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5th Workshop of the TRY Initiative:
Quantifying and Scaling Global Plant Trait Diversity
3 – 5 September 2013 Leipzig, Germany

Summary

The 5th workshop of the Global Plant Trait Initiative (TRY; www.try-db.org) aimed at examining recent developments in the context of TRY, supporting cooperation on core research topics and further refining the TRY initiative, in particular the intellectual property guidelines and access to data stored in the trait database. The workshop was hosted by the German Centre for Integrative Biodiversity Research (iDiv), with support from DIVERSITAS and the Max Planck Institute for Biogeochemistry.

The first day of the workshop started with an introduction to the TRY initiative and its database. The TRY initiative started in 2007 as IGBP Fast-Track Initiative on Refining Plant Functional Classifications (PFT-FTI). In 2008, the name was changed to TRY, and a new goal was developed: the development of a global plant trait database to make data available for trait-based approaches in ecology and the design of a new generation of DGVMs. In conjunction with this, Intellectual Property Guidelines were developed to overcome psychological barriers and provide incentives for data sharing. Over the last few years, TRY has gained considerable momentum. It is now a global research network with 591 participants from more than 200 institutes worldwide.

The introduction to the TRY initiative was followed by presentations from other data sharing initiatives in ecology: DataONE (William Michener), LEDA (Michael Kleyer), GBIF (Eamon O'Tuama), MetaPhenomics (Hendrik Poorter) and FLUXNET (Markus Reichstein). These presentations also provided the background for discussion on potential collaborations of TRY with these initiatives.

A number of participants were given the opportunity to present their latest research based on using data via the TRY initiative either in talks or in a poster session. Topics covered functional biogeography of traits, trait-environment relationships, and the integration of aspects of functional biodiversity into dynamic vegetation modelling.

The second day of the workshop was dedicated to in-depth discussions in working groups on:

- Plant traits and vegetation modelling (lead: Colin Prentice, Nicolas Viovy)
- Plant trait prediction and gap-filling (lead: Arindam Banerjee)
- The global spectrum of plant function (lead: Sandra Diaz, Sandra Lavorel)
- Plant traits and phylogenetic analyses (lead: William Pearse)
- Next generation trait screening projects (lead: Joe Craine)
- Tropical Forest Traits (lead: Christopher Baratolo)
- Linking Plant traits to plot data (lead: Oliver Purschke)

Detailed reports are provided at the end of this workshop summary. Several collaborations have arisen from the working groups, and manuscripts on the global spectrum of plant functional traits and trait screening projects are in preparation.

The final day of the workshop focused on refining the TRY initiative, in particular with respect to data availability, data access and data quality and the integration of TRY with other data sharing initiatives. Several suggestions to improve the TRY initiative have been discussed during the workshop, including a move towards open access. The intellectual property guidelines are currently updated to take these suggestions into account. The draft document will be circulated to workshop participants and to the TRY community for approval.

Data quality shall be improved by better consolidation of meta-data and auxiliary data, as well as taxonomic information. There are currently efforts under way to develop a thesaurus of plant traits and link this to the TRY database. In parallel there is a need to make contributed datasets citable, e.g. via assigning DOIs or publishing data papers, and to allow them being cited in the context of scientific journals and being identified by relevant scientific indices, e.g. the Web of Knowledge.

The TRY database shall further be amended and expanded by linking plant traits to inventory and plot data, linking specimens to trait data, and complementing the compilation of trait data, e.g. with a focus on root traits and conducting systematic gap analyses.

The workshop ended with a guided tour to the botanical garden of the University of Leipzig.

<u>Reports from working groups:</u>

Working group: “Plant traits and vegetation modelling” *(lead: Colin Prentice, Nicolas Viovy)*

Given the failure of current DGVMs and coupled climate-carbon cycle models to produce consistent results, it has to be recognized that there is a convergence of interest (and an urgent requirement) for plant functional ecologists and model developers to work together towards a deeper *understanding* of key processes. *We need to develop – together – a better understanding of the trade-offs, and the optimality principles, that are needed both to explain trait correlation patterns and to predict the consequences of environmental change for plants and ecosystems.*

There has been an imbalance in the research concerns of the wider DGVM community: concerns originating in the biogeochemistry community (notably nutrient “constraints”) have dominated while biodiversity issues have been mainly neglected. Yet the limitations of current models (a) have *not* been resolved by the inclusion of nutrient cycling and (b) may stem as much from simplistic treatment of biodiversity as they do from simplistic treatment of biogeochemical cycles!

In particular, there may well be undesirable consequences from the representation of all co-existing plants by one or two PFTs. A few groups are beginning to explore this issue.

A key area of research urgently in need of attention is the controls of species distribution. Can we predict species distributions from measurable traits, and if so, are the relevant traits in TRY? A lively discussion ensued. Key traits include vessel diameter, wood density, leaf size…. but understanding of the linkages between these properties and climate is incomplete. Moreover, we seem to lack traits to predict the very important constraint of extreme cold tolerance.

It was easily agreed that it is not a good idea to use species distributions to predict species distributions, and yet this is exactly what niche models do! There are possible “work-arounds” including the prior specification of independent environmental constraints, followed by the use of distributional data to define numerical values of these constraints. But the best approach would surely be to try to predict species’ distributions from entirely independent measurements. This has never been done to our knowledge.

Two main approaches have emerged for the use of trait data in model development. One is to use data to provide better estimates of key parameters for PFTs. This has been done with some success, but its scope is limited. In particular, it is quite possible to “improve” the representation of one process in a DGVM only to expose further problems in other processes, leading to worse rather than better model performance. The other approach is far more radical and consists of using trait data to create a new generation of models “from the ground up” using either theoretical or empirical methods or some combination thereof. Only a few groups are doing this at the moment. We cannot predict their success in the long run but early results are encouraging.

One principle that can be adopted in new model development is the separation of time scales (at the stage of initial model development and evaluation against observations). For example, fast flux predictions can be tested independently on vegetation distributions or dynamics. However, in the end, it is important that submodels with different time scales can be coupled, and that different communities do not develop models applicable to one time scale without cognizance of processes operating at other time scales… which was what used to happen. We do not want to turn the clock back to before the days of DGVM development. We *do* want to use the power of observations and the power of models to achieve a more transparent and robust model development than is currently the case with the present generation of DGVMs, aka "Frankenmodels"…

Working group: "Plant trait prediction and gap-filling" *(lead: Arindam Banerjee)*

Participants:

Arindam Banerjee, Victor Brovkin, Bradley Evans, Siddeswara Guru, Martin Jung, Jens Kattge, Koen Kramer, Ingolf Kühn, Miguel Mahecha, Kiona Ogle, Franziska Schrodt, Carlos Sierra, Nathan Swenson, Susanne Tautenhahn, Marjan van de Weg, Colleen Webb, Claus Weiland

Motivation:

Plant traits are morphological, anatomical, biochemical, physiological or phenological features of individuals or their component organs or tissues, e.g., the height of a mature plant, the mass of a seed or the nitrogen content of leaves. They result from adaptive strategies and determine how the primary producers respond to environmental factors, affect other trophic levels, and influence ecosystem functioning. Plant traits therefore are a key to understand and predict the adaptation of ecosystems to ongoing and expected environmental changes. To improve the empirical data basis for such projections, in 2007 the TRY project (http://www.try-db.org) was initiated, aimed at bringing together different plant trait databases worldwide. Since then the TRY database has accomplished an unprecedented coverage. The consolidated database is likely to become a standard resource for the ecological community and to substantially improve research in quantitative and predictive ecology and global change science.

Despite its large coverage, TRY data are highly sparse, which constrains the usefulness of the joint trait database. Since traits are correlated and they do not vary independently, quite a few quantitative or predictive tasks in ecology require each "referenced" object (it could be an individual plant or a species at a site, but we only use the plant as an example in the following) to have multiple traits fully available. However, in the TRY database, the number of plants with more than three traits available for any referenced object is extremely small, making it tricky to perform such tasks on TRY data directly. There are three possible solutions: The first is aggregating data, e.g., on the level of species or functional groups. The second strategy is "chopping", i.e., removing all plants with target traits missing. Such a simple strategy results in reduced statistical power and may significantly alter parameter estimates and model selection, and for TRY this would actually reduce the data available to a nearly uselessly low number of plants. The third strategy is ``filling'', i.e., based on the non-missing trait entries, filling in the missing entries with predicted values, which yields a complete data set for further processing.

Primary Goal:

The goal of the working group is to investigate statistical machine learning methods for gap-filling in the TRY database. Such methods will also be suitably extended to incorporate additional information including taxonomic and/or phylogenetic information, and information regarding local environmental factors, including climate and soil properties. The methods may also consider trait-trait correlations. Further, the methods will be generalized for upscaling of traits to new locations based on species distribution or related maps.

Current Work:

Current work on trait gap-filling has considered a Bayesian hierarchical model over low-rank latent factorizations of the observed plant-trait data matrix with missing values. The method has been shown to outperform species mean, a widely used baseline for gap-filling. The work was published at the International Conference on Machine Learning (http://arxiv.org/abs/1206.6439).

Future Directions:

While the preliminary results are promising, significant amount of additional work and ideas are needed to better understand the accuracy and trade-offs in gap-filling, how other statistical methods may perform, how to incorporate additional information on individuals, traits, and local environment, and how to upscale traits to new spatial locations.

The working group considered and actively discussed the following aspects for future directions:

- Benchmarking gap filling: The goal of benchmarking is to understand the relative strengths and weaknesses of methods for gap-filling, along with establishing protocols and practices for evaluation of new methodologies. The planned work can be broadly divided into three components:
    - Comparative study: One can investigate the application of a variety of regression and imputation methods for the purposes of gap-filling. Such methods include multiple linear regression, neutral networks, Gaussian processes, boosted regression trees, random forests, and classical approaches to multiple imputation. One can also consider combinations or ensemble of such methods, with the possibility of leveraging the unique strengths of each approach.
    - Evaluation methodology: The structure of missing entries in a gap-filling context is important. The simplest assumption is Missing Completely at Random (MCAR), where any entry can be missing with equal probability. For real world scenarios, the MCAR scenario needs not be valid. Proper investigation of the structure of missing entries is needed, along with appropriate methods for stratified sampling for cross-validation of gap-filling methods. Stratification may have to be done based on taxonomic or

  phylogenetic information (say, species or family), and geographic regions. Too much stratification can lead to small datasets, which in turn can lead to non-robust results and/or unreliable evaluation.

  - Using Synthetic datasets: Synthetic datasets can be used to evaluate gap-filling methodology. Such datasets can be created using suitable dependencies among tree traits, possibly based on phylogenetic profiles.

- Bayesian Hierarchical Models with Phylogenies: An important consideration in any gap-filling approach is a model for the species-species similarity matrix. The taxonomic information has been used in past work to serve as a surrogate to such a similarity/correlation matrix. A promising direction will be to consider such similarities characterized by phylogenetic hierarchies, possibly parameterized differently. Such a construction may potentially be considered as part of a Bayesian hierarchical model where one will also be able to obtain posteriors over the parameterizations.
- Trait Upscaling: A key focus of future work will be upscaling of traits to geospatial locations where no measurements have been made. Given the spatial sparsity of the TRY database, the work is necessary and challenging. Several ideas were discussed for spatial upscaling of traits. One can use spatial information, including latitude/longitude and/or environmental variables as predictors for upscaling. Another possible idea is to use latitude/longitude as "traits" and use a gap-filling algorithm where, for new locations, the lat/long will be the only available traits. A concern regarding such an approach is that the lat/long information may overwhelm the true trait information. For any suitable local regression model used, the spatial covariance structure in traits can be captured by spatial statistics models, such as conditional auto-regressive (CAR) models.
- Trait dependence on environmental variables: Improved understanding of the dependence of traits on environmental variables such as temperature and precipitation is an important problem. In addition to helping in trait upscaling, such understanding can have implications for better vegetation modelling. A key consideration in the study of trait dependence on environmental factors is the resolution and/or representation of vegetation. For example, considering functional groups, such as trees, shrubs, may lead to more meaningful dependencies as opposed to individuals or species.
- Species distributions: Knowledge of spatial species distributions will play a key role in trait prediction, especially in the context of trait upscaling. Initial work can leverage existing species distribution maps, along with associated uncertainty and abundance information as available. Going forward, one can consider building hybrid/joint statistical models of both species distribution and trait prediction. Such models may be able to improve over existing species distribution maps.

Working group: “Plant traits and phylogenetic analyses” *(lead: William Pearse)*

Participants:

Christopher Baraloto, Markus Bernhardt, Jeannine Cavender-Bares, Will Cornwall, Sonja Knapp, Koen Kramer, Guofang Liu, Talie Musavi, Ulo Niinemets, Kiona Ogle, Yusuke Onoda, Will Pearse, Hendrik Poorter, Oliver Purschke, Christine Roemermann, Stephanie Stuart, Marten Winter, Amy Zanne

Focusing initially on the kinds of evolutionary questions we would like to address with the TRY database, we identified a few major themes: (1) what are the rates (fast, slow, initial burst followed by stasis, etc.) and patterns (Brownian motion, Ornstein-Uhlenbeck, etc.) of trait evolution, (2) what are the rates and patterns of evolution along niche/resource axes, (3) how much variation is attributable to phylogeny and intraspecific variation, (4) is there variation in the answers to questions 1, 2, and 3 among phylogenetic clades, and (5) how can extinction risk and invasiveness be related to trait evolution. We also discussed how to build a phylogeny to address these questions, as well as the comparative methods required to test these hypotheses. We considered the overlap between species coverage in TRY, GenBank, and GBIF, and decided exploring mismatches in these datasets might drive future research questions.

Next steps planned:

- January 2014: submit TRY proposal for data
- June 2014: preliminary taxonomic cleaning, data sorting, workshop funding proposals
- December 2014: final cut-off for taxonomic cleaning, data sorting

Working group: “Next generation trait screening projects” *(lead: Joe Craine)*

The working group “Next-generation trait screening projects” met for approximately 3 hours. The purpose of the group was to begin to lay out the principles of how to improve proposals for future trait screening experiments. One of the bottlenecks in getting trait screening experiments is explaining choices for experimental designs to reviewers. To this end, a manuscript has been initiated that will lay out the general principles for decisions on the general design of trait screening experiments. These different approaches would take the forms of scenarios that can be easily referenced. For example, for a given amount of effort, trait screening experiments can either focus on sampling as many species as possible (Scenario A.1) or maximizing replication within species (Scenario A.2). Questions about the relationships of traits among species would favor selecting Scenario A.1, while questions that seek to compare individual species selected from a constrained pool, such as a pre-determined experimental design, would favor Scenario A.2. Additional work is necessary to lay out the principles for selecting species with respect to phylogeny and growth conditions.

The second half of the working group’s time was dedicated to broader questions of promoting plant trait research. Discussions related to the logic of selecting key traits to promote people to measure. One suggestion was to potentially survey TRY members about key traits they think should be measured more and lay out the rationale to focus effort there. If a new set of traits could be agreed upon, researchers globally could measure them on their flora, broadening the geographic and taxonomic distribution of those traits. Which traits and why need more discussion.

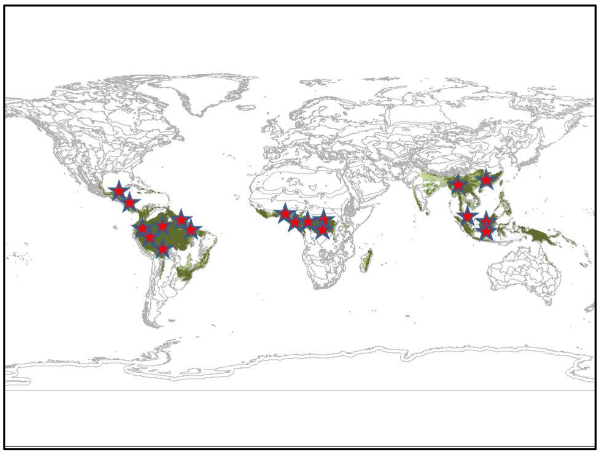
Another line of discussion which carried on during coffee focused on the need to find a way to improve the number of traits that are measured for a given species to begin to examine cross-trait relationships on a global scale. In genomics, this general need was met by selecting model species. To this purpose, model species sets could fill this role. In a model species set, a number of species would be delimited as the model species set, allowing individuals to explore traits they think are important, while allowing later comparisons of different traits. Model species sets could be delimited for grasses, herbaceous eudicots, or woody species. A lot more thinking is necessary for this to become a reality.

Actions: Following up from this workshop, a letter has been written to New Phytologist describing the idea of model species sets and their role in furthering our understanding of trait relationships. A second paper on designing trait experiments is in progress. Over the next year, we hope to lay the groundwork for delineating the first model species sets so that they can be implemented soon.

Working group: “Tropical Forest Traits” *(lead: Christopher Baraloto)*

Participants:

24 participants from 17 countries, representing tropical forests plots with > 3000 species.



Tropical Forests and TRY

- High diversity and lot of data
- Control for some biogeographic noise
- Clear link with plot data
- Well defined gradients – altitude, succession
- Important conservation questions

Tropical needs from TRY

- Taxonomic standardization – voucher accessions, codes of certainty
- Plant age
- Hierarchical data: plot-individual-tissue-replicate (sometimes temporal)
- Standardizing environmental measures
- Repeated environmental measures

Some plans

- Collecting participants' metadata
- Discussing integration of data in TRY
- Building dataset
- Defining protocol standardization
- Identifying gaps – traits, geography, gradients
- Verifying functional strategies across datasets
- Trait variation across gradients (altitude, succession) and by continent
- Trait space and rarity

Working group: "Linking Plant traits to plot data" *(lead: Oliver Purschke)*

Participants:

Oliver Purschke, Helge Bruelheide, Jürgen Dengler, Ute Jandt, Jitendra Gaikwad, Markus Bernhardt-Römermann, Alice Boit, Christopher Baraloto, Dylan Craven, Nikos Fyllas, Gabriela Gonzalez-Lopez, Anke Hildebrandt, Pete Manning, Mike Perring, Valerio Pillar, Lourens Poorter, Christine Römermann, Peter van Bodegom, Cristabel Durán Rangel, Kathryn Luckett, Vania Torrez, Elizabeth Kearsley, Boris Sakschewski

This working group addressed a range of topics related to linking plant trait and environmental data on the basis of vegetation plot data, with emphasis on global scale analysis. Compared to existing global studies of trait-environment relationships, that were done at the species- and/or grid-level, plot-based studies include reliable information on species absence and co-occurrence and will therefore allow for the first global-scale assessment of community-levels properties, such as community-weighted trait means (CWM) and functional diversity (FD) as well as their response to environmental drivers. Such analyses will soon become possible as there are coordinated efforts underway to generate a global vegetation-plot database (sPlot), that includes vegetation (species co-occurrence) data from the various bioclimatic regions of the world.

The topics discussed by the group included issues related to vegetation plot size, quantification of trait diversity, testable hypotheses, model-data integration as well as data availability. The group agreed that in a global-scale analysis grassland and forest plots need to be analysed separately. Although CWM is unbiased by plot size, this will not be the case for FD; appropriate null models, however, can correct for this source of bias. To this end, functional beta diversity can be used as a complementary approach to address the spatial scaling issue. Because existing FD metrics are usually based on a Gaussian response along environmental gradients, alternative ways to quantify trait distributions, beyond the mean and spread, were discussed (e.g. Laughlin et al. 2012 Ecol. Lett.). Although descriptions of trait distributions will be informative, mechanisms can hardly be inferred. Further, a framework to linking traits to the environment (Pillar et al. 2010 Ecol. Lett.), beyond simple trait means or classical fourth-corner approaches, was presented.

We further discussed the hypothesis whether functional diversity increases or decreases with increasing environmental (i.e. climatic) variability and how such relationships are expected to change across biomes, and across different temporal scales at which environmental variability occurs. The question was posed whether the latter topic should be approached from an effect- instead of a response-trait-perspective, as vegetation time series are hardly available. Anyway, we agreed that it will be reasonable to tackle this questions from a response-trait perspective as present-day diversity patterns always represent a legacy of past events.

Finally, the potential for model-data-integration was discussed. An individual-based model (LPJml, PIK-Potsdam), has revealed relationships between FD and environmental variability similar to the one expected from a conceptional model previously developed by some of the working groups participants. LPJml could be used as an experiment that generates trait distributions, which may help to develop hypotheses about the shape of trait responses to environmental factors that can serve as a basis for the development of novel metrics of functional diversity.

Workshop Program

Tuesday **3rd September**	
9:00am	**Welcome by organizers** (iDiv – Christian Wirth, MPI-BGC – Markus Reichstein, DIVERSITAS – Paul Leadley)
9:45am	**The current state of the TRY database and initiative** (Jens Kattge, Gerhard Bönisch)
10:30am	*Coffee Break*
11:00am	**Initiatives related to TRY** • DataONE: Empowering the discovery and management of environmental data (William Michener, *keynote*) • The LEDA Traitbase - vision, success, perspectives (Michael Kleyer) • GBIF (Eamon O'Tuama) • Phenomics and meta-phenomics at the Jülich Plant Phenotyping Centre (Hendrik Poorter) • FLUXNET (Markus Reichstein)
12:30pm	*Lunch Break*
2:00pm	**TRY related projects: functional biogeography** • A brief history of trait ecology (Mark Westoby) • Large-scale patterns of forest functional diversity and identity (Christian Wirth) • Plant traits and ecosystem function (Marjan van de Weg) • Can plant traits predict ecosystem carbon stocks and fluxes? (Pete Manning) • Global distribution of resprouting types: changes along disturbance gradients (Susana Paula) • Savanna woody plant trait responses to bottom-up and top-down controls (Ben Wigley)
3:30pm	*Coffee Break*
4:00pm	**TRY related projects: plot data / vegetation modelling** • BIEN - The Botanical Information and Ecology Network (Brian Enquist, *remotely from Tucson*) • Why do we need to link traits and tropical forest plot data? The RAINFOR and AfriTRON perspective (Gabriela Lopez-Gonzalez)

	• sPlot - Plant trait-environment relationships across the world's biomes (Helge Bruelheide) • DIVGRASS - trait pattern of French grasslands at community scale (Eric Garnier) • Use of plant trait data in the ORCHIDEE model (Nicolas Viovy) • Refining PFTs in JSBACH-DGVM (Peter van Bodegom) • Performance of a trait-based vegetation model in (rain)forest systems at landscape scale (Alice Boit) • The role of biodiversity for the carbon cycle: Implementation of functional diversity in a dynamic vegetation model (Boris Sakschewski)
6:00pm	*End of the session*
6:30pm	**Poster session and finger-food dinner** • Multi-scale phylogenetic structure in coastal dune plant communities across the globe (Jeannine Cavender-Bares) • A key Leaf-Scale Functional Trait to Estimate Ecosystem Gross Primary Production (Juan Posada) • Plant trait variation in Chinese arid and semiarid ecosystems (Guofang Liu) • The TOPIC Network (Isabelle Aubin) • Phylogenetic relatedness influences the strength of priority effects in heathland communities (Vania Torrez) • Linking plant functional traits and forest carbon stocks in the Congo Basin (Elizabeth Kearsley) • GIVD - The global index of vegetation-plot databases (Jürgen Dengler) • Linking plant traits at ecosystem scale to ecosystem functions as observed by eddy covariance measurements (Talie Musavi) • Mechanisms underlying global temperature-related patterns in leaf longevity (Yusuke Onoda) • Traits of clonal growth – the missing element in the analysis of functional diversity (Jitka Klimešová)

Wednesday 4th September	
9:00am	**Short presentations to introduce the working groups** • Plant traits and vegetation modelling (Colin Prentice, Nicolas Viovy) • Plant trait prediction and gap-filling (Arindam Banerjee) • The global spectrum of plant function (Sandra Diaz, Sandra Lavorel, *closed session to finalize analyses*) • Plant traits and phylogenetic analyses (William Pearse) • Next generation trait screening projects (Joe Craine)

	• Linking plant traits to vegetation plot data (Oliver Purschke) • Tropical forest trait group (Christopher Baraloto)
10:30am	*Coffee Break*
11:00am	**Working groups**
12:30pm	*Lunch Break*
2:00pm	**Working groups (continued)**
3:30pm	*Coffee Break*
4:00pm	**Refining the TRY initiative** • Five years of TRY development: experiences and challenges (Jens Kattge) • Suggestion for an improved workflow for proposal management and data access (Gerhard Bönisch) • TERN data management and access policy (Siddeswara Guru)
6:00pm	*End of the session*

Thursday **5th September**	
9:00am	**Refining the TRY initiative**
10:30am	*Coffee Break*
11:00am	**Refining the TRY initiative** Outlook: Remotely sensed trait data in TRY? (Shaun Levick)
12:30pm	*Lunch Break*
2:00pm	**Presentations from Working groups, wrap-up and workshop closing**
4:00pm	*Coffee Break*
4:30pm	**Guided tour to the botanical garden of Leipzig University**
5:30pm	*End of the workshop*

Workshop participants:

	Name	Affiliation
1	Isabelle Aubin	Great Lakes Forestry Centre, Sault Ste. Marie, Canada
2	Arindam Banerjee	University of Minnesota, Minneapolis/StPaul, USA
3	Christopher Baraloto	INRA, Kourou, France
4	Markus Bernhardt	University of Regensburg, Regensburg, Germany
5	Alice Boit	Potsdam Institute for Climate Change (PIK), Potsdam, Germany
6	Gerhard Bönisch	Max Planck Institute for Biogeochemistry, Jena, Germany
7	Victor Brovkin	Max Planck Institute for Meteorology, Hamburg, Germany
8	Helge Bruelheide	University of Halle, Halle, Germany
9	Natalia Carrasco	UFZ – Helmholtz Centre for Environmental Research, Halle, Germany
10	Nuno Carvalhais	Max Planck Institute for Biogeochemistry, Jena, Germany
11	Jeannine Cavender-Bares	University of Minnesota, Minneapolis/StPaul, USA
12	Hans Cornelissen	Vrije Universiteit Amsterdam, Amsterdam, The Netherlands
13	Will Cornwell	Vrije Universiteit Amsterdam, Amsterdam, Australia
14	Joseph Craine	Kansas State University, Manhattan, USA
15	Dylan Craven	Yale University, New Haven, USA
16	Eduardo de Mattos	Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil
17	Jürgen Dengler	University of Bayreuth, Bayreuth, Germany
18	Sandra Diaz	Universidad Nacional de Cordoba, Cordoba, Argentina
19	Cristabel Durán Rangel	University of Freiburg, Freiburg, Germany
20	Brian Enquist*	University of Arizona, Tucson, USA
21	Abeje Eshete	Ethiopian Institute of Agricultural Research, Addis Ababa, Ethopia
22	Bradley Evans	Macquarie University, Sydney, Australia
23	Katrin Fleischer	Vrije Universiteit Amsterdam, Amsterdam, Netherlands
24	Nikos Fyllas	University of Athens, Athens, Greece
25	Jitendra Gaikwad	University of Jena, Jena, Germany
26	Eric Garnier	Centre d'Ecologie Fonctionelle et Evolutive, Montpellier, France
27	Maren Gleisberg	Global Biodiversity Information Facility (GBIF) , Berlin, Germany
28	Gabriela Gonzalez-Lopez	University of Leeds, Leeds, UK
29	Volker Grimm	UFZ – Helmholtz Centre for Environmental Research, Leipzig, Germany
30	Angela Günther	Max Planck Institute for Biogeochemistry, Jena, Germany
31	Siddeswara Guru	Terrestrial Ecosystem Research Network, St Lucia, Australia
32	Alvaro Gutierrez	Swiss Federal Institute of Technology, Zurich, Switzerland
33	Anke Hildebrandt	Max Planck Institute for Biogeochemistry, Jena, Germany
34	Steven Jansen	University of Ulm, Ulm, Germany
35	Martin Jung	Max Planck Institute for Biogeochemistry, Jena, Germany
36	Jens Kattge	Max Planck Institute for Biogeochemistry, Jena, Germany
37	Elizabeth Kearsley	University of Ghent, Ghent, Belgium
38	Michael Kleyer	University of Oldenburg, Oldenburg, Germany
39	Jitka Klimesova	Institute of Botany, Třeboň, Czech Republik
40	Stefan Klotz	UFZ – Helmholtz Centre for Environmental Research, Leipzig, Germany
41	Sonja Knapp	UFZ – Helmholtz Centre for Environmental Research, Leipzig, Germany
42	Cornelia Krug	DIVERSITAS, Paris, France
43	Ingolf Kühn	UFZ – Helmholtz Centre for Environmental Research, Leipzig, Germany
44	Sandra Lavorel	Universite Joseph Fourrier, Grenoble, France
45	Paul Leadley	Universite Paris-Sud XI, Orsay, France
46	Shaun Levick	Max Planck Institute for Biogeochemistry, Jena, Germany
47	Guofang Liu	Beijing Academy of Sciences, Beijing, China
48	Yolanda López-Maldonadc	Ludwig-Maximilians-Universität , München, Germany
49	Kathryn Luckett	Imperial College, London, UK
50	Xiaotao Lyu	Institute of Applied Ecology, Chinese Academy of Sciences, Beijing, China
51	Miguel Mahecha	Max Planck Institute for Biogeochemistry, Jena, Germany
52	Yadvinder Malhi	University of Oxford, Oxford, UK
53	Pete Manning	University of Bern, Bern, Switzerland

54	William Michener	University of New Mexico, Albuquerque, USA
55	Vanessa Minden	University of Oldenburg, Oldenburg, Germany
56	Christian Mulder	National Institute for Public Health and Environment, Bilthoven, The Netherlands
57	Talie Musavi	Max Planck Institute for Biogeochemistry, Jena, Germany
58	Ülo Niinemets	Estonian University of Life Sciences, Tartu, Estonia
59	Eamonn O'Tuama	Global Biodiversity Information Facility (GBIF), Copenhagen, Denmark
60	Kiona Ogle	Arizona State University, Tempe, USA
61	Yusuke Onoda	University of Kyoto, Kyoto, Japan
62	Robin Pakeman	The James Hutton Institute, Aberdeen, UK
63	Susana Paula	Universidad Austral de Chile, Valdivia, Chile
64	William Pearse	University of Minnesota, Minneapolis/StPaul, USA
65	Mike Perring	University of Western Australia, Perth, Australia
66	Valerio Pillar	Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil
67	Hendrik Poorter	Forschungszentrum Jülich, Jülich, Germany
68	Lourens Poorter	Universiteit Wageningen, Wageningen, The Netherlands
69	Juan Posada	Universidad del Rosario, Bogota, Colombia
70	Colin Prentice	Imperial College/Macquarie University, London/Sydney, UK/Australia
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