

## Introduction:

Phenology—the timing of recurrent seasonal events in an organism—is largely driven by regional climatic conditions, such as temperature, sunlight availability and precipitation.

Anthropogenic changes in climate are causing species to shift their phenology in different ways, leading to phenological mismatches. In mutualistic species, which rely on having matched phenology, these mismatches can lead to declines in population growth and overall ecosystem health. Greater phenological variation within a species could decrease the likelihood of phenological mismatches; for instance, a population of trees with variations in individual's flowering times could be less susceptible to disruptions in pollinator timings. Although intraspecific phenological variations are common, its causes are widely unknown—though one candidate is variation in the microclimatic conditions that drive phenology.

To investigate the effect of variation in microclimatic conditions, this study will focus on the flowering phenology of *Liriodendron tulipifera* (tulip trees) across several large study sites ( $>10\text{km}^2$ ). Phenological studies are generally conducted on small sites, not at this large scale. However, with the advent of computer vision techniques, along with fine-scale remote sensing technologies such as LiDAR and hyperspectral imagery, we can assess how phenology varies across individuals at a large-scale. The National Ecological Observatory Network (NEON) provides data products for this goal—phenological data on a small study site and remote sensing data on the larger surrounding area. The proposed research aims to leverage these two scales of NEON data to (1) construct a flowering phenology map over a large area and (2) collect data on the microclimatic features within the site. These data will then be used to investigate the relationship between these microclimatic features and variations in flowering phenology in tulip trees.

## Background:

Since the late 20th century, scientists and global leaders have grown increasingly concerned about the implications of anthropogenic current climate trends and the potential threats posed to biodiversity and ecosystem health (Grimm et al. 2016). One pervasive response to the changing climatic conditions is shifts in phenology, the timing of recurrent seasonal events in an organism (Visser and Both 2005; Parmesan 2006; Walther et al. 2002). Phenology is largely driven by regional climatic conditions such as temperature and precipitation; for instance, plants may flower sooner with heavier rain, or birds may migrate later due to a warmer winter. However, phenological transitions are driven by different environmental cues in different species. Because of this, species will respond to climate change in different ways, and thus phenological shifts are variable within ecosystems (Thackeray et al. 2016; 2010; Visser, Both, and Lambrechts 2004).

If different species exhibit different responses to the same climatic changes, phenological mismatches can arise between mutualistic species, causing detrimental effects in population growth and ecosystem health . Furthermore, individuals within a species can exhibit different phenology even in the same regional climatic conditions (Moran, Hartig, and Bell 2016; Xie, Thammavong, and Park 2022). This intraspecific phenological variation could reduce the risk of phenological mismatch; for instance, if either species of a mutualistic pair shows variations in their phenology, the risks of a mismatch due to climate-mediated phenological shifts decreases. Intraspecific variations in phenology have been shown to have implications on ecosystem health in a number of ways: for instance by broadening niches and the range of interactions between species (Moran, Hartig, and Bell 2016), strengthening mutualistic networks (Arroyo-Correa, Jordano, and Bartomeus 2023), and in network robustness in phenological shifts (Xie,

Thammavong, and Park 2022). Despite its importance, the causes of intraspecific variation in phenology are relatively understudied.

One possible explanation for intraspecific phenological variations is variations in the underlying microclimatic conditions which drive phenology. For instance, topography has been shown to be an important driver of phenological variation on small study sites, especially those with highly variable elevation, and consequently snowmelt timing (Hwang et al. 2011; Ward, Schulze, and Roy 2018; O’Leary, Kellermann, and Wayne 2018; Billings and Bliss 1959; Sherwood et al. 2017). Soil properties that vary on a fine spatial scale can also influence which vary influence intraspecific phenological variability; for instance, properties such as pH (Arend, Gessler, and Schaub 2016), moisture (Bernal, Estiarte, and Peñuelas 2011; Wheeler et al. 2015; Cortés-Flores et al. 2017), and temperature (O’Connell, Alber, and Pennings 2020). Despite exhaustive research showing that intraspecific phenological variation at this microscale exists, little work has been done to conclude which abiotic factors are driving this variation, and whether these factors may be helpful for predicting how variable phenologies will respond to a changing climate.

Due to the difficulty of collecting individual level data, large scale phenological studies estimate population statistics by assessing mean changes, such as analyzing continent-wide trends over many years. Studies which do collect individual level data generally do so on small scale study sites. As a result, there is a lack of individual level data across a large scale—the kind of data which would be useful for assessing intraspecific phenological variation at scale. However, recent advances in remote sensing techniques allow researchers to collect data from a distance, creating the potential for phenological and topographical studies to be conducted at a much larger range. For instance, researchers may use mean greenness of a region to make

predictions of mean phenology metrics at scale—generally, the greenness of a plant changes with its stages in phenology in predictable ways (Orusa et al. 2023). Greenness, or other visual properties of plants, is often measured with hyperspectral imagery, which involves sampling reflected wavelengths across the entire spectrum of light (rather than just the visible spectrum) (Orusa et al. 2023; Luo and Yu 2017; Peng et al. 2021). However, this kind of data is still insufficient to this study's end, as it doesn't contain individual-level information on phenology, but rather population-level information. Machine learning and computer vision techniques, such as segmentation and classification models, can aid in extracting individual-level data from remote sensing data.

Machine learning has been previously used to extract individual level phenology data from remote sensing data (Dixon et al. 2021). To do this, the remote sensing data must be segmented into individuals of a species of interest, then these individuals are assessed for some phenology metric, such as flowering. This kind of process is commonly done in phenological studies by segmenting the data into contiguous parts (representing where individuals are in the data) and classifying the individuals into their species. For this research, segmentation and classification will be conducted using LiDAR and hyperspectral imagery, respectively. LiDAR data, which describes three-dimensional geometries by mapping distances from a reflective laser grid. In phenological studies, segmentation, or more specifically, tree delineation models are generally unsupervised models which delineate LiDAR data into its contiguous parts, which represent the objects present in that data. In recent years, LiDAR systems have been increasingly applied in remote sensing applications, such as the modeling of forest structure (Lim et al. 2003; Ediriweera et al. 2014), topography (Flood and Gutelius 1997), burn patterns (Park and Sim 2023), and habitats (Vierling et al. 2008). In phenological studies, LiDAR can be used to gain

insights into regional topography (Paynter et al. 2016; Risse et al. 2018), tree delineation (Jakubowski et al. 2013; Li et al. 2012), and species classification (Scholl et al. 2020; Maschler, Atzberger, and Immitzer 2018). Hyperspectral imagery, as mentioned prior, is used often in remote sensing for predicting large scale mean phenological metrics (Orusa et al. 2023; Luo and Yu 2017; Peng et al. 2021). Additionally, many classification models have been developed to leverage hyperspectral imagery for species classification (Scholl et al. 2020; Maschler, Atzberger, and Immitzer 2018; Marconi et al. 2022; Landmann et al. 2015; Fricker et al. 2019), and for flowering classification (Dixon et al. 2021; Landmann et al. 2015; Gallmann et al. 2022).

To take advantage of the high potential of remote sensing data, the National Ecological Observatory Network (NEON) was built in an effort to track ecological (including phenological) changes at a continental scale (Zedler 2011; Kampe et al. 2010). The network includes 81 field sites across the U.S. which produce a variety of data products in a highly structured and consistent manner. Of interest to this study, the data products include in-situ observations of phenology as well as remote sensing data such as LiDAR and hyperspectral imagery. NEON data is free to use and extensive, offering high spatial resolution information across time and the U.S. With regard to this research, NEON will be leveraged through three data products. Phenology data is available on a subsection of each site, representing the flowering information on some individuals of the entire population—i.e., the ground truth labels. LiDAR and hyperspectral imagery data is available across the entire site, which together will provide the ground truth and unlabeled data. Furthermore, LiDAR data can be analyzed to extract topographical features of the land, which can later be used to quantify the effects of these features on flowering phenology.

I aim to develop machine learning methods which leverage the extensive remote sensing data available through NEON to extract individual-level flowering phenology data at a large

scale. Individual-level phenology data at this scale would enable researchers to investigate questions about intraspecific phenological variation in ways previously impossible. To extract this information, there are three rough steps. (1) Segments of individuals must be extracted from the large-scale remote sensing data, (2) then be classified as a species of interest, (3) and finally be classified into their phenological state. NEON remote sensing and phenology data supplies the necessary data for these models to be trained and ultimately ran on. The final output of this research, a map of flowering states for a species of interest, will be combined with information on the spatial abiotic factors which make up NEON sites. This map can be analyzed using statistical methods such as regression models.

#### Proposed work:

The proposed research aims to develop a pipeline which can extract flowering phenology data from NEON data, then combine that data with a map of spatial, abiotic factors such as topology (fig 1). The pipeline begins with ground truth data, representing all information we have about the subset of labeled individuals within a site. After filtering the data to a species of interest, a segmentation model will be applied to the ground truth map. This data, which represents the typical appearance of individuals of the species in different flowering states (either

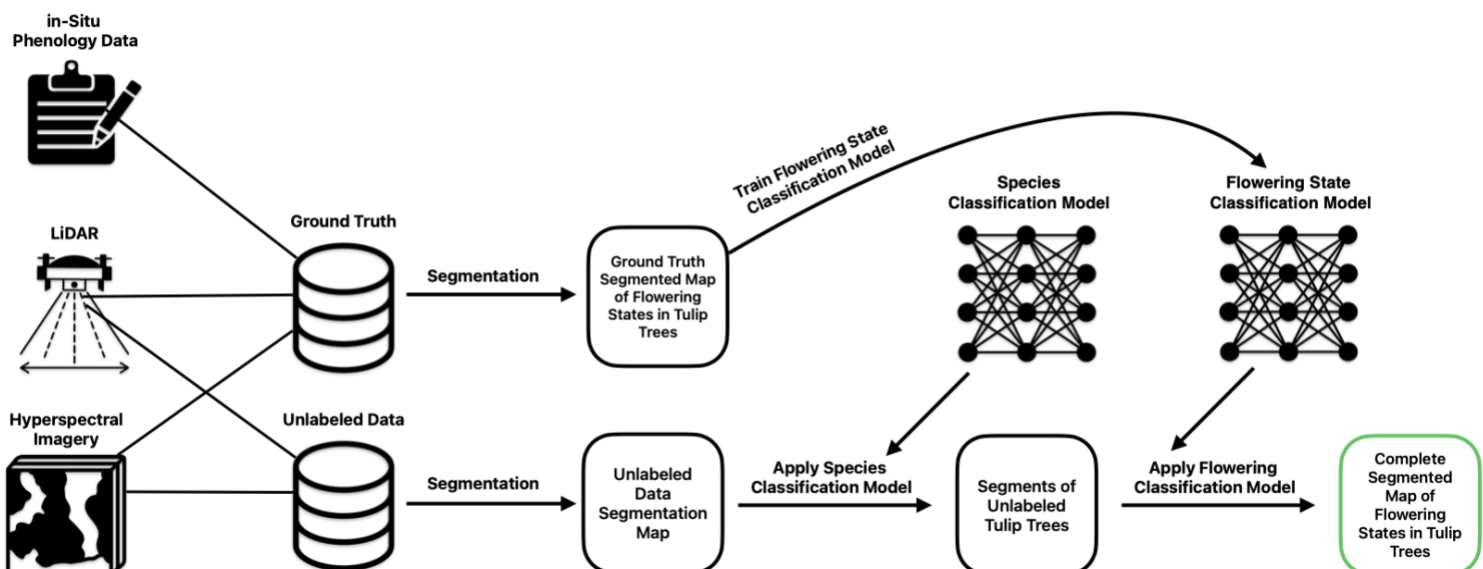


Figure 1. Proposed machine learning pipeline.

flowering, yet to flower, or already flowered), will then be used to train a flowering classification model. This flowering classification model, in addition to the species classification model and segmentation model, can be applied to unlabeled data to extract flowering phenology data on an individual level across the entire site.

While this work is largely concerned with the development of methods to be used in phenological studies, I have selected a single species to work on with the potential to extend the findings to other species. Most work thus far has been concerned with selecting this species and a subset of NEON sites which contain data on the species. The hope is that, because NEON data is collected in a highly standardized manner, the methods developed herein will be applicable to other species in future studies.

To select a study species, I began with surveying phenological data from all of the NEON sites for the species which were included. While each site has many species present within it, phenology data is only collected on a handful of those species (and only on a subset of individuals of those species). After constructing a list of species with individual phenology data, I selected the study species using 3 criteria. First, the study species must be a tree, as trees are large and thus are best suited for extracting individual-level data (without conflating overlapping individuals). Second, the study species must have visually detectable flowering patterns, as I ultimately aim to classify the flowering state of trees with imagery—this rules out trees which do not rely on showy flowers to attract pollinators, such as conifers and wind-pollinated trees like oak. Third, we want to maximize the number of sites which include this tree in the phenology data in order to gather information on many individuals across a diverse set of sites. Under these criteria, I selected *Liriodendron tulipifera* (tulip trees) as a potential candidate for a study species.

*Liriodendron tulipifera* is a tall deciduous tree native to the U.S. which produces showy yellow flowers from May to June. Phenology data for *L. tulipifera* is available in a number of NEON sites in the eastern United States: Great Smoky Mountains National Park (GRSM), Oak Ridge National Laboratory (ORNL), Smithsonian Conservation Biology Institute (SCBI), and Smithsonian Environmental Research Center (SERC). To confirm that *L. tulipifera* is an adequate study species, I wanted to check whether *L. tulipifera* is in variable flowering states when remote sensing data is collected for each site (once per year). For training a model to predict whether a tree has flowered or not, I need adequate data for three categories: flowering, yet to flower, and already flowered. Using the phenology data, I determined the flowering observation closest to the AOP flyover data for each individual in each site/year pairing. Across

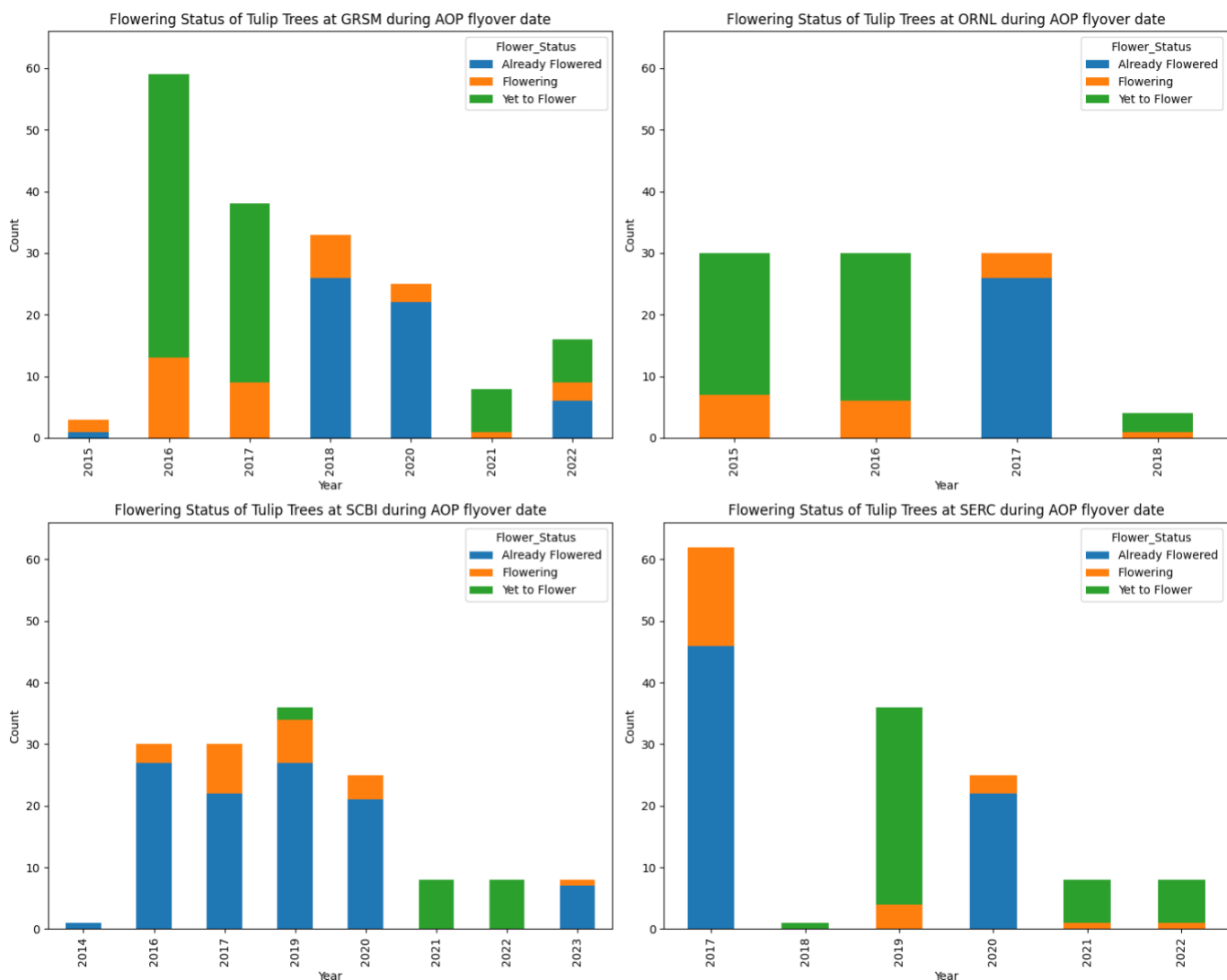


Figure 2. Flowering status of tulip trees in each site for every year with an AOP flyover (ie, all available ground truth data).



the sites there is variable flowering states throughout the years, likely due to differences in the AOP flyover dates from year to year (fig 2).

To begin the pipeline, a ground truth map must be constructed by integrating the in-situ phenology data, LiDAR, and hyperspectral imagery. The phenology data is used to determine flowering states as described for *L tulipifera*. The exact location of each individual can be extracted by utilizing NEON's API (Lunch, Sokol and Hondula, 2007). Once the exact locations have been determined, the LiDAR and hyperspectral imagery data can be overlaid on top of the phenology map. Together, these three data products form the ground truth map of flowering states in tulip trees. This ground truth represents the actual flowering state of trees at a given date, and the hyperspectral imagery (what the region looks like) as well as the LiDAR (the topography of the region).

In order to train the later models, we must segment the ground truth map to locate the actual shapes and appearance of each individual tree. This will be done with a segmentation model, a common task in computer vision. A segmentation model aims to delineate some data into its contiguous parts, which represent the discrete objects present in that data. In this case, I aim to segment 3d point clouds from LiDAR into individual trees using the segmentation model outlined in (Li et al. 2012). Validation of the model will be conducted both by manually labeling segments and by comparing the LiDAR segmentation method with computed segments from NEON tree crown data as in (Scholl et al. 2020). Furthermore, previously computed segments for my chosen NEON sites are available for validation of the model (Weinstein et al. 2023). The hyperspectral imagery from the segmented ground truth data will be used to train two models: one to classify species, and one to classify flower states in *L. tulipifera*. The segmented map identifies where to sample the hyperspectral imagery from to correspond to each individual.

The species classification will be adapted from a model designed in Marconi et al. 2022. Marconi et al. developed a general species classification model for NEON data using hyperspectral imagery—it incorporates a suite of previously developed classifiers: a random forest classifier (Belgiu and Drăguț 2016), a k-nearest neighbors classifier (Laaksonen and Oja 1996), a histogram gradient boosting classifier (Guryanov 2019), a fully connected multilayer perceptron (Pacifico, Macario, and Oliveira 2018), and a bagging classifier with support vector machine as base estimators, using tools from the scikit-learn python package (Pedregosa et al. 2011). Marconi et al. developed a general classifier and site-specific classifier. While the general classifier has the benefit of using more training data, the site-specific classifier outperforms the general model on specific sites, likely due to site-specific effects; for instance, the time of day during data collection, cloud coverage, or in leaf biochemical features (which can affect reflectance under hyperspectral imagery) (Marconi et al. 2022; Sims and Gamon 2002). Because of the increased performance on higher specified training data, I will adapt the site-specific model to my sites of interest. Additionally, Marconi et al.'s model uses elevation as a predictor, but given my interest of relating topography to phenology, I will leave out elevation from the model. The model will be trained and validated on ground truth data from all species in a site, including the in-situ phenology data and other NEON data products, such as vegetation structure, which includes more labeled species.

The flowering state classification model will similarly be based on Marconi et al.'s model architecture but rather than predicting species, predicting whether an individual is flowering, not yet flowering, or yet to flower. However, because there is only flowering data on a small subset (10-20) of the individuals present within each site/year pairing, it is likely to be unfeasible to train and validate a specific model for each site/year pairing. A general model can be adapted

according to the protocol in Marconi et al., which is trained from multiple site/year pairings, then applied to each site/year pairing individually. Following Marconi et al., I can correct for site/year specific effects in this case by including site information in the flowering classification model, such as a nominal identifier for each site/year pairing. This nominal identifier can then be transformed into a real-valued number (to be included in the model inputs) based on the correlation between the categorical variable (site id) and the species classification for each site (Marconi et al. 2022; Wright and König 2019). The flower state classification model will be validated in the same way as the species classification model.

The final output of this pipeline will be a segmented map of flowering state in tulip trees across the entire site for each site/year pairing present in the available data. This output represents a data product which has previously been unavailable for phenological studies—fine-scale spatial information on flowering phenology across a large region. This kind of data allows for analysis of how features such as fine-scale abiotic variation may influence phenology, or more specifically, the timing of flowering events. For instance, a regression model could be developed focusing on the spatial abiotic factors present in a site such as topography and soil properties, with the dependent variable being the flowering state of tulip trees. Through this model, we could quantitatively assess the impact of each abiotic factor on tulip tree flowering phenology. For instance, we could find that certain soil pH levels or elevations are conducive to earlier blooming. Models such as these could elucidate the causes of intraspecific variation in phenology, and in turn motivate future large-scale studies of fine-scale phenology.

Timeline:

Due Date	Writing Tasks	Computation Tasks
1/22/2024		Construct ground truth maps
1/29/2024	Outline of methods	Build segmentation model
2/5/2024		Segment ground truth maps
2/12/2024	Draft of methods	Build species classification model
2/19/2024	Outline results	Classify unknown species
2/26/2024	Draft of introduction	Segment identified species
3/4/2024	Draft of results	Build flowering state classification model
3/11/2024	Spring break!	
3/18/2024	Outline of discussion	Construct final flowering maps
4/1/2024	First draft of final report	
4/8/2024	Draft of presentation	
4/15/2024	Second draft of final report	
4/22/2024	Final report due	
4/29/2024	Final presentation	

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