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The data used to create graphs from Box 1 are openly available in Environmental Data Initiative (EDI) at http://doi.org/[doi in progress], reference number [reference number in progress]. Additionally, the data derived in this article are available from USA-National Phenology Network at http://doi.org/10.5066/F78S4N1V, National Ecological Observatory Network at https://www.neonscience.org/data, Dryad at https://datadryad.org/stash, and EDI at https://edirepository.org/. These data were derived from the following resources available in the public domain:

Switzer J, Chamberlain S, Marsh L, Wong K (2024). _rnpn: Interface to the National 'Phenology' Network 'API'_. R package version 1.2.8.0, <https://CRAN.R-project.org/package=rnpn>.

NEON (National Ecological Observatory Network). 2024. Plant phenology observations, DP1.10055.001 (RELEASE-2023). 2013-2021 for Region: Contiguous United States. Dataset accessed May 2023 via the USA National Phenology Network at http://doi.org/10.5066/F78S4N1V.

Park, Isaac et al. (2023). Herbarium-Derived Phenological Data in North America [Dataset]. Dryad. https://doi.org/10.25349/D9WP6S. Accessed Feb 2023

Park, D., A. Williams, E. Law, A. Ellison, and C. Davis. 2023. Assessing Plant Phenological Patterns in the Eastern United States Over the Last 120 Years ver 5. Environmental Data Initiative. https://doi.org/10.6073/pasta/bfb70a1701ef23f686fcc73840e6ae17 (Accessed 2023-08).

Bridging data silos to holistically model plant macrophenology

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Summary

- Phenological shifts to global climate change impact ecosystem functions. There are various data sources from which spatiotemporal, and taxonomic phenological data may be obtained: mobilized herbaria, community-science initiatives, observatory networks, and remote-sensing. However, analyses conducted to date have generally relied on single sources of data, thus treating alternative data sources as isolated silos.
- Siloed treatment of data in analyses may be due to the lack of harmonization across different data sources, that offer partially non-overlapping information and are often complementary. Such treatment precludes a deeper understanding of phenological responses at macroecological scales. Here, we describe data harmonization as the direct integration of disparate sources of phenological data using a common schema.
- We highlight existing methods for data harmonization that can be applied to phenological data: data-design patterns, metadata standards, and ontologies. We describe how harmonized data from multiple sources can be integrated into analyses using existing methods and discuss the use of automated extraction techniques.
- Data harmonization is not a new concept in ecology but the harmonization of phenological data is long overdue. We aim to highlight the need for better data harmonization providing a roadmap for how harmonized phenological data may fill data gaps while simultaneously integrated into analyses.

Keywords: Data harmonization, Data management, Ontologies, Scales, SDMs

Introduction

Many biological interactions depend on phenological patterns that reflect ecological and evolutionary responses to climatic conditions (e.g., Chmura *et al.*, 2019). For example, plant phenology — the recurring seasonal timing of leaf-out, flowering, fruiting, and leaf senescence — is a key set of genetically- and environmentally-controlled traits that are central to plant reproduction, plant-pollinator interactions, and availability of resources to herbivores. Plant phenology is also linked directly to ecosystem processes and services relevant to human society, such as carbon sequestration, seasonal allergies, and food security (e.g., Fatima *et al.*, 2020; Gray

& Ewers, 2021; Cope *et al.*, 2022). Because plant phenology is very sensitive to ongoing rapid environmental change, there is an urgent need to better quantify and predict plant phenological dynamics (e.g., Gallinat *et al.*, 2021; Park *et al.*, 2021).

A major challenge to quantifying and predicting phenology lies in its scale-dependence (D. S. Park *et al.*, 2021). Like many other ecological phenomena, inferences made about phenology depend on how data are combined across space, time, or taxa (Levin, 1992; D. S. Park *et al.*, 2021). Furthermore, environmental drivers of phenology (e.g., temperature, precipitation, solar insolation) can vary across space and time (e.g., Chamberlain & Wolkovich, 2023), and plastic organismal responses to these drivers can differ among individuals, populations, species, and communities (Ramirez-Parada *et al.*, 2024). Studying the effects of phenology on ecological processes at global scales is the objective of a growing field known as macrophenology; such inferences differ qualitatively from studies focused on more local scales (Doi *et al.* 2017; Gallinat *et al.* 2021). Understanding and analyzing this scale-dependence requires macrophenological data that span scales of space, time, taxonomy, and levels of biological organization.

Data sources at each of these scales do exist although they rarely have been analyzed simultaneously. For plant phenological data, these include herbarium specimens, community science initiatives, observatory networks, and remote-sensing platforms (e.g., Gray & Ewers, 2021; Reyes-González *et al.*, 2021; Davis *et al.*, 2022). Different data types capture disparate scales as a result of their sampling design and effort. For instance, remote sensing may provide continuous monitoring over a long period of time, whereas observatory networks may provide periodic sampling with field surveys that vary in their temporal extent (Fig. 1). These scale mismatches often hinder data harmonization—the direct integration of disparate data types under a common schema. The Lack of harmonization across datasets limits our ability to assess phenological responses to climate at various scales.

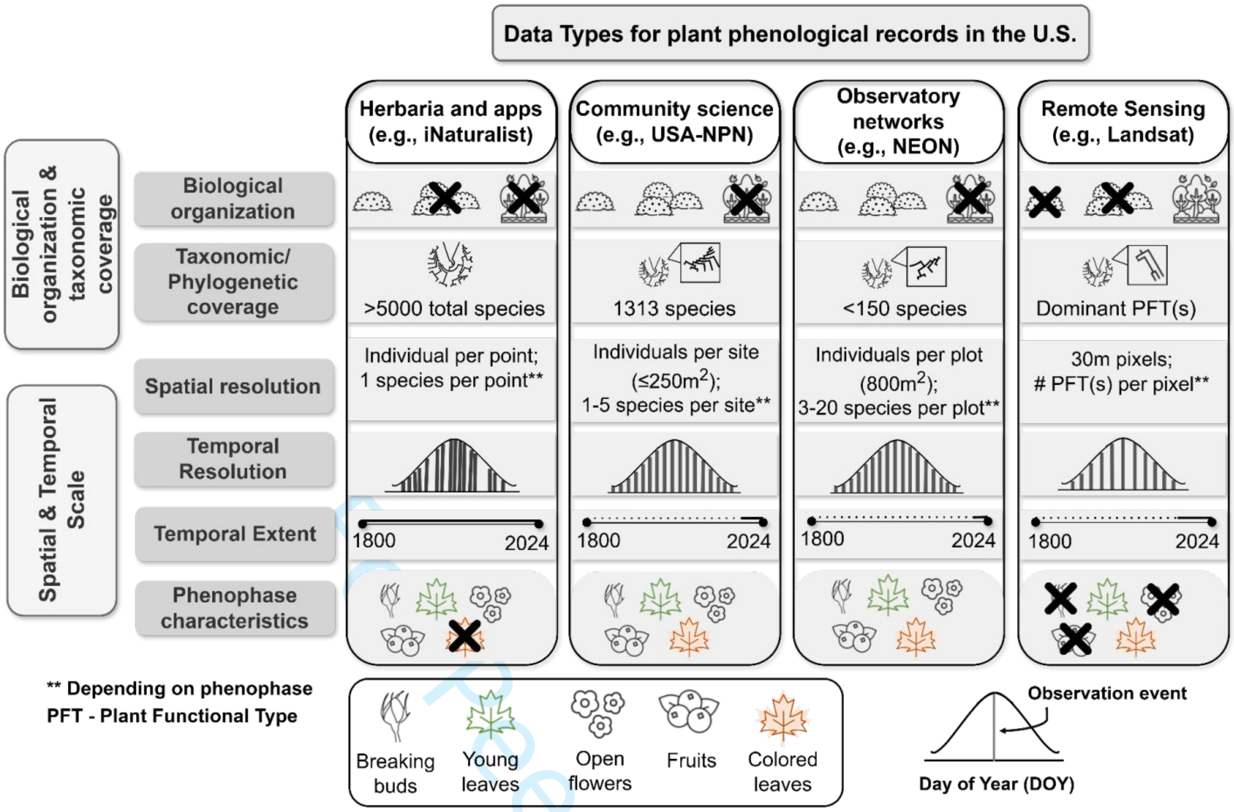


Figure 1. Data aspects across phenological data types with example datasets. Each data type offers a distinct level of biological, taxonomic, spatial, temporal, and phenophase information. Each level contains example-specific information comparing the similarities and differences across data types. Differences between data types (across columns) highlight gaps where data harmonization would benefit and maximize coverage within each level. We use a bell-curve to exemplify the sampling frequency within the duration of a phenophase. Young leaves also include fully opened green leaves.

We assert that data harmonization is critical for improving our understanding of the impacts of climatic change on macrophenology (Gallinat *et al.*, 2021). In this Viewpoint, we focus on plant phenological datasets collected predominantly in the United States, although similar data have been collected at sites worldwide. We explore the characteristics of these data and reveal the unintentional data silos that limit our ability to answer a range of important ecological and evolutionary questions about phenology. Additionally, we identify how bringing together multiple data sources will enable us to answer new questions. To move toward a common goal of phenological data harmonization, we provide a road map describing methods for harmonization, how harmonization can help to fill gaps in phenological data across space and time, and methods for integrating harmonized data into analyses. We end with a call for harmonization of phenological data to rapidly advance phenological research.

A multiplicity of data sources with different strengths and weaknesses

Phenological data have provided invaluable insights into the varying effects of changing climate on the timing of phenology (D. Li *et al.*, 2019; Zohner *et al.*, 2023), and recent papers highlight potential new insights to be made from each independent data type (Davis *et al.*, 2022; Dronova & Taddeo, 2022; Binley & Bennett, 2023; Zhu & Song, 2023). Because of gaps within any single data type, we cannot get a complete picture of phenology without integrating across data types. In this section, we draw attention to the strengths, weaknesses, and gaps of each data type with respect to space, time, taxonomy, life history, and levels of biological organization.

Herbarium Specimens

Herbarium specimens provide irreplaceable historical climate baselines and they have been mobilized to study phenological sensitivity to local climatic conditions and climatic change (e.g., Chmura *et al.*, 2019; Lenters *et al.*, 2021; Davis, 2023) at broad spatial scales (e.g., Davis *et al.*, 2015; Willis *et al.*, 2017; Zhu & Song, 2023). Many of the large herbarium collections in the U.S. have increased the accessibility of phenology data contained in these specimens through massive efforts to digitize millions of physical specimens and the information contained in their labels with the centralization of data into repositories (e.g., the Global Biodiversity Information Facility [GBIF], Southwestern Environmental Information Network [SEINet]) (GBIF; SEINet Portal Network, 2023; Hedrick *et al.*, 2020). However, smaller collections or those from countries with less digital infrastructure in place are less accessible or less frequently digitized, leading to biogeographical biases in spatial coverage (Daru *et al.* 2018; Davis *et al.* 2022). Despite the large taxonomic coverage at the species level, herbarium specimens provide relatively coarse phenophase information, represent single “snapshots” of phenology in space and time, and may exhibit sampling biases that make it unclear whether a specimen represents an early, median, or late observation relative to its source population (Daru *et al.*, 2018; Ramirez-Parada *et al.*, 2022; I. W. Park *et al.*, 2024; Fig. 1). Moreover, as specimens represent single observations of individuals distributed widely in space and time, variation in phenology among specimens represents both within- and among-population differences. Thus, identifying the level of ecological organization associated with relationships between phenology and environmental variables–and the mechanisms underlying such relationships–requires careful statistical design and interpretation of results (Ramirez-Parada *et al.* 2024). Another limitation of herbarium-derived data for use in phenological studies is the difficulty in identifying dates of occurrence for phenological phases other than flowering and fruiting for most species. Additionally, the patchy temporal and spatial coverage limits their use at global or local scales and depends on the sampling biases (Daru *et al.* 2018).

Community-science initiatives

Community-science initiatives harness the power of volunteers to record phenological data across broad spatial extents while providing high-resolution phenophase information from a variety of taxa (Reyes-González *et al.*, 2021; Domingo-Marimon *et al.*, 2022). Such initiatives vary in the degree of standardization used in data collection. For instance, image contributors for community-sourced app-based records (e.g., iNaturalist) do not follow specific protocols for capturing phenophases. In contrast, the USA National Phenology Network (USA-NPN) is an example of a community-science initiative with volunteer engagement across the country through their Nature's Notebook platform (Crimmins *et al.*, 2017; https://www.usanpn.org/). It has a standardized protocol to facilitate repeated observations of specific individuals (or patches) at a chosen site (Crimmins *et al.*, 2017; Fig. 1). These data provide estimates of date onset, termination, and duration of multiple phenophases at high temporal resolution and national coverage (Fig. 1). However, while these data encompass observations for thousands of species, most correspond to a narrow set of indicator species for which specific observational protocols have been developed. Furthermore, investment by volunteers leads to large variations in taxonomic coverage and duration of observations (e.g., a single versus multiple years). These data often contain observation bias and inconsistencies in protocol implementation that can limit their application (Reyes-González *et al.*, 2021; Domingo-Marimon *et al.*, 2022). In some cases, participants might record the phenological status of only one individual at one site many times per year (sometimes less), but they might not sample multiple individuals at a given site, thus greatly limiting population-level inferences.

Observatory Networks

Observatory networks provide systematic, long-term field data that follow individuals throughout their phenological cycle (Gallinat *et al.*, 2021), thus providing opportunities to quantify inter- and intraspecific variation in phenology across ecoregions. The U.S. National Science Foundation's National Ecological Observatory Network (NEON) is one such long-term, ecological monitoring network designed to collect data through 2049 (Elmendorf *et al.*, 2016). NEON works closely with the USA-NPN and Phenocam networks to collect data and has adopted their standards and protocols (Richardson *et al.*, 2007). This offers an exciting example of how different phenological monitoring systems can coordinate efforts for standardized observations (Richardson *et al.*, 2007). Similar to NPN, NEON provides high-resolution phenological information through repeated measures in their field sampling design (Fig. 1). NEON also records co-located information on a suite of other biological and physical variables relevant to phenology (e.g., beetle pollinator abundance, climatic variables, carbon dioxide flux) (Nagy *et al.*, 2021). Despite the continental scale and projected 30-year lifespan scale of NEON, their NPN-style field observations are limited in i.) taxonomic coverage due to resource constraints; ii.) spatial coverage as data are collected only at the several dozen established NEON sites; and iii.) current temporal range due to the relatively recent establishment of the network in 2019 (Fig. 1). The Long-term Ecological Research Network has some sites that collect phenological information, but these data are not collected with a standardized protocol and synthesis of them is challenging (Mulder *et al.*, 2021; Schulze, 2023; but see Keenan et al., 2014). Moving forward, NEON promises to be an irreplaceable long-term reference for fine-resolution phenological data compatible with all data amassed by the USA-NPN through their active partnership and delivering NEON data through the USA-NPN portal.

Remote Sensing

Remotely-sensed data are capable of capturing continental and interannual changes in phenology, yet the spatial resolution of the data is often too coarse to discern phenological changes at the species-level (Gallinat *et al.*, 2021; Reyes-González *et al.*, 2021). Satellites, near-Earth imagery, and biologging devices have allowed for spatially continuous observations with improving temporal resolution (Zarnetske *et al.*, 2019; Lechner *et al.*, 2020; Latifi *et al.*, 2023).

Remote-sensing techniques related to phenology have been applied successfully to detect the start and end of the growing season (i.e., leaf out and leaf off) for either dominant tree taxa or functional types, and primarily in temperate deciduous and tropical dry forests (Dronova & Taddeo, 2022). Recent applications of deep-learning algorithms to high-resolution hyperspectral and red-green-blue images (1-m and 0.25-m, respectively) from near-Earth (i.e., airborne) remote sensing of NEON sites enable the segmentation and identification of individual tree crowns (Weinstein *et al.*, 2024), paving the way for the detection of individual tree-crown phenology from frequent near-Earth image acquisition (e.g., by drones). Furthermore, the National Aeronautics and Space Administration's Surface Biology and Geology High Frequency Time Series (SHIFT) near-Earth remote-sensing campaign in 2023 enabled the detection of superblooms in the grasslands of coastal California from weekly flyovers (Angel *et al.*, 2024). Although hyperspectral sensors have broadened the possibilities of remotely-sensed phenological monitoring, such efforts remain limited to specific sites (e.g., NEON sites) or campaigns with high spatial and temporal resolution. Another limitation is that the earliest remote sensing data are limited to the 1970's (i.e. Landsat 1 products) and do not provide substantial pre-global warming information comparable to point-based herbarium data.

Moving forward: bridging data silos in macrophenology

Data Harmonization

Data harmonization is not a new concept in ecology. For decades there has been tremendous interest across the scientific community in pooling and harmonizing plant trait data. For instance, the TRY database has excelled in aggregating trait data and supported extensive advances in trait-based plant ecology, but lacks a common format that limits compatibility between data sets (Kattge *et al.*, 2011, 2020). More recently, ecologists have recognized the importance of considering intraspecific trait variation, emphasizing the coordination of open science efforts around individual-level trait information (Violle *et al.*, 2012; Cope *et al.*, 2022). Except by remote-sensing networks, phenological data are collected from individual organisms and allow for exploration of intraspecific trait variation. This makes phenological data an excellent test bed for developing and testing approaches for data harmonization of individual-level traits. Various approaches exist for harmonizing ecological data that could be applied to phenological data. Many of these approaches incorporate common terminology and structures (i.e., design patterns) representing relational tables tracking organismal information (e.g., taxonomy, measurement [i.e., trait, number of individuals]) and other important metadata (e.g, geographic locations and differences in sampling methodologies (O'Brien *et al.*, 2021; Keller *et al.*, 2023)(Fig. 2).

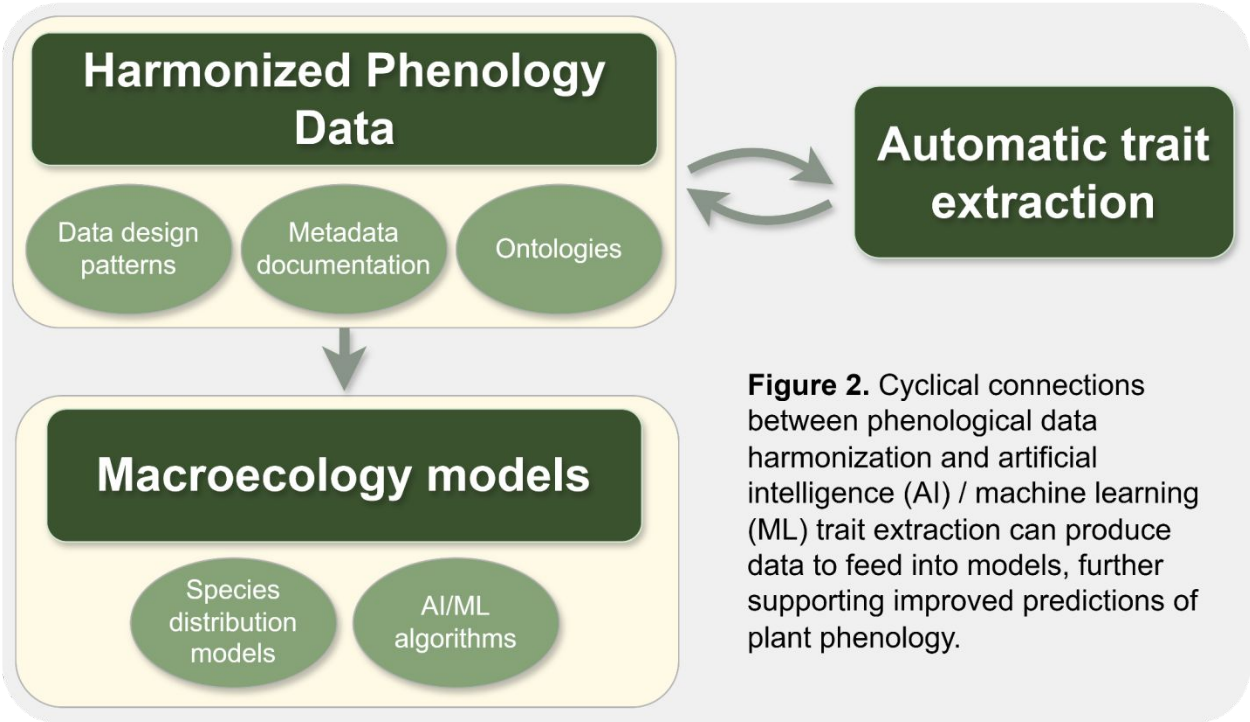


Figure 2. Cyclical connections between phenological data harmonization and artificial intelligence (AI) / machine learning (ML) trait extraction can produce data to feed into models, further supporting improved predictions of plant phenology.

Using common terminology and notation is a key aspect of harmonizing phenological data to make it easier for researchers (and algorithms) to discover and use data. Ontologies provide a structured, formal language for the standardization of terminology and concepts related to data management (see Stucky *et al.*, 2018; Schneider *et al.*, 2019; O'Brien *et al.*, 2021; Lenters *et al.*, 2021; Dumschott *et al.*, 2023; Keller *et al.*, 2023). To our knowledge, the most well-developed catalog for ontologies in plant phenology was made available by Stucky *et al.* (2018), who assembled a robust framework of aggregated vocabulary from global phenological records. Contributions towards such efforts are crucial for dispelling uncertainties in naming conventions for phenophases. For example, intensity-based vocabulary may require a minimum percentage of reproductive organs to be displayed as “open flowers” for an individual’s phenophase to be identified as “flowering”, whereas qualitative assessments of flowering status may simply require the presence of a single open flower. The ontology of Stucky *et al.* (2018) could also be combined with more vocabulary pertaining more widely to ecological traits to capture other important information (e.g., the location of observation). The Ecological Trait Data Standard (ETS) is a common vocabulary to facilitate trait data harmonization and is implemented in some trait data integration networks (Open Traits Network; Gallagher *et al.*, 2020). Notably, ETS incorporates terms used by the Darwin Core Standard (DwC), a glossary of terms to facilitate sharing information about biodiversity maintained by the Biodiversity Information Standards Taxonomic Databases Working Group. Common vocabularies propagate a shared understanding of phenological phenomena that lay the groundwork for the harmonization of data into a common structure.

A robust data design pattern (i.e., relational structure) will empower the increased integration of harmonized data into derived data products that may make it easier to account for differences in sampling effort or biases in downstream analyses. Although there are various data design patterns for plant traits (e.g., structural traits of palms incorporating the ETS [Lenters *et al.* 2021]), there is not a well-adopted data design pattern for plant phenological traits. We propose a phenological trait extension of the Ecological Community Data Design Pattern (ecocomDP), which was developed for harmonizing community ecology biodiversity data (O’Brien *et al.*, 2021). The original ecocomDP model is extended with two features: 1) reconfiguring the table for mapping variables to external dictionaries to allow any variable attribute (e.g., a trait) to be recorded and linked to an external dictionary of concepts, such as the ontologies mentioned above, and 2) adding additional descriptive fields to the dataset summary table (Fig. 3). Because ecocomDP already accommodates community-level analyses, this extension would enable researchers to ask questions across levels of biological organization (e.g., from individuals to populations to communities). Another advantage of incorporating trait data into ecocomDP is that existing NEON and Long Term Ecological Research (LTER) Network data from various taxa are already harmonized with ecocomDP, making it a good candidate for the future incorporation of phenological traits as well as additional individual-level traits. ecocomDP also employs concepts used by ETS and DwC, making data harmonized into its structure easily convertible to the DwC-Archive. Finally, ecocomDP strongly emphasizes metadata, which is essential to ensure that downstream users can determine the relevance of the data for their study objectives through filtering.

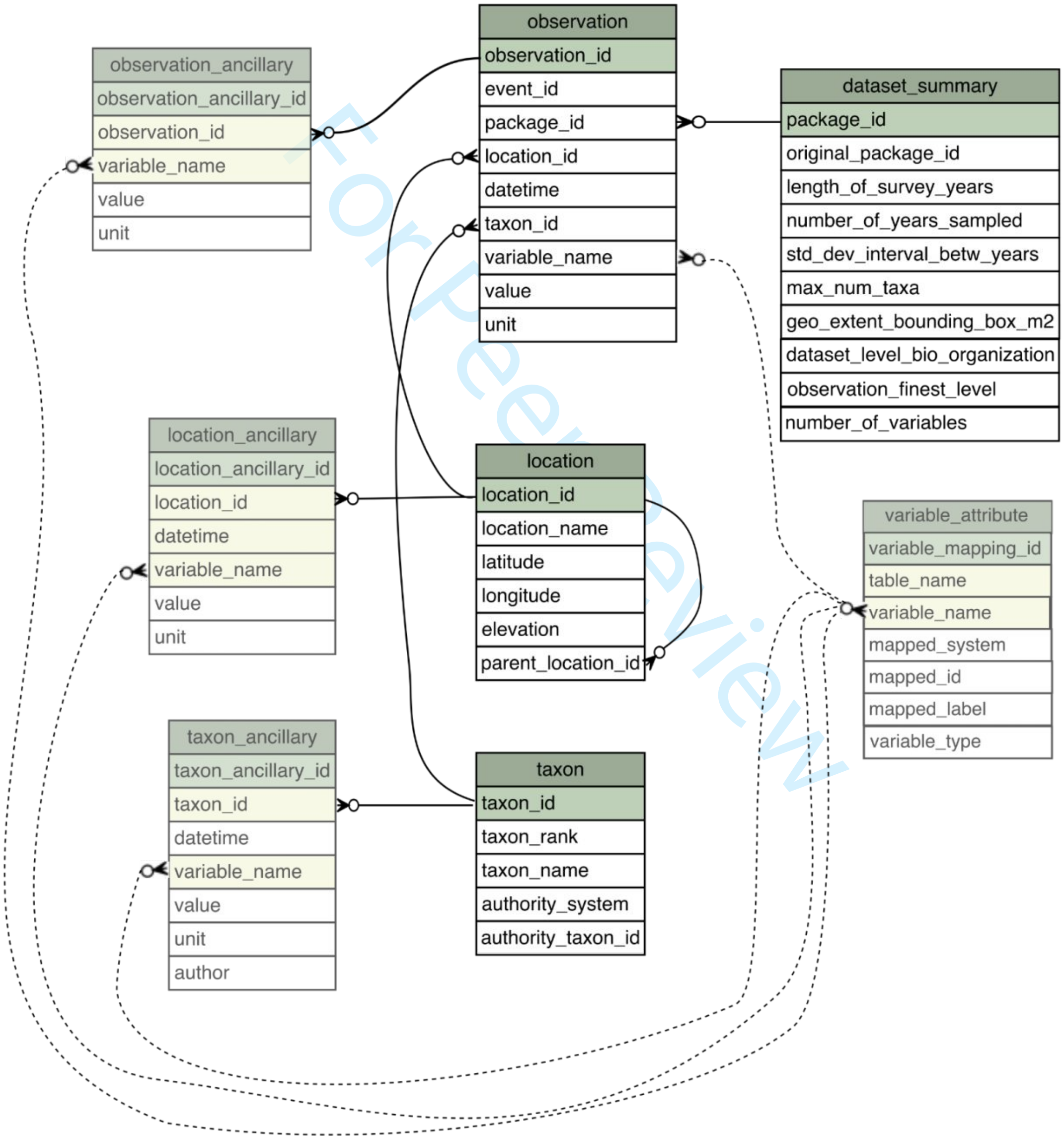


Figure 3. Schema of the updated ecocomDP data design pattern with the extension to accommodate traits (O'Brien *et al.*, 2021). Added fields in the dataset summary table allow users to include the level of biological organization, level of observation, and the number of

variables associated with the trait. The variable attribute (previously variable_mappling) now includes variable type to indicate the type of trait measured (e.g. start and end dates).

With phenological measurements, the protocol for observing the phenophase is a key aspect to consider. For instance, when combining community-science and observatory-network data in analyses, it is incumbent to know the difference between observation methods because each has different levels of observation uncertainty (Binley & Bennett, 2023). Accessible information about sampling design would help compare levels of uncertainty between data types and assess their degree of interoperability for specific research objectives (Fig. 4). Sharing reproducible methods in open platforms such as protocol.io (https://protocols.io; Accessed June 3, 2024) will contribute towards the development of standard disciplinary formats that are useful in metadata curation. Shared protocols between NEON and NPN are a notable example, but even their metadata is found only on site-specific publications or their websites. Furthermore, any protocols used in the collection or curation of herbarium specimens (including their digital records) that are relevant to plant phenology should be included in the metadata or the specimen label. This fits perfectly with the concept of the Global Metaherbarium and the Extended Specimen concept (Davis, 2023). Protocol standards with accessible metadata information and sampling disclosures will be key in supporting data integration and harmonization among data sources while highlighting commonalities and differences in observations (Schneider *et al.*, 2019; Dumschott *et al.*, 2023; Keller *et al.*, 2023;).

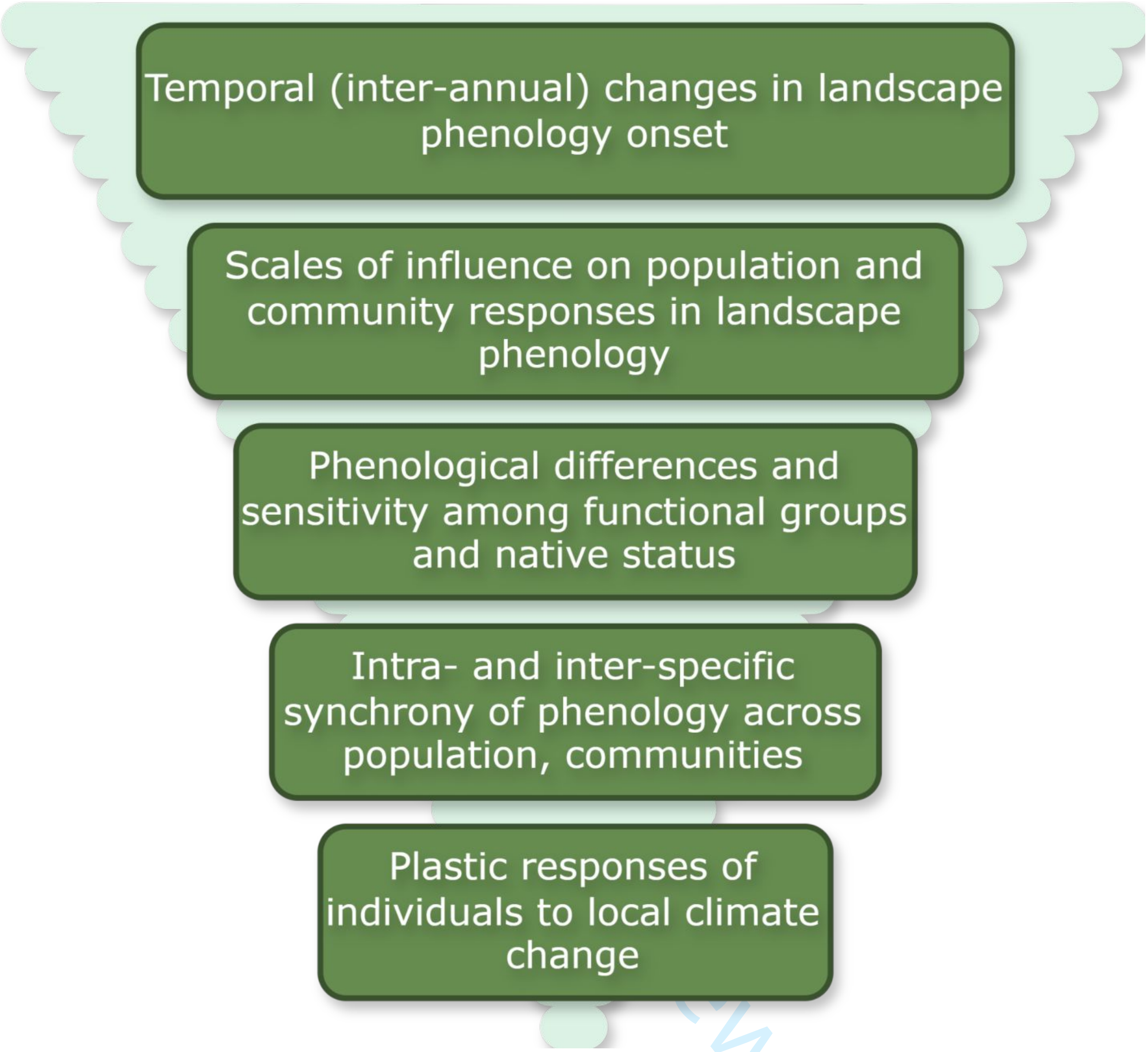


Figure 4. Hierarchy of general objectives in plant macrophenology, from broad to specific. The phenophase event of interest may determine the data types appropriate for achieving the objective.

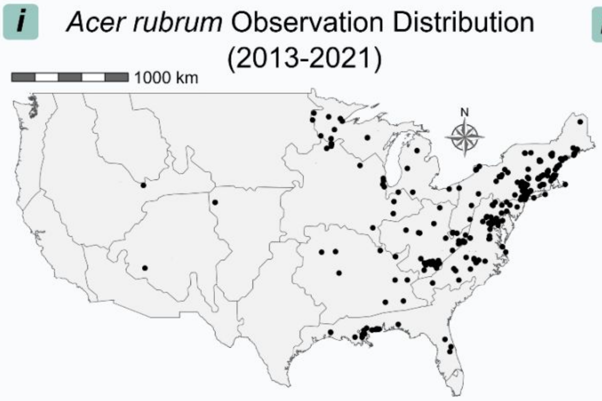
Methods for integrating harmonized phenological data into analyses

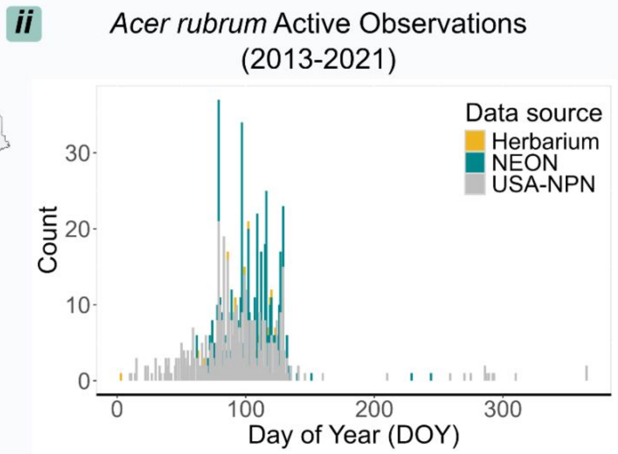
When modeling phenology we need to expand our perspective on where we can apply observations beyond classic phenological models (i.e., location-specific growing degree day models; Chamberlain & Wolkovich, 2023). With the integration of different data types into analyses, models must account for underlying biases from different data containing information on phenology and its drivers across spatial and temporal scales. Here we discuss macroecological approaches to solving two challenges: 1) differences in how phenophases are recorded and 2) spatial and temporal mismatches between phenological, geographic, and climatic data. These hurdles greatly impede efforts of macroscale phenology studies as they limit the geographic scope and questions that may be explored (Gallinat *et al.*, 2021). To address the first challenge of differences in how phenophases are recorded, there are many methods phenologists could adapt from species distribution modeling (SDM). Instead of modeling a response of species occurrence or abundance, we can model the probability of occurrence of a phenophase throughout the year. For instance, such a model could be used to create rasterized forecasts of species-level phenological point observations from herbarium, community science, or observatory network data into a spatially gridded dataset that is compatible with remote sensing data (Peng *et al.*, 2024). For example, Yoder *et al.* (2024) used herbarium and community-science data to create gridded predictions of whether Joshua trees are expected to have masted or flowered for each year and location. These rasterized predictions of mast events can then be compared to remotely-sensed gridded data on leaf phenology (i.e., peak greenness).

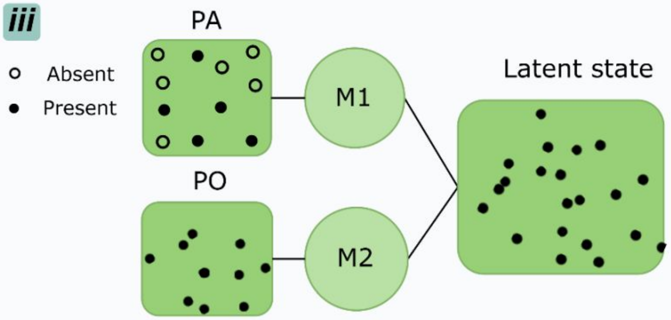
Another approach to account for differences in how phenophases are recorded is occupancy modeling (OM), which is widely used in the field of macroecology to model species distributions and provides a rich methodology by addressing imperfect detection and incorporating geographic location error from specimens for analyses of harmonized phenological data with differences in sampling effort (Erickson & Smith, 2021). One difference in sampling effort presented by phenological data is that some data types only record presence-only (PO) information on phenophases (e.g., herbarium records; iNaturalist), whereas others record both presences and absences (PA) of phenophases (e.g., NPN, NEON). With an OM framework, differences in sampling effort can be accounted for by treating each data type as a designated survey or method to account for differences in detection. Recent advances with integrated SDMs that model PO and PA responses provide a powerful approach for combining data types with differences in sampling effort (Miller *et al.*, 2019; Isaac *et al.*, 2020; Mäkinen *et al.*, 2024). Integrated SDMs could be a powerful way to combine disparate phenological data types (Box 1) and overcome the challenge of accounting for differences in how phenophases are recorded.

Box 1. ISDM roadmap for harmonized models

Understanding phenology at local and global scales is imperative towards connecting multi-scaled issues like climate change. Macrophenology can be better studied through leveraging data harmonization as it provides the potential to fill gaps in coverage across space and time. Phenological data types have different biases that should be considered when using them in a common analysis. For example, different data sources vary in the precision with which phenophases are observed (i.e., presence-only (PO) observations of flowering vs. presence-absence (PA) of flowering). Fortunately, frameworks exist for modeling data with varying levels of precision in detection, such as integrated species distribution models (ISDMs) that allow for both PO and PA responses. To illustrate how ISDMs could be used to simultaneously model different types of phenological data, we present a roadmap to constructing a harmonized model using open flowers of red maples (*Acer rubrum*) using open-source data types that differ in detection of flowering (herbarium [PO] and field observations from NEON and USA-NPN [PA]). To better understand the heterogeneity across data types, it is important to first understand where observations occur in space in time to guide model parameterization (*panel i, ii*). Visualizations of observations for each data source depict disparities in sampling effort across time. The main assumption for an ISDM is that the data observed are modeling the same ecological state where the true distribution is unknown (i.e. latent state; *panel iii*). The common parameters shared between each model address the assumption of observations pertaining to the same ecological state (*panel iv*). The ISDM incorporates shared spatial biases and any known sampling biases into the species-specific models to predict the probability of flowering occurring across space at a point in time (*panel iv*) to produce a probabilistic map of flowering across space at that time.


i *Acer rubrum* Observation Distribution (2013-2021)


ii *Acer rubrum* Active Observations (2013-2021)



iv

M1 $y \sim Binomial(p_i)$

$log(p_i) = \beta_0 + \beta 1 * x_i + \zeta_{shared}$

M2 $y \sim Poisson(\omega(s) * e^{\lambda\_p(s)})$

$\lambda_p(s) = \beta_0 + \beta 1 * x_i + \zeta_{shared} + \zeta_{bias}$

Where p_i the probability of presence in location i, x_i is a coefficient value at location i, ζ_{shared} is the shared spatial bias, w(s) is a thinning parameter, ζ_{bias} is the spatial random field to account for sampling bias,

A second challenge is that phenological data and drivers of phenological responses are often measured at different temporal scales and spatial scales (and therefore, levels of biological organization) (Fig. 5). Automated integration and synthesis tools have begun to be developed to facilitate cross-scale phenological studies. For instance, the Pheno-Synthesis Software Suite (PS3) summarizes ground-based phenological observations into gridded climate and phenological indices (Morisette *et al.*, 2021). One consideration in using such software is understanding what spatial and temporal resolutions and extents have the greatest influence on phenology; to explore the optimal spatial scale between phenological data and its drivers (e.g., climate, land use topography), different grains (e.g., varying radii around a central phenological observation point or pixel) and extents (e.g., continental, ecoregion, site for NPN or NEON) that are then compared in analyses (Zarnetske *et al.*, 2019; Read *et al.*, 2020; Z. Li, 2022).

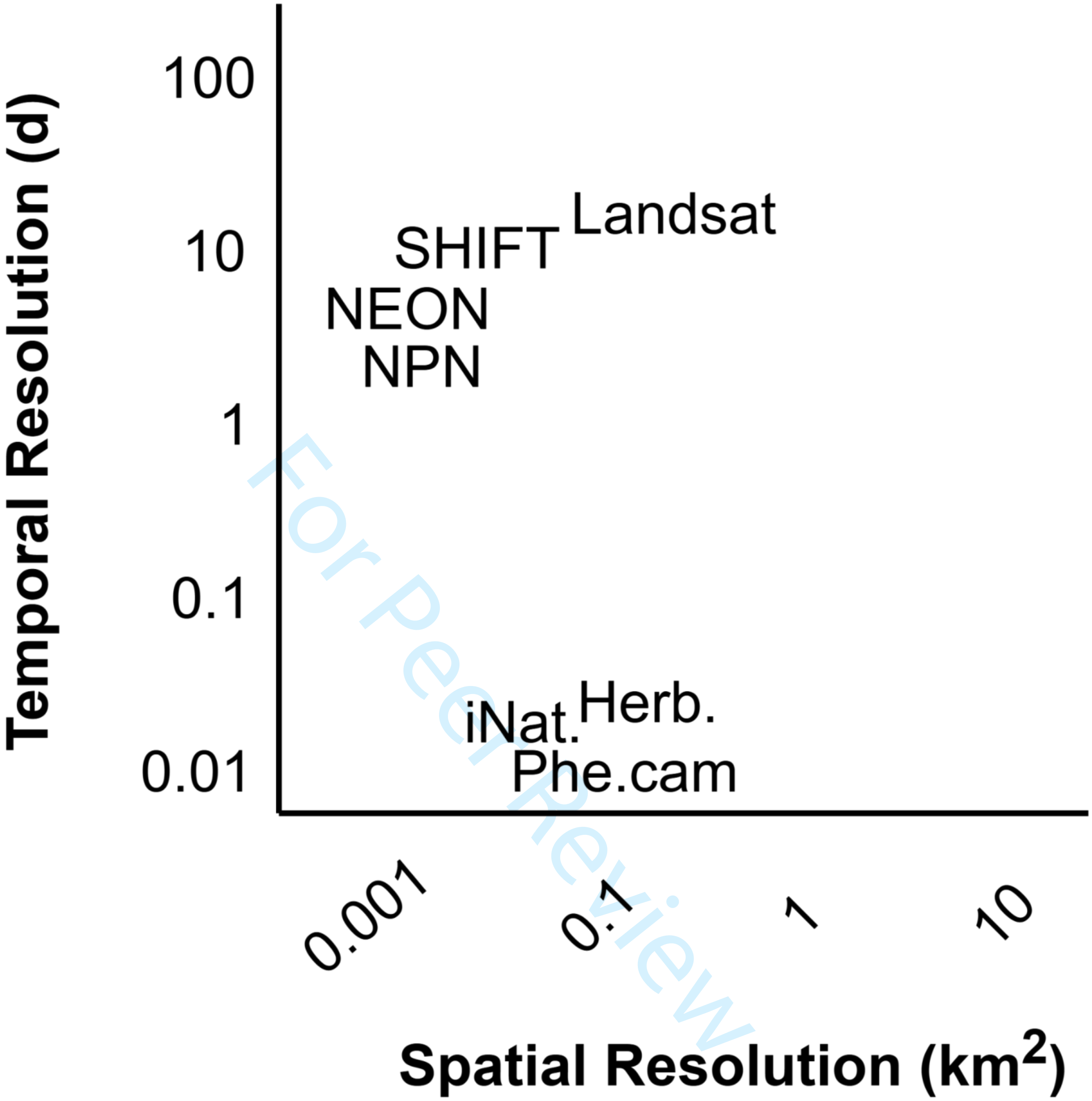


Figure 5. Temporal and spatial resolution mismatches between phenological attributes. Abbreviations: Herb. - Herbarium, Phe.cam - Phenocam, iNat. - iNaturalist.

A promising approach for exploring scales of space and time simultaneously is through interpretable machine learning (ML). Interpretable ML aims to understand what input data characteristics are most important in driving predictions of output data. Local interpretation with ML—wherein the prediction of a model for a single observation in space and time is considered, as opposed to trying to understand the overall predictive behavior of the model across the entire dataset—is especially relevant for exploring spatio-temporal drivers of geo-referenced phenological data. This allows for the visualization and estimation of interactions between location features (i.e., spatial coordinates of phenological data points or grid cells) and other model features (e.g., temperature data represented by different spatial resolutions or temporal lags; Z. Li, 2022). An example of a local interpretation method comes from an extension of the Shapley value in game theory (Shapley 1953), which evaluates how contributions of different players collectively result in a contest's outcome. SHapley Additive exPlanations (SHAP), a recent ML offshoot of Shapley values, quantifies how much each feature collectively contributes to averaged model predictions (Štrumbelj & Kononenko, 2014). Historical phenological data could be used as features in such a model to predict contemporary or future phenological responses. The Shapley value and other local interpretability methods (e.g., Local Interpretable Model-agnostic Explanation or LIME; Ribeiro *et al.*, 2016) offer an exciting new opportunity to simultaneously explore spatiotemporal effects of drivers of harmonized phenological data. Overall, existing modeling approaches from macrosystems ecology and data informatics pose unique solutions to challenges by the integration of phenological data simultaneously into analyses.

Concluding remarks

Predicting plant phenological responses to global change is important given its close ties to ecosystem processes and human health. However, given the scale-dependence of plant phenology, it is difficult to make informed predictions in the absence of data that spans space, time, taxa, and levels of biological organization. Fortunately, such data are at our fingertips through various efforts in recording plant phenology at different scales and with different methods of observation, but the distinct types of phenological data need to be harmonized to unlock their full potential. Efforts to bridge phenological data silos can benefit from successful examples from other subdisciplines in ecology. Approaches to harmonize data can be adopted from existing ecological data design patterns, metadata standards, and ontologies. Biogeographic and macroecological studies offer many solutions for integrating disparate data with unique sampling biases into models. They provide a rich methodology for tackling imperfect detection and incorporating geographic location error from specimens (Erickson & Smith, 2021). Data informatic approaches towards multimodal and big data fusion are other promising tools to automate data extraction and harmonization while improving predictions of plant phenology through pattern detection. Data interoperability is not a new concept in ecology, and phenological data harmonization is long overdue.

Glossary

Data design pattern: A blueprint that captures the essential data characteristics so that a centralized workflow can access, reformat, and structure data (O'Brien *et al.*, 2021).

Data harmonization: Direct integration of different plant phenological data categories (e.g., community science, herbarium, remote sensing) under a common schema

Data integration (or data interoperability): Disparate data sources that may be used in tandem and are readably applicable in modeling or management frameworks (Brenskelle *et al.*, 2019; Stucky *et al.*, 2018; Wilkinson *et al.*, 2016).

Data management: The organization and handling of data that supports its continuous discovery, evaluation, and reuse (Wilkinson *et al.*, 2016).

Machine learning (ML): A subset of methodologies that use algorithms to automate learning predictions about data (e.g., Deep Learning, random forest; "Artificial Intelligence (AI) vs. Machine Learning," n.d.; Pearson *et al.*, 2020).

Occupancy model (OM): A spatially explicit model that determines the occupation of an organism using presence and absence information.

Ontology: Standardized vocabulary and a language framework using formal logic that relates terms to concepts and allows for the integration of different data (Madin *et al.*, 2008; Stucky *et al.*, 2018).

Plant phenology: The timing of recurring life stages (reproductive or growth) of a plant; with a focus on angiosperms.

Phenophase: The phenological stage of a plant or animal, that details a particular life cycle stage (e.g., leaf emergence, migration, breeding).

Species Distribution Model (SDM): A form of occupancy modeling that predicts species distributions over space based on the attributes of the locations where they are currently known to occur.

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Conflict of Interest Statement

L. G. A. and S. R. are in a working group with Daijiang Li, Kai Zhu, and Tong Qui who may appear as potential reviewers. The authors have no other conflicts of interest to disclose.

Author Contributions

L.G.A., A.M.E, C.C.D. conceived the initial ideas which were further developed and refined with S.J.M., I.W.P., T.R-P., and S.R. L.G.A. designed and developed outlines which were further refined by S.R., C.C.D., A.M.E., I.W.P., S.J.M., and T.R-P. L.G.A. and M.O'B drafted and compiled figures which were further refined by S.R., C.C.D., A.M.E., I.W.P., S.J.M., T.R-P, C.A.S, and E.R.S. L.G.A. led the writing of the manuscript and S.R., C.C.D., A.M.E., I.W.P., S.J.M, M.O'B, C.A.S., and E.R.S. contributed significantly to the subsequent revisions. S.R. served as Ph.D. advisor for L.G.A. All authors contributed critically to the drafts and gave final approval for publication.

Data Availability

The data used to create graphs from Box 1 are openly available in Environmental Data Initiative (EDI) at http://doi.org/[***doi in progress***], reference number [***reference number in progress***]. Additionally, the data derived in this article are available from USA-National Phenology Network at http://doi.org/10.5066/F78S4N1V, National Ecological Observatory Network at https://www.neonscience.org/data, Dryad at https://datadryad.org/stash, and EDI at https://edirepository.org/. These data were derived from the following resources available in the public domain:

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