



**iDiv**

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Integrative Biodiversity Research (iDiv)  
Halle-Jena-Leipzig



# **sPlot - The Global Vegetation Database**

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# Outline

- Why sPlot?
- What (and who) is sPlot?
- Challenges
- Applications and perspectives



# Aims of sPlot

analysis of plant  
community trait -  
environment  
relationships

across the world's  
biomes

on the basis of  
fine-grain  
vegetation plot data.





Credits: E. Del Vico

## Why sPlot?

- Global patterns of e.g. taxonomic, functional or phylogenetic diversity may differ when compared to single species data.
- Vegetation plot data allows to derive true-absences and explore species co-occurrences patterns
- Joins fine grain with large extent
- Accounts for relative species abundances
- Huge amount of data collected over decades but scattered



Credits: S. Burrascano



## Trait community data *versus* grid cell mean trait values

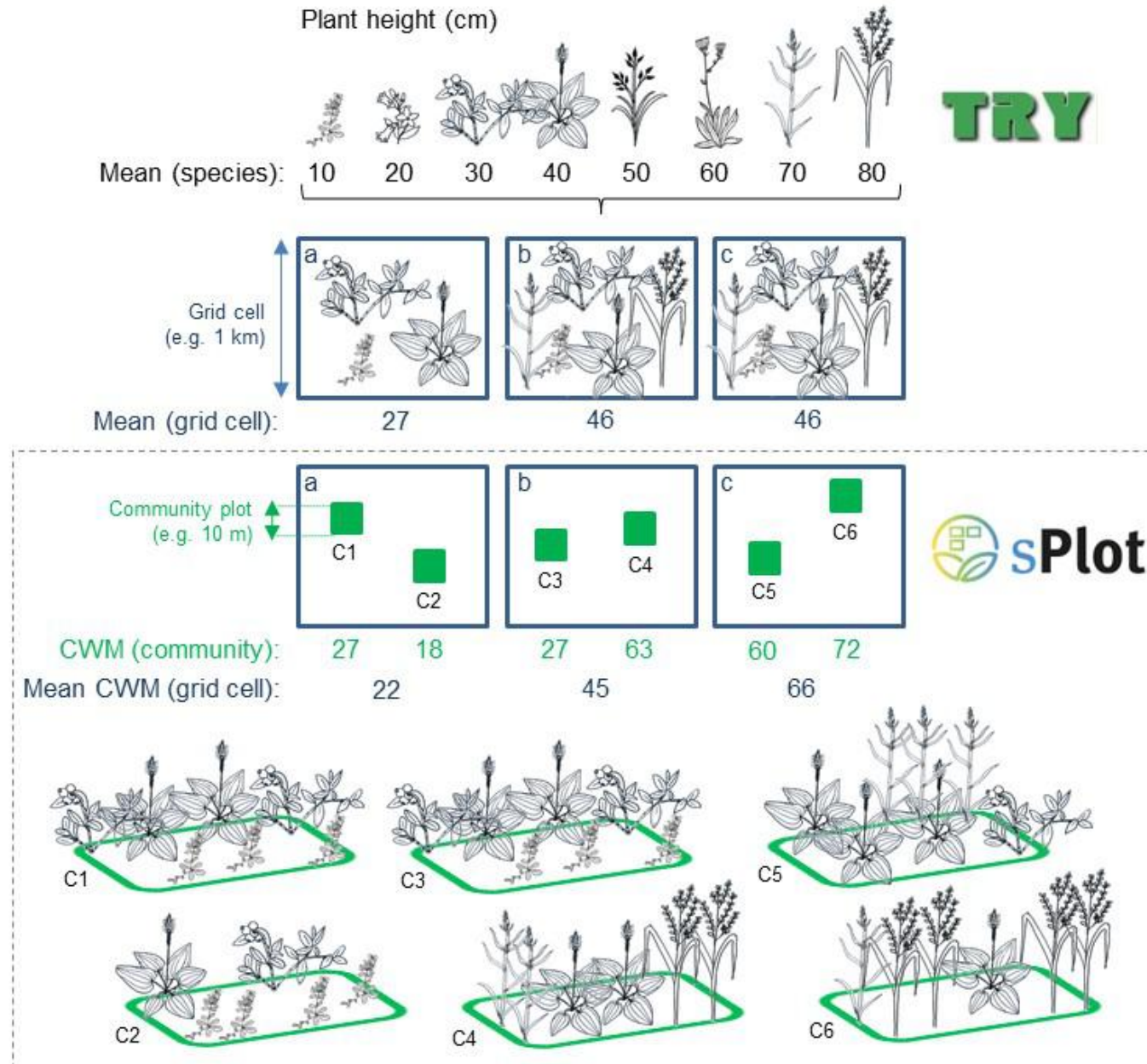
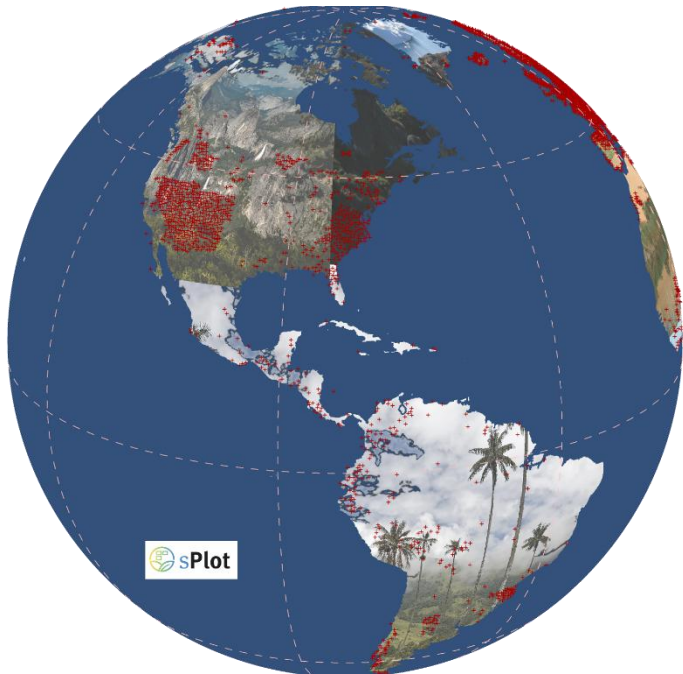
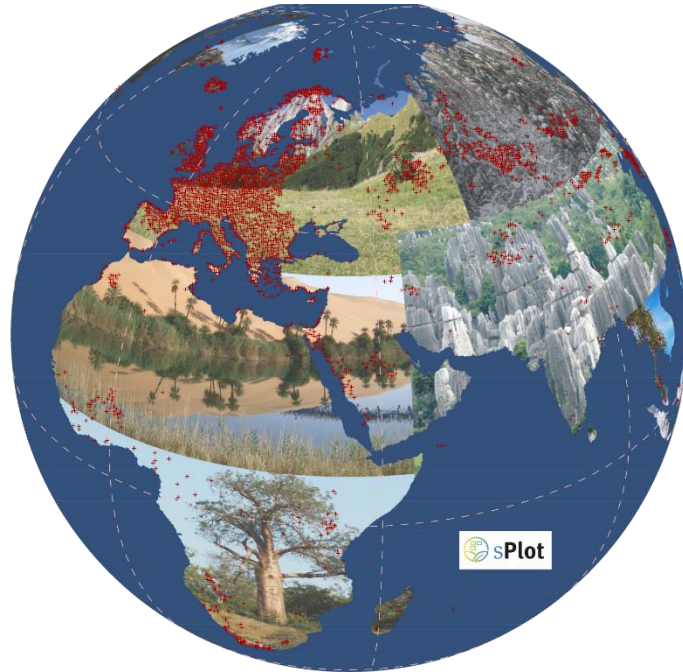


Fig. 1 from Bruelheide, Dengler, Jiménez-Alfaro, Purschke et al. (in prep.): sPlot – the global vegetation-plot database. - Under review in Global Change Biology.

# What (and who) is sPlot?



- Relational database including species lists recorded in plots and header data (geographic and environmental information)
- linked with functional traits provided by TRY and phylogenetic data
- Software - Turboveg 3
- 111 databases (and counting)
- 199 members



# Challenges

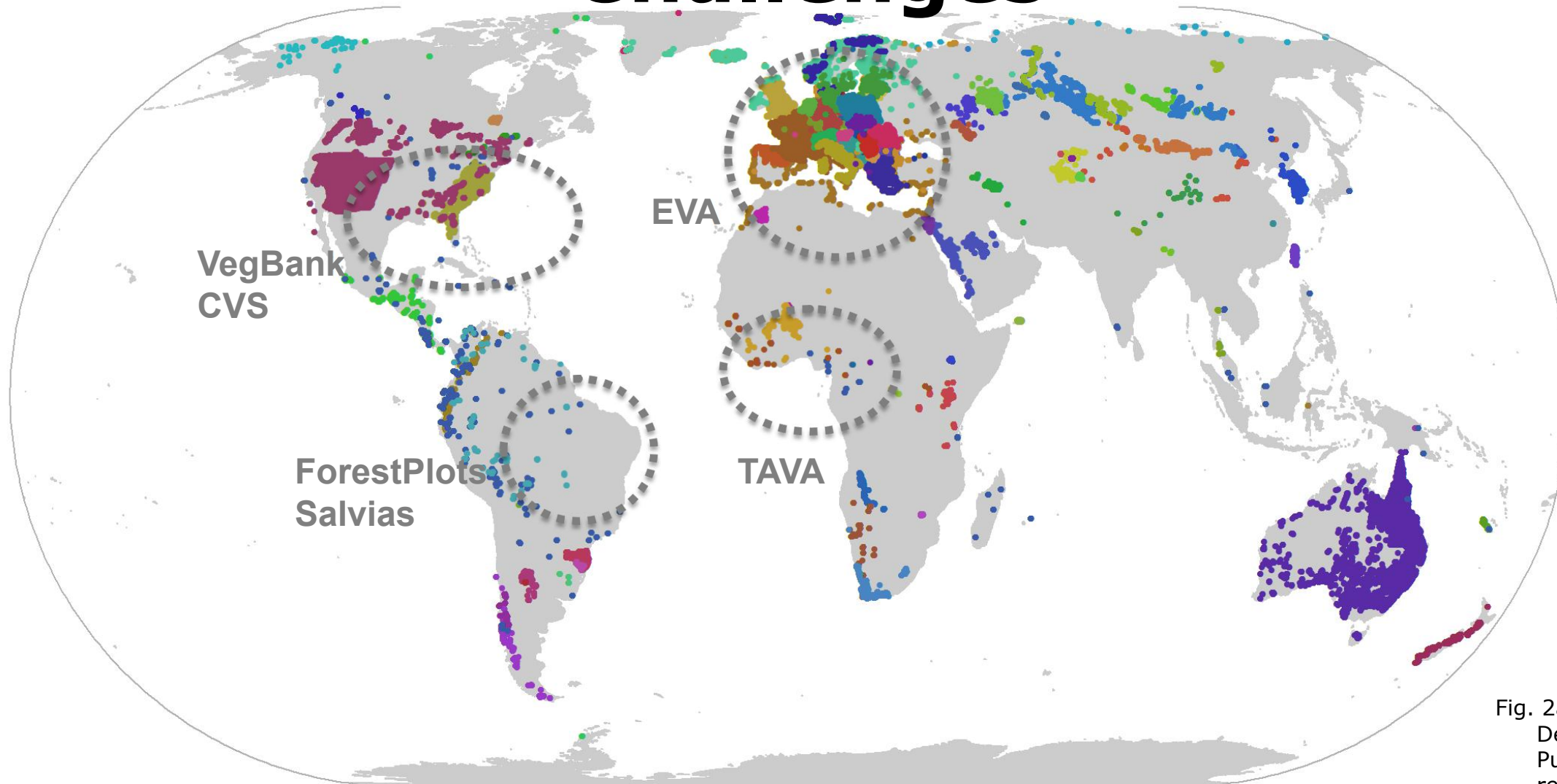
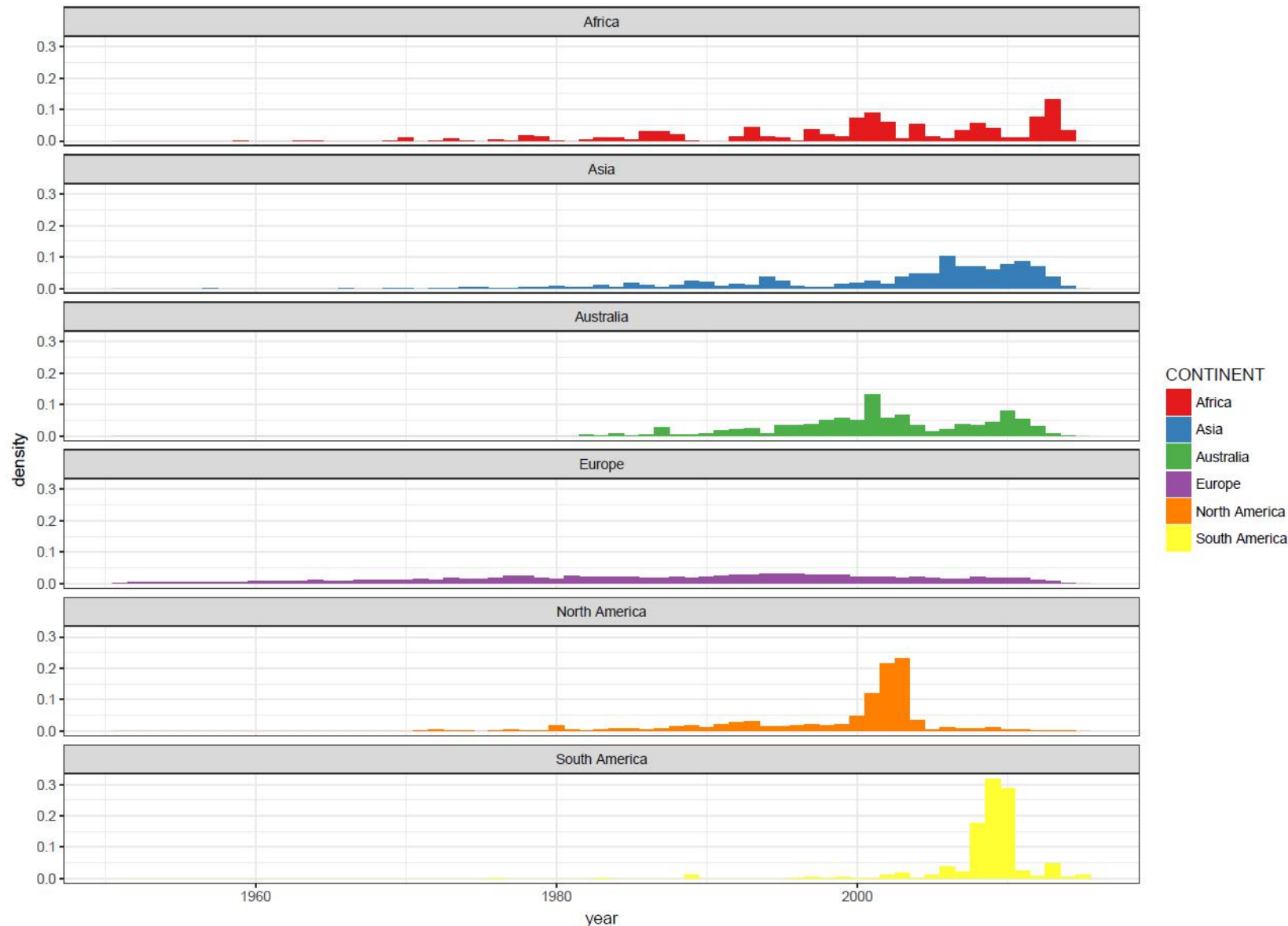


Fig. 2a from Bruelheide, Dengler, Jiménez-Alfaro, Purschke et al. (under review): sPlot – the global vegetation-plot database. - Global Change Biology.

1,121,244 vegetation plots - (23,586,216 species × plot observations)



# Temporal coverage of sPlot 2.1



Relative frequency  
of plots per year  
by continent



## Traits from TRY 3.0

### Gap-filled data through matrix factorization

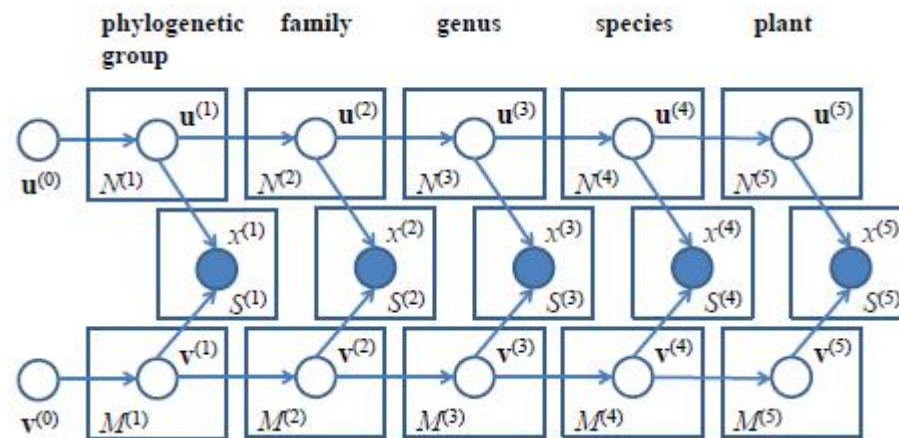


Fig 2. in Schrodte, F., et al. (2015) "BHPMF—a hierarchical Bayesian approach to gap-filling and trait prediction for macroecology and functional biogeography." *Global Ecology and Biogeography*

Total number of taxa with gap-filled traits in TRY: **52,032**

Of these **26,632** are in sPlot

Total number of records in sPlot2 (=entries): **23,586,216**

Total number of records with resolved species names without non-vascular plants: **22,195,966** (94.10% of all entries)

Total number of records with a gap-filled trait value: **21,050,474**  
(89.25% of all entries)

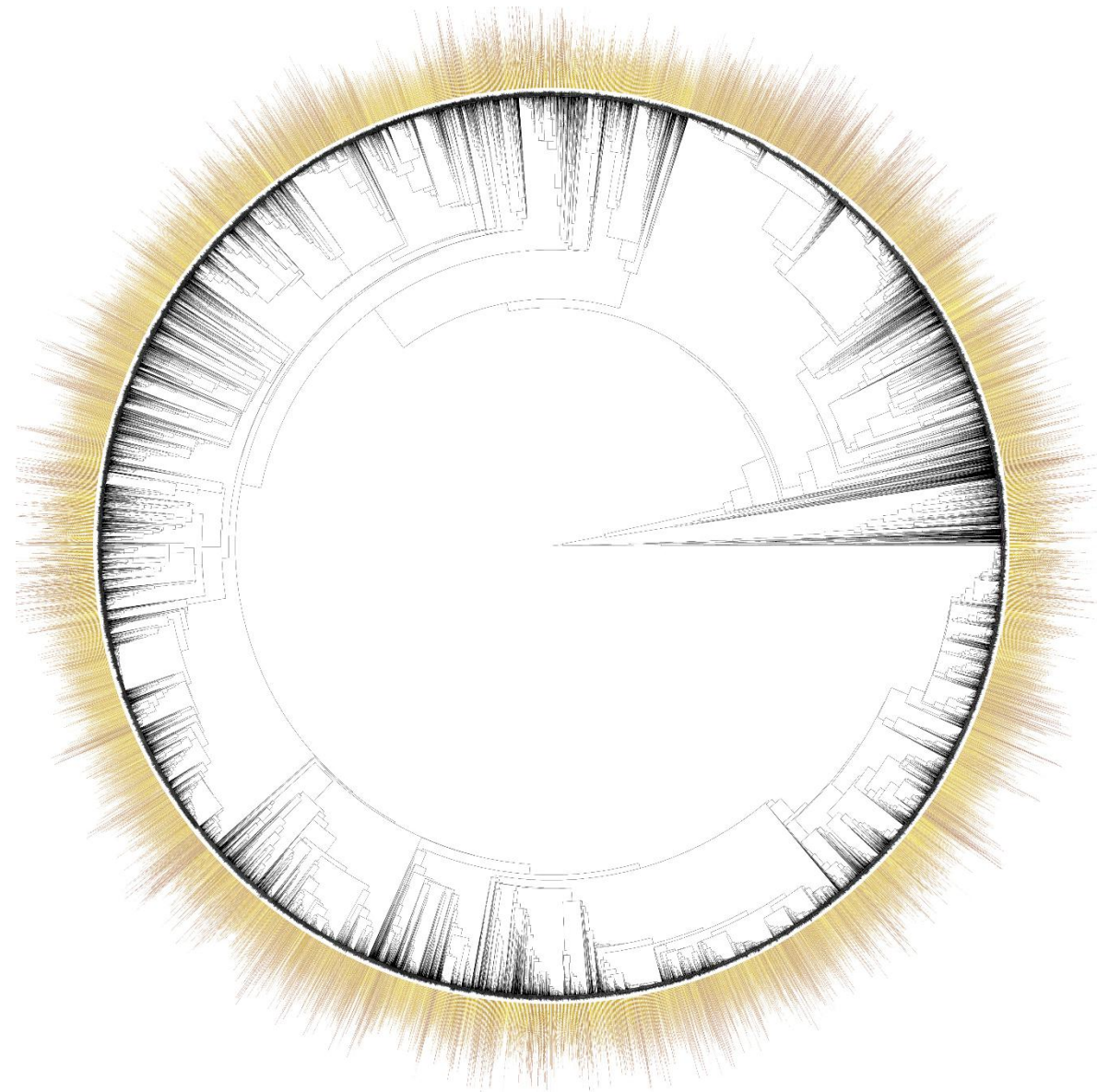


## Taxonomic coverage of sPlot 2.1

Total number of species  
names: **86,432**

After resolving names with  
TRNS 4.0 **54,519 taxon  
names** remained.

For **50,167 taxa** we could  
construct a phylogenetic  
tree.



Appendix S6, Fig. 1 from Bruelheide,  
Dengler, Jiménez-Alfaro, Purschke et  
al. (Under review): sPlot – the global  
vegetation-plot database.  
- Global Change Biology.

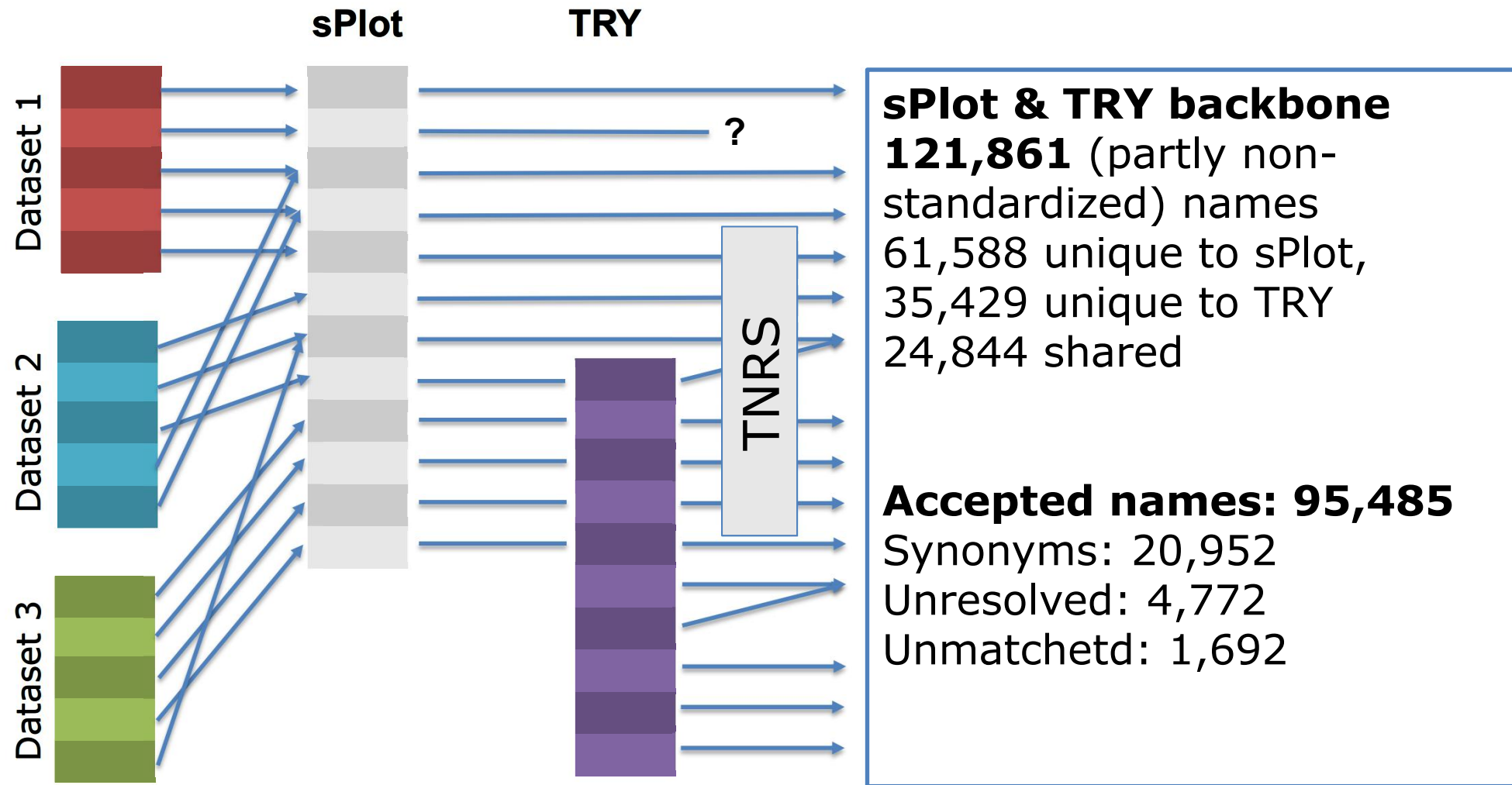


## Challenges

- Different database systems
- Different header data structure
- Different species taxonomies
- Different sampling protocols
- Heterogeneous abundance measures
- Heterogeneous (or incomplete) header data
- Heterogeneous geographic precision (~1 m to 10s of Km!)
- Different sampling intensities (e.g. Plot size)
- Biased distribution of relevés (within and across datasets)
- Missing information on vegetation types



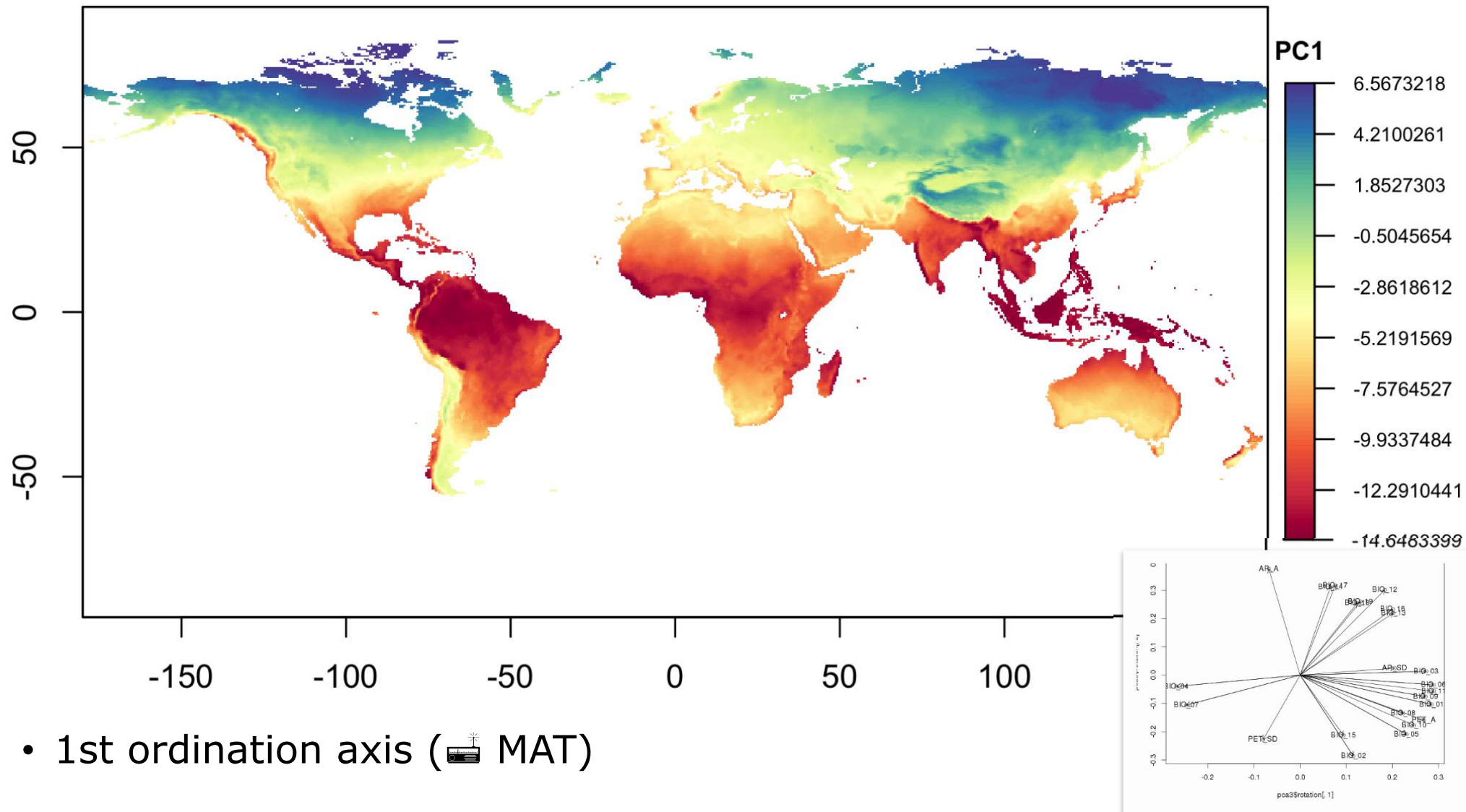
# Taxonomic Backbone





## Biased distribution of plots

- Based on 8,384,404 raster cells at 2.5 arc min

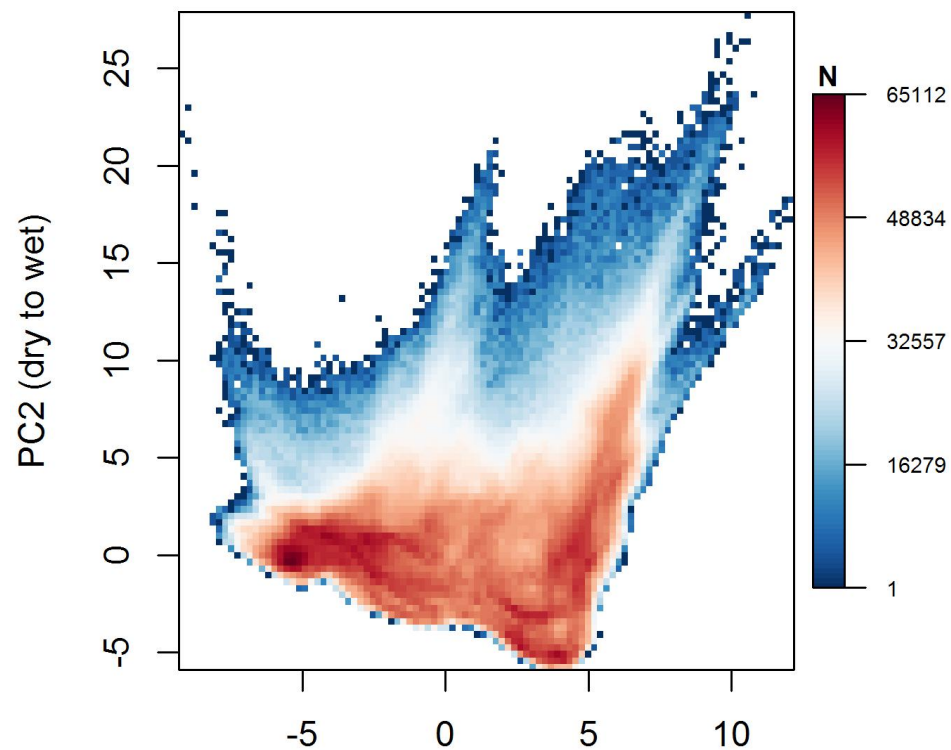




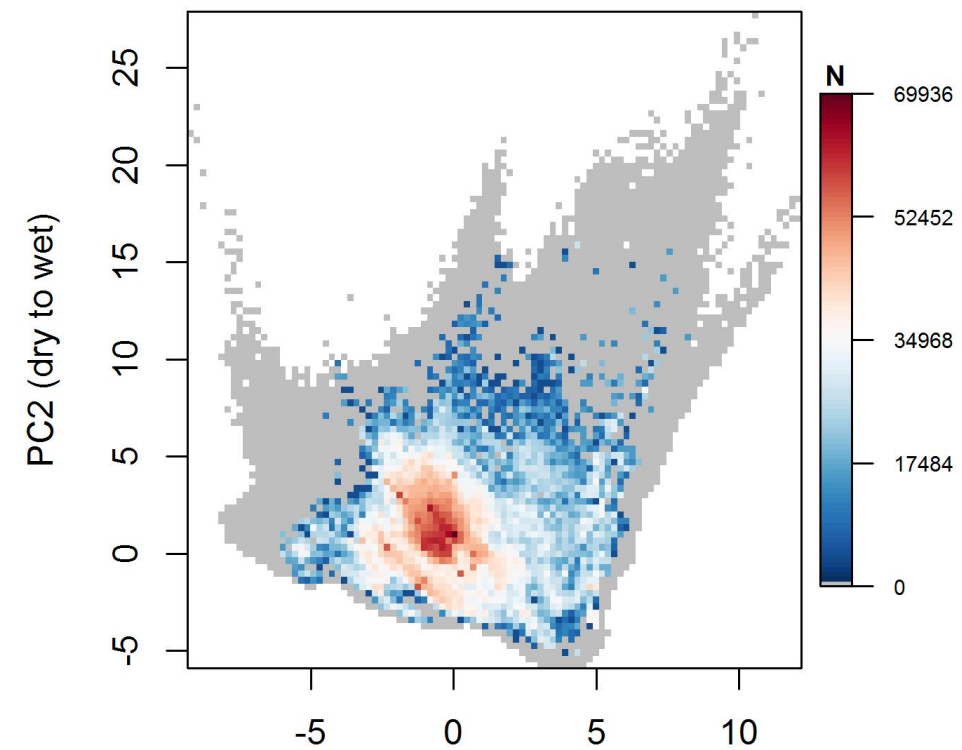
## Biased distribution of plots

a) all terrestrial 2.5 arc-minute cells, b) plots in sPlot 2.1 in the principal component analysis (PCA) space defined on all 30 environmental variables.

a) Number of 2.5 arc-minute environmental cells globally (log scale)



b) Number of plots in sPlot per environmental cell (log scale)



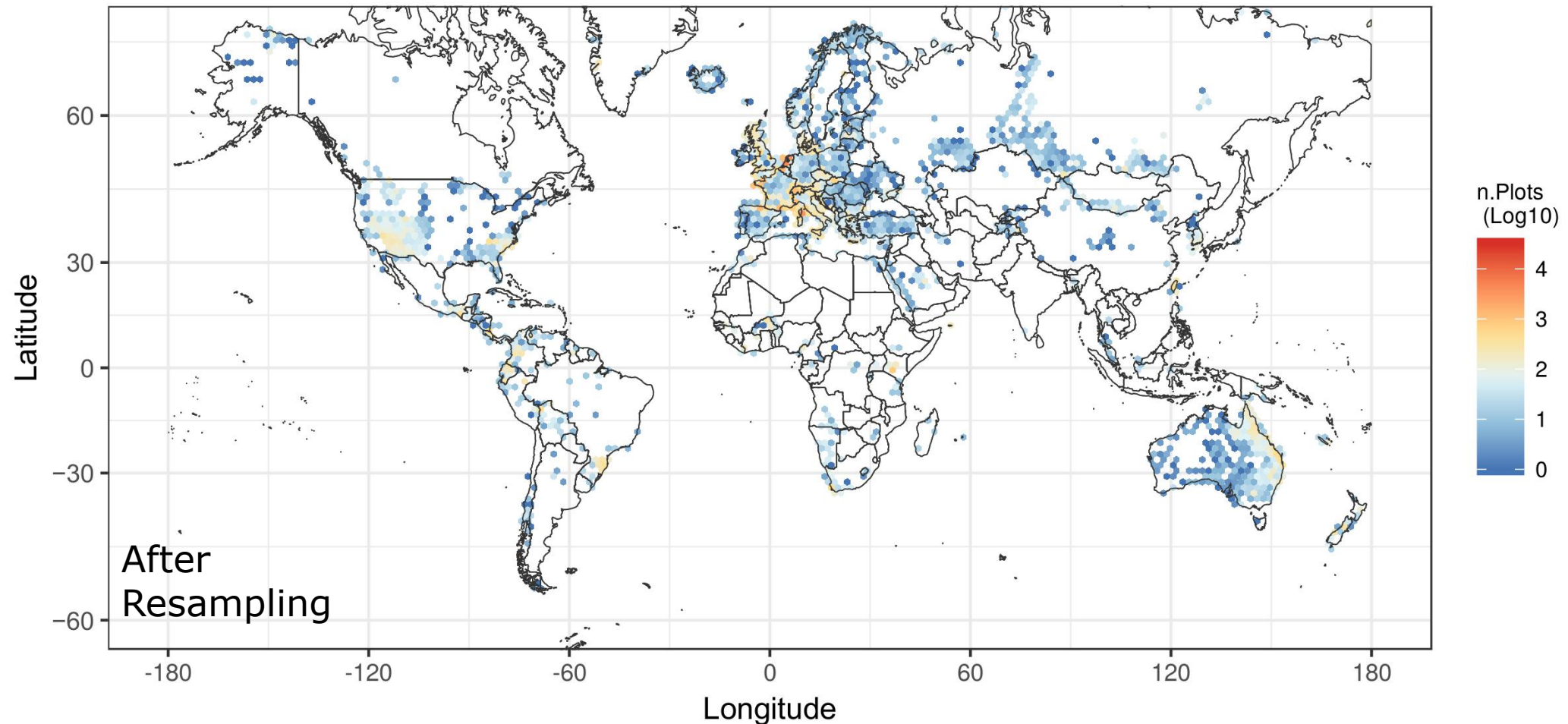
PC1 (cold and seasonal to hot and stable)

PC1 (cold and seasonal to hot and stable)



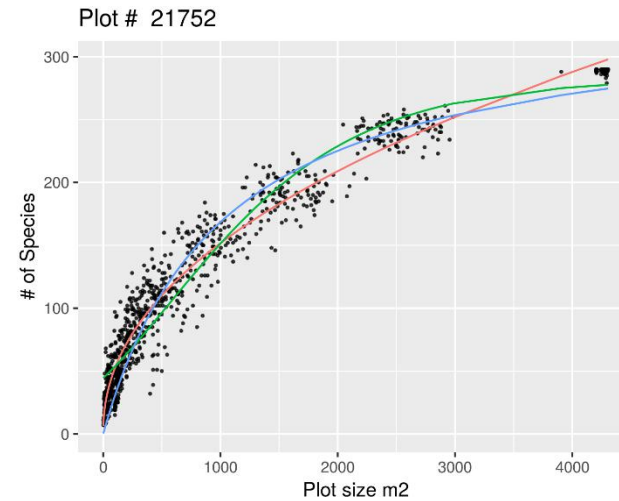
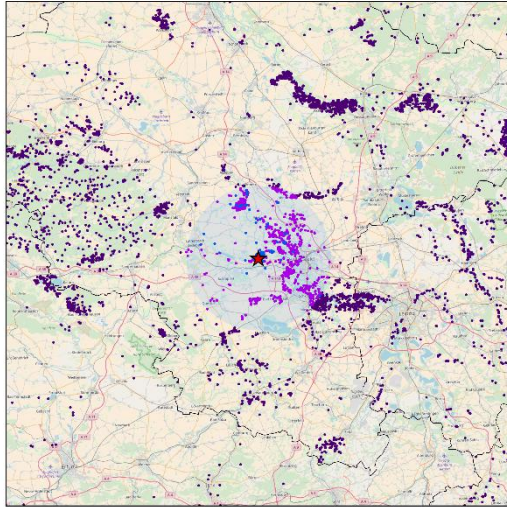
# Biased distribution of plots

Systematic sampling within the environmental space to capture a subset of plots representative of the available environmental variability.

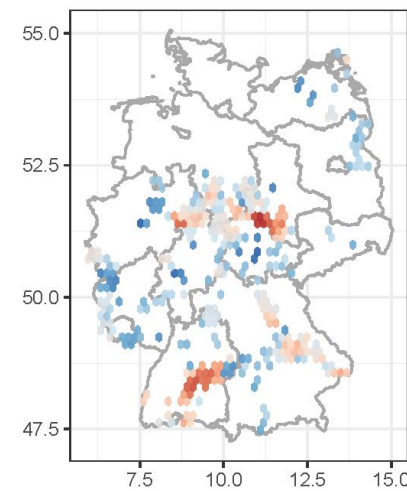
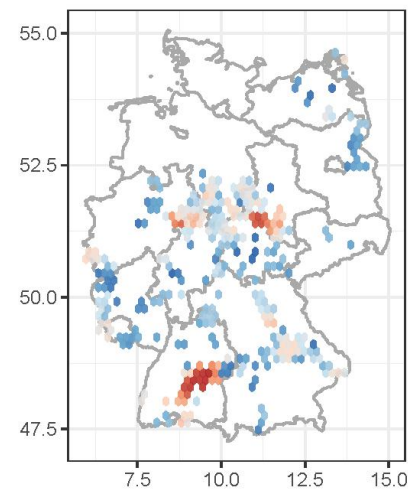
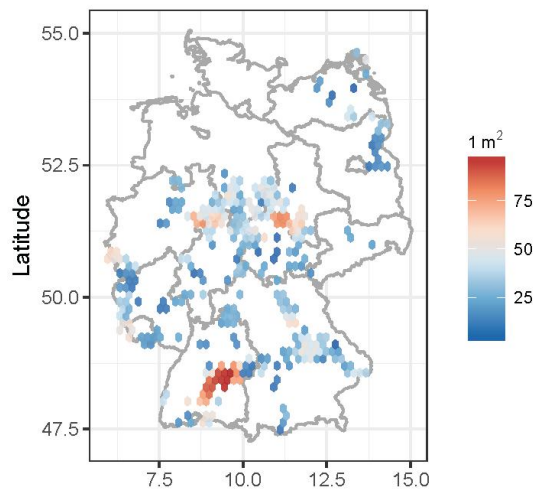




# Plot-specific species Pools



- Rarefaction & Species pools to control for sampling intensity
- Probabilistic species pools (Beal's smoothing algorithm)







# Applications & Perspectives

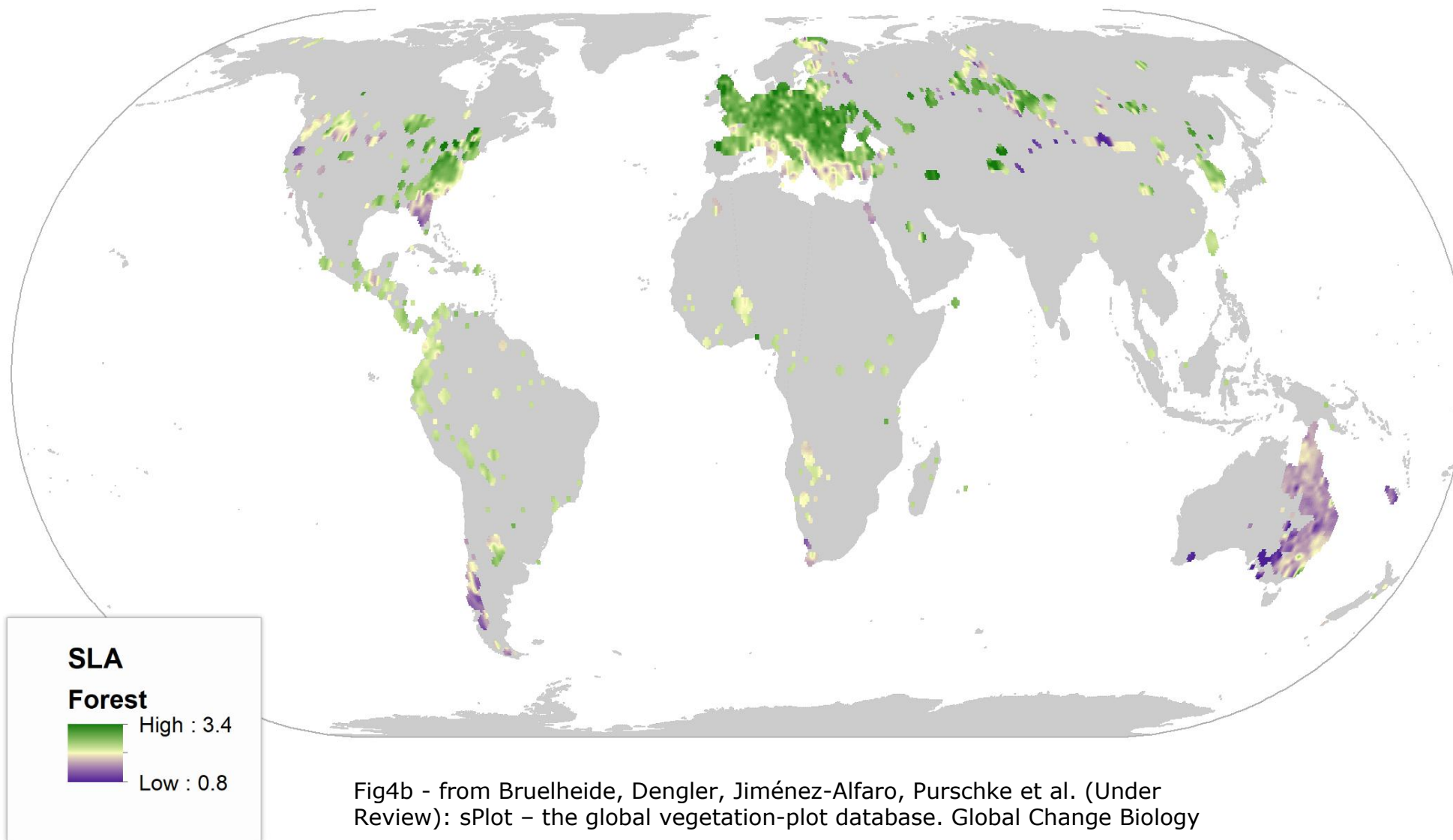


Fig4b - from Bruelheide, Dengler, Jiménez-Alfaro, Purschke et al. (Under Review): sPlot – the global vegetation-plot database. Global Change Biology

# Applications & Perspectives

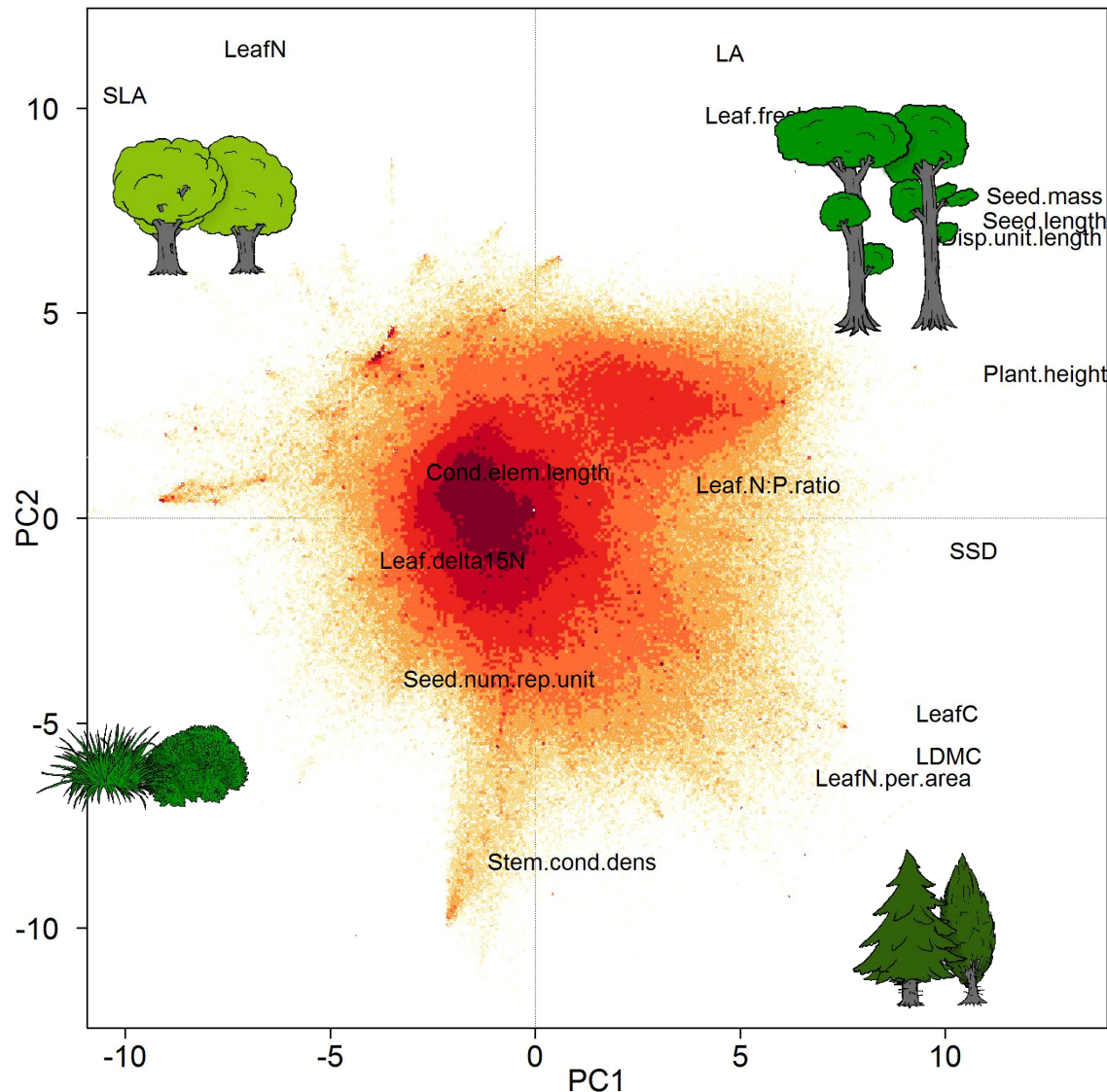


Fig. 1 from Bruelheide, ... & Jandt (Accepted): Global trait-environment relationships of plant communities. - Nature, Ecology and Evolution.

## PCA of all CWMs

Community-weighted means of 18 traits explained by the first two axes = **49.81%**

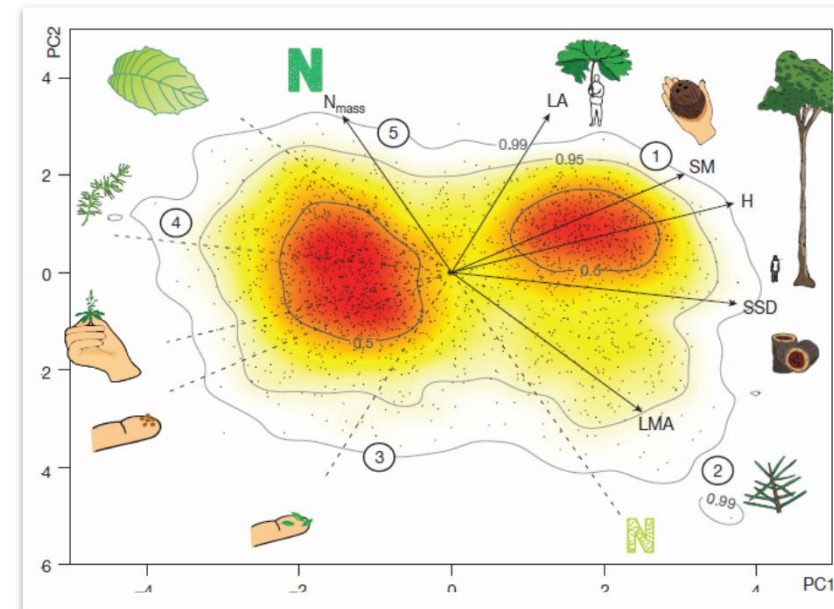
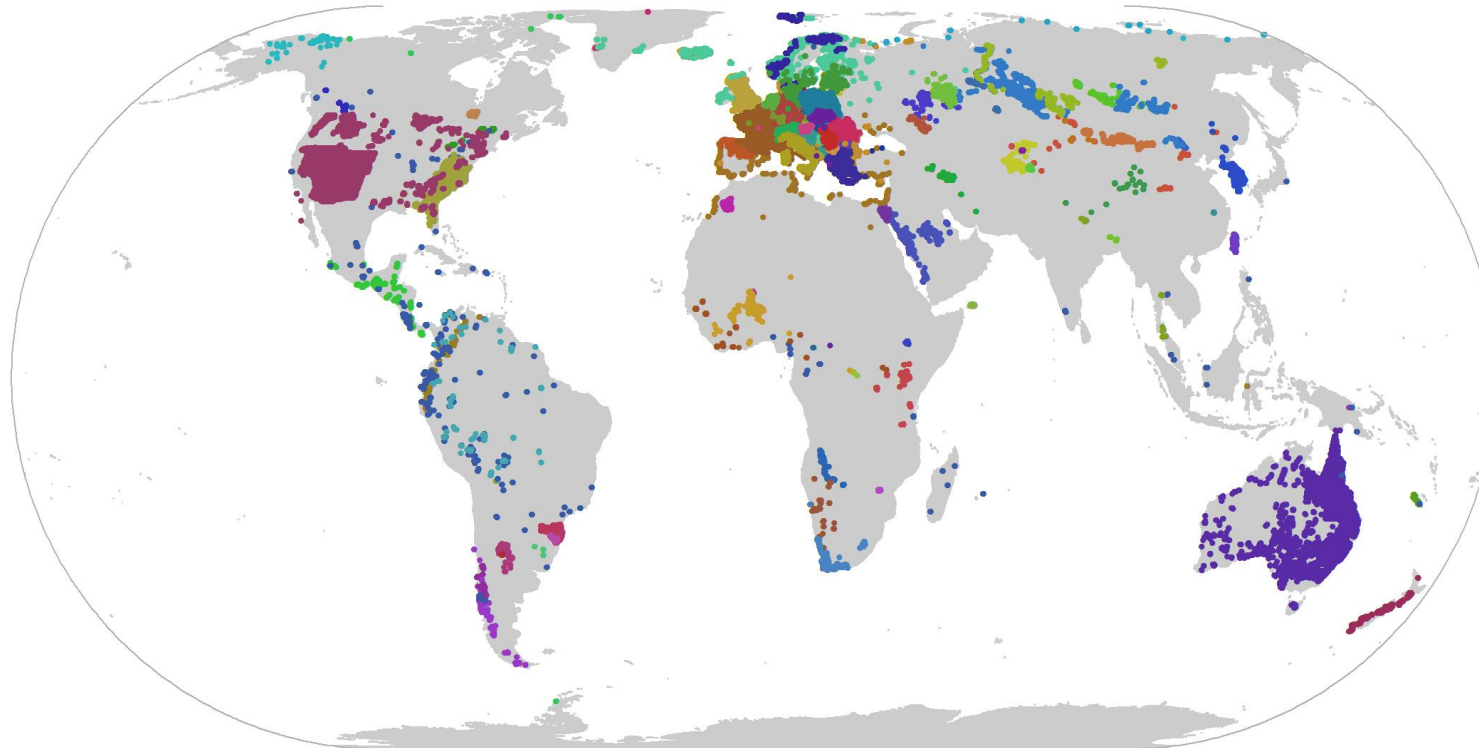


Fig. 2a from Díaz et al. (2016): The global spectrum of plant form and function. Nature 529: 167-171.



# Applications & Perspectives



**Towards  
sPlot 3.0**

Filling the  
gaps

Expected release 1<sup>o</sup> quarter 2019



## Acknowledgements

*German Research Foundation (DFG)*



[www.idiv.de/sdiv/working\\_groups/wg\\_pool/splot.html](http://www.idiv.de/sdiv/working_groups/wg_pool/splot.html)



@sPlot\_iDiv

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## Ongoing projects

### Providing sPlot data for integrative biodiversity research

#1 [sPlot – the global vegetation-plot database \(Bruehlheide, Dengler, Jimenez-Alfaro, Purschke et al.\)](#)

#2 A resampling procedure for big data (Lenoir et al.)

### Testing global patterns in plant diversity

#3 [Patterns on global trait composition \(Bruehlheide et al.\)](#)

#5 Earth observation data and diversity (Sandel et al.)

#6 Phylogenetic similarity of native and invasive plants (van der Sande et al.)

#8a Grassland productivity and functional diversity (Engel, Pillar et al.)

#10 Local richness on fern diversity at large scales (Kessler et al.)

#13 Global patterns of aquatic macrophyte diversity (Schrodt et al.)

#16 Projecting tree diversity and distributions in a changing world (Schrodt, Serra-Diaz et al.)

#17 Spatial patterns of plant assemblages in mountains (Peyre et al.)

#18 Global patterns of taxonomical and funct. diversity in alpine veg. (Atorre, Testolin et al.)

#19 Building a Vegetation <> Land-use converter for Europe (Joswig, Mimet et al.)

### Scaling plant diversity in space and time

#8b Effect of climatic stability in vegetation (Pillar et al.)

#9 Downscaling of distribution modelling from regional to plot level (Monnet, Sandel et al.)

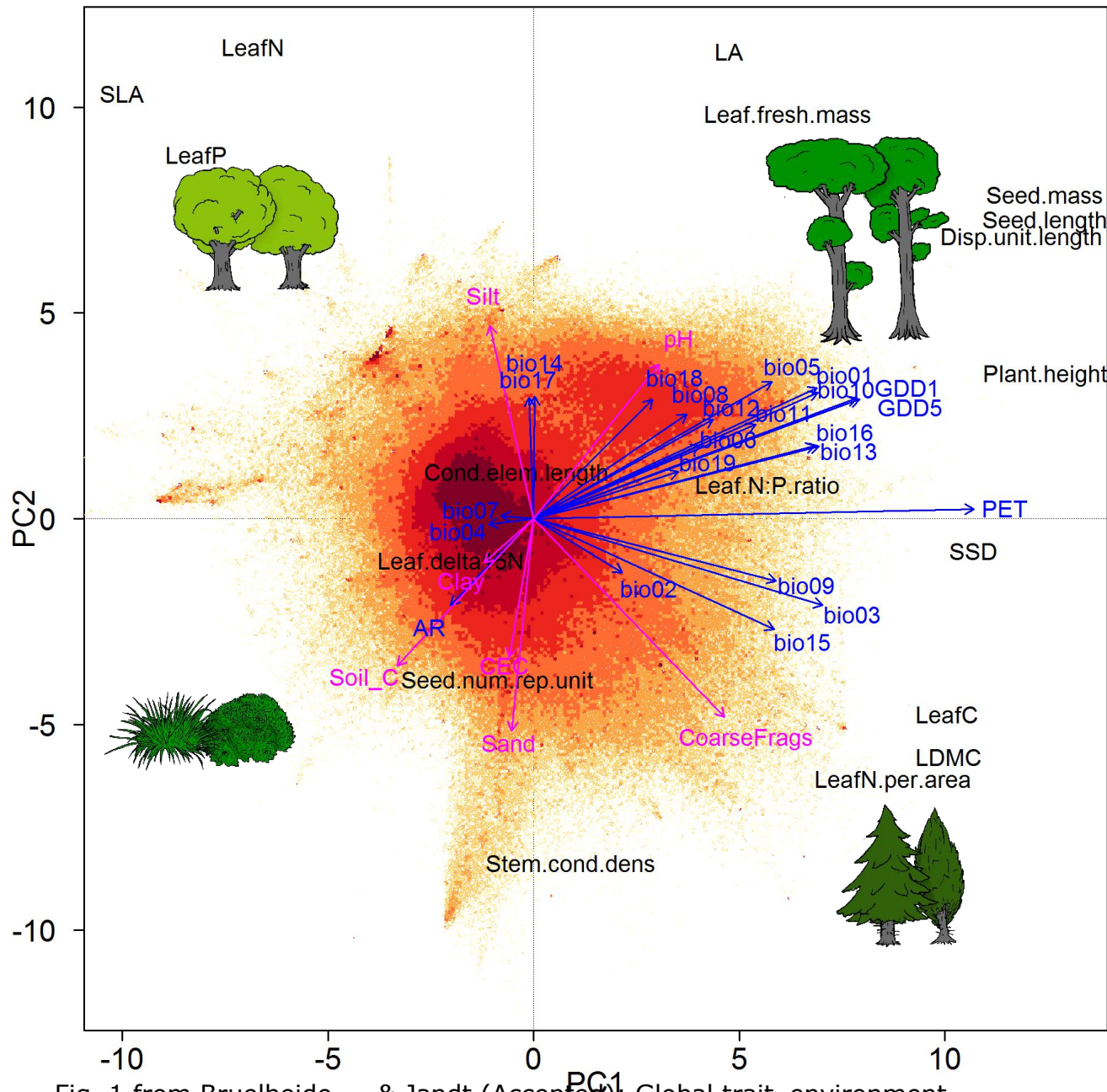
#11 [Probabilistic species pools at the plot level \(Bruehlheide et al.\)](#)

#12 Temperate deciduous forests of the northern hemisphere (Peet et al.)

#14 Functional convergence of terrestrial ecosystems in world biomes (Jimenez-Alfaro et al.)

#15 Cross-scale transferability of species niche breadth estimates (Kambach et al.)

#20 Trait-dependent extinctions across flowering plants in biodiversity hotspots



## PCA of all CWMs

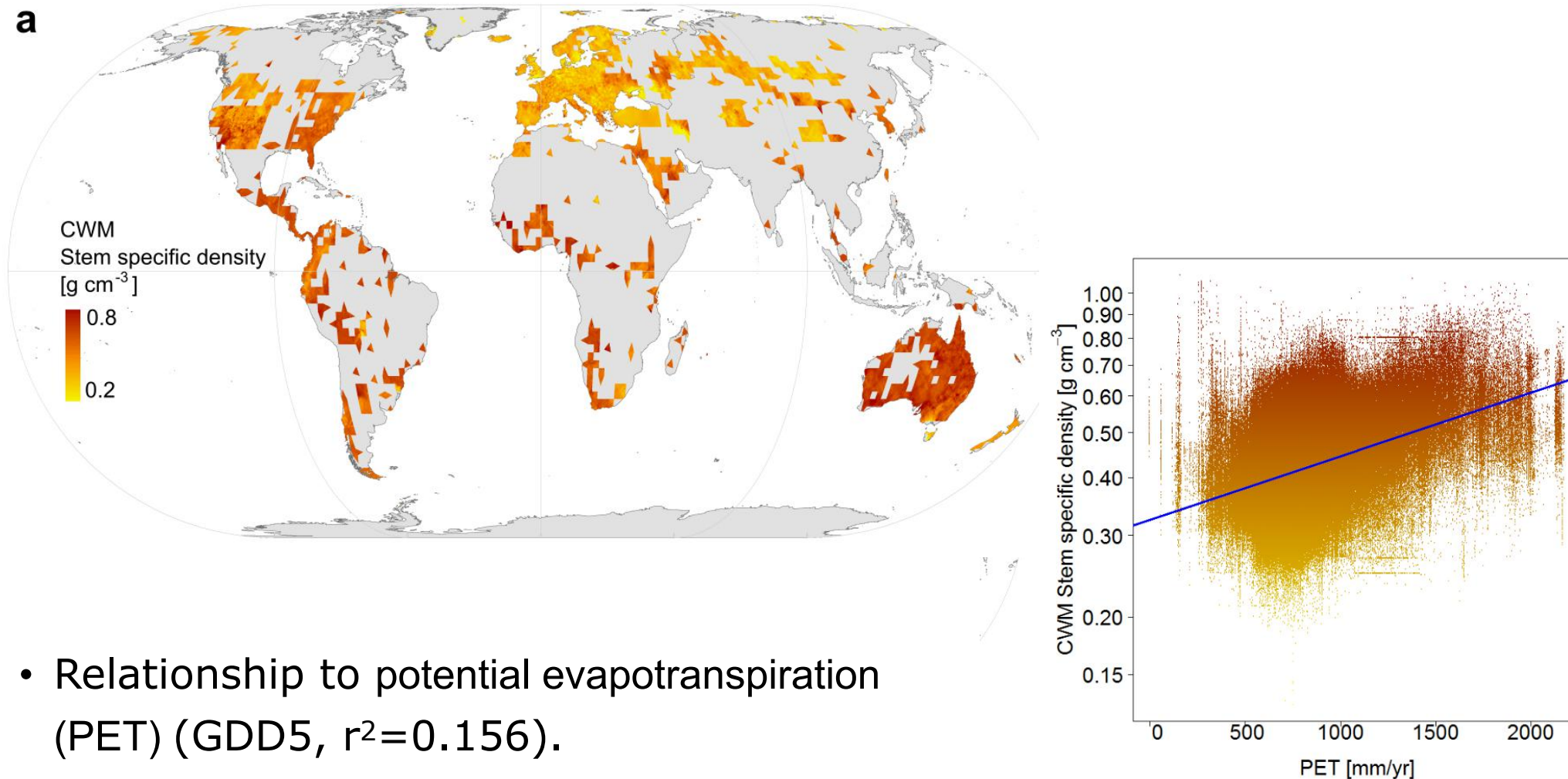
Cumulative variance in a Redundancy Analysis (RDA) explained by the first two constrained axes of 30 environmental variables = 10.8%.

Fig. 1 from Bruelheide, ... & Jandt (Accepted): Global trait-environment relationships of plant communities. - Nature, Ecology and Evolution.



## Community-weighted mean values of stem specific density (CWM SSD)

- Based on **1,114,304** plots, SSD  $\log_e$  transformed



- Relationship to potential evapotranspiration (PET) (GDD5,  $r^2=0.156$ ).