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# The Tree Biodiversity Network (BIOTREE-NET): prospects for biodiversity research and conservation in the Neotropics

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**Abstract:** Biodiversity research and conservation efforts in the tropics are hindered by the lack of knowledge of the assemblages found there, with many species undescribed or poorly known. Our initiative, the Tree Biodiversity Network (BIOTREE-NET), aims to address this problem by assembling georeferenced data from a wide range of sources, making these data easily accessible and easily queried, and promoting data sharing. The database (GIVD ID NA-00-002) currently comprises ca. 50,000 tree records of ca. 5,000 species (230 in the IUCN Red List) from >2,000 forest plots in 11 countries. The focus is on trees because of their pivotal role in tropical forest ecosystems (which contain most of the world's biodiversity) in terms of ecosystem function, carbon storage and effects on other species. BIOTREE-NET currently focuses on southern Mexico and Central America, but we aim to expand coverage to other parts of tropical America. The database is relational, comprising 12 linked data tables. We summarise its structure and contents. Key tables contain data on forest plots (including size, location and date(s) sampled), individual trees (including diameter, when available, and both recorded and standardised species name), species (including biological traits of each species) and the researchers who collected the data. Many types of queries are facilitated and species distribution modelling is enabled. Examining the data in BIOTREE-NET to date, we found an uneven distribution of data in space and across biomes, reflecting the general state of knowledge of the tropics. More than 90% of the data were collected since 1990 and plot size varies widely, but with most less than one hectare in size. A wide range of minimum sizes is used to define a 'tree'. The database helps to identify gaps that need filling by further data collection and collation. The data can be publicly accessed through a web application at <http://portal.biotreenet.com>. Researchers are invited and encouraged to contribute data to BIOTREE-NET.

**Keywords:** Central America; data linking; data sharing; relational database; southern Mexico; species distribution modelling; tropical forest.

Received: 12 January 2011 – Accepted: 30 September 2011 – Co-ordinating Editor: Gabriela Lopez-Gonzalez.

## Introduction

One of the main problems in conservation biology is a shortage of data on organisms (Myers et al. 2000, Brooks et al. 2001,

Olson & Dinerstein 2002, Funk et al. 2005). Many species are not yet formally named and catalogued (the 'Linnaean shortfall', Brown & Lomolino 1998), and a large proportion of those that have been

taxonomically described lack adequate data on their global, regional or even local distribution (the 'Wallacean shortfall', Lomolino 2004). Not surprisingly, collection and monitoring efforts in some parts

of the world have been insufficient to produce reliable, systematic range maps across much of the earth's surface – even for the relatively heavily studied higher plants (Whittaker et al. 2005). The Convention for Biological Diversity (United

Nations 1992) aimed “to achieve by 2010 a significant reduction in biodiversity loss at the global, regional and national levels”. However, these goals have not been met and extinction rates are likely to increase further in the future (Pereira et al.

2010). Reversing these trends requires, among other things, effective monitoring schemes, yet we currently lack the comprehensive data needed (Pereira & Cooper 2006).

GIVD Database ID: NA-00-002		Last update: 2012-07-16
Tree Biodiversity Network (BIOTREE-NET)		
<b>Scope:</b> BIOTREE-NET is a network of forest inventory plots in southern Mexico and Central America. Its major goal is to promote biodiversity research and conservation in the tropics by stimulating data sharing and collaboration between scientists from different parts of the world.		
<b>Status:</b> completed and continuing		<b>Period:</b> 1969-2009
<b>Database manager(s):</b> Luis Cayuela (luis.cayuela@urjc.es)		
<b>Owner:</b> Public		
<b>Web address:</b> <a href="http://portal.biotreenet.com/">http://portal.biotreenet.com/</a>		
<b>Availability:</b> free online	<b>Online upload:</b> no	<b>Online search:</b> yes
<b>Database format(s):</b> PostgreSQL	<b>Export format(s):</b> SQL, CSV file, plain text file	
<b>Publication:</b> Since BIOTREE-NET pools together several datasets, there are publications describing the data for most of the individual datasets (see list of primary sources), but there is not yet any publication describing all the data within BIOTREE-NET as a whole.		
<b>Plot type(s):</b> normal plots		<b>Plot-size range:</b> 100-54000 m <sup>2</sup>
<b>Non-overlapping plots:</b> 2,019	<b>Estimate of existing plots:</b> [NA]	<b>Completeness:</b> [NA]
<b>Total plot observations:</b> 2,019	<b>Number of sources:</b> 53	<b>Valid taxa:</b> 1,188
<b>Countries:</b> BZ: 1.6%; CR: 10.2%; HN: 6.9%; MX: 65.9%; NI: 2.1%; PA: 9.9%; SV: 3.4%		
<b>Forest:</b> 100% — <b>Non-forest:</b> aquatic: 0%; semi-aquatic: 0%; arctic-alpine: 0%; natural: 0%; semi-natural: 0%; anthropogenic: 0%		
<b>Guilds:</b> only trees and shrubs: 100%		
<b>Environmental data:</b> [NA]		
<b>Performance measure(s):</b> presence/absence only: 10%; number of individuals: 90%; measurements like diameter or height of trees: 21%		
<b>Geographic localisation:</b> GPS coordinates (precision 25 m or less): 75%; point coordinates less precise than GPS, up to 1 km: 20%; small grid (not coarser than 10 km): 5%		
<b>Sampling periods:</b> 1960-1969: 0.0%; 1980-1989: 0.4%; 1990-1999: 33.0%; 2000-2009: 59.9%; unknown: 6.9%		
Information as of 2012-07-19; further details and future updates available from <a href="http://www.givd.info/ID/NA-00-002">http://www.givd.info/ID/NA-00-002</a>		

Data shortfalls are especially characteristic of tropical areas (Bawa et al. 2004), where most of the world's megadiverse areas occur (Myers et al. 2000, Funk and Fa 2010), and where rates of habitat loss and environmental degradation are highest (Laurance 1999, Brooks et al. 2002, Sodhi et al. 2004, Wright & Muller-Landau 2006, Hoffmann et al. 2010). Species loss in the tropics is difficult to quantify (Laurance 2007, Stork 2010), but at least half of the species in these areas are threatened with extinction (Bradshaw et al. 2009). Reducing the further loss of irreplaceable tropical biodiversity has never been more compelling. Accordingly, there is an urgent need, particularly in these regions, to assemble and share information on biodiversity, increase collaborations between tropical biologists and stakeholders, and develop research tools to assist conservation planning, policy development and implementation (Bawa et al. 2004, Boreux et al. 2009, Shanley & Lopez 2009).

Recently several initiatives have tried to address these information gaps at supra-national or global scales. One such initiative, the Global Biodiversity Infor-

mation Facility (GBIF, <http://www.gbif.org>), has collated millions of data entries from natural history collections, library materials, and databases (Yesson et al. 2007). However, a large proportion of the information currently available in GBIF refers to developed countries, whereas huge information gaps remain in many developing countries, particularly those in the tropics (Cayuela et al. 2009). Therefore, more work is needed to identify and fill these gaps. The effectiveness and utility of global initiatives is enhanced when complementary networks work, at smaller scales, to improve the structure and content of datasets that focus on specific regions or taxa. One of the best regional examples of this is the Biodiversity and Environmental Resource Database System (BERDS) of Belize (<http://www.biodiversity.bz/>), which uses a spatially explicit, relational database for data storage, display, and analysis. Other examples that demonstrate effective collaboration and data sharing are the RAINFOR initiative (Malhi et al. 2002), and the Amazon Plot Network (Ter Steege et al. 2006). Data from these smaller but more specific and thus more

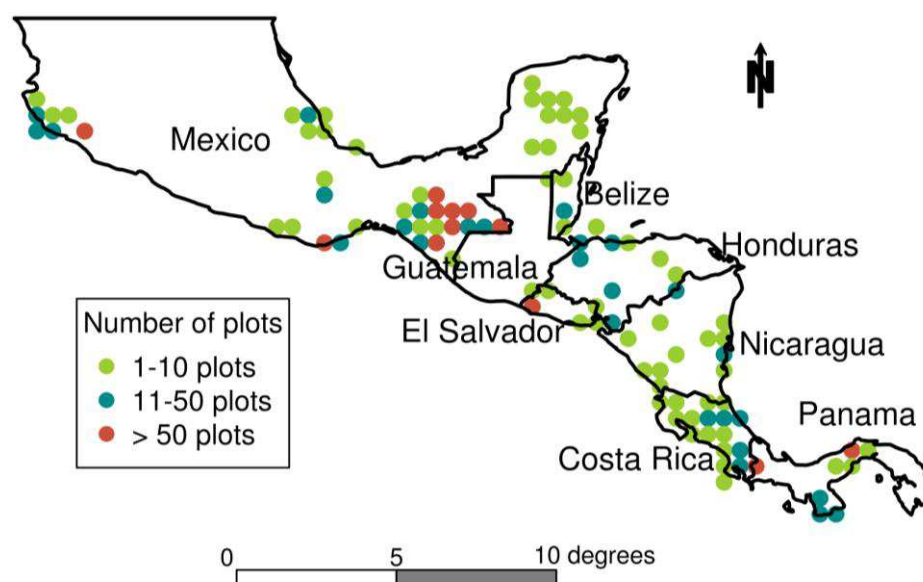
manageable databases can be integrated into larger exchange programmes, such as the ForestPlots.net database (Lopez-Gonzalez et al. 2012) or the Group on Earth Observations – Biodiversity Observation Network (GEO BON, Scholes et al. 2009, <http://www.earthobservations.com/geobon.shtml>).

It is in this context that the Tree Biodiversity Network (BIOTREE-NET) emerged as an international initiative whose objective is to organise and store tree data from forest inventory plots in a structured and standardised manner, including spatial information. BIOTREE-NET was developed to contain information on trees (and eventually lianas) from a wide range of tropical forests, including primary and secondary forests, across southern Mexico and Central America. Soon the geographical scope will be expanded to include tropical countries from northern South America, to cover the full distributional range of most neotropical species. The ultimate goal of the BIOTREE-NET project is to provide researchers, managers, and conservation practitioners access to biodiversity data from one of the most diverse and under-explored regions of the

world. The specific aims of the project are to: (1) collate existing information on tree biodiversity data and make them accessible to the wider scientific community; (2) integrate, standardise and organise forest plot data, providing relevant meta-data; (3) provide users with data analysis and

modelling tools, including species distribution modelling functionality; (4) link spatial tree data with the latest information on species' biological traits; (5) promote data sharing among the scientific community; (6) identify information gaps and formulate research proposals to ad-

dress those gaps; and (7) contribute to global programmes of biodiversity data sharing with well-structured, comprehensive data. The purpose of this paper is to review the scope, data, and key features of the BIOTREE-NET database.



**Fig. 1: Distribution of forest plots, aggregated in 0.5 x 0.5 degree cells, across Central America and southern Mexico (including the states of Colima, Jalisco, Quintana Roo, Yucatan, Campeche, Tabasco, Veracruz, Chiapas, Oaxaca, Guerrero, and Michoacan).**

## Scope

BIOTREE-NET contains tree abundance or presence-absence data from plots located in tropical forests of southern Mexico and Central America (Fig. 1). This region requires urgent biodiversity research and conservation initiatives. Despite containing an estimated 7% of global biodiversity on less than 1% of the world's land surface (Myers et al. 2000), this region experiences rates of deforestation and environmental degradation that are among the highest in the world (DeClerck et al. 2010, Hoffmann et al. 2010). Yet there are insufficient human and financial resources to explore even the most basic ecological aspects of most of the species that occur in the region (Cayuela et al. 2009).

BIOTREE-NET focuses mostly on trees, instead of other taxa, for several reasons. First, trees are important globally, as species of conservation interest in

themselves, especially in the tropics. Second, trees provide habitat, refuge and food for many other species (e.g. insects, Novotny et al. 2006), and provide structural support for other life-forms, such as epiphytes (Sporn et al. 2010), lianas (Dewalt et al. 2000) and fungi (Zhao et al. 2003). Consequently, understanding tree diversity is crucial to understanding the overall biodiversity of tropical forests (e.g. Erwin 1982, Kissling et al. 2010). Third, trees control erosion and help regulate the local climate, mitigating large-scale environmental problems such as pollution and climate change (Bonan 2008, Ponette-Gonzalez et al. 2010). Fourth, as sessile, conspicuous organisms, trees are relatively easy to study compared to more elusive organisms (Lughadha et al. 2005). Finally, trees account for the majority of the biomass in terrestrial ecosystems (Lughadha et al. 2005). As a result, there is generally a larger amount of information available

about trees in tropical regions, compared with other plant groups such as herbs or fungi. Focusing on trees therefore provides a useful, attainable starting point for comprehensive data compilation.

At present, over 40 independent researchers from 11 countries have contributed to the BIOTREE-NET initiative (see Acknowledgements). Data from forest inventory plots contained in this database vary in their nature (abundance, presence-absence), shape and extent of sampling area, minimum diameter at breast height (dbh) at which trees are recorded, and data quality. Some inventory plots have been resampled throughout time, and others have not.

## Database structure and data storage

BIOTREE-NET is based on a relational database that includes 12 tables (Fig. 2).

The tables store information about each individual plot, the botanical name of each individual tree, diameter measurements, and biological traits of the species. Not all of these data are available for all individual plots.

Given that the data amassed into BIOTREE-NET are forest plot data, we start our description of the database structure with the table inventory. This contains plot information, including location, sampling area and sampling protocol. It is linked to the table projects, which refer to groups of forest plots that have been surveyed largely by the same researcher(s) within a certain time-period; in turn, this table links to one called institution, giving more information about those projects. The table inventory also links to one called people (name and contact details of the researcher(s) responsible for each forest plot), via the intermediary inventory\_people. The table inventory also links to temporal, which contains information about the date of sampling and minimum dbh criterion; if a forest plot has been sampled *n* times, there are *n* entries with the same inventory id in this table.

Information at the individual tree level is stored in an observation table, where each species is assigned a unique identifier (Fig. 2). Contrary to other biodiversity databases, a typical entry in the BIOTREE-NET database does not correspond to an individual tree, but to an identified species, for which there is either information on the number of individuals that were recorded in a forest plot (i.e. abundance data) or a record indicating that the species was present in that plot (i.e. presence-absence data). This approach allows us to more easily focus on species-specific patterns within and across plots. The name of the person(s) that carried out the taxonomic identification of each species is also included in this table. If information about diameter measurements is available, it is stored in the table observation\_dbh. This table includes the dbh measurement of individual trees, so the unique identifier for each species (from table observation) appears in the table observation\_dbh as many times as individuals of this species with dbh information have been registered. The table observation is also linked (via the intermediary inventory\_people) to the table taxon, which holds taxonomic information about tree species after standardising species names and correcting misspellings and typographical errors (see below). Fi-

nally, the table ecoprofiles stores data on the biological traits and taxonomic description of species that are stored in the table taxon, e.g. habit, scientific description, habitat, endemism, mean plant height, fire tolerance, stem density, mean seed length, leaf size, deciduousness and dispersal syndrome. Information on ecoprofiles is being compiled by a team of expert botanists and ecologists from different countries and it is therefore generated independently from the plot data. These data are linked to each species in the table taxon to provide relevant ecological information, and to increase the usefulness of the database by identifying all registered species that have a particular trait, such as a particular dispersal syndrome, through just one search query. Images of the ecoprofiles are contained in the final table, imagesecoprofiles. More-detailed information on the BIOTREE-NET relational database can be found in Cayuela et al. (2010).

## Taxonomic standardisation

Data by themselves are not sufficient for competent, high-level research and management recommendations. Given the considerable taxonomic variability arising from the use of different systems and the rapid changes in nomenclature, it is necessary to standardise this information and correct spelling mistakes and typographical errors as much as possible, in order to make reliable inferences. Acquisition of pertinent information, processing, quality control, archiving, timely access and database management are important components that will make the information valuable and usable in research and operational programs (Doraiswamy et al. 2000).

In BIOTREE-NET we used the Plant List (<http://www.theplantlist.org/>) to accomplish this task. The Plant List is a working list of all known plant species, which provides the accepted Latin name for most species, with links to all known synonyms for that species. It also includes unresolved names for which the contributing data sources did not contain sufficient evidence to decide whether they are accepted or synonyms.

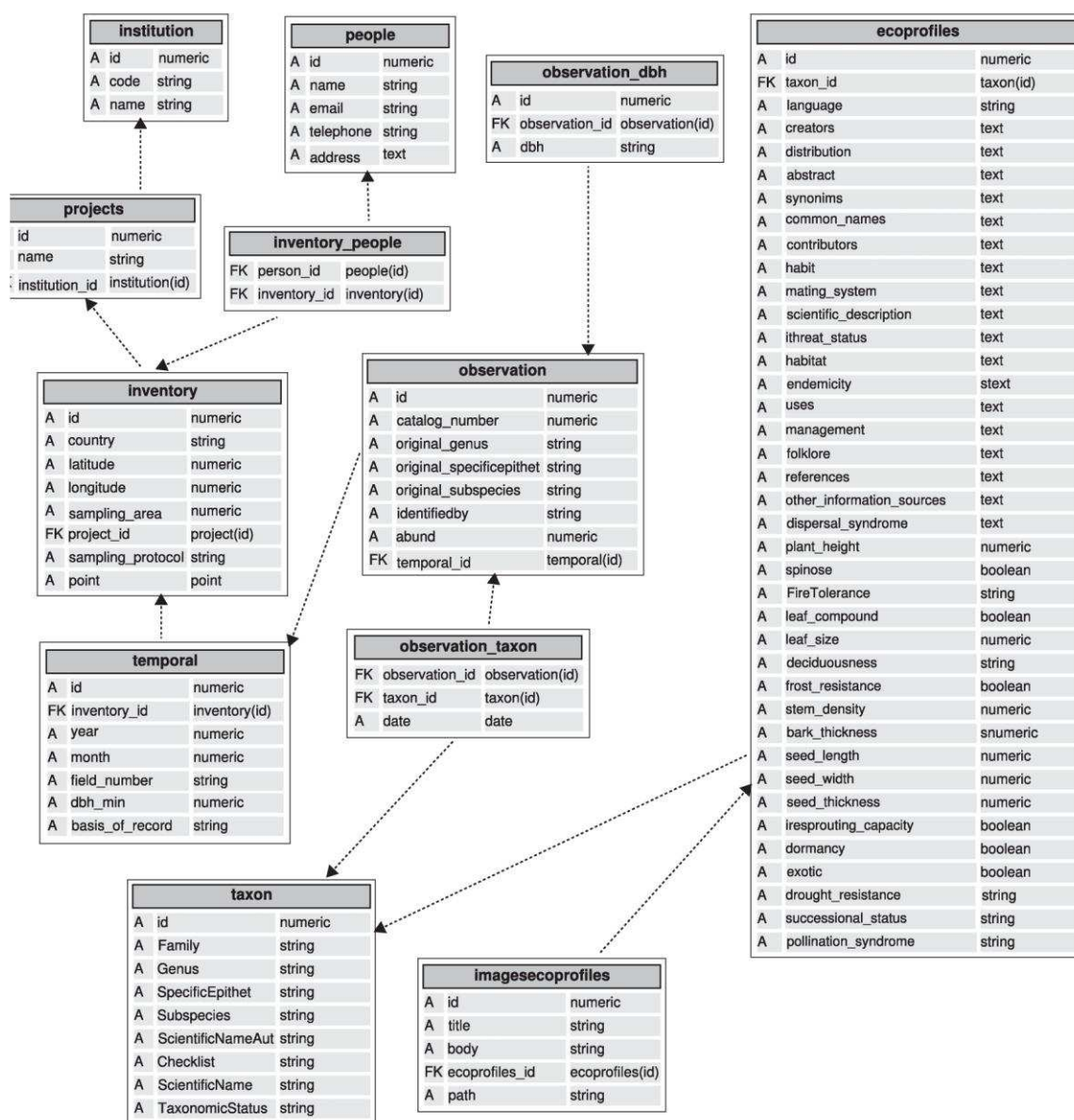
We wrote an automated procedure in the R environment (Cayuela 2012) to cross-check all species names in our database against the Plant List database (Fig. 3). If the species name was contained in the Plant List, then we extracted

information on whether the species name was accepted, a synonym or unresolved. In case the species was a synonym, the validated name was also obtained from the Plant List.

For the species that were not found in the Plant List, we searched for approximate matches to all species within the genus, provided that this information was available and correctly written, using the Approximate String Matching (agrep) function in R (R Development Core Team 2011). This enables automatic identification and correction of typographical errors. For the remaining species, we conducted a non-automated revision of species names to identify: (1) further typographical errors not detected automatically in the previous step; (2) morphospecies, i.e. species identified to genus or family level based on morphological traits; and (3) existing species names which are not currently included in the Plant List. In the case of morphospecies we reassigned the species and gave it a unique name for further analyses. For instance, consider that researcher A and researcher B have identified a species based on morphological traits and labelled it as *Persea* sp1. These two identifications can refer to different species because researcher A and B have not cross-checked their identifications. Therefore, in order to avoid commission errors, the name of the project is added to the species name in table 'taxon', e.g. *Persea* sp1\_CBR vs *Persea* sp1\_TZA. In case a species name is not included in the Plant List, other taxonomic checklists will be examined (Fig. 3), such as the Chicago Botanical Garden or the New York Botanical Garden databases.

## Technical specification

The BIOTREE-NET project aims to address the needs of researchers and end users. Therefore, we designed a system that is accessible from the Internet (<http://portal.biotreenet.com>), which provides a web interface and a set of web services that allow both human-machine and machine-machine interactions. The system development has followed a three-layer architecture that is widely used in software development: model, view and controller (Leff & Rayfield 2001). This architecture allows the management of different layers independently so that changes in one layer do not affect other layers.



**Fig. 2: The BIOTREE-NET data tables and their inter-relationships.** Dotted lines show how tables are linked, with arrows indicating directionality of subordination between tables. Some tables are designed only to link the main data tables together (see text). The main data tables all contain identifier fields labelled 'id'. In the table *inventory* this identifies the forest plot; in *temporal* it identifies the sample/census; in *observation* it refers to the recorded (raw) species identification, while in *taxon* it refers to the corrected species identification; in *observation\_dbh* it identifies the dbh measurement; in *ecoprofiles* it identifies the trait and in *imagesecoprofiles* it refers to an image of that trait. These and other fields are marked as attributes with an 'A', except for fields in subordinate tables that link to the 'master' table (the dotted lines); these fields are labelled 'FK'.

The framework used for the development of the system is Ruby on Rails (RoR, Ruby et al. 2009). RoR enables agile software development by abstracting the functionality of the model, view and controller layers. The differentiation into layers allows for greater control and security as well as the implementation of, independent modules that complement the

functionality of the project. Advantages to this framework include authentication multi-language, security layer, abstract model layer, large development community and open source.

The model layer is implemented in PostgreSQL and PostGIS (Fig. 4) to cover alphanumeric and spatial data. In reference to forest plots, spatial data are repre-

sented by a point vector layer indicating the plot centroid. In addition, a set of auxiliary layers are also managed from PostGIS, including administrative boundaries (countries, states, counties), forest types (Arino et al. 2008), ecoregions (WWF 2010), and natural protected areas (WDPA 2010). Raster layers, including climatic and topographical data (Hijmans



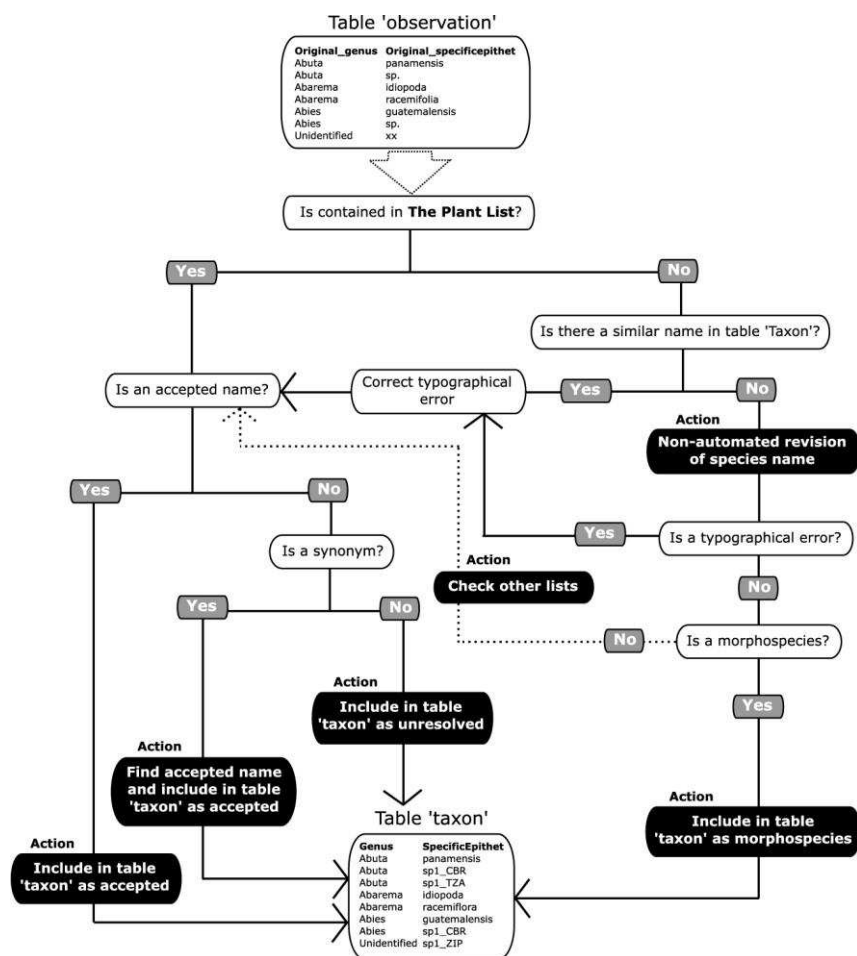


Fig. 3: Protocol for taxonomic standardisation of species names in BIOTREE-NET.

et al. 2005), will be also included within a global spatial data infrastructure. Spatial vector and raster layers cannot be made publicly available within BIOTREE-NET because intellectual property rights are protected in most cases, but project participants will be given privileged access.

The view layer (front-web and web in services) provides an interface for the user or machine with the BIOTREE-NET project (Fig. 4). This layer is implemented in Dynamic HTML, CSS and Javascript for the front-web, and SOAP for Web Services. The controller layer manages requests through the view layer, performs the required actions, and when necessary, provides access to the model layer. The controller layer is mainly managed in Ruby (Fig. 4). Other technologies (such as

R, GRASS and Python) will be used to complete the project information, for example by fitting statistical models to predict species distribution ranges.

### Basic statistical summary of the tree data

All figures given in this section refer to the state of the BIOTREE-NET database as of 27 December 2010. These data are stored in, and available from, the BIOTREE-NET database, with the ID NA-00-002 in the Global Index of Vegetation-Plot Databases (Dengler et al. 2011). By this date, the database contained 2,019 forest inventory plots from southern Mexico and Central America. Most plots are

from Mexico (65.9%), followed by Costa Rica (10.2%), Panama (9.9%), Honduras (6.9%), El Salvador (3.4%), Belize (2.1%) and Nicaragua (1.6%) (Fig. 5a). Figures change slightly if we look at the total sampled area by country, with Mexico holding the largest total sampled area (135.89 ha), followed by Panama (114.16 ha), Costa Rica (29.43 ha), Honduras (12.29 ha), El Salvador (6.39 ha), Nicaragua (6.15 ha) and Belize (5.33 ha). No data have yet been collated from Guatemala but some forest plots have already been identified and new research projects are to be launched in this country in the near future. Forest plots and total sampled area are also unevenly distributed across ecoregions (Table 1); this probably represents a general pattern in forest data. Five out of the 42 ecoregions present in this area account for 64.6% of all forest plots, and 14 ecoregions have no information (listed in Table 1 legend). This disparity in plot distribution is due mainly to the specific interests of researchers and access to large datasets of particular regions, such as the Central American pine-oak forests ecoregion (Plate A), the Peten-Veracruz moist forests, or the Isthmian-Atlantic and Isthmian-Pacific moist forests (Plate B). Even within these large ecoregions, forest plots are unevenly distributed. For example, in Central American pine-oak forests, more than 90% of the plots are concentrated in southern Mexico, while (as previously indicated), no plots are available for Guatemala, and only a few plots are located in Honduras and El Salvador. Around 68% of all the forest plots are outside protected areas. Some protected areas are, however, relatively well sampled, such as El Triunfo (92 plots), and Sierra de Manantlán Biosphere Reserve (87 plots), in Mexico. The vast majority of forest plots (ca. 98%) in the BIOTREE-NET database have been censused only once. Most forest plots were sampled between 2001 and 2010 (59.9%) and 1991-2000 (39.0%) (Fig. 5b). Only a few plots from Palo Verde National Park in Costa Rica (0.39%; Hartshorn 1983) and north central Yucatan in Mexico (0.05%; White and Hood 2004) were sampled prior to 1990.



**B**



**C**



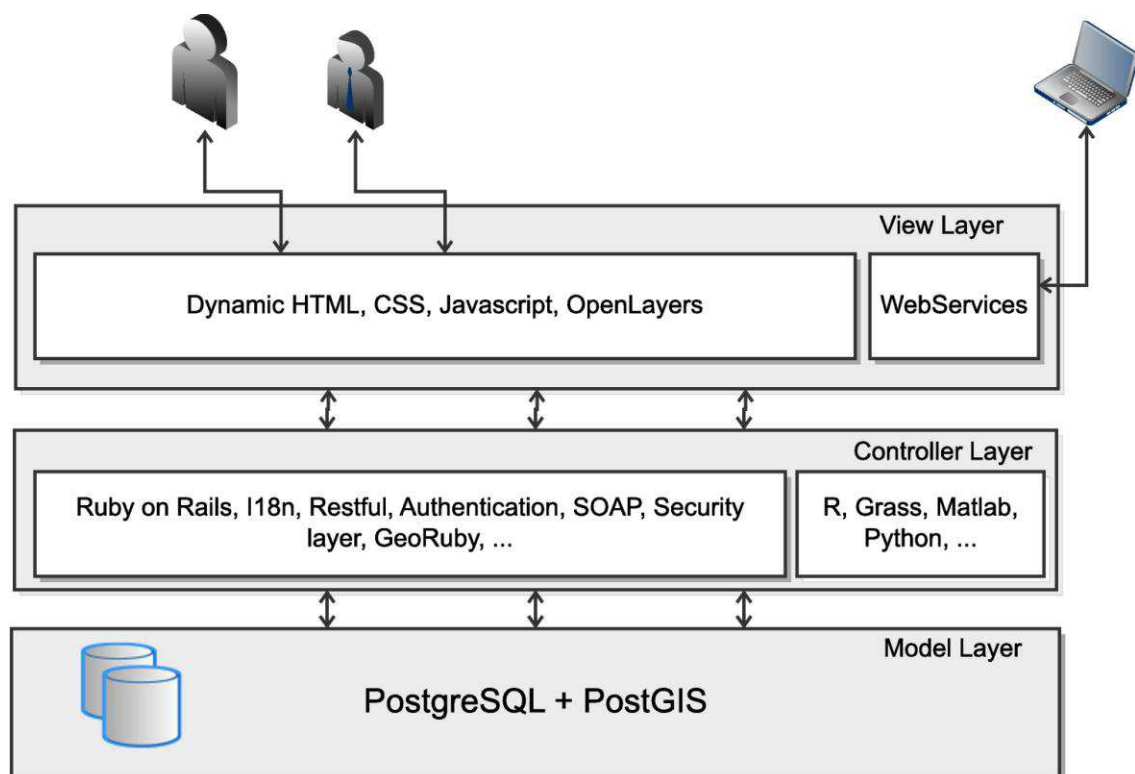
**Plate:** Some of the most common vegetation types featured by the BIOTREE-NET database (GIVD ID NA-00-002).

**A:** Central American pine-oak forest in the Huitepec Reserve, southern Mexico (Photo: N. Ramírez-Marcial).

**B:** Isthmian-Pacific moist forest in Cerro La Tronosa, Panama (Photo: C. Garibaldi).

**C:** Chiapas Depression dry forest in Jiquipilas, southern Mexico (Photo: N. Ramírez-Marcial).





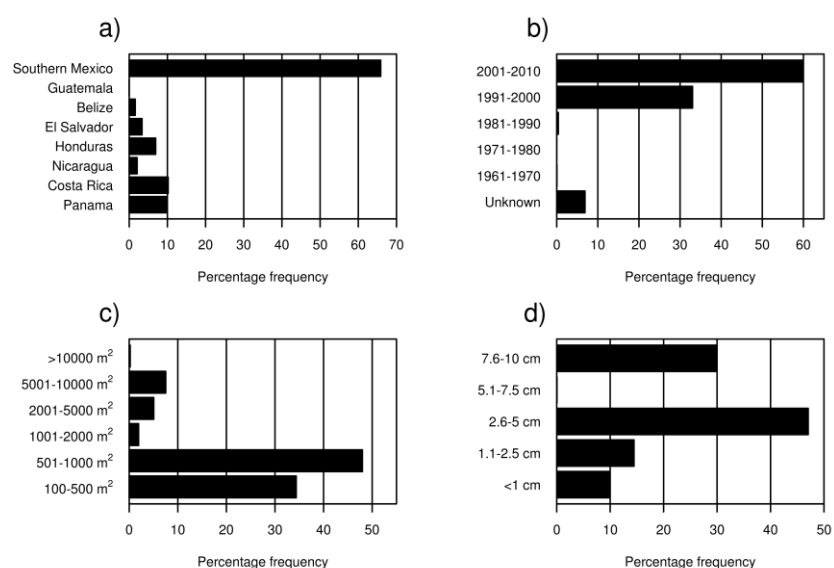
**Fig. 4: Technical specification of the BIOTREE-NET project and global view of the system, including the model, view and controller layers.**

Nearly 7% of forest plots were undated. Sampling protocols and the type of data collected vary considerably within the BIOTREE-NET forest inventory plots. Most of the forest plots contain data on tree species abundance (90.4%), the rest being presence-absence data only. In the plots with abundance data, 73.5% contain fewer than 100 stems, followed by plots with 100-500 stems (23.6%), plots with 500-1,000 stems (1.7%), and plots with 1,000-5,000 stems (1.2%). Around 20% of the forest plots have information on tree diameter. Plot shape also varies considerably, and sampling protocols include circular plots, quadrats, nested plots, transects and rapid biodiversity surveys. There is also a wide variation in sampling area (Fig. 5c). A large proportion of forest plots are small, with sampled areas of 0.05-0.1 ha (48.0%) or 0.01-0.05 ha (34.4%). Larger plots are less common, with 1.9% in the range 0.1-0.2 ha, 5.1% 0.2-0.5 ha, 7.5% 0.5-1 ha and only 0.2% of the plots being larger than 1 ha. The largest sampled areas often correspond to a set of smaller sub-samples for which detailed tree species data have been pooled. In such cases, geographical coordinates often indicate the centroid of all sub-samples. More detailed information from these forest plots may be available in a near future. The minimum dbh at

which individual trees were recorded for most of the plots was 5 cm (47.1%) or 10 cm (29.8%); however, some plots included smaller trees (Fig. 5d).

Of the forest plots, 68.8% were obtained from published scientific papers. Of these, only 6% were available for

download via the Internet. Around 14.6% were unpublished forest plot data from degree and master theses or technical reports. Finally, ca. 17% of all forest plots come from unpublished surveys carried out by researchers and conservation organisations.



**Fig. 5: Percent frequency of forest plots included in the BIOTREE-NET database according to: (a) country; (b) decade (1961 to 2010); (c) individual plot size; and (d) minimum dbh of trees measured.**

**Table 1: Ecoregions (WWF 2010) for which there are forest inventory plots in the BIOTREE-NET database and total sampled area (ha). Ecoregions are defined as large areas of land or water that contain a geographically distinct assemblage of natural communities that: (a) share a large majority of their species and ecological dynamics; (b) share similar environmental conditions, and; (c) interact ecologically in ways that are critical for their long-term persistence (Dinerstein et al. 2000). There is no information available for the following 14 ecoregions: Bajo dry forests, Balsas dry forests, Chimalapas montane forests, Choco-Darien moist forests, Motagua valley thornscrub, Northern Mesoamerican Pacific mangroves, Panamanian dry forests, Pantanos de Centla, Sierra Madre Occidental pine–oak forests, Sierra Madre Oriental pine–oak forests, Sinaloa dry forests, South American Pacific mangroves, Tehuacan valley matorral, Veracruz montane forests. Eighteen plots need revised geographical coordinates and, consequently, could not be assigned yet to a specific ecoregion.**

Ecoregion	Number of plots	Total sampled area (ha)
Central American pine–oak forests	709	69.80
Isthmian-Atlantic moist forests	199	114.91
Peten–Veracruz moist forests	154	12.50
Chiapas montane forests	125	13.74
Isthmian-Pacific moist forests	119	10.71
Sierra Madre de Chiapas moist forests	95	9.60
Trans-Mexican Volcanic Belt pine–oak forests	88	4.42
Southern Pacific dry forests	85	12.25
Central American Atlantic moist forests	80	3.87
Talamancan montane forests	70	9.37
Chiapas Depression dry forests	53	5.20
Jalisco dry forests	51	7.11
Central American montane forests	32	3.10
Oaxacan montane forests	30	2.88
Central American dry forests	27	11.42
Yucatan moist forests	26	3.93
Mesoamerican Gulf–Caribbean mangroves	14	0.77
Costa Rican seasonal moist forests	12	2.20
Veracruz dry forests	10	1.00
Yucatan dry forests	6	1.86
Southern Mesoamerican Pacific mangroves	5	0.75
Belizian pine forests	3	2.43
Veracruz moist forests	2	0.20
Sierra Madre del Sur pine–oak forests	2	0.25
Eastern Panamanian montane forests	1	1.00
Miskito pine forests	1	0.15
Sierra de los Tuxtlas	1	0.10
Sierra Madre de Oaxaca pine–oak forests	1	1.00
<b>Total</b>	<b>2001</b>	<b>306.52</b>

The BIOTREE-NET database is a valuable source of floristic information. There are more than 5,000 species names in the database, although a large proportion (20–30%) corresponds to morphospecies. A list of the 20 most frequent species in the database is presented in Table 2, which mostly correspond to montane pine–oak forest species. In total there are 49,982 observations (each observation refers to an identified species within a forest plot, for which there is associated information on either abundance or presence). Two hundred and thirty of the tree species are included in the IUCN Red List of Threatened Species (IUCN 2010) under the categories of extinct in the wild (1), critically endangered (9), endangered (50), vulnerable (87), near threatened (2), low

risk (73), least concern (3), and data deficient (5).

## Future outlook

We are now working on an improved structure for the BIOTREE-NET database, developing web applications and data analysis tools. Data quality control is an important issue that needs on-going work and periodical evaluation. Some taxonomic errors can be identified by means of potential species distribution models. The accuracy of geographical coordinates also needs to be assessed. Geographical misallocations of a few dozens of meters can be irrelevant for macroecological analyses, but larger errors can have important consequences for

data analyses, particularly in the context of species distribution modelling (Guisan et al. 2007). Information about biological and ecological attributes of species is currently being generated. This information is already available for ca. 300 species (N. Ramírez-Marcial, unpublished data), but the target is to reach 1,000 species by the end of the project and to enable an editing system to allow researchers to continue generating and editing this information in the future. This will be especially relevant for species conservation, for example, through the design of restoration protocols that consider seed dispersal mechanisms, and shade or drought tolerance of seedlings.

We strongly believe that a free, readily available and comprehensive database such as BIOTREE-NET may encourage

more proactive conservation measures in those countries where scientific effort (e.g. inventories) is limited by economic and accessibility constraints. As more data become part of the network, it will allow for the identification of knowledge gaps with respect to specific geographical areas and/or tree families and species, and this in turn will help focus resources to maximise the usefulness of results. It will also help identify new sources of information, and promote interactions between researchers and research institutions from different areas through common research and technical activities. Through BIOTREE-NET, scientists working in Central America and southern Mexico will be able to identify and contact other researchers working towards common goals and/or in similar areas, and we hope this will promote collaborations and further exchanges of data and ideas. Although governmental and non-governmental conservation agencies fund academic research, they often do not use the results of such research to guide conservation policies in practice (Prendergast et al. 1999). Since BIOTREE-NET aims to include data from all suitable sources, we will try to involve as many regional/national government bodies as possible, so that data that may be obscured in official reports become readily available to researchers. Additionally, it may help politicians and

wildlife managers establish collaborations with other regions or countries when planning species-specific conservation plans.

As an open-access database, BIOTREE-NET can be extremely useful for Researchers can also use BIOTREE-NET to investigate ecological communities, analyse species turnover along environmental gradients, and assist in identifying comparable forest ecosystems by matching information amongst research sites. Because BIOTREE-NET incorporates plots of different sizes, such research implies the use of methods that enable comparison of samples of unequal size. We are at present working on the development of rarefaction methods for this purpose (L. Cayuela et al., unpublished results). Taxonomic uncertainty can be also incorporated to the analyses of ecological communities by randomly re-assigning non identified species in each site to any of the other species found in the remaining sites in an iterative fashion. This allows estimation of a range of plausible values for the parameter of interest under different scenarios of re-assigned species identities (Cayuela et al. 2011).

A set of tools that provides a database with the ability to run spatial queries will be incorporated into the database through the use of PostGIS. The results of queries will be fed directly into the open source

statistical language R within which spatial models can be built and evaluated. Implemented models will include GAMs, tree-based models (CART), generalized linear models and maximum entropy models. Scripts will be implemented on the server and results presented to users in the form of maps and graphical outputs based on submitted queries. The R language will also be incorporated within the PostgreSQL database using the PL/R package. Dynamic overlays will be possible online through spatial queries that allow data to be combined in various ways to address complex research questions. Visualisation of the results of online queries will be provided in the form of web pages and downloadable data files. This output will help resolve specific data needs.

Because a major goal of the project is to provide a powerful and flexible framework that will meet a variety of research needs, researchers with knowledge of SQL will be permitted and encouraged to build and submit their own spatial queries to the system in order to address specific questions. To that end, full documentation regarding the database scheme and structure will be provided for users with the appropriate privileges. The documentation will also include examples on the use of the modelling structure.

**Table 2: The twenty most frequent species in the forest plots of the BIOTREE-NET database and the number of plots in which each species is present.**

Species	Number of plots
<i>Dendropanax arboreus</i> (L.) Decne. & Planch.	354
<i>Quercus segoviensis</i> Liebm.	328
<i>Pinus oocarpa</i> Schiede ex Schltdl.	261
<i>Quercus crispipilis</i> Trel.	252
<i>Bursera simaruba</i> (L.) Sarg.	241
<i>Cordia alliodora</i> (Ruiz & Pav.) Oken	238
<i>Brosimum alicastrum</i> Sw.	230
<i>Pinus maximinoi</i> H.E. Moore	222
<i>Cleyera theoides</i> (Sw.) Choisy	210
<i>Pinus tecunumanii</i> F. Schwardt. ex Eguluz & J.P. Perry	189
<i>Virola sebifera</i> Aubl.	178
<i>Quercus crassifolia</i> Humb. & Bonpl.	176
<i>Lacistema aggregatum</i> (Bergius) Rusby	171
<i>Cecropia obtusifolia</i> Bertol.	171
<i>Persea americana</i> Mill.	165
<i>Simarouba amara</i> Aubl.	164
<i>Pinus pseudostrobus</i> Lindl.	161
<i>Cornus disciflora</i> DC.	161
<i>Guazuma ulmifolia</i> Lam.	160
<i>Cassipourea elliptica</i> (Sw.) Poir.	154

## Contributing to the BIOTREE-NET project

Anyone who wishes to contribute to the BIOTREE-NET project with forest inventory data is welcome to participate in this initiative. The BIOTREE-NET database is now publicly available (<http://portal.biotreenet.com>). The website contains clear instructions for how to get and use the data. Access to GIS layers will be however restricted to data contributors and project participants. It is important to note that contributors must sign an agreement to share and make their data public. This agreement guarantees free distribution of data as long as they are used for non-commercial purposes, and authorship is duly acknowledged whenever used. If data from BIOTREE-NET aim to be used in a scientific publication, data contributors must be given the opportunity to collaborate in such publication. Further information on the participation and data use agreement as well as on intellectual property rights can be found in the BIOTREE-NET website (<http://www.biotreenet.com/english/html>).

## Acknowledgements

The original idea of the paper was conceived by L.C., D.J.G. and L.G.B. The technical specifications of the database were developed by R.P.P. In addition, F.S.A., R.A.Z., N.R.M., C.G., M.G.E., F.J.B., J.M.R.B. and R.Z. have contributed significantly to the development of the relational structure of the database, the definition of the taxonomic standardisation protocol, and the elaboration of the participation and data use agreement. This paper was written by L.C. with significant input from R.F., L.G.B., D.M.G., P.B., E.V., J.M.R.B., S.A.S., B.F.R., M.O.V., D.L.K., G.A.I., G.W.L., R.A.Z., C.G., and W.F.G. The data stored in BIOTREE-NET have been provided by L.C., D.J.G., N.R.M., M.G.E., P.B., S.W.B., A.C.C., M.A.C., I.C., B.J., R.C. I.C., J.F., R.F., B.F.R., W.F.G., L.G.J., T.W.G., B.G.R., J.E.G., D.M.G., J.H., G.A.I., D.L.K., J.L., S.G.L., S.M., J.A.M., E.V.M., V.M., S.O.G., M.O.V., C.J.P., V.R.G., K.A.S., S.A.S., F.T.D., E.V., K.M.V., D.A.W., J.N.W. and G.W.L. BIOTREE-NET development has been supported primarily by Fundación BBVA (project BIOCON08\_044). We thank Gabriela Lopez-Gonzalez and an anonymous reviewer for their comments and suggestions.

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