**BIEN 3 derived data**

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# Introduction

This document summarizes the major high-level standardizations, validations and other derived data products of the BIEN3 database. By "derived", I mean data in addition to the original raw data. These are data based on or calculated from the raw data, but in most cases, not present in the original dataset. By "high-level", I mean that generating these data requires specialized domain knowledge, involves complex algorithms, or both. These attributes of domain-specific knowledge and complexity distinguish high-level derived data from low-level, generic validations and standardizations, such as determining if coordinates fall within the range of valid latitude and longitude (a low-level validation) or converting valid coordinates from degrees, minutes, seconds to decimal degrees (a low-level standardization). As illustrated by the preceding example, "validations" check if the data meet a set rules and flag them accordingly; "standardizations" change the data. Other derived data products include complex data such as species range models; although based in part on the raw data, theuy represent entirely new datasets. Typically complex derived data involves aggregation, such that the derived dataset contains many fewer rows than the raw data.

Derived data may be as simple as a yes/no flag indicating whether geocoordinate fit within their declared political divisions, or as complex as a species range map based on millions of input rows, numerous input layers and hundreds or thousands of programming steps. For the purposes of most research questions, the derived data are as important as the raw data. None are frills nor "nice to haves"; all are required for at least one planned analysis. Some, such as taxonomic validation, geovalidation or the detection of cultivated specimens, are essential; the BIEN database cannot be used without them.

Below, I provide a general overview of the purpose and methods behind each major type of derived data in BIEN 3. Full details will be provided in appendices at the end of this document. Ulimately, this information should be made available via the BIEN website. Doing so will allow researchers using BIEN data to (a) understand fully how the data they are using was prepared and (b) describe these methods, when appropriate, in their publications. We therefore urge anyone responsible for the BIEN 3 data to provide a detailed description of their methods.

# Overview of BIEN 3 derived data

## 1. Taxonomy

##### Taxonomic names must be corrected and standardized before species observations can be used. Correction include fixing spelling errors and removing extraneous information such as comments and question marks that prevent names from matching. Standardizations include using a only one abbreviated form for an authority, and only one of several variant spellings, even when such alternative are all technically considered correct under the rules of nomenclature.

These corrections and standardizations are performed using the Taxonomic Name Resolution Service (TNRS, <http://tnrs.iplantcollaborative.org/>), a tool developed under a BIEN-iPlant collaboration. Values that should be stored in the BIEN database include:

* The verbatim original name
* The matched name
* TNRS overall match score for the matched name
* Taxonomic status, if provided, of the matched name (i.e., "Accepted", "Synonym", "Invalid", etc.)
* The accepted name; if no accepted name is provided, use the matched name
* Unmatched unmatched terms
* The most probably morphospecies, formed by concatenating the accepted name with unmatched terms, if any.
* TNRS metadata: taxonomic source(s), date of access of the TNRS, versions of TNRS application and database

For the matched and accepted name, in addition to the lowest-level taxon (e.g., species, subspecies, variety, etc.), the following taxonomic levels should also be stored: Family, Genus, Species, Authority of the lowest level taxon.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

## 2. Phylogeny

### 2.a. NCBI phylogeny

To aid in filtering by higher taxon, the final accepted name returned by the TNRS is joined to the most recent NCBI plant phylogeny (Viridiplantae) at the genus level, or, failing a match at the genus level, by family. Taxa in BIEN joining neither by genus nor family are assumed not to belong to the Viridiplantae.

This filtering requires that the Viridiplantae subset of the NCBI phylogeny be cached locally as part of the BIEN database, and indexed in a manner that allowed retrieval of both ancestor and descendent taxa to arbitrary depth. Right and left indexes generated using a modified-preorder tree traversal algorithm are one indexing methods; others are possible.

As an additional shortcut to assist users in filtering by higher taxa, the link to the NCBI backbone should also be used to populate on or more columns with values conforming to a closed vocabulary representing major clades of plants likely to be of interest to researchers. An example of one such division into major clades is "mosses, liverworts, hepatics", "lycophytes", "ferns", "gymnosperms", "angiosperms".

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

### 2.b. BIEN species-level phylogeny

Whereas the NCBI phylogeny merely splices BIEN taxa by genus or family onto the NCBI phylogenetic backbone, the BIEN species-level phylogeny is an attempt to resolve relationships among all species in BIEN using a variety of complex algorithms. The BIEN species-level phylogeny is the product of a BIEN-iPlant collaboration, with primary development by Bill Piel.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

## 3. Geography

For BIEN 3, the principal derived geographic data are: geographic name resolution and geovalidation.

### 3.a. Geographic name resolution

##### Geographic name resolution discovers and standardizes names of political divisions within 3-level hierarchy (e.g., Country, State, County). Names are standardized and indexed according to the GeoNames database (<http://www.geonames.org/>). This standardization if performed for **both** BIEN data and the political division names within the GADM political division shapefile database used for the later step of geovalidation (see 3b, below). The end product of geographic name resolution is a standadized names and identifier for each of the three political division Country, StateProvince and CountyParish. These values are required for the subsequent step of geovalidation, which determines if the coordinates of a given taxon observation fall within its declared political divisions. The details of geographic name resolution are provided in Appendix @gnrs.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

### 3.b. Geovalidation

Geovalidation verifies that the geocoordinates (latitude and longitue) of a taxon observation falls within the known limits of its declared political division. Geovalidation is performed as a GIS operation by joining the spatial point (as indicated by its geocoordinates) to the polygon (shapefile) of its declared political division and determining if the point falls inside or outside of that polygon, and, if outside, its distance from the nearest point along the boundary of the polygon.

The political division polygons used for BIEN geovalidation are from the GADM database (<http://www.gadm.org/>). Because the GADM database uses non-standard political division names, GADM names must also be standardized to UniversalNames standards by geographic names resolution, prior to geovalidation (see 3a, above). Geographic name resolution and geovalidation are thus intimately linked as steps 1 and 2 of the same geographic standardization pipeline.

The end product of the geographic name resolution plus geovalidation is two new fields for each of the three political divisions: an integer field indicating if a standard name was matched for that political division, and if so, if the associated point fell in or out of the political division, and, for points falling outside, a decimal value indicating km from nearly boundary point. In addition, a seventh integer field indicates whether or not the record as a whole passed validation. Passing validation requires that the point either fall within all declared political divisions or outside but within an allowable distance from the boundary. Allowing this small amount of error recognizes the inherent imprecision in political shapeful boundaries, thereby avoiding the exclusion of potentially important collections or observations of species near country borders.

Geographic name resolution and geovalidation were initially developed by Brad Boyle and John Donoghue for internal use within the BIEN 2 database, and later improved and optimized by Jim Regetz for BIEN 3. A longer term "nice-to-have" for BIEN will be to provide access to both of these utilities via a publcly-accessible web service and web interface.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

### 3.c. New World localities

Most analysis based on the BIEN 3 database will require filtering out of taxon observations from Old World localities. There, each taxon observation will be flagged is inside or outside the New World, based on a reference list of New World countries. The result is a field called `isNewWorld`, which has a value of 1 for New World localities and 0 for non-New World localities. For BIEN purposes, Greenland is considered part of the New World.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

## 4. Cultivated specimens and anthropogenic (planted, cultivated or otherwise strongly human-influenced) plant community samples

Taxon observations representing plants sewn and cultivated by humans, especially when outside their native range, are a serious source of error for most analyses. For this reason, every effort must be made to detect and remove or flag such observations. To this end, we perform two main sets of validations, one set for specimen observations, and a second set of (currently customized specifically for the FIA database, which is known to contain numerous plots in plantations or forests subject o logging or sivicultural treatments.

### 4.a. Cultivated specimens

Currently, we use a variety of methods to detect and flag specimen observations known or suspected to represent cultivated plants. The end product of this validation is the field `isCultivated` which takes on three values: 0='Definitely knot cultivated", 1="Cultivated", NULL="unknown". These methods were originally developed for the BIEN 2 database by Brad Boyle, and have been transferred mostly unchanged to BIEN 3. The methods are as follows:

**4.a.i. Indications of cultivated status by original data provider.** Unlike most othe BIEN 3 derived data operations, this method must be implemented during the loading stage on a source-specific basis. Different herbaria use different fields or combinations of fields to indicate cultivated specimens, and in fact most herbaria do not record this information at all. Nonetheless, when present, such information should always be preserved as it is the highest-confidence means of detecting cultivated specimens.

*Scope of implementation*: Source-specific. These operations must be performed at the loading stage using rules specific to individual data providers. Applies to specimen observations only.

**4.a.ii. Key words in locality description.** This method searches on the both the locality description and specimen description fields for key words matching a black list of terms possibly indicating that the specimen was collected from a farm, garden or plantation (e.g., "garden", "plantation", etc.). Although this method has a high rate of both false positives and false negatives, it has still proven effective at removing cultivated specimens not detected by other methods.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded. Applies to specimen observations only.

**4.a.iii. Proximity to herbarium.** This method was designed specifically to remedy the problem of a large number of vouchers specimens of (cultivated) plants from botanical gardens. Lacking a database of the locations of botanical gardens, we instead used locality information for world herbaria from Index Herbariorum, removing from the database (or rather, flagging as cultivated) any specimen observation within 3 km of a herbarium. As many botanical gardens are associated with herbaria, this approach has proven effective at removing cultivated specimens not detected by other methods.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded. Applies to specimen observations only.

**4.a.iv. Flagging of species outside their known range.** A "black list" of countries where a given species is known not to occur is used to mark species as cultivated. For example, pines do not occur naturally south of Nicaragua; therefore, any occurrence of a pine in a country south of Nicaragua is flagged as cultivated.

Currently, this method has been implemented on a very limited scale for a small set of higher taxa, such as pines and oaks, with well-known country-level distributions. In the future, it may be worth using a more detailed "white list" approach, in the form of state or county distribution records. Although this approach would provide much more thorough filtering of cultivated specimens, the danger of false positives should not be ignored. The user could have the option of inspecting and, if desired, retaining observations which he or she believes to be wrongly labelled as cultivated. Such record-by-record inspection may not be feasible for large data extracts, and the extremely damaging effects of even a single cultivated specimen should be weighed against the slght loss of information due to rejecting a few records from a large dataset.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded. Applies to specimen observations only.

**4.a.v. Other methods for detecting cultivated specimens.** One other potential method for excluding cultivated specimens, not yet implemented, is the use of outlier analysis to detect and flag unusual occurrence records. However, given the many tropical species that are know only from a handful of widely dispersed occurrences, the consequences of false positives are not trivial. This approach is perhaps be best implement for species with collection records above a certain minimum sample size threshold.

### 4b. Cultivated, planted and otherwise disturbed plots

Currently, this operation applies only to plot observations from the Forest Inventory and Analysis (FIA) database. Numerous plots in this database—perhaps the majority—represent plantations, logging operations or silvicultural treatments and therefore must be excluded for most analyses. Originally implemented in BIEN 2 by Brad Boyle, with assistance from Bob Peet and Brian McGill, this algorithm with revised extensively for BIEN 3 with assistance from Jes Coyle, Bob Peet and Margaret Evans.

This operation uses a complex series of rules based on metadata specific to the FIA database, in particular the COND table, and is therefore implemented at the loading stage for this source only (see Appendix @FIA for details). The rules are applied to entire plots, not to individual taxon observations. In BIEN 3, the offending plots are marked isCultivated=1, as for cultivated specimens. The majority of plots in FIA are quality as "cultivated" for one or more reasons, and user should take great care to exclude these samples.

*Scope of implementation*: Source-specific. These operations must be performed at the loading stage using rules specific to individual data providers. Applies to specimen observations only.

## 5. Successional status

We currently have no standardized fields in BIEN 3 for indicating successional status of plant community samples. Such metadata are urgently needed, as many datasets currently loaded in BIEN 3 are known to represent secondary forest (for example, the Susan Letcher La Selva Secondary Forest Transect Database, from SALVIAS).

## 6. Conservation status

##### **6.a.** IUCN **Threatened and endangered status**

##### The BIEN 3 database will be pre-populated with threatened & endangered status codes from the from latest IUCN Red List (http://www.iucnredlist.org/).

### 6.b. BIEN estimated candidate IUCN status

##### One of the bien research products currently in preparation is an algorithmic approach to estimating IUCN threatened & endangered status based on BIEN species range models. IUCN status would be estimated for the subset of categories pertaining to range extent, size and fragmentation. This information will be made available via the bien database and website.

##### In addition, we are exploring the possibility of using demographic information from plots to provide more comprehensive estimates of IUCN status for the subset of species with sufficiently robust samples sizes.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

### 6.c. Other sources of T&E status

We are also considering providing access to other indicators of threatened and endandered status from country, state, regional, NGOs lists.

## 7. Demography

##### A variety of values pertaining to local abundance in plots are not directly present in most plot data sources and must be calculated using domain-specific knowledge regarding how specific types of plot data area collected, how these datasets are structured, and the acceptable and non-acceptable ways of combining and aggregating data. In BIEN 2, calculated fields summarizing abundance in plots included: individuals >= 1cm dbh, individuals >=2 cm dbh, individuals >= 10 cm dbh. In BIEN 3 we will want to include these and other calculated fields as well. However, these values must be calculated with extreme care, as differences in plot methodology will affect how the values are calculated, and in some cases may rended inappropriate the aggregation of data from different plots and datasets. For example, the plots in BIEN 3 sample a range for different areas, and abundance must therefore be scaled accordingly. More critically, plots using different inclusion/exclusion criteria **cannot** be compared, without additional subsampling. In many cases, and subsampling not be possible. Managing all of the complications successfully requires a detailed knowledge of plot methods, covered in the next section.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded. Note however that successful implementation of aggregation operations depends critically on accurate metadata pertaining to methods, most of which is source-specific. Applies to plots only.

## 8. Methods

##### As discussed above, differences in plot sampling methods affect critically how data from different plots are aggregated, and whether the data can be combined at all. BIEN 3 would benefit from a standardized vocabulary for describing the enormous variety of plot methods.

### 8.a. Sampling methods

##### A sampling method is a specific way of measuring a specific attribute within a plot. Categories of sampling methods include:

##### Plot size and shape

##### Inclusion & exclusion criteria

##### Presence, dimensions and spatial orientation of subplots. Subplots are typically spatially discrete subdivisions of a plot

##### Presence, dimensions and spatial orientation of strata. Strata are typically divisions in the vertical dimension of different sizes, heights or growth forms of plants. They are often spatially overlapping in various ways

It should be possible to tag a given individual plot with a specific value for one or more of these method categories. For example, a plot could have `plotAreaHa`="1 ha", `shape`="square", `minimumStemDiameter`="10 cm dbh", etc.

### 8.b. Standard methodologies

A methodology is a complete set of sampling methods. For BIEN users, it will be important to identify and index sets of plots belonging to a single, well established or "standard" methodology. In most cases, different datasets collected using the same methodology can be safely merged and aggregated. For BIEN 3, we will need one or a set of metadata elements which identify plots that belong to one of these standard methodologies. Example methodologies include "1 ha/10 cm dbh tree plot", "0.1 ha Gentry transect", "Braun-Blanque Releve". Plots belongomng to a standard method should inherit the set of methods belonging to that methodology

Belonging to a single standard methodology does not necessarily imply that all methods used are identical for all plots. For example, Al Gentry sampled fewer alle standard 10 subplots in many of his high altitude "0.1 ha" transects (for a total area of <0.a ha). For this reason, it should be possible to add method variants to individual plots which would over-ride one or more inherited methods. In the case of the high altitude Gentry plots just mention, the standard methodology would be "0.1 ha Gentry transect", with a method variant of `plotAreaHa`="0.08 ha".

## 9. Data provenance, ownership, attribution and access conditions

##### Information on data provenance, ownership, attribution and access conditions is central to BIEN's goal of encouraging collaboration while respecting intellectual property and data access conditions. Furthermore, proper attribution is a requirement of access to data provided by GBIF, the major source of specimen data used by BIEN. For this reason, the BIEN schema must support tracking of following information:

* Immediate data provider: who gave the data to BIEN?
* Immediate data provider type. Are they an indexer (aggregator) such as GBIF, or a primary data provider such as Missouri Botanical Garden?
* If the data provider is an indexers, who are the primary data providers of each component dataset?
* Intellectual property. Who are the data owners? In some cases, this may be the same as the primary data providers, or there may be multiple data owners in addition to the primary data provider.
* Are any data access conditions attached by the primary data provider? Other data owners? Data indexers?

Although we may lack some or most of this information for a given data set, we should have somewhere to put it when we get it. GBIF requires us to support all of this information. Having this information will enable us to quickly generate lists of data providers and data owners that must be cited in a publication, and will enable us to "link back" from publications to their data providers, to produce a list of publications citing a given source within a given years. Herbaria in particular are particularly keen on getting this information in exchange for use of their data.

Changes to the BIEN 3 core schema will be required to support metadata pertaining to data provenance, ownership, attribution and access conditions.

*Scope of implementation*: Source-specific. These operations must be performed at the loading stage using rules specific to individual data providers. However, to be useful, source-specific methods must be mapped to universal sets of method descriptors.

## 10. Inferred traits

##### Although Cyrille Violle has already compiled a separate BIEN database of trait values from other trait database and the scientific literature, ultimately, we will be able to begin inferring many species-level trait values from the BIEN database itself. Examples of such inferred trait values includes:

##### **Growth form (habit).** Barbara Dobrin is has developed algorithms that infer species growth habits by comparing habit designations in BIEN, other specimens databases not in BIEN, and a variety of other sources such as regional floras.

*Scope of implementation*: Universal and source-specific. Some operations must be performed at the loading stage using rules specific to individual data providers (the detection of source-specific habit fields). Other operations may be performed on the entire database (search the specimen description field for information on growth form).

##### **Phenology**. Cyrille is taking the lead in inferring flowering phenology based on collection dates and specimen descriptions of flowering and fruiting condition. Determining this trait will require a combinations of universal and source-specific operations and validation. Universal intepretation involves parsing of phenological trait descriptors in specimen description fields. Source-specific operations will require identifying, standardizing to a common vocabulary and saving to the core database any field unique to particular data sources which provide information of phenological status. Many herbarium databases contain information on whether the plant in a particular specimen was in flower, in fruit or sterile. This information must not be discarded.

*Scope of implementation*: Universal and source-specific. Some operations must be performed at the loading stage using rules specific to individual data providers (the detection of source-specific phenological status fields). Other operations may be performed on the entire database (search the specimen description field for information on phenological status).

##### **Abundance.** Many plots provide data on relative or absolute abundance. These data must be handled with extreme caution, as there are many wrong ways and few right ways to aggregate abundance data collected using different methodologies.

##### **Height of individual plants.** This information is sometimes recorded in tree plots. In addition, many cover plot record data by height strata; this information may be useful for inferring average height or maximum height of a species.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

##### **Stem diameter.** Average and maximum stem diameters, as well as derived values such as basal area, con be inferred for species based on values recorded in tree plots.

*Scope of implementation*: Universal. These operations should be performed on the entire database, once all data have been loaded.

##### **Geographic distributions**. Species distributions, however complex their determination, are another form of inferred trait. Species distributions can in turn be broken down into such products as range maps, range size statistics, such as mean, variance and skewness. Etc., etc.

# Appendices