



5th workshop of the TRY initiative

Quantifying and scaling global plant trait diversity

Workshop Report (compiled by Cornelia Krug)

Welcome by organizers

Christian Wirth, Managing Director iDIV, welcomed participants to the 5th meeting of the TRY initiative, held at the sDIV centre of iDIV. He introduced the newly established iDIV and its two mission statements – How and Why - to the participants, and provided an overview over the functioning of iDIV (www.idiv-biodiversity.de)

Marten Winter, scientific coordinator of the synthesis centre, sDIV, introduced the role and functioning of sDIV within iDIV, and announced joint sDIV/SESYNC call for workshops on biodiversity and ecosystem services.

Christian Wirth provided an introduction to the workshop, and an overview over the programme. He called to consider making the TRY data base “open access”.

Paul Leadley, chair of the bioDISCOVERY core project of DIVERSITAS, gave an overview over the activities of bioDISCOVERY, and how TRY fits within the bioDISCOVERY research framework and activities.

Markus Reichstein, director of the department of biogeochemical integration at MPI-BCG provided an overview over the Earth System Science conducted at MPI-BCG, the interaction between land surface and climate/atmosphere, and the integration of atmosphere and biosphere research within the MPI-BCG.

The current state of the TRY database and initiative

History and State of the TRY initiative - Jens Kattge

Origin of TRY initiative: apparent mismatch of “actual” biodiversity and representation of biodiversity in DGVMs. Started in 2007 as IGBP fast-track initiative on “refining plant functional classifications” (PFT-FTI). In 2008, name was changed to TRY, which is not an acronym, but statement of sentiment, and enlarging of scope – new goal: a global plant trait database to make data available for trait-based approaches in ecology and the design of a new generation of DGVMs.

Intellectual Property Guidelines developed to overcome psychological barriers, and to provide incentives for data contributions.

TRY database is a relational database, with Star-Schema. Data processing mechanism is provided as a “service” to data contributors. Categorical plant trait look up table available on <http://www.try-db.org/TryWeb/Data.php>

TRY has gained momentum over the last few years, it is now a global research network with 591 participants from more than 200 institutes worldwide.

Perspectives for 2013/2014 include the improvement of data processing and process of data release, as well as further development of TRY as “role model” in the ecological community.

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Interactive website - Gerhard Boenisch

Introducing new explorative function on TRY website – Data explorer (<http://www.try-db.org/de/de.php>)

Initiatives related to TRY

DataONE – Bill Michener

DataONE: Empowering the discovery and management of environmental data (<http://www.dataone.org/>). Challenges faces by data sharing initiatives: data entropy; data integration; exploration, visualisation, analysis of data; Community perceptions (Data sharing by scientists: practices and perceptions, Tenopir et al., 2011, PLOSOne): although scientists would like to share their data, they rarely do so – don't know and how and where, and want credit.

Currently, movement towards open science; Dryad repository for journal data available; promotion of data citations via Dryad

DataONE is a NSF 10-year programme, established to provide access data on the environment on earth. Aims are 1) building community, 2) developing sustainable data discovery – coordination nodes, member nodes, investigator toolkit, 3) novel solutions for data management. DataONE ensures metadata interoperability through an extensible system enabling the inclusion of different types of meta-data. Metadata are indexed in central location.

A number of different tools have been developed to facilitate data sharing – see <http://www.dataone.org/investigator-toolkit>:

- DMPTool (<http://www.dataone.org/software-tools/dmp-tool>) – data management tool
- DATAUp (<http://dataup.cdlib.org/>) – website to upload scientific data – NB only works for WINDOWS.
- ONEMercury (<https://cn.dataone.org/onemercury/>) – dataONE search tool for scientific data
- Vistrails (http://www.vistrails.org/index.php/Main_Page) - Analysis, Visualitions and Explorations – vistrails

A list of data sharing Best Practices (<http://www.dataone.org/best-practices>) and a software tools catalogue (<http://www.dataone.org/all-software-tools>) have also been made available on dataone.org. Furthermore, education modules for data management and data sharing are available (<http://www.dataone.org/education-modules>).

The LEDA Traitbase – history and lessons learnt - Michael Kleyer

LEDA – started in 2000, database of floral traits of NW Europe, covering:

- whole plant traits
- stem and leaf traits
- seed traits
- dispersability traits
- clonal traits

Early metadata documented in book (downloadable at LEDA website – www.leda-traitbase.org)

Project ended in 2005, however, extensive data quality control and error checking still necessary

In 2008, LEDA datasets integrated into TRY

IN 2010, support for database abandoned

In 2013, LEDA will be fully integrated into TRY, if this is technically possible.

Lessons learnt ++++

- Matrix of species with traits
- public database retrievable from web
- "trait owners" - quality control of all traits

Lessons learnt ---

- Underestimated costs of long-term maintenance of database
- no updating after 2005 possible

Caveats for TRY

- quality control – risk of double entries
- collection and measurement protocols, and assigned experts for traits

GBIF - Eamon O'Tuama

GBIF vision: "A world in which biodiversity information is freely and universally available for science, society and a sustainable future." (www.gbif.org)

GBIF is connected community, informatics infrastructure, window on biodiversity, tool for science and society.

GBIF deals with three types of biodiversity data:

- Metadata (data about data)
- Occurrences (observations, specimens etc)
- Checklists (names)

Data Quality is focus in 2014 GBIF work programme:

- expert communities → fitness for use working groups
- metrics and indicators for assessing relevance of data
- inclusion of authoritative checklists to verify taxonomic data
- solving licencing issue – CC0 licence
- unique identifiers for data sets

Allocation DOIs to data sets makes them searchable

Tracking use of GBIF data → distributions, climate impact studies

GBIF and TRY

GBIF as complementary data source for representing trait data

TRY species occurrences shared with GBIF → re-direct to TRY for trait info

Use of Integrated publishing toolkit

Vocabulary and ontology management – semantic media wiki - <http://terms.gbif.org/wiki/>
bioportal establishes biodiversity slice - <http://bioportal.bioontology.org/projects/168>

Phenomics and meta-phenomics at the Jülich Plant Phenotyping Centre – Hendrik Poorter

Phenotyping bottleneck – manual handling and field experiments time consuming and costly.

High-throughput phenomics – automated plant handling

Ecological aspects

- plant growth conditions
- recommendations on descriptions for environmental conditions in experiments

Meta-phenomics:

data base of 1000 species, 60 traits, aimed at controlled experiments, individual plants, different levels of environmental factors, long-term adjustment, broad coverage of past literature

Main goals: establish dose-response curves, rank effects of different environmental factors, differentiate between functional groups of species

Proof of concept: Plasticity index – how trait changes with changes in environmental factor, orthogonal trait relationships

FLUXNET meets TRY... why? - Markus Reichstein

FluxNet (www.fluxdata.org) is a network network of eddy-covariance sites for measuring flux and meteorological data at ecosystem level – see www.fluxdata.org. Extended data sets are accessible under the free and fair use of data policy.

Data are upscaled from plot to global level by integration with remote sensing data. Approach allows to investigate of ecosystem functional properties, and to link traits and organisms to fluxes. It allows for spatial upscaling of traits to ecosystem level.

TRY related projects: functional biogeography

A brief history of trait ecology - Mark Westoby

Trait ecology has a long history, but has been reinvented since 1995, for 3 reasons: 1) understanding of community function and 2) assembly rules, and 3) using traits directly as strategy axes. Not achieved was 1) a consensus on a strategy scheme, 2) a short list of (most important) traits and 3) theory predicting constellation of trait-space occupied at site. TRY data

Large-scale patterns of forest functional diversity and identity - Christian Wirth

Processes and traits act as filters at different levels. To date, approaches are focussed on large scales modelling, and only recently efforts have been made to include “real” data. Use of traits to understand species occurrences, and to estimate bioclimatic limits for trait values, allowing identification of

- trait-based “no-go-areas”
- species exclusion maps
- shifts of traits spectra under global change

On community assembly level, trait richness maps indicate functional diversity (keeping in mind that species richness \neq functional diversity).

Proposed approaches also aid in the identification of large-scale productivity pattern.

Plant traits and ecosystem function - Marjan van de Weg

Carbon and Water flux at happen at different scales. TRY and FLUX data are linked through traits (traits measured at sites, and plain mean traits). Data types are then scaled to same scale. There are some data challenges, however, as not all data are of the same quality, or data sets are not complete. Remote sensing products are validated using auxiliary data.

Can plant traits predict ecosystem carbon stocks and fluxes? - Pete Manning

Carbon stocks are used as example to link plant traits to ecosystem function. The effects of grassland management on grassland ecosystem services are investigated by comparing the

total carbon pools in different sites. A hierarchy of controls is used to explain the variation in soil carbon and microbial communities. Carbon stocks can indeed be predicted from environmental conditions and plant traits, the proposed approach is currently being refined through biodiversity exploratories.

Global distribution of resprouting types: changes along disturbance gradients - Susana Paula

A number of different types of resprouting exist, and the complexity of resprouting changes with disturbance severity. The evolution of resprouting can be linked to flammable ecosystems, but resprouting can also be a function of exploitation, storage, persistence, or splitting. Data on resprouting capability have been captured in the the BROT database (<http://www.uv.es/jgpausas/brot.htm>). Currently, the most resprouting traits in occur in the mediterranean region.

Savanna woody plant trait responses to bottom-up and top-down controls - Ben Wigley

Savanna dynamics are controled through top-down and bottom-up processes / mechanisms - nutrients, fire and herbivory. Interactions and feedbacks of drivers exist, and traits respond to disturbances. Study sites were not separated based on their leaf traits. The observed pattern was not strong, and not in the direction expected. A high intra-site variability could be observed, and no trade-off related to soil nutrients could be found.

Leaf traits seem to be driven by herbivory rather than nutrients, and leaf quality was impacted on by browsing. Defence traits showed a trade-off with soil nutrients, and meso-browsers seem more important than mega-browsers in shaping leaf traits.

TRY related projects: plot data / vegetation modelling

BIEN - The Botanical Information and Ecology Network - Brian Enquist (remote presentation)

Problem: the “dark underbelly of bioinformatics”, which includes poor data quality (data is error prone and biased), taxonomy, a lack of standardisation in use of species names, bad data and sampling bias in general. There was also a need for a standardised and publishable workflow.

BIEN (<http://bien.nceas.ucsb.edu/bien/>) is the longest running NCEAS working group, its goals are

- 1) address specific science questions merging herbarium, plot and trait data
- 2) development of technology necessary
- 3) longer-term programme development

The workflow includes a considerable amount of quality control

Deliverables include

- Botanical Informatics
 - tools
 - integrated database
 - repeatable workflow
- Derived products
 - standardised species list
 - species level phylogeny
 - species ranges maps

The current version BIEN 2.0 includes the following tools:

- taxonomic name resolution service <http://tnrs.iplantcollaborative.org/>
- Species distribution overview
- Phylogeny and Phylogenetic diversity
- trait component – 24 traits

A version BIEN 3.0 is currently being developed.

A project linking TRY and BIEN is currently underway, with the aim of assigning life forms/habitat to BIEN data. There are also efforts underway to “cyberlink” the two initiatives through the integration of TRY trait records into BIEN.

Why do we need to link traits and tropical forest plot data? The RAINFOR and AfriTRON perspective - Gabriela Lopez-Gonzalez

Introduction to the Amazon Forest Inventory Network (RAINFOR - <http://www.rainfor.org/>) and African Tropical Observation Network (AfriTRON - <http://www.geog.leeds.ac.uk/projects/afritron/>). Both are international research networks that conduct permanent plot monitoring, taxonomic identification and soil sampling in the tropical rain forests for of Latin America and Africa. Both are partners in the FORESTPLOTS.net (<http://www.forestplots.net/forestplots.net>) initiative, where the plot data are made available.

FORESTPLOTS.net provides private and publicly available data, mostly plot metadata, and holds voucher specimens linked to plot data. Traits and plot data are linked, and a functional traits database was developed, but never directly linked to plot data.

A number of challenges have been encountered, in terms of:

- data standardisation
 - improve taxonomic information
 - managing and standardising of duplicate datasets
 - managing datasets with different methodologies
 - standardising trait names; and
- data sharing
 - acknowledgement of data collectors
 - increasing sharing of data sets – allocating DOIs
 - balancing data sharing requirement of different funding bodies
 - funding and time limitations

Proposal to link TRY and Forestplots.net, how and why still need to be fleshed out.

sPlot - Plant trait-environment relationships across the world's biomes - Helge Bruelheide

The first workshop held at the new sDIV focussed on plant trait environment relationships across the world. Aim was to establish a global plot data base, and making use of TRY to link the plot data to trait data. The initiative includes a wide range of scientists, covering theory, application and modelling. Community plot data is also needed, as traits not only filtered by environment, but also by community at a site. Suggestions for data analysis include the comparison of mean species trait values vs. mean community trait values and the interaction of factors influencing trait values. There are plans to expand to remote sensing of plots and to include ecosystem functions. Data sharing could be done via the TRY data base, however, there are still gaps especially on the Southern Hemisphere.

DIVGRASS - trait pattern of French grasslands at community scale - Eric Garnier

The DIVGRASS initiative links species and communities data with modelling of ecosystem properties. Research is mainly conducted in French permanent grasslands, and focussed on primarily on management and conservation issues. A number of different data bases, containing trait data, botanical releve data and climate data are linked.

An example for a potential integration is the investigation of the importance of Leaf Dry Matter Content for digestibility. Data availability was limited, as there is no centralised data base for DIVGrass. Trait data from TRY and DivHerbe were compared, and a good congruence of data was found. This allowed for the comparison of two digestibility predictors. The extrapolation to large spatial scale will depend on the availability and quality of data. Potential other opportunities are the application of the method to other ecosystem properties, however, this relies on the identification of relevant traits.

Use of plant trait data in the ORCHIDEE model - Nicolas Viovy

Current limitation of dynamic vegetation modelling are the static trait values used in the models. A Step-wise approach was taken to improve trait representation:

1. refining PFTs – splitting into new PFTs
2. variability of traits – NPP at species level
3. spatial distribution of traits / trait values

DIVGRASS & CAMELEON were used to determine the sensitivity of simulated fluxes to trait variability. Next steps are to explore relationships between traits and environment, and to re-define PFTs based on differences in parametrisation.

Refining PFTs in JSBACH-DGVM - Peter van Bodegom

Trait variation is only partly captured in PFT/biome classification currently applied in DGVMs. However, the inclusion of trait variation accounts for acclimatisation and adaptation of species to environmental conditions. To test this, 3 key leaf traits (SLA/VCM_{max}/J_{max}) were selected, PFT-specific empirical trait-environment relationships derived and compared to observed mean variation. Results (Verheijen et al., 2013, BioGeoSciences) show that variability is truly incorporated, as the mean varies from default setting. This variability has considerable effects on model output, e.g. the predictions of future carbon sink differ when trait variation is considered. Research Idea: comparison of inclusion of trait variation in different models.

Scaling up functional biodiversity from landscape to global scal with DGVM LPJmL - Alice Boit

Aim of project was to test sensitivity of trait combinations to parametrisation. LPJmL was re-implemented at DGVM gap model (see ROBIN Project <http://robinproject.info/home/>), and gap model dynamics were up-scaled.

The role of biodiversity for the carbon cycle: Implementation of functional diversity in a dynamic vegetation model - Boris Sakschewski

TRY was used to select plant that might be of interest in model. A number of leaf traits were selected, and a “correlation corridor” (not fixed regression) constructed. This approach provided 100 different plant types. Competition dynamics were tested, and outcomes of test patches scaled up to grid cells. Modelled and observed SLA were compared. The approach allowed to implement trait variability, and to reproduce local SLA distribution, and contributes to explaining functional diversity and feedbacks.

Working groups (for outcomes, see also detailed reports of working groups)

Plant traits and vegetation modelling (Colin Prentice, Nicolas Viovy)

Aim: Brain-storming “good” way forward on how to improve plant trait diversity representation in models

Outcomes: linking TRY to models through identification of key traits that could be parametrised for models. Currently, most traits used are related to photosynthesis, but there are others, such as root traits, or traits related to cold tolerance that might be worth considering.

Plant trait prediction and gap-filling (Arindam Banerjee)

Aim: Improving gap-filling & Out-of-sample prediction

Outcomes: Discussed approaches for Out-of-sample predictions, Trait dependence on environmental variables, combining distributions and trait predictions to improve species distribution predictions, benchmarking gap filling and Bayesian Hierarchical Models with phylogenies.

The global spectrum of plant function (Sandra Diaz, Sandra Lavorel, *closed session to finalize analyses*)

Aim: Identification of whole plant trait pattern at global scale

Outcomes: analysis of TRY data fairly advanced – 6-dimensional trait space with gaps. Traits covered include LMA, Leaf nitrogen, wood density, leaf area, seed mass, plant height. Null-models developed to fill trait-space, manuscript hopefully finalised by end of the year.

Plant traits and phylogenetic analyses (William Pearse)

Aims: examination of phylogenetic signal in plant traits, examination of variation explained by phylogeny, and by plasticity, and determining fast and slow evolving traits

Outcomes: Series of interrelated questions developed on how traits evolved, developed approaches to “trait-based” conservation, discussed potential overlaps between GBIF, genbank, and TRY, discussion of methodological approaches and key hypotheses to drive these phylogenetic analyses.

Next generation trait screening projects (Joe Craine)

Aims: Set up practices to guide trait screening, lay out different ways for screening experiments for different situations, develop guidelines and ensure that good stream of data is flowing into TRY

Outcomes: development of principles for designing research to measure plant traits, three ways to deal with replication – 1) maximise no of species, 2) uneven sampling of species, 3) constrained species set

Linking Plant traits to plot data (Oliver Purschke)

Aims: improve need for understanding of processes that generate community functional composition by linking functional trait data and plot data, and by conducting large-scale analysis that link trait data to species occurrences

Outcomes: discussion focussed on methodological side - plot size, quantification of trait diversity. Plot size matters when calculating functional diversity, but not community weighted means. Discussed relationship between community traits and environmental drivers, and alternative way to link traits with environmental variables. Parametrisation of LPJmL for different biomes informs which functional diversity measure could be used. The

model will be developed by Nikolaos Fyllas, and outputs of the two models will be compared. Needed still are plots along environmental gradients in the tropics

Tropical Forest Trait Group (Christopher Baratolo)

Aims: improve trait sampling and measuring (to be guided by TRY), and overcome obstacles to linking traits to plot data

Outcomes:

Benefits to TRY:

- tropical forests and TRY
- high diversity and lot of data
- control from some biogeographic noise
- clear link with plot data
- well defined gradients
- important conservation questions

Required by Tropical Forest Group

- taxonomic standardisation
- plant age
- hierarchical data
- standardising environmental measures
- repeated environmental measures

Way forward

- establish group together
- integration of data into TRY
- building of data sets
- defining protocol
- id gaps
 - functional strategies across data sets
 - trait variation across gradients and continents
 - trait space and rarity

Refining the TRY initiative

Five years of TRY development: experiences and challenges – Jens Kattge

TRY – Psychology: moving from “my data – are you nuts?” to “my data – sure!”

TRY experienced both growth in community and gain in momentum of data base growth. However, some time lag in data release / manuscript publication. TRY approach to data sharing seen as overly complicated and restricted. BUT: open access does not come without obligations!

Topic addressed during discussions:

1. Data availability
 1. Intellectual property guidelines
 2. Proposal management
2. Data Quality
 1. meta data and auxiliary data
 2. taxonomic data
3. Integration of TRY with other Data sharing initiatives

Current model – data ownership remains with data contributors, give-and-take systems (apart from modelling), and proposal approval system. Incentives for contribution of data were use of data contained in data base, citation, and potential co-authorship.

Proposed new model - Data ownership remains with data contributors, and give-and-take system (in case with non-public data) is established. Three levels of data availability will be implemented: 1) permission (of data owner) required in each case, 2) permission is granted by default, and 3) data are made publicly available. Incentives for data contribution include the use of non-public data from joint data base, citation, and potential co-authorship. However, journals only allow a restricted number of references. Revised authorship regulations need to be reflected in intellectual property guidelines. Distinction between "data projects" and "modelling projects" will no longer be made, and proposals will in future be approved by data owners.

Gerhard Boenisch presented open access website and three settings for data availability, as well as scheme for current and envisaged data management.

Move towards open access welcomed by the participants, however, the need to cite and acknowledge data sources was stressed and suggestions were made on how this could be achieved. The best way forward would be **assigning DOIs to the data sets**. FLUXNET has shown that the open access model (with obligations attached to it) is working, and this could be used as a model. Early career researchers depositing data in TRY should be protected, and their data only released with their permission (and they be potentially offered co-authorship by users of their data).

TERN data management and access policy - Siddeswara Guru

TERN (<http://www.tern.org.au/>) was established in 2009, as a national infrastructure to store data and knowledge of Australian terrestrial ecosystems.

Both the Data discovery portal (<http://portal.tern.org.au>) and the Australian Centre for Ecological Analysis and Synthesis (ACEAS - <http://www.aceas.org.au/>) provide the room for a shared and collaborative research infrastructure to address Australia's critical ecosystem science and management challenges. They also contributed to efficiency gain in the ecosystem science research cycle.

Key elements of data infrastructure include publishing as web-feature service and a DOI minting facility (however, not all data sets have DOIs assigned).

The TERN data licensing policy is open access, with a least restrictive licence option, but users are required to attribute source of the data. Protection of sensitive data is allowed under justifiable conditions (18 months quarantine period). Challenge is to identify whether copyrights subsists with the data.

TERN developed a data licence suite that covers all licensed materials including materials not subjected to copy right. For data policy, see

http://www.tern.org.au/rs/7/sites/998/user_uploads/File/Data%20Licensing%20Documents/TERN%20Data%20Licensing%20Policy%20v1_0.pdf

It accounts for domain specific management, includes flexible licensing policy and links to the national research data catalogue. The approach allows to provide:

- citable data with DOI
- scalable and replicable infrastructure
- standardised data collection and analysis
- new continental data sets
- knowledge science for management

Refining the proposed new approach

Under the new model, proposals submitted are for information only for the data base management, and will no further be approved by the SC. However, as the proposals are also send to the data owner, the proposal should convince him to release the data. Ownership of the data will remain with data contributor / custodian.

Establishment of a new "Give and Take system" with three levels of data availability (see above). Propositions for implementation:

- 1) to streamline and speed up data release, an email with request to owners should include a the url to the website where release can be approved
- 2) metadata: DOI assigned to data contributions
- 3) development of alternative approach to co-authorship

Currently, data contribution does not automatically lead to co-authorship, but you will be contacted to give you opportunity to contribute intellectually in the manuscript. TRY has also established a 10% rule. i.e. if the data contributed amounts to more than 10% of the total data released, the owner will be offered authorship. However, the ability of collecting data does not reflect ability to contribute to project / manuscript. Doing away with the 10% rule would facilitate involvement of early career researchers in manuscripts.

Suggestion to *invite all data owners to contribute*, but they have to respond timely and adequately, and in the case of collective data sets, custodians are required to pass the invitations on to data contributors. This, however, would potentially lead to a large group of co-authors, only those that are making meaningful contributions early on should be included. As this might not be practical in many cases, it might be sufficient to cite the relevant publications, and not include co-authorship. Also acknowledgement that paper was a community effort (less rule, more moral)

The most practical solution is to *assign DOIs* either to whole data sets, or contributed data sets of a collective data set. It might be necessary to find an solution that individually fits the collective data sets. In case of public data sets, only a citation is required. Publication of data papers would allow for a DOI to be assigned to the data set, and make it citable. *Option to be taken forward*, but publication will need to be updated on a regular basis. Consider *other incentives* that could entice people to contribute to TRY.

Way forward: move towards open access, but place some restrictions on certain types of data. Public access data will have guidelines for good practice attached, which are facilitated by TRY. Handling of acknowledgement of data with restricted access is responsibility of both data owner and data user, they will need come to an agreement.

Need to find ways to make data sets "*citable*", e.g. via assigning DOIs or publishing data papers. Intellectual property guidelines to be updated accordingly, a small group will work on draft, which will be circulated to workshop participants and the TRY Community. Draft document to be circulated to work shop participants and TRY community.

Safeguarding against use of complete TRY dataset will need to be considered. Potentially establish an advisory board that provide guidance on the issues raised.

Improving data quality

This includes improving meta data and auxiliary data, as well as taxonomic information. There are currently efforts underway on standardising terminology within TRY. Quality control takes place during curation, when data are checked for consistency, and trait names used in data base are assigned.

Further considerations for expansion of TRY data:

- Metadata
 - TRY only needs coarse information as metadata
 - Auxiliary data for required for each data point
 - Provide meta data documents for original data sets
 - Use EML standards for meta data
 - Add information on trait categories used
- Directly link plant thesaurus to TRY data base
- Link traits to plot data (e.g. via plot id)
- Linking specimens to traits
- Complementing trait data
 - Root trait data
 - "shopping list" of traits
 - Conduct gap analysis
- Dealing with "Pseudo-traits"
 - Clear distinction between actual and modelled traits needed
 - categorical, continuous and computational traits
 - include error / uncertainty measurement
 - Derivation of new traits
- Inclusion of remote sensing measurements

Outlook: Remotely sensed trait data in TRY? - Shaun Levick

Development of Carnegie Airborne Observatory (Greg Asner, <http://cao.stanford.edu/>), enables sampling in remote places. The move towards high resolution satellite and air-borne imagery, e.g. LiDAR allows to obtain information on vegetation structure, but also on terrain. Data collection can be organised similar to data collection in the field.

Contributions of remote sensing to TRY

- probe areas where little data is available
- explaining variation in plant traits → enhancing link between TRY and modelling

Wrap-up and workshop closing

Christian Wirth closed workshop thanked everyone, in particular Jens and Gerhard for their work for the TRY initiative.

Gerhard and Jens to implement changes suggested at workshop.

Steering committee to synthesise discussion around property guidelines and mechanism

Appendix 1 Workshop participants:

	Participant	Affiliation
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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
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Appendix 2

Working Group Report **Plant trait prediction and gap-filling**

Participants:

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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. **It contains 2.88 million trait entries for 750 traits of 1 million plants, representing 70,000 plant species.** 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 TRY database, the number of plants with more than same three traits available is extremely small, making it tricky to perform such tasks on TRY data directly. There are two possible solutions: The first 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 second 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 regarding the trees, including taxonomic, phylogenetic, and/or genomic 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 trees, 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 methodology. 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, neural 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 need 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 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. 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 individual trees/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.

Appendix 3a

Working Group Report Next generation Trait Screening

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 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.

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Appendix 3a

Working Group Report

Notes from Trait screening working group (afternoon session)

There is enough time that has passed since last good screening programs. There was a consensus among the group that there is a need for a new strong screening program that allows answer current key ecological questions.

We discussed about the current trend of funding agency to neglect financing data acquisition such as a screening program and prioritise re-use of data/data synthesis. The down side effect of this is that it may reduce datasets availability for future data synthesis work.

We had a short discussion on how we should select the traits that should be part of a screening project The key one to answer current key questions may not necessary be those that are more documented in TRY.

We had discussion on some key traits that are currently not well documented/represented in TRY (e.g all root traits) and for many of which we don't have a standardised measurement protocols available.

A survey was suggested as a way to identify which traits should be measured. This survey should be based on the following questions (to avoid that everybody simply identifies the trait they are currently measuring as the priority):

- What question would you like to address
- Which traits do you need to measure to address this?
- What should be the experimental design and environmental data needed to answer this

This survey may help get funding for a screening program (we can show that there is a need to measure those traits).

We had a discussion on which traits to be measured in the future. Two aspects that has been identified to influence which traits to be measured are:

- New scientific questions
- New methodology available to measure hard traits

It is hard to quantify the relative importance of a given trait. There is a trade off between technology (could be costly= replication) and simple cheap measure that could be made at larger scale.

We had a short discussion on where/how should those traits measured and on new ways of data management (importance of metadata) to facilitate integration of this information.



Appendix 4

Working Group Report **Phylogeny**

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.

Workshop 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.

Appendix 5

Working Group Report **Modelling**

Key points from the traits/modelling Working Group

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 tradeoffs, 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



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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”...

Appendix 6

Working Group Report **Linking plant traits to vegetation plots**

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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 conceptual 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 FD-metrics.