

TreeGenes: Past, Present, and Future Development

Jill Wegrzyn

Plant and Animal Genome Conference

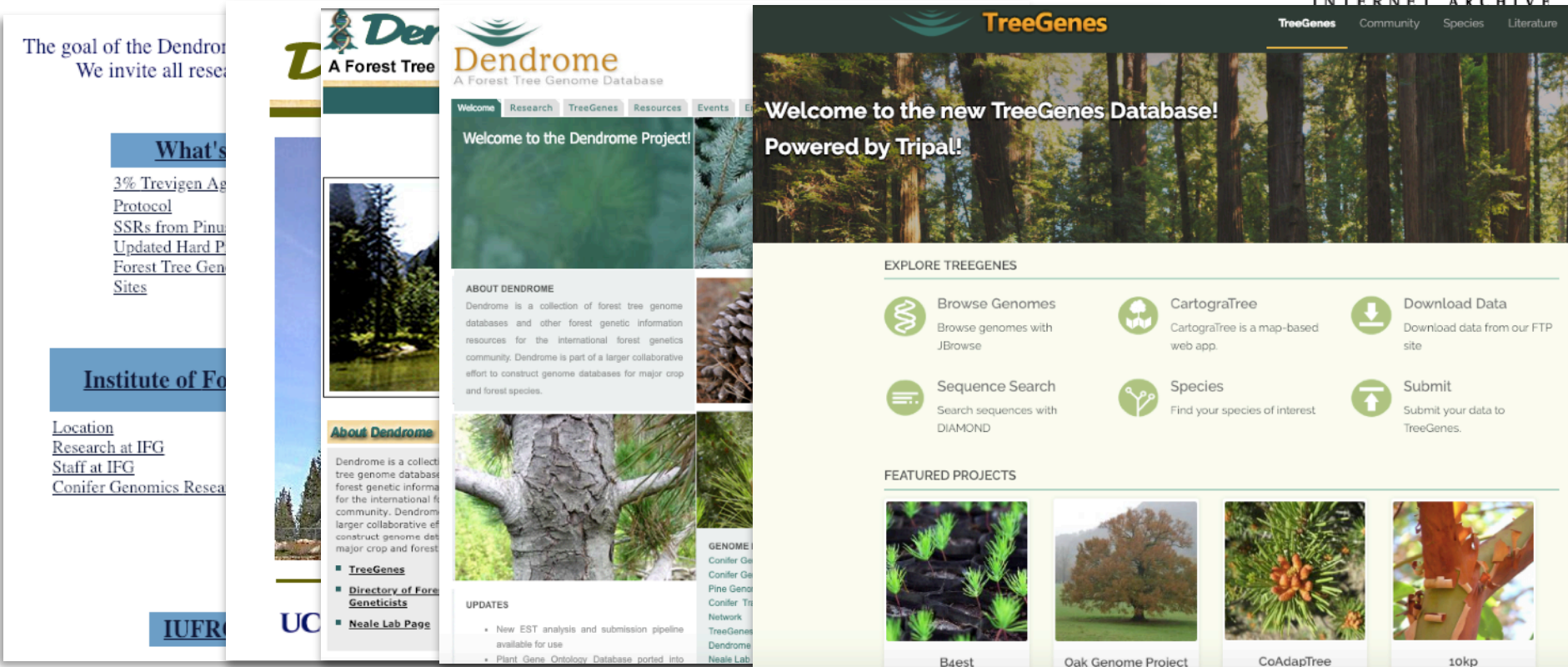
January 14th 2019



**Dendrome/TreeGenes was the original
three USDA-ARS databases**



So much time...so many technologies!



1991:
Dendrome
(stand-
alone
software)



1995:
Database
Online
(ACEDB)



2001:
Oracle
Database



2005:
MySQL



2009:
PostgreSQL



2015:
Tripal
Framework



So much time...so many data types!

Colleague
Directory
Literature
Database
Markers
(SSR, AFLP)

**Genetic
Maps,
Community
Markers
(SSR, AFLP,
RAPD)
ESTs**

Genetic Maps,
Community
Markers,
Community
ESTs
cDNAs

Genetic Maps,
Markers,
Community
ESTs
cDNAs
Phenotypes

Genetic
Maps,
Markers,
Community
ESTs
cDNAs
Phenotypes
**SNPs
Genomes**

Genetic
Maps,
Markers,
Community
ESTs
cDNAs
Phenotypes
SNPs
Genomes
Environmental

1991:
Dendrome
(stand-
alone
software)



1995:
Database
Online
(ACEDB)



2001:
Oracle
Database



2005:
MySQL



2009:
PostgreSQL



2015:
Tripal
Framework

dendrome.ucdavis.edu

**Treegenes.
ucdavis.edu**

**Treegenesd
b.org**

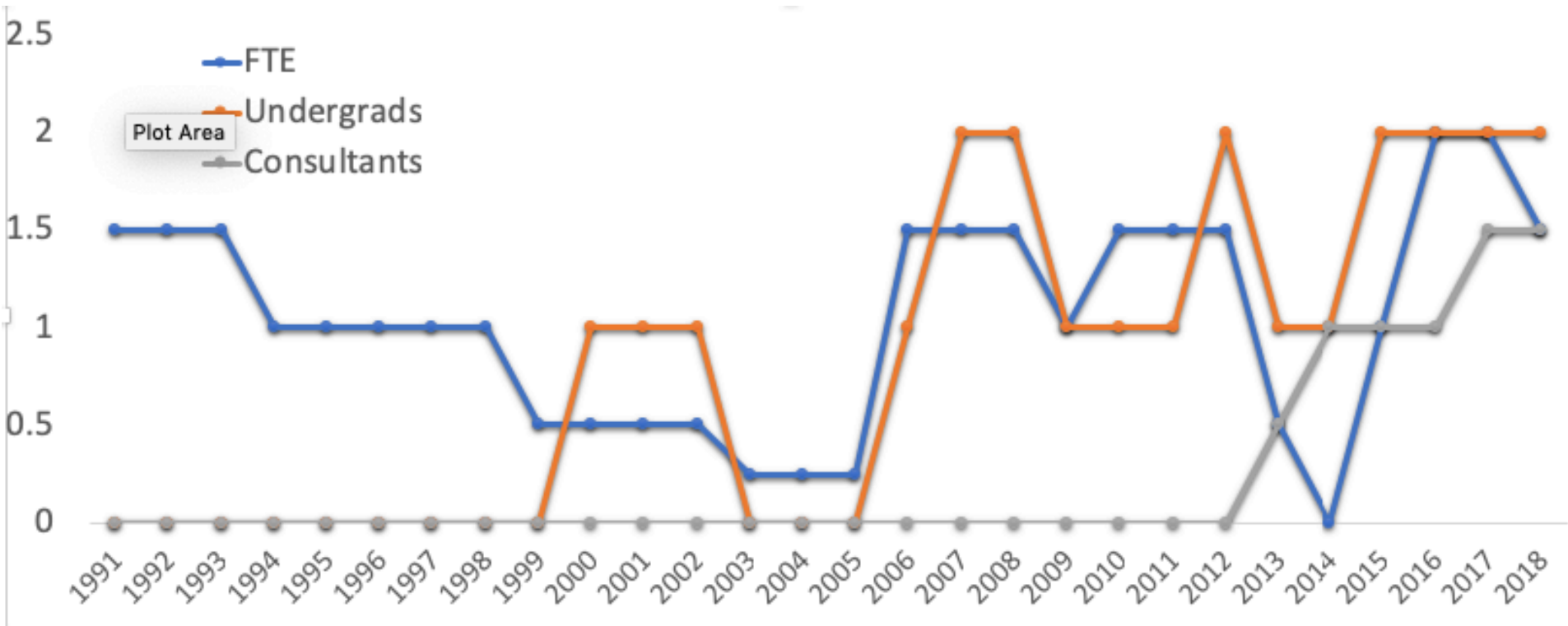


TreeGenes Audience

- Academic Research Labs
- Non-profit research institutions
- US Forest Service
- Industry
 - Timber companies
- JGI/DOE
 - Data exchange
- Genbank
 - Data exchange



TreeGenes Staffing



BT Era (Before Tripal)



Primary Structure

Web

- Custom Frontends
- Search Fields/ Summary Pages
- Advanced Interface (DiversiTree)

Database

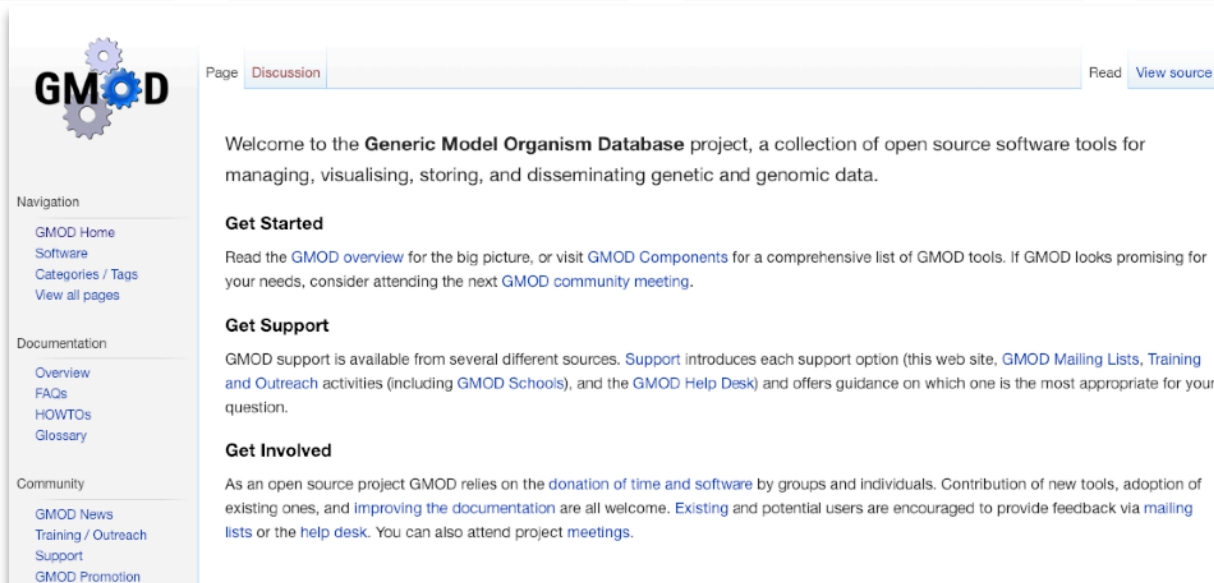
- Custom Schema
- GMOD components:
 - Genetic Maps (CMap)
 - Genomes (Gbrowse/ Jbrowse)

Scope

- Genetic Maps
- Sequence
- Phenotypes
- Genotypes
- Conifers/Forest Trees

Funding

- No *dedicated* funding
 - Forest Service
 - USDA CAP
 - NSF Projects
 - Inbetween? plugging along (i.e. Maintenance)



The screenshot shows the GMOD (Generic Model Organism Database) website. The header features the GMOD logo (three interlocking gears) and navigation links: GMOD Home, Software, Categories / Tags, and View all pages. The main content area is titled "Discussion" and includes a welcome message, a "Get Started" section with links to the GMOD overview and components, a "Get Support" section with links to support options, and a "Get Involved" section with links to donation, documentation, and feedback. The footer contains links for GMOD News, Training / Outreach, Support, and GMOD Promotion.

GMOD

Page [Discussion](#) [Read](#) [View source](#)

Welcome to the **Generic Model Organism Database** project, a collection of open source software tools for managing, visualising, storing, and disseminating genetic and genomic data.

Get Started

Read the [GMOD overview](#) for the big picture, or visit [GMOD Components](#) for a comprehensive list of GMOD tools. If GMOD looks promising for your needs, consider attending the next [GMOD community meeting](#).

Get Support

GMOD support is available from several different sources. [Support](#) introduces each support option (this web site, [GMOD Mailing Lists](#), [Training and Outreach](#) activities (including [GMOD Schools](#)), and the [GMOD Help Desk](#)) and offers guidance on which one is the most appropriate for your question.

Get Involved

As an open source project GMOD relies on the [donation of time and software](#) by groups and individuals. Contribution of new tools, adoption of existing ones, and [improving the documentation](#) are all welcome. [Existing](#) and potential users are encouraged to provide feedback via [mailing lists](#) or the [help desk](#). You can also attend project [meetings](#).

Navigation

- [GMOD Home](#)
- [Software](#)
- [Categories / Tags](#)
- [View all pages](#)

Documentation

- [Overview](#)
- [FAQs](#)
- [HOWTOs](#)
- [Glossary](#)

Community

- [GMOD News](#)
- [Training / Outreach](#)
- [Support](#)
- [GMOD Promotion](#)



AT Era (After Tripal)

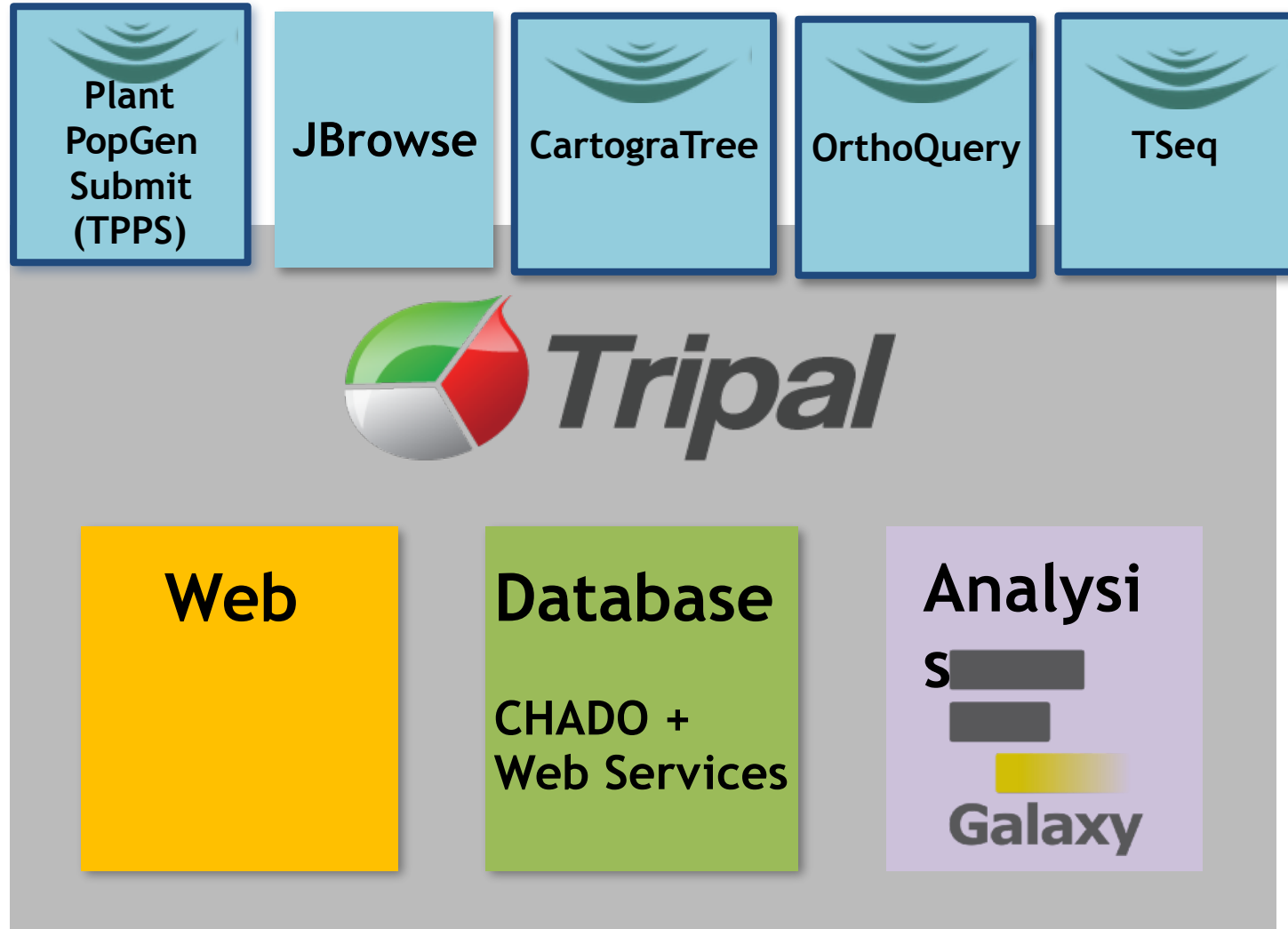


Current Funding

- **NSF PGRP (2015-2019)**
 - Conversion to Tripal
 - Ontologies
 - CartograTree
- **NSF DIBBS (2014-2018)**
 - Tripal Galaxy
 - Module development
 - CartograTree
- **USDA AFRI - PineSNP**
 - Partial project support



Tripal v3 Framework in TreeGenes



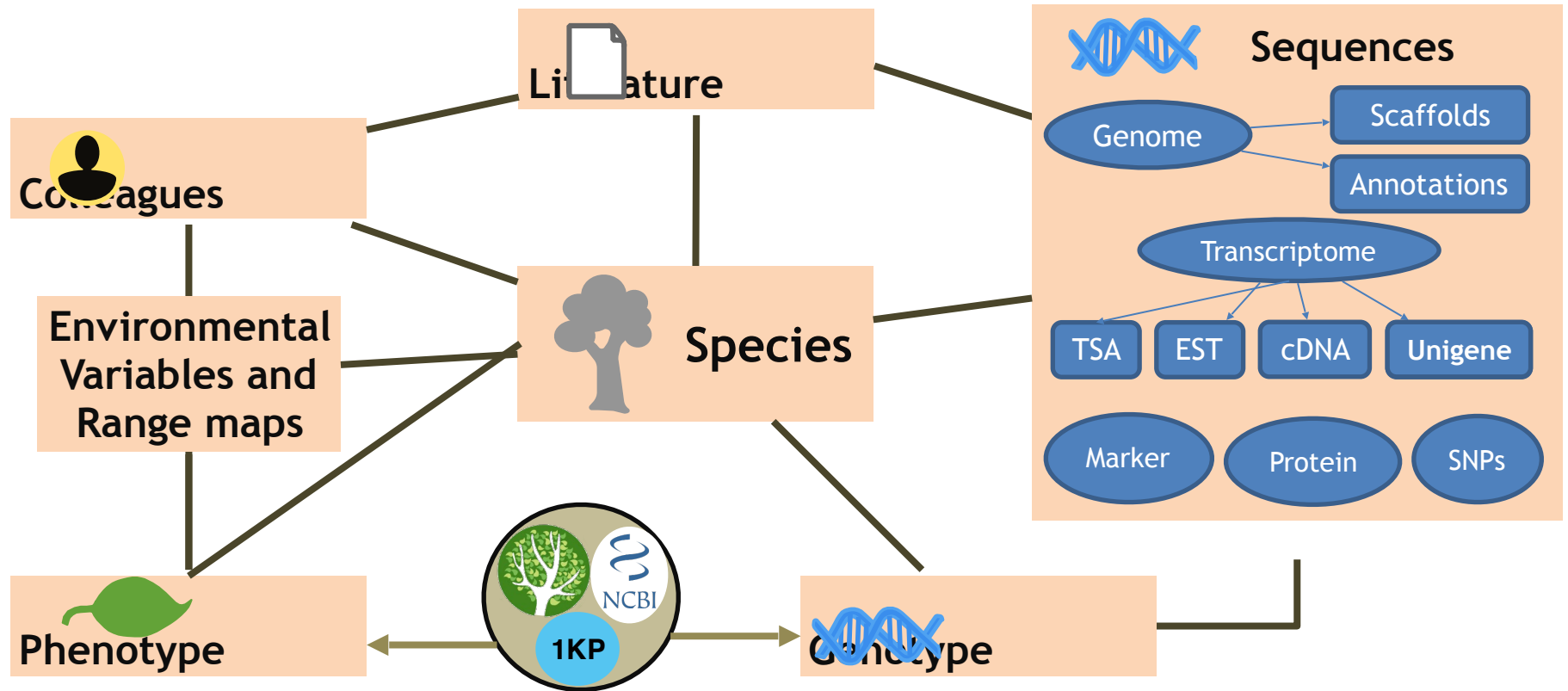
TreeGenes Database: Species

treegenesdb.org



- 1,850 species from 112 genera
 - At least one genetic artifact from each species
- Full genome sequence: 35 species
- Transcriptome/Expression resources: 6,920,817 sequences from 322 species
- 101 genetic maps from 37 species
- **Population studies**
 - Georeferenced trees
 - Extensive genotypic (GBS and array) and phenotypic data

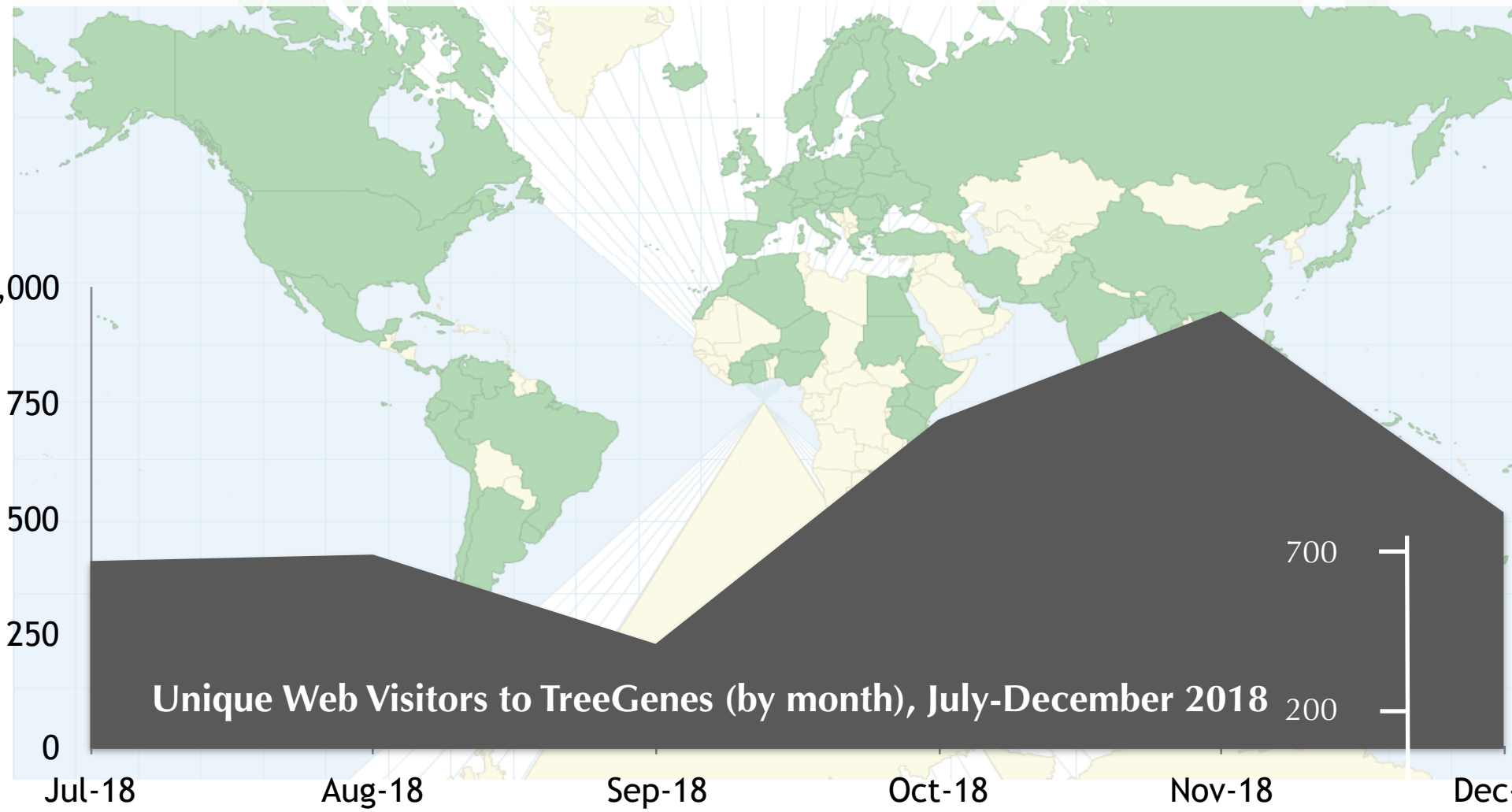
Relational Data in TreeGenes



TreeGenes Database: Users

treegenesdb.org

3,100 unique visitors from 116 countries



Unique Web Visitors to TreeGenes (by month), July-December 2018

Welcome to the new TreeGenes Database!
Powered by Tripal!

EXPLORE TREEGENES



Browse Genomes

Browse genomes with
JBrowse



CartograTree

CartograTree is a map-based
web app.



Download Data

Download data from our FTP
site



Sequence Search

Search sequences with
DIAMOND



Species

Find your species of interest



Submit

Submit your data to
TreeGenes.

MEETINGS

PAG XXVII

January 12 to 16 2019
San Diego, USA

2019 SFTIC

June 3 to 6 2019
Lexington, USA

- [View more meetings](#)

FEATURED PROJECTS



B4est



Oak Genome Project



CoAdapTree



10kp

LATEST LITERATURE

Genetic variation and
signatures of natural selection
in populations of European
beech (*Fagus sylvatica* L.)
along precipitation gradients.
(2018) Tree Genetics &
Genomes

Community Resources: Colleague directory, mailing
list, meetings, employment listings, and literature



Welcome!

[Home](#)

[View](#)
[Edit](#)
[Manage display](#)
[Devel](#)

Welcome to



You're now logged in and ready to go!

USER MENU

[Edit Profile](#) >

[Log out](#) >

[My account](#) >

[Add new job posting](#) >

[Add new meeting posting](#) >

MEETINGS

PAG XXVII

January 12 to 16 2019
San Diego, USA

2019 SFTIC

June 3 to 6 2019
Lexington, USA

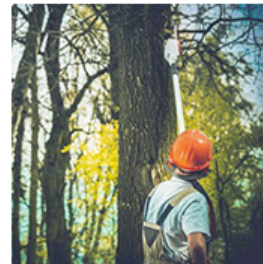
• [View more meetings](#)



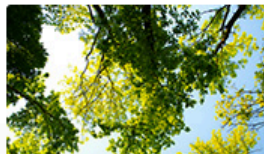
[Add/Edit Profile](#)



[Add/Edit Workshop/Conference](#)



[Add/Edit Employment Listings](#)



Free account to: edit profile, add listings, submit data!

Eucalyptus grandis

Summary

Genome

Transcriptome

Literature

TPPS



Species: Eucalyptus grandis

Common Name: Grand Eucalyptus

TreeGenes Code: Eugr

Lineages: Viridiplantae; Streptophyta; Streptophytina; Embryophyta; Tracheophyta; Euphyllophyta; Spermatophyta; Magnoliophyta; Mesangiospermae; eudicotyledons; Gunneridae; Pentapetalae; rosids; malvids; Myrtales; Myrtaceae; Myrtoideae; Eucalypteae; Eucalyptus

Haploid Chromosome Number: 12

GBIF: <https://www.gbif.org/species/3177028>

Bioproject Records: 50

Biosample Records: 130



TreeGenes: Genome Access



Betula nana

Version: v1.0
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)



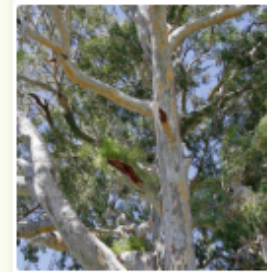
Carica papaya

Version: v0.4
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)



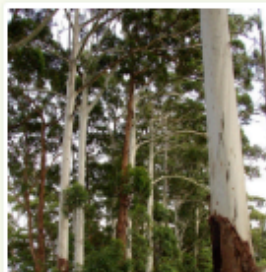
Elaeis guineensis

Version: v1.0
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)



Eucalyptus camaldulensis

Version: v1.0
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)



Eucalyptus grandis

Version: v1.0
Organism Detail | JBrowse
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)



Fraxinus excelsior

Version: v0.5
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)



Ginkgo biloba

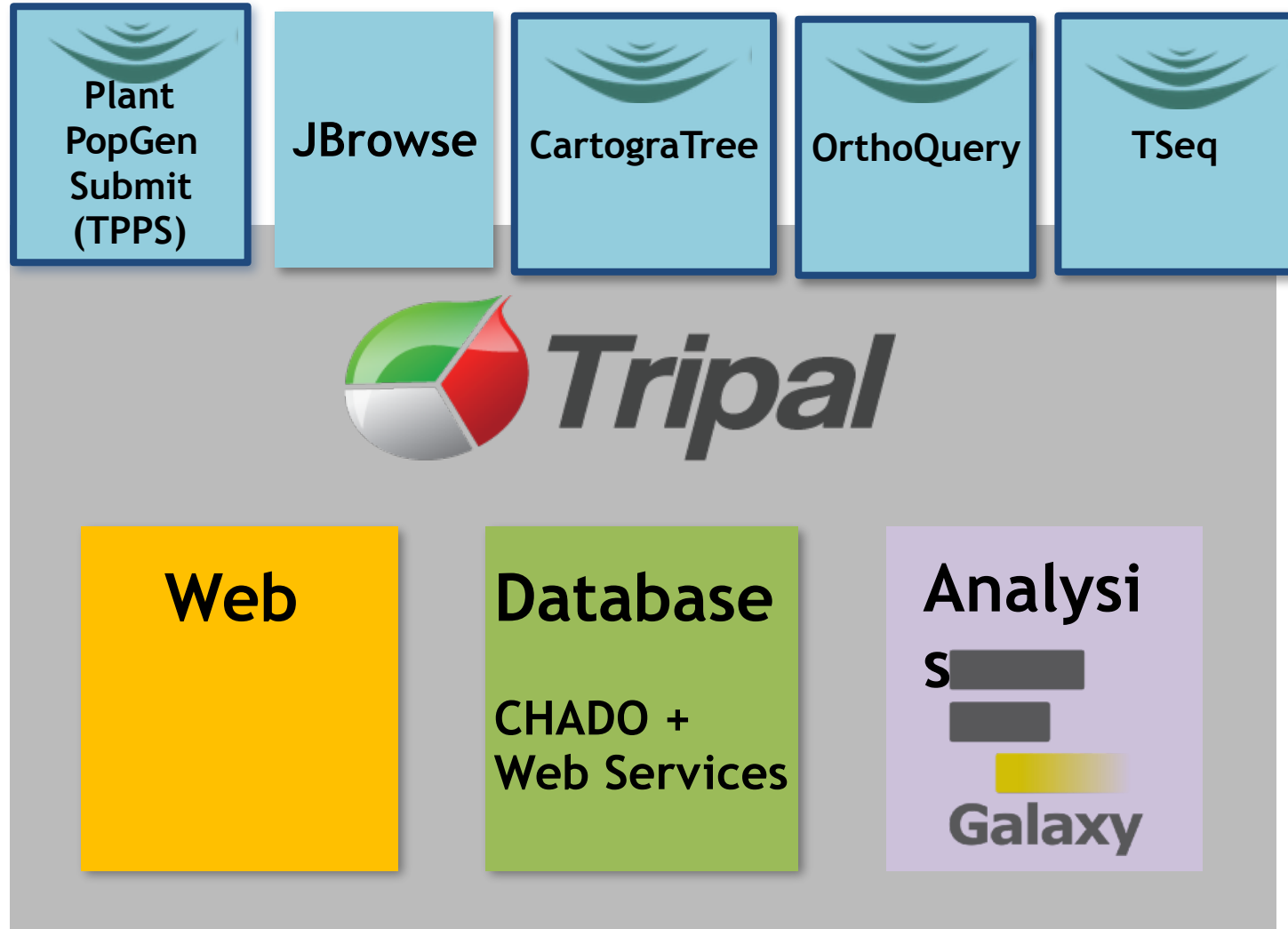
Version: v1.0
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)



Gnetum montanum

Version: v1.0
Organism Detail | JBrowse
📄 Genome FASTA
📄 Annotation (GFF3)
📄 Genes (FASTA)
📄 Proteins (FASTA)

Tripal v3 Framework in TreeGenes



TSeq

Diamond search

BLASTp/x


Faster performance

BLAST

BLASTn

**Analysis on remote
(non-web) server**



 **TreeGenes**

TSeq: Tripal Sequence Similarity Search

▼ SIMILARITY SEARCH OVERVIEW

Sequence similarity search is supported in TreeGenes against genes, transcripts (BLASTN) while protein or translated protein searches are executed with BLASTx (BLASTX) at a similar sensitivity. Both packages accept similar input parameters. You can provide FASTA formatted sequences for searching. You can select from a list of databases provided in FASTA format and formatted for you.

SEQUENCE QUERY TYPE

☐ Protein

☒ Nucleotide (coding or whole genome)

Database Search Type

PROVIDE/LOAD QUERY SEQUENCE

```
ccgaagtccttgctaagtatttccgggtcatcccatgctttctcaaggatccttcatgcattatgtt
tttcatgtatgtgtctcacccgggcaagctatccgtataaaccaattatccaagcattccctcgattt
```

No file chosen

TARGET/DATABASE SELECTION

Protein

Protein (UniGene)

Protein (TSA)

TreeGenes UniGenes to OrthoQuery

TreeGenes: OrthoQuery Module



3 Primary Uses Cases for the OrthoQuery Module



Input: Small Set of Protein Sequences

Question: Which gene family does it belong to?

Process:

1. Map existing orthogroups to the protein sequence(s)
2. Provide visualization
3. Assign functional annotation

Input: Transcriptome/Gene Set

Question: Orthologous genes, expansion/contraction of gene families

Process:

1. Construct Proteome
2. Discover new orthogroups with existing tools
3. Provide visualization & statistical results

Input: Proteome

Question: Orthologous genes, expansion/contraction of gene families

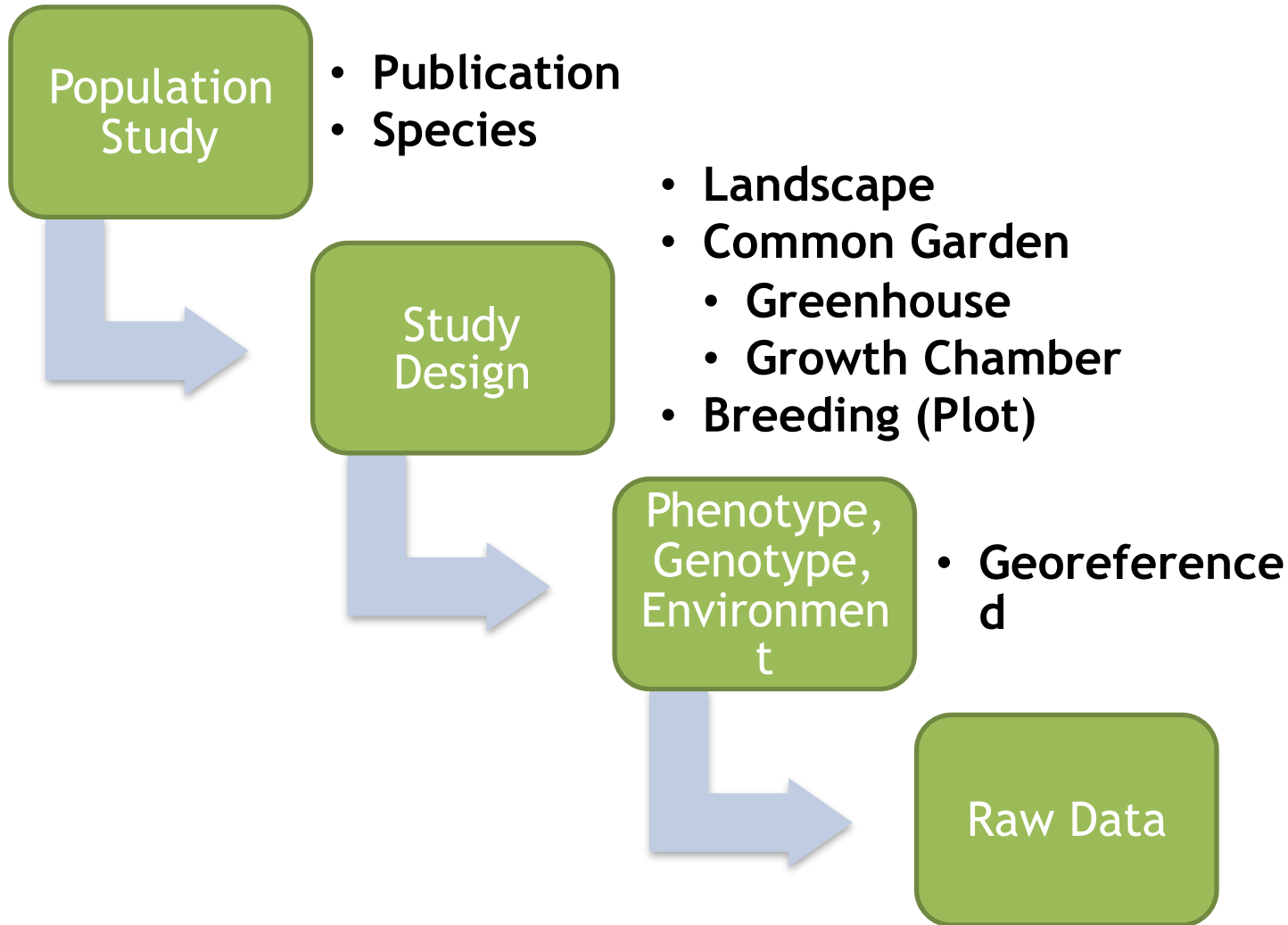
Process:

1. Discover new orthogroups with existing tools
2. Provide visualization & present statistical results

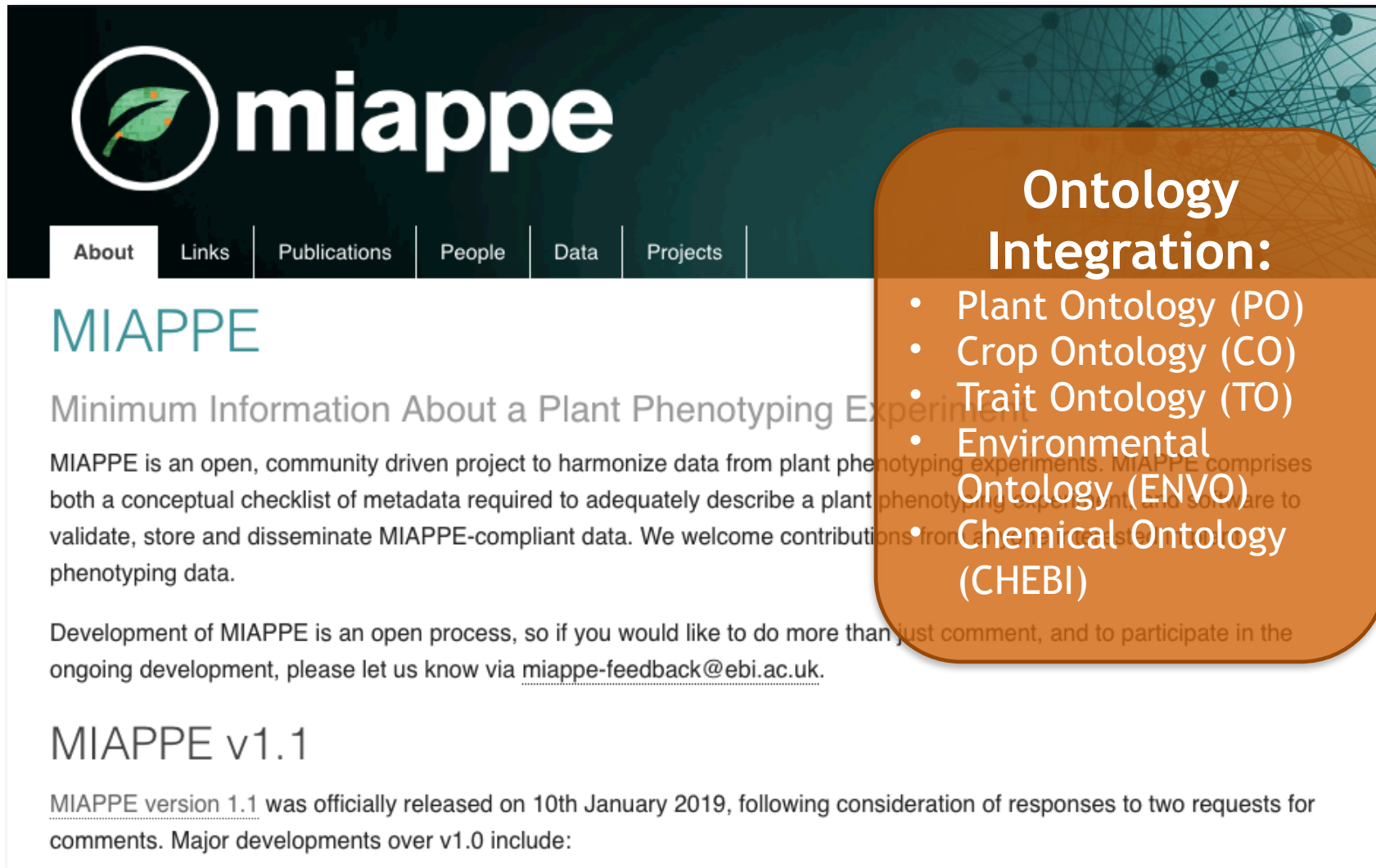
DEMO

CONTINUE TO ORTHOQUERY

Tripal Plant PopGen Submit (TPPS)



Minimal Information About a Plant Phenotyping Experiment (MIAPPE)



The image shows a screenshot of the MIAPPE website. The header features the MIAPPE logo, which consists of a green leaf icon inside a white circle, followed by the text "miappe" in a bold, white, sans-serif font. Below the logo is a navigation bar with links: "About", "Links", "Publications", "People", "Data", and "Projects". The main content area has the heading "MIAPPE" in a large, teal, sans-serif font, followed by the subtitle "Minimum Information About a Plant Phenotyping Experiment". A paragraph describes MIAPPE as an open, community-driven project to harmonize data from plant phenotyping experiments. An orange rounded rectangle is overlaid on the right side of the page, containing the text "Ontology Integration:" followed by a bulleted list of four ontologies: Plant Ontology (PO), Crop Ontology (CO), Trait Ontology (TO), and Environmental Ontology (ENVO). Below this list, the text "Chemical Ontology (CHEBI)" is also visible. At the bottom of the page, the text "MIAPPE v1.1" is displayed, followed by a paragraph stating that MIAPPE version 1.1 was officially released on 10th January 2019.

miappe

About | Links | Publications | People | Data | Projects

MIAPPE

Minimum Information About a Plant Phenotyping Experiment

MIAPPE is an open, community driven project to harmonize data from plant phenotyping experiments. MIAPPE comprises both a conceptual checklist of metadata required to adequately describe a plant phenotyping experiment, and software to validate, store and disseminate MIAPPE-compliant data. We welcome contributions from the plant phenotyping community.

Development of MIAPPE is an open process, so if you would like to do more than just comment, and to participate in the ongoing development, please let us know via miappe-feedback@ebi.ac.uk.

MIAPPE v1.1

MIAPPE version 1.1 was officially released on 10th January 2019, following consideration of responses to two requests for comments. Major developments over v1.0 include:

Ontology Integration:

- Plant Ontology (PO)
- Crop Ontology (CO)
- Trait Ontology (TO)
- Environmental Ontology (ENVO)
- Chemical Ontology (CHEBI)

TreeGenes Ontology Integration

TreeGenes Phenotype and Structure Ontology Directory

TREEGENES PHENOTYPE AND STRUCTURE ONTOLOGY DIRECTORY

TreeGenes is actively curating submitted traits and structures and assigning these traits to the following ontologies: Plant Ontology (structure), Trait Ontology (traits), Crop Ontology (woody trait ontology), and PATO (descriptive ontology). When possible, assignments are made to existing terms that are curated by the [Planteome](#) and [Crop Ontology](#) projects. For terms that are not yet assigned to Assignment of individual measurements and structures to an ontological framework provides improved recovery of data downstream for all users. This also enables comprehensive analytical pipelines that can efficiently integrate across a multitude of independent studies. To submit your phenotype and/or genotype study, please use the [TriPal Plant Population Genetics Submit Pipeline](#).

We currently have **306** unique phenotypes described on **22** unique structures representing a total of **724265** phenotypic measures from **41451** samples representing **18** species.

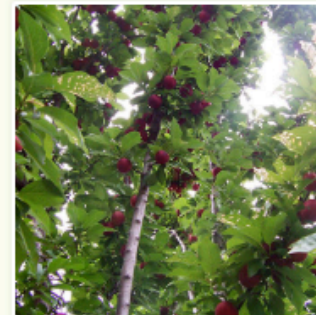
ONTOLOGY TERM SEARCH



Plant Ontology (PO)



Trait Ontology (TO)



Crop Ontology (CO)

Tripal Plant PopGen Submit (TPPS)

Phenotype Metadata File: Please upload a file containing columns with the name, attribute, description, and units of each of your phenotypes: *

 phenotype metadata.xlsx **REMOVE**

File Upload empty field: NA

By default, TPPS will treat cells with the value "NA" as empty. If you used a different empty value indicator, please provide it here.

▼ DEFINE DATA

Please define which columns hold the required data: Phenotype name

name	attribute	units	
Phenotype Name/Identifier	Attribute	Units	Description
phenotype 1	age	years	quantitative
phenotype 2	age	years	quantitative
phenotype 3	age	years	quantitative

**TreeGenes Data
Repository Accession
(TGDR####) -> DOI**

Phenotype file below:

Phenotype 2 Attribute: *

Some examples of attributes include: "amount", "width", "mass density", "area", "height", "age", "broken", "time", "color", "composition", etc.

Phenotype 2 Description: *

Please provide a short description of Phenotype 2

Phenotype 2 Units: *

☐ Humidity regime

[Click here to view trees on map!](#)



Map data ©2018 Google, IN Terms of Use

FAIR
Findable
Accessible



TreeGenes to CartograTree

TPPS/TGDR DETAILS FOR TGDR001

Attribute	Details
Accession	TGDR001
Title	Association genetics of traits controlling lignin and cellulose biosynthesis in black cottonwood (<i>Populus trichocarpa</i> , Salicaceae) secondary xylem.
Species	<i>Populus trichocarpa</i>
Study Type	GxP
File Downloads	<ul style="list-style-type: none">✓ ASSOCIATION RESULTS FILE 1 FILE✓ GENOTYPES SNP✓ GPS COORDINATES✓ HAPLOTYPE DATA FILE✓ PHENOTYPES✓ PHENOTYPES DEFINITIONS
CartograTree	View in CartograTree
Tree Count	1376
Phenotype Count	4032
Unique Phenotypes	3



CartograTree: Integrating environmental layers with georeferenced trees

The screenshot displays the CartograTree web application interface. The top navigation bar includes the TreeGenes logo, the application name 'CartograTree', and links for 'Analyze' and 'About'. A 'Login' button is located in the top right corner.

The left sidebar contains several sections:

- Map Options:** Includes a 'LAYERS +' button and a 'Map Summary' toggle (OFF/ON).
- Tree Dataset Sources:** Lists 'TreeGenes', 'TreeSNAP', and 'DRYAD', each with an 'OFF/ON' toggle.
- Organisms:** Features a 'Family' dropdown menu and a list of taxonomic levels: 'Family', 'Genus', 'Species', and 'Publications'.

The central 'LAYERS' panel is highlighted with an orange border and lists various environmental data layers:

- WorldClim v.2
 - Precipitation (WorldClim v2) ▾
 - Temperature (WorldClim v2) ▾
 - Solar Radiation (WorldClim v2) ▾
 - Solar radiation January: OFF/ON toggle, Opacity 39% slider.
 - Wind Speed (WorldClim v2) ▾
 - Water Vapor (WorldClim v2) ▾
- Major Soil Types (Conservation Biology Institute) ▾
- Species Range Maps ▾
- Land Cover ▾
- PET and Aridity (CGIARCSI) ▾
- Canopy Height ▾

The main map area shows a geographical view of the Southeastern United States (Kentucky, Tennessee, Alabama, Georgia, North Carolina, South Carolina, Virginia). Numerous pink tree icons are plotted on the map. A pop-up window for a specific tree is displayed, showing:

- Latitude: 36.959 | Longitude: -86.338
- Coordinate type: approximate
- Species: **Celtis occidentalis**
- ID: treesnap.194
- Buttons: DEL, ADD, and a '1 of 1' indicator.

On the right side of the map, there is a 'CartograTree Map Summary' panel with a table:

Publication Datasets	Count
White Sulphur Springs	0
Beckley	0
Bluefield	0
Roanoke	0
Rocky Mount	0
Wytheville	0
South Boston	0
South Hill	0
Farmville	0
Myrtle Beach	0
Wilmington	0
Charleston	0
Walterboro	0
Beaufort	0
Savannah	0
Douglas	0
Albany	0
Eufaula	0
Montgomery	0
Troy	0
Greenville	0
Greensboro	0
Winston-Salem	0
Fayetteville	0
Lumberton	0
Whiteville	0
Wilmington	0
Myrtle Beach	0
Wilmington	0
Myrtle Beach	0

A 'SAVE' button is located below the table. A color scale legend for 'nodata' is visible on the far right.



CartograTree: Integrating environmental layers with georeferenced trees

The screenshot displays the CartograTree web application interface. The top navigation bar includes the TreeGenes logo, the CartograTree name, and links for 'Analyze' (highlighted with a red circle) and 'About'. The left sidebar contains several panels: 'Phenotypes' with an 'Additive' toggle set to 'ON', 'Phenotype & Trait Ontology' with a search bar, 'Plant Ontology' with a search bar, and 'Plant Ontology' with a list of selected terms: 'inflorescence bud' (306), 'leaf' (1201), and 'bud burst stage' (435). At the bottom left, there is a 'Marker Type' dropdown and a 'Collapse' button. The main area is a map of Europe showing several tree markers. A detailed popup window is open for a tree marker in the Netherlands, displaying the following information:

- Latitude: 49.25 | Longitude: 3.1
- Coordinate type: exact
- Fagus sylvatica (angiosperm)**
- Family: Fagaceae
- ID: TGDR069-190141
- DEL ☒ ADD
- Environmental Data:
- 1 of 15

The map shows the Netherlands, Luxembourg, and France, with various cities and geographical features labeled. The TreeGenes logo is visible in the bottom right corner of the map area.

CartograTree: Save searches locally and select for meta-analysis

The image displays the CartograTree web application interface, which is a Forest Tree Map Utility. The interface is divided into several sections:

- Left Panel (TreeGenes CartograTree):** Contains a sidebar with various ontology categories and their associated trait counts.
 - Phenotypes:** Additive (OFF/ON toggle), Phenotype (1201), Phenotype & Trait Ontology (1201), Plant Ontology (435).
 - Plant Ontology:** Inflorescence bud (308), leaf (1201), bud burst stage (435).
 - Marker Type:** Collapse button.
- Main Panel (CartograTree Analysis):** Displays a map of France with tree locations marked. The map is titled "CartograTree Analysis" and "A Forest Tree Map Utility".
- Analysis Workflow:** The main panel shows a sequence of steps: "Select State of Map", "Additional Options", and "Summary and Confirm".
- Current Map State:** A table showing the current state of the map.

# Trees	# Species	# Layers
1201	0	1
- Load Saved Searches:** A table showing saved searches.

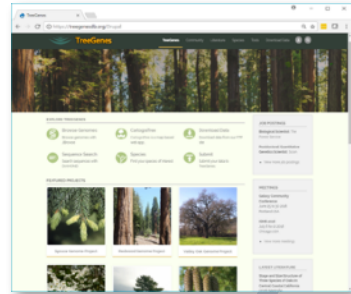
Date	Title	# Trees	# Species
- Analysis type:** A dropdown menu showing "Landscape GxE".
- Publications Selected:** A table showing selected publications.

ID	Title	Author	Year	# Trees	Study type	Status
- Environmental variables:** A table showing environmental variables.

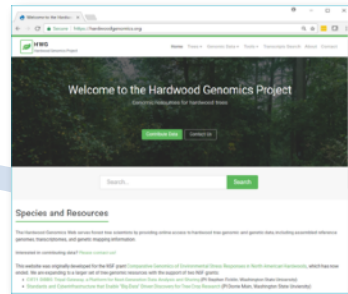
Layer name	Source	Environmental values
Solar radiation January	http://worldclim.org/version2	<input checked="" type="checkbox"/> Solar_radiation
- Navigation:** Buttons for "BACK", "NEXT", and "CLOSE".



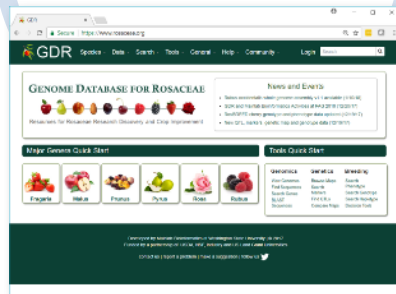
Bringing Analytical Capacity to the Data



Tree Genes

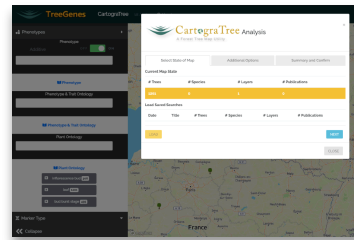


Hardwood Genomics



Genome Database for Rosaceae

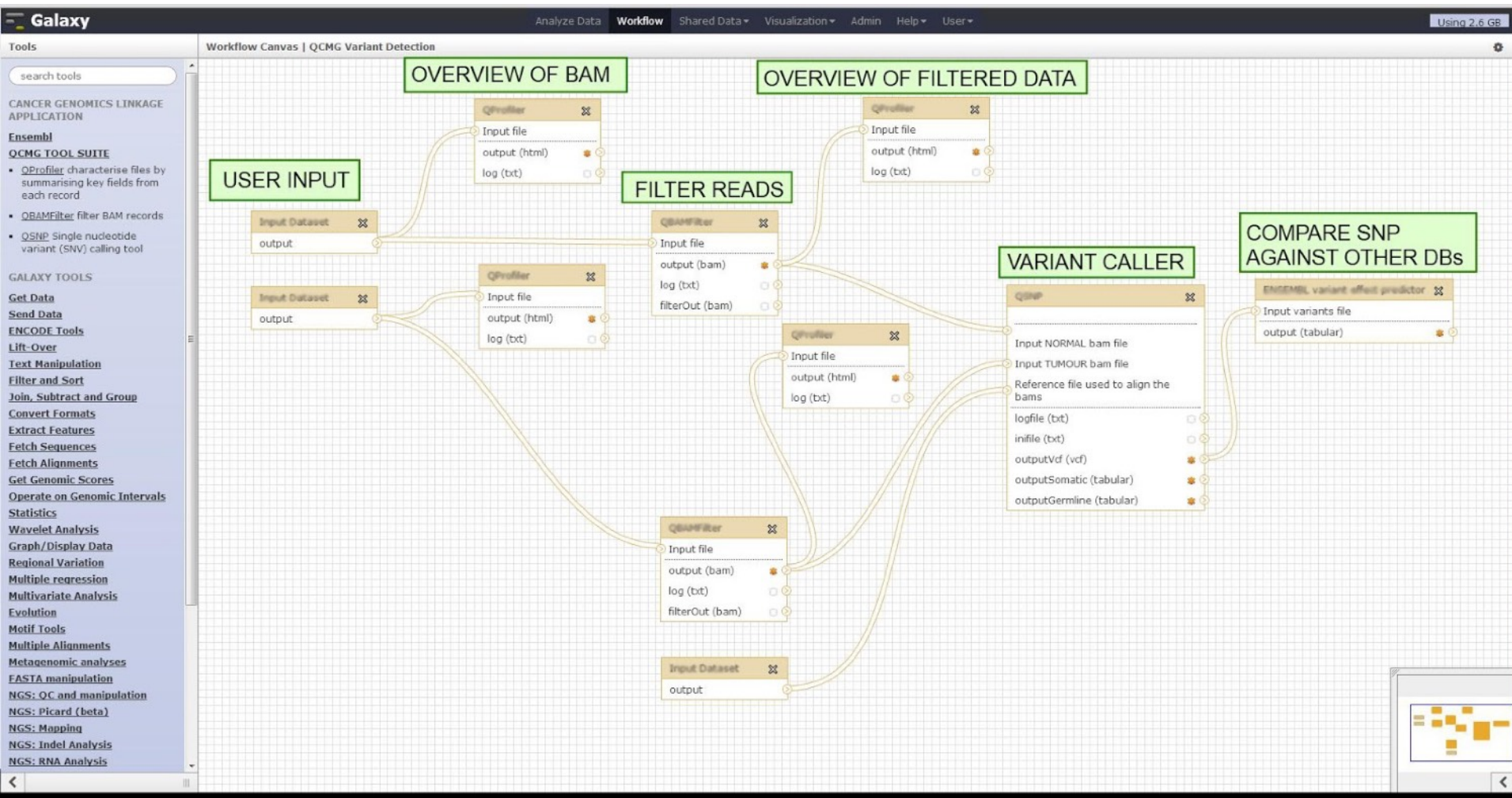
CartograTree



Galaxy
PROJECT



Galaxy: Open Source Web-based Platform for Bioinformatic Analysis



Workflows for Landscape Genomics: Integrating across diverse datasets

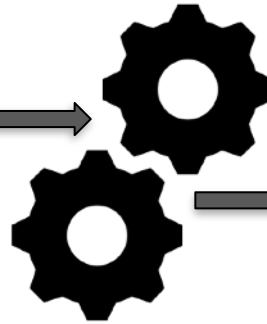
	SNP1	SNP2	SNP3	SNP4	SNP5	SNP6	SNP7	SNP8	SNP9	SN
TREE1	0	0	0	0	0	0	0	0	0	0
TREE2	1	0	0	0	0	0	0	0	0	0
TREE3	1	0	0	0	0	0	0	1	1	0
TREE4	1	0	0	0	0	0	0	0	0	0
TREE5	1	0	0	0	0	0	0	0	0	0
TREE6	1	0	0	0	0	0	0	1	0	0
TREE7	0	0	0	0	0	0	0	1	1	0
TREE8	0	0	0	0	0	0	0	0	1	0
TREE9	1	0	1	1	0	1	0	0	1	0
TREE10	0	0	0	1	0	0	0	0	0	0

Genotypic data

	PC1	PC2	PC3	PC4	PopStr
TREE1	-8.648228102	3.173037266	3.66273579	-0.177338137	-8.554180345
TREE2	-8.554180345	2.43752863	0.93398487	0.04374811	0.37830172
TREE3	3.94101741	0.4768156	0.093398487	0.04374811	0.37830172
TREE4	0.4768156	0.093398487	0.04374811	0.37830172	0.37830172
TREE5	0.093398487	0.04374811	0.37830172	0.37830172	0.37830172
TREE6	0.04374811	0.37830172	0.37830172	0.37830172	0.37830172
TREE7	0.37830172	0.37830172	0.37830172	0.37830172	0.37830172
TREE8	0.37830172	0.37830172	0.37830172	0.37830172	0.37830172
TREE9	-8.570749832	2.761219441	4.189358619	0.120877968	-9.732114439
TREE10	-8.570749832	2.761219441	4.189358619	0.120877968	-9.732114439

Environmental data

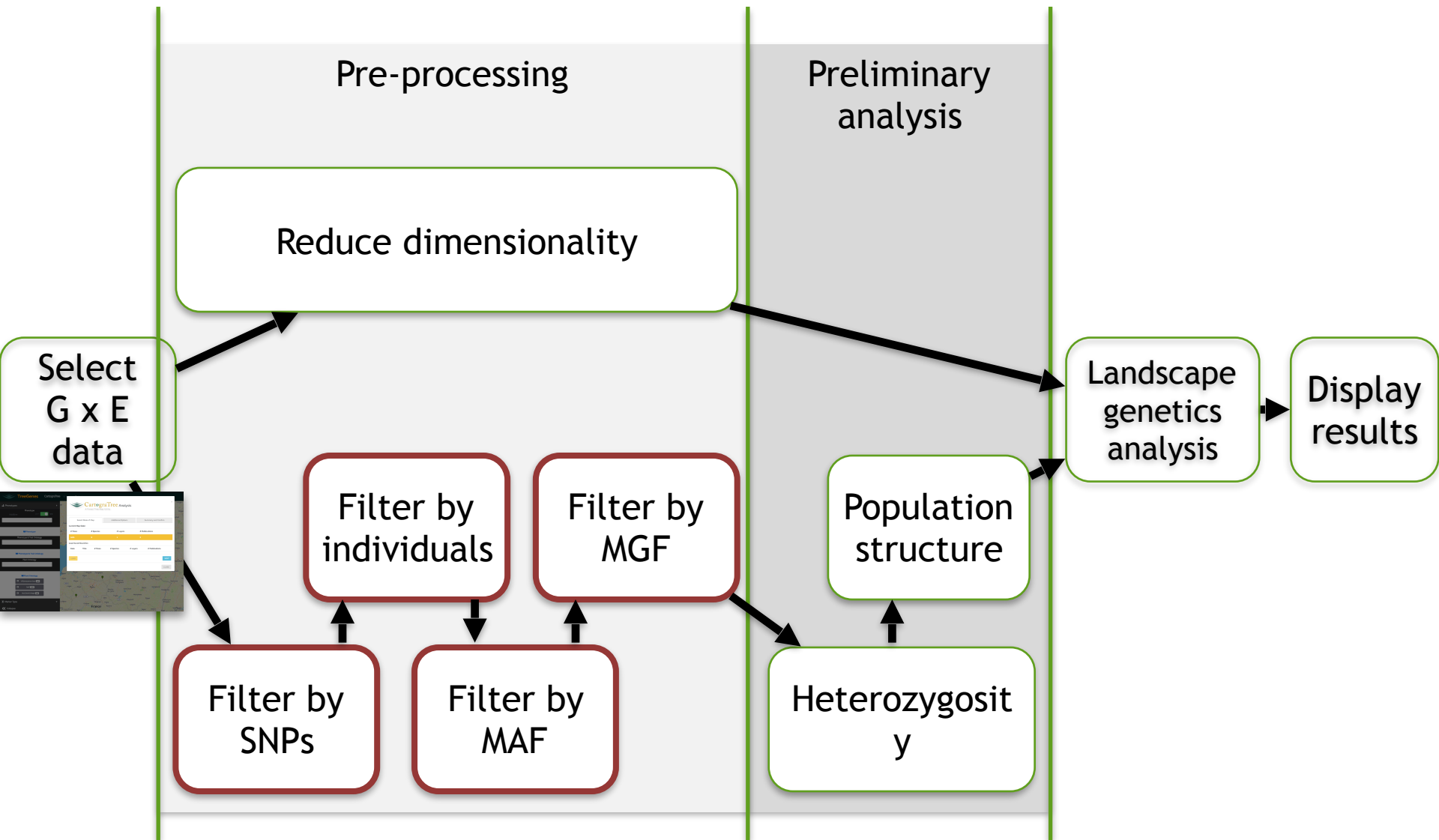
Galaxy



Marker	Env_1	Env_2	Loglikelihood	Gscore	WaldScore	NumError	Efron	McFadden	M
SNP1	PC1	PC3	-439.2146473	31.677384	30.54585431	0	0.192739468	0.034806126	0
SNP2	PC1	PopStr	-351.0	0	0	0	0.248893702	0.037839423	0
SNP3	PC4	PopStr	-350.0	0	0	0	0.231231003	0.041423415	0
SNP4	PC3	PopStr	-376.0	0	0	0	0.345328702	0.029909067	0
SNP5	PC1	PC3	-495.0	0	0	0	0.104945853	0.020848599	0
SNP6	PC1	PC4	-439.0	0	0	0	0.093285957	0.020636018	0
SNP7	PC3	PopStr	-423.0	0	0	0	0.267726345	0.023629761	0
SNP8	PC3	PopStr	-355.0	0	0	0	0.20534412	0.025734199	0
SNP9	PC1	PC3	-454.1183637	18.47638759	17.29764504	0	0.045307766	0.019937548	0

Correlated markers

Workflows: Executed in Galaxy with metadata



Sustainability?



Sustainability

Funding

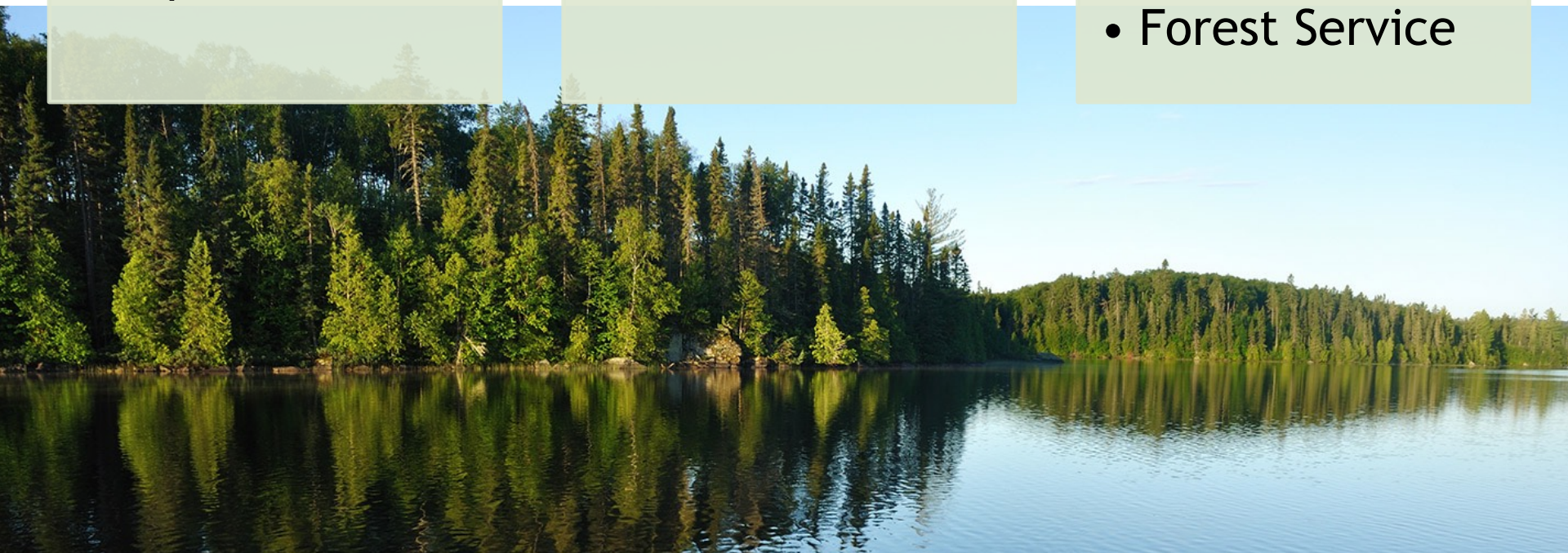
- CartograTree
- Modules + APIs
- Tripal Core

Collaborative

- Consultant
- DMP
Coordination

Industry/NGO/Gov

- Industry
partners?
- GTTN
- Forest Service



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