Mapping changes in forest diversity and disease in North American temperate forests

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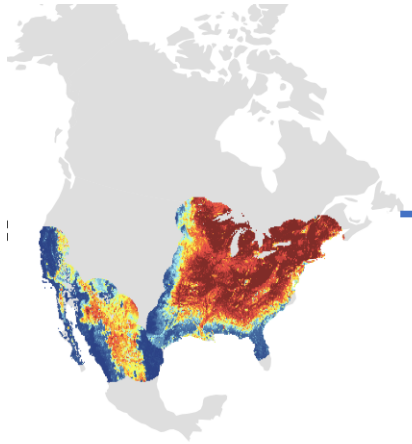
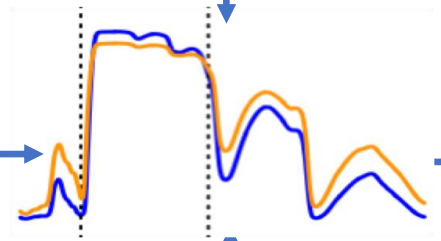
Phil Townsend

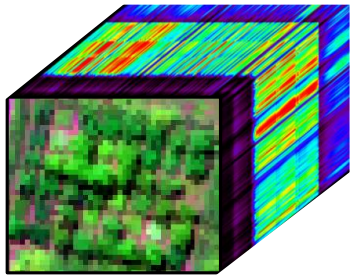
Minnesota Invasive Terrestrial Plants and Pests Center

Species and lineage identification from spectra

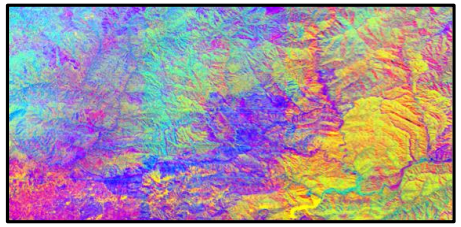
Species distribution modeling





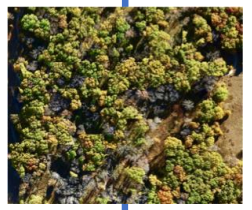


Community composition mapping using phylogenetically conserved spectral regions

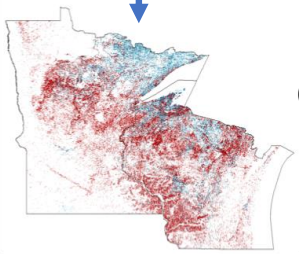


Threat detection

Leaf



Canopy



Communities

Compelling reasons to map lineages – important units of conservation for ecosystem function, easier to classify than species and critical for disease detection

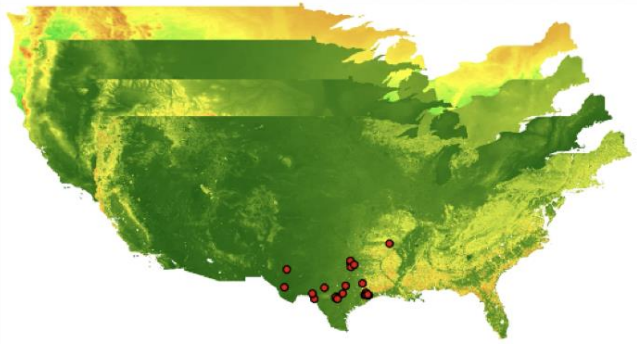
Predicting species distributions and community composition using satellite products

NextGen SDMs

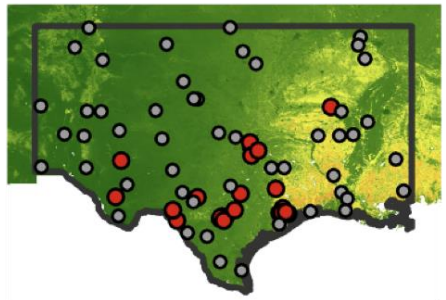
Remotely sensed environmental covariates

Delimit accessible area for each species

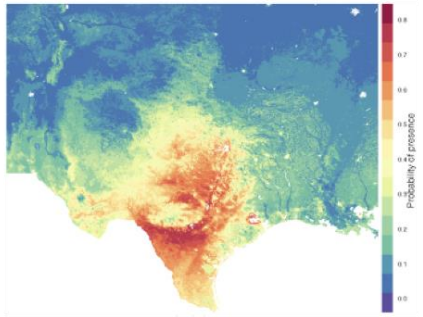
Species Distribution Model



- MOD 11C3 - Temperature
- CHIRPS - Precipitation
- MOD 15A2 - DHI-LAI
- SRTM - Altitude



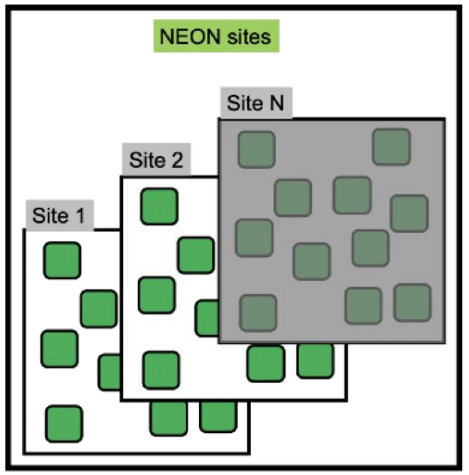
- Crop covariates to M
- Pseudo-absences generation



Probability of species presence

GBIF and **iDigBIO** species occurrence data

B) NEON and FIA and plots



Validate with **NEON** and **FIA** occurrence data

C) Assemblage predictions evaluation

Ensemble S-SDMs
- Binary
- Probability
- Constrained - PRR

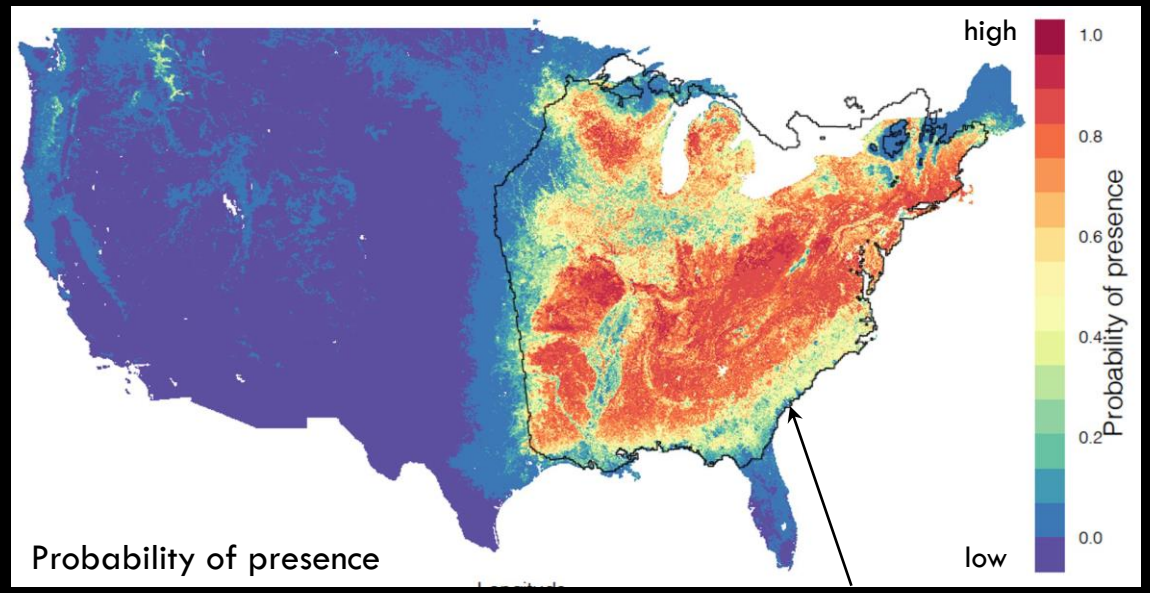
- Species richness
- Species composition

- SR deviation, change
- Indices of accuracy

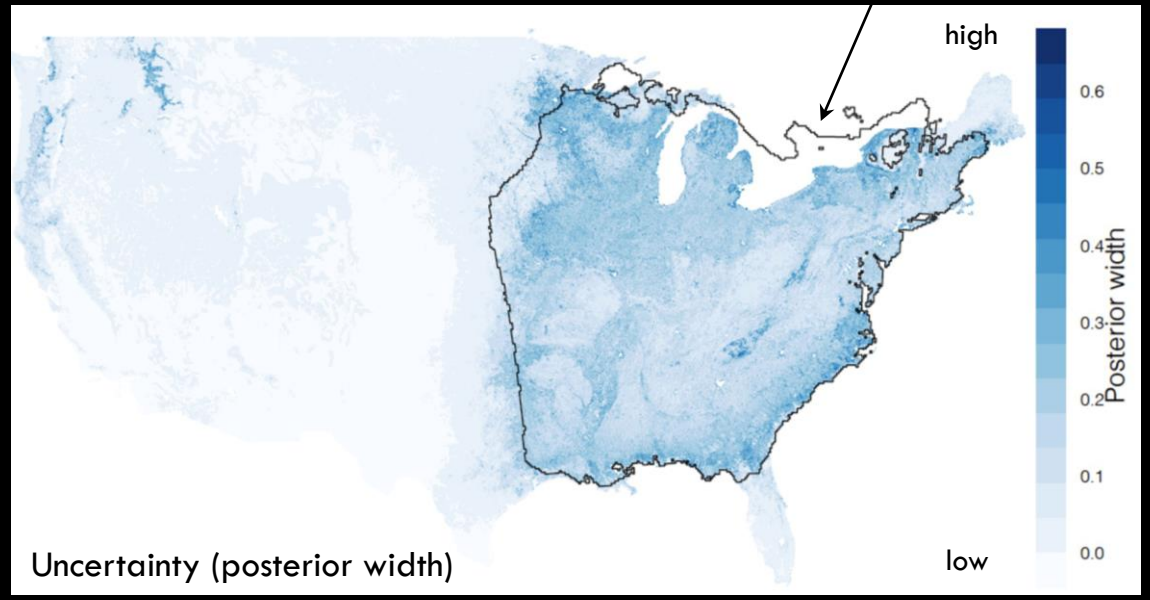
Pinto-Ledezma and Cavender-Bares 2021

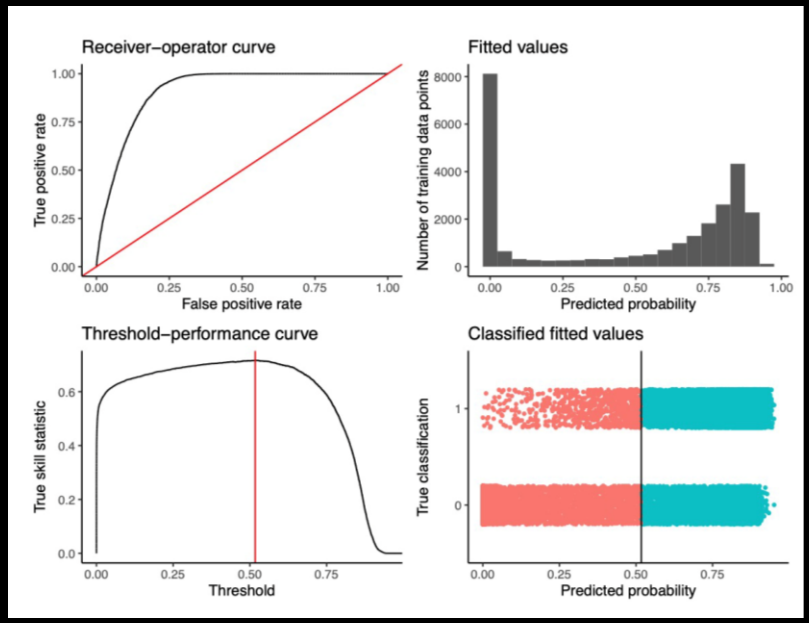
https://github.com/jesusNPL/BayesianSDMs_Oaks

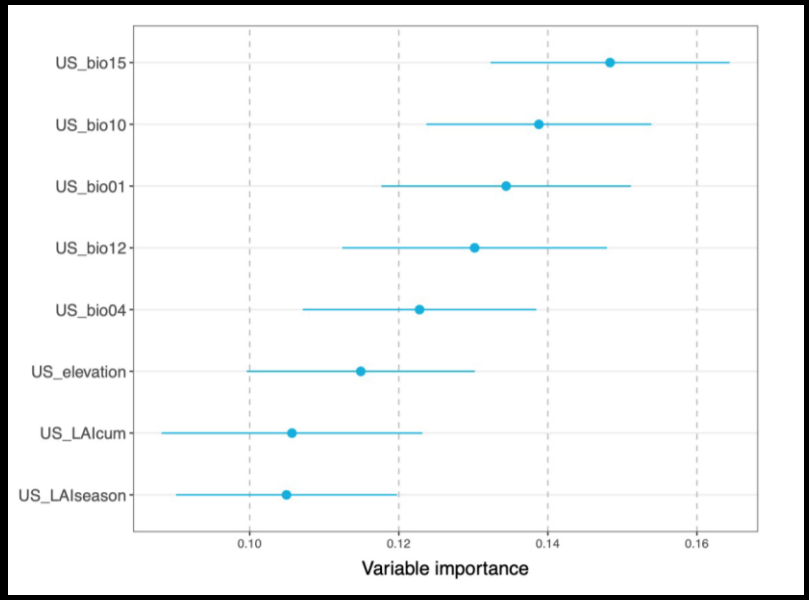
Predicted probability of presence of white oak (*Quercus alba*)



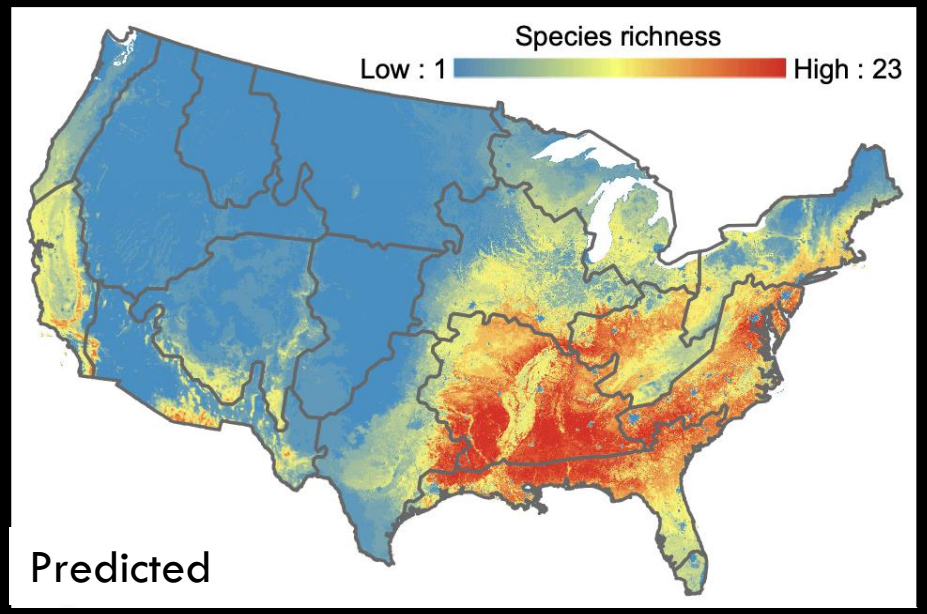
Polygon: BIEN estimated species range

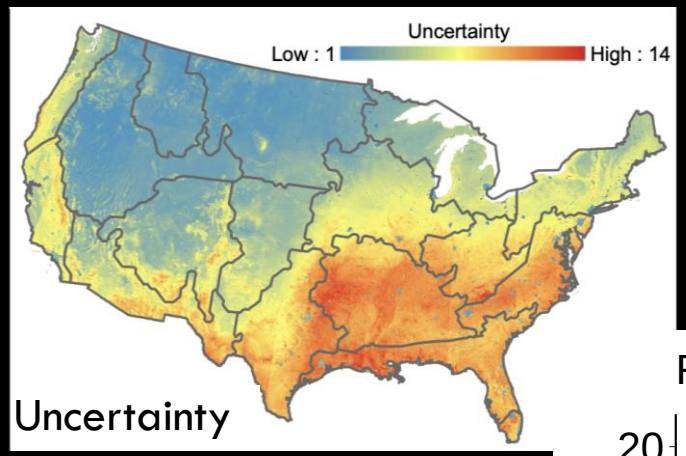


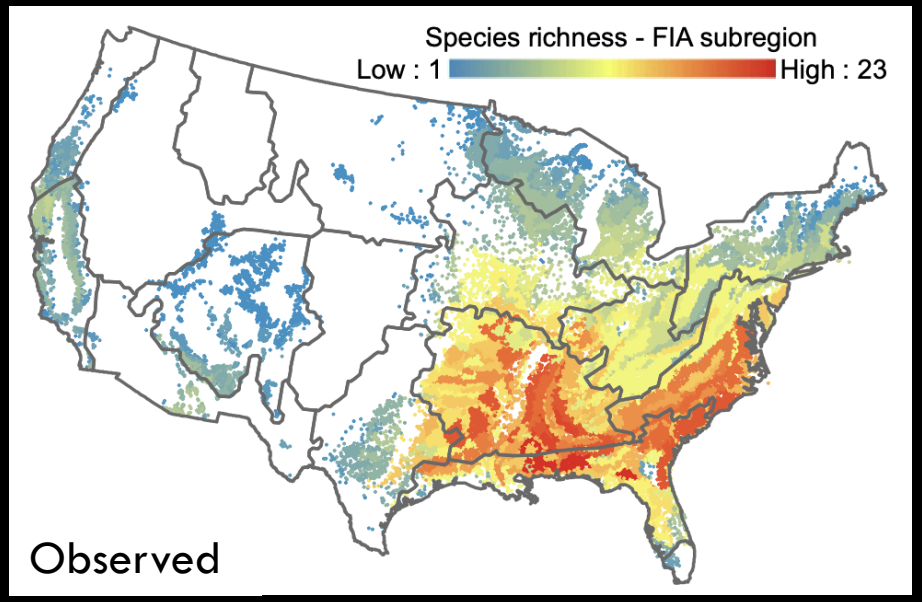


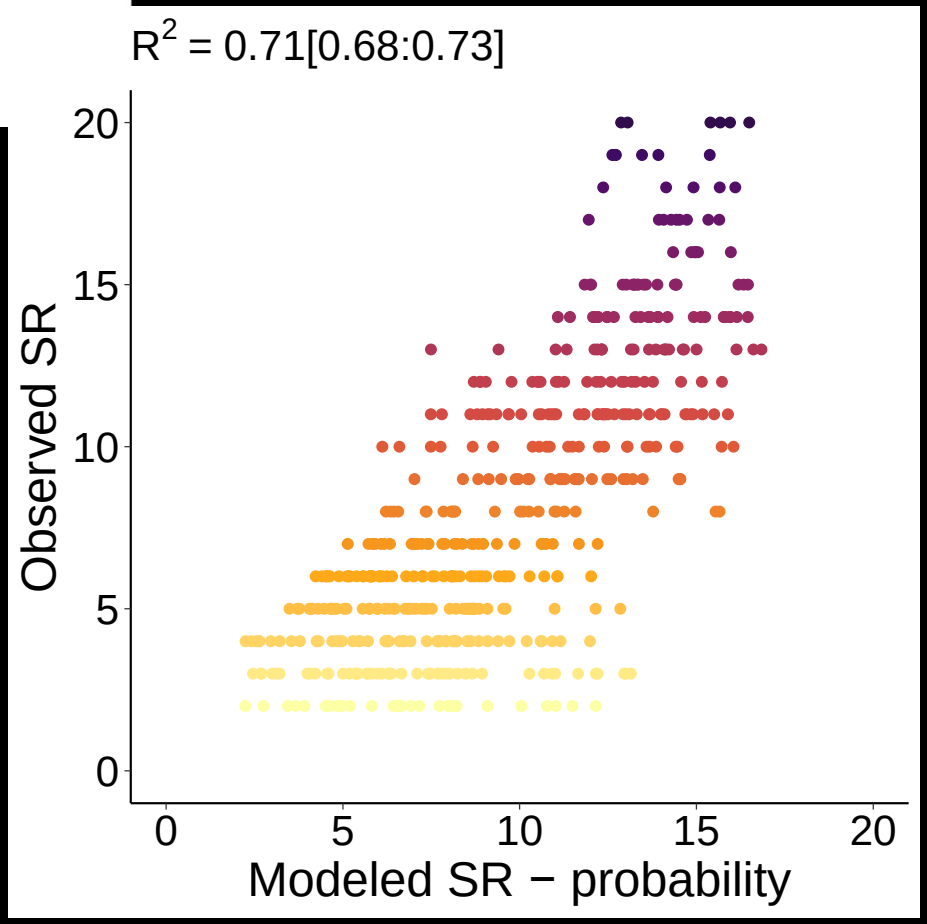


Stacked NextGen SDMs from GBIF+iDigBio predict observed species richness (FIA and NEON)

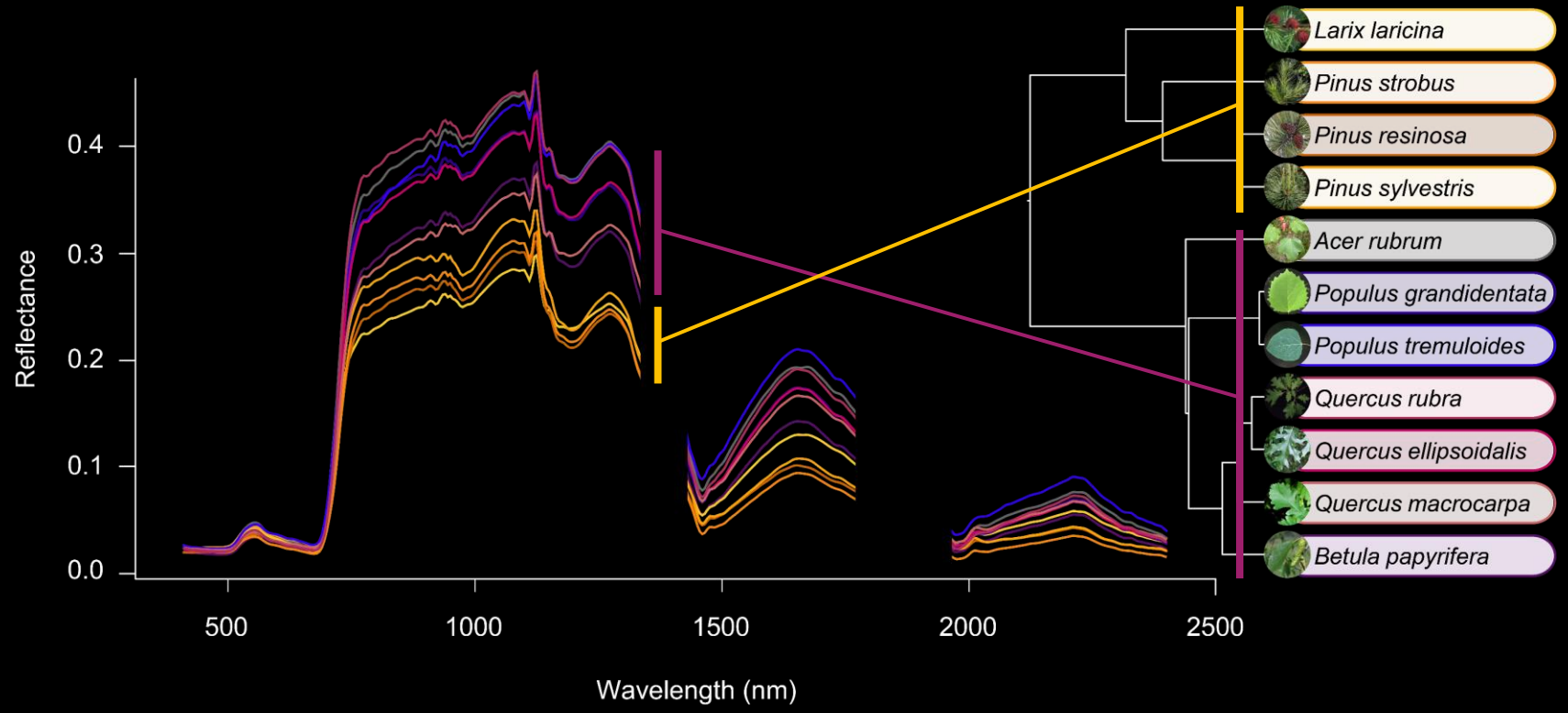


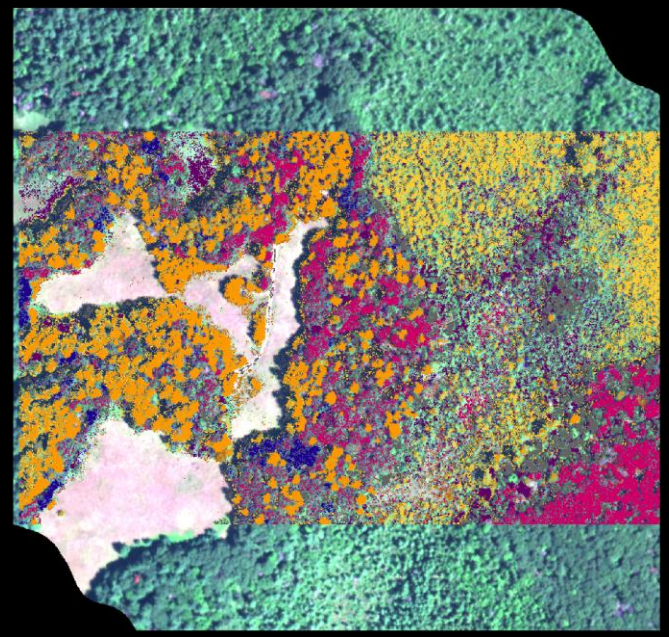




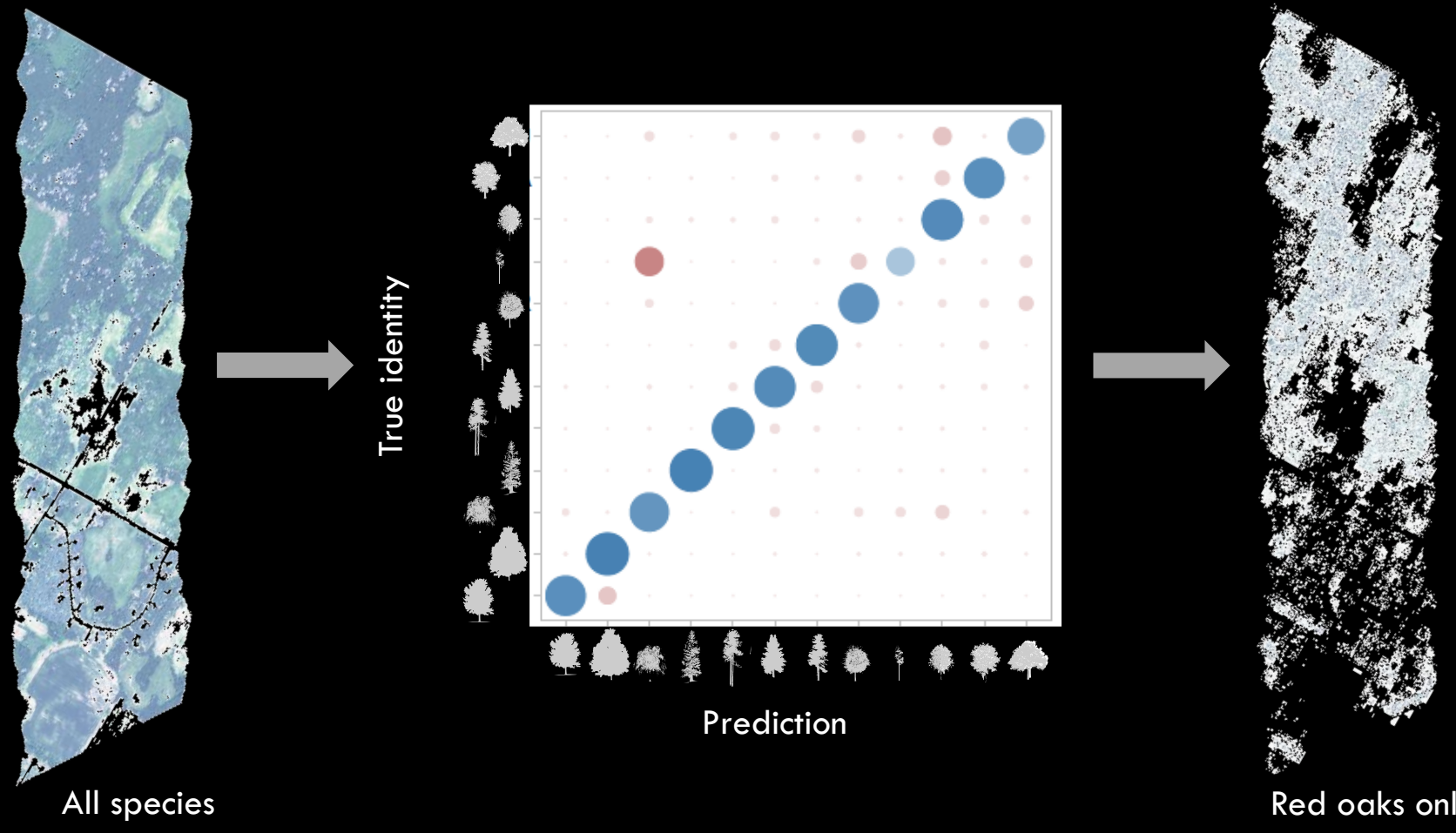


Detection of species and lineages from airborne data (AVIRIS NG)





In a mixed deciduous forest in Minnesota, tree species are accurately classified using PLSDA



Oak wilt (*Bretziella fagacearum*) is the most lethal threat to oaks in the U.S.

Image: Antonio Guzmán

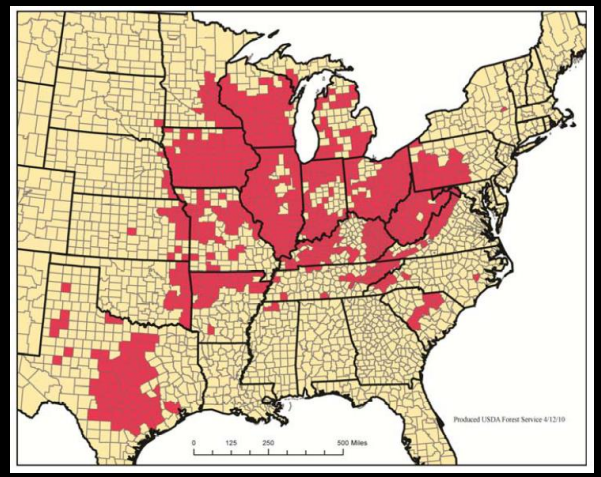
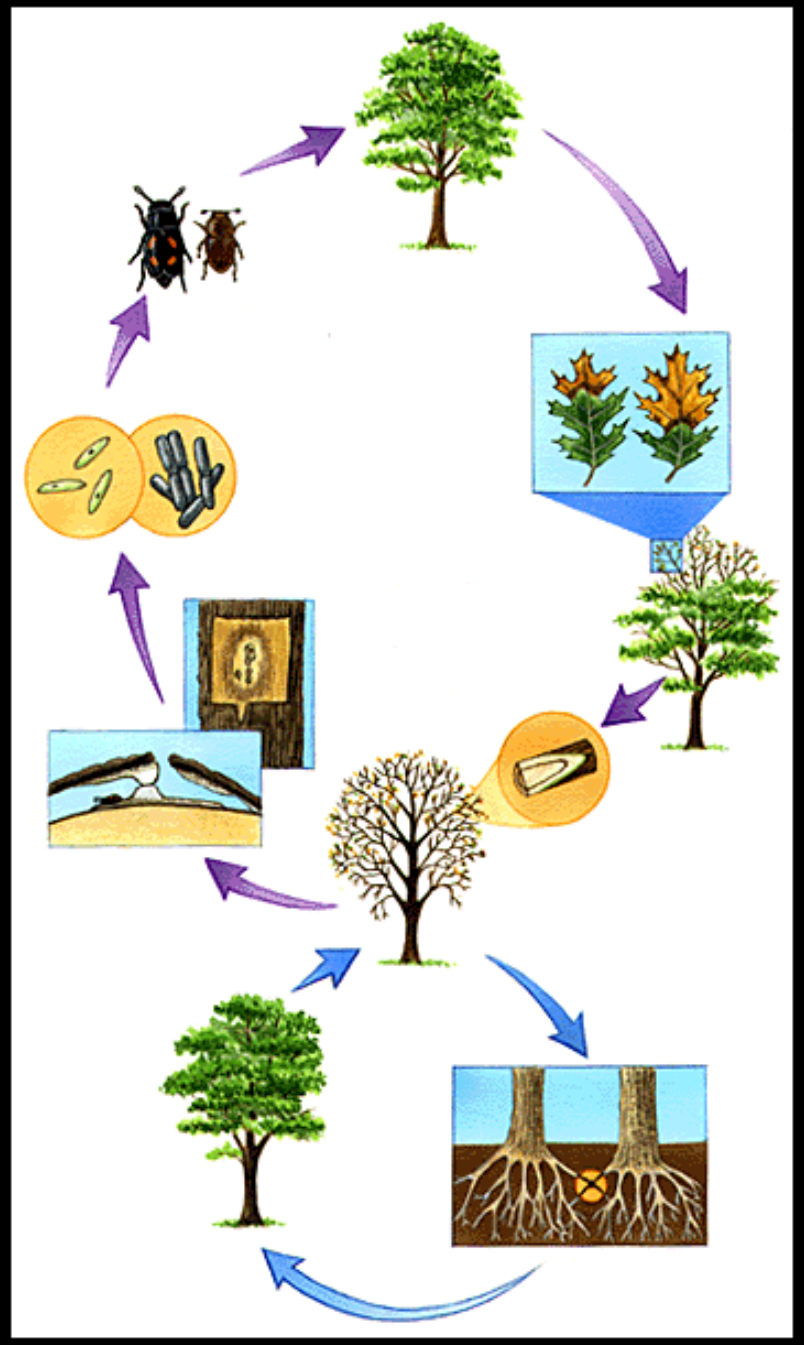


Photo: Dave Mausel

Annual ecosystem service values of US trees

Cavender-Bares…Polasky SESYNC working group, 2022, *PLoS Sustainability & Transformations*

Common Name	Scientific Name	Aggregate	Climate Regulation	Air Quality Regulation	Wood Products
Pine	*Pinus*	$25.3 billion	$10.6 billion	$7.4 billion	$7.4 billion
Oak	***Quercus***	**$22.3 billion**	**$10.7 billion**	**$11 billion**	**$577 million**
Maple	*Acer*	$11 billion	$5.2 billion	$5.5 billion	$297 million
Douglas-fir	*Pseudotsuga*	$8.6 billion	$5.9 billion	$1.5 billion	$1.2 billion
Hemlock	*Tsuga*	$4.5 billion	$3 billion	$1.2 billion	$234 million



Julie Martinez - USDA-FS

Overland spread

Movement of spores from fungal mats by sapsucking beetles – sexual reproduction of fungus

Credit: David Mausel

Credit: Sandra Jensen

Belowground spread

Very rapid spread through grafted roots – causes oak wilt "pockets"

Credit: Ronald F. Billings

Possible to manage effectively—depends on efficient detection

Oak wilt treatment – if detected early

Chainsaw girdling – Rapid Response

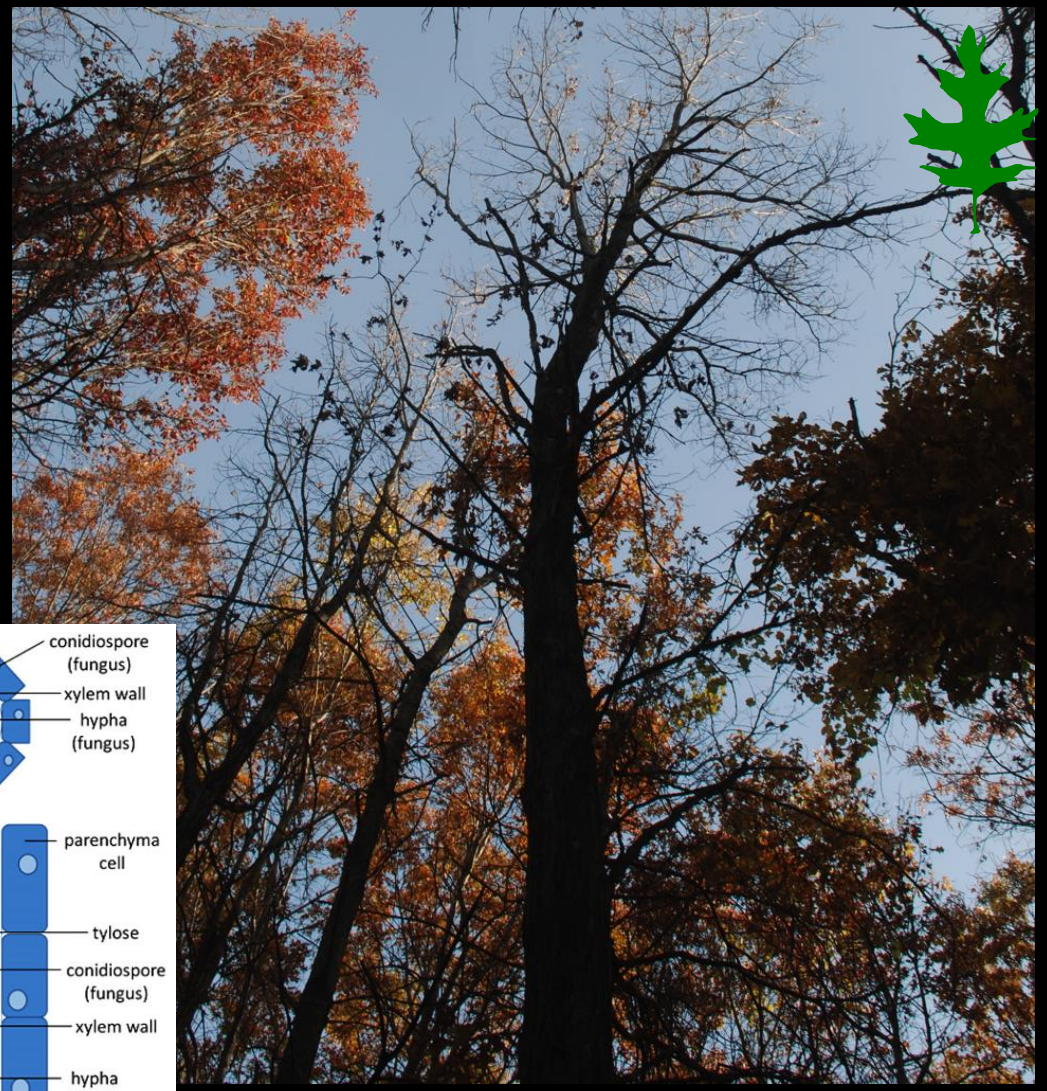
Herbicide treatment

Photos from J. Juzwik

Vibratory plow to severe root connections between neighboring trees

Phylogenetic lineages differ in disease susceptibility

Red oaks like *Quercus ellipsoidalis* – highly susceptible



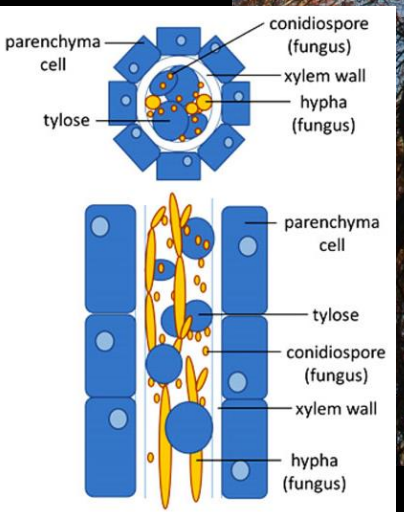
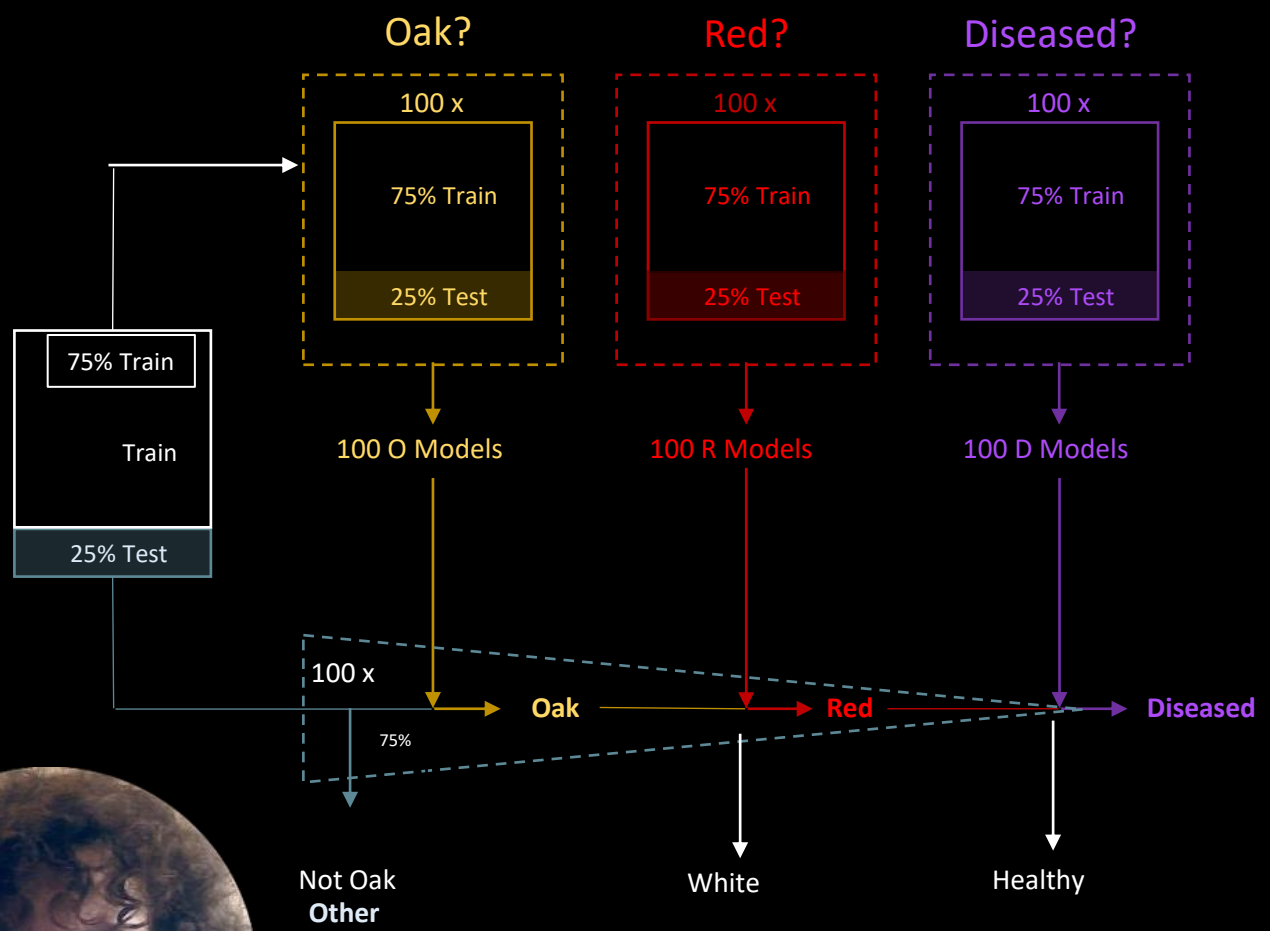


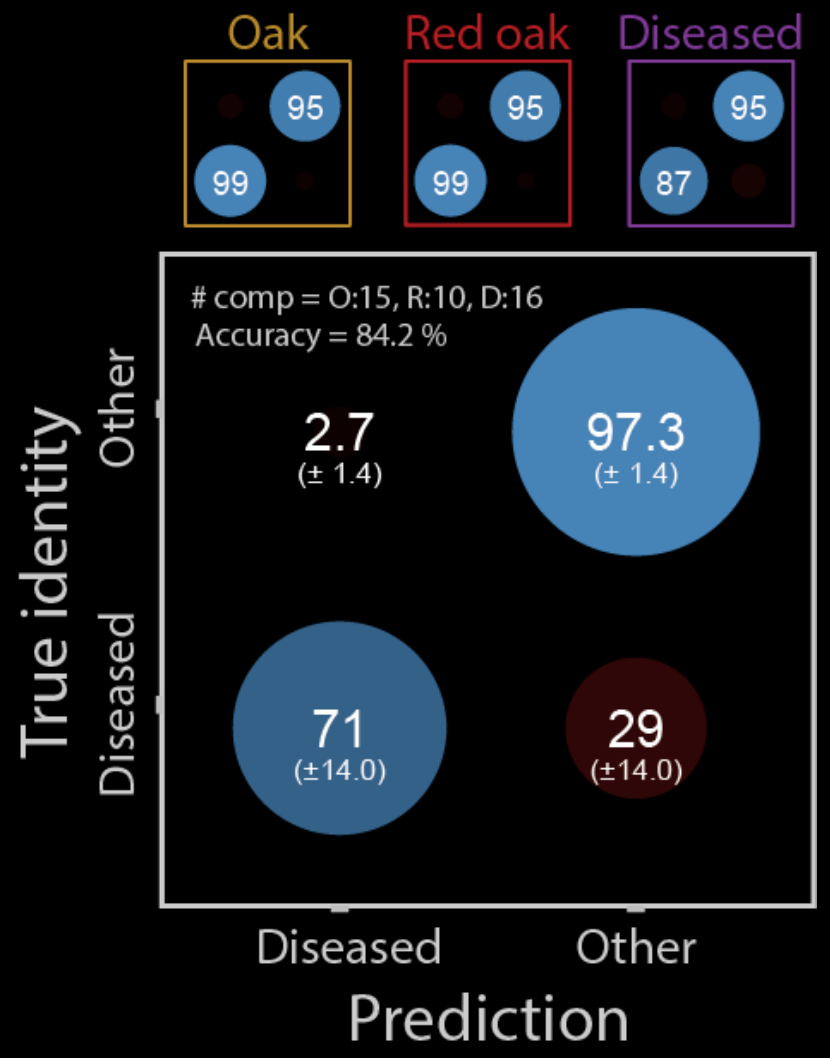
Photo: J. Cavender-Bares

White oaks like *Quercus macrocarpa* – resistant

Photo: Brian Schwingle

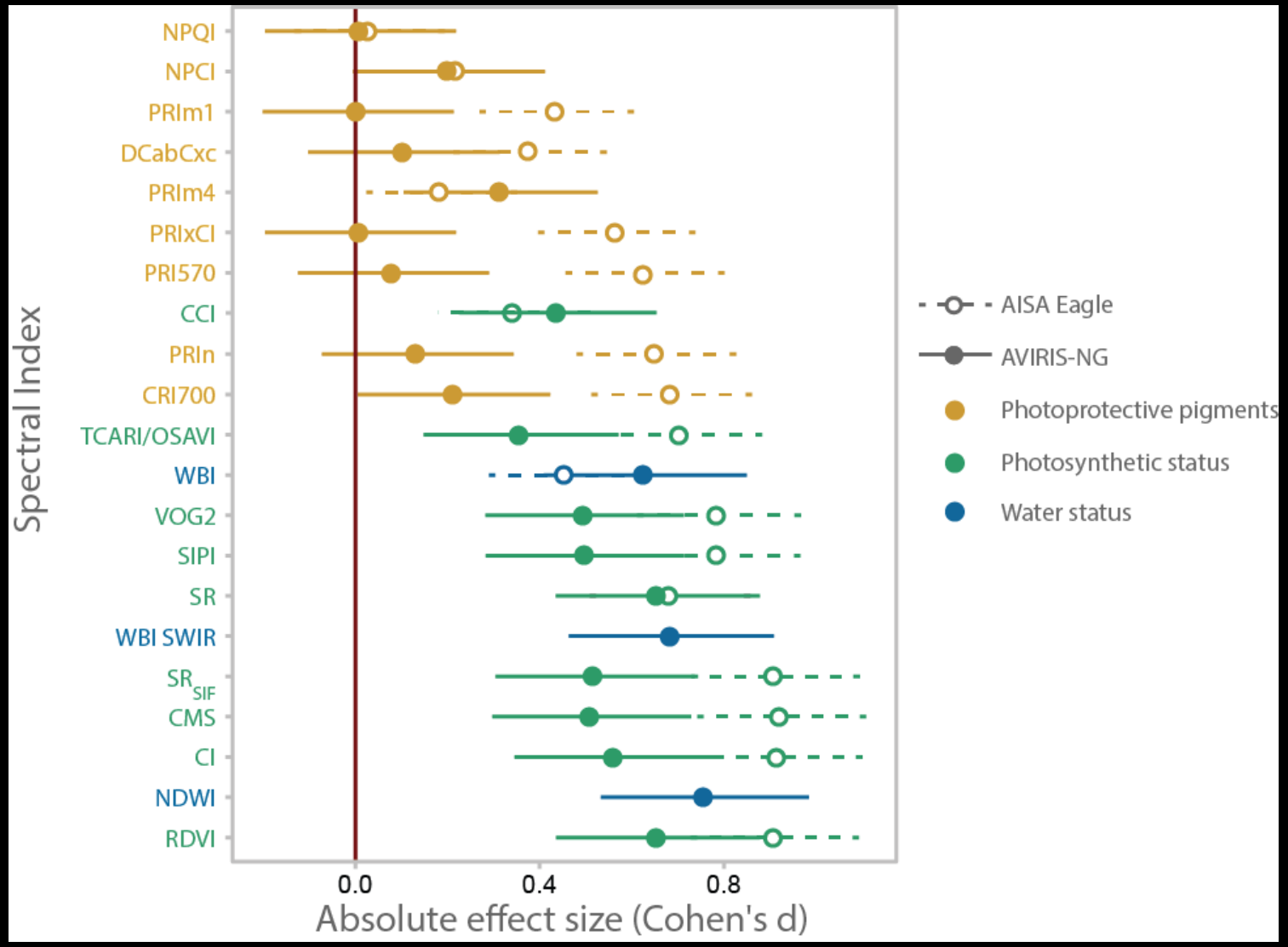
Spectral phylogeny + spectral physiology enables oak wilt detection across the landscape



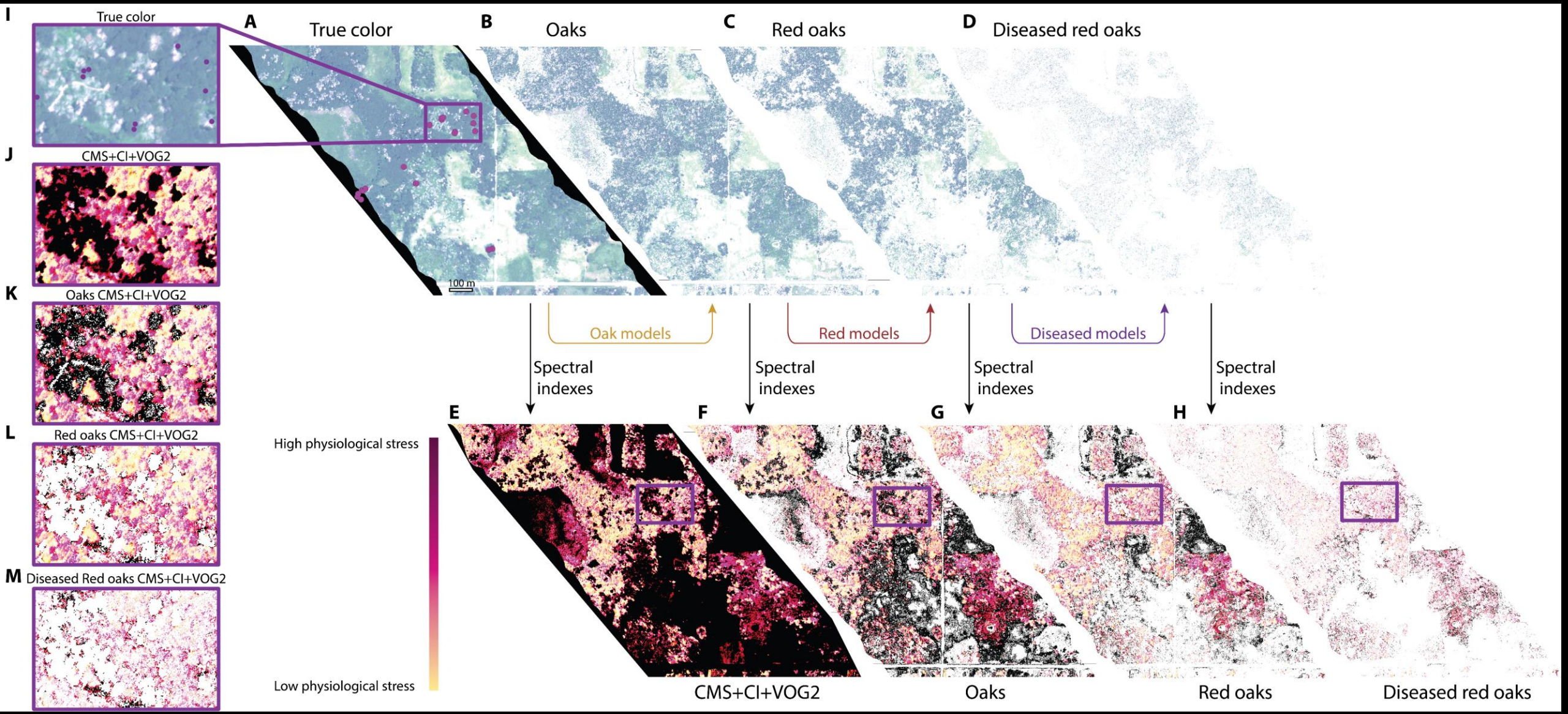


Sapes et al., 2022, *Remote Sensing of Environment*

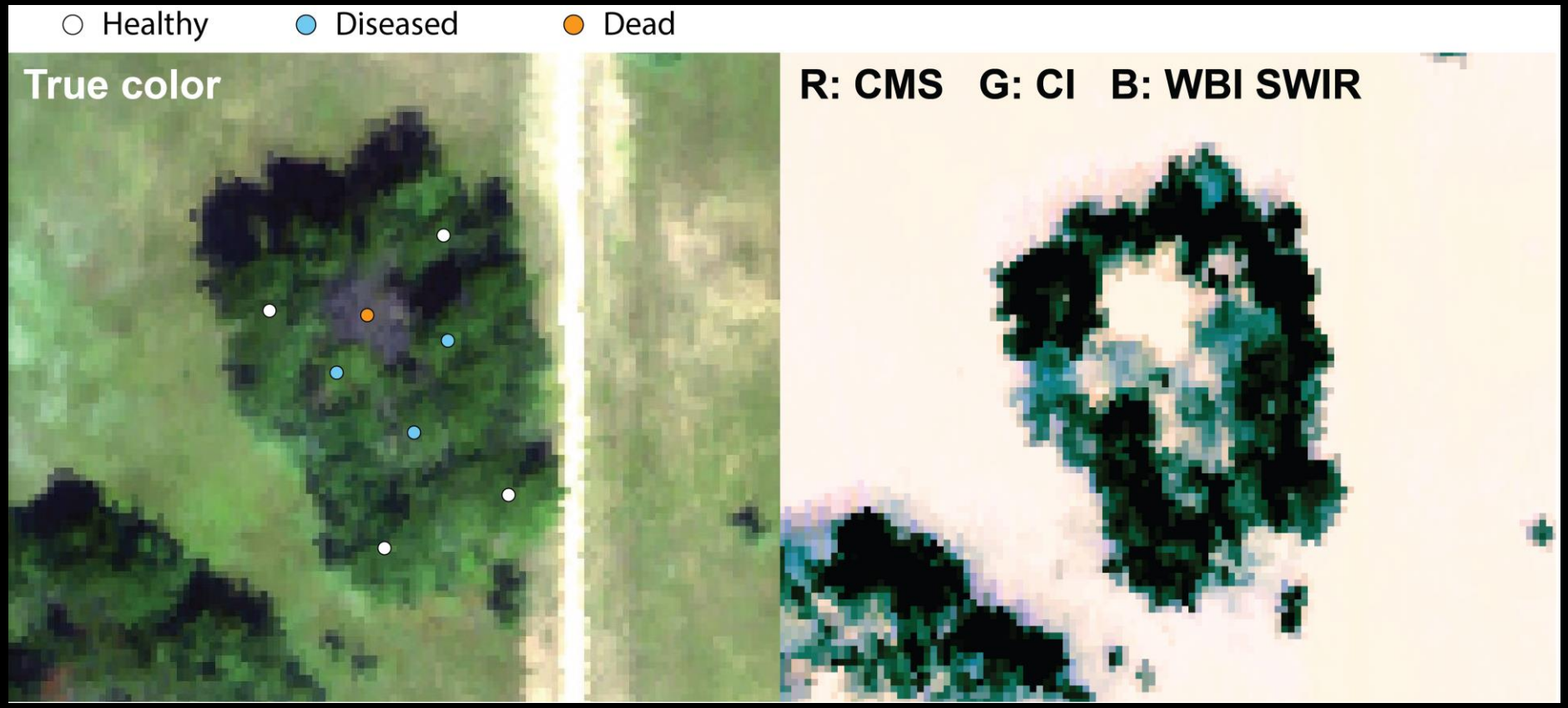
Spectral indices associated with photosynthetic (green) and water status (blue) readily differentiated diseased red oaks from healthy red oaks



Sapes et al. 2022



Sapes et al. 2022



Sapes et al., 2022

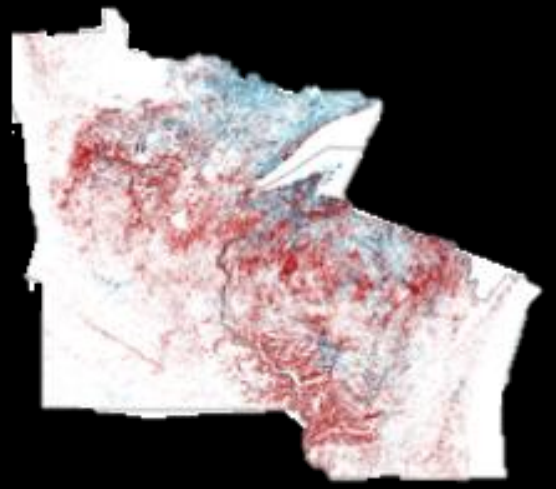
Scaling up physiological symptoms to satellite data

Organ

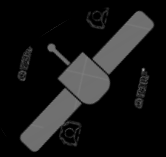
Tissue

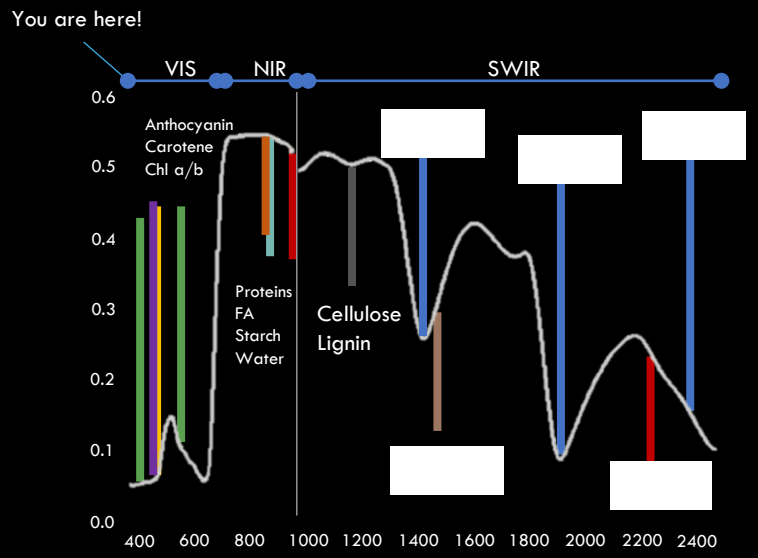
Individual

Landscape

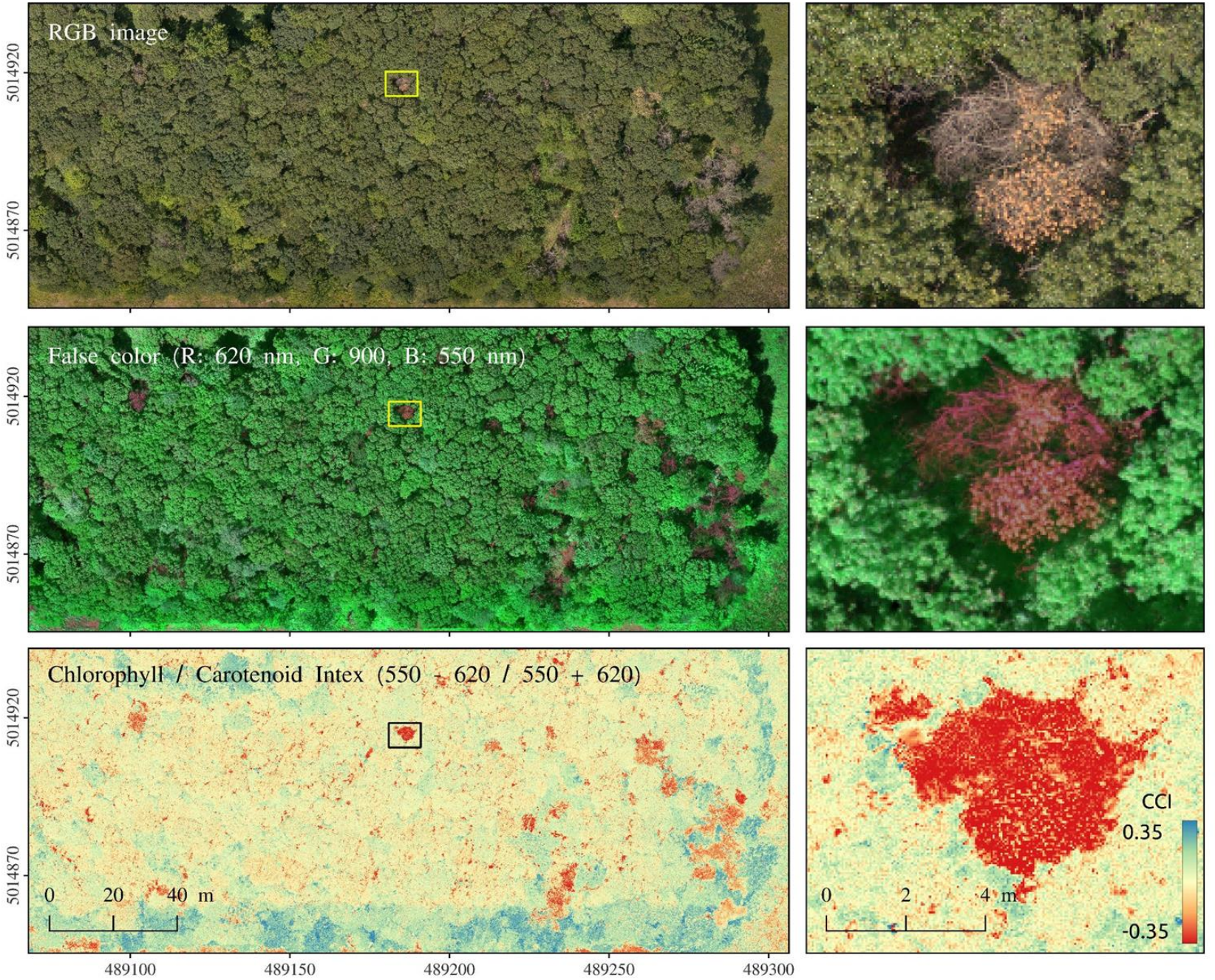


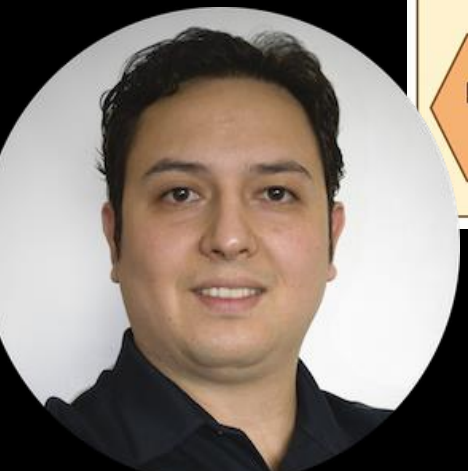
Region

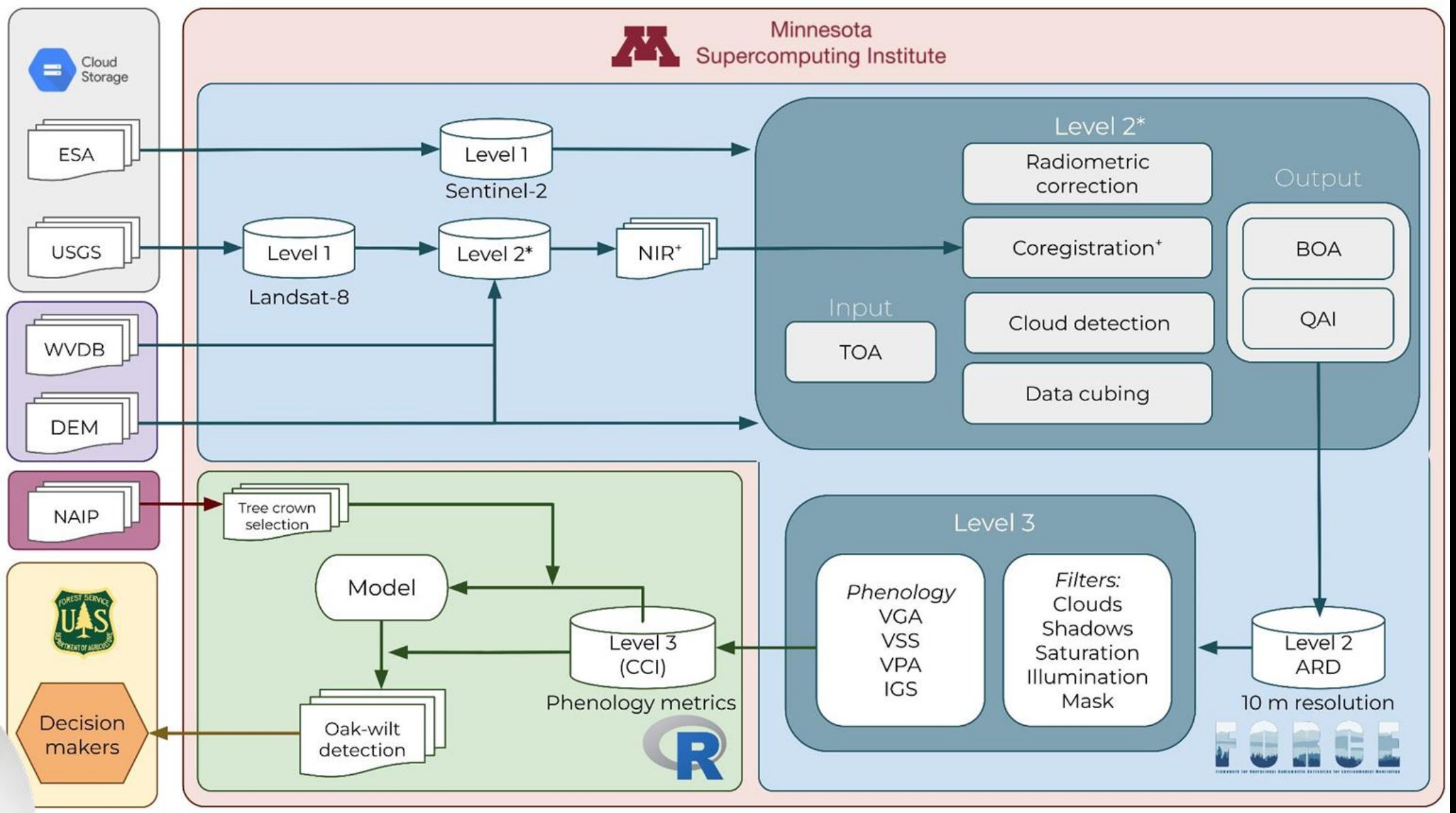




Using a phenological approach







Workflow for acquiring, processing, and analyzing Landsat 8 and Sentinel-2 imagery for mapping of oak wilt.

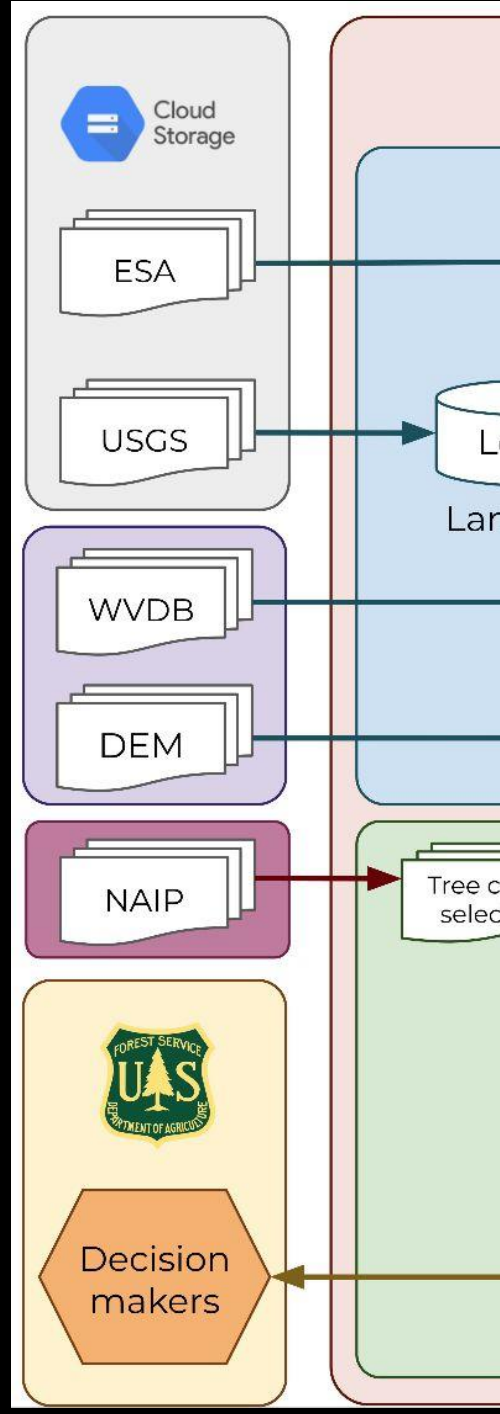
ESA - Sentinel-2

NASA-USGS - Landsat-8

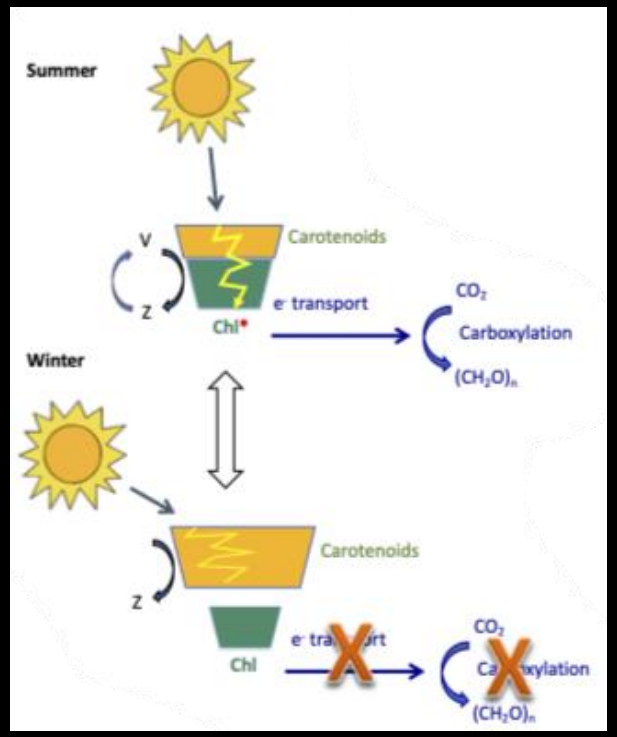
NASA - MODIS (MODIS Water Vapor Database from Terra and Aqua MODIS Total Precipitable Water Vapor products)

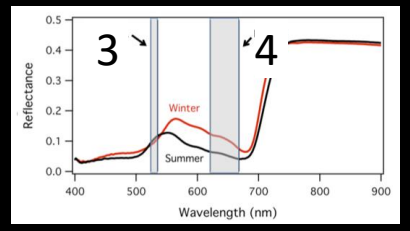
NASA - Shuttle Radar Topography Mission (SRTM) / A Digital Elevation Model

USGS - National Agriculture Imagery Program

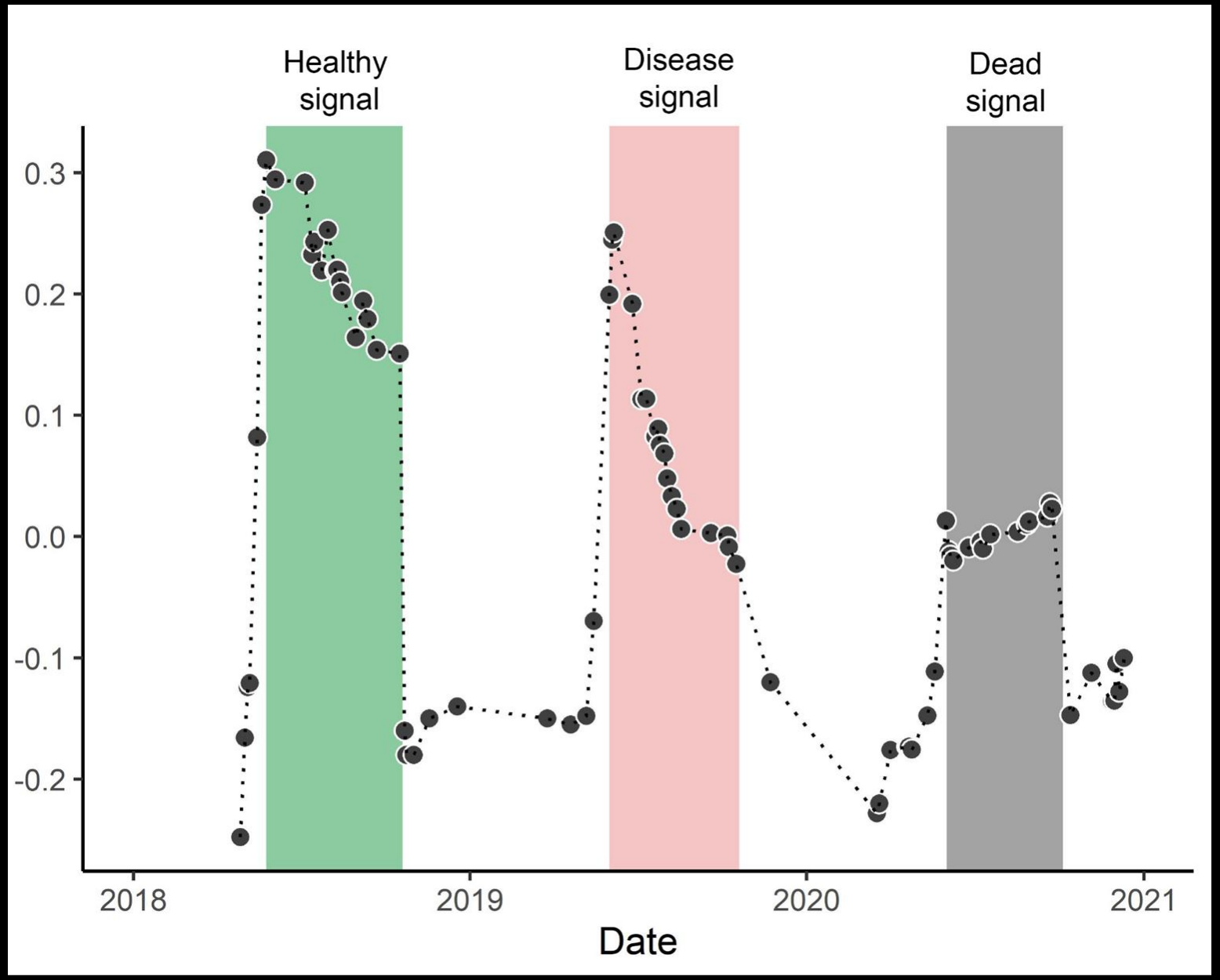


Chlorophyll/Carotenoid Index
tracks changes in pigments and photosynthetic activity (Sentinel2)





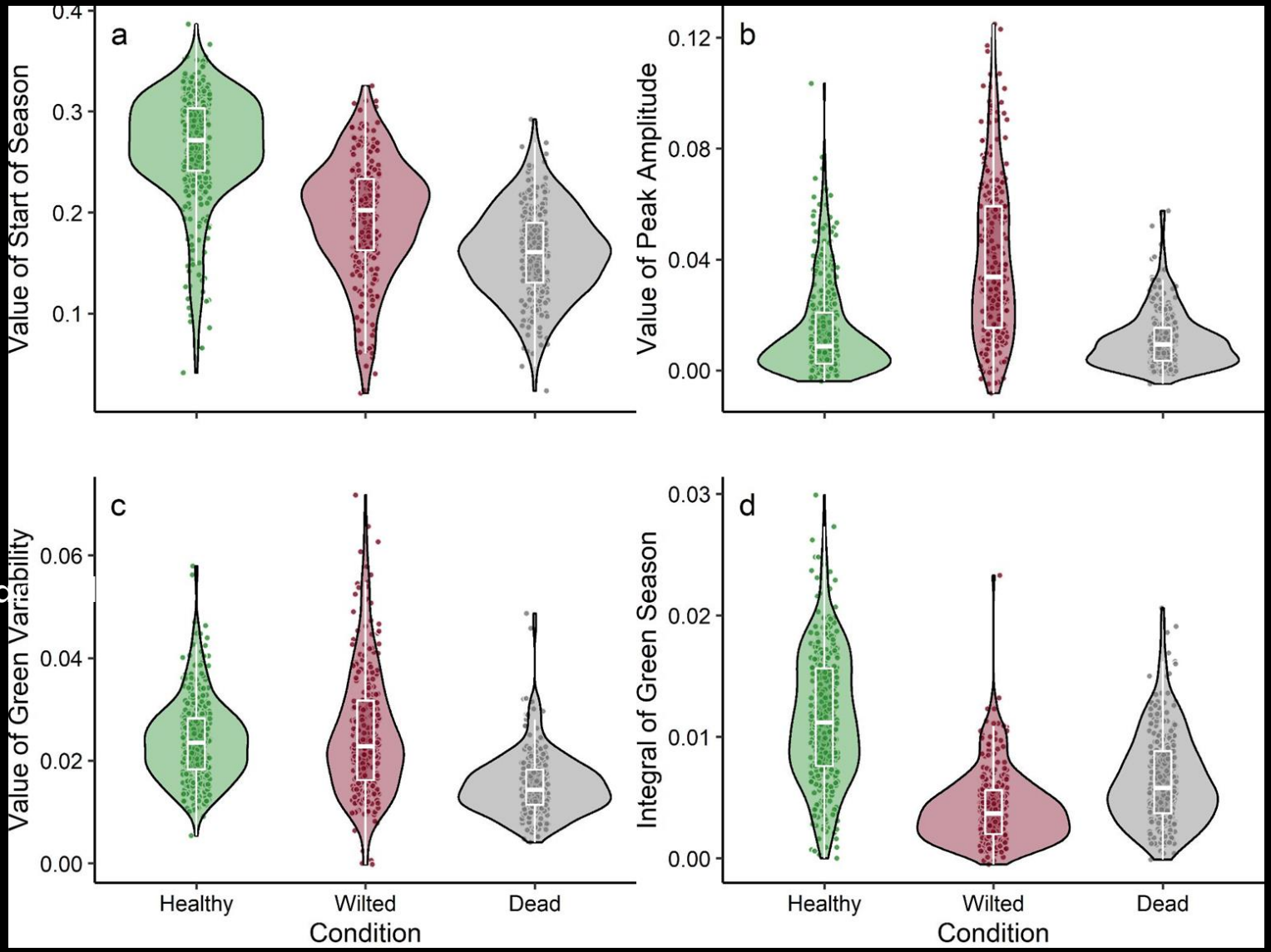
Gamon et al 2016



Time series of CCI for a single oak tree (pixel) that died from oak wilt

VSS value at start of the season

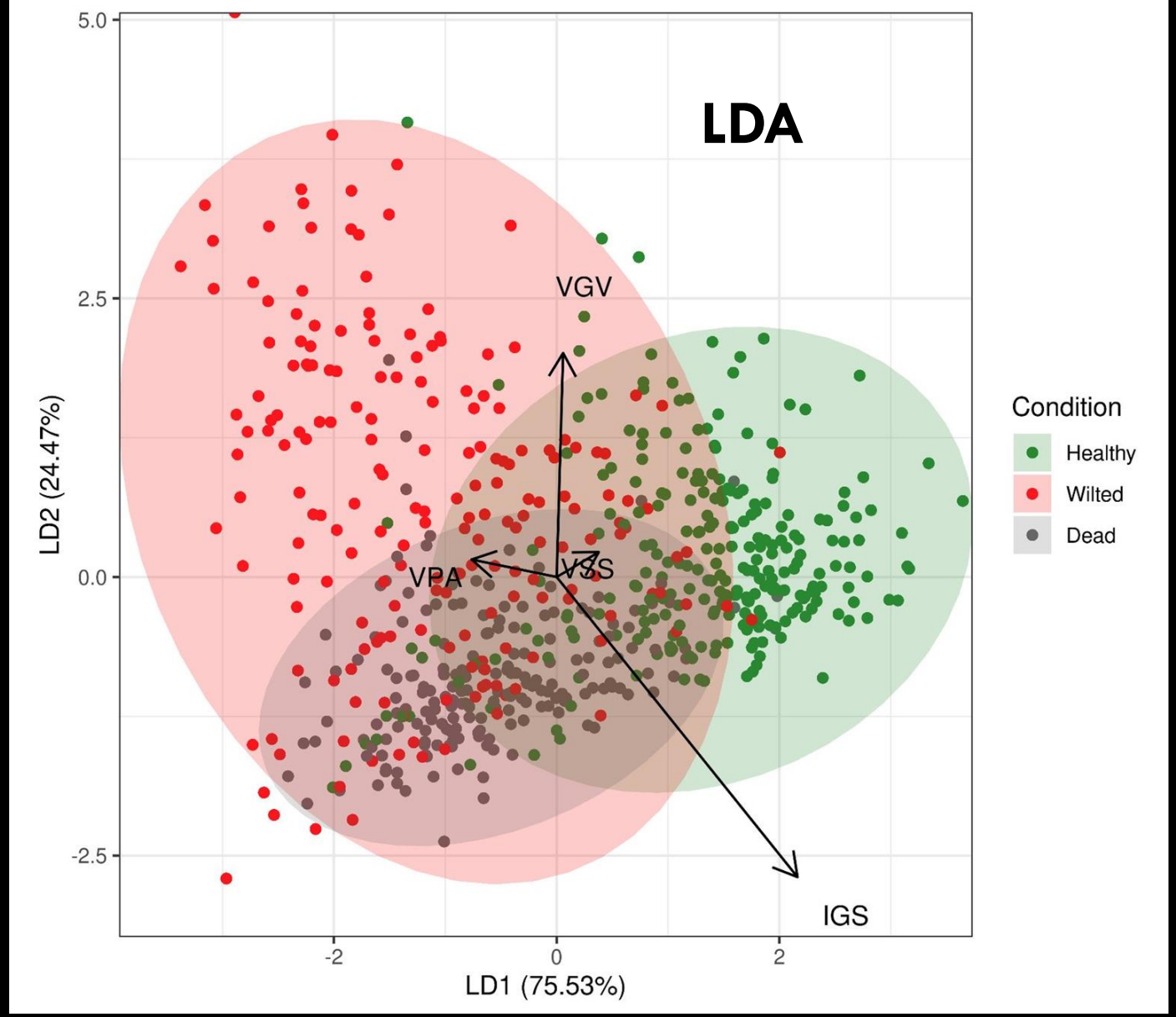
VGV value of green va



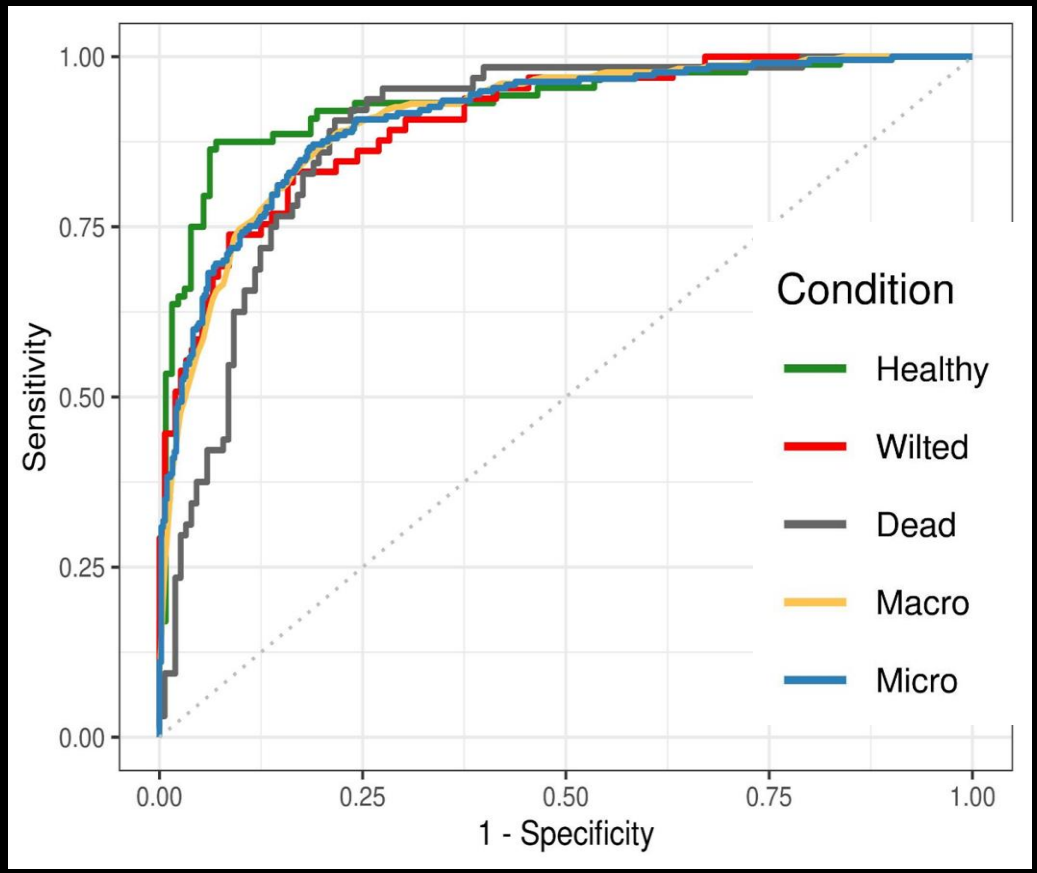
VPA value of peak amplitude

IGS integral of growing season

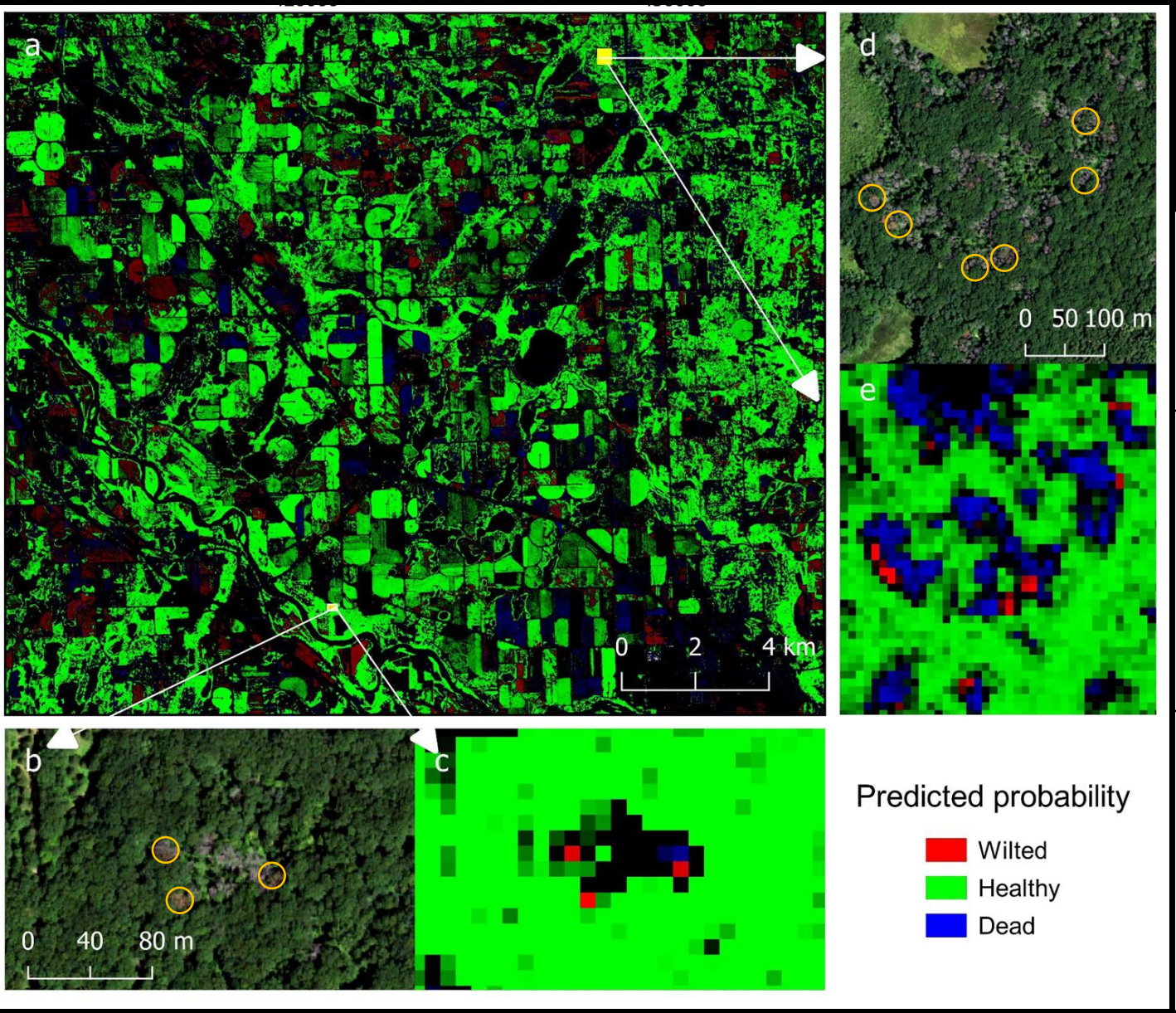
4 phenological metrics using CCI that differentiate **healthy**, **diseased**, and **dead** oaks



Receiver Operating Characteristic curves



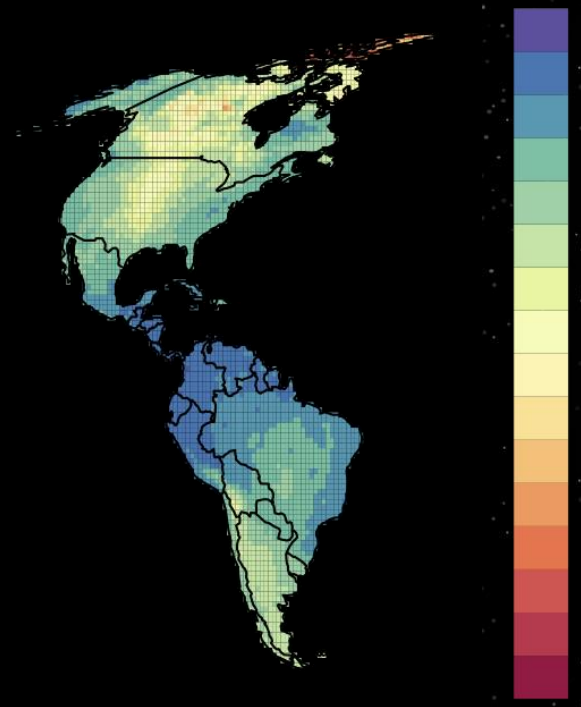
Linear Discrimination Analysis on the training dataset summarizes the variability of the phenological signal between healthy, wilted, and dead oak trees

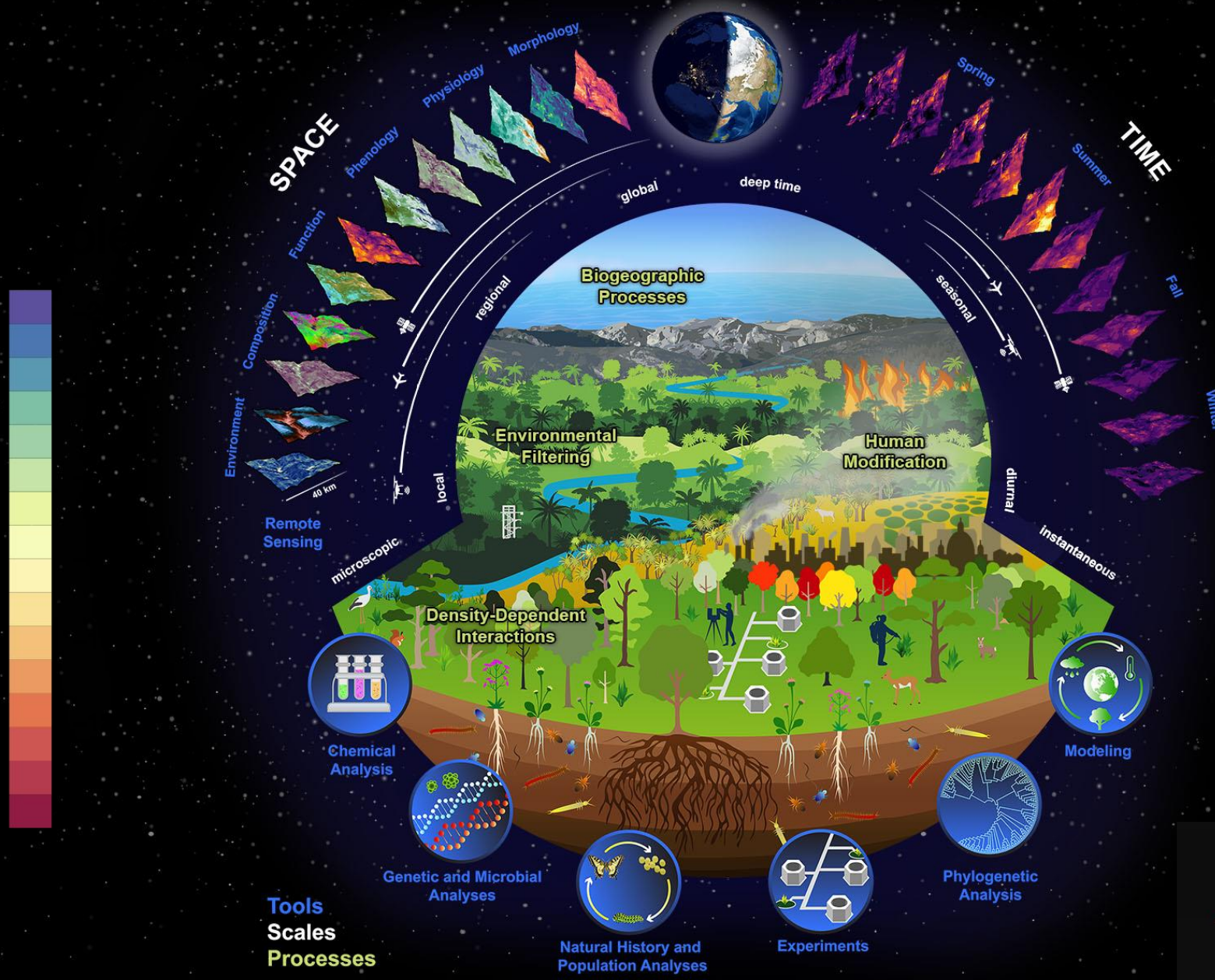


Oak wilt detection
Sherburne County, MN

Dataset	Metric	Condition		
		Healthy	Wilted	Dead
Training	Accuracy	0.86	0.85	0.78
	Sensitivity	0.82	0.84	0.66
	Specificity	0.91	0.85	0.90
Testing	Accuracy	0.85	0.84	0.76
	Sensitivity	0.79	0.86	0.64
	Specificity	0.91	0.82	0.88

Engaging with folks at the Minnesota State Fair




SPACE
TIME
Morphology
Physiology
Phenology
Function
Composition
Environment
40 km
Remote Sensing
microscopic
local
regional
global
deep time
seasonal
diurnal
instantaneous
Spring
Summer
Fall
Winter
Biogeographic Processes
Environmental Filtering
Human Modification
Density-Dependent Interactions
Chemical Analysis
Genetic and Microbial Analyses
Natural History and Population Analyses
Experiments
Phylogenetic Analysis
Modeling
Tools
Scales
Processes