCGR & USDA-ARS)**



Medicago truncatula HapMap



**Medicago genome (JCVI)**



**PeanutBase (ISU & USDA-ARS)**



SoyBase



## But what is a federation, really?

- Communication (human and computer) and cooperation.
- Sharing data and software components.
- Agreement on data exchange formats, terms, web service APIs, requirements for data deposit (e.g. use of standard repositories, metadata, integrity).
- Caring for full lifecycle of a web resource, which may include porting to a more permanent resource at the end of funding.
- Respect a level of autonomy.



## Why federate?

- Data management grows ever more expensive.
- Extend limited personnel and resources.
- Proliferation of specialized but useful web resources.
- Need for domain experts.
- Help for smaller members.



# Why federate legume web resources?

- Legumes are extremely important:

- high-protein food
- forage and feed
- improve soil

- **Many research communities**

*Medicago truncatula*, *Lotus japonicus*, adzuki bean, alfalfa, apios, bambara groundnut, birdsfoot trefoil, black gram, carob, chickpea, clovers, common bean, cowpea, faba bean, fenugreek, grass pea, guar, horse gram, indigo, lablab, lentil, licorice, lima bean, lupin, moth bean, mesquite, mung bean, pea, peanut, pigeon pea, rice bean, scarlet runner bean, soybean, tamarind, tepary bean, yellow pea, vetch, winged bean

- Taxonomic relatedness enables comparative research



# The Legume Federation



- Communication, coordination and collaboration
- Data and metadata standardization and exchange
- Data repository
- Linking data across legume species
- Development
- Training

# The Legume Federation



- **Communication, coordination and collaboration\***
- **Data and metadata standardization and exchange\***
- Data repository
- Linking data across species
- **Development\***

# The Legume Federation



- Communication, coordination and collaboration
- Data and metadata standardization and exchange
- Data repository
- **Linking data across species\***
- Development

# The Legume Federation



Also...

- Provides web resources for small research communities
- Provides web resources for long-term projects generating significant quantities of data
  - Developing sharable data curation practices
- Supports full lifecycle of web resource



# The Legume Federation

Also...

- Provide web resources for small research communities\*
- Provide web resources for long-term projects generating significant quantities of data\*
  - Develop sharable data curation practices
- Support full lifecycle of web resource\*

# Communication, coordination and collaboration



- Coordinate and communicate across legume web resources
- Share development efforts
- Engage major data generators
- Communicate with research communities

# Communication, coordination and collaboration



- Coordinate and communicate across legume data centers  
[GMOD community](#)
- Share development efforts  
[Tripal/Chado](#), [InterMine](#)
- Engage major data generators  
[Provide VMs of website/database with data loaders](#)
- Communicate to research communities

# Data and metadata standardization and exchange



- Standardization of metadata
- Standardization of data exchange
- Use of established ontologies
- Use of common data collection templates



# Data and metadata standardization and exchange



- Standardization of metadata  
Tripal, ?
- Standardization of data exchange  
GBrowse, JBrowse, Tripal web services, Chado, ?
- Use of established ontologies  
Tripal, ?
- Use of common data collection templates  
Collaborations with other dbs, Tripal



## Data repository

- A central location where researchers can find and download datasets
- Support PURLs, currently planning to use ARKs for major datasets
- Internal IDs for derived data and for attaching metadata directly to files
- Requires good metadata, at least semi-standardized
- Partnering with CyVerse

# Data repository – internal IDs

Concept: file name includes an opaque ID which links to its metadata.



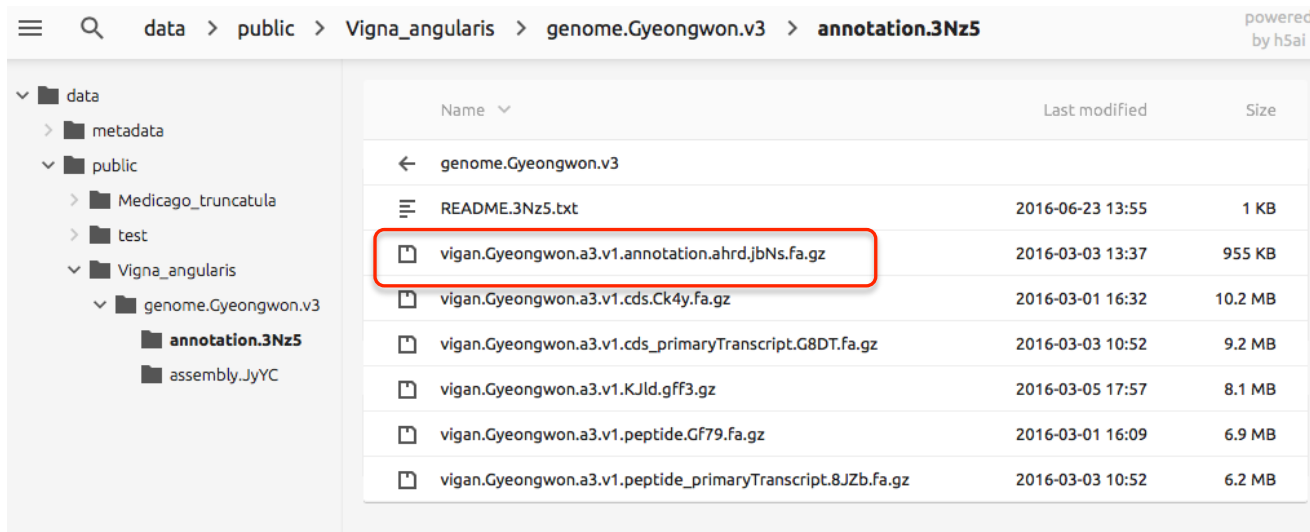
The screenshot shows a file repository interface with a breadcrumb path: data > public > Vigna\_angularis > genome.Gyeongwon.v3 > assembly.JyYC. The interface is powered by h5ai. On the left, a sidebar shows a tree view of the directory structure. The main area displays a table of files and folders:

Name	Last modified	Size
← genome.Gyeongwon.v3		
☰ README.JyYC.txt	2016-06-23 13:38	1 KB
📄 vigan.Gyeongwon.a3.genome.JyYC.fa.gz	2016-03-04 14:57	123.1 MB

A file containing a *Vigna angularis* pseudomolecule sequence. The ID “jyYC” is linked to metadata about this file, including its original filename (required) and information about the project which produced it.

# Data repository – internal IDs

Concept: file name includes an opaque ID which links to its metadata.



The screenshot shows a file repository interface. The breadcrumb path is: data > public > Vigna\_angularis > genome.Gyeongwon.v3 > annotation.3Nz5. The interface is powered by h5ai. On the left, a sidebar shows the directory tree: data > metadata > public > Medicago\_truncatula > test > Vigna\_angularis > genome.Gyeongwon.v3 > annotation.3Nz5 (selected) > assembly\_JyYC. The main area displays a table of files:

Name	Last modified	Size
← genome.Gyeongwon.v3		
☰ README.3Nz5.txt	2016-06-23 13:55	1 KB
📄 vigan.Gyeongwon.a3.v1.annotation.ahrd.jbNs.fa.gz	2016-03-03 13:37	955 KB
📄 vigan.Gyeongwon.a3.v1.cds.Ck4y.fa.gz	2016-03-01 16:32	10.2 MB
📄 vigan.Gyeongwon.a3.v1.cds_primaryTranscript.G8DT.fa.gz	2016-03-03 10:52	9.2 MB
📄 vigan.Gyeongwon.a3.v1.KJld.gff3.gz	2016-03-05 17:57	8.1 MB
📄 vigan.Gyeongwon.a3.v1.peptide.Gf79.fa.gz	2016-03-01 16:09	6.9 MB
📄 vigan.Gyeongwon.a3.v1.peptide_primaryTranscript.8JZb.fa.gz	2016-03-03 10:52	6.2 MB

This is a file generated by LIS to complement this *V. angularis* genome annotation. The ID “jbNs” links to metadata describing the genome annotation, and an explanation of how this file was created.

# Development



Enable sharing of development efforts, encourage good development practices, increase use of existing software.



# Development

## CMapII

JavaScript | In design

## InterMine instances (<http://mines.legumeinfo.org/>)

Working [development instances](#): BeanMine, SoyMine, PeanutMine, LegumeMine

Established instances: [MedicMine](#), [ThaleMine](#)

## Tripal modules: BLAST, Ontology Search, QTL, Phylotree, Domain Search

All in active use; QTL module will be re-written by Main lab

## Context viewer

JavaScript+Django | In active use.

## CViTjs (whole genome viewer)

JavaScript | Beta expected this month



# Development

## CMapII

*USDA-ARS & NCGR - Steven Cannon, Andrew Farmer, Sudhansu Dash, Ethy Cannon, Alex Rice, Alan Cleary, Andrew Wilkey, David Grant*

- JavaScript
- Will read GFF files
- Support all CMap features + SoyBase CMap extensions
- Handle large numbers of features
- Would like comparative views

**Dorrie Main's lab is developing a Tripal map viewer with all features from CMap, which will pull map data from Chado.**

**Contact us if you would like to be involved with the design.**



# Development

InterMine instances (<http://mines.legumeinfo.org/>)

NCGR - Sam Hokin & Andrew Farmer | JCVI - Vivek Krishnakumar

BeanMine  
MedicMine  
PeanutMine  
SoyMine  
ThaleMine

**PeanutMine** v0.3 A mine with peanut data from LIS Peanutbase

Home Templates Lists QueryBuilder Regions Data Sources API MyMine Other LIS Mines | LIS Home | Contact Us | Log in

Search: e.g Aradu.000JC GO

**Search**  
Search this mine. Enter names, identifiers or keywords.  
Examples: Aradu.000JC, Aradu.000JC.1, GM1069  
e.g. X, Y, Z  
SEARCH

**Analyze**  
Enter a list of identifiers.  
Gene  
e.g. Aradu.000JC  
advanced  
ANALYSE

**Welcome to the LIS PeanutMine!**  
This mine integrates many types of data for **peanuts**. It is currently under development by LIS/NCGR as a demo built from Peanutbase, via chado and GFF files. database. Contact Sam Hokin shokin at ncgr dot org.  
TRY THIS TEMPLATE!

**Latest updates (v0.3, 1 June 2016)**  
• Added Plant Reactome pathways to polypeptides with external links to Plant Reactome





# Development - Tripal

Tripal modules: **BLAST**, Ontology Search, QTL, Phylotree, Domain Search

**Lead developer:** Lacey Sanderson (Usask)  
Available and in use.

▸ See Results from a Recent BLAST

▾ Request a New BLAST

▾ Enter *Protein* Query Sequence

*Enter one or more queries in the top text box or use the browse button to upload a file from your local disk. The file may contain a single sequence or a list of sequences. In both cases, the data must be in [FASTA format](#)®.*

Enter FASTA sequence(s)  Show an Example Sequence

Enter query sequence(s) in the text area.

**Or upload your own query FASTA:**

No file chosen

The file should be a plain-text FASTA (.fasta, .fna, .fa, .fas) file. In other words, it cannot have formatting as is the case with MS Word (.doc, .docx) or Rich Text Format (.rtf). It cannot be greater than 2MB in size. **Don't forget to press the Upload button before attempting to submit your BLAST.**

▾ Choose Search Target

*Choose from one of the protein BLAST databases listed below.*

**Protein BLAST Databases:**

Arachis duranensis - proteins ▾

▸ Advanced Options



# Development - Tripal

Tripal modules: **BLAST**, Ontology Search, QTL, Phylotree, Domain Search

Download: [Alignment](#), [Tab-Delimited](#), [XML](#)

Query Information: /tmp/2016Jun28\_175505\_query.fasta

Search Target: Arachis duranensis - proteins

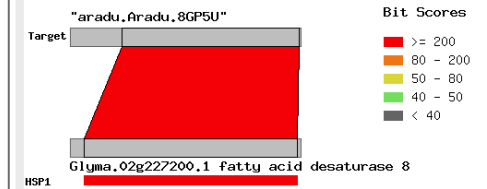
Submission Date: Tue, 06/28/2016 - 17:55

BLAST Command executed: blastp -max\_target\_seqs 10 -evalue 0.001 -word\_size 3 -gapopen 7 -gapextend 2 -culling\_limit 0 -matrix PAM30

The following table summarizes the results of your BLAST. Click on a *triangle* on the left to see the alignment and a visualization of the hit, and click the *target name* to get more information about the target hit.

#	Query Name (Click for alignment & visualization)	Target Name	E-Value
▼ 1	Glyma.02g227200.1 fatty acid desaturase 8	Aradu.i67U0	0
▲ 2	Glyma.02g227200.1 fatty acid desaturase 8	Aradu.8GP5U	3.10536E-177

Hit Visualization



The image above shows the relationship between query and target for this particular BLAST hit.

Alignment

HSP 1

Identity= 258/351 (73.5%) , Positive= 278/351 (79.2%) Query Matches 24 to 374 Hit Matches = 103 to 453

```
Query: 24 DFDPSPAPPPFKIAEIRASIPKHCWVKNPWSLSYVLRDLVIALVAATHFDMMLLMI 83
      +FDP APPFF A+IRA IPKHCWVK+PW S+SYV RDV V+ L A A + WL W
Sbjct: 103 EFDPGAPPPFNLAIRAIPKHCWVKDPKSMYSYVARDVIVVLGLAAGAAVLSNMLVWPL 162

Query: 84 YCPIQQTMFALFVLGHDCGHSFSDSPLLSLVGHILHSSILVPHGWRIHRTHQNH 143
      Y QQTMFALFVLGHDCGHSF+ LNS VGH LHSSILVPHGWRIHRTHQNH
Sbjct: 163 YMAAGCCMREAYRUCGDCGCGCSSENGKTSKICWLTLSKSTVHVVWCGWLTGHRTHQNH 222
```



# Development - Tripal

Tripal modules: **BLAST**, Ontology Search, QTL, Phylotree, Domain Search

REST Web services:

*Prateek Gupta*

- **GET** list of target databases
- **GET** available **BLAST** options
- **POST** job
- **GET** status
- **GET** results

Download: [Alignment](#), [Tab-Delimited](#), [XML](#)

Query Information: /tmp/2016Jun28\_175505\_query.fasta  
Search Target: Arachis duranensis - proteins  
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HSP1

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      +FDP APPFF A+IRA IPKHCWVK+PW S+SYV RDV V+ L A A + WL W
Sbjct: 103 EFDPGAPPPFNLAIRAIPKHCWVKDPKMSYVARDVIVVLGLAAGAAVLSNVLVWFL 162

Query: 84 YCPIQQTMFWALFVLGHDCGHSFSDSPLLSLVGHILHSSILVPHGWRIHRTHQNH 143
      Y QQTMFWALFVLGHDCGHSF+ LNS VGH LHSILVPHGWRIHRTHQNH
Sbjct: 163 YMAAQQMFWALFVLGHDCGHSFSDSPLLSLVGHILHSSILVPHGWRIHRTHQNH 322
```



# Development - Tripal

Tripal modules: **BLAST**, Ontology Search, QTL, Phylotree, Domain Search

REST Web services:

*Prateek Gupta*

Status: testing and documenting.

Release: end of summer?

Next: consume CoGe BLAST Web services. (LegFed customization)

Download: [Alignment](#), [Tab-Delimited](#), [XML](#)

Query Information: /tmp/2016Jun28\_175505\_query.fasta  
Search Target: Arachis duranensis - proteins  
Submission Date: Tue, 06/28/2016 - 17:55  
BLAST Command executed: blastp -max\_target\_seqs 10 -evalue 0.001 -word\_size 3 -gapopen 7 -gapextend 2 -culling\_limit 0 -matrix PAM30

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+EDP APPFF A+IRA IPKHCWVK+PW S+SYV RDV V+ L A A + WL W
Sbjct: 103 EFDPGAPPPFNLAIRAAIPKHCWVKDPKMSYVARDVIVVGLAAGAAVLSNMLVWPL 162

Query: 84 YCPIQQTMFWALFVLGHDCGHSFSDSPLLSLVGHILHSSILVPHGWRIHRTHQNH 143
Y QQTMFWALFVLGHDCGHSF+ LNS VGH LHSSILVPHGWRIHRTHQNH
Sbjct: 163 YMAAQQCMWALYKLVGHDCGHSFSDSPLLSLVGHILHSSILVPHGWRIHRTHQNH 322
```



# Development - Tripal

**Tripal modules: BLAST, Ontology Search, QTL, Phylotree, Domain Search**


*ISU & Washington State - Ethy Cannon & Sook Jung*

- Preliminary QTL modules exist at CoolSeasonFoodLegumes, and PeanutBase/LegumeInfo (adapted from the CSFL module).
- New QTL data dictionary developed jointly by Ethy and Sook Jung with input from other groups.
- Tripal module for the new data dictionary will be developed by Dorrie Main's group after Tripal 3 is released.




# Development - Tripal

Tripal modules: BLAST, Ontology Search, **QTL**, Phylotree, Domain Search  
*ISU & Washington State - Ethy Cannon & Sook Jung*



## LIS - Legume Information System

Information about legume traits for crop improvement

Newsletter signup 

- Home
- Species
- Genomes
- Traits & Maps
- Germplasm
- Search
- Download
- Submit Data
- Community
- Contact
- Help


### Search for Legume QTL

Search for chickpea (*Cicer arietinum*) QTL at [CoolSeasonFoodLegumes](#)

Search for faba bean (*Vicia faba*) QTL [CoolSeasonFoodLegumes](#)

Search for lentil (*Lens culinaris*) QTL [CoolSeasonFoodLegumes](#)

Search for pea (*Pisum sativa* and other *Pisum* sp.) QTL [CoolSeasonFoodLegumes](#)



All fields are optional and partial names are accepted. Click column headers to sort.

Total QTL count: 222

- Arachis hypogaea (PeanutBase)
- Arachis spp. (PeanutBase)
- Glycine max (SoyBase)
- ✓ Phaseolus vulgaris

Trait Class	QTL name	QTL Symbol in Pub	Trait Name in Pub	From this Pub	Apply
Organism	Trait Class	QTL name	QTL Symbol in Publication	Trait Name in Publication	Citation
Phaseolus vulgaris	whole-plant	Branching 1-1	Brn1	Branch number	<a href="#">Checa and Blair, 2008a</a>
Phaseolus vulgaris	whole-plant	Canopy width 1-1	pw6.1	Plant width	<a href="#">Blair, Iriarte et al., 2006a</a>
Phaseolus vulgaris	whole-plant	Canopy width 1-2	pw6.2	Plant width	<a href="#">Blair, Iriarte et al., 2006a</a>
Phaseolus vulgaris	whole-plant	Canopy width 1-3	pw7.1	Plant width	<a href="#">Blair, Iriarte et al., 2006a</a>
Phaseolus vulgaris	whole-plant	Climbing 1-1	Cab1-1	Climbing ability 45 days after planting	<a href="#">Checa and Blair, 2008a</a>



# Development - Tripal


Tripal modules: BLAST, Ontology Search, **QTL**, Phylotree, Domain Search  
*ISU & Washington State - Ethy Cannon & Sook Jung*

The screenshot shows the LIS - Legume Information System website. The header includes the title "LIS - Legume Information System" and the tagline "Information about legume traits for crop improvement". A navigation menu contains links for Home, Species, Genomes, Traits & Maps, Germplasm, Search, Download, Submit Data, Community, Contact, and Help. The main content area is titled "Search for Legume QTL" and lists search options for chickpea, faba bean, lentil, and pea. Below this, it states "Total QTL count: 262". The search form includes a "Species" dropdown menu (highlighted with a red box) set to "Glycine max (SoyBase)", a "QTL name" text input field containing "oil", and an "Apply" button.



# Development - Tripal

Tripal modules: BLAST, Ontology Search, [QTL](#), Phylotree, Domain Search  
*ISU & Washington State - Ethy Cannon & Sook Jung*

**SoyBase and the Soybean Breeder's Toolbox**  
Integrating Genetics and Molecular Biology for Soybean Researchers Follow us on Twitter @SoyBaseDatabase

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[SoyBase Home](#) [Help & Tutorials](#) [Genetic Map](#) [Sequence Map](#) [Expression](#) [Mutants](#) [Projects](#) [Tools](#) [Community](#) [Site Map](#)

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**Search Soybase**

Category	Term	Details	Trait	Annotation	Expression	Mutants	Genomic Map	Genetic Map
QTL	oil	188	3	8				188





# Development - Tripal

**Tripal modules: BLAST, [Ontology Search](#), QTL, Phylotree, Domain Search**  
*ISU - Shivan Gunda and Ethy Cannon; idea by David Grant*

Takes advantage of the structure of ontology trees to improve searching of data objects with attached ontology terms.

1. Find all terms in selected ontologies that contain the search text.
2. Find all children of those terms.
3. Retrieve data objects annotated with those terms.

**Bonus:** sibling terms provide user with related terms that might more closely match what is being sought.

**Intended to be used as a library**  
Core functionality can be used outside Tripal



# Development - Tripal

Tripal modules: BLAST, **Ontology Search**, QTL, Phylotree, Domain Search  
*ISU - Shivan Gunda and Ethy Cannon; idea by David Grant*

## Basic functionality:

- SetOntologies(ontology-list)
- SearchTerms(search-text)
- GetChildren(term)
- GetSiblings(term)
- GetParents(term)

Hope to release at the end of this summer



# Development - Tripal

Tripal modules: BLAST, [Ontology Search](#), QTL, Phylotree, Domain Search  
*ISU - Shivan Gunda and Ethy Cannon*

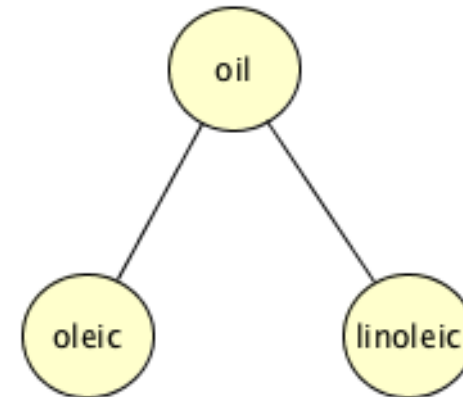
Implemented in QTL search at PeanutBase

Old way:

“oil” → only traits containing the word “oil”

New way:

“oil” → traits containing the words “oil”, “linoleic” and “oleic”





# Development - Tripal

Tripal modules: BLAST, [Ontology Search](#), QTL, Phylotree, Domain Search  
*ISU - Shivan Gunda and Ethy Cannon*

Species	Trait Class	Trait	QTL Symbol in Pub	Trait Name in Pub	From this Pub
- Any -	- Any -	seed			- Any -
<input type="button" value="Search"/>					
<input type="checkbox"/> Use narrow search (if checked, only traits containing the requested text will be returned)					

Sibling terms can give additional hints:

Arachis spp.	yield	Seeds per plant 1-1	SN_WW_a05	Seed number	Fonckea, Tossim et al., 2012a
<b>Related traits: Aboveground weight, Pods per plant, Stature, Plant weight</b>					



# Development - Tripal

## Tripal modules: BLAST, Ontology Search, QTL, Phylotree, **Domain Search**

NCGR: Pooja Umale & Andrew Farmer

Available and in use at  
LegumeInfo.org and  
PeanutBase.org.

**Protein Domain Search**

This page provides a search tool and information about protein domain annotations that are derived from InterproScan analysis. We have also provided here the count of number of genes per species that are associated with each of these domains, which when clicked will redirect you to gene and gene\_family information.

---

<b>Domain ID</b> Is equal to <input type="text"/>	<b>Domain Name</b> Contains <input type="text"/>
(e.g. [is equal to]: PF00139)	(e.g. [Contains]: Zinc finger)
<b>Interpro term</b> Is equal to <input type="text"/>	<b>Description</b> Contains all words <input type="text"/>
(e.g. [is equal to]: IPR027278)	(e.g. [Contains all words]: disease resistance)

<b>Family Count</b> Is equal to <input type="text"/>	<b>Gene Count</b> Is equal to <input type="text"/>	<b>Medtr Count</b> Is equal to <input type="text"/>	<b>Lotja Count</b> Is equal to <input type="text"/>
<b>Cicar (CDCFrontier) Count</b> Is equal to <input type="text"/>	<b>Tripr Count</b> Is equal to <input type="text"/>	<b>Vigan Count</b> Is equal to <input type="text"/>	<b>Vigra Count</b> Is equal to <input type="text"/>
<b>Phavu Count</b> Is equal to <input type="text"/>	<b>Glyma Count</b> Is equal to <input type="text"/>	<b>Cajca Count</b> Is equal to <input type="text"/>	<b>Aradu Count</b> Is equal to <input type="text"/>
<b>Araip Count</b> Is equal to <input type="text"/>			

Domain ID	Domain Name	Interpro	Family	Gene	Medtr	Lotja	Cicar	Tripr	Vigan	Vigra	Glyma	Phavu	Cajca	Aradu	Araip
-----------	-------------	----------	--------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------



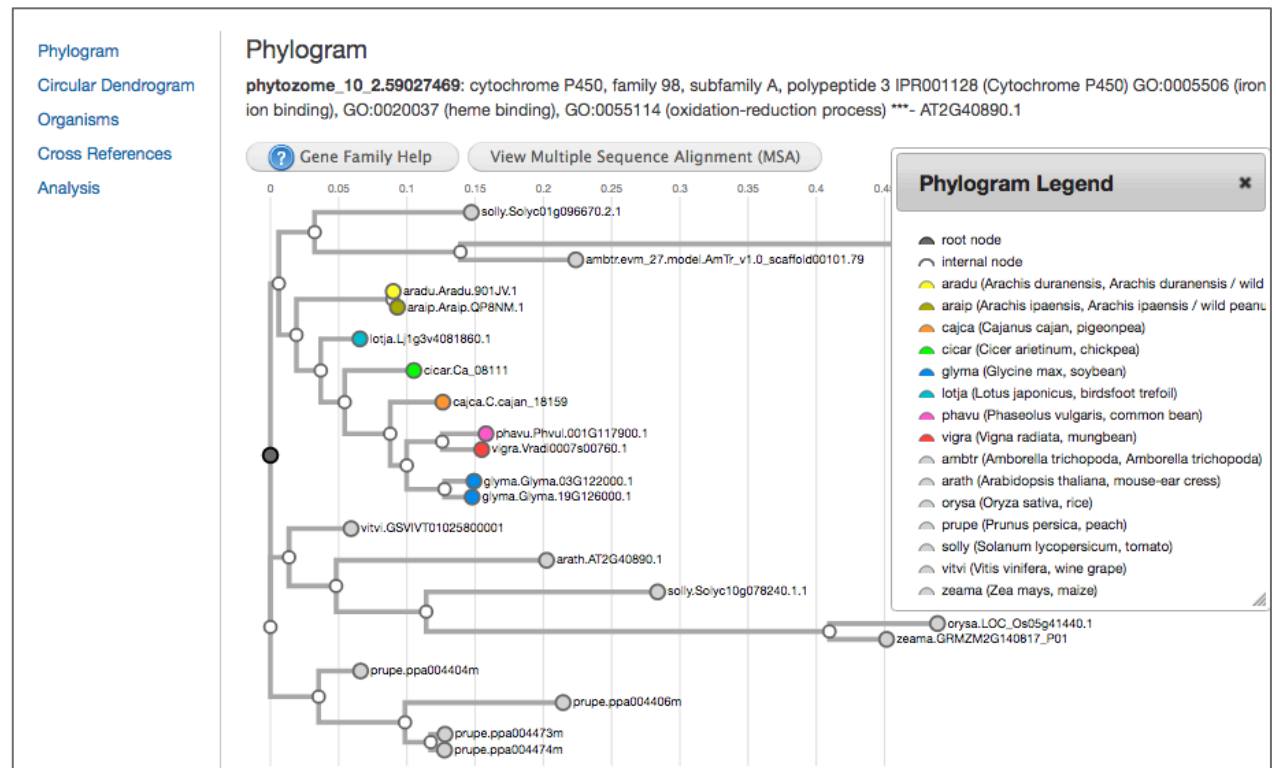
# Development - Tripal

Tripal modules: BLAST, Ontology Search, QTL, **Phylo**tree, Domain Search

*NCGR - Alex Rice & Andrew Farmer*

Available at **LegumeInfo.org**

Ready to become a full-fledged Tripal module but first needs a volunteer to implement it at a new website.





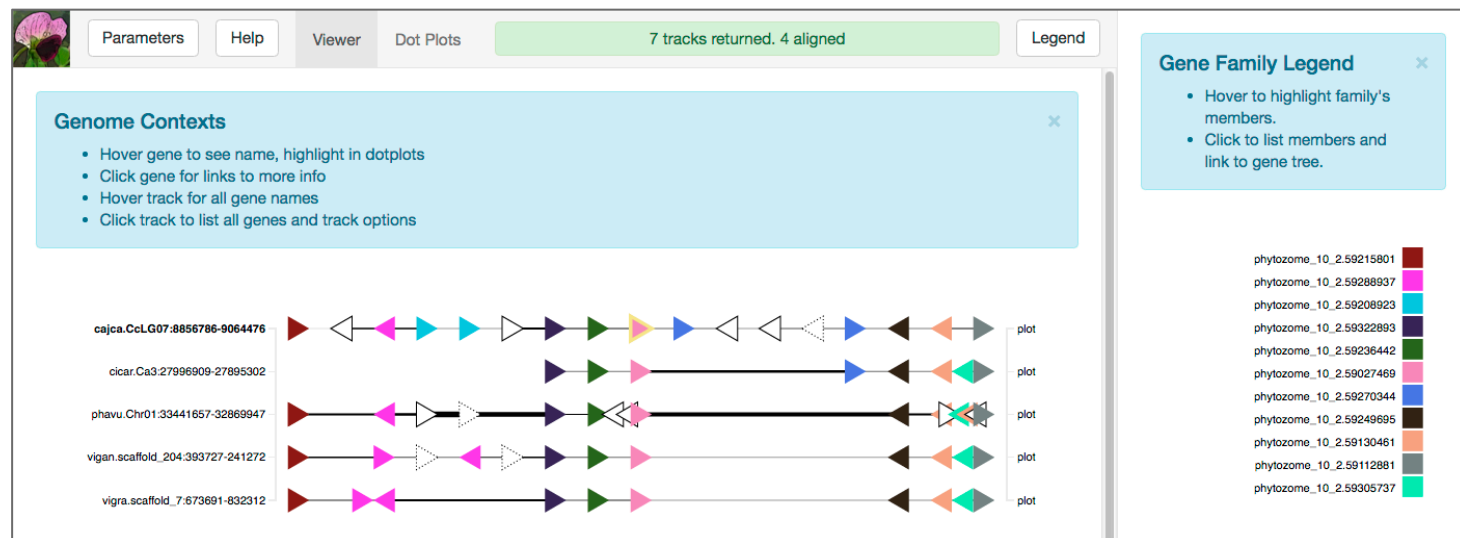
# Development

## Genomic context viewer

NCGR - Alan Cleary and Andrew Farmer

Django + Javascript

Displays gene synteny among the species hosted at LegumeInfo.org.





# Development

## CViTjs (whole genome viewer)

*ISU - Andrew Wilkey, Ethy Cannon & Steven Cannon*

An interactive JavaScript version of CViT.

### Software stack:

RequireJS  
Paper.js  
jQuery  
Bootstrap







# Development

## CViTjs (whole genome viewer)

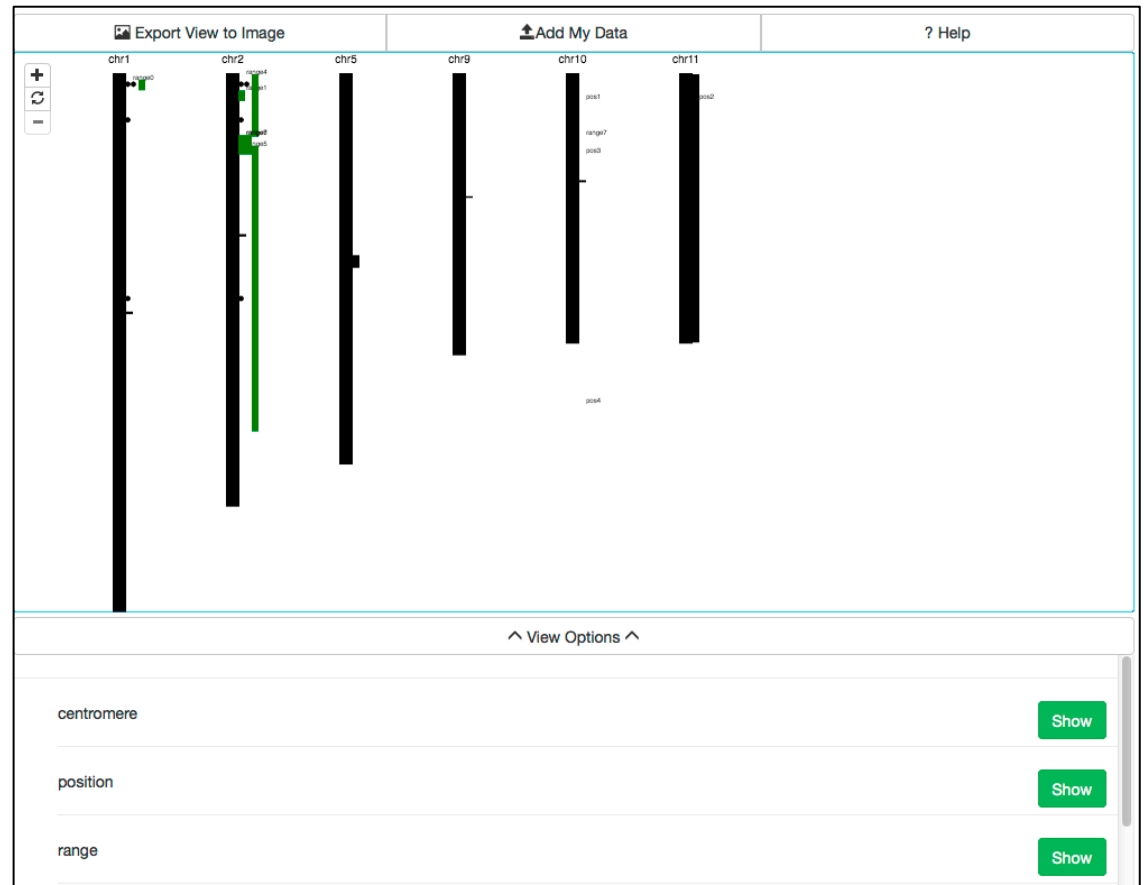
ISU - Andrew Wilkey, Ethy Cannon & Steven Cannon

An interactive JavaScript version of CViT.

### Status:

Approaching beta.

<https://github.com/awilkey/cvitjs>





## Iowa State University

Jacqueline Campbell, Ethy Cannon, **David Fernandez-Baca\***, Shivan Gunda, Prateek Gupta, Wei Huang, Andrew Wilkey, Akshay Yadov



## National Center for Genomic Research

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