

CartograTree: Enabling Landscape Genomics for Forest Trees

Nic Herndon¹, Emily S. Grau¹, Iman Batra¹, Steven A. Demurjian Jr.¹, Hans A. Vasquez-Gross², Margaret E. Staton³, and Jill L. Wegrzyn¹

¹University of Connecticut, Department of Ecology and Evolutionary Biology, Storrs, CT, USA

²University of California, Davis, Department of Plant Sciences, Davis, CA, USA

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

ABSTRACT

Forest trees cover just over 30% of the earth's surface and are studied by researchers around the world for both their conservation and economic value. With the onset of high throughput technologies, tremendous phenotypic and genomic data sets have been generated for hundreds of species. These long-lived and immobile individuals serve as ideal models to assess population structure and adaptation to environment. Despite the availability of comprehensive data, researchers are challenged to integrate genotype, phenotype, and environment in one place. Towards this goal, CartograTree was designed and implemented as an open repository and open-source analytic framework for genomic, phenotypic, and environmental data for forest trees. One of its key components, the integration of geospatial data, allows the display of environmental layers and acquisition of environmental metrics relative to the positions of georeferenced individuals. Currently, CartograTree uses the Google Maps API to load environmental data. Limitations inherent to this API are driving new development with a focus on functionality to provide efficient queries of numerous environmental metrics.

Keywords: CartograTree, open data, open-source software, landscape genomics, genotype, phenotype, environment, association mapping, forest trees, GIS.

BACKGROUND

Forest trees have a major ecological and economic impact worldwide. They are critical for CO₂ sequestration, prevention of soil erosion, maintenance of watersheds, and promotion of biodiversity. From an economic point of view, they are necessary for timber production as well as an alternative source of biofuels. In light of climate change, populations of forest trees are being subjected to longer droughts, as well as increased damage from introduced and native pests and pathogens. From a production perspective, there is a desire to improve breeding populations through the identification of loci contributing to the growth and wood quality traits of interest.

Association genetics identifies correlations between genotypes and phenotypes in large populations, i.e., it finds the relationship between a set of genes or genome regions that contribute to a trait or a disease. A similar association mapping, between the genotype and the environment, known as landscape genetics (Manel et al., 2003), enables a better understanding of the factors that influence adaptation. With the adoption of next generation sequencing technologies, which have led to increasing availability of genomic and transcriptomic sequences, the bottleneck has shifted from data

generation to data storage and analysis. Increases in phenotypic and environmental data have been seen as a result of advancements in high throughput genotyping, remote sensing tools and geographic information systems. The availability of these data as well as more recent concerns around the impact of climate change, led to recent growth in landscape genomics studies (for a review, see Sork and Waits (2010)). The associations sought in forest trees are further enabled by their large, diverse outcrossing populations as well as their extended longevity in the same environment. This allows the association of genotype to phenotype as well as genotype to environment. For example, Evans et al. (2014) investigated the adaptive variation in growth, phenology and physiological traits of black cottonwood across the species' latitude range, and found that warmer climates are associated with earlier bud flush and later bud set. Salicoid duplicate genes had distinctive patterns of adaptive variation, and specific genomic regions were associated with adaptive traits. Similarly, Holliday et al. (2010) found associations between 28 genes and phenotypic variance in two dormancy-related traits, autumn cold hardiness and budset timing, for Sitka spruce, across its range. Eckert et al. (2009) identified associations between genes and cold-hardiness related traits for coastal Douglas fir.

The ability to perform these studies on a large-scale and in a comparative framework, requires extensive data integration across disciplines. CartograTree (Vasquez-Gross et al., 2013) was developed from a collaboration among forest tree ecologists, geneticists, breeders, and physiologists who identified both integration and analysis as the critical bottlenecks. CartograTree aims to use open-source tools to integrate genomic and phenotypic data for forest trees, along with environmental data through a map-based visualization platform. The tool does not only enable visualization and search capabilities, but also the ability to perform association mapping analysis through the use of semantic technologies and high performance computing resources offered by Cyverse (Goff et al., 2011).

CARTOGRATREE DATA

Currently, two primary repositories are responsible for the acquisition and curation of tree genomics data. The TreeGenes database (<http://treegenesdb.org>, Wegrzyn et al. (2008, 2012)) currently hosts 13 genome assemblies, transcriptome resources for 262 species, 95 genetic maps, over 110 million genotypes, and nearly 200,000 phenotypic evaluations. While TreeGenes hosts data for over 1,200 species, the most substantial genotype and phenotype resources have been curated for conifer species. The Hardwood Genomics Web (HWG, <http://www.hardwoodgenomics.org>, Sanderson et al. (2013)) houses deep RNASeq data from phylogenetically diverse forest tree species. In addition, low coverage genome sequence data, resulting genotypes, and genomic SSRs are available for key hardwood species. Permanent mapping and reference populations (genetic linkage maps) are in development for green ash, tulip poplar, honeylocust, black walnut and northern red oak. Both repositories rely on open-source technologies to store and display the data. The Chado relational database schema (Mungall et al., 2007) is used for storing data and was specifically designed for representing biological information. Standardization around this schema enables seamless integration across the two repositories. For visualizing the data, TreeGenes and HWG use another open-source technology, Tripal (Sanderson et al., 2013; Ficklin et al., 2011), which integrates Chado through specific templates designed in the Drupal content management system.

The genotype and phenotype data is delivered to the databases through the TreeGenes Data Repository (TGDR) which takes the scientist through a vetted workflow that collects both association

raw data and experimental metadata on existing studies. The majority of the individual tree accessions are associated with georeference coordinates that are requested during the submission. Data is also made available through collaborative studies whose data storage is facilitated by TreeGenes or HWG. Following submission, public studies or datasets are available for geospatial presentation and access in CartograTree.

In addition to the phenotypes delivered through TGDR, TreeGenes collects phenotypes for species with genotype data that also have geo-referenced individuals in TRY-DB. The TRY initiative is a collection of both published and unpublished datasets from a wide variety of trait databases, including: LEDA, GlopNET, BiolFlor, SID, and EcoFlora (Kattge et al., 2011).

Environmental data can be accessed via the WorldClim dataset which contains summarized temperatures and precipitations, and biologically relevant variables for past, current, and future conditions (Hijmans et al., 2005). In addition, the CartograTree application fully integrates the Ameriflux project which includes a total of 156 stations spread across North and South America (<http://ameriflux.lbl.gov>). This information will be coupled with metrics from user-submissions and collaborative projects which may be tracking specific information, such as soil samples.

A system overview of the CartograTree is shown in Figure 1.

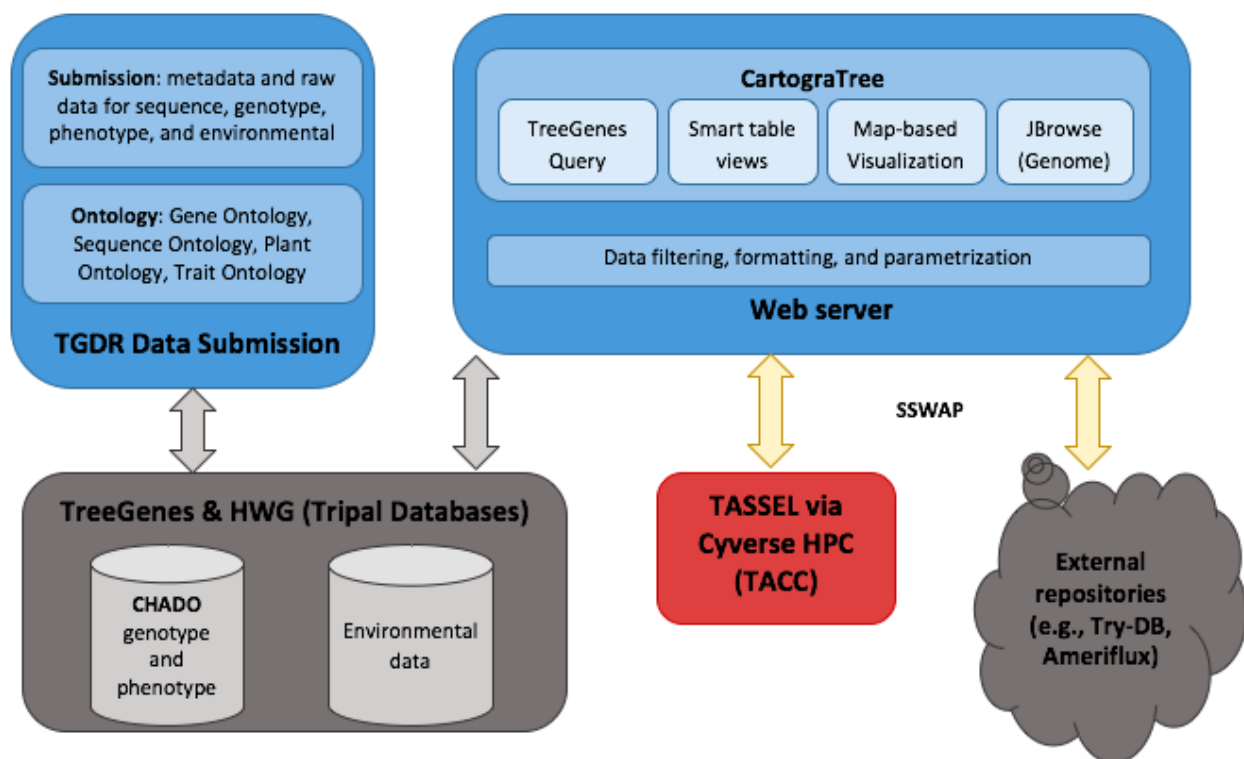


Figure 1. Architectural view of CartograTree. Users can upload data into the Triplal databases using the TreeGenes Data Repository module (TGDR). These databases and other external repositories can be queried and the results visualized using the web interfaces. Users can also further analyze the data using TASSEL.

CARTOGRATREE SERVICES

CartograTree allows scientists to view georeferenced tree accessions, along with metadata via the Google Maps API, as shown in Figure 2. The web interface allows one to select specific studies, species, regions, specific phenotypes, and more. Researchers can select, filter, combine, and inspect data through basic and more complex queries. Although Google Maps API is free to use and generates maps that load and update quickly, several limitations exist:

- Character limits prohibit implementation of a RESTful system.
- All source code is controlled and modified by Google.
- Compatible ArcGIS layers cannot be directly queried through the API.

Further data exploration with CartograTree is enabled through interaction with web services in the form of the open-source SSWAP semantic discovery pipeline. Data is semantically tagged as a set, and formatted appropriately for analytical applications. Currently, the platform supports multiple sequence alignment, phylogenetic analysis, and association genetics. TASSEL, the open-source application of choice for association genetics, can operate on various combinations of genotypic, phenotypic, and environmental files (Bradbury et al., 2007). Web service entry points are semantically tagged for TASSEL and hosted at the Texas Advanced Computing Center's (TACC) High Performance Computing resources using the Agave API (<http://agaveapi.co>). Semantic TASSEL is automatically discovered by SSWAP (Gessler et al., 2009), and the association data is marshaled to the service. This is a drag-and-drop operation for the scientist that negates the need to enter file names, stage, or manually copy the data. The scientist initiates the association mapping analysis, SSWAP monitors the job, and places the final results in the data store hosted by Cyverse.

FUTURE DEVELOPMENTS

While CartograTree presents an important framework for data integration and association mapping analysis, further development is needed to ensure its utility to the broader community. Current work is focused on developing a more advanced geospatial framework, including performance, metrics, and the ability to query across high resolution GIS layers. In addition, we are addressing the need for more parameterization of the association mapping runs. This should include the ability to generate population structure information, select a variety of statistical models, examine phenotypic distributions, and filter for missing data. This collaborative project between TreeGenes and Hardwood Genomics Web will enable researchers to integrate these diverse and valuable datasets to address the numerous threats facing forests worldwide.

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Users can filter displayed data by publication, taxa, datatype and data source.

Trees of interest are selected via the map interface.

Selected trees are displayed in the table below. Genotype, phenotype and environmental data can be accessed from the table.

Users can launch web services to launch analyses such as TASSEL and MUSCLE.

Type	ID	Latitude	Longitude	Total sequences	Total genotypes	Total phenotypes
✓	TGDR001-2199.0	47.7330	-121.9830	0	874	3
✓	TGDR001-2019.1	45.3170	-122.5670	0	874	3
✓	TGDR001-2143.2	48.8170	-122.2170	0	874	3
✓	TGDR001-2415.3	46.1170	-123.0000	0	874	3
✓	TGDR001-2312.4	48.7170	-122.2000	0	874	3
✓	TGDR001-2402.5	47.1670	-122.3830	0	874	3
✓	TGDR001-2212.6	47.0830	-122.2330	0	874	3
✓	TGDR001-2046.7	46.7330	-121.9000	0	874	3
✓	TGDR001-2178.8	47.6830	-121.9170	0	874	3
✓	TGDR001-2371.9	46.0500	-121.9330	0	874	3

Figure 2. User interface of CartograTree. Users can select the trees of interest using the GUI, filter them through the web form, and select trees for further analyses.

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