



Mapping intraspecific genetic variation in *Populus tremuloides*

Sponsorship Project Report

ID 1b09e2

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Context

- More extreme, prolonged, and widespread droughts are accelerating tree mortality across biomes
- Our current ability to predict when and where mortality will occur is low
 - This limits our capacity to sustainably manage landscapes for continuity of ecosystem services!
- Current predictive models are based on environmental variables alone
- **Hypothesis:** including variables describing genetic variation alongside environmental predictors will improve our predictive capacity
 - Resource-intensive methods requiring field campaigns and laboratory analyses have historically prevented scientists from gathering spatially explicit datasets describing genetic variation at large scales

Objectives

- Pioneer methods for using genetic field data, multi-scale remote sensing data, and deep learning methods to map intraspecific genetic diversity
- Test the hypothesis that our ability to forecast when and where vegetation will experience mortality from extreme climatic conditions improves when we include metrics of intraspecific genetic variation as predictors

Project Goals - 1b09e2

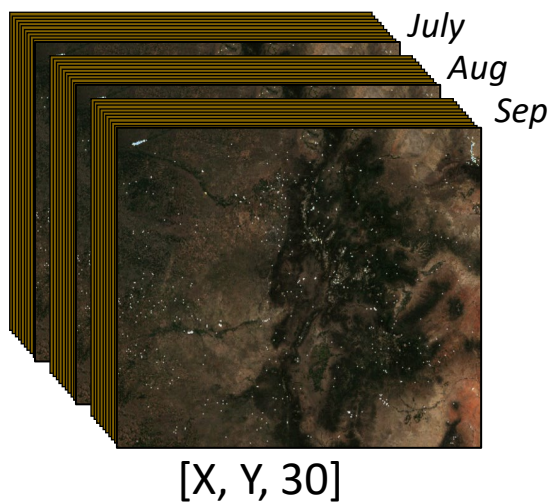
- (1) Map intraspecific variation in cytotype (number of chromosome copies) in quaking aspen (*Populus tremuloides*) in southwestern Colorado, USA.
- (2) Test if the spectral signal of cytotype is consistent across years.

Process

Feature:

Sentinel-2

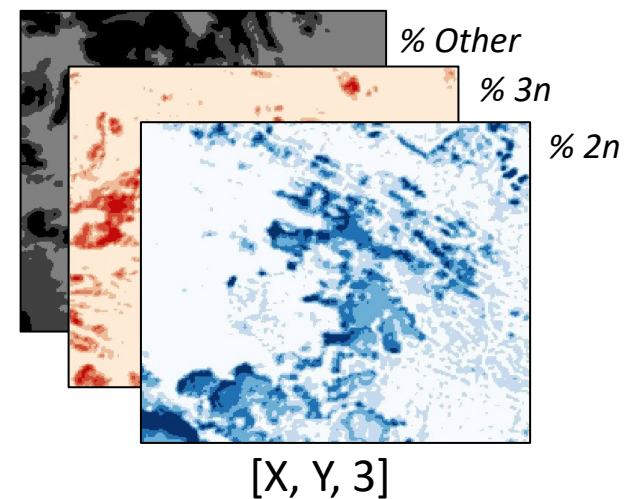
- 10-bands (10, 20m)
- 5-day revisit
- Phenology stack



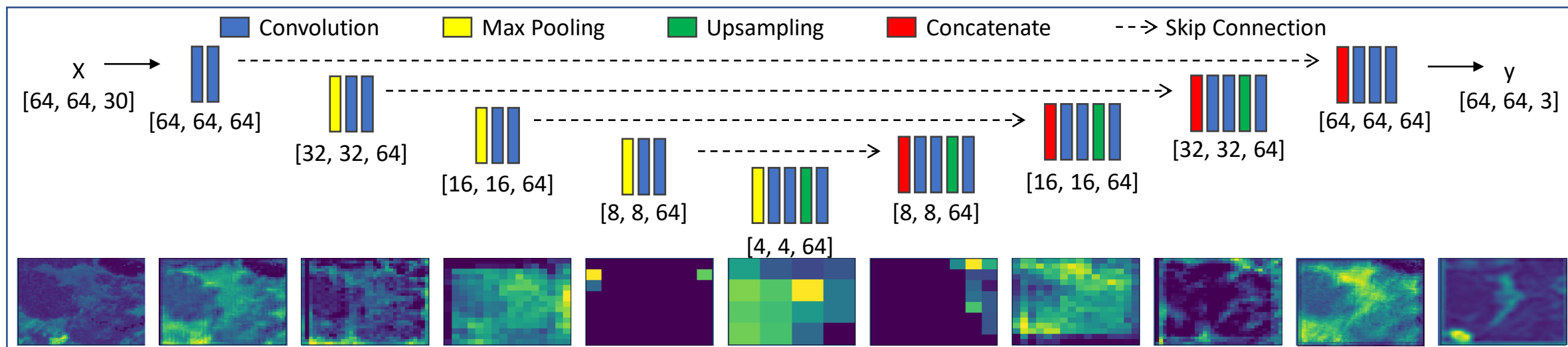
Response:

Blonder et al. (2022)

- Upscaled to 10m



Ensemble of FCNNs

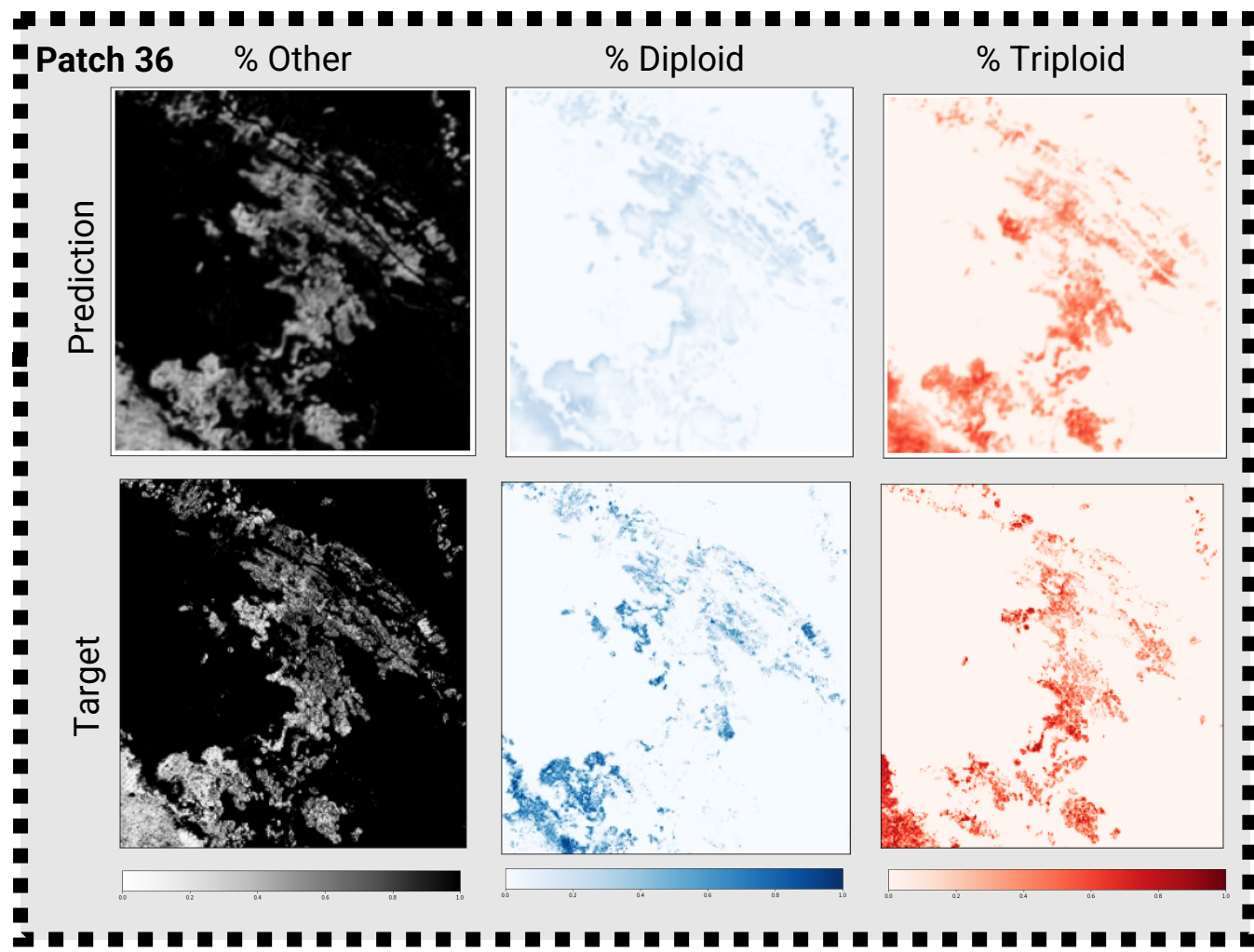
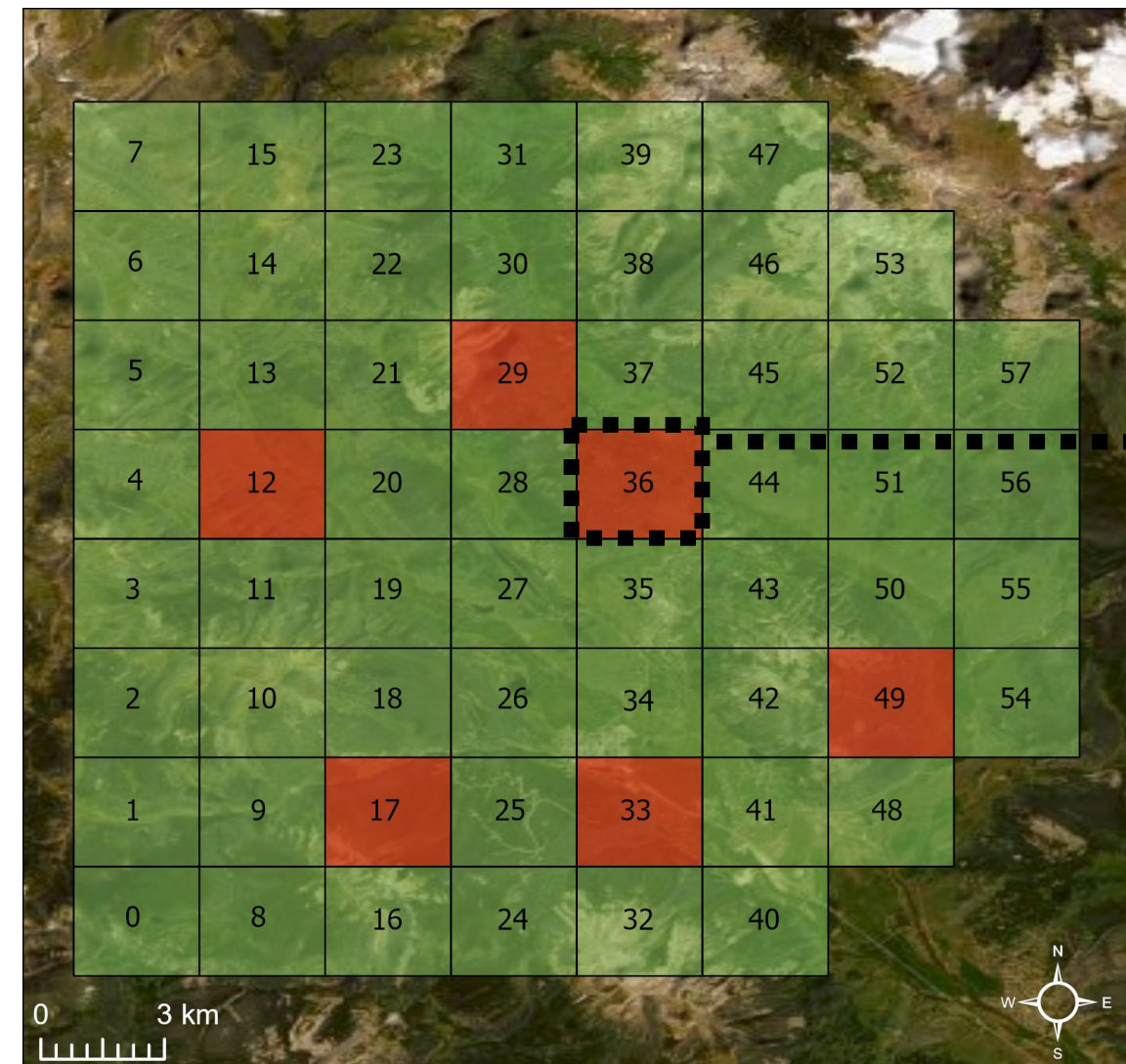


Accessing data via the SentinelHub python package enabled me to efficiently collect and preprocess massive amounts of Sentinel-2 imagery over our study area. I was able to mosaic the best pixels for every month of imagery available since the sensor began collecting in 2017, and seamlessly feed that data into my ensemble of fully convolutional networks as annual tiled phenology stacks. Calling only the final mosaics from the cloud to my home computer meant that I could sort through massive amounts of data without overloading my personal computer, and the python integration allowed for trackable, shareable, integrated workflows start to finish.

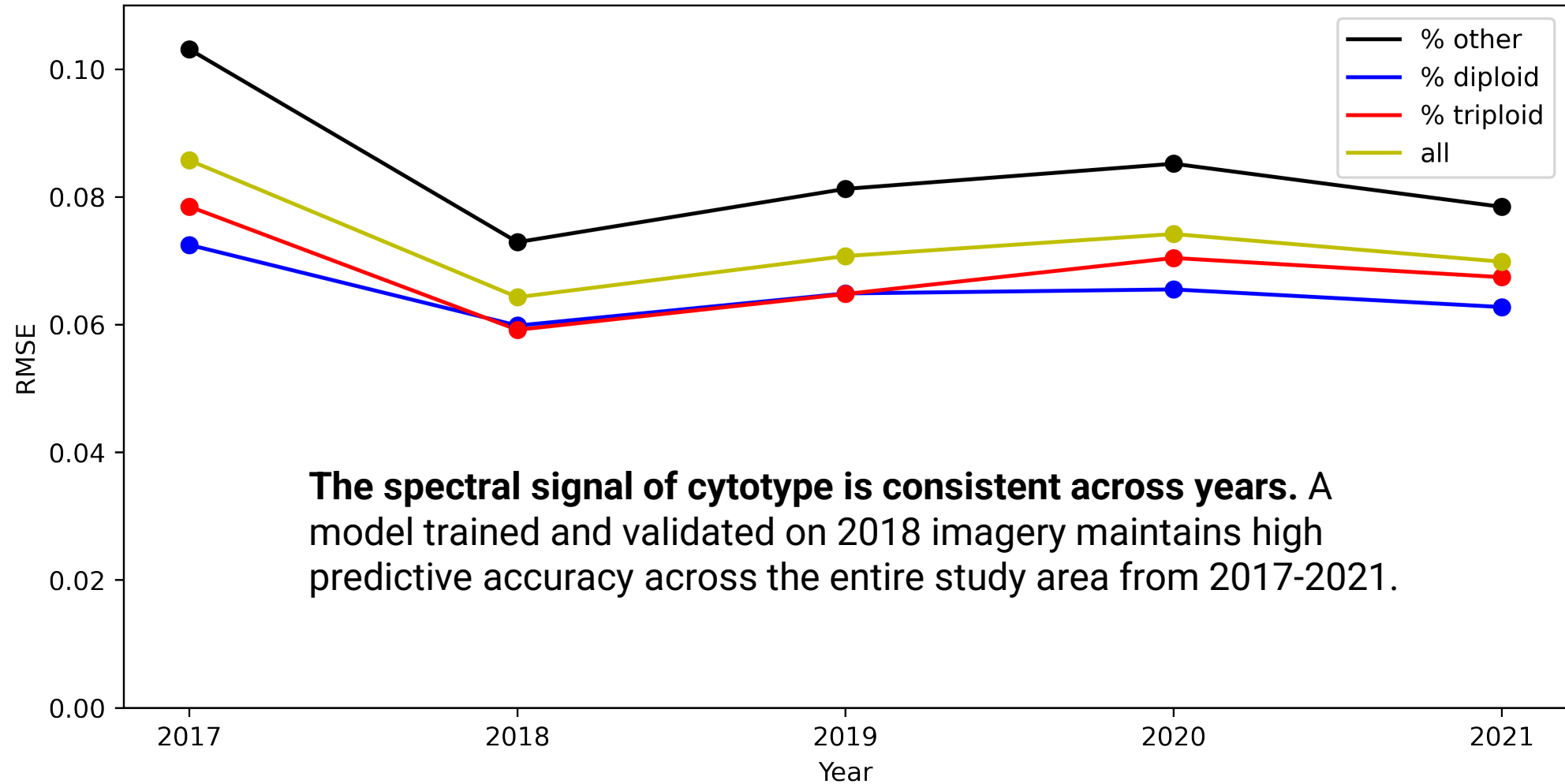
Results

We classify cytotype with <10% RMSE in a spatially-explicit hold out test set

All	Diploid	Triploid	Other
0.083	0.089	0.074	0.084



Results



Highlights

- Presented results at the Ecological Society of America 2022 Annual Meeting in Montreal, Canada
- Presented results to the United State Forest Service Grand Mesa Uncompahgre and Gunnison National Forest management teams to plan future collaborative management actions

Next Steps

- Incorporate Sentinel-1 imagery into the feature space
- Test the spatial and temporal limits of model transferability across the western United States
- Map annual mortality in the species as time below a threshold combined NDVI/NDMI
- Model mortality as a function of cytotype and environment, compare accuracy to a model predicting mortality based on environmental variables alone