CartograPlant: Integrating, visualizing, and analyzing genotype, phenotype, and environmental data for georeferenced plants

Jill Wegrzyn



Team!

- Irene Cobo-Simon Postdoctoral Scholar
- Rish Ramnath Lead Developer
- Vlad Savitsky

 TPPS/TPPSc Developer
- Emily Grau Lead Database Administrator of TreeGenes
- Gabe Barrett Analytic workflow developer
- Sean Buehler Tripal Developer
- Shay Muhonen TreeGenes/CartograPlant Coordinator
- Meg Staton Lab (UTK) TreeSnap! Noah Caldwell

Biocuration Team Lead (UConn): Meghan Myles

- Curation Team: Victoria Burton, Maddie Gadomski, Isabella Harding, Jeff Gamer, and Rachel Wolther
- Nic Herndon Lab (ECU)!



Funded by USDA-NIFA #2018-09223 Funded by AG2PI



Today's Schedule (in EST!)

11:00-11:20 Introduction to CartograPlant - Dr. Jill Wegrzyn

11:20-11:40 Introduction to Data Submission with TPPS/TPPSc - Emily Grau

11:40-12:00 Introduction to Data Collection/Mobile Phenotyping with TreeSnap - Dr.

Margaret Staton

12:00-12:15 Break

12:15-12:35 Behind the Scenes of CartograPlant - Environmental Layers and Data - Risharde

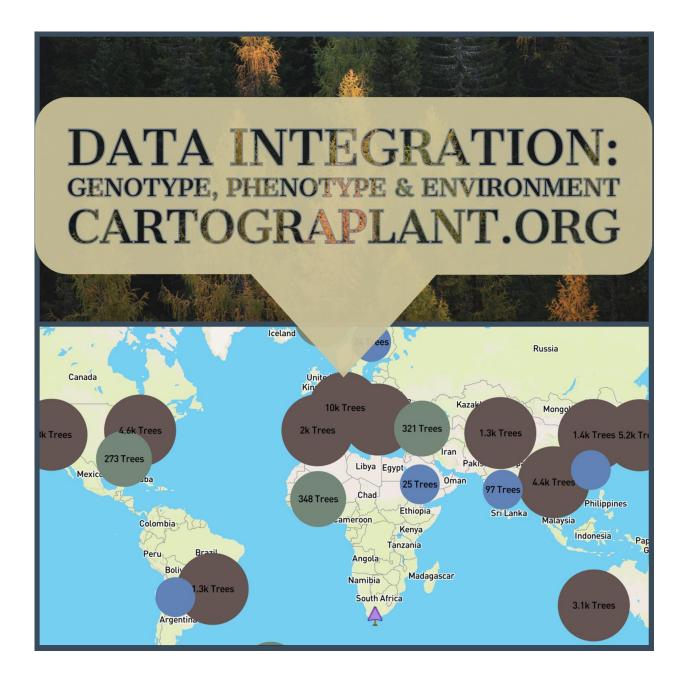
Ramnath

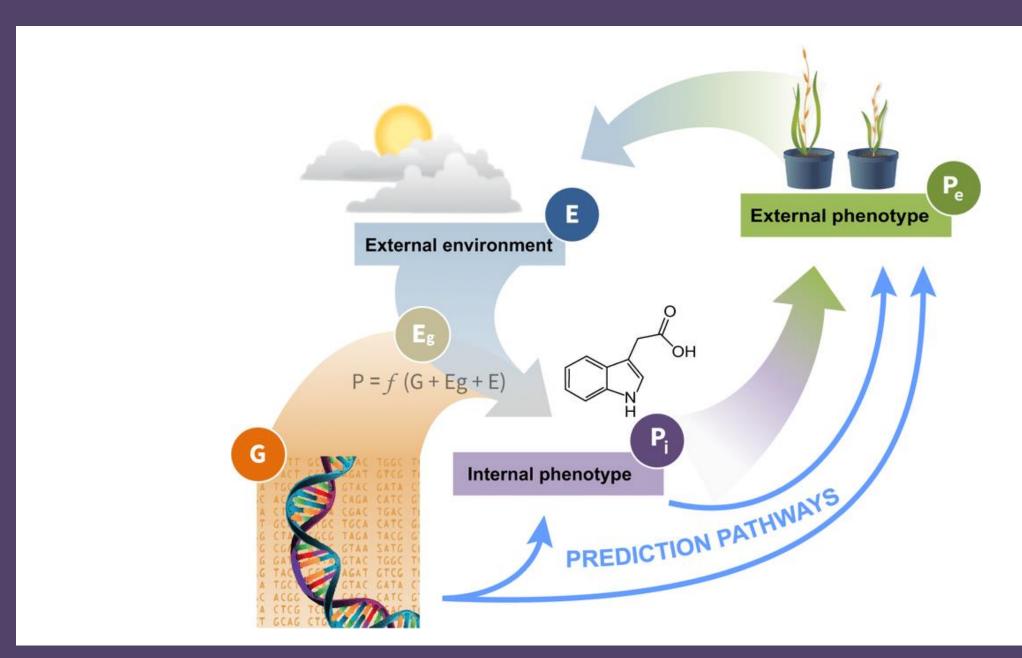
12:35-12:55 Analytics with CartograPlant (GWAS and GEA). Part 1 - Gabriel Barrett

12:55-1:15 Analytics with CartograPlant (GWAS and GEA). Part 2 – Dr. Irene Cobo-Simon

CartograPlant

Web-based and mapbased platform to facilitate metaanalysis across scales (genes to environment)





Who needs this data integration?

Researchers that study georeferenced plant populations!

- Pests and Pathogens
- Breeding
- Assisted migration
- Invasive plants
- Climate adaptation
- Timber tracking





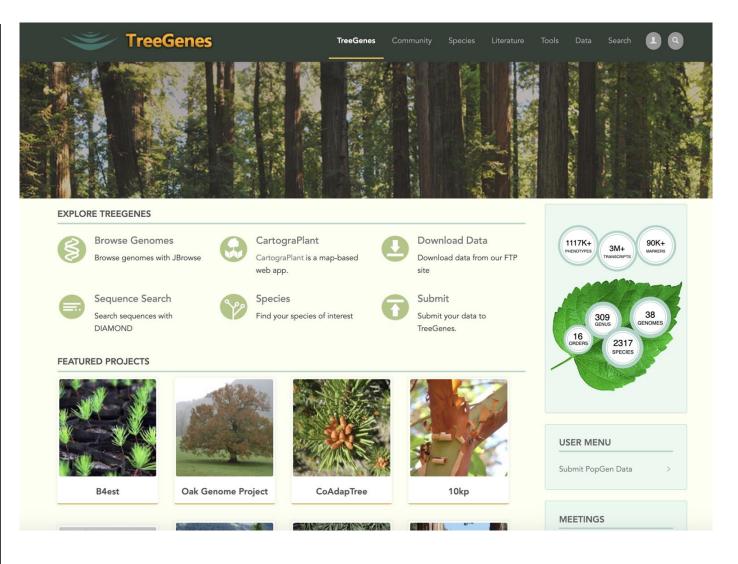
CartograTree -> CartograPlant

TreeGenes treegenesdb.org

Integrated resource for forest tree genetics

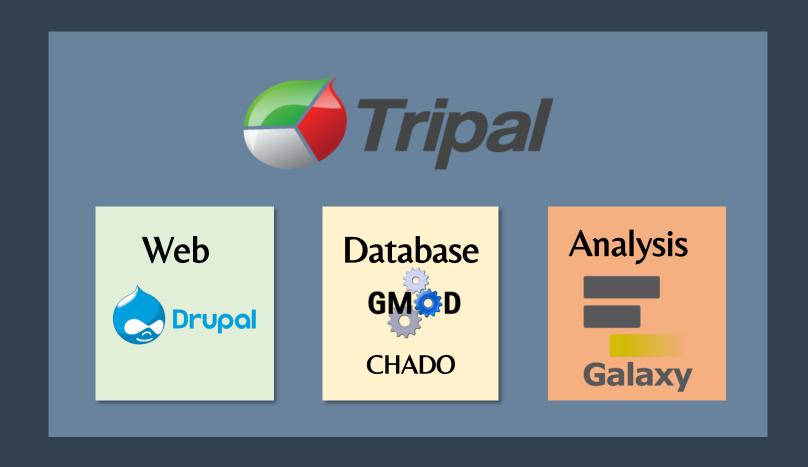
2300 species
genomes, genes, genetic
maps, proteins, SNPs,
traits

Tripal Database





Tripal is a software framework for biological databases





Features Citations Dow

Download & Install

Support

API

Blog

About

Demo Site

Home

User's Guide Developer's Handbook Extension Modules Tripal Community Tripal @ gitHub.com

Tripal @ drupal.org

Tripal is a toolkit for construction of online biological (genetics, genomics, breeding, etc), community database web portals, and is a member of the GMOD family of tools. Use Tripal out-of-the box to create a basic genomics site (with no programming) or customize using Tripal's Application Programming Interface (API). Tripal is free and open-source (GNU General Public License version 2), allows for extensive customization and is backed by a helpful user community. A strength of Tripal is our community of developers. Customization and extension of Tripal can be created and shared with other sites as modules allowing you to create your own tools and visualizations or leverage those developed by groups around the world. To see what features Tripal provides, see the Tripal User's Guide and the Developer's Guide! If you have any questions, thoughts, or concerns, we would love to hear from you on our GitHub Issue Queue!

Sites Using Tripal

Tripal sites are found worldwide.

News

Tripal v4 Compatibility

Aug 15, 2022

Tripal 4 will be keep up with Drupal releases!



Technical Blog Posts

Introducing the Helium Data Exporter Tripal Module

An additional way to visualize pedigree and phenotypic data stored in a Tripal web portal.

DOI 10.5281/zenodo.6611672

The Helium Visualization Framework is a visualization tool for large-scale plant pedigree data with the option to overlay categorical data. We developed the Helium Data Exporter module to transform germplasm and raw





KnowPulse



Mimubase



PeanutBase



Plant Fungal Pathogen Genomics Project





Legume Information System



Musa Germplasm Informati



Active Tripal Websites







Rice Genome Hub





Citrus Genome Database

00000

Genome Database for Vaccinium





CottonGen



DivSeek Canada



Genome Database for Rosaceae

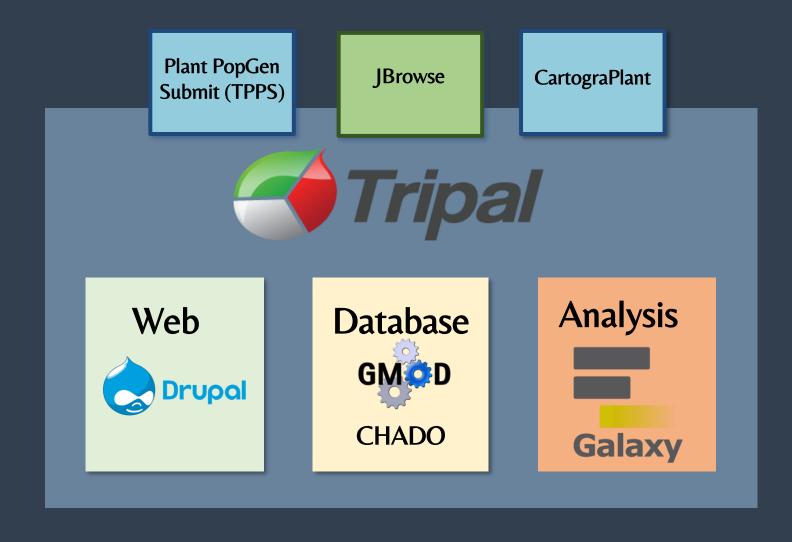


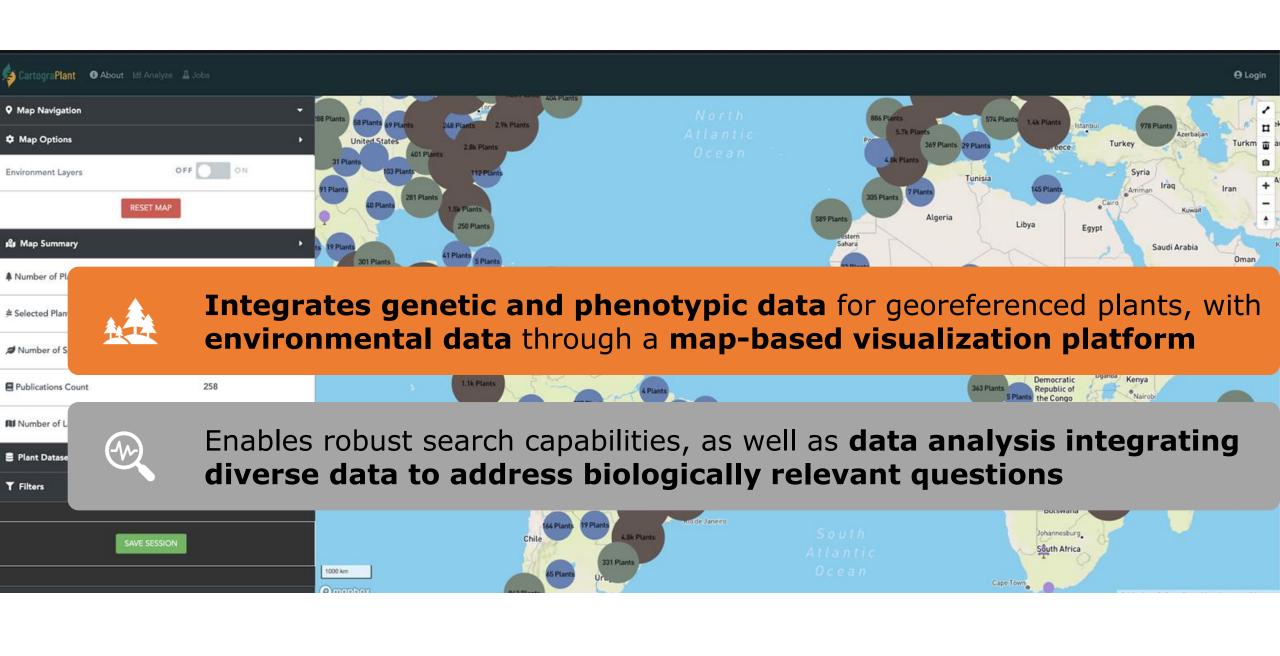
Hardwood Genomics Project



TreeGenes:

Tripal is a software framework for biological databases







CartograPlant

Integration of genomic, phenomic, and environmental data for georeferenced plants

CartograPlant.Org CartograPlantsOrg

ig-lived and sessile plant species serve as ideal models to assess population structure and adaptation to the environment. Despite the availability of comprehensive data, the researchers who study them are challenged to integrate data describing genotype, phenotype, and the environment. Towards this goal, the web application CartograTree (now known as CartograPlant), was designed and implemented as an open repository and open-source analytic web-based framework for all three.

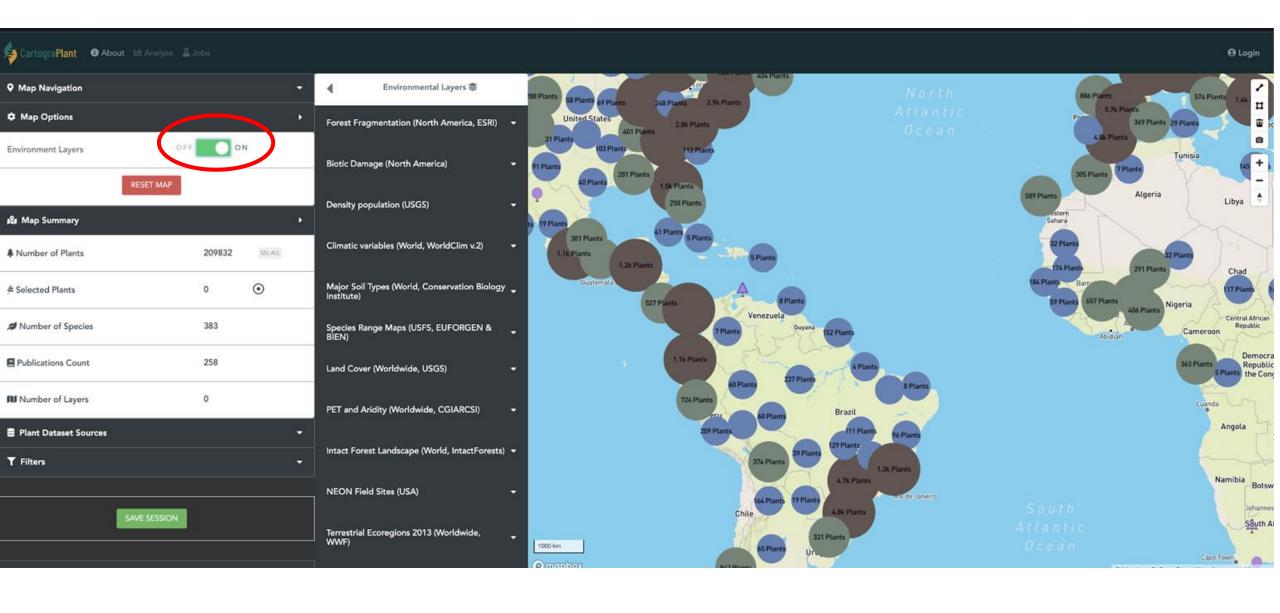


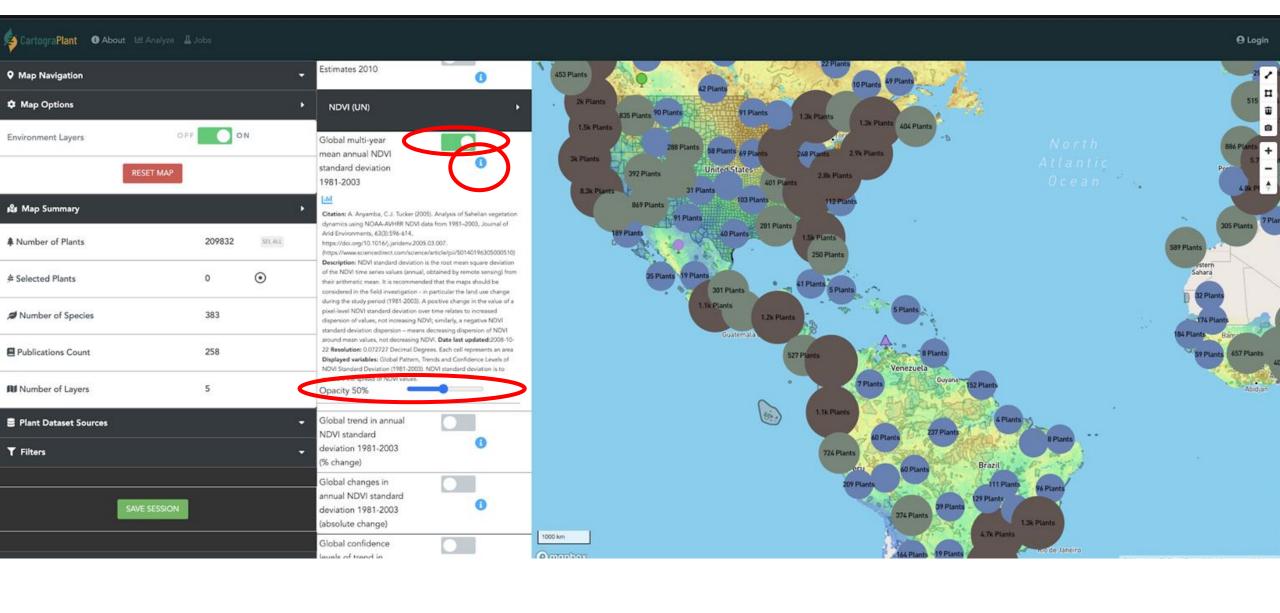
Submit Submit data for analysis

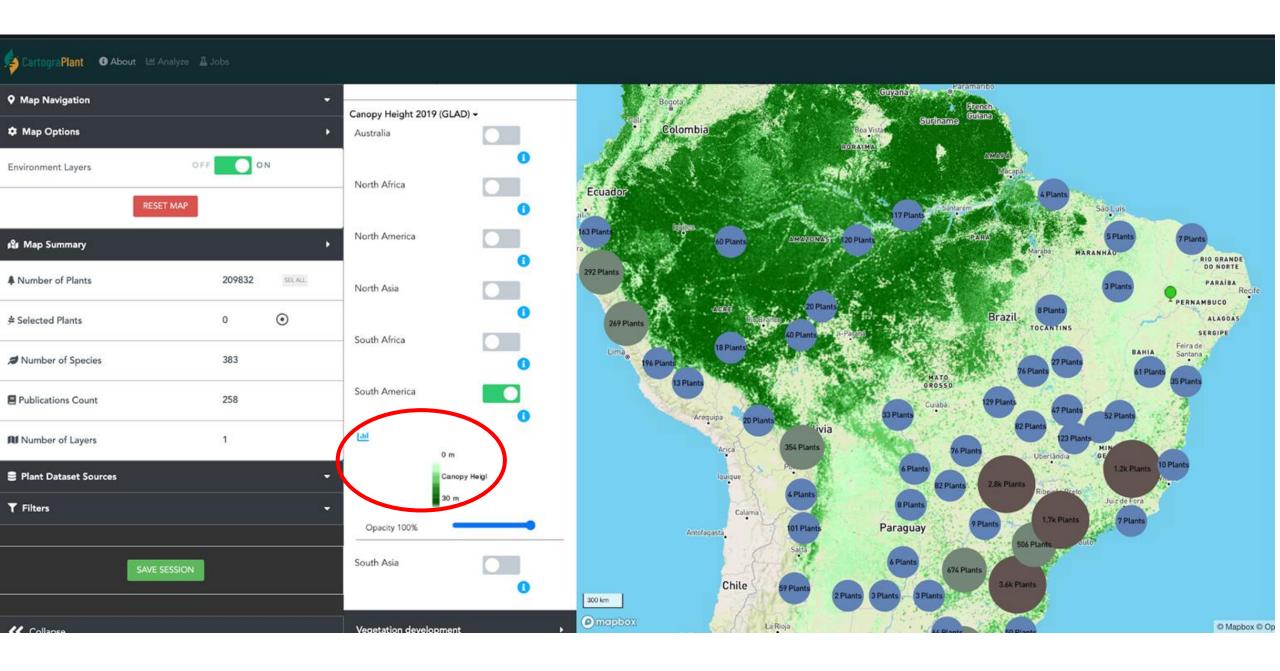


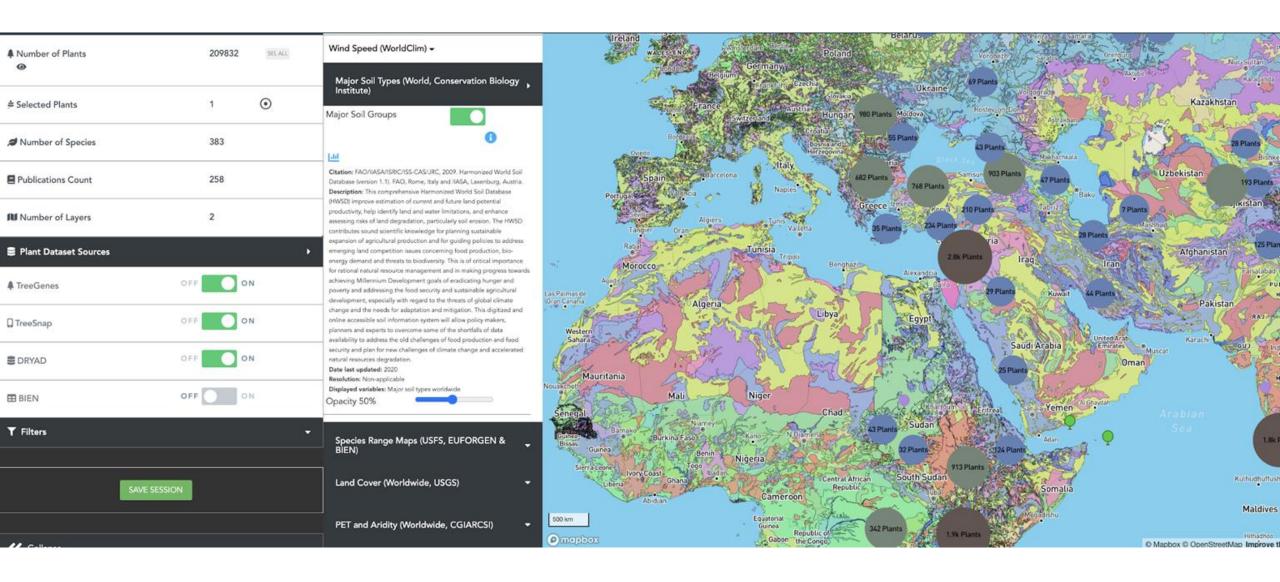
Browse or search CartograPlant here

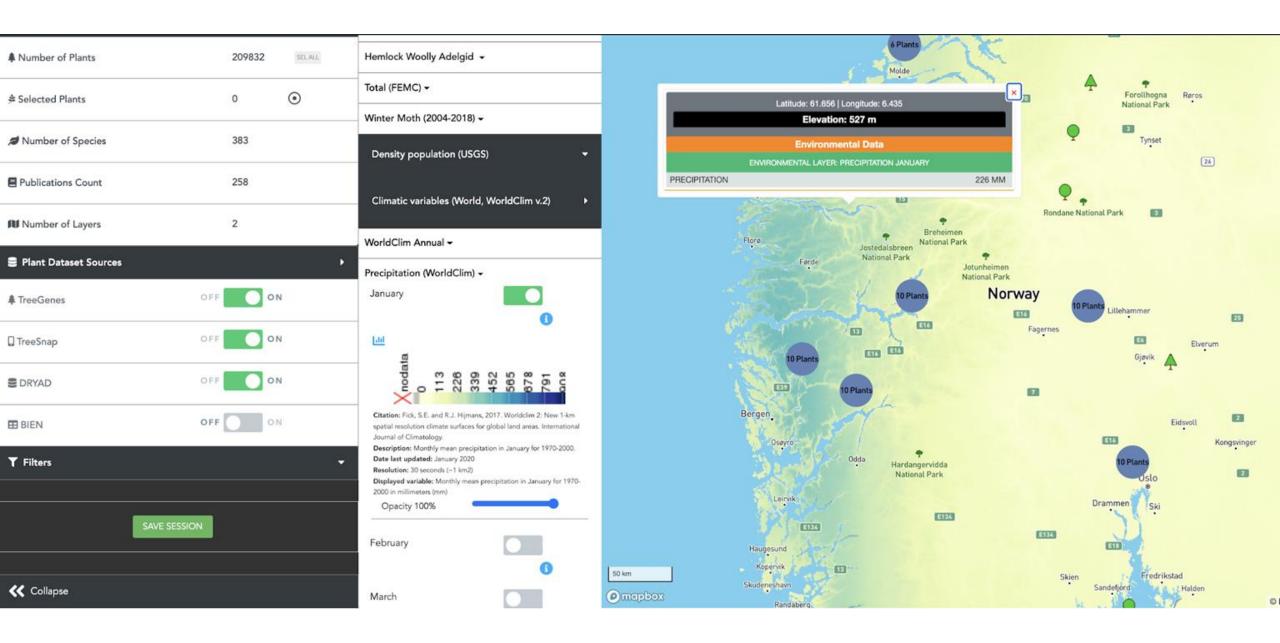
Detailed documentation, tutorials and resources

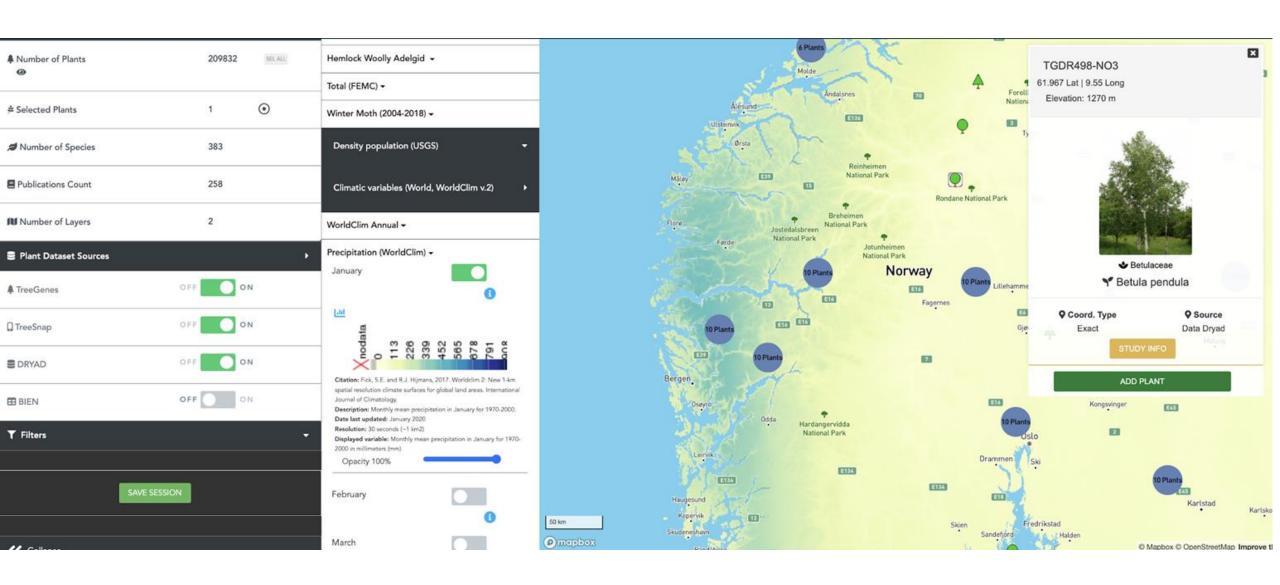


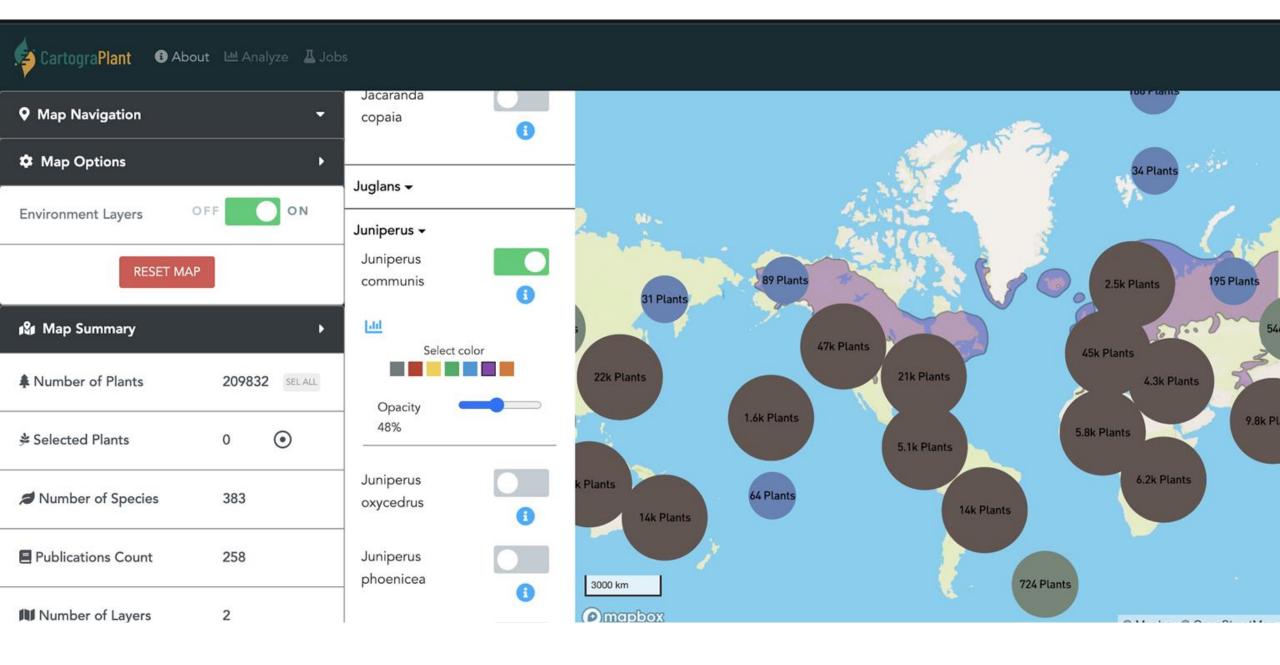








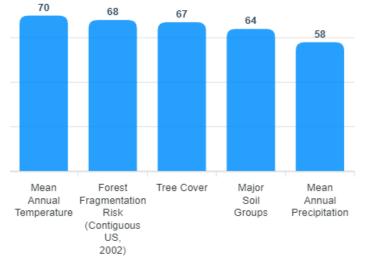




CartograPlant Layers Statistics

Frequently Accessed Environmental Layers







OVER 900 Layers and counting!

Where do the plants come from?

Multiple Sources!

Provide a mechanism for georeferenced plant data to be imported from:

- Directly from scientists!
- Mobile applications (citizen science and research based)
- Public Repositories (curation)



Study Types

- Landscape Genomics
- Population Structure
- Association Mapping
- Diversity Estimates

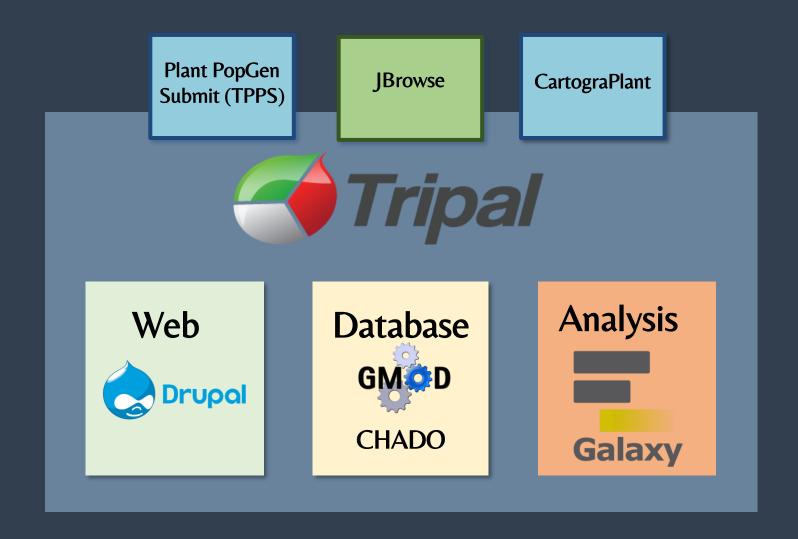




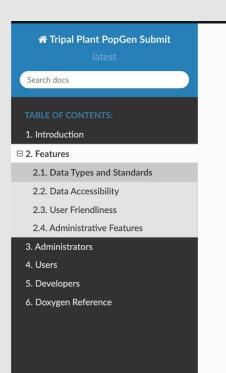




TreeGenes: Tripal is a software framework for biological databases



TPPS Data Import



Docs » 2. Features

Edit on GitLab

2. Features

TPPS has many features that make data collection easier for administrators. Here are a few notable ones:

2.1. Data Types and Standards

- Support for genotype, phenotype, and environmental data and metadata
- Support for population, association, and landscape genetics studies
- Support for ontology standards, including the Minimum Information About a Plant Phenotyping Experiment (MIAPPE)
- Support for standard genotyping file formats, such as .VCF
- Automatically submits data according to the Tripal CHADO database schema

2.2. Data Accessibility

- Data is standardized and stored in the local database so that other tools, for example,
 CartograPlant, can easily collect and analyze it
- Restricted access to approved users of the site
- · Accepted studies are associated and stored in the database with longterm accessions that can

Tripal Plant PopGen Submit Pipeline

- Public version
- Curation team version
- Ontologies (controlled vocabularies)
 - Generates standardizes storage to improve queries and provide a framework for meta-analysis across studies
- Experimental Design
- Raw Data
- Works with existing primary databases
- Generates DOI
- Metadata + Data

FAIR DATA



FINDABLE

Data has rich metadata and unique identifier



ACCESSIBLE

Data can be easily downloaded or used by using standard protocols



INTEROPERABLE

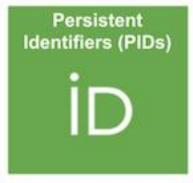
Metadata use an accessible and standard language



REUSABLE

Data is well-described and provides clear usage of licences













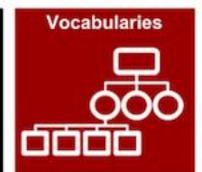








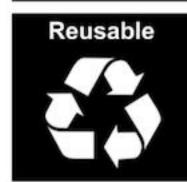






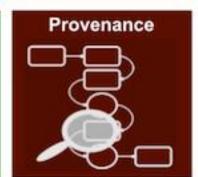






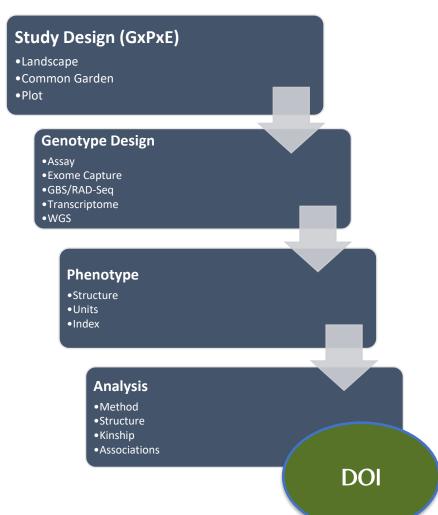


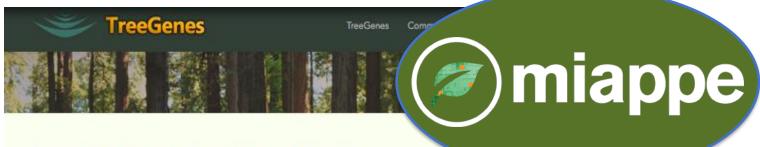






Data and metadata collection in TPPS





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 <u>Planteome</u> and <u>Crop Ontology</u> 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 <u>Tripal Plant Population Genetics Submit Pipeline</u>.

We currently have 343 unique phenotypes described on 36 unique structures representing a total of 1061193 phenotypic measures from 57234 samples representing species.

ONTOLOGY TERM SEARCH

SEARC









Proper metadata collection – flanking sequences, positions, genome versions allows re-mapping to the new genomes

Mobile Applications



Dr. Meg Staton
(UTK)
&
Noah Caldwell
(UTK)

AVAILABLE NOW

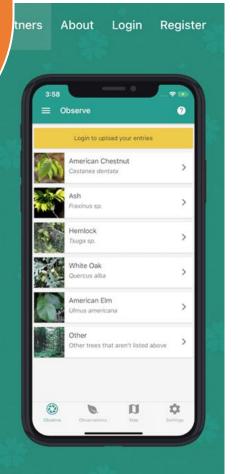
Help Our Nation's Trees!

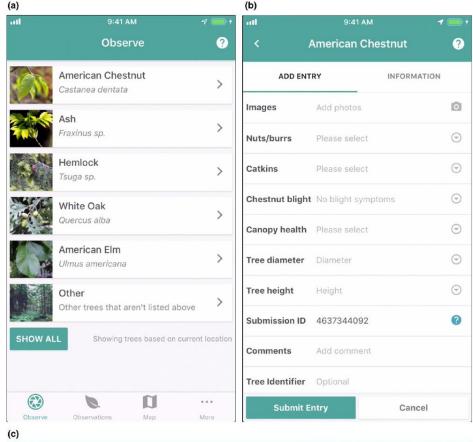
Invasive diseases and pests threaten the health of America's forests. Scientists are working to understand what allows some individual trees to survive, but they need to find healthy, resilient trees in the forest to study. That's where concerned foresters, landowners, and citizens (you!) can help. Tag trees you find in your community, on your property, or out in the wild using TreeSnap! Scientists will use the data you collect to locate trees for research projects like studying the genetic diversity of tree species and building better tree breeding programs.

Meet the scientists that use TreeSnap data









TreeShap Map Satellite ONTARIO ONTAR

Template and custom views (target species)

Received: 1 February 2019 | Revised: 10 April 2019 | Accepted: 16 April 2019

DOI: 10.1002/ppp3.41

BRIEF REPORT

Plants People Planet PPP

TreeSnap: A citizen science app connecting tree enthusiasts and forest scientists

Ellen Crocker^{1,2} | Bradford Condon³ | Abdullah Almsaeed³ | Benjamin Jarret⁴ | C. Dana Nelson^{2,5} | Albert G. Abbott² | Doreen Main⁶ | Margaret Staton³ ©

¹Department of Forestry and Natural Resources, University of Kentucky, Lexington, Kentucky, USA

²Forest Health Research and Education Center, University of Kentucky, Lexington, Kentucky, USA

³Department of Entomology and Plant Pathology, University of Tennessee, Institute of Agriculture, Knoxville, Tennessee, USA

⁴The American Chestnut Foundation, Asheville, North Carolina, USA

⁵USDA Forest Service, Southern Research Station, Lexington, Kentucky, USA

⁶Department of Horticulture, Washington State University, Pullman, Washington, USA

Correspondence

Margaret Staton, Department of Entomology and Plant Pathology, University of Tennessee, Institute of Agriculture, Knoxville, Tennessee, USA. Email: e.crocker@uky.edu

Funding information

National Science Foundation, Grant/Award Number: 1444573; U.S. Forest Service; University of Kentucky; University of Connecticut; Washington State University; Oregon State University

Societal Impact Statement

The scientists that study and work to improve forest health need information on where pests and diseases are spreading, as well as where healthy, resilient trees remain. TreeSnap is a citizen science project and mobile app created to meet this need by enabling citizens to easily submit global positioning system (GPS) locations, photos, and observational information about trees of interest to scientists. The app was designed and built to ensure that the data being collected directly helps scientists engaged in a number of forest health research activities, including studying the genetic diversity of tree species, breeding trees, and monitoring tree health.

KEYWORDS

citizen science, forest health, chestnut, treesnap, mobile app, restoration breeding

1 | INTRODUCTION

Citizen science engages non-professional scientists in scientific research (Bonney et al., 2009; Conrad & Hilchey, 2011; Dickinson et al., 2012; Dickinson, Zuckerberg, & Bonter, 2010; McKinley et al., 2017). For researchers, citizen science offers exciting opportunities to expand the range and scope of data collected and involve a broader and more diverse group of observers and data contributors (Pocock,

Tweddle, Savage, Robinson, & Roy, 2017). By incorporating a large number of interested people working in parallel, citizen science has the potential to accelerate the pace or expand the scope of research projects. In today's world of constrained research funding, communicating the value of scientific research to the public is increasingly important yet avenues for sharing scientific research with general audiences are few and researchers typically have little institutional support for education and outreach activities, despite outreach

Ellen Crocker, Bradford and Abdullah Almsaeed Condon contributed equally to this work.

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Plants, People, Planet. 2019;00:1-6.

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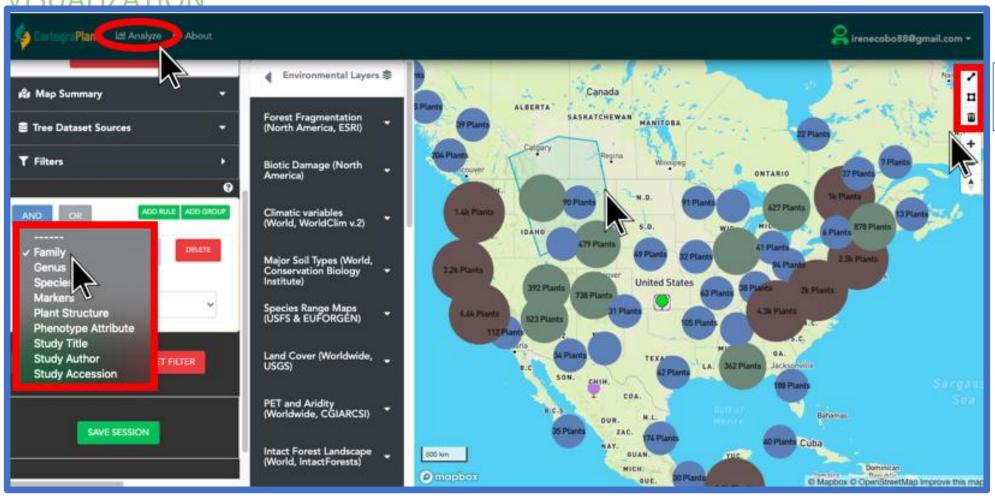
South Africa

Mapbox OpenStreetMap Improve this map

https://cartograplant.org/

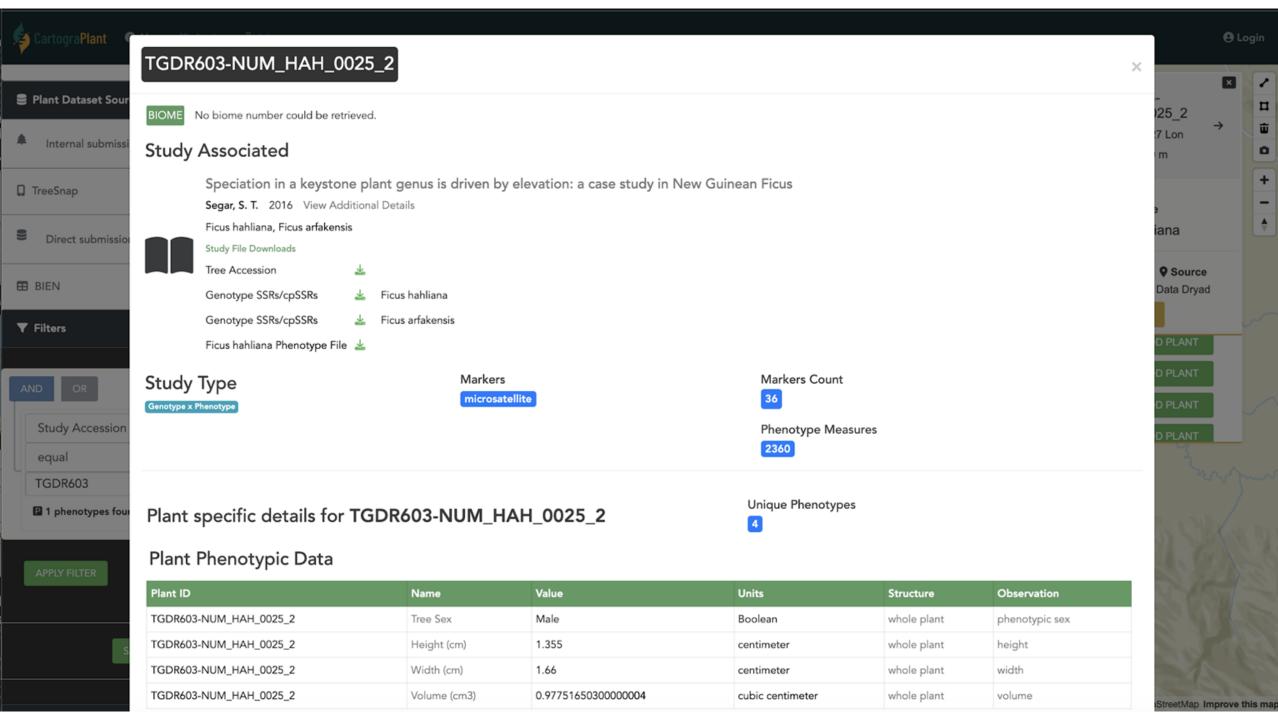
INTERFACE AND DATA

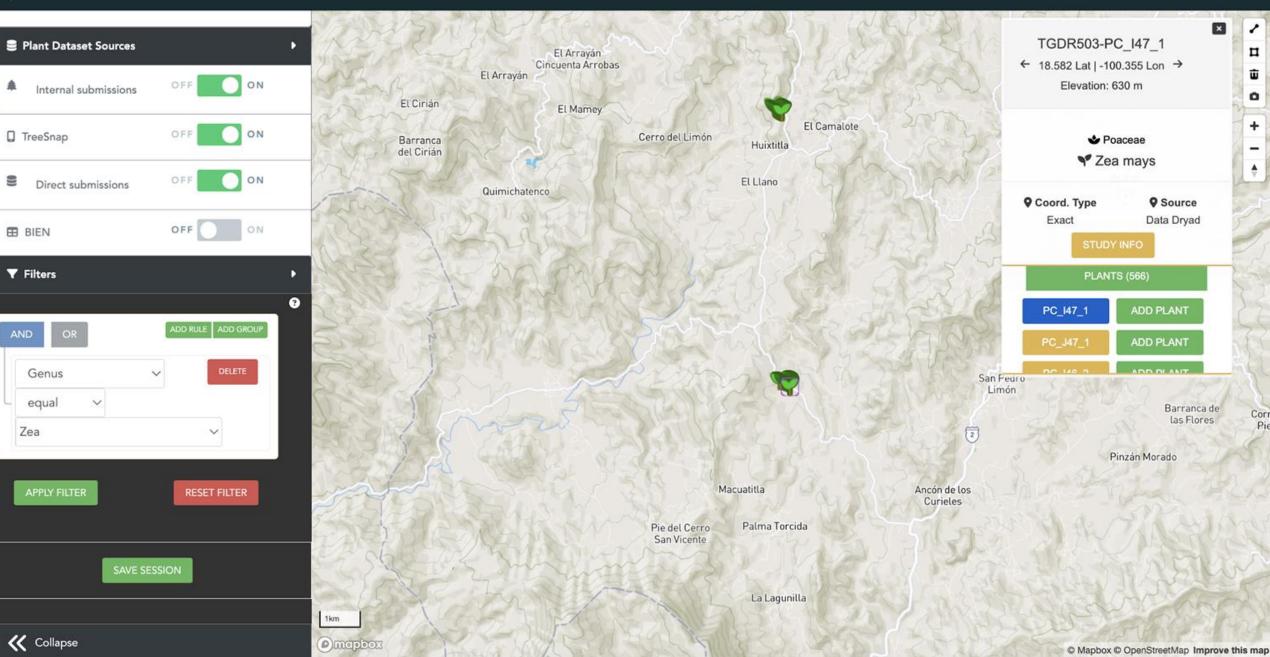
VISUALIZATION

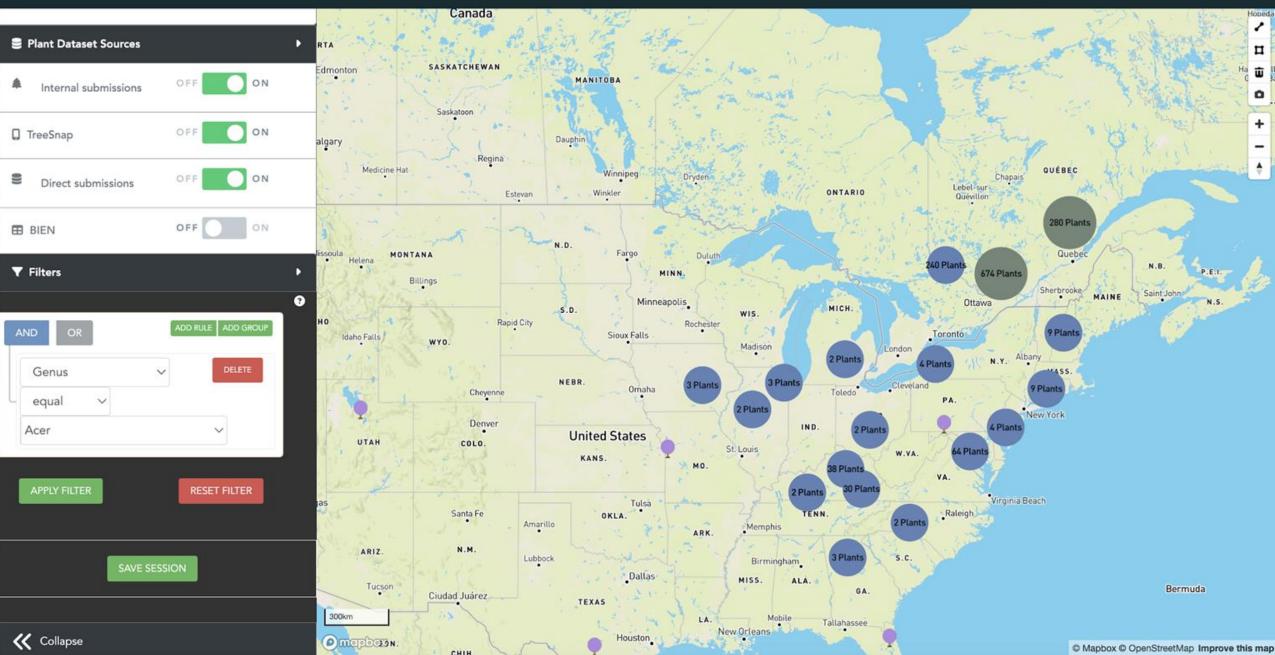


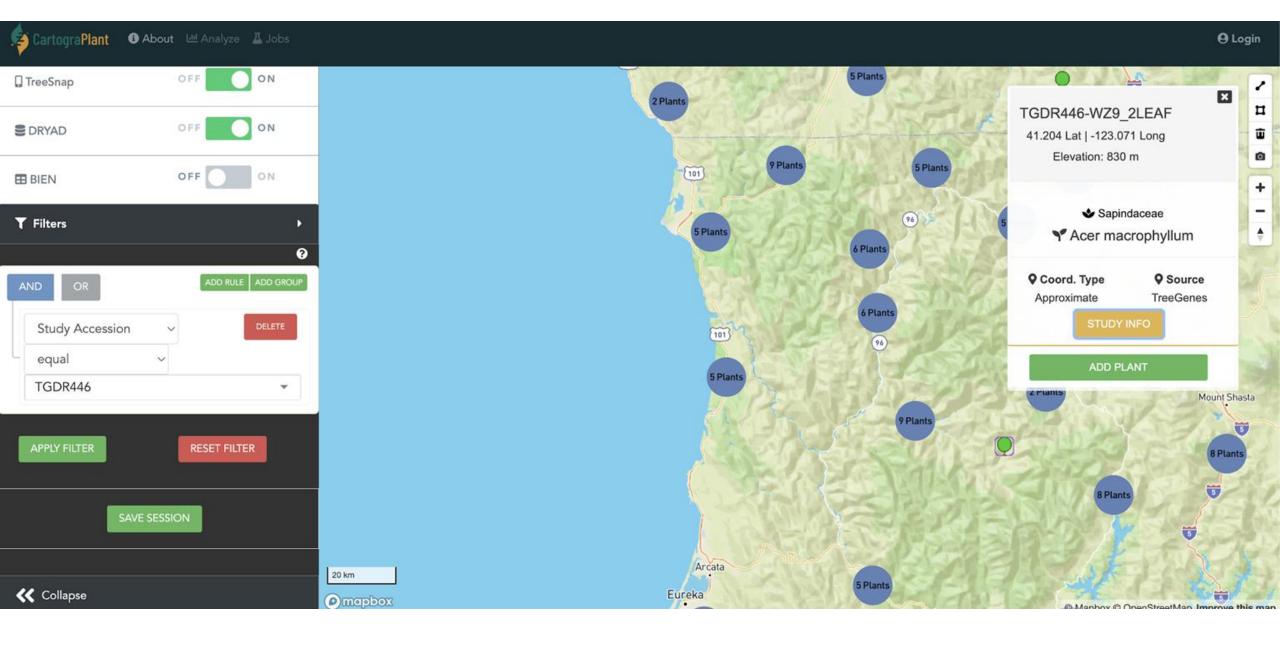
Polygon drawing on the map

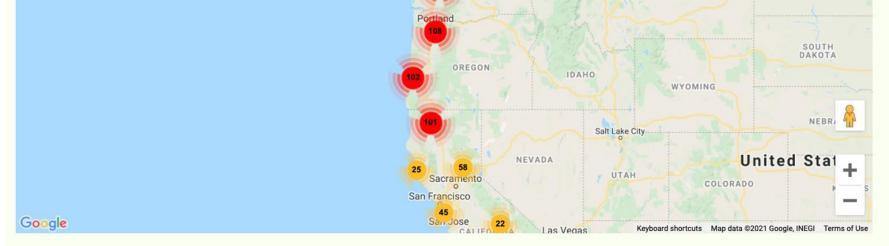
DATA SELECTION FOR ANALYSIS











RANGE-WIDE ASSESSMENT OF A SNP PANEL FOR INDIVIDUALIZATION AND GEOLOCALIZATION OF BIGLEAF MAPLE (ACER MACROPHYLLUM PURSH)

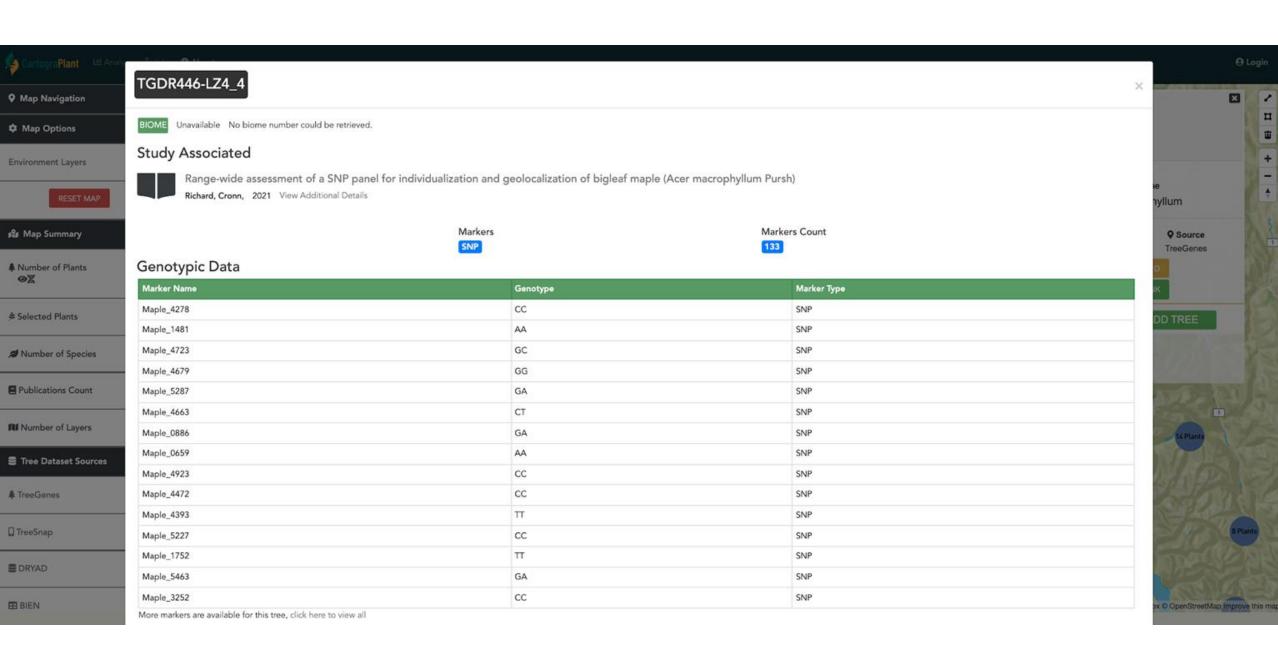
Cronn, Richard, Kristen N. Finch, Laura L. Hauck, Meaghan Parker-Forney, Brook G. Milligan, Jenélle Dowling, Adventure Scientists Published 2021, in Forensic Science International: Animals and Environments

Click to show abstract
View in CartograPlant
Download compressed raw files

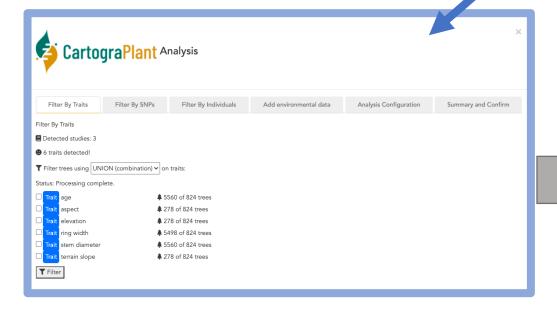
Species Study Details Plants Genotypes

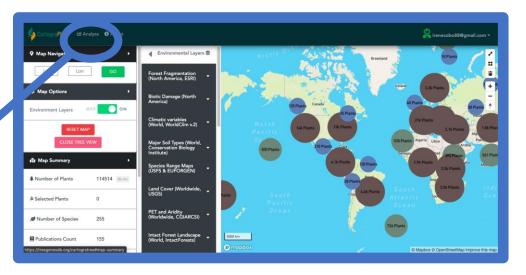
Accession TGDR446

Accession	TGDR446
Title	Range-wide assessment of a SNP panel for individualization and geolocalization of bigleaf maple (Acer macrophyllum Pursh)
Authors	Cronn, Richard, Kristen N. Finch, Laura L. Hauck, Meaghan Parker-Forney, Brook G. Milligan, Jenélle Dowling, Adventure Scientists
Species	Acer macrophyllum
Data Type	Genotype
Study Type	Natural Population (Landscape)
File Downloads	TGDR446_Plant_Accession_Acer_macrophyllum.csv TGDR446_Genotype_SNPs_Assay_Acer_macrophyllum.csv
Population Size	1158



Analytics in CartograPlant







Summary

- Integrate relevant environmental layers from curated public sources
- Provide a mechanism for georeferenced plant data to be imported (FAIR)
- HPC supported workflows that are useraccessible and reproducible
- Future
 - More regional and higher resolution layers
 - Population structure
 - Improved/Additional Analytics
 - Respond to community needs!





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