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sPlot – a new tool for global vegetation analyses

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Complete List of Authors:	Bruelheide, Helge; Institute of Biology, Geobotany and Botanical Garden Dengler, Jürgen; Zurcher Hochschule fur Angewandte Wissenschaften Life Sciences und Facility Management, Institute of Natural Resource Management (IUNR); Universitat Bayreuth Bayreuther Centrum fur Okologie und Umweltforschung, Plant Ecology; German Centre for Integrative Biodiversity Research (iDiv) Jiménez-Alfaro, Borja; University of Oviedo; Martin-Luther-Universitat Halle-Wittenberg Institut fur Biologie; German Centre for Integrative Biodiversity Research (iDiv) Purschke, Oliver Hennekens, Stephan; Alterra, Wageningen University and Research Centre, Wageningen Environmental Research (Alterra) Chytrý, Milan; Masaryk University, Department of Botany and Zoology Pillar, Valerio; Universidade Federal do Rio Grande do Sul, Ecologia Jansen, Florian; Universitat Rostock, Faculty of Agriculture and Environmental Sciences Kattge, Jens; Max Planck Institute for Biogeochemistry; German Centre for Integrative Biodiversity Research (iDiv) Sandel, Brody; Santa Clara University, Department of Biology Aubin, Isabelle; Canadian Forest Service, Natural Resources Canada, Great Lakes Forestry Centre Biurrun, Idoia; University of the Basque Country, Plant Biology and Ecology Field, Richard; University of Nottingham, Geography Haider, Sylvia; Martin-Luther-Universitat Halle-Wittenberg Institut fur Biologie Jandt, Ute; Martin-Luther-Universitat Halle-Wittenberg Institut fur Biologie Lenoir, Jonathan; Jules Verne University of Picardie, Ecologie et Dynamiques des Systèmes Anthropisés (EDYSAN, UMR 7058 CNRS-UPJV) Peet, Robert; University of North Carolina, Deparment of Biology Peyre, Gwendolyn; University of the Andes, Department of Civil and Environmental Engineering Sabatini, Francesco; Martin-Luther-Universitat Halle-Wittenberg Institut fur Biologie; German Centre for Integrative Biodiversity Research (iDiv) Schmidt, Marco; Senckenberg Biodiversity and Climate Research Centre (BiK-F), Data and Modelling Centre Schrodt, Franziska; University of Nottingham, School of Geography Winter, Marten; German Centre for Integrative Biodiversity Research

(iDiv),
Aćić, Svetlana; University of Belgrade, Faculty of Agriculture, Department of Agrobotany
Agrillo, Emiliano; University of Roma "La Sapienza", Department of Environmental Biology
Alvarez, Miguel; University of Bonn, Plant Nutrition, INRES
Ambarli, Didem; Düzce University, Department of Agricultural Biotechnology
Angelini, Pierangela; ISPRA, Biodiversity Conservation Department
Apostolova, Iva; Bulgarian Academy of Sciences, Institute of biodiversity and ecosysytem research
Arfin Khan, Mohammed A.S. ; Shahjalal University of Science & Technology, Forestry & Environmental Science; University of Bayreuth, Disturbance Ecology, Bayreuth Center of Ecology and Environmental Research (BayCEER)
Arnst, Elise; Manaaki Whenua - Landcare Research
Attorre, Fabio; Sapienza University of Rome, Department of Environmental Biology
Baraloto, Christopher; The Kampong of the National Tropical Botanical Garden, International Center for Tropical Botany (ICTB); Florida International University, Department of Biological Sciences
Beckmann, Michael; UFZ-Helmholtz Centre for Environmental Research, Landscape Ecology,
Berg, Christian; University of Graz, Botanical Garden
Bergeron, Yves; Université du Québec en Abitibi-Témiscamingue, Forest Research Institute
Bergmeier, Erwin; University of Goettingen, Vegetation Ecology and Phytodiversity
Bjorkman, Anne; Aarhus Universitet, Center for Biodiversity Dynamics in a Changing World (BIOCHANGE) & Section for Ecoinformatics & Biodiversity, Department of Bioscience
Bondareva, Viktoria; Institute of Ecology of the Volga River Basin, Laboratory of Phytocoenology
Borchardt, Peter; University of Hamburg, Institute of Geography, CEN - Center for Earth System Research and Sustainability
Botta-Dukát, Zoltán; Centre for Ecological Research, Hungarian Academy of Sciences, Institute of Ecology and Botany
Boyle, Brad; University of Arizona, Ecology and Evolutionary Biology
Breen, Amy; University of Alaska, International Arctic Research Center
Brisse, Henry; Faculté des Sciences, MEP
Byun, Chaeho; Seoul National University, Biological Sciences
Cabido, Marcelo; Multidisciplinary Institute for Plant Biology (IMBIV - CONICET), University of Cordoba - CONICET
Casella, Laura; ISPRA, Biodiversity Conservation Department
Cayuela, Luis; Universidad Rey Juan Carlos, Department of Biology, Geology, Physics and Inorganic Chemistry
Černý, Tomáš; Faculty of Forestry and Wood Sciences, Czech University of Life Sciences, Department of Forest Ecology
Chepinoga, Victor; The V.B. Sochava Institute of Geography SB RAS, Laboratory of Physical Geography and Biogeography
Csiky, Janos; University of Pécs, Department of Ecology
Curran, Michael; Swiss Federal Institute of Technology (ETH) Zürich, Institute of Environmental Engineering
Ćušterevska, Renata; Institute of Biology, Faculty for Natural Science and Mathematics, Skopje., Department of Botany
Dajić Stevanović, Zora; University of Belgrade, Faculty of Agriculture, Department of Agrobotany
De Bie, Els; Research Institute for Nature and Forest (INBO), Departement of Biodiversity and Natural Environment
de Ruffray, Patrice; IBMP
De Sanctis, Michele; Sapienza University of Rome, Department of

	Environmental Biology Dimopoulos, Panayotis; University of Patras, Institute of Botany, Division of Plant Biology, Department of Biology Dressler, Stefan; Senckenberg Research Institute Frankfurt, Department of Botany and molecular Evolution Ejrnaes, Rasmus; Aarhus University, Department of Bioscience El Sheikh, Mohamad; College of Science, King Saud University, Botany and Microbiology Department; Damanhour University, Botany Department Enquist, Brian; University of Arizona, Department of Ecology and Evolutionary Biology Ewald, Jörg; University of Applied Sciences Weihenstephan-Triesdorf, Hochschule Weihenstephan-Triesdorf Fagúndez, Jaime; University of A Coruña, Faculty of Science Finckh, Manfred; University of Hamburg, Biodiversity, Ecology and Evolution of Plants, Institute for Plant Science & Microbiology Font, Xavier; Universitat de Barcelona, Plant Biodiversity Resource Centre Forey, Estelle; Normandie University, Laboratoire Ecodiv, EA 1293 URA IRSTEA Fotiadis, Georgios; TEI of Sterea Ellada, Department of Forestry & Natural Environment Management GARCIA-MIJANGOS, ITZIAR; Universidad del Pais Vasco, Plant Biology and Ecology de Gasper, André Luis; Regional University of Blumenau, Departament of Natural Science Golub, V.B.; Institute of Ecology of the Volga River Basin, Laboratory of Phytocoenology Gutierrez, Alvaro; Universidad de Chile, Departamento de Ciencias Ambientales y Recursos Naturales Renovables, Facultad de Ciencias Agronomicas Hatim, Mohamed Z.; Tanta University, Botany, Faculty of Science, He, Tianhua; Curtin University, School of Molecular and Life Sicences Higuchi, Pedro; Universidade do Estado de Santa Catarina, Forestry Department Michalcová, Dana; Masaryk University, Department of Botany and Zoology Hölzel, Norbert; University of Muenster, Institute of Landscape Ecology Homeier, Jürgen; University of Göttingen, Plant Ecology and Ecosystems Research Indreica, Adrian; Universitatea Transilvania din Brasov, Department of Silviculture Işık Gürsoy, Deniz; Celal Bayar University, Biology Jansen, Steven; Universitat Ulm Fakultat fur Naturwissenschaften, Institute of Systematic Botany and Ecology Janssen, John; Wageningen University and Research, Wageningen Environmental Research (Alterra) Jedrzejek, Birgit; University of Münster, Institute of Landscape Ecology Jiroušek, Martin; Masaryk University, Inst. of Botany and Zoology; Mendelova univerzita v Brne, Department of Plant Biology Jürgens, Norbert; University of Hamburg, Biodiversity, Ecology and Evolution of Plants, Institute for Plant Science & Microbiology Kącki, Zygmunt; University of Wroclaw, Botanical Garden Kavgacı, Ali; Southwest Anatolia Forest Research Institute, Silviculture and Forest Botany Kearsley, Elizabeth; Ghent University, Department of Environment Kessler, Michael; Zurich University, Department of Systematic and Evolutionary Botany Knollová, Ilona; Masaryk University, Department fo Botany and Zoology Kolomiychuk, Vitaliy; O. V. Fomin Botanical Garden at the Educational and Scientific Centre «Institute of Biology», Taras Shevchenko National

University of Kyiv,
Korolyuk, Andrei; Central Siberia Botanical Garden, Russian Academy of Sciences, Geosystem Laboratory
Kozhevnikova, Maria; Kazanskij federal'nyj universitet, Institute of Environmental Sciences
Kozub, Lukasz; Uniwersytet Warszawski Wydzial Biologii, Department of Plant Ecology and Environmental Conservation
Krstonošić, Daniel; University of Zagreb, Faculty of forestry
Kühl, Hjalmar; Max Planck Institute for Evolutionary Anthropology (MPI-EVA), Primatology; Martin-Luther-Universitat Halle-Wittenberg Institut fur Biologie; German Centre for Integrative Biodiversity Research (iDiv)
Kühn, Ingolf; Helmholtz Centre for Environmental Research - UFZ, Community Ecology (BZF); Martin-Luther-Universitat Halle-Wittenberg Institut fur Biologie; German Centre for Integrative Biodiversity Research (iDiv)
Kuzemko, Anna; M.G. Kholodny Institute of Botany NAS of Ukraine
Küzmič, Filip; Scientific Research Centre of the Slovenian Academy of Sciences and Art, Institute of Biology
Landucci, Flavia; Masaryk University, Department of Botany and Zoology
Lee, Michael; NatureServe
Levesley, Aurora; University of Leeds, School of Geography
Li, Ching-Feng; National Taiwan University, School of Forestry and Resource Conservation
Liu, Hongyan; Peking University, College of Urban and Environmental Sciences
Lopez-Gonzalez, Gabriela; University of Leeds, School of Geography
Lysenko, Tatiana; Institute of Ecology of the Volga River Basin RAS, Phytodiversity Problems
Macanović, Armin; University of Sarajevo, Center for Ecology and Natural Resources - Academician Sulejman Redžić, Department of Biology
Mahdavi, Parastoo; C.v.O. Universität Oldenburg, Dept. of Ecology and Environmental Science
Manning, Peter; Senckenberg Research Institute, Project Group Causes and Consequences of Climate Change
Marcenò, Corrado; University of the Basque Country UPV/EHU, Plant Biology and Ecology
Martynenko, Vassiliy; Ufa Institute of Biology of Ufa Federal Scientific Centre of the Russian Academy of Sciences
Mencuccini, Maurizio; Institucio Catalana de Recerca i Estudis Avancats, Centre Research Ecology and Forestry Applications (CREAF)
Minden, Vanessa; Carl von Ossietzky-University Oldenburg, Institute of Biology an Environmental Sciences
Moeslund, Jesper; Aarhus University, Department of Bioscience
Moretti, Marco; Swiss Federal Research Institute WSL, Biodiversity and Conservation Biology
Müller, Jonas V.; Royal Botanic Gardens, Kew, Conservation Science
Munzinger, Jérôme; Université Montpellier, AMAP - Botany and Modelling of Plant Architecture and Vegetation, IRD, CIRAD, CNRS, INRA,
Niinemets, Ülo; Estonian University of Life Sciences, Chair of Crop Science and Plant Biology
Nobis, Marcin; Jagiellonian University, Institute of Botany
Noroozi, Jalil; University of Vienna , Department of Botany and Biodiversity Research
Nowak, Arkadiusz; Polish Academy of Sciences, Botanical Garden
Onyshchenko, Viktor; M.G.Kholodny Institute of Botany, NAS of Ukraine
Overbeck, Gerhard; Universidade Federal do Rio Grande do Sul, Department of Ecology
Ozinga, Wim; Wageningen Environmental Research, Team Vegetation, Forest and Landscape Ecology
Pauchard, Anibal; Universidad de Concepcion, Laboratorio de Invasiones

	Biológicas (LIB) Pedashenko, Hristo Penuelas, Josep; CSIC, Global Ecology Unit CREAF-CSIC-UAB; CREAF Pérez-Haase, Aaron; University of Barcelona, Department of Evolutionary Biology, Ecology and Environmental Sciences; Spanish Research Council (CEAB-CSIC), Center for Advanced Studies of Blanes Peterka, Tomáš; Masaryk University, Faculty of Science, Department of Botany and Zoology Petřík, Petr; The Czech Academy of Sciences, Department of GIS and Remote Sensing, Institute of Botany Phillips, Oliver; University of Leeds, School of Geography Prokhorov, Vadim; Kazanskij federal'nyj universitet, Institute of Environmental Sciences Rašomavičius, Valerijus; Gamtos tyrimr centras, Institute of Botany Revermann, Rasmus; University of Hamburg, Biodiversity, Ecology and Evolution of Plants, Institute for Plant Science & Microbiology Rodwell, John Ruprecht, Eszter; Babes-Bolyai University, Hungarian Department of Biology and Ecology, Faculty of Biology and Geology Rūsiņa, Solvita; University of Latvia, Department of Geography Samimi, Cyrus; University of Bayreuth, Climatology, Bayreuth Center of Ecology and Environmental Research (BayCEER) Schaminée, Joop; Alterra, Wageningen University and Research Centre Schmiedel, Ute; University of Hamburg, Biodiversity, Evolution and Ecology of Plants, Institute for Plant Science and Microbiology Šibík, Jozef; Plant Science and Biodiversity Centre Slovak Academy of Sciences, Institute of Botany Šilc, Urban; Research Centre of the Slovenian Academy of Sciences and Arts, Institute of Biology Škvorc, Željko; Faculty of Forestry, University of Zagreb, Smyth, Anita; University of Adelaide, TERN Sop , Tenekwetche; Max Planck Institute for Evolutionary Anthropology (MPI-EVA), Primatology; German Centre for Integrative Biodiversity Research (iDiv) Sopotlieva, Desislava; Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Department of Plant and Fungal Diversity and Resources Sparrow, Ben; University of Adelaide, TERN Stančić, Zvjezdana; University of Zagreb, Faculty of Geotechnical Engineering Svenning, Jens-Christian; Aarhus University, Center for Biodiversity Dynamics in a Changing World (BIOCHANGE) & Section for Ecoinformatics & Biodiversity, Department of Bioscience Swacha, Grzegorz; University of Wroclaw, Botanical Garden Tang, Zhiyao; Peking University, Dept. of Ecology, College of Urban and Environmental Sciences Tsiripidis, Ioannis; Aristolte University of Thessaloniki, School of Biology Turtureanu, Pavel Dan; Babeș-Bolyai University, A. Borza Botanical Garden Ugurlu, Emin; Bursa Teknik Universitesi, Forest Engineering Department, Faculty of Forestry Uogintas, Domas; Nature Research Centre, Institute of Botany Valachovič, Milan; Plant Science and Biodiversity Centre Slovak Academy of Sciences, Institute of Botany Vanselow, Kim; University of Erlangen-Nuremberg, Department of Geography Vashenyak, Yulia; Khmelnytskyi Institute of Interregional Academy of Personnel Management Vassilev, Kiril; Balgarska academija na naukite, Department of Plant and Fungal Diversity and Resources, Institute of Biodiversity and Ecosystem Research

	Vélez-Martin, Eduardo; Universidade Federal do Rio Grande do Sul, Department of Ecology Venanzoni, Roberto; Universita degli Studi di Perugia, Department of Chemistry, Biology and Biotechnology Vibrans, Alexander Christian; Universidade Regional de Blumenau, Departamento de Engenharia Florestal Violle, Cyrille; Universite Paul-Valery Montpellier, CNRS - Université de Montpellier, EPHE, Centre d'Ecologie Fonctionnelle et Evolutive (UMR5175) Virtanen, Risto; University of Oulu, Ecology and Genetics Research Unit, Biodiversity Unit; Helmholtz Center for Environmental Research - UFZ, Department of Physiological Diversity; German Centre for Integrative Biodiversity Research (iDiv) von Wehrden, Henrik; Leuphana Universitat Luneburg, Institute of Ecology Wagner, Viktoria; University of Alberta, Department of Biological Sciences Walker, Donald; University of Alaska Fairbanks, Institute of Arctic Biology Wana, Desalegn; Addis Ababa University, Department of Geography & Environmental Studies Weiher, Evan; University of Wisconsin - Eau Claire, Department of Biology Wesche, Karsten; Senckenberg Museum of Natural History, Botany; German Centre for Integrative Biodiversity Research (iDiv); Technische Universitat Dresden, International Institute Zittau Whitfeld, Timothy; Brown University, Department of Ecology and Evolutionary Biology, Brown University Herbarium Willner, Wolfgang; VINCA, Wiser, Susan; Manaaki Whenua - Landcare Research Wohlgemuth, Thomas ; Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Research Unit Forest Dynamics Yamalov, Sergey; Ufa Scientific Centre, Russian Academy of Sciences, Laboratory of Wild-Growing Flora, Botanical Garden-Institute Zizka, Georg; Senckenberg Research Institute Frankfurt, Department of Botany and molecular Evolution Zverev, Andrei; Tomskij gosudarstvennyj universitet, Department of Botany
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JVS-R-04700 Response letter

L549: Not sure this is the best reference, it is about bird occurrences in different sources and not about local communities nor about vegetation.

> We deleted the reference. Since this sentence states something that is missing, there is no need of using any reference here.

L560: But some species might be dormant (belowground organs only). Truly absent from the aboveground vegetation?

> We added the suggested specification

L563: Only if exact coordinates are known! In a way, GBIF occurrences are also spatially explicit and can be resurveyed.

> A significant proportion of sPlot plots have precise coordinates (see Fig. S2.2). We do not claim that all plots would allow exact relocalisation. We however added "many plots"

L566: For plots which has exact locations only! Do you have data how precise are coordinates?

> See above.

L567: This is also not unique to plots, you can sample a taxon from another trophic level from the very same point where a plant taxon has been recorded in gbif!

> We believe that a plot of a certain size can contain multiple taxa, but a point cannot. To clarify this, we now say "vegetation plots represent a snapshot of the primary producers of a terrestrial ecosystem"

L569a: This reference is about N and P concentration in leaves and roots in response to drought, elevated CO2, and fertilization. This is relevant to decomposers but no other trophic levels included to the study!

> We agree and have changed this reference.

L569b: I doubt that this is the best reference for multi trophic level sampling.

> Yes, the Bruelheide e al. (2018) reference was cited in the wrong place.

L591: If you will use only "species pool", many readers understand this as all plant species in the dataset, or perhaps in the whole Denmark. Use "site-specific species pool", or, since the absent portion of this is considered in the paper, you might consider calling this "dark diversity".

> Done – thanks for the suggestion

L596: current? (i.e. not LGM precipitation)?

> Actually it is current precipitation, which now has been added

L609: This depends on research question. If the aim is to find CWM for grid cell species composition, it is fine. If a such study aims to explain traits in local communities, there is likely a bias.

> Our sentence describes the likely biases of the approach used so far. We deleted the last sentence to avoid confusion.

Table 1a: You can also use just a single vegetation plot and get all measures what you have in the left column? Here listing additional information only?

We added the new line “to derive information on…” to clarify that our meaning is slightly different from what you understood. We hope that the table is clearer now.

Table 1b: Well, direct interaction of plant species has often demonstrated for very fine scales (comparable to plant size).

Admittedly, the larger plots in sPlot are probably not suited for this purpose, but one indeed needs plots.

Table 1c: Also depends on sampling intensity? If all vegetation types are well sampled, this can form local flora better than more random inventories.

We added a qualifier, but we believe that you will not find any grid in sPlot where it is really possible. We added sampling intensity here.

Table 1d: of the grid cell?

Now clarified by the second head line

Table 1e: + the grid cell (if sampling is intense enough). Even for habitat-specific species pools sampling need to be intense enough!

Yes, in principle you are right. But the aim of our table is not to describe all rare exceptions but the typical things that can or cannot be done with a database like sPlot. If we would add all rare exceptions, the table would get very long and uniformative, we believe.

Table 1f: Remove "I"

Done

Table 1g: and also dark diversity!

You are right, but dark diversity does not fit into the line with alpha, beta and gamma diversity, so we prefer not to add it here.

Table 1h: + frequency in the grid cell

Added, good point.

Table 1i: And also grid cell (if sampling intensity is enough).

See response on Table 1e.

L629: Since this is a Report, I suggest to replace traditional "Materials and Methods" and "Results" with more descriptive headings (e.g. "Compilation of the sPlot database", "General description of the sPlot data" or something similar)

Done

L638: Put the full stop after "S"

Done

L645: Why not visible?

Because the authors opted not to make this information public. Still we use GIVD as our tool for metadata.

L648: Use "S1"

Appendix 1 (different from Appendix S1) was a remainder from the original submission to GEB. GEB uses printed appendices to present references to data sources in small print in the main paper (which will be used by Web of Science etc.). Since JVS does not have such a separation into two reference lists, we included the references to the databases into the main reference list and dissolved Appendix 1. Please note that the sPlot Rules force us to print one reference per database if required by these, so there would be no way to transfer these references to an online-only appendix.

L658: Cite also Appendix (S2)

Done

L691: This function is using the same the Plant List web application?

Yes, the tpf function connects to the plant list website.

L795: Did not find the shape file!

We have uploaded the shapefile now as Appendix S 5

L857: Is it possible to assign a likely plot size for the rest (or range? or with uncertainty?)

No, unfortunately no plot size means that we have no information on it. However, one can assume that in each region of the world the plots without plot size information do not differ systematically in size from those where the information has been recorded in the database.

L872: Even if a single plot is in the 1-degree cell?

There are only a very few cells consisting on a single plot (n=142/2633). We provide this information now in the Caption of Fig. 4. This can also be seen from the maps in Figure 3 for plot density.

L914: I understand these rules. However, while keeping the advantage of having co-occurrence data, I strongly suggest that you will make occurrence data available through GBIF. You can discuss with GBIF how this can be done without revealing co-occurrence in plots (perhaps using a certain resolution of coordinates?)

Please note that the sPlot Rules do not allow this currently. The sPlot Steering Committee is fully aware of the strong potential sPlot would have for GBIF, but we would have to leave this to future developments of the sPlot Consortium and its rules.

We would also like to point out that since 2 years, GBIF can also handle co-occurrence data, using the Darwin core. For example, the vegetation plots of the Netherlands have been uploaded already. We believe that we should take time to discuss who will upload the data, to avoid multiple entries. We think that doing this should be the responsibility of the data base curators, as it would be also them to update these data.

L928: What about previous versions? If some data has withdrawn from a previous version, reproducibility is not functioning any more?

We keep all previous sPlot versions. sPlot Rules do not allow withdrawing data from already started projects. Our understanding is that this includes the right of sPlot to maintain the specific sPlot version used in a project for studies that aim at reproduction/testing this study.

L946: This is partly overlapping with Introduction and Table 1. Can this be combined?

We would like to keep this part because it explains “what to do with the data” while the Intro presents “why the data is necessary”. However, we agree that is makes sense to shorten this part and have removed some sections.

L984: This is not plot specific feature?

We believe that it is, see comment on L567

L1001: Is it possible to add few lines at which research questions these shortcomings are most critical, what can be done to minimize their effects?

Actually, L996-1001 already contained some core research questions that would suffer from such limitations and potential remedies. We have now expanded a little bit on that, but we generally believe that the limitations and the remedies are very case-specific and this report is not the appropriate place to elaborate in detail on them. Each of the ongoing sPlot paper projects, of course, unavoidably will have to address them.

L1002: What about BIEN? It was designed for Americas but include some other regions as well?

While BIEN indeed contains (few) plot data, they hitherto have only used the plot data to enrich their species occurrence data and they were not able to export the plot data in any meaningful way. sPlot had signed a MoU with BIEN that they should contribute their plot data, but after long trials they admitted that they are not able to do so and we got the majority of their plot data from their contributing databases, like VegBank, directly. Moreover, the amount of plot data and the spatial coverage of sPlot and BIEN are not comparable. While sPlot has perhaps 90% of the plots that are in BIEN, BIEN has only perhaps 10% of the plots of sPlot.

L1003: adding "relatively" Methods still vary a lot.

Done

L1005: BIEN?

See response to L1002

L1008: Strange to have alien species topic "In summary" paragraph without any prior mentioning. Can this be discussed above a bit?

Indeed, this was strange. We added this topic now already under point (1) of Expected Impact.

L1235: Please list all appendices with short titles.

Done

S2.1: It would be good to have some more information how this was assigned post hoc.

We have added this information. Post-hoc assignment of plot uncertainty was based on the number of decimal places of the given coordinates. We have added this information now.

TITLE PAGE

REPORT PAPER

sPlot – a new tool for global vegetation analyses

Helge Bruelheide[x,1,2], Jürgen Dengler[x,3,4,2], Borja Jiménez-Alfaro[x,5,1,2], Oliver Purschke[x,6], Stephan M. Hennekens[7], Milan Chytrý[8], Valério D. Pillar[9], Florian Jansen[10], Jens Kattge[11,2], Brody Sandel[12], Isabelle Aubin[13], Idoia Biurrun[14], Richard Field[15], Sylvia Haider[1], Ute Jandt[1], Jonathan Lenoir[16], Robert K. Peet[17], Gwendolyn Peyre[18], Francesco Maria Sabatini[1,2], Marco Schmidt[19], Franziska Schrodt[15], Marten Winter[2], Svetlana Aćić[20], Emiliano Agrillo[21], Miguel Alvarez[22], Didem Ambarlı[23], Pierangela Angelini[24], Iva Apostolova[25], Mohammed A.S. Arfin Khan[26,27], Elise Arnst[28], Fabio Attorre[21], Christopher Baraloto[29,30], Michael Beckmann[31], Christian Berg[32], Yves Bergeron[33], Erwin Bergmeier[34], Anne D. Bjorkman[35], Viktoria Bondareva[36], Peter Borchardt[37], Zoltán Botta-Dukát[38], Brad Boyle[39], Amy Breen[40], Henry Brisse[41], Chaeho Byun[42], Marcelo R. Cabido[43], Laura Casella[24], Luis Cayuela[44], Tomáš Černý[45], Victor Chepinoga[46], János Csiky[47], Michael Curran[48], Renata Ćušterevska[49], Zora Dajić Stevanović[20], Els De Bie[50], Patrice De Ruffray[51], Michele De Sanctis[21], Panayotis Dimopoulos[52], Stefan Dressler[53], Rasmus Ejrnæs[54], Mohamed Abd El-Rouf Mousa El-Sheikh[55,56], Brian Enquist[39], Jörg Ewald[57], Jaime Fagúndez[58], Manfred Finckh[59], Xavier Font[60], Estelle Forey[61], Georgios Fotiadis[62], Itziar García-Mijangos[14], André Luis de Gasper[63], Valentin Golub[36], Alvaro G. Gutierrez[64], Mohamed Z. Hatim[65], Tianhua He[66], Pedro Higuchi[67], Dana Holubová[8], Norbert Hölzel[68], Jürgen Homeier[69], Adrian Indreica[70], Deniz Işık Gürsoy[71], Steven Jansen[72], John Janssen[7], Birgit Jedrzejek[68], Martin Jiroušek[8,73], Norbert Jürgens[59], Zygmunt Kącki[74], Ali Kavgacı[75], Elizabeth Kearsley[76], Michael Kessler[77], Ilona Knollová[8], Vitaliy Kolomiychuk[78], Andrey Korolyuk[79], Maria Kozhevnikova[80], Łukasz Kozub[81], Daniel Krstonošić[82], Hjalmar Kühl[83,2], Ingolf Kühn[84,1,2], Anna Kuzemko[85], Filip Küzmič[86], Flavia Landucci[8], Michael T. Lee[87], Aurora Levesley[88], Ching-Feng Li[89], Hongyan Liu[90], Gabriela Lopez-Gonzalez[88], Tatiana Lysenko[91], Armin Macanović[92], Parastoo Mahdavi[93], Peter Manning[94], Corrado Marcenò[14], Vassiliy Martynenko[95], Maurizio Mencuccini[96], Vanessa Minden[97], Jesper Erenskjold Moeslund[54], Marco Moretti[98], Jonas V. Müller[99], Jérôme Munzinger[100], Ülo Niinemets[101], Marcin Nobis[102], Jalil Noroozi[103], Arkadiusz Nowak[104], Viktor Onyshchenko[85], Gerhard E. Overbeck[9], Wim A. Ozinga[105], Anibal Pauchard[106], Hristo Pedashenko[107], Josep Peñuelas[108,109], Aaron Pérez-Haase[110,111], Tomáš Peterka[8], Petr Petřík[112], Oliver L. Phillips[88], Vadim Prokhorov[80], Valerijus Rašomavičius[113], Rasmus Revermann[59], John Rodwell[114], Eszter Ruprecht[115], Solvita Rūsiņa[116], Cyrus Samimi[117], Joop H.J. Schaminée[7], Ute Schmiedel[59], Jozef Šibík[118], Urban Šilc[86], Željko Škvorc[82], Anita Smyth[119], Tenekwetche Sop[83,2], Desislava Sopotlieva[25], Ben Sparrow[119], Zvjezdana Stančić[120], Jens-Christian Svenning[35], Grzegorz Swacha[74], Zhiyao Tang[90], Ioannis Tsiripidis[121], Pavel Dan Turtureanu[122], Emin Ugurlu[123], Domas Uogintas[113], Milan Valachovič[118], Kim André Vanselow[124], Yulia Vashenyak[125], Kiril Vassilev[25], Eduardo Vélez-Martin[9], Roberto Venanzoni[126], Alexander Christian Vibrans[127], Cyrille Violle[128], Risto Virtanen[129,130,2], Henrik von Wehrden[131], Viktoria Wagner[132], Donald A. Walker[133], Desalegn Wana[134], Evan Weiher[135], Karsten Wesche[136,2,137], Timothy Whitfeld[138], Wolfgang Willner[139], Susan Wiser[28], Thomas Wohlgemuth[140], Sergey Yamalov[141], Georg Zizka[53], Andrei Zverev[142]

[x] Helge Bruelheide, Jürgen Dengler, Borja Jiménez-Alfaro and Oliver Purschke should be considered joint first authors

AFFILIATIONS

[1]Institute of Biology / Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle, Germany

[2]German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany

[3]Vegetation Ecology Group, Institute of Natural Resource Sciences (IUNR), Zurich University of Applied Sciences (ZHAW), Wädenswil, Switzerland

[4]Plant Ecology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany

[5]Research Unit of Biodiversity (CSUC/UO/PA), University of Oviedo, Mieres, Spain

[6]Leipzig, Germany

[7]Wageningen Environmental Research (Alterra), Wageningen University and Research, Wageningen, Netherlands

[8]Department of Botany and Zoology, Masaryk University, Brno, Czech Republic

[9]Department of Ecology, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil

[10]Faculty of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany

[11]Max Planck Institute for Biogeochemistry, Jena, Germany

[12]Department of Biology, Santa Clara University, Santa Clara, CA, United States

[13]Great Lakes Forestry Centre, Canadian Forest Service, Natural Resources Canada, Sault Ste Marie (Ontario), Canada

[14]Plant Biology and Ecology, University of the Basque Country UPV/EHU, Bilbao, Spain

[15]School of Geography, University of Nottingham, Nottingham, United Kingdom

[16]Ecologie et Dynamiques des Systèmes Anthropisés (EDYSAN, UMR 7058 CNRS-UPJV), Université de Picardie Jules Verne, Amiens, France

[17]Department of Biology, University of North Carolina, Chapel Hill, NC, United States

[18]Department of Civil and Environmental Engineering, University of the Andes, Bogota, Colombia

[19]Data and Modelling Centre, Senckenberg Biodiversity and Climate Research Centre (BiK-F), Frankfurt am Main, Germany

[20]Department of Agrobotany, Faculty of Agriculture, Belgrade-Zemun, Serbia

[21]Department of Environmental Biology, "Sapienza" University of Rome, Rome, Italy

[22]Plant Nutrition, INRES, University of Bonn, Bonn, Germany

[23]Department of Agricultural Biotechnology, Faculty of Agriculture and Natural Sciences, Düzce University, Düzce, Turkey

[24]Biodiversity Conservation Department, ISPRA - Italian National Institute for Environmental Protection and Research, Rome, Italy

[25]Department of Plant and Fungal Diversity and Resources, Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria

[26]Forestry & Environmental Science, Shahjalal University of Science & Technology, Sylhet, Bangladesh

[27]Disturbance Ecology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany

[28]Manaaki Whenua -- Landcare Research, Lincoln, New Zealand

[29]International Center for Tropical Botany (ICTB), The Kampong of the National Tropical Botanical Garden, Coconut Grove, Florida, United States

[30]Department of Biological Sciences, Florida International University, Miami, Florida, United States

[31]Landscape Ecology, Helmholtz Centre for Environmental Research - UFZ, Leipzig, Germany

[32]Botanical Garden, University of Graz, Graz, Austria

[33]Forest Research Institute, Université du Québec en Abitibi-Témiscamingue , Rouyn-Noranda, Canada

[34]Vegetation Ecology and Phytodiversity, University of Göttingen, Göttingen, Germany

[35]Center for Biodiversity Dynamics in a Changing World (BIOCHANGE) & Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Aarhus C, Denmark

[36]Laboratory of Phytocoenology, Institute of Ecology of the Volga River Basin, Toljatty , Russian Federation

[37]Institute of Geography, CEN - Center for Earth System Research and Sustainability, University of Hamburg, Hamburg, Germany

[38]Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary

[39]Ecology and Evolutionary Biology, University of Arizona, Tucson, United States

[40]International Arctic Research Center, University of Alaska, Fairbanks, United States

[41]Faculté des Sciences, MEP, Marseille cedex 20, France

[42]School of Civil and Environmental Engineering, Yonsei University, Seoul, South Korea

[43]Multidisciplinary Institute for Plant Biology (IMBIV - CONICET), University of Cordoba - CONICET, Cordoba, Argentina

[44]Department of Biology, Geology, Physics and Inorganic Chemistry, Universidad Rey Juan Carlos, Móstoles, Spain

[45]Department of Forest Ecology, Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Praha 6 - Suchdol, Czech Republic

[46]Laboratory of Physical Geography and Biogeography, V.B. Sochava Insitute of Geography SB RAS, Irkutsk, Russian Federation

[47]Department of Ecology, University of Pécs, Pécs, Hungary

[48]Institute of Environmental Engineering, Swiss Federal Institute of Technology (ETH) Zürich, Zürich, Switzerland

[49]Institute of Biology, Faculty of Natural Sciences and Mathematics, Skopje, Republic of Macedonia

[50]Departement of Biodiversity and Natural Environment, Research Institute for Nature and Forest (INBO), Brussels, Belgium

[51]IBMP, Strasburg, France

[52]Institute of Botany, Division of Plant Biology, Department of Biology, University of Patras, Patras, Greece

[53]Dept. Botany and Molecular Evolution, Senckenberg Research Institute, Frankfurt am Main, Germany

[54]Department of Bioscience, Aarhus University, Roende, Denmark

[55]Botany and Microbiology Department, College of Science, King Saud University, Riyadh, Saudi Arabia

[56]Botany Department, Faculty of Science, Damanhour University, Damanhour, Egypt

[57]Hochschule Weihenstephan-Triesdorf, University of Applied Sciences, Freising, Germany

[58]Faculty of Science, University of A Coruña, A Coruña, Spain

[59]Biodiversity, Ecology and Evolution of Plants, Institute for Plant Science & Microbiology, University of Hamburg, Hamburg, Germany

[60]Plant Biodiversity Resource Centre, University of Barcelona, Barcelona, Spain

[61]Laboratoire Ecodiv, EA 1293 URA IRSTEA, Normandie University, Mont-Saint-Aignan, France

[62]Department of Forestry & Natural Environment Management, TEI of Sterea Ellada, Karpenissi, Greece

[63]Departament of Natural Science, Regional University of Blumenau, Blumenau, Brazil

[64]Departamento de Ciencias Ambientales y Recursos Naturales Renovables, Facultad de Ciencias Agronomicas, Universidad de Chile, Santiago, Chile

[65]Botany, Faculty of Science, Tanta University, Tanta, Egypt

[66]School of Molecular and Life Sicences, Curtin University, Bentley, WA, Australia

[67]Forestry Department, Santa Catarina State University, Lages, Brazil

[68]Institute of Landscape Ecology, University of Münster, Münster, Germany

[69]Plant Ecology and Ecosystems Research, University of Göttingen, Göttingen, Germany

[70]Department of Silviculture, Transilvania University of Brasov, Brasov, Romania

[71]Department of Biology, Celal Bayar University, Manisa, Turkey

[72]Institute of Systematic Botany and Ecology, Ulm University, Ulm, Germany

[73]Department of Plant Biology, Mendel University in Brno, Brno, Czech Republic

[74]Botanical Garden, University of Wrocław, Wrocław, Poland

[75]Silviculture and Forest Botany, Soutwest Anatolia Forest Research Institute, Antalya, Turkey

[76]Department of Environment, Ghent University, Gent, Belgium

[77]Department of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland

[78]O.V. Fomin Botanical Garden, Taras Shevchenko National University of Kyiv, Kyiv, Ukraine

[79]Geosystem Laboratory, Central Siberian Botanical Garden, Siberian Branch, Russian Academy of Sciences , Novosibirsk, Russian Federation

[80]Institute of Environmental Sciences, Kazan Federal University, Kazan, Russian Federation

[81]Department of Plant Ecology and Environmental Conservation, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Warsaw, Poland

[82]Faculty of Forestry, University of Zagreb, Zagreb, Croatia

[83]Primatology, Max Planck Institute for Evolutionary Anthropology (MPI-EVA, Leipzig, Germany)

[84]Dept. Community Ecology, Helmholtz Centre for Environmental Research - UFZ, Halle, Germany

[85]M.G. Kholodny Institute of Botany, National Academy of Sciences of Ukraine, Kyiv, Ukraine

[86]Institute of Biology, Research Centre of Slovenian Academy of Sciences and Arts (ZRC SAZU), Ljubljana, Slovenia

[87]NatureServe, Durham, United States

[88]School of Geography, University of Leeds, Leeds, United Kingdom

[89]School of Forestry and Resource Conservation, National Taiwan University, Hsinchu, Taiwan

[90]College of Urban and Environmental Sciences, Peking University, Beijing, China

[91]Dept. of the Phytodiversity Problems, Institute of Ecology of the Volga River Basin RAS, Togliatti, Russian Federation

[92]Center for Ecology and Natural Resources - Academician Sulejman Redžić, Department of Biology, University of Sarajevo, Sarajevo, Bosnia and Herzegovina

[93]Research Group Vegetation Science & Nature Conservation, Dept. of Ecology and Environmental Science, Carl von Ossietzky-University Oldenburg, Oldenburg, Germany

[94]Project Group Causes and Consequences of Climate Change, Senckenberg Research Institute, Frankfurt am Main, Germany

[95]Ufa Institute of Biology of Ufa Federal Scientific Centre of the Russian Academy of Sciences, Ufa, Russian Federation

[96]Centre Research Ecology and Forestry Applications (CREAF), ICREA, Barcelona, Spain

[97]Institute of Biology an Environmental Sciences, Carl von Ossietzky-University Oldenburg, Oldenburg, Germany

[98]Biodiversity and Conservation Biology, Swiss Federal Research Institute WSL, Birmensdorf, Switzerland

[99]Conservation Science, Royal Botanic Gardens, Kew, Ardingly, West Sussex, United Kingdom

[100]AMAP - Botany and Modelling of Plant Architecture and Vegetation, IRD, CIRAD, CNRS, INRA, Université Montpellier, Montpellier, France

[101]Chair of Crop Science and Plant Biology, Estonian University of Life Sciences, Tartu, Estonia

[102]Institute of Botany, Jagiellonian University, Kraków, Poland

[103]Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria

[104]Botanical Garden - Center for Biological Diversity Conservation, Polish Academy of Sciences, Warszawa, Poland

[105]Team Vegetation, Forest and Landscape Ecology, Wageningen Environmental Research, Wageningen, Netherlands

[106]Laboratorio de Invasiones Biológicas (LIB), University of Concepción, Concepción, Chile

[107]Amsterdam, Netherlands

[108]Global Ecology Unit CREAF-CSIC-UAB, CSIC, Bellaterra, Spain

[109]CREAF, Cerdanyola del Vallès, Spain

[110]Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain

[111]Continental Ecology, Center for Advanced Studies of Blanes, Spanish Research Council (CEAB-CSIC), Blanes, Girona, Spain

[112]Department of GIS and Remote Sensing, Institute of Botany, The Czech Academy of Sciences, Průhonice, Czech Republic

[113]Institute of Botany, Nature Research Centre, Vilnius, Lithuania

[114]Lancaster, United Kingdom

[115]Hungarian Department of Biology and Ecology, Faculty of Biology and Geology, Babeș-Bolyai University, Cluj-Napoca, Romania

[116]Department of Geography, University of Latvia, Riga, Latvia

[117]Climatology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany

[118]Institute of Botany, Plant Science and Biodiversity Centre Slovak Academy of Sciences, Bratislava, Slovakia

[119]TERN, University of Adelaide, Adelaide, Australia

[120]Faculty of Geotechnical Engineering, University of Zagreb, Varaždin, Croatia

[121]School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece

[122]A. Borza Botanical Garden, Babeș-Bolyai University, Cluj-Napoca, Romania

[123]Forest Engineering Department, Faculty of Forestry, Bursa Technical University, Yıldırım, Bursa, Turkey

[124]Department of Geography, University of Erlangen-Nuremberg, Erlangen, Germany

[125]Khmelnytskyi Institute of Interregional Academy of Personnel Management, Khmelnytskyi, Ukraine

[126]Department of Chemistry, Biology and Biotechnology, University of Perugia, Perugia, Italy

[127]Departamento de Engenharia Florestal, Universidade Regional de Blumenau, Blumenau, Brazil

[128]Centre d'Ecologie Fonctionnelle et Evolutive (UMR5175), CNRS - Université de Montpellier - Université Paul-Valéry Montpellier - EPHE, Montpellier, France

[129]Ecology and Genetics Research Unit, Biodiversity Unit, University of Oulu, Oulu, Finland

[130]Department of Physiological Diversity, Helmholtz Center for Environmental Research - UFZ, Leipzig, Germany

[131]Institute of Ecology, Leuphana University of Lüneburg, Lüneburg, Germany

[132]Department of Biological Sciences, University of Alberta, Edmonton, Canada

[133]Institute of Arctic Biology, University of Alaska, Fairbanks, United States

[134]Department of Geography & Environmental Studies, Addis Ababa University, Addis Ababa, Ethiopia

[135]Department of Biology, University of Wisconsin - Eau Claire, Eau Claire, WI, United States

[136]Botany Department, Senckenberg Museum of Natural History Görlitz, Görlitz, Germany

[137]International Institute Zittau, Technische Universität Dresden, Zittau, Germany

[138]Department of Ecology and Evolutionary Biology/Brown University Herbarium, Brown University, Providence, United States

[139]Vienna Institute for Nature Conservation & Analyses, Vienna, Austria

[140]Research Unit Forest Dynamics, Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland

[141]Laboratory of Wild-Growing Flora, Botanical Garden-Institute, Ufa Scientific Centre, Russian Academy of Sciences, Ufa, Russian Federation

[142]Department of Botany, Tomsk State University, Tomsk, Russian Federation

Correspondence:

Helge Bruelheide, Institute of Biology / Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Am Kirchtor 1, 06108 Halle, Germany

Email: helge.bruelheide@botanik.uni-halle.de

ORCID:

Helge Bruelheide http://orcid.org/0000-0003-3135-0356

Jürgen Dengler http://orcid.org/0000-0003-3221-660X

Borja Jiménez-Alfaro http://orcid.org/0000-0001-6601-9597

Oliver Purschke http://orcid.org/0000-0003-0444-0882

Milan Chytrý http://orcid.org/0000-0002-8122-3075

Valério D. Pillar http://orcid.org/0000-0001-6408-2891

Jens Kattge http://orcid.org/0000-0002-1022-8469

Idoia Biurrun http://orcid.org/0000-0002-1454-0433

Richard Field http://orcid.org/0000-0003-2613-2688

Jonathan Lenoir http://orcid.org/0000-0003-0638-9582

Francesco M. Sabatini http://orcid.org/0000-0002-7202-7697

Marco Schmidt http://orcid.org/0000-0001-6087-6117

Franziska Schrodt http://orcid.org/0000-0001-9053-8872

Emiliano Agrillo http://orcid.org/0000-0003-2346-8346

Miguel Alvarez http://orcid.org/0000-0003-1500-1834
Pierangela Angelini http://orcid.org/0000-0002-5321-9757
Mohammed A.S. Arfin Khan http://orcid.org/0000-0001-6275-7023
Fabio Attorre http://orcid.org/0000-0002-7744-2195
Michael Beckmann http://orcid.org/0000-0002-5678-265X
Yves Bergeron http://orcid.org/0000-0003-3707-3687
Erwin Bergmeier http://orcid.org/0000-0002-6118-4611
Zoltán Botta-Dukát http://orcid.org/0000-0002-9544-3474
Chaeho Byun http://orcid.org/0000-0003-3209-3275
Laura Casella http://orcid.org/0000-0003-2550-3010
Luis Cayuela http://orcid.org/0000-0003-3562-2662
Victor Chepinoga http://orcid.org/0000-0003-3809-7453
Michele De Sanctis http://orcid.org/0000-0002-7280-6199
Jaime Fagúndez http://orcid.org/0000-0001-6605-7278
Xavier Font http://orcid.org/0000-0002-7253-8905
Estelle Forey http://orcid.org/0000-0001-6082-3023
André Luis de Gasper http://orcid.org/0000-0002-1940-9581
Alvaro G. Gutierrez http://orcid.org/0000-0001-8928-3198
Tianhua He http://orcid.org/0000-0002-0924-3637
Pedro Higuchi http://orcid.org/0000-0002-3855-555X
Norbert Hölzel http://orcid.org/0000-0002-6367-3400
Steven Jansen http://orcid.org/0000-0002-4476-5334
Martin Jiroušek http://orcid.org/0000-0002-4293-478X
Norbert Jürgens http://orcid.org/0000-0003-3211-0549

Ali Kavgacı http://orcid.org/0000-0002-4549-3668

Elizabeth Kearsley http://orcid.org/0000-0003-0046-3606

Michael Kessler http://orcid.org/0000-0003-4612-9937

Ingolf Kühn http://orcid.org/0000-0003-1691-8249

Flavia Landucci http://orcid.org/0000-0002-6848-0384

Ching-Feng Li http://orcid.org/0000-0003-0744-490X

Peter Manning http://orcid.org/0000-0002-7940-2023

Corrado Marcenò http://orcid.org/0000-0003-4361-5200

Maurizio Mencuccini http://orcid.org/0000-0003-0840-1477

Vanessa Minden http://orcid.org/0000-0002-4933-5931

Jesper Erenskjold Moeslund http://orcid.org/0000-0001-8591-7149

Marco Moretti http://orcid.org/0000-0002-5845-3198

Jérôme Munzinger http://orcid.org/0000-0001-5300-2702

Ülo Niinemets http://orcid.org/0000-0002-3078-2192

Arkadiusz Nowak http://orcid.org/0000-0001-8638-0208

Gerhard E. Overbeck http://orcid.org/0000-0002-8716-5136

Wim A. Ozinga http://orcid.org/0000-0002-6369-7859

Hristo Pedashenko http://orcid.org/0000-0002-6743-0625

Josep Penuelas http://orcid.org/0000-0002-7215-0150

Aaron Pérez-Haase http://orcid.org/0000-0002-5974-7374

Petr Petřík http://orcid.org/0000-0001-8518-6737

Oliver L. Phillips http://orcid.org/0000-0002-8993-6168

Jozef Šibík http://orcid.org/0000-0002-5949-862X

Urban Šilc http://orcid.org/0000-0002-3052-699X

Jens-Christian Svenning http://orcid.org/0000-0002-3415-0862

Emin Ugurlu http://orcid.org/0000-0003-0824-1426

Eduardo Vélez-Martin http://orcid.org/0000-0001-8028-8953

Roberto Venanzoni http://orcid.org/0000-0002-7768-0468

Risto Virtanen http://orcid.org/0000-0002-8295-8217

Evan Weiher http://orcid.org/0000-0002-5375-9964

Susan Wiser http://orcid.org/0000-0002-8938-8181

email:

Helge Bruelheide: helge.bruelheide@botanik.uni-halle.de

Jürgen Dengler: juergen.dengler@uni-bayreuth.de

Borja Jiménez-Alfaro: jimenezalfaro.borja@gmail.com

Oliver Purschke: oliverpurschke@web.de

Stephan M. Hennekens: stephan.hennekens@wur.nl

Milan Chytrý: chytry@sci.muni.cz

Valério De Patta Pillar: vpillar@ufrgs.br

Florian Jansen: florian.jansen@uni-rostock.de

Jens Kattge: jkattge@bgc-jena.mpg.de

Brody Sandel: bsandel@scu.edu

Marten Winter: marten.winter@idiv.de

Isabelle Aubin: isabelle.aubin@canada.ca

Idoia Biurrun: idoia.biurrun@ehu.es

Richard Field: Richard.Field@nottingham.ac.uk

Sylvia Haider: sylvia.haider@botanik.uni-halle.de

Ute Jandt: ute.jandt@botanik.uni-halle.de

Jonathan Lenoir: jonathan.lenoir@u-picardie.fr
Robert K. Peet: peet@unc.edu
Gwendolyn Peyre: gf.peyre@uniandes.edu.co
Francesco M. Sabatini: francesco.maria.sabatini@botanik.uni-halle.de
Marco Schmidt: marco.schmidt@stadt-frankfurt.de
Franziska Schrodt: f.i.schrodt@gmail.com
Svetlana Aćić: acic@agrif.bg.ac.rs
Emiliano Agrillo: emiliano.agrillo@uniroma1.it
Miguel Alvarez: malvarez@uni-bonn.de
Didem Ambarlı: didemambarli@duzce.edu.tr
Pierangela Angelini: pierangela.angelini@isprambiente.it
Iva Apostolova: iva.apostolova@gmail.com
Mohammed A.S. Arfin Khan: nobelarfin@yahoo.com
Elise Arnst: arnste@landcareresearch.co.nz
Fabio Attorre: fabio.attorre@uniroma1.it
Christian Berg: christian.berg@uni-graz.at
Yves Bergeron: yves.bergeron@uqat.ca
Erwin Bergmeier: erwin.bergmeier@bio.uni-goettingen.de
Anne D. Bjorkman: annebj@gmail.com
Viktoria Bondareva: bondarevavictoria@yandex.ru
Peter Borchardt: pbo1@gmx.de
Zoltán Botta-Dukát: botta-dukat.zoltan@okologia.mta.hu
Brad Boyle: bboyle@email.arizona.edu
Amy Breen: albreen@alaska.edu
Henry Brisse: brisse.henry@orange.fr
Marcelo R. Cabido: mcabido@imbiv.unc.edu.ar

Laura Casella: laura.casella@isprambiente.it

Luis Cayuela: luis.cayuela@urjc.es

Tomáš Černý: cernyt@fld.czu.cz

Victor Chepinoga: victor.chepinoga@gmail.com

János Csiky: moon@ttk.pte.hu

Michael Curran: currmi01@gmail.com

Renata Ćušterevska: renatapmf@yahoo.com

Zora Dajić Stevanović: dajic@agrif.bg.ac.rs

Els De Bie: els.debie@inbo.be

Patrice De Ruffray: patrice.de-ruffray@wanadoo.fr

Michele De Sanctis: michedes@gmail.com

Panayotis Dimopoulos: pdimopoulos@upatras.gr

Stefan Dressler: stefan.dressler@senckenberg.de

Rasmus Ejrnæs: rasmus@bios.au.dk

Mohamed Abd El-Rouf Mousa El-Sheikh: el_sheikh_eg@yahoo.co.uk

Brian Enquist: benquist@email.arizona.edu

Jörg Ewald: joerg.ewald@hswt.de

Manfred Finckh: manfred.finckh@uni-hamburg.de

Xavier Font: xfont@ub.edu

Georgios Fotiadis: gfotiad95@gmail.com

Itziar García-Mijangos: itziar.garcia@ehu.es

André Luis de Gasper: algasper@furb.br

Valentin Golub: vbgolub2000@mail.ru

Alvaro G. Gutierrez: bosqueciencia@gmail.com

Mohamed Z. Hatim: mohamed.zakaria@science.tanta.edu.eg

Norbert Hölzel: nhoelzel@uni-muenster.de

Dana Holubová: danmich@sci.muni.cz
Jürgen Homeier: jhomeie@gwdg.de
Adrian Indreica: adrianindreica@unitbv.ro
Deniz Işık Gürsoy: biodeniz-04@hotmail.com
John Janssen: john.janssen@wur.nl
Birgit Jedrzejek: siegb@uni-muenster.de
Martin Jiroušek: machozrut@mail.muni.cz
Norbert Jürgens: norbert.juergens@uni-hamburg.de
Zygmunt Kącki: zygmunt.kacki@uwr.edu.pl
Ali Kavgacı: alikavgaci1977@yahoo.com
Elizabeth Kearsley: elizabeth.kearsley@ugent.be
Michael Kessler: michael.kessler@systbot.uzh.ch
Ilona Knollová: ikuzel@sci.muni.cz
Vitaliy Kolomiychuk: vkolomiychuk@ukr.net
Andrey Korolyuk: akorolyuk@rambler.ru
Maria Kozhevnikova: mania_kazan@mail.ru
Łukasz Kozub: kozub.lukasz@gmail.com
Daniel Krstonošić: dkrstonosic@sumfak.hr
Hjalmar Kühl: kuehl@eva.mpg.de
Anna Kuzemko: anyameadow.ak@gmail.com
Filip Küzmič: filip.kuzmic@zrc-sazu.si
Flavia Landucci: flavia.landucci@gmail.com
Michael T. Lee: michael_lee@natureserve.org
Aurora Levesley: a.levesley@leeds.ac.uk
Ching-Feng Li: chingfeng.li@gmail.com
Hongyan Liu: lhy@urban.pku.edu.cn

Gabriela Lopez-Gonzalez: g.lopez-gonzalez@leeds.ac.uk

Tatiana Lysenko: ltm2000@mail.ru

Parastoo Mahdavi: parastoo.mahdavi@uni-oldenburg.de

Armin Macanović: arminecology@gmail.com

Corrado Marcenò: marceno.corrado@ehu.eus

Vassiliy Martynenko: vasmar@anrb.ru

Jesper Erenskjold Moeslund: jesper.moeslund@bios.au.dk

Jonas V. Müller: j.mueller@kew.org

Jérôme Munzinger: jerome.munzinger@ird.fr

Marcin Nobis: m.nobis@uj.edu.pl

Jalil Noroozi: noroozi.jalil@gmail.com

Arkadiusz Nowak: anowak@uni.opole.pl

Viktor Onyshchenko: labzap@ukr.net

Gerhard E. Overbeck: gerhard.overbeck@ufrgs.br

Anibal Pauchard: pauchard@udec.cl

Hristo Pedashenko: hristo_pedashenko@yahoo.com

Aaron Pérez-Haase: aaronperez@ub.edu

Tomáš Peterka: peterkatomasek@seznam.cz

Petr Petřík: petr.petrik@ibot.cas.cz

Oliver L. Phillips: o.phillips@leeds.ac.uk

Vadim Prokhorov: vadim.prokhorov@gmail.com

Valerijus Rašomavičius: valerijus.rasomavicius@botanika.lt

Rasmus Revermann: rasmus.revermann@gmail.com

John Rodwell: johnrodwell@tiscali.co.uk

Eszter Ruprecht: eszter.ruprecht@ubbcluj.ro

Solvita Rūsiņa: rusina@lu.lv

Cyrus Samimi: cyrus.samimi@uni-bayreuth.de

Joop H.J. Schaminée: joop.schaminee@wur.nl

Ute Schmiedel: ute.schmiedel@uni-hamburg.de

Jozef Šibík: jozef.sibik@savba.sk

Urban Šilc: urban@zrc-sazu.si

Željko Škvorc: skvorc@sumfak.hr

Anita Smyth: anita.smyth@adelaide.edu.au

Tenekwetche Sop : tenekwetche_sop@eva.mpg.de

Desislava Sopotlieva: desislava.sopotlieva@iber.bas.bg

Ben Sparrow: ben.sparrow@adelaide.edu.au

Zvjezdana Stančić: zvjezdana.stancic@gfv.hr

Jens-Christian Svenning: svenning@bios.au.dk

Grzegorz Swacha: gswacha@gmail.com

Zhiyao Tang: zytang@urban.pku.edu.cn

Ioannis Tsiripidis: tsiripid@bio.auth.gr

Pavel Dan Turtureanu: turtureanudan@gmail.com

Emin Ugurlu: emin.ugurlu@btu.edu.tr

Domas Uogintas: domas.uogintas@botanika.lt

Milan Valachovič: milan.valachovic@savba.sk

Kim André Vanselow: kim.vanselow@fau.de

Yulia Vashenyak: vasheniyak@mail.ru

Kiril Vassilev : kiril5914@abv.bg

Eduardo Vélez-Martin: velezedu@portoweb.com.br

Roberto Venanzoni: roberto.venanzoni@unipg.it

Alexander Christian Vibrans: acv@furb.br

Cyrille Violle: cyrille.violle@cefe.cnrs.fr

Risto Virtanen: risto.virtanen@oulu.fi
Henrik von Wehrden: henrik.von_wehrden@leuphana.de
Viktoria Wagner: viktoria.wagner@ualberta.ca
Donald A. Walker: dawalker@alaska.edu
Desalegn Wana: deswana2002@yahoo.com
Karsten Wesche: karsten.wesche@senckenberg.de
Timothy Whitfeld: timothy_whitfeld@brown.edu
Wolfgang Willner: wolfgang.willner@vinca.at
Susan Wiser: wisers@landcareresearch.co.nz
Thomas Wohlgemuth: thomas.wohlgemuth@wsl.ch
Sergey Yamalov: yamalovsm@mail.ru
Georg Zizka: georg.zizka@senckenberg.de
Andrei Zverev: ibiss@rambler.ru

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AUTHOR CONTRIBUTIONS

H.Bru. had the original idea and led the consortium from the start, while O.Pu. and J.D. coordinated the sPlot workshops. J.D., S.M.H. and U.J. compiled the databases to be included in sPlot. J.D. and later B.J.-A. and F.M.S. coordinated the network and the database. O.P. prepared the taxonomic and phylogenetic data. S.M.H programmed the Turboveg software. B.Sa., F.J., H.Bru., J.D., J.K., M.Ch., and V.D.P. organized the network in the Steering Committee. B.J.-A. and H.Bru. led the writing together with J.D. and input from S.M.H., O.Pu., M.Ch., F.J., J.K., V.D.P., B.Sa., I.Au., I.B., R.K.P., R.F., S.H., U.J., J.L., G.P., F.M.S., M.S., F.S. and M.W. The rest of authors (ordered alphabetically) contributed the plot and trait data. All authors agreed with the final manuscript.

BIOSKETCH

sPlot is a consortium established during three workshops held at the German Centre of Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig. The consortium currently comprises 110 member databases, two data aggregators and 43 personal members, including plant ecologists, biogeographers, field botanists and data analysts. More information about the consortium and its projects can be accessed at www.idiv.de/splot.

SHORT RUNNING TITLE

sPlot – the global vegetation database

ABSTRACT

Questions: Vegetation-plot records provide information on presence and cover or abundance of plants co-occurring in the same community. Vegetation-plot data are spread across research groups, environmental agencies and biodiversity research centers, and thus, are rarely accessible at continental or global scales. Here we present the sPlot database, which collates vegetation plots worldwide to allow for the exploration of global patterns in taxonomic, functional and phylogenetic diversity at the plant community level.

Location: sPlot version 2.1 contains records from 1,121,244 vegetation plots, which comprise 23,586,216 records of plant species and their relative cover or abundance in plots collected between 1885 and 2015.

Methods: We complemented the information for each plot by retrieving environmental conditions (i.e. climate and soil) and the biogeographic context (i.e. biomes) from external sources, and by calculating community-weighted means and variances of traits using gap-filled data from the global plant trait database TRY. Moreover, we created a phylogenetic tree for 50,167 out of the 54,519 species identified in the plots.

Results: We present the first maps of global patterns of community richness and community-weighted means of key traits.

Conclusions: The availability of vegetation plot data in sPlot offers new avenues for vegetation analysis at the global scale.

KEYWORDS

Biodiversity; community ecology; ecoinformatics; functional diversity; global scale; macroecology; phylogenetic diversity; plot database; sPlot; taxonomic diversity; vascular plant; vegetation relevé.

INTRODUCTION

Studying global biodiversity patterns is at the core of macroecological research (Kreft & Jetz, 2007; Wiens, 2011; Costello, Wilson & Houlding, 2012), since their exploration may provide insights into the ecological and evolutionary processes acting at different spatio-temporal scales (Ricklefs, 2004). The opportunities enabled by the compilation of large collections of biodiversity data into widely accessible global (GBIF, www.gbif.org) or continental databases (e.g. BIEN, www.bien.nceas.ucsb.edu/bien) have recently advanced our understanding of global biodiversity patterns, especially for vertebrates, but also for vascular plants (Swenson et al., 2012; Lamanna et al., 2014; Engemann et al., 2016; Butler et al., 2017). Although this development has led to the formulation of several macroecological theories (Currie et al., 2004; Pärtel, Bennett & Zobel, 2016), a more mechanistic understanding of how assembly processes shape ecological communities and consequently global biodiversity patterns, is still missing (Lessard, Belmaker, Myers, Chase & Rahbek, 2012).

Understanding the links between biodiversity patterns and assembly processes requires fine-grain data on the co-occurrence of species in ecological communities, sampled across continental or global spatial extents (Beck et al., 2012; Wisz et al., 2013). For example, such co-occurrence data have been used to compare changes in vegetation composition over time spans of decades (Jandt, von Wehrden & Bruelheide 2011; Perring et al. 2018). Unfortunately, information on fine-grain vegetation data up to now has not been readily available, as most of the continental to global biodiversity datasets have been derived from occurrence data (i.e. presence-only data), and after being aggregated spatially, have a relatively coarse-grain scale (e.g. 1-degree grid cells) and no information on species co-occurrence at the meaningful scale of local communities. In contrast, vegetation-plot data record the cover or abundance of each plant species that occurs in a plot of a given size at the date of the survey, representing the main reservoir of plant community data worldwide (Dengler et al., 2011).

Vegetation-plot data differ in fundamental ways from databases of occurrence records of individual species aggregated at the level of grid cells or regions of hundreds or thousands of square kilometers (**Figure 1**). First, vegetation plots usually provide information on species relative cover or relative abundance, allowing for the testing of central theories of biogeography, such as the abundance-range size relationship (Gaston & Curnutt, 1998) or the relationship between local abundance and niche breadth (Gaston et al., 2000). Second, they contain information on which plant species co-occur in the same locality (Chytrý et al., 2016), which is a necessary precondition for direct biotic interactions among plant individuals. Third, unrecorded species can be considered truly absent from the aboveground vegetation at this scale because the standardized methodology of taking a vegetation record requires a systematic search for all species in a plot, or at least all species of the dominant functional group. Fourth, many plots are spatially explicit and can be resurveyed through time to assess possible consequences of land use and climate change (Steinbauer et al. 2018; Perring et al. 2018). Fifth, vegetation plots represent a snapshot of the primary producers of a terrestrial ecosystem, which can be functionally linked to organisms from different trophic groups sampled in the same plots (e.g. multiple taxa surveys) and related processes and services both below (e.g. decomposition, nutrient cycling) and above ground (e.g. herbivory, pollination) (e.g. Schuldt et al. 2018).

Recently several projects at the regional to continental scale have demonstrated the potential of using vegetation-plot databases for exploring biodiversity patterns and the underlying assembly processes. Using vegetation data of French grasslands, Borgy et al. (2017) demonstrated that weighting leaf traits by species abundance in local communities is pivotal to capture leaf trait–environment relationships. Analyzing United States forest assemblages surveyed at the community level, Šímová, Rueda & Hawkins (2017) were able to relate cold or drought tolerance to leaf traits, dispersal traits and traits related to stem hydraulics. Using plot-based tree inventories of the United States forest service, Zhang, Niinemets, Sheffield & Lichstein (2018) found that shifts in tree functional composition amplifies the response of forest biomass to droughts. Based on >15.000 plots from a wide number of habitat types in Denmark, Moeslund et al. (2017) showed that typical plant species that are part of the site-specific species pool, but are absent in a community tend to depend on mycorrhiza, are mostly adapted to low light and low nutrient levels, have poor dispersal abilities and are ruderals and stress intolerant. By collating >40,000 vegetation plots sampled in European beech forests, Jiménez-Alfaro et al. (2018) found that current local community diversity and species pool sizes calculated at different scales were mainly explained by proximity to glacial refugia and current precipitation.

Although large collections of vegetation-plot data are now available from national to continental levels (e.g. Schaminée, Hennekens, Chytrý & Rodwell, 2012; Peet, Lee, Jennings & Faber-Langendoen, 2012; Schmidt et al., 2012; Chytrý et al., 2016; Enquist, Condit, Peet, Schildhauer & Thiers, 2016), they are rarely used in global-scale biodiversity research (Wiser, 2016; Franklin, Serra-Díez, Syphard & Regan, 2017). This is unfortunate because vegetation-plot data may reveal important patterns that cannot be captured by grid-based datasets (**Table 1**). Functional composition patterns, for instance, may differ substantially when considering vegetation-plot data rather than single species occurrences aggregated at the level of coarse-grain grid cells. Using plant height for illustration reveals that the trait means calculated on all the species occurring in a grid cell may differ strongly from the community-weighted means (CWMs) averaged across local communities (**Figure 1**). Nevertheless, only the grid-based approach has been used to date in studies of the geographic distribution of trait values (Swenson et al., 2012, 2017; Wright et al., 2017).

Here, we present sPlot, a global database for compiling and integrating plant community data. We describe (i) main steps in integrating vegetation-plot data in a repository that provides taxonomic, functional and phylogenetic information on co-occurring plant species and links it to global environmental drivers; (ii) principal sources and properties of the data and the procedure for data usage; and (iii) expected impacts of the database in future ecological research. To illustrate the potential of sPlot we also show global diversity patterns that can be readily derived from the current content.

2. COMPILATION OF THE sPlot DATABASE

2.1 Vegetation-plot data

The sPlot consortium currently collates 110 vegetation-plot databases of regional, national or continental extents. Some of the databases have been previously aggregated by and contributed through two (sub-) continental database initiatives (**Table 2** and **Appendix S1** in Supporting Information). All data from Europe and nearby regions were contributed via the European Vegetation Archive (EVA), using the SynBioSys taxon database as a standard taxonomic backbone (Chytrý et al., 2016). Three African databases were contributed via the Tropical African Vegetation Archive (TAVA). In addition, multiple U.S. databases were contributed through the VegBank archive maintained in support of the U.S. National Vegetation Classification (Peet et al. 2012). The data from other regions (South America, Asia) were contributed as separate databases.

We stored the vegetation-plot data from the individual databases in the database software TURBOVEG v2 (Hennekens & Schaminée, 2001). Our general procedure was to preserve the original structure and content of the databases as much as possible in order to facilitate regular updates through automated workflows. The individual databases were then integrated into a single SQLite database using TURBOVEG v3 (S.M. Hennekens, ALTERRA, The Netherlands; www.synbiosys.alterra.nl/turboveg3/help/en/index.html). TURBOVEG v3 combines the species lists from the original databases in a single repository and links the plot attributes (so-called header data) to 58 descriptors of vegetation-plots (**Table S2.1 in Appendix S2**). The metadata of the databases collated in sPlot were managed through the Global Index of

Vegetation-Plot Databases (GIVD; Dengler et al. 2011), using the GIVD ID as the identifier. The current sPlot version 2.1 was created in October 2016 and contains 1,121,244 vegetation plots with 23,586,216 plant species × plot observations (i.e. ords of a species in a plot). Most records (1,073,737; 95.8%) have information on cover, 29,288 on presence/absence, 5,854 on basal area, 3,265 on counts of individuals, 148 on importance value, 1,895 on per cent frequency, 4,883 on number of stems, and further 2,174 have a mix of these types of these different metrics.

2.2 Taxonomic standardization

To combine the species lists of the different databases in sPlot, we constructed a taxonomic backbone. To link co-occurrence information in sPlot with plant traits, we expanded this backbone to integrate plant names used in the TRY database (Kattge et al., 2011). The taxon names (without nomenclatural authors) from sPlot 2.1 and TRY 3.0 were first concatenated into one list, resulting in 121,861 names, of which 61,588 (50.5%) were unique to sPlot; 35,429 (29.1%) unique to TRY; and 24,844 (20.4%) shared between TRY and sPlot. Taxon names were parsed and resolved using the Taxonomic Name Resolution Service web application (TNRS version 4.0; Boyle et al., 2013; iPlant Collaborative, 2015), using the five TNRS standard sources ranked by default. We allowed for (i) partial matching to the next higher rank (genus or family) if the full taxon name could not be found and (ii) full fuzzy matching, to return names that were matched within a maximum number of four single-character edits (Levenshtein edit distance of 4), which corresponds to the minimum match accuracy of 0.05 in TNRS, with 1 indicating a perfect match.

We accepted all names that were matched, or converted from synonyms, with an overall match score of 1. In case with no exact match (i.e. the overall match score was <1), names were inspected on an individual basis. All names that matched at taxonomic ranks lower than species (e.g. subspecies, varieties) were accepted as correct names. The name matching procedure was repeated for the uncertain names (i.e. with match accuracy scores below the threshold value from the first matching run), with a preference on first using the source 'Tropicos'(Missouri Botanical Garden; http://www.tropicos.org/; accessed 19 Dec 2014) because here matching scores were often higher for names of low taxonomic rank. The remaining 9,641 non-matched names were resolved using (i) the additional source 'NCBI' (Federhen, 2010) within TNRS, (ii) the matching tools in the Plant List web application (The Plant List 2010), (iii) the 'tpl'-function within the R-package 'Taxonstand' (Cayuela, Stein & Oksanen, 2017) and (iv) manual inspection (i.e. to resolve vernacular names). All subspecies were aggregated to the species level. Names that could not be matched were classified as 'No suitable matches found'. Because sPlot and TRY contain taxa of non-vascular plants, we tagged vascular plant names based on their family and phylum affiliation, using the 'rgbif' library in R (Chamberlain, 2017). Of the full list of plant names in sPlot and TRY, 79,171 (94.6%) plant names were matched at the species level, 4,343 (5.2%) at the genus level, 152 (0.2%) at the family level and 13 names at higher taxonomic levels. Overall, this led to 58,066 accepted taxon names in sPlot. Family affiliation was classified according to APG III (Bremer et al., 2009). A detailed description of the workflow, including R-code, is available in Purschke (2017a).

One potential shortcoming of our taxonomic backbone is that for most regions it was necessary to standardize taxa using standard sets of taxonomic synonyms. Thus, if a taxonomic name represents multiple taxonomic concepts, e.g. such as created by the splitting and lumping of taxa, or a name has been misapplied in a region, we must trust that this problem has been addressed in our component databases (Franz, Peet & Weakley, 2004; Jansen & Dengler, 2010).

2.3 Physiognomic information

To achieve a classification into forests vs. non-forests that is applicable to all plots irrespective of the structural and habitat data provided by the source database, we defined as forest all plot records that had >25% absolute cover of the tree layer, making use of the attribute data of sPlot. This threshold is similar to the classification of Ellenberg & Müller-Dombois (1967), who defined woodland formations with trees covering more than 30%. There were 16,244 tree species in the sPlot database. There were 16,244 tree species in the sPlot database. As tree layer cover was available for only 25% of all plots, we additionally used the information whether the taxa present in a plot were trees (usually defined as being taller than 5 m), using the plant growth form information from TRY (see below). Thus, plots lacking tree cover information were defined as forests if the sum of relative cover of all tree taxa was >25%. Similarly, we defined non-forests by calculating the cover of all taxa that were not defined as trees or shrubs (also taken from the TRY plant growth form information) and that were not taller than 2 m, using the TRY data on mean plant height. In total, 21,888 taxa belonged to this category. We defined all plots as non-forests if the sum of relative cover of these low-stature, non-tree and non-shrub taxa was >90%. As we did not have the growth form and height information for all taxa, a fraction of about 25% of the plots remained unassigned (i.e. was neither forest, nor non-forest. In addition, more detailed classifications of plots into physiognomic formations (**Table S3.2 in Appendix S3**) and naturalness (**Table S3.3 in Appendix S3**) were derived from various types of plot-level or database-level information provided by the sources and stored in five separate fields (see **Table S2.1 in Appendix S2**).

2.4 Phylogenetic information

We developed a workflow to generate a phylogeny of the vascular plant species in sPlot, using the phylogeny of Zanne et al. (2014), updated by Qian & Jin (2016). Species present in sPlot but missing from this phylogeny were added next to a randomly selected congener (see also Maitner et al., 2018). This approach has been demonstrated to introduce less bias into subsequent analyses than adding missing species as polytomies to the respective genera (Davies et al., 2012). We only added species based on taxonomic information on the genus level, thus not making use of family affiliation. Because of the absence of congeners in the reference phylogeny, 7,147 species could not be added (11.7% of all resolved taxa in sPlot and TRY). This resulted in a phylogeny with 54,067 resolved taxon names from 61,214 standardized taxa in the combined list of sPlot and TRY. The tree was finally pruned to the vascular plant taxa of the current sPlot version 2.1, resulting in a phylogenetic tree for 53,489 out of the 58,066 taxa in sPlot. Of these 53,489 names, 16,026 are also found among the 31,389 taxa in the phylogenetic tree of Qian & Jin (2016), i.e. 51.1%. The full procedure and the R code is available in Purschke (2017b).

2.5 Associated environmental plot information

To complement the plot data, we harmonized geographical coordinates (in decimal degrees), elevation (m above sea level), aspect (degrees) and slope (degrees) as provided by the contributing databases. All other variables were too sparsely and too inconsistently sampled across databases to be combined in the global set, but were retained in the original data sources and can be retrieved for particular purposes.

We used the geographic coordinates to create a geodatabase in ArcGIS 14.1 (ESRI, Redlands, CA) to link sPlot 2.1 to these climate and soil data. We retrieved data for all the 19 bioclimatic variables provided by CHELSA v1.1 (Karger et al., 2017) by averaging climatic data from the period 1979–2013 at 30 arc seconds (about 1 km in grid cells near to the equator). These variables are the same as the ones used in WorldClim (www.worldclim.org; Hijmans, Cameron, Parra, Jones & Jarvis, 2005), but calculated with a downscaling approach based on estimates of the ERA-Interim climatic reanalysis. While the CHELSA climatological data have a similar accuracy as other products for temperature, they are more precise for precipitation patterns (Karger, et al. 2017). We also calculated growing degree days for 1 °C (GDD1) and 5 °C (GDD5), according to Synes & Osborne (2011) and based on CHELSA data, and included the index of aridity and potential evapotranspiration extracted from the CGIAR-CSI website (www.cgiar-csi.org). In addition, we extracted seven soil variables from the SOILGRIDS project (https://soilgrids.org/; licensed by ISRIC – World Soil Information), downloaded at 250-m resolution and then converted to the same 30-arc second grid format of CHELSA. To explore the distribution of sPlot data in the global environmental space, we subjected all 30 climate and soil variables of the global terrestrial surface rasterized on a 2.5 arc-minute grid resolution to a principal component analysis (PCA) on standardized and centered data. We subsequently created a grid of 100 × 100 cells within the bi-dimensional environmental space defined by the first two PCA axes (PC1 and PC2) and counted the number of terrestrial cells per environmental grid cell of the PC1-PC2 space. Then, we counted the number of plots in sPlot in the same PCA grid (**Figure 2**).

We linked all vegetation plots to two global biome classifications. We used the World Wildlife Fund (WWF) spatial information on terrestrial ecoregions (Olson et al., 2001) to assign plots to one of the 867 ecoregions, 14 biomes and eight biogeographic realms. The WWF approach is based on a bottom-up expert system using various regional biodiversity sources to define ecoregions, which in turn are grouped into realms and biomes (Olson et al., 2001). In addition, we created a shapefile for the ecozones defined by Schultz (2005) to represent major biomes in response to global climatic variation. Since these zones are climatically heterogeneous in mountain regions, we differentiated an additional “alpine” biome for mountain areas above the lower mountain thermal belt, as defined in the classification of world mountain regions by Körner et al. (2017). This resulted in a distinction of 10 major biomes (**Fig. S4.5 in Appendix S4**), whose shape file is freely available (**Appendix S5)**.

2.6 Trait information

To broaden the potential applications of the global vegetation database in functional contexts, we linked sPlot to TRY. We accessed plant trait data from TRY version 3.0 on August 10, 2016 and included 18 traits that describe the leaf, wood and seed economics spectra (Westoby, 1998;

Reich, 2014; **Table S6.4 in Appendix S6**), and are known to affect different key ecosystem processes and to respond to macroclimatic drivers. These traits were represented across all species in the TRY database by at least 1,000 trait records. We excluded trait records from manipulative experiments and outliers (Kattge et al., 2011), which resulted in a matrix with 632,938 individual plant records on 52,032 taxa in TRY, having data records for an average of 3.08 for the 18 selected traits. On average, each trait has been measured at least once in 17.1% of all taxa. In order to attain data for these 18 traits for all species with at least one trait value in TRY, we employed hierarchical Bayesian modelling, using the R package 'BHPMF' (Schrodt et al., 2015; Fazayeli, Banerpee, Kattge, Schrodt & Reich, 2017), to fill a gap in the matrix of individual plant records in TRY. Gap-filling allows to obtain trait values for a species on which this trait has not been measured, but for which other traits were available. To assess gap-filling quality, we used the probability density distributions provided by BHPMF for each imputation and removed highly uncertain imputations with a coefficient of variation >1. We then $\log_e$-transformed all gap-filled trait values and averaged them by taxon. For taxa recorded at genus level only, we calculated genus means, resulting in a full trait matrix for 26,632 out of the 54,519 taxa in sPlot (45.9%), with 6, 1,510 and 25,116 taxa at the family, genus and species level, respectively. These species covered 88.7% of all species-by-plot combinations.

For every trait *j* and plot *k*, we calculated the community-weighted mean (CWM) and the community-weighted variance (CWV) for each of the 18 traits in a plot (Enquist et al., 2015):

$$CWM_{j,k} = \sum_{i}^{n_k} p_{i,k} t_{i,j}$$

$$CWV_{j,k} = \sum_{i}^{n_k} p_{i,k}\,(t_{i,j} - CWM_{j,k})^2$$

where n_k is the number of species with trait information in plot *k*, $p_{i,k}$ is the relative abundance of species *i* in plot *k* calculated as the species' fraction in cover or abundance of total cover or abundance, and $t_{i,j}$ is the mean value of species *i* for trait *j*. CWMs and CWVs were calculated for

18 traits in 1,117,369 and 1,099,463 plots, respectively, the second being a smaller number as at least two taxa were needed for CWV calculation.

3. CONTENT OF sPlot 2.1

3.1 Plot community data

sPlot 2.1 contains 1,121,244 vegetation plots from 160 countries and from all continents (**Figure 3**). The global coverage is biased towards Europe, North America and Australia, reflecting unequal sampling effort across the globe (**Table 1**). At the ecoregion level, major gaps occur in the wet tropics of South America and Asia, as well as in subtropical deserts worldwide and in the North American taiga. Although the plots are highly clustered geographically, their coverage in the environmental space is much more representative: the highest concentration of plots is found in environments that are most abundant globally (**Figure 2**), while they are lacking in the very moist parts of the environmental space, which are also spatially rare, and in the very cold parts, which are sparsely vegetated.

In most cases (98.4%), plot records in sPlot include full species lists of vascular plants, while 1.6% had only wood species above a certain diameter or only the most dominant species recorded. Terricolous bryophytes and lichens were additionally identified in 14% and 7% of plots, respectively. (**Table S2.1 in Appendix S2**). Forest and non-forest plots comprise 330,873 (29.7%) and 513,035 (46.0%) of all plots in sPlot, respectively. In most cases, species abundance was estimated using different variants of the Braun-Blanquet cover-abundance scale (66%), followed by percentage cover (15%) and 55 other numeric or ordinal scales. The temporal extent of the data spans from 1885 to 2015, but >94% of vegetation plots were recorded later than 1960 (**Fig. S2.1 in Appendix S2**). Almost all plots are georeferenced (1,120,686) and most plots have location uncertainty of 10 m or less (**Fig. S2.2 in Appendix S2**).

Vascular plant richness per plot ranges from 1 to 723 species (median = 17 species). The most frequent richness class is between 20 and 25 species (**Fig. S2.3 in Appendix S2**). Plot size is reported in 65.4% of plots, ranging from less than 1 m^2 to 25 ha, with a median of 36 m^2. While forest plots have plot sizes $\geq$100 m^2, and in most cases $\leq$1,000 m^2, non-forest plots range between $\geq$5 and $\leq$100 m^2 (**Fig. S2.4 in Appendix S2**). When using these size ranges, forest plots tend to be richer in species (**Figure 4a**). The fact that the gradient in richness found in our plots was at least one order of magnitude stronger than differences that could be expected by the differences in plot sizes, prompted us to produce the first global maps of plot-scale species richness, separately for forests and non-forests (**Figure 4a**). While plots with complete vascular species composition are largely lacking from the wet tropics, for the remaining biomes the plot-scale richness data do not show the typical latitudinal richness gradient in either formation. Particularly species-rich forests are found in the wet subtropics (such as SE United States, Taiwan and the East coast of Australia) as well as in some mountainous regions of the nemoral and steppic biomes of Eurasia. Likewise, non-forest communities, have a particularly high mean vascular plant species in mountainous regions of the nemoral and steppic biomes of Eurasia.

3.2 Phylogenetic information

The phylogenetic tree for sPlot was produced from 53,489 vascular plant names contained in the database, comprising 5518 genera (**Appendix S7**). Moderately to highly frequent species in sPlot 2.1 are equally distributed across the phylogeny (corresponding to yellowish to reddish colors for low and high peaks, respectively, in **Fig. S7.6 in Appendix S7**). Coverage of species included in the phylogeny ranges from 89% of species that occur only once in all plots to 100% of species with a frequency >10,000 plots (**Fig. S7.7 in Appendix S7**).

3.3 Functional information

The proportion of species with trait information increases with the species' frequency in plots. Gap-filled trait information is available for 77.2% and 96.2% for taxa that occurred in more than 100 and 1,000 plots, respectively. Trait coverage is similar across biomes (**Fig. S8.8 in Appendix S8**). Across all biomes, the proportion of species for which gap-filled trait data are available increases with the species' frequency across plots. Compared to gap-filled data, trait coverage for the original trait data is considerably lower, being highest for height, seed mass, leaf area and specific leaf area (SLA, **Fig. S8.9 in Appendix S8**).

The high representation of the 18 traits in the gap-filled trait data and the high degree of trait coverage for frequent species across all biomes (>75%) made us confident to produce the first maps of global patterns of community-weighted means (CWMs) (**Figure 4b–d**). The maps show the main trait dimensions of SLA, height and seed mass, separately for forests and non-forests, for those regions of the world that are already sufficiently covered by sPlot data. Accordingly, CWMs of SLA are quite similar for forest and non-forest plots, being highest in western North America and Europe and lowest in eastern North America, East and South Australia (**Figure 4b**). Non-forest vegetation shows lowest CWMs of SLA in the desert regions of the Namib and Sinai. Forests with highest CWMs of canopy height are found along the western and eastern coast of North America, some regions in Europe, East Asia and southern Australia (**Figure 4c**). These areas only partly coincide with those of highest seed masses for forests, while seed mass in non-forests is highest in the eastern Mediterranean Basin and in Central Asia (**Figure 4d**). The corresponding patterns for CWV are shown in Appendix **Fig. S9.10 in Appendix S9**.

4. DATA USAGE

The sPlot database (the vegetation-plot data, including the environmental information for each plot and the species phylogeny) is released in fixed versions to allow reproducibility of results, but also due to the enormous effort needed for data integration and harmonization and for updating the phylogeny. By delivering few fixed versions while keeping older versions available, the sPlot consortium ensures that the same data can be used in parallel projects and that the data underlying a specific study remain accessible in the future, thus allowing re-analysis. Each new version will be matched to the current TRY database.

Data access to sPlot is regulated by the Governance and Data Property Rules (www.idiv.de/sPlot) to ensure a fair balance between the interests of data contributors and data analysts. In brief, the sPlot Rules state that: (1) all contributing vegetation-plot databases become members of the sPlot consortium, represented by their custodian and deputy custodian; (2) vegetation-plot data contributed to sPlot remain the property of the data contributors and can be withdrawn at any time except for approved projects; (3) other scientists (e.g. data managers or participants of the sPlot workshops) with particular responsibilities may also be appointed as personal members to the sPlot consortium; (4) sPlot data can be requested for projects that involve at least one member of the sPlot consortium; (5) whenever a project has been proposed, all sPlot consortium members will be informed and can declare their interest in becoming co-authors of manuscripts resulting from this project and then becoming actively involved in data evaluation and writing; and (6) if also the matched gap-filled or original trait data from TRY are requested for a project, likewise members from the TRY consortium can opt-in as co-authors. The sPlot database is, therefore, available according to a 'give-and-receive' system. Moreover, the data are available to any researcher by establishing a collaboration that includes and is supported by at least one sPlot consortium member.

The sPlot consortium is governed by a Steering Committee elected by all consortium members for two-year, renewable terms. Project proposals can be submitted to the Steering Committee, which ensures that the sPlot Rules are followed and redundant work between overlapping projects is avoided. The lists of databases, sPlot consortium members and the Steering Committee members are updated regularly on the sPlot website, as are the sPlot Rules and the list of approved projects.

5. EXPECTED IMPACT AND LIMITATIONS

The main aim of the sPlot database is to catalyze a collaborative network for understanding global diversity patterns of plant communities in space and time. sPlot provides a unique, integrated global repository of data that would otherwise be fragmented in unconnected and structurally inconsistent databases at regional, national or continental levels. Together with the provision of harmonized phylogenetic, functional and environmental information, sPlot allows, for the first time, global analyses of plant community data. Compared to approaches using data aggregated from species occurrences in grid cells, sPlot will significantly advance ecological analyses and future interdisciplinary research in at least four different ways.

1.) Using sPlot, one can predict the species that can co-exist in a community and also the frequencies of their co-occurrence (Breitschwerdt, Jandt & Bruelheide, 2015) or niche overlap (Broennimann et al., 2012). In addition, emerging tools such as Markov networks can be used to infer strengths of interspecific interactions (Harris, 2016). When investigating community assembly rules, the same information can be used to derive species pools for specific vegetation types (de Bello et al., 2016; Lewis, Szava-Kovats & Pärtel, 2016; Karger et al., 2016). Moreover, the co-occurrence data from sPlot can be used to address fundamental patterns and drivers of plant invasions better than information on large geographic entities (e.g. van Kleunen et al., 2015) alone could.

2.) sPlot data can be aggregated across all types of plots, by grid cells, ecoregions, environment, or even vegetation type or formation. Furthermore, replicated plots within grid cells, ecoregions, or any other subdivision of environmental conditions or vegetation types allow users to derive measures of compositional differences between plant communities within grid cells (= beta diversity; **Table 1**). Thus, the community data are an important complement to regional-scale species occurrence data (e.g. Kreft & Jetz, 2007; Enquist et al., 2016).

3.) sPlot data provide information on the proportion of species in communities. When combined with functional trait information, relative abundance of species allows calculation of community abundance-weighted mean trait values (Bruelheide et al. 2018). Information on the relative contribution of species to a community-aggregated trait value is particularly necessary when traits are used as proxies for vegetation functions and processes, allowing to test, among other things, the mass ratio hypothesis (Grime, 1998; Garnier et al., 2004) and to assess the role of divergent traits (Díaz et al., 2007; Kröber et al., 2015).

4.) Plant species within plots can be linked to traits that predict interactions with organisms from other trophic groups, both belowground (mycorrhizae, soil decomposers) and aboveground (herbivores and pollinators). This will allow to link vegetation plot information to ecosystem processes and services such as pest control, pollination and nutrient cycling (e.g. de Bello et al., 2010).

Despite the large amount of available data and its potential suitability for global research, a number of limitations must be considered by future users of sPlot, such as i) biases towards certain regions and communities, ii) near-complete lack of plots with complete vascular plant species composition for certain regions (e.g. the wet tropics), iii) identification or sampling errors by the surveyors and incomplete records because the detection of some species may be precluded in certain seasons by their phenology, iv) taxonomic uncertainty particularly in the tropics, v) strongly varying plot sizes employed in different studies and regions, vi) lack of trait measures at the plot level. For example, patterns of diversity components are typically affected by grain size. This means that using sPlot data for such studies either requires filtering for plots with identical or at least similar size or accounting for the plot-size effects in the statistical model. In addition, analyses of functional diversity with sPlot data is limited by the absence of trait data for a (small) portion of the species and by the lack of plot-specific trait measures. Furthermore, the non-random and geographically and ecologically very unequal distribution of the plots contained in sPlot call for stratified resampling to balance records of different environments (e.g. stratified by climate, **Figure 2**) or physiognomic formations (**Figure 4**). Users of sPlot need to be aware of these and other limitations and to correct potential biases for their specific research question.

6. CONCLUSION

sPlot is a unique global database of plant community records sampled with relatively similar methods widely used in vegetation ecology. The integration of co-occurrence data into a unified database that can be directly linked to environmental, functional and phylogenetic information, makes sPlot an unprecedented and essential tool for analyzing global plant diversity, the structure of plant communities and the co-occurrence of plant species. The compatibility of this consolidated database with other global databases, e.g. via a joint taxonomic backbone with TRY and the Global Naturalized Alien Flora (GloNAF; van Kleunen et al., 2015) (via taxon names), or via standardized geo-reference with databases of environmental information such as CHELSA, WorldClim or SoilGrids (Bruelheide et al. 2018), facilitates data integration and creates new research opportunities. The adaptive management of the database employed by the sPlot consortium allows regular incorporation of new data, resulting in a dynamic platform for storing and analyzing the most comprehensive compilation of plant community data worldwide.

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DATA ACCESSIBILITY

The data contained in sPlot (the vegetation-plot data complemented by species phylogeny and environmental information) are available by request, through contacting any of the consortium members for submitting a paper proposal. The proposals should follow the Governance and Data Property Rules of the sPlot Working Group, which are available on the sPlot website (www.idiv.de/sPlot). After acceptance, the respective data will be provided. In addition to the plot data, CWMs and CWVs of 18 plant traits are available for every plot.

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

Appendix S1 Additional references, attributions and disclaimers for datasets included in sPlot 2.1

Appendix S2 Data associated to the vegetation plot records stored in sPlot 2.1

Appendix S3 Details on the workflow for setting up plot definitions in sPlot 2.1

Appendix S4 Biome classification created for sPlot 2.1

Appendix S5 Zip file of the biome classification of Appendix S4 containing the shapefile (Geospatial vector data for geographic information system (GIS) software) and accompanying accessory files (database, projection etc.).

Appendix S6 Trait information in sPlot 2.1

Appendix S7 Phylogenetic information in sPlot 2.1

Appendix S8 Gap-filled trait information

Appendix S9 Global patterns of community-weighted variances

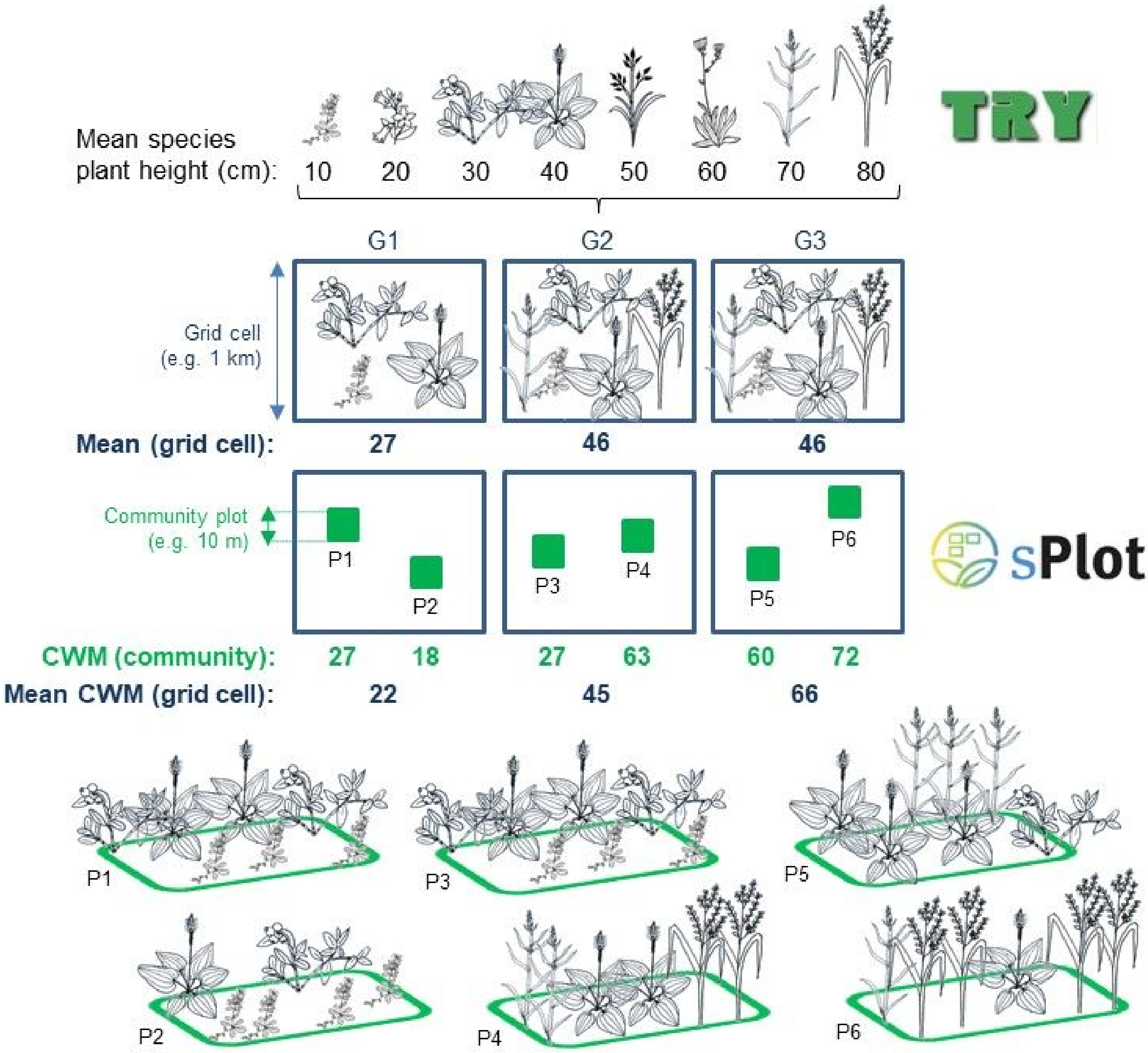
Mean species
plant height (cm):
10
20
30
40
50
60
70
80
TRY
G1
G2
G3
Grid cell
(e.g. 1 km)
Mean (grid cell):
27
46
46
Community plot
(e.g. 10 m)
P1
P2
P3
P4
P5
P6
sPlot
CWM (community):
27
18
27
63
60
72
Mean CWM (grid cell):
22
45
66
P1
P3
P5
P2
P4
P6

Figure 1. Conceptual figure visualizing how functional composition (in this case plant height) differs between calculations based on mean traits for grid cells and community data sampled in vegetation plots. Occurrence data (e.g. from distribution atlases, GBIF, etc.) can be used to calculate mean trait values in grid cells G1–G3. However, community weighted means (CWMs) of traits differ across local plots (P1–P6), while the mean values of CWMs in the grid cells differ from the unweighted values calculated in the grid cells. This example is simplified by showing few species and few plots. In reality, differences are generally more pronounced.

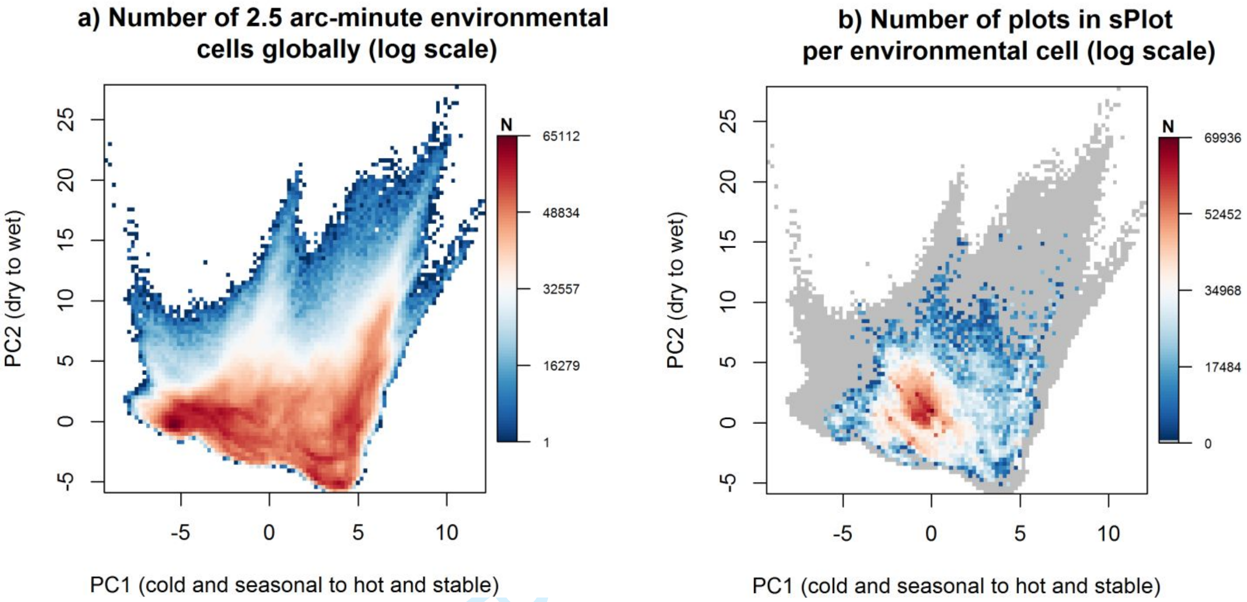

Figure 2. Distribution of vegetation plots from sPlot 2.1 in the global environmental space. Comparison of the distribution of all terrestrial 2.5 arc-minute cells (a) and plots in sPlot 2.1 (b) in the principal component analysis (PCA) space defined on 30 environmental (climate and soil) variables. The PCA space was divided into a 100 × 100 regular grid. For each element of this grid, the graphs show the number of 2.5 arc-minute cells (a) and plots (b), respectively. Colors refer to the logarithm of number of plots, with the legend showing untransformed number of plots. The first and second PCA axis explained 48.6% and 27.3% of the total variance**.**

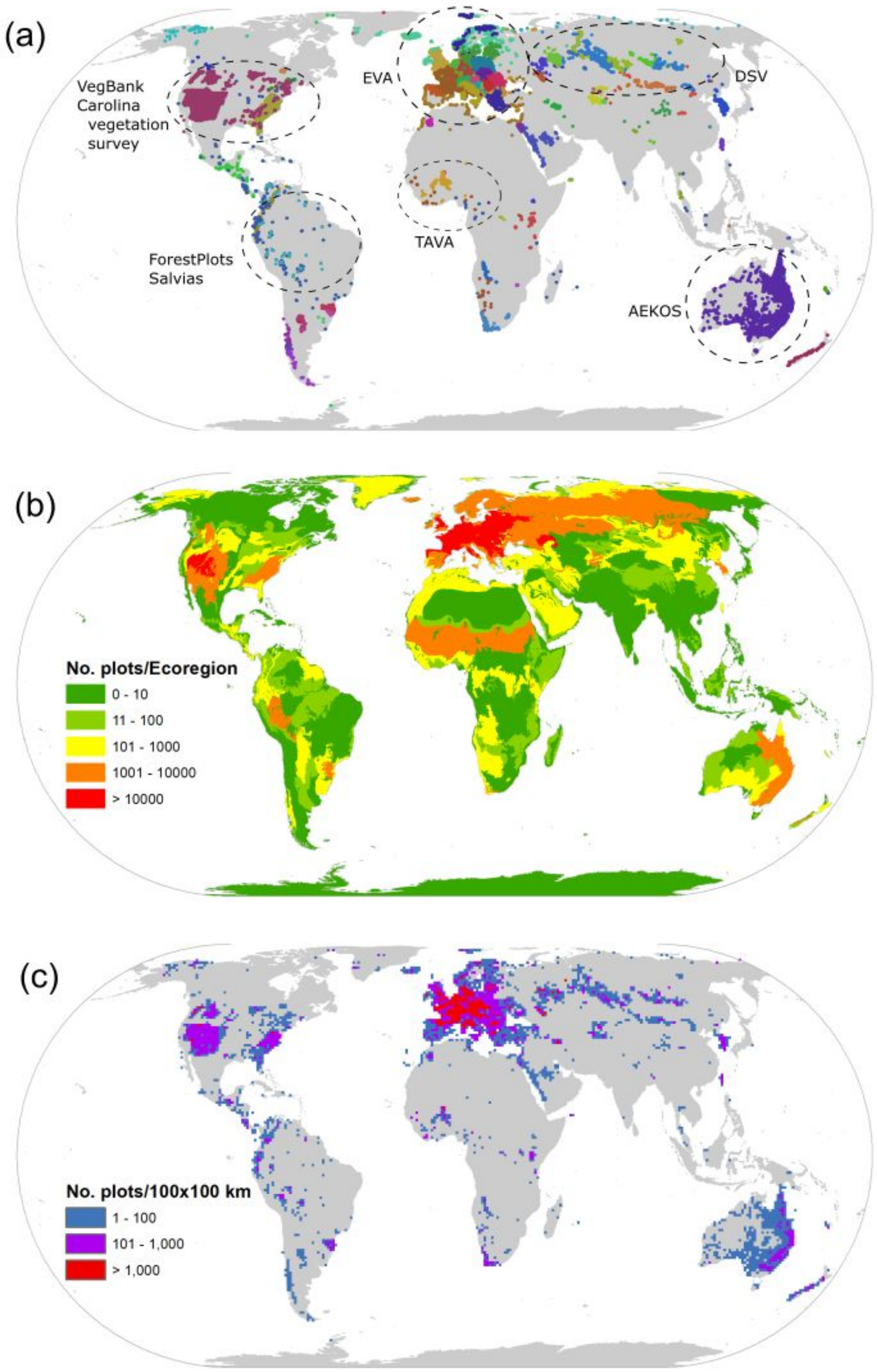

Figure 3. Global coverage of sPlot 2.1; (a) contributing databases identified by different colours with indication of the two data aggregators (EVA, TAVA) and a few particularly large individual databases; (b) available plot numbers per WWF Ecoregion; and (c) available plot density in grid cells of 100 km × 100 km.

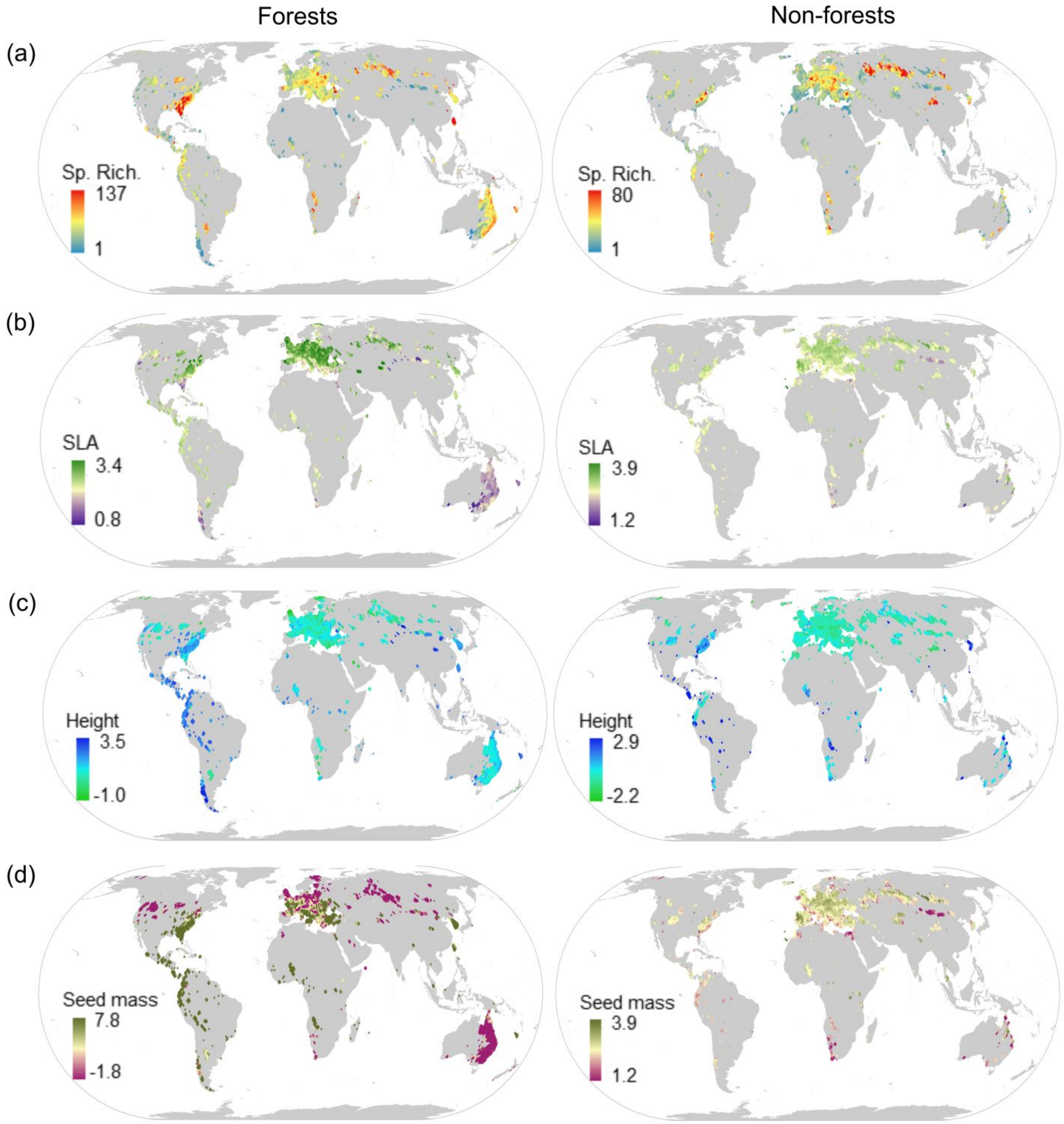

Figure 4. Examples of global community-level patterns that can be derived from (a) sPlot alone and (b–d) sPlot combined with TRY, here shown as raw data averaged by 1-degree grid cells. There are only a very few cells (142 out of 2633) comprising only a single plot. For the maps, only plots with full vascular species composition and spatial accuracy < 5 km were used. They are based on 148,474 and 218,051 plots for forests and non-forests respectively. Note that these maps are not corrected for biases caused by the facts that not all community types were

recorded in all grid cells and that plot sizes as well as the fraction of species with available trait data varied spatially. Maps show patterns of (a) fine-grain alpha diversity, expressed as vascular plant species richness (only plots with plot sizes of 100–1000 m² for forests and 5–100 m² for non-forests); (b) community-weighted means (CWMs) for $\log_e$-transformed trait values of specific leaf area (SLA, m^2 kg^{-1}), (c) plant height (m) and (d) seed mass (mg).

Table 1. Types of information provided by single vegetation plots, vegetation plots aggregated within grid cells (or other geographic units) and single species occurrence records aggregated within grid cells. The three levels are illustrated in Figure 1.

Information from...	Single vegetation plots	Set of vegetation plots aggregated within grid cells	Grid-cell data from floristic inventories
To derive information on the …	Plot level	Grid cell level	Grid cell level
Type of occurrence	Co-occurrence, occurrence by vegetation type	Occurrence by vegetation type	Occurrence
Community assembly rules	Yes (co-occurrence is a prerequisite for species interactions)	No	No
Absences	Yes (for the target plant group in a study)	No (except for intensive sampling schemes)	Depending on sampling intensity
Floristic composition …	… of the local community	… of the species pools of vegetation types	… of the total set of species
Diversity	α	β, γ	γ
Species abundance	Local cover-abundance	Mean cover-abundance and frequency by vegetation type	Occurrence only
Combination with traits	Functional composition of the local community (traits unweighted or weighted by cover: CWM, CWV)	Functional composition of the species pool (unweighted or weighted)	Functional composition of the total set of species (unweighted only)
Environmental filtering …	… at the local level	… at the regional level	… at the regional level

Table 2. Plot datasets included in sPlot 2.1. GIVD ID refers to the ID in the Global Index of Vegetation-Plot Databases (http://www.givd.info), which manages the metadata for sPlot and provides updated online descriptions of these databases; * after the GIVD ID indicates that the respective database description is currently not visible on the GIVD website. Datasets contributed in harmonized format from a continental data aggregator ("collective database" according to the sPlot Rules) are listed under its name. Further references, attributions and disclaimers for particular datasets are found Appendix S1.

GIVD ID	Database name	# of plots in sPlot 2.1	Custodian	Deputy custodian	Reference
[Aggregator]	**European Vegetation Archive (EVA)**	**950,001**	**Milan Chytrý**	**Ilona Knollová**	**Chytrý et al. (2016)**
00-00-004	Vegetation Database of Eurasian Tundra	1,132	Risto Virtanen		
00-RU-001	Vegetation Database Forest of Southern Ural	1,102	Vassiliy Martynenko		
00-RU-003	Database Meadows and Steppes of Southern Ural	2,354	Sergey Yamalov	Mariya Lebedeva	
00-TR-001	Forest Vegetation Database of Turkey - FVDT	919	Ali Kavgacı		
00-TR-002*	Non-forest Vegetation Database of Turkey	3,018	Deniz Işık	Didem Ambarlı	
AS-TR-002	Vegetation Database of Oak Communities in Turkey	1,181	Emin Uğurlu		
EU-00-002	Nordic-Baltic Grassland Vegetation Database (NBGVD)	7,675	Jürgen Dengler	Łukasz Kozub	Dengler & Rūsiņa (2012)
EU-00-011	Vegetation-Plot Database of the University of the Basque Country (BIOVEG)	18,441	Idoia Biurrun	Itziar García-Mijangos	Biurrun et al. (2012)
EU-00-013	Balkan Dry Grasslands Database	7,683	Kiril Vassilev	Armin Macanović	Vassilev et al. (2012)
EU-00-016	Mediterranean Ammophiletea Database	7,359	Corrado Marcenò	Borja Jiménez-Alfaro	Marcenò & Jiménez-Alfaro (2017)
EU-00-017	European Coastal Vegetation Database	4,624	John Janssen		
EU-00-018	The Nordic Vegetation Database	5,477	Jonathan Lenoir	Jens-Christian Svenning	Lenoir et al. (2013)
EU-00-019	Balkan Vegetation Database	9,118	Kiril Vassilev	Hristo Pedashenko	Vassilev et al. (2016)
EU-00-020	WetVegEurope	14,111	Flavia Landucci		Landucci et al. (2015)
EU-00-022	European Mire Vegetation Database	10,147	Tomáš Peterka	Martin Jiroušek	Peterka et al. (2015)
EU-AL-001	Vegetation Database of Albania	290	Michele De Sanctis	Giuliano Fanelli	De Sanctis et al. (2017)
EU-AT-001	Austrian Vegetation Database	34,458	Wolfgang Willner	Christian Berg	Willner et al. (2012)
EU-BE-002	INBOVEG	25,665	Els De Bie		
EU-BG-001	Bulgarian Vegetation Database	5,254	Iva Apostolova	Desislava Sopotlieva	Apostolova et al. (2012)
EU-CH-005	Swiss Forest Vegetation Database	14,193	Thomas Wohlgemuth		Wohlgemuth (2012)

EU-CZ-001	Czech National Phytosociological Database	104,697	Milan Chytrý	Dana Holubová	Chytrý & Rafajová (2003)
EU-DE-001	VegMV	53,822	Florian Jansen	Christian Berg	Jansen et al. (2012)
EU-DE-013	VegetWeb Germany	23,078	Jörg Ewald		Ewald et al. (2012)
EU-DE-014	German Vegetation Reference Database (GVRD)	30,840	Ute Jandt	Helge Bruelheide	Jandt & Bruelheide (2012)
EU-DK-002	National Vegetation Database of Denmark	24,264	Jesper Erenskjold Moeslund	Rasmus Ejrnæs	
EU-ES-001	Iberian and Macaronesian Vegetation Information System (SIVIM) Wetlands	6,560	Aaron Pérez-Haase	Xavier Font	
EU-FR-003	SOPHY	209,864	Henry Brisse	Patrice De Ruffray	Brisse et al. (1995)
EU-GB-001	UK National Vegetation Classification Database	28,533	John S. Rodwell		
EU-GR-001	KRITI	292	Erwin Bergmeier		
EU-GR-005	Hellenic Natura 2000 Vegetation Database (HelNatVeg)	5,168	Panayotis Dimopoulos	Ioannis Tsiripidis	Dimopoulos & Tsiripidis (2012)
EU-GR-006	Hellenic Woodland Database	3,199	Georgios Fotiadis	Ioannis Tsiripidis	Fotiadis et al. (2012)
EU-HR-001	Phytosociological Database of Non-Forest Vegetation in Croatia	5,057	Zvjezdana Stančić		Stančić (2012)
EU-HR-002	Croatian Vegetation Database	8,734	Željko Škvorc	Daniel Krstonošić	
EU-HU-003	CoenoDat Hungarian Phytosociological Database	8,505	János Csiky	Zoltán Botta-Dukát	Lájer et al. (2008)
EU-IT-001	VegItaly	15,332	Roberto Venanzoni	Flavia Landucci	Landucci et al. (2012)
EU-IT-010	Italian National Vegetation Database (BVN/ISPRA)	3,562	Laura Casella	Pierangela Angelini	Casella et al. (2012)
EU-IT-011	Vegetation-Plot Database Sapienza University of Rome (VPD-Sapienza)	12,780	Emiliano Agrillo	Fabio Attorre	Agrillo et al. (2017)
EU-LT-001	Lithuanian Vegetation Database	7,821	Valerijus Rašomavičius	Domas Uogintas	
EU-LV-001	Semi-natural Grassland Vegetation Database of Latvia	5,594	Solvita Rūsiņa		Rūsiņa (2012)
EU-MK-001	Vegetation Database of the Republic of Macedonia	1,417	Renata Ćušterevska		
EU-NL-001	Dutch National Vegetation Database	102,327	Joop H.J. Schaminée	Stephan M. Hennekens	Schaminée et al. (2006)
EU-PL-001	Polish Vegetation Database	22,229	Zygmunt Kącki	Grzegorz Swacha	Kącki & Śliwiński (2012)
EU-RO-007	Romanian Forest Database	6,017	Adrian Indreica	Pavel Dan Turtureanu	Indreica et al. (2017)
EU-RO-008	Romanian Grassland Database	1,921	Eszter Ruprecht	Kiril Vassilev	Vassilev et al. (2018)
EU-RS-002	Vegetation Database Grassland Vegetation of Serbia	5,587	Svetlana Aćić	Zora Dajić Stevanović	Aćić et al. (2012)
EU-RU-002	Lower Volga Valley Phytosociological Database	14,853	Valentin Golub	Viktoria Bondareva	Golub et al. (2012)
EU-RU-003	Vegetation Database of the Volga and the Ural Rivers Basins	1,516	Tatiana Lysenko		Lysenko et al. (2012)
EU-RU-011	Vegetation Database of Tatarstan	7,471	Vadim Prokhorov	Maria Kozhevnikova	Prokhorov et al. (2017)
EU-SI-001	Vegetation Database of Slovenia	10,986	Urban Šilc	Filip Küzmič	Šilc (2012)
EU-SK-001	Slovak Vegetation Database	36,405	Milan Valachovič	Jozef Šibík	Šibík (2012)
EU-UA-001	Ukrainian Grasslands Database	4,043	Anna Kuzemko	Yulia Vashenyak	Kuzemko (2012)
EU-UA-006	Vegetation Database of Ukraine and Adjacent Parts of Russia	3,326	Viktor Onyshchenko	Vitaliy Kolomiychuk	

[Aggregator]	**Tropical African Vegetation Archive (TAVA)**	**6,677**	**Marco Schmidt**	**Stefan Dressler**	**Janßen et al. (2011)**
AF-00-001	West African Vegetation Database	3,129	Marco Schmidt	Georg Zizka	Schmidt et al. (2012)
AF-00-008	PANAF Vegetation Database	2,469	Hjalmar Kühl	TeneKwetche Sop	
AF-BF-001	Sahel Vegetation Database	1,079	Jonas V. Müller	Marco Schmidt	Müller (2003)
	Other databases	**164,566**			
00-00-001	RAINFOR data managed by ForestPlots.net	1,827	Oliver L. Phillips	Aurora Levesley	Lopez-Gonzalez et al. (2011)
00-00-003	SALVIAS	4,883	Brian Enquist	Brad Boyle	
00-00-005	Tundra Vegetation Plots (TundraPlot)	577	Anne D. Bjorkman	Sarah Elmendorf	Elmendorf et al. (2012)
00-RU-002	Database of Masaryk University`s Vegetation Research in Siberia	1,547	Milan Chytrý		Chytrý (2012)
AF-00-003	BIOTA Southern Africa Biodiversity Observatories Vegetation Database	1,666	Norbert Jürgens	Gerhard Muche	Muche et al. (2012)
AF-00-006	SWEA-Dataveg	2,704	Miguel Alvarez	Michael Curran	
AF-00-009	Vegetation Database of the Okavango Basin	590	Rasmus Revermann	Manfred Finckh	Revermann et al. (2016)
AF-CD-001	Forest Database of Central Congo Basin	292	Elizabeth Kearsley	Hans Verbeeck	Kearsley et al. (2013)
AF-ET-001	Vegetation Database of Ethiopia	74	Desalegn Wana	Anke Jentsch	Wana & Beierkuhnlein (2011)
AF-MA-001	Vegetation Database of Southern Morocco	1,337	Manfred Finckh		Finckh (2012)
AF-ZA-003*	SynBioSys Fynbos Vegetation Database	3,810	John Janssen		
AF-ZW-001*	Vegetation Database of Zimbabwe	36	Cyrus Samimi		Samimi (2003)
AS-00-001	Korean Forest Database	4,885	Tomáš Černý	Petr Petřík	Černý et al. (2015)
AS-00-003	Vegetation of Middle Asia	1,381	Arkadiusz Nowak	Marcin Nobis	Nowak et al. (2017)
AS-00-004	Rice Field Vegetation Database	179	Arkadiusz Nowak		
AS-BD-001	Tropical Forest Dataset of Bangladesh	211	Mohammed A.S. Arfin Khan	Fahmida Sultana	
AS-CN-001	China Forest-Steppe Ecotone Database	148	Hongyan Liu	Fengjun Zhao	Liu et al. (2000)
AS-CN-002	Tibet-PaDeMoS Grazing Transect	146	Karsten Wesche		Wang et al. (2017)
AS-CN-003*	Vegetation Database of the BEF China Project	27	Helge Bruelheide		Bruelheide et al. (2011)
AS-CN-004*	Vegetation Database of the Northern Mountains in China	485	Zhiyao Tang		
AS-CN-005*	Database Steppe Vegetation of Xinjiang	129	Kohei Suzuki		
AS-EG-001	Vegetation Database of Sinai in Egypt	926	Mohamed Z. Hatim		Hatim (2012)
AS-ID-001	Sulawesi Vegetation Database	24	Michael Kessler		
AS-IR-001	Vegetation Database of Iran	2,335	Jalil Noroozi	Parastoo Mahdavi	
AS-KG-001	Vegetation Database of South-Western Kyrgyzstan	452	Peter Borchardt	Udo Schickhoff	Borchardt & Schickhoff (2012)
AS-KZ-001	Database of Meadow Vegetation in the NW Tian Shan Mountains	94	Viktoria Wagner		Wagner (2009)
AS-MN-001	Southern Gobi Protected Areas Database	1,516	Henrik von Wehrden	Karsten Wesche	von Wehrden et al. (2009)
AS-RU-001	Wetland Vegetation Database of Baikal Siberia (WETBS)	2,381	Victor Chepinoga		Chepinoga (2012)

AS-RU-002	Database of Siberian Vegetation (DSV)	9,116	Andrey Korolyuk	Andrei Zverev	
AS-RU-004	Database of the University of Münster - Biodiversity and Ecosystem Research Group's Vegetation Research in Western Siberia and Kazakhstan	445	Norbert Hölzel	Wanja Mathar	
AS-SA-001*	Vegetation Database of Saudi Arabia	919	Mohamed Abd El-Rouf Mousa El-Sheikh		
AS-TJ-001	Eastern Pamirs	282	Kim André Vanselow		Vanselow (2016)
AS-TW-001	National Vegetation Database of Taiwan	930	Ching-Feng Li	Chang-Fu Hsieh	
AS-YE-001	Socotra Vegetation Database	396	Michele De Sanctis	Fabio Attorre	De Sanctis & Attorre (2012)
AU-AU-002	TERN AEKOS	21,261	Anita Smyth	Ben Sparrow	Turner et al (2017)
AU-NC-001	New Caledonian Plant Inventory and Permanent Plot Network (NC-PIPPN)	201	Jérôme Munzinger	Philippe Birnbaum	Ibanez et al. (2014)
AU-NZ-001	New Zealand National Vegetation Databank	1,895	Susan Wiser		Wiser et al. (2001)
AU-PG-001	Forest Plots from Papua New Guinea	63	Timothy Whitfeld	George Weiblen	Whitfeld et al. (2014)
NA-00-002	Tree Biodiversity Network (BIOTREE-NET)	1,757	Luis Cayuela		Cayuela et al. (2012)
NA-CA-003	Database of Timberline Vegetation in NW North America	110	Viktoria Wagner	Toby Spribille	agner et al. (2014)
NA-CA-004	Understory of Sugar Maple Dominated Stands in Quebec and Ontario (Canada)	156	Isabelle Aubin		Aubin et al. (2007)
NA-CA-005*	Boreal Forest of Canada	89	Yves Bergeron	Louis De Grandpré	
NA-GL-001	Vegetation Database of Greenland	664	Birgit Jedrzejek	Fred J.A. Daniëls	Sieg et al. (2006)
NA-US-002	VegBank	67,352	Robert K. Peet	Michael T. Lee	Peet et al. (2012a)
NA-US-006	Carolina Vegetation Survey Database	17,221	Robert K. Peet	Michael T. Lee	Peet et al. (2012b)
NA-US-014	Alaska-Arctic Vegetation Archive	1,363	Donald A. Walker	Amy Breen	Walker et al. (2016)
SA-00-002	VegPáramo	2,643	Gwendolyn Peyre	Xavier Font	Peyre et al. (2015)
SA-AR-002	Vegetation Database of Central Argentina	218	Marcelo R. Cabido	Alicia Acosta	
SA-BO-003	Bolivia Forest Plots	75	Michael Kessler	Sebastian Herzog	
SA-BR-002	Forest Inventory, State of Santa Catarina, Brazil (IFFSC Project)	1,669	Alexander Christian Vibrans	André Luis de Gasper	Vibrans et al. (2010)
SA-BR-003	Grasslands of Rio Grande do Sul, Brazil	320	Eduardo Vélez-Martin	Valério De Patta Pillar	
SA-BR-004	Grassland Database of Campos Sulinos	161	Gerhard E. Overbeck	Valério De Patta Pillar	
SA-CL-002	SSAForests_Plots_db	261	Alvaro G. Gutierrez		
SA-CL-003*	Chilean Park Transects - Fondecyt 1040528	165	Aníbal Pauchard	Alicia Marticorena	Pauchard et al. (2003)
SA-EC-001	Ecuador Forest Plot Database	172	Jürgen Homeier		

TITLE PAGE

REPORT PAPER

sPlot – a new tool for global vegetation analyses

Helge Bruelheide[x,1,2], Jürgen Dengler[x,3,4,2], Borja Jiménez-Alfaro[x,5,1,2], Oliver Purschke[x,6], Stephan M. Hennekens[7], Milan Chytrý[8], Valério D. Pillar[9], Florian Jansen[10], Jens Kattge[11,2], Brody Sandel[12], Isabelle Aubin[13], Idoia Biurrun[14], Richard Field[15], Sylvia Haider[1], Ute Jandt[1], Jonathan Lenoir[16], Robert K. Peet[17], Gwendolyn Peyre[18], Francesco Maria Sabatini[1,2], Marco Schmidt[19], Franziska Schrodt[15], Marten Winter[2], Svetlana Aćić[20], Emiliano Agrillo[21], Miguel Alvarez[22], Didem Ambarlı[23], Pierangela Angelini[24], Iva Apostolova[25], Mohammed A.S. Arfin Khan[26,27], Elise Arnst[28], Fabio Attorre[21], Christopher Baraloto[29,30], Michael Beckmann[31], Christian Berg[32], Yves Bergeron[33], Erwin Bergmeier[34], Anne D. Bjorkman[35], Viktoria Bondareva[36], Peter Borchardt[37], Zoltán Botta-Dukát[38], Brad Boyle[39], Amy Breen[40], Henry Brisse[41], Chaeho Byun[42], Marcelo R. Cabido[43], Laura Casella[24], Luis Cayuela[44], Tomáš Černý[45], Victor Chepinoga[46], János Csiky[47], Michael Curran[48], Renata Ćušterevska[49], Zora Dajić Stevanović[20], Els De Bie[50], Patrice De Ruffray[51], Michele De Sanctis[21], Panayotis Dimopoulos[52], Stefan Dressler[53], Rasmus Ejrnæs[54], Mohamed Abd El-Rouf Mousa El-Sheikh[55,56], Brian Enquist[39], Jörg Ewald[57], Jaime Fagúndez[58], Manfred Finckh[59], Xavier Font[60], Estelle Forey[61], Georgios Fotiadis[62], Itziar García-Mijangos[14], André Luis de Gasper[63], Valentin Golub[36], Alvaro G. Gutierrez[64], Mohamed Z. Hatim[65], Tianhua He[66], Pedro Higuchi[67], Dana Holubová[8], Norbert Hölzel[68], Jürgen Homeier[69], Adrian Indreica[70], Deniz Işık Gürsoy[71], Steven Jansen[72], John Janssen[7], Birgit Jedrzejek[68], Martin Jiroušek[8,73], Norbert Jürgens[59], Zygmunt Kącki[74], Ali Kavgacı[75], Elizabeth Kearsley[76], Michael Kessler[77], Ilona Knollová[8], Vitaliy Kolomiychuk[78], Andrey Korolyuk[79], Maria Kozhevnikova[80], Łukasz Kozub[81], Daniel Krstonošić[82], Hjalmar Kühl[83,2], Ingolf Kühn[84,1,2], Anna Kuzemko[85], Filip Küzmič[86], Flavia Landucci[8], Michael T. Lee[87], Aurora Levesley[88], Ching-Feng Li[89], Hongyan Liu[90], Gabriela Lopez-Gonzalez[88], Tatiana Lysenko[91], Armin Macanović[92], Parastoo Mahdavi[93], Peter Manning[94], Corrado Marcenò[14], Vassiliy Martynenko[95], Maurizio Mencuccini[96], Vanessa Minden[97], Jesper Erenskjold Moeslund[54], Marco Moretti[98], Jonas V. Müller[99], Jérôme Munzinger[100], Ülo Niinemets[101], Marcin Nobis[102], Jalil Noroozi[103], Arkadiusz Nowak[104], Viktor Onyshchenko[85], Gerhard E. Overbeck[9], Wim A. Ozinga[105], Anibal Pauchard[106], Hristo Pedashenko[107], Josep Peñuelas[108,109], Aaron Pérez-Haase[110,111], Tomáš Peterka[8], Petr Petřík[112], Oliver L. Phillips[88], Vadim Prokhorov[80], Valerijus Rašomavičius[113], Rasmus Revermann[59], John Rodwell[114], Eszter Ruprecht[115], Solvita Rūsiņa[116], Cyrus Samimi[117], Joop H.J. Schaminée[7], Ute Schmiedel[59], Jozef Šibík[118], Urban Šilc[86], Željko Škvorc[82], Anita Smyth[119], Tenekwetche Sop[83,2], Desislava Sopotlieva[25], Ben Sparrow[119], Zvjezdana Stančić[120], Jens-Christian Svenning[35], Grzegorz Swacha[74], Zhiyao Tang[90], Ioannis Tsiripidis[121], Pavel Dan Turtureanu[122], Emin Ugurlu[123], Domas Uogintas[113], Milan Valachovič[118], Kim André Vanselow[124], Yulia Vashenyak[125], Kiril Vassilev[25], Eduardo Vélez-Martin[9], Roberto Venanzoni[126], Alexander Christian Vibrans[127], Cyrille Violle[128], Risto Virtanen[129,130,2], Henrik von Wehrden[131], Viktoria Wagner[132], Donald A. Walker[133], Desalegn Wana[134], Evan Weiher[135], Karsten Wesche[136,2,137], Timothy Whitfeld[138], Wolfgang Willner[139], Susan Wiser[28], Thomas Wohlgemuth[140], Sergey Yamalov[141], Georg Zizka[53], Andrei Zverev[142]

[x] Helge Bruelheide, Jürgen Dengler, Borja Jiménez-Alfaro and Oliver Purschke should be considered joint first authors

AFFILIATIONS

[1]Institute of Biology / Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Halle, Germany

[2]German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany

[3]Vegetation Ecology Group, Institute of Natural Resource Sciences (IUNR), Zurich University of Applied Sciences (ZHAW), Wädenswil, Switzerland

[4]Plant Ecology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany

[5]Research Unit of Biodiversity (CSUC/UO/PA), University of Oviedo, Mieres, Spain

[6]Leipzig, Germany

[7]Wageningen Environmental Research (Alterra), Wageningen University and Research, Wageningen, Netherlands

[8]Department of Botany and Zoology, Masaryk University, Brno, Czech Republic

[9]Department of Ecology, Universidade Federal do Rio Grande do Sul, Porto Alegre, Brazil

[10]Faculty of Agricultural and Environmental Sciences, University of Rostock, Rostock, Germany

[11]Max Planck Institute for Biogeochemistry, Jena, Germany

[12]Department of Biology, Santa Clara University, Santa Clara, CA, United States

[13]Great Lakes Forestry Centre, Canadian Forest Service, Natural Resources Canada, Sault Ste Marie (Ontario), Canada

[14]Plant Biology and Ecology, University of the Basque Country UPV/EHU, Bilbao, Spain

[15]School of Geography, University of Nottingham, Nottingham, United Kingdom

[16]Ecologie et Dynamiques des Systèmes Anthropisés (EDYSAN, UMR 7058 CNRS-UPJV), Université de Picardie Jules Verne, Amiens, France

[17]Department of Biology, University of North Carolina, Chapel Hill, NC, United States

[18]Department of Civil and Environmental Engineering, University of the Andes, Bogota, Colombia

[19]Data and Modelling Centre, Senckenberg Biodiversity and Climate Research Centre (BiK-F), Frankfurt am Main, Germany

[20]Department of Agrobotany, Faculty of Agriculture, Belgrade-Zemun, Serbia

[21]Department of Environmental Biology, "Sapienza" University of Rome, Rome, Italy

[22]Plant Nutrition, INRES, University of Bonn, Bonn, Germany

[23]Department of Agricultural Biotechnology, Faculty of Agriculture and Natural Sciences, Düzce University, Düzce, Turkey

[24]Biodiversity Conservation Department, ISPRA - Italian National Institute for Environmental Protection and Research, Rome, Italy

[25]Department of Plant and Fungal Diversity and Resources, Institute of Biodiversity and Ecosystem Research, Bulgarian Academy of Sciences, Sofia, Bulgaria

[26]Forestry & Environmental Science, Shahjalal University of Science & Technology, Sylhet, Bangladesh

[27]Disturbance Ecology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany

[28]Manaaki Whenua -- Landcare Research, Lincoln, New Zealand

[29]International Center for Tropical Botany (ICTB), The Kampong of the National Tropical Botanical Garden, Coconut Grove, Florida, United States

[30]Department of Biological Sciences, Florida International University, Miami, Florida, United States

[31]Landscape Ecology, Helmholtz Centre for Environmental Research - UFZ, Leipzig, Germany

[32]Botanical Garden, University of Graz, Graz, Austria

[33]Forest Research Institute, Université du Québec en Abitibi-Témiscamingue , Rouyn-Noranda, Canada

[34]Vegetation Ecology and Phytodiversity, University of Göttingen, Göttingen, Germany

[35]Center for Biodiversity Dynamics in a Changing World (BIOCHANGE) & Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University, Aarhus C, Denmark

[36]Laboratory of Phytocoenology, Institute of Ecology of the Volga River Basin, Toljatty , Russian Federation

[37]Institute of Geography, CEN - Center for Earth System Research and Sustainability, University of Hamburg, Hamburg, Germany

[38]Institute of Ecology and Botany, MTA Centre for Ecological Research, Vácrátót, Hungary

[39]Ecology and Evolutionary Biology, University of Arizona, Tucson, United States

[40]International Arctic Research Center, University of Alaska, Fairbanks, United States

[41]Faculté des Sciences, MEP, Marseille cedex 20, France

[42]School of Civil and Environmental Engineering, Yonsei University, Seoul, South Korea

[43]Multidisciplinary Institute for Plant Biology (IMBIV - CONICET), University of Cordoba - CONICET, Cordoba, Argentina

[44]Department of Biology, Geology, Physics and Inorganic Chemistry, Universidad Rey Juan Carlos, Móstoles, Spain

[45]Department of Forest Ecology, Faculty of Forestry and Wood Sciences, Czech University of Life Sciences Prague, Praha 6 - Suchdol, Czech Republic

[46]Laboratory of Physical Geography and Biogeography, V.B. Sochava Insitute of Geography SB RAS, Irkutsk, Russian Federation

[47]Department of Ecology, University of Pécs, Pécs, Hungary

[48]Institute of Environmental Engineering, Swiss Federal Institute of Technology (ETH) Zürich, Zürich, Switzerland

[49]Institute of Biology, Faculty of Natural Sciences and Mathematics, Skopje, Republic of Macedonia

[50]Departement of Biodiversity and Natural Environment, Research Institute for Nature and Forest (INBO), Brussels, Belgium

[51]IBMP, Strasburg, France

[52]Institute of Botany, Division of Plant Biology, Department of Biology, University of Patras, Patras, Greece

[53]Dept. Botany and Molecular Evolution, Senckenberg Research Institute, Frankfurt am Main, Germany

[54]Department of Bioscience, Aarhus University, Roende, Denmark

[55]Botany and Microbiology Department, College of Science, King Saud University, Riyadh, Saudi Arabia

[56]Botany Department, Faculty of Science, Damanhour University, Damanhour, Egypt

[57]Hochschule Weihenstephan-Triesdorf, University of Applied Sciences, Freising, Germany

[58]Faculty of Science, University of A Coruña, A Coruña, Spain

[59]Biodiversity, Ecology and Evolution of Plants, Institute for Plant Science & Microbiology, University of Hamburg, Hamburg, Germany

[60]Plant Biodiversity Resource Centre, University of Barcelona, Barcelona, Spain

[61]Laboratoire Ecodiv, EA 1293 URA IRSTEA, Normandie University, Mont-Saint-Aignan, France

[62]Department of Forestry & Natural Environment Management, TEI of Sterea Ellada, Karpenissi, Greece

[63]Departament of Natural Science, Regional University of Blumenau, Blumenau, Brazil

[64]Departamento de Ciencias Ambientales y Recursos Naturales Renovables, Facultad de Ciencias Agronomicas, Universidad de Chile, Santiago, Chile

[65]Botany, Faculty of Science, Tanta University, Tanta, Egypt

[66]School of Molecular and Life Sicences, Curtin University, Bentley, WA, Australia

[67]Forestry Department, Santa Catarina State University, Lages, Brazil

[68]Institute of Landscape Ecology, University of Münster, Münster, Germany

[69]Plant Ecology and Ecosystems Research, University of Göttingen, Göttingen, Germany

[70]Department of Silviculture, Transilvania University of Brasov, Brasov, Romania

[71]Department of Biology, Celal Bayar University, Manisa, Turkey

[72]Institute of Systematic Botany and Ecology, Ulm University, Ulm, Germany

[73]Department of Plant Biology, Mendel University in Brno, Brno, Czech Republic

[74]Botanical Garden, University of Wrocław, Wrocław, Poland

[75]Silviculture and Forest Botany, Soutwest Anatolia Forest Research Institute, Antalya, Turkey

[76]Department of Environment, Ghent University, Gent, Belgium

[77]Department of Systematic and Evolutionary Botany, University of Zurich, Zurich, Switzerland

[78]O.V. Fomin Botanical Garden, Taras Shevchenko National University of Kyiv, Kyiv, Ukraine

[79]Geosystem Laboratory, Central Siberian Botanical Garden, Siberian Branch, Russian Academy of Sciences , Novosibirsk, Russian Federation

[80]Institute of Environmental Sciences, Kazan Federal University, Kazan, Russian Federation

[81]Department of Plant Ecology and Environmental Conservation, Faculty of Biology, Biological and Chemical Research Centre, University of Warsaw, Warsaw, Poland

[82]Faculty of Forestry, University of Zagreb, Zagreb, Croatia

[83]Primatology, Max Planck Institute for Evolutionary Anthropology (MPI-EVA, Leipzig, Germany)

[84]Dept. Community Ecology, Helmholtz Centre for Environmental Research - UFZ, Halle, Germany

[85]M.G. Kholodny Institute of Botany, National Academy of Sciences of Ukraine, Kyiv, Ukraine

[86]Institute of Biology, Research Centre of Slovenian Academy of Sciences and Arts (ZRC SAZU), Ljubljana, Slovenia

[87]NatureServe, Durham, United States

[88]School of Geography, University of Leeds, Leeds, United Kingdom

[89]School of Forestry and Resource Conservation, National Taiwan University, Hsinchu, Taiwan

[90]College of Urban and Environmental Sciences, Peking University, Beijing, China

[91]Dept. of the Phytodiversity Problems, Institute of Ecology of the Volga River Basin RAS, Togliatti, Russian Federation

[92]Center for Ecology and Natural Resources - Academician Sulejman Redžić, Department of Biology, University of Sarajevo, Sarajevo, Bosnia and Herzegovina

[93]Research Group Vegetation Science & Nature Conservation, Dept. of Ecology and Environmental Science, Carl von Ossietzky-University Oldenburg, Oldenburg, Germany

[94]Project Group Causes and Consequences of Climate Change, Senckenberg Research Institute, Frankfurt am Main, Germany

[95]Ufa Institute of Biology of Ufa Federal Scientific Centre of the Russian Academy of Sciences, Ufa, Russian Federation

[96]Centre Research Ecology and Forestry Applications (CREAF), ICREA, Barcelona, Spain

[97]Institute of Biology an Environmental Sciences, Carl von Ossietzky-University Oldenburg, Oldenburg, Germany

[98]Biodiversity and Conservation Biology, Swiss Federal Research Institute WSL, Birmensdorf, Switzerland

[99]Conservation Science, Royal Botanic Gardens, Kew, Ardingly, West Sussex, United Kingdom

[100]AMAP - Botany and Modelling of Plant Architecture and Vegetation, IRD, CIRAD, CNRS, INRA, Université Montpellier, Montpellier, France

[101]Chair of Crop Science and Plant Biology, Estonian University of Life Sciences, Tartu, Estonia

[102]Institute of Botany, Jagiellonian University, Kraków, Poland

[103]Department of Botany and Biodiversity Research, University of Vienna, Vienna, Austria

[104]Botanical Garden - Center for Biological Diversity Conservation, Polish Academy of Sciences, Warszawa, Poland

[105]Team Vegetation, Forest and Landscape Ecology, Wageningen Environmental Research, Wageningen, Netherlands

[106]Laboratorio de Invasiones Biológicas (LIB), University of Concepción, Concepción, Chile

[107]Amsterdam, Netherlands

[108]Global Ecology Unit CREAF-CSIC-UAB, CSIC, Bellaterra, Spain

[109]CREAF, Cerdanyola del Vallès, Spain

[110]Department of Evolutionary Biology, Ecology and Environmental Sciences, University of Barcelona, Barcelona, Spain

[111]Continental Ecology, Center for Advanced Studies of Blanes, Spanish Research Council (CEAB-CSIC), Blanes, Girona, Spain

[112]Department of GIS and Remote Sensing, Institute of Botany, The Czech Academy of Sciences, Průhonice, Czech Republic

[113]Institute of Botany, Nature Research Centre, Vilnius, Lithuania

[114]Lancaster, United Kingdom

[115]Hungarian Department of Biology and Ecology, Faculty of Biology and Geology, Babeș-Bolyai University, Cluj-Napoca, Romania

[116]Department of Geography, University of Latvia, Riga, Latvia

[117]Climatology, Bayreuth Center of Ecology and Environmental Research (BayCEER), University of Bayreuth, Bayreuth, Germany

[118]Institute of Botany, Plant Science and Biodiversity Centre Slovak Academy of Sciences, Bratislava, Slovakia

[119]TERN, University of Adelaide, Adelaide, Australia

[120]Faculty of Geotechnical Engineering, University of Zagreb, Varaždin, Croatia

[121]School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece

[122]A. Borza Botanical Garden, Babeș-Bolyai University, Cluj-Napoca, Romania

[123]Forest Engineering Department, Faculty of Forestry, Bursa Technical University, Yıldırım, Bursa, Turkey

[124]Department of Geography, University of Erlangen-Nuremberg, Erlangen, Germany

[125]Khmelnytskyi Institute of Interregional Academy of Personnel Management, Khmelnytskyi, Ukraine

[126]Department of Chemistry, Biology and Biotechnology, University of Perugia, Perugia, Italy

[127]Departamento de Engenharia Florestal, Universidade Regional de Blumenau, Blumenau, Brazil

[128]Centre d'Ecologie Fonctionnelle et Evolutive (UMR5175), CNRS - Université de Montpellier - Université Paul-Valéry Montpellier - EPHE, Montpellier, France

[129]Ecology and Genetics Research Unit, Biodiversity Unit, University of Oulu, Oulu, Finland

[130]Department of Physiological Diversity, Helmholtz Center for Environmental Research - UFZ, Leipzig, Germany

[131]Institute of Ecology, Leuphana University of Lüneburg, Lüneburg, Germany

[132]Department of Biological Sciences, University of Alberta, Edmonton, Canada

[133]Institute of Arctic Biology, University of Alaska, Fairbanks, United States

[134]Department of Geography & Environmental Studies, Addis Ababa University, Addis Ababa, Ethiopia

[135]Department of Biology, University of Wisconsin - Eau Claire, Eau Claire, WI, United States

[136]Botany Department, Senckenberg Museum of Natural History Görlitz, Görlitz, Germany

[137]International Institute Zittau, Technische Universität Dresden, Zittau, Germany

[138]Department of Ecology and Evolutionary Biology/Brown University Herbarium, Brown University, Providence, United States

[139]Vienna Institute for Nature Conservation & Analyses, Vienna, Austria

[140]Research Unit Forest Dynamics, Swiss Federal Institute for Forest, Snow and Landscape Research WSL, Birmensdorf, Switzerland

[141]Laboratory of Wild-Growing Flora, Botanical Garden-Institute, Ufa Scientific Centre, Russian Academy of Sciences, Ufa, Russian Federation

[142]Department of Botany, Tomsk State University, Tomsk, Russian Federation

Correspondence:

Helge Bruelheide, Institute of Biology / Geobotany and Botanical Garden, Martin Luther University Halle-Wittenberg, Am Kirchtor 1, 06108 Halle, Germany

Email: helge.bruelheide@botanik.uni-halle.de

ORCID:

Helge Bruelheide http://orcid.org/0000-0003-3135-0356

Jürgen Dengler http://orcid.org/0000-0003-3221-660X

Borja Jiménez-Alfaro http://orcid.org/0000-0001-6601-9597

Oliver Purschke http://orcid.org/0000-0003-0444-0882

Milan Chytrý http://orcid.org/0000-0002-8122-3075

Valério D. Pillar http://orcid.org/0000-0001-6408-2891

Jens Kattge http://orcid.org/0000-0002-1022-8469

Idoia Biurrun http://orcid.org/0000-0002-1454-0433

Richard Field http://orcid.org/0000-0003-2613-2688

Jonathan Lenoir http://orcid.org/0000-0003-0638-9582

Francesco M. Sabatini http://orcid.org/0000-0002-7202-7697

Marco Schmidt http://orcid.org/0000-0001-6087-6117

Franziska Schrodt http://orcid.org/0000-0001-9053-8872

Emiliano Agrillo http://orcid.org/0000-0003-2346-8346

Miguel Alvarez http://orcid.org/0000-0003-1500-1834

Pierangela Angelini http://orcid.org/0000-0002-5321-9757

Mohammed A.S. Arfin Khan http://orcid.org/0000-0001-6275-7023

Fabio Attorre http://orcid.org/0000-0002-7744-2195

Michael Beckmann http://orcid.org/0000-0002-5678-265X

Yves Bergeron http://orcid.org/0000-0003-3707-3687

Erwin Bergmeier http://orcid.org/0000-0002-6118-4611

Zoltán Botta-Dukát http://orcid.org/0000-0002-9544-3474

Chaeho Byun http://orcid.org/0000-0003-3209-3275

Laura Casella http://orcid.org/0000-0003-2550-3010

Luis Cayuela http://orcid.org/0000-0003-3562-2662

Victor Chepinoga http://orcid.org/0000-0003-3809-7453

Michele De Sanctis http://orcid.org/0000-0002-7280-6199

Jaime Fagúndez http://orcid.org/0000-0001-6605-7278

Xavier Font http://orcid.org/0000-0002-7253-8905

Estelle Forey http://orcid.org/0000-0001-6082-3023

André Luis de Gasper http://orcid.org/0000-0002-1940-9581

Alvaro G. Gutierrez http://orcid.org/0000-0001-8928-3198

Tianhua He http://orcid.org/0000-0002-0924-3637

Pedro Higuchi http://orcid.org/0000-0002-3855-555X

Norbert Hölzel http://orcid.org/0000-0002-6367-3400

Steven Jansen http://orcid.org/0000-0002-4476-5334

Martin Jiroušek http://orcid.org/0000-0002-4293-478X

Norbert Jürgens http://orcid.org/0000-0003-3211-0549

Ali Kavgacı http://orcid.org/0000-0002-4549-3668

Elizabeth Kearsley http://orcid.org/0000-0003-0046-3606

Michael Kessler http://orcid.org/0000-0003-4612-9937

Ingolf Kühn http://orcid.org/0000-0003-1691-8249

Flavia Landucci http://orcid.org/0000-0002-6848-0384

Ching-Feng Li http://orcid.org/0000-0003-0744-490X

Peter Manning http://orcid.org/0000-0002-7940-2023

Corrado Marcenò http://orcid.org/0000-0003-4361-5200

Maurizio Mencuccini http://orcid.org/0000-0003-0840-1477

Vanessa Minden http://orcid.org/0000-0002-4933-5931

Jesper Erenskjold Moeslund http://orcid.org/0000-0001-8591-7149

Marco Moretti http://orcid.org/0000-0002-5845-3198

Jérôme Munzinger http://orcid.org/0000-0001-5300-2702

Ülo Niinemets http://orcid.org/0000-0002-3078-2192

Arkadiusz Nowak http://orcid.org/0000-0001-8638-0208

Gerhard E. Overbeck http://orcid.org/0000-0002-8716-5136

Wim A. Ozinga http://orcid.org/0000-0002-6369-7859

Hristo Pedashenko http://orcid.org/0000-0002-6743-0625

Josep Penuelas http://orcid.org/0000-0002-7215-0150

Aaron Pérez-Haase http://orcid.org/0000-0002-5974-7374

Petr Petřík http://orcid.org/0000-0001-8518-6737

Oliver L. Phillips http://orcid.org/0000-0002-8993-6168

Jozef Šibík http://orcid.org/0000-0002-5949-862X

Urban Šilc http://orcid.org/0000-0002-3052-699X

Jens-Christian Svenning http://orcid.org/0000-0002-3415-0862

Emin Ugurlu http://orcid.org/0000-0003-0824-1426

Eduardo Vélez-Martin http://orcid.org/0000-0001-8028-8953

Roberto Venanzoni http://orcid.org/0000-0002-7768-0468

Risto Virtanen http://orcid.org/0000-0002-8295-8217

Evan Weiher http://orcid.org/0000-0002-5375-9964

Susan Wiser http://orcid.org/0000-0002-8938-8181

email:

Helge Bruelheide: helge.bruelheide@botanik.uni-halle.de

Jürgen Dengler: juergen.dengler@uni-bayreuth.de

Borja Jiménez-Alfaro: jimenezalfaro.borja@gmail.com

Oliver Purschke: oliverpurschke@web.de

Stephan M. Hennekens: stephan.hennekens@wur.nl

Milan Chytrý: chytry@sci.muni.cz

Valério De Patta Pillar: vpillar@ufrgs.br

Florian Jansen: florian.jansen@uni-rostock.de

Jens Kattge: jkattge@bgc-jena.mpg.de

Brody Sandel: bsandel@scu.edu

Marten Winter: marten.winter@idiv.de

Isabelle Aubin: isabelle.aubin@canada.ca

Idoia Biurrun: idoia.biurrun@ehu.es

Richard Field: Richard.Field@nottingham.ac.uk

Sylvia Haider: sylvia.haider@botanik.uni-halle.de

Ute Jandt: ute.jandt@botanik.uni-halle.de

Jonathan Lenoir: jonathan.lenoir@u-picardie.fr

Robert K. Peet: peet@unc.edu

Gwendolyn Peyre: gf.peyre@uniandes.edu.co

Francesco M. Sabatini: francesco.maria.sabatini@botanik.uni-halle.de

Marco Schmidt: marco.schmidt@stadt-frankfurt.de

Franziska Schrodt: f.i.schrodt@gmail.com

Svetlana Aćić: acic@agrif.bg.ac.rs

Emiliano Agrillo: emiliano.agrillo@uniroma1.it

Miguel Alvarez: malvarez@uni-bonn.de

Didem Ambarlı: didemambarli@duzce.edu.tr

Pierangela Angelini: pierangela.angelini@isprambiente.it

Iva Apostolova: iva.apostolova@gmail.com

Mohammed A.S. Arfin Khan: nobelarfin@yahoo.com

Elise Arnst: arnste@landcareresearch.co.nz

Fabio Attorre: fabio.attorre@uniroma1.it

Christian Berg: christian.berg@uni-graz.at

Yves Bergeron: yves.bergeron@uqat.ca

Erwin Bergmeier: erwin.bergmeier@bio.uni-goettingen.de

Anne D. Bjorkman: annebj@gmail.com

Viktoria Bondareva: bondarevavictoria@yandex.ru

Peter Borchardt: pbo1@gmx.de

Zoltán Botta-Dukát: botta-dukat.zoltan@okologia.mta.hu

Brad Boyle: bboyle@email.arizona.edu

Amy Breen: albreen@alaska.edu

Henry Brisse: brisse.henry@orange.fr

Marcelo R. Cabido: mcabido@imbiv.unc.edu.ar

Laura Casella: laura.casella@isprambiente.it

Luis Cayuela: luis.cayuela@urjc.es

Tomáš Černý: cernyt@fld.czu.cz

Victor Chepinoga: victor.chepinoga@gmail.com

János Csiky: moon@ttk.pte.hu

Michael Curran: currmi01@gmail.com

Renata Ćušterevska: renatapmf@yahoo.com

Zora Dajić Stevanović: dajic@agrif.bg.ac.rs

Els De Bie: els.debie@inbo.be

Patrice De Ruffray: patrice.de-ruffray@wanadoo.fr

Michele De Sanctis: michedes@gmail.com

Panayotis Dimopoulos: pdimopoulos@upatras.gr

Stefan Dressler: stefan.dressler@senckenberg.de

Rasmus Ejrnæs: rasmus@bios.au.dk

Mohamed Abd El-Rouf Mousa El-Sheikh: el_sheikh_eg@yahoo.co.uk

Brian Enquist: benquist@email.arizona.edu

Jörg Ewald: joerg.ewald@hswt.de

Manfred Finckh: manfred.finckh@uni-hamburg.de

Xavier Font: xfont@ub.edu

Georgios Fotiadis: gfotiad95@gmail.com

Itziar García-Mijangos: itziar.garcia@ehu.es

André Luis de Gasper: algasper@furb.br

Valentin Golub: vbgolub2000@mail.ru

Alvaro G. Gutierrez: bosqueciencia@gmail.com

Mohamed Z. Hatim: mohamed.zakaria@science.tanta.edu.eg

Norbert Hölzel: nhoelzel@uni-muenster.de

Dana Holubová: danmich@sci.muni.cz

Jürgen Homeier: jhomeie@gwdg.de

Adrian Indreica: adrianindreica@unitbv.ro

Deniz Işık Gürsoy: biodeniz-04@hotmail.com

John Janssen: john.janssen@wur.nl

Birgit Jedrzejek: siegb@uni-muenster.de

Martin Jiroušek: machozrut@mail.muni.cz

Norbert Jürgens: norbert.juergens@uni-hamburg.de

Zygmunt Kącki: zygmunt.kacki@uwr.edu.pl

Ali Kavgacı: alikavgaci1977@yahoo.com

Elizabeth Kearsley: elizabeth.kearsley@ugent.be

Michael Kessler: michael.kessler@systbot.uzh.ch

Ilona Knollová: ikuzel@sci.muni.cz

Vitaliy Kolomiychuk: vkolomiychuk@ukr.net

Andrey Korolyuk: akorolyuk@rambler.ru

Maria Kozhevnikova: mania_kazan@mail.ru

Łukasz Kozub: kozub.lukasz@gmail.com

Daniel Krstonošić: dkrstonosic@sumfak.hr

Hjalmar Kühl: kuehl@eva.mpg.de

Anna Kuzemko: anyameadow.ak@gmail.com

Filip Küzmič: filip.kuzmic@zrc-sazu.si

Flavia Landucci: flavia.landucci@gmail.com

Michael T. Lee: michael_lee@natureserve.org

Aurora Levesley: a.levesley@leeds.ac.uk

Ching-Feng Li: chingfeng.li@gmail.com

Hongyan Liu: lhy@urban.pku.edu.cn

Gabriela Lopez-Gonzalez: g.lopez-gonzalez@leeds.ac.uk

Tatiana Lysenko: ltm2000@mail.ru

Parastoo Mahdavi: parastoo.mahdavi@uni-oldenburg.de

Armin Macanović: arminecology@gmail.com

Corrado Marcenò: marceno.corrado@ehu.eus

Vassiliy Martynenko: vasmar@anrb.ru

Jesper Erenskjold Moeslund: jesper.moeslund@bios.au.dk

Jonas V. Müller: j.mueller@kew.org

Jérôme Munzinger: jerome.munzinger@ird.fr

Marcin Nobis: m.nobis@uj.edu.pl

Jalil Noroozi: noroozi.jalil@gmail.com

Arkadiusz Nowak: anowak@uni.opole.pl

Viktor Onyshchenko: labzap@ukr.net

Gerhard E. Overbeck: gerhard.overbeck@ufrgs.br

Anibal Pauchard: pauchard@udec.cl

Hristo Pedashenko: hristo_pedashenko@yahoo.com

Aaron Pérez-Haase: aaronperez@ub.edu

Tomáš Peterka: peterkatomasek@seznam.cz

Petr Petřík: petr.petrik@ibot.cas.cz

Oliver L. Phillips: o.phillips@leeds.ac.uk

Vadim Prokhorov: vadim.prokhorov@gmail.com

Valerijus Rašomavičius: valerijus.rasomavicius@botanika.lt

Rasmus Revermann: rasmus.revermann@gmail.com

John Rodwell: johnrodwell@tiscali.co.uk

Eszter Ruprecht: eszter.ruprecht@ubbcluj.ro

Solvita Rūsiņa: rusina@lu.lv

Cyrus Samimi: cyrus.samimi@uni-bayreuth.de

Joop H.J. Schaminée: joop.schaminee@wur.nl

Ute Schmiedel: ute.schmiedel@uni-hamburg.de

Jozef Šibík: jozef.sibik@savba.sk

Urban Šilc: urban@zrc-sazu.si

Željko Škvorc: skvorc@sumfak.hr

Anita Smyth: anita.smyth@adelaide.edu.au

Tenekwetche Sop : tenekwetche_sop@eva.mpg.de

Desislava Sopotlieva: desislava.sopotlieva@iber.bas.bg

Ben Sparrow: ben.sparrow@adelaide.edu.au

Zvjezdana Stančić: zvjezdana.stancic@gfv.hr

Jens-Christian Svenning: svenning@bios.au.dk

Grzegorz Swacha: gswacha@gmail.com

Zhiyao Tang: zytang@urban.pku.edu.cn

Ioannis Tsiripidis: tsiripid@bio.auth.gr

Pavel Dan Turtureanu: turtureanudan@gmail.com

Emin Ugurlu: emin.ugurlu@btu.edu.tr

Domas Uogintas: domas.uogintas@botanika.lt

Milan Valachovič: milan.valachovic@savba.sk

Kim André Vanselow: kim.vanselow@fau.de

Yulia Vashenyak: vasheniyak@mail.ru

Kiril Vassilev : kiril5914@abv.bg

Eduardo Vélez-Martin: velezedu@portoweb.com.br

Roberto Venanzoni: roberto.venanzoni@unipg.it

Alexander Christian Vibrans: acv@furb.br

Cyrille Violle: cyrille.violle@cefe.cnrs.fr

Risto Virtanen: risto.virtanen@oulu.fi
Henrik von Wehrden: henrik.von_wehrden@leuphana.de
Viktoria Wagner: viktoria.wagner@ualberta.ca
Donald A. Walker: dawalker@alaska.edu
Desalegn Wana: deswana2002@yahoo.com
Karsten Wesche: karsten.wesche@senckenberg.de
Timothy Whitfeld: timothy_whitfeld@brown.edu
Wolfgang Willner: wolfgang.willner@vinca.at
Susan Wiser: wisers@landcareresearch.co.nz
Thomas Wohlgemuth: thomas.wohlgemuth@wsl.ch
Sergey Yamalov: yamalovsm@mail.ru
Georg Zizka: georg.zizka@senckenberg.de
Andrei Zverev: ibiss@rambler.ru

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AUTHOR CONTRIBUTIONS

H.Bru. had the original idea and led the consortium from the start, while O.Pu. and J.D. coordinated the sPlot workshops. J.D., S.M.H. and U.J. compiled the databases to be included in sPlot. J.D. and later B.J.-A. and F.M.S. coordinated the network and the database. O.P. prepared the taxonomic and phylogenetic data. S.M.H programmed the Turboveg software. B.Sa., F.J., H.Bru., J.D., J.K., M.Ch., and V.D.P. organized the network in the Steering Committee. B.J.-A. and H.Bru. led the writing together with J.D. and input from S.M.H., O.Pu., M.Ch., F.J., J.K., V.D.P., B.Sa., I.Au., I.B., R.K.P., R.F., S.H., U.J., J.L., G.P., F.M.S., M.S., F.S. and M.W. The rest of authors (ordered alphabetically) contributed the plot and trait data. All authors agreed with the final manuscript.

BIOSKETCH

sPlot is a consortium established during three workshops held at the German Centre of Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig. The consortium currently comprises 110 member databases, two data aggregators and 43 personal members, including plant ecologists, biogeographers, field botanists and data analysts. More information about the consortium and its projects can be accessed at www.idiv.de/splot.

SHORT RUNNING TITLE

sPlot – the global vegetation database

ABSTRACT

Questions: Vegetation-plot records provide information on presence and cover or abundance of plants co-occurring in the same community. Vegetation-plot data are spread across research groups, environmental agencies and biodiversity research centers, and thus, are rarely accessible at continental or global scales. Here we present the sPlot database, which collates vegetation plots worldwide to allow for the exploration of global patterns in taxonomic, functional and phylogenetic diversity at the plant community level.

Location: sPlot version 2.1 contains records from 1,121,244 vegetation plots, which comprise 23,586,216 records of plant species and their relative cover or abundance in plots collected between 1885 and 2015.

Methods: We complemented the information for each plot by retrieving environmental conditions (i.e. climate and soil) and the biogeographic context (i.e. biomes) from external sources, and by calculating community-weighted means and variances of traits using gap-filled data from the global plant trait database TRY. Moreover, we created a phylogenetic tree for 50,167 out of the 54,519 species identified in the plots.

Results: We present the first maps of global patterns of community richness and community-weighted means of key traits.

Conclusions: The availability of vegetation plot data in sPlot offers new avenues for vegetation analysis at the global scale.

KEYWORDS

Biodiversity; community ecology; ecoinformatics; functional diversity; global scale; macroecology; phylogenetic diversity; plot database; sPlot; taxonomic diversity; vascular plant; vegetation relevé.

INTRODUCTION

Studying global biodiversity patterns is at the core of macroecological research (Kreft & Jetz, 2007; Wiens, 2011; Costello, Wilson & Houlding, 2012), since their exploration may provide insights into the ecological and evolutionary processes acting at different spatio-temporal scales (Ricklefs, 2004). The opportunities enabled by the compilation of large collections of biodiversity data into widely accessible global (GBIF, www.gbif.org) or continental databases (e.g. BIEN, www.bien.nceas.ucsb.edu/bien) have recently advanced our understanding of global biodiversity patterns, especially for vertebrates, but also for vascular plants (Swenson et al., 2012; Lamanna et al., 2014; Engemann et al., 2016; Butler et al., 2017). Although this development has led to the formulation of several macroecological theories (Currie et al., 2004; Pärtel, Bennett & Zobel, 2016), a more mechanistic understanding of how assembly processes shape ecological communities and consequently global biodiversity patterns, is still missing (Lessard, Belmaker, Myers, Chase & Rahbek, 2012).

Understanding the links between biodiversity patterns and assembly processes requires fine-grain data on the co-occurrence of species in ecological communities, sampled across continental or global spatial extents (Beck et al., 2012; Wisz et al., 2013). For example, such co-occurrence data have been used to compare changes in vegetation composition over time spans of decades (Jandt, von Wehrden & Bruelheide 2011; Perring et al. 2018). Unfortunately, information on fine-grain vegetation data up to now has not been readily available, as most of the continental to global biodiversity datasets have been derived from occurrence data (i.e. presence-only data), and after being aggregated spatially, have a relatively coarse-grain scale (e.g. 1-degree grid cells) and no information on species co-occurrence at the meaningful scale of local communities. In contrast, ~~(Boakes et al., 2010).~~v

~~V~~egetation-plot data ~~are~~ record~~s~~ ~~of~~ the cover or abundance of each plant species that occurs in a plot of a given size at the date of the survey, representing ~~. They represent~~ the main reservoir of plant community data worldwide (Dengler et al., 2011).

~~These~~ Vegetation-plot data differ in fundamental ways from databases of occurrence records of individual species aggregated at the level of grid cells or regions of hundreds or thousands of square kilometers (**Figure 1**). First, vegetation plots usually provide information on species relative cover or relative abundance, allowing for the testing of central theories of biogeography, such as the abundance-range size relationship (Gaston & Curnutt, 1998) or the relationship between local abundance and niche breadth (Gaston et al., 2000). Second, they contain information on which plant species co-occur in the same locality (Chytrý et al., 2016), which is a necessary precondition for direct biotic interactions among plant individuals. Third, unrecorded species can be considered truly absent from the aboveground vegetation at this scale because the standardized methodology of taking a vegetation record requires a systematic search for all species in a plot, or at least all species of the dominant functional group. Fourth, ~~they~~ many plots are spatially explicit and can be resurveyed through time to assess possible consequences of land use and climate change (Steinbauer et al. 2018; Perring et al. 2018). ~~While, so far, sPlot only contains plots that have been surveyed only once, it presents a global baseline for future resurveys.~~ Fifth, ~~they~~ vegetation plots represent ~~important~~ a snapshot of ~~an~~the primary producers of a terrestrial ecosystem, which~~ patch~~ ~~sources of information that~~ can be functionally linked to organisms from different trophic groups sampled in the same plots (e.g. multiple taxa surveys) and related processes and services both below (e.g. decomposition, nutrient cycling) and above ground (e.g. herbivory, pollination) (~~Sardans et al. 2017,~~e.g. ~~Bruelheide~~ Schuldt et al. 2018).

Recently several projects at the regional to continental scale have demonstrated the potential of using vegetation-plot databases for exploring biodiversity patterns and the underlying assembly processes. Using vegetation data of French grasslands, Borgy et al. (2017) demonstrated that weighting leaf traits by species abundance in local communities is pivotal to capture leaf trait–environment relationships. Analyzing United States forest assemblages surveyed at the community level, Šímová, Rueda & Hawkins (2017) were able to relate cold or drought tolerance to leaf traits, dispersal traits and traits related to stem hydraulics. Using plot-based tree inventories of the United States forest service, Zhang, Niinemets, Sheffield & Lichstein (2018) found that shifts in tree functional composition amplifies the response of forest biomass to droughts. Based on >15.000 plots from a wide number of habitat types in Denmark, Moeslund et al. (2017) showed that typical plant species that are part of the site-specific species pool, but are absent in a community tend to depend on mycorrhiza, ~~be~~ are mostly adapted to low light and low nutrient levels, have poor dispersal abilities and ~~be~~ are ruderals and stress intolerant. By collating >40,000 vegetation plots sampled in European beech forests, Jiménez-Alfaro et al. (2018) found that current local community diversity and species pool sizes calculated at different scales were mainly explained by proximity to glacial refugia and current precipitation.

Although large collections of vegetation-plot data are now available from national to continental levels (e.g. Schaminée, Hennekens, Chytrý & Rodwell, 2012; Peet, Lee, Jennings & Faber-Langendoen, 2012; Schmidt et al., 2012; Chytrý et al., 2016; Enquist, Condit, Peet, Schildhauer & Thiers, 2016), they are rarely used in global-scale biodiversity research (Wiser, 2016; Franklin, Serra-Díez, Syphard & Regan, 2017). This is unfortunate~~,~~ because vegetation-plot data may reveal important patterns that cannot be captured by grid-based datasets (**Table 1**). Functional composition patterns, for instance, may differ substantially when considering vegetation-plot data rather than single species occurrences aggregated at the level of coarse-grain grid cells. Using plant height for illustration reveals that the trait means calculated on all the species occurring in a grid cell may differ strongly from the community-weighted means (CWMs) averaged across local communities (**Figure 1**). Nevertheless, only the grid-based approach has been used to date in studies of the geographic distribution of trait values (Swenson et al., 2012, 2017; Wright et al., 2017)~~, even though it disregards varying species abundances in local communities and the relative spatial extent of different communities~~.

~~Compiling a global database of vegetation plots is technically and conceptually challenging as it requires the integration of data from heterogeneous sources, collected and stored according to different standards, and often based on inconsistent taxonomic nomenclatures.~~ Here, we present ~~an attempt to overcome these challenges with~~ sPlot, a global database ~~of plant co-occurrence data,~~for compiling and integrating plant community data. We describe (i) main steps in integrating vegetation-plot data in a repository that provides taxonomic, functional and phylogenetic information on co-occurring plant species and links it to global environmental drivers; (ii) principal sources and properties of the data and the procedure for data usage; and (iii) expected impacts of the database in future ecological research. To illustrate the potential of sPlot we also show global diversity patterns that can be readily derived from the current content.

2. ~~MATERIAL AND METHODS~~ COMPILATION OF THE sPlot DATABASE

2.1 Vegetation-plot data

The sPlot consortium currently collates 110 vegetation-plot databases of regional, national or continental extents. Some of the databases have been previously aggregated by and contributed through two (sub-) continental database initiatives (**Table 2** and **Appendix S1** in Supporting Information). All data from Europe and nearby regions were contributed via the European Vegetation Archive (EVA), using the SynBioSys taxon database as a standard taxonomic backbone (Chytrý et al., 2016). Three African databases were contributed via the Tropical African Vegetation Archive (TAVA). In addition, multiple U.S. databases were contributed through the VegBank archive maintained in support of the U.S~~.~~. National Vegetation

Classification (Peet et al. 2012). The data from other regions (South America, Asia) were contributed as separate databases.

We stored the vegetation-plot data from the individual databases in the database software TURBOVEG v2 (Hennekens & Schaminée, 2001). Our general procedure was to preserve the original structure and content of the databases as much as possible in order to facilitate regular updates through automated workflows. The individual databases were then integrated into a single SQLite database using TURBOVEG v3 (S.M. Hennekens, ALTERRA, The Netherlands; www.synbiosys.alterra.nl/turboveg3/help/en/index.html). TURBOVEG v3 combines the species lists from the original databases in a single repository and links the plot attributes (so-called header data) to 58 descriptors of vegetation-plots (**Table S2.1** in Appendix S2). The metadata of the databases collated in sPlot were managed through the Global Index of Vegetation-Plot Databases (GIVD; Dengler et al. 2011), using the GIVD ID as the identifier. The current sPlot version 2.1 was created in October 2016 and contains 1,121,244 vegetation plots with 23,586,216 plant species × plot observations (i.e. ords of a species in a plot). Most records (1,073,737; 95.8%) have information on cover, 29,288 on presence/absence, 5,854 on basal area, 3,265 on counts of individuals, 148 on importance value, 1,895 on per cent frequency, 4,883 on number of stems, and further 2,174 have a mix of these types of these different metrics.

2.2 Taxonomic standardization

To combine the species lists of the different databases in sPlot, we constructed a taxonomic backbone. To link co-occurrence information in sPlot with plant traits, we expanded this backbone to integrate plant names used in the TRY database (Kattge et al., 2011). The taxon names (without nomenclatural authors) from sPlot 2.1 and TRY 3.0 were first concatenated into one list, resulting in 121,861 names, of which 61,588 (50.5%) were unique to sPlot; 35,429 (29.1%) unique to TRY; and 24,844 (20.4%) shared between TRY and sPlot. Taxon names were parsed and resolved using the Taxonomic Name Resolution Service web application (TNRS version 4.0; Boyle et al., 2013; iPlant Collaborative, 2015), using the five TNRS standard sources ranked by default. We allowed for (i) partial matching to the next higher rank (genus or family) if the full taxon name could not be found and (ii) full fuzzy matching, to return names that were matched within a maximum number of four single-character edits (Levenshtein edit distance of 4), which corresponds to the minimum match accuracy of 0.05 in TNRS, with 1 indicating a perfect match.

We accepted all names that were matched, or converted from synonyms, with an overall match score of 1. In case with no exact match (i.e. the overall match score was <1), names were inspected on an individual basis. All names that matched at taxonomic ranks lower than species (e.g. subspecies, varieties) were accepted as correct names. The name matching procedure was repeated for the uncertain names (i.e. with match accuracy scores below the threshold value from the first matching run), with a preference on first using the source ‘Tropicos’(Missouri Botanical Garden; http://www.tropicos.org/; accessed 19 Dec 2014) because here matching scores were often higher for names of low taxonomic rank. The remaining 9,641 non-matched names were resolved using (i) the additional source ‘NCBI’ (Federhen, 2010) within TNRS, (ii) the matching tools in the Plant List web application (The Plant List 2010), (iii) the ‘tpl’-function within the R-package ‘Taxonstand’ (Cayuela, Stein & Oksanen, 2017) and (iv) manual inspection (i.e. to resolve vernacular names). All subspecies were aggregated to the species level. Names that could not be matched were classified as ‘No suitable matches found’. Because sPlot and TRY contain taxa of non-vascular plants, we tagged vascular plant names based on their family and phylum affiliation, using the ‘rgbif’ library in R (Chamberlain, 2017). Of the full list of plant names in sPlot and TRY, 79,171 (94.6%) plant names were matched at the species level, 4,343 (5.2%) at the genus level, 152 (0.2%) at the family level and 13 names at higher taxonomic levels. Overall, this led to 58,066 accepted taxon names in sPlot. Family affiliation was classified according to APG III (Bremer et al., 2009). A detailed description of the workflow, including R-code, is available in Purschke (2017a).

One potential shortcoming of our taxonomic backbone is that for most regions it was necessary to standardize taxa using standard sets of taxonomic synonyms. Thus, if a taxonomic name represents multiple taxonomic concepts, e.g. such as created by the splitting and lumping of taxa, or a name has been misapplied in a region, we must trust that this problem has been addressed in our component databases (Franz, Peet & Weakley, 2004; Jansen & Dengler, 2010).

2.3 Physiognomic information

To achieve a classification into forests vs. non-forests that is applicable to all plots irrespective of the structural and habitat data provided by the source database, we defined as forest all plot records that had >25% absolute cover of the tree layer, making use of the attribute data of sPlot. This threshold is similar to the classification of Ellenberg & Müller-Dombois (1967), who defined woodland formations with trees covering more than 30%. There were 16,244 tree species in the sPlot database. There were 16,244 tree species in the sPlot database. As tree layer cover was available for only 25% of all plots, we additionally used the information whether the taxa present in a plot were trees (usually defined as being taller than 5 m), using the plant growth form information from TRY (see below). Thus, plots lacking tree cover information were defined as forests if the sum of relative cover of all tree taxa was >25%. Similarly, we defined non-forests by calculating the cover of all taxa that were not defined as trees or shrubs (also taken from the TRY plant growth form information) and that were not taller than 2 m, using the TRY data on mean plant height. In total, 21,888 taxa belonged to this category. We defined all plots as non-forests if the sum of relative cover of these low-stature, non-tree and non-shrub taxa was >90%. As we did not have the growth form and height information for all taxa, a fraction of about 25% of the plots remained unassigned (i.e. was neither forest, nor non-forest. In addition, more detailed classifications of plots into physiognomic formations (**Table S3.2** in Appendix S3) and naturalness (**Table S3.3** in Appendix S3) were derived from various types of plot-level or database-level information provided by the sources and stored in five separate fields (see **Table S2.1** in Appendix S2).

2.4 Phylogenetic information

We developed a workflow to generate a phylogeny of the vascular plant species in sPlot, using the phylogeny of Zanne et al. (2014), updated by Qian & Jin (2016). Species present in sPlot but missing from this phylogeny were added next to a randomly selected congener (see also Maitner et al., 2018). This approach has been demonstrated to introduce less bias into subsequent analyses than adding missing species as polytomies to the respective genera (Davies et al., 2012). We only added species based on taxonomic information on the genus level, thus not making use of family affiliation. Because of the absence of congeners in the reference phylogeny, 7,147 species could not be added (11.7% of all resolved taxa in sPlot and TRY). This resulted in a phylogeny with 54,067 resolved taxon names from 61,214 standardized taxa in the combined list of sPlot and TRY. The tree was finally pruned to the vascular plant taxa of the current sPlot version 2.1, resulting in a phylogenetic tree for 53,489 out of the 58,066 taxa in sPlot. Of these 53,489 names, 16,026 are also found among the 31,389 taxa in the phylogenetic tree of Qian & Jin (2016), i.e. 51.1%. The full procedure and the R code is available in Purschke (2017b).

2.5 Associated environmental plot information

To complement the plot data, we harmonized geographical coordinates (in decimal degrees), elevation (m above sea level), aspect (degrees) and slope (degrees) as provided by the contributing databases. All other variables were too sparsely and too inconsistently sampled across databases to be combined in the global set, but were retained in the original data sources and can be retrieved for particular purposes.

We used the geographic coordinates to create a geodatabase in ArcGIS 14.1 (ESRI, Redlands, CA) to link sPlot 2.1 to these climate and soil data. We retrieved data for all the 19 bioclimatic variables provided by CHELSA v1.1 (Karger et al., 2017) by averaging climatic data from the period 1979–2013 at 30 arc seconds (about 1 km in grid cells near to the equator). These variables are the same as the ones used in WorldClim (www.worldclim.org; Hijmans, Cameron, Parra, Jones & Jarvis, 2005), but calculated with a downscaling approach based on estimates of the ERA-Interim climatic reanalysis. While the CHELSA climatological data have a similar accuracy as other products for temperature, they are more precise for precipitation patterns (Karger, et al. 2017). We also calculated growing degree days for 1 °C (GDD1) and 5 °C (GDD5), according to Synes & Osborne (2011) and based on CHELSA data, and included the index of aridity and potential evapotranspiration extracted from the CGIAR-CSI website (www.cgiar-csi.org). In addition, we extracted seven soil variables from the SOILGRIDS project (https://soilgrids.org/; licensed by ISRIC – World Soil Information), downloaded at 250-m resolution and then converted to the same 30-arc second grid format of CHELSA. To explore the distribution of sPlot data in the global environmental space, we subjected all 30 climate and soil variables of the global terrestrial surface rasterized on a 2.5 arc-minute grid resolution to a principal component analysis (PCA) on standardized and centered data. We subsequently created a grid of 100 × 100 cells within the bi-dimensional environmental space defined by the first two PCA axes (PC1 and PC2) and counted the number of terrestrial cells per environmental grid cell of the PC1-PC2 space. Then, we counted the number of plots in sPlot in the same PCA grid (**Figure 2**).

We linked all vegetation plots to two global biome classifications. We used the World Wildlife Fund (WWF) spatial information on terrestrial ecoregions (Olson et al., 2001) to assign plots to one of the 867 ecoregions, 14 biomes and eight biogeographic realms. The WWF approach is based on a bottom-up expert system using various regional biodiversity sources to define ecoregions, which in turn are grouped into realms and biomes (Olson et al., 2001). In addition, we created a shapefile for the ecozones defined by Schultz (2005) to represent major biomes in response to global climatic variation. Since these zones are climatically heterogeneous in mountain regions, we differentiated an additional "alpine" biome for mountain areas above the lower mountain thermal belt, as defined in the classification of world mountain regions by Körner et al. (2017). This resulted in a distinction of 10 major biomes (**Fig. S4.5 in Appendix S4**), whose shape file is freely available ~~(from https://www.idiv.de/en/sdiv/working_groups/wg_pool/splot/materials.html)~~**Appendix S5)**.

2.6 Trait information

To broaden the potential applications of the global vegetation database in functional contexts, we linked sPlot to TRY. We accessed plant trait data from TRY version 3.0 on August 10, 2016 and included 18 traits that describe the leaf, wood and seed economics spectra (Westoby, 1998; Reich, 2014; **Table S6~~5~~.4 in Appendix S6~~5~~**), and are known to affect different key ecosystem processes and to respond to macroclimatic drivers. These traits were represented across all species in the TRY database by at least 1,000 trait records. We excluded trait records from manipulative experiments and outliers (Kattge et al., 2011), which resulted in a matrix with 632,938 individual plant records on 52,032 taxa in TRY, having data records for an average of 3.08 for the 18 selected traits. On average, each trait has been measured at least once in 17.1% of all taxa. In order to attain data for these 18 traits for all species with at least one trait value in TRY, we employed hierarchical Bayesian modelling, using the R package 'BHPMF' (Schrodt et al., 2015; Fazayeli, Banerpee, Kattge, Schrodt & Reich, 2017), to fill a gap in the matrix of individual plant records in TRY. Gap-filling allows to obtain trait values for a species on which this trait has not been measured, but for which other traits were available. To assess gap-filling quality, we used the probability density distributions provided by BHPMF for each imputation and removed highly uncertain imputations with a coefficient of variation >1. We then $\log_e$-transformed all gap-filled trait values and averaged them by taxon. For taxa recorded at genus level only, we calculated genus means, resulting in a full trait matrix for 26,632 out of the 54,519 taxa in sPlot (45.9%), with 6, 1,510 and 25,116 taxa at the family, genus and species level, respectively. These species covered 88.7% of all species-by-plot combinations.

For every trait *j* and plot *k*, we calculated the community-weighted mean (CWM) and the community-weighted variance (CWV) for each of the 18 traits in a plot (Enquist et al., 2015):

$$CWM_{j,k} = \sum_{i}^{n_k} p_{i,k} t_{i,j}$$

$$CWV_{j,k} = \sum_{i}^{n_k} p_{i,k}\ (t_{i,j} - CWM_{j,k})^2$$

where n_k is the number of species with trait information in plot *k*, $p_{i,k}$ is the relative abundance of species *i* in plot *k* calculated as the species' fraction in cover or abundance of total cover or abundance, and $t_{i,j}$ is the mean value of species *i* for trait *j*. CWMs and CWVs were calculated for 18 traits in 1,117,369 and 1,099,463 plots, respectively, the second being a smaller number as at least two taxa were needed for CWV calculation.

3. ~~RESULTS~~CONTENT OF sPlot 2.1

3.1 Plot community data

sPlot 2.1 contains 1,121,244 vegetation plots from 160 countries and from all continents (**Figure 3**). The global coverage is biased towards Europe, North America and Australia, reflecting unequal sampling effort across the globe (**Table 1**). At the ecoregion level, major gaps occur in the wet tropics of South America and Asia, as well as in subtropical deserts worldwide and in the North American taiga. Although the plots are highly clustered geographically, their coverage in the environmental space is much more representative: the highest concentration of plots is found in environments that are most abundant globally (**Figure 2**), while they are lacking in the very moist parts of the environmental space, which are also spatially rare, and in the very cold parts, which are sparsely vegetated.

In most cases (98.4%), plot records in sPlot include full species lists of vascular plants, while 1.6% had only wood species above a certain diameter or only the most dominant species recorded. Terricolous bryophytes and lichens were additionally identified in 14% and 7% of plots, respectively. (**Table S2.1** **in Appendix S2**). Forest and non-forest plots comprise 330,873 (29.7%) and 513,035 (46.0%) of all plots in sPlot, respectively. In most cases, species abundance was estimated using different variants of the Braun-Blanquet cover-abundance scale (66%), followed by percentage cover (15%) and 55 other numeric or ordinal scales. The temporal extent of the data spans from 1885 to 2015, but >94% of vegetation plots were recorded later than 1960 (**Fig. S2.1** **in Appendix S2**). Almost all plots are georeferenced (1,120,686) and most plots have location uncertainty of 10 m or less (**Fig. S2.2** **in Appendix S2**).

Vascular plant richness per plot ranges from 1 to 723 species (median = 17 species). The most frequent richness class is between 20 and 25 species (**Fig. S2.3** **in Appendix S2**). Plot size is reported in 65.4% of plots, ranging from less than 1 m^2 to 25 ha, with a median of 36 m^2. While forest plots have plot sizes ≥100 m^2, and in most cases ≤1,000 m^2, non-forest plots range between ≥5 and ≤100 m^2 (**Fig. S2.4** **in Appendix S2**). When using these size ranges, forest plots tend to be richer in species (**Figure 4a**). The fact that the gradient in richness found in our plots was at least one order of magnitude stronger than differences that could be expected by the differences in plot sizes, prompted us to produce the first global maps of plot-scale species richness, separately for forests and non-forests (**Figure 4a**). While plots with complete vascular species composition are largely lacking from the wet tropics, for the remaining biomes the plot-scale richness data do not show the typical latitudinal richness gradient in either formation. Particularly species-rich forests are found in the wet subtropics (such as SE United States, Taiwan and the East coast of Australia) as well as in some mountainous regions of the nemoral and steppic biomes of Eurasia. Likewise, non-forest communities, have a particularly high mean vascular plant species in mountainous regions of the nemoral and steppic biomes of Eurasia.

3.2 Phylogenetic information

The phylogenetic tree for sPlot was produced from 53,489 vascular plant names contained in the database, comprising 5518 genera (**Appendix S7**~~6~~). Moderately to highly frequent species in sPlot 2.1 are equally distributed across the phylogeny (corresponding to yellowish to reddish colors for low and high peaks, respectively, in **Fig. S7**~~6~~**.6 in Appendix S**~~6~~**7**). Coverage of species included in the phylogeny ranges from 89% of species that occur only once in all plots to 100% of species with a frequency >10,000 plots (**Fig. S7**~~6~~**.7 in Appendix S**~~6~~**7**).

3.3 Functional information

The proportion of species with trait information increases with the species' frequency in plots. Gap-filled trait information is available for 77.2% and 96.2% for taxa that occurred in more than 100 and 1,000 plots, respectively. Trait coverage is similar across biomes (**Fig. S8**~~7~~**.8 in Appendix S**~~7~~**8**). Across all biomes, the proportion of species for which gap-filled trait data are available increases with the species' frequency across plots. Compared to gap-filled data, trait coverage for the original trait data is considerably lower, being highest for height, seed mass, leaf area and specific leaf area (SLA, **Fig. S8**~~7~~**.9 in Appendix S**~~7~~**8**).

The high representation of the 18 traits in the gap-filled trait data and the high degree of trait coverage for frequent species across all biomes (>75%) made us confident to produce the first maps of global patterns of community-weighted means (CWMs) (**Figure 4b–d**). The maps show the main trait dimensions of SLA, height and seed mass, separately for forests and non-forests, for those regions of the world that are already sufficiently covered by sPlot data. Accordingly, CWMs of SLA are quite similar for forest and non-forest plots, being highest in western North America and Europe and lowest in eastern North America, East and South Australia (**Figure 4b**). Non-forest vegetation shows lowest CWMs of SLA in the desert regions of the Namib and Sinai. Forests with highest CWMs of canopy height are found along the western and eastern coast of North America, some regions in Europe, East Asia and southern Australia (**Figure 4c**). These areas only partly coincide with those of highest seed masses for forests, while seed mass in non-forests is highest in the eastern Mediterranean Basin and in Central Asia (**Figure 4d**). The corresponding patterns for CWV are shown in Appendix **Fig. S9~~8~~.10 in Appendix S9~~8~~**.

4. DATA USAGE

The sPlot database (the vegetation-plot data, including the environmental information for each plot and the species phylogeny) is released in fixed versions to allow reproducibility of results, but also due to the enormous effort needed for data integration and harmonization and for updating the phylogeny. By delivering few fixed versions while keeping older versions available, the sPlot consortium ensures that the same data can be used in ~~numerous~~ parallel projects and that the data underlying a specific study remain accessible in the future, thus allowing re-analysis. Each new version will be matched to the current TRY database~~, thus providing CWMs and CWVs for all plots~~.

Data access to sPlot is regulated by the Governance and Data Property Rules (www.idiv.de/sPlot) to ensure a fair balance between the interests of data contributors and data analysts. In brief, the sPlot Rules state that: (1) all contributing vegetation-plot databases become members of the sPlot consortium, represented by their custodian and deputy custodian; (2) vegetation-plot data contributed to sPlot remain the property of the data contributors and can be withdrawn at any time except for approved projects; (3) other scientists (e.g. data managers or participants of the sPlot workshops) with particular responsibilities may also be appointed as personal members to the sPlot consortium; (4) sPlot data can be requested for projects that involve at least one member of the sPlot consortium; (5) whenever a project has been proposed, all sPlot consortium members will be informed and can declare their interest in becoming co-authors of manuscripts resulting from this project and then becoming actively involved in data evaluation and writing; and (6) if also the matched gap-filled or original trait data from TRY are requested for a project, likewise members from the TRY consortium can opt-in as co-authors. The sPlot database is, therefore, available according to a ‘give-and-receive’ system. Moreover, the data are available to any researcher by establishing a collaboration that includes and is supported by at least one sPlot consortium member.

The sPlot consortium is governed by a Steering Committee elected by all consortium members for two-year, renewable terms. Project proposals can be submitted to the Steering Committee, which ensures that the sPlot Rules are followed and redundant work between overlapping projects is avoided. The lists of databases, sPlot consortium members and the Steering Committee members are updated regularly on the sPlot website, as are the sPlot Rules and the list of approved projects.

5. EXPECTED IMPACT AND LIMITATIONS

The main aim of the sPlot database is to catalyze a collaborative network for understanding global diversity patterns of plant communities in space and time. sPlot provides a unique, integrated global repository of data that would otherwise be fragmented in unconnected and structurally inconsistent databases ~~of institutions~~ at regional, national or continental levels. Together with the provision of harmonized phylogenetic, functional and environmental information, sPlot allows, for the first time, global analyses of plant community data. Compared to approaches using data aggregated from species occurrences in grid cells, sPlot will significantly advance ecological analyses and future interdisciplinary research in at least four different ways.

1.) ~~Co-occurrence information in every plot allows for the identification of species that potentially interact with each other (**Table 1**).~~ Using ~~this information~~sPlot, one can predict the species that can co-exist in a community and also the frequencies of their co-occurrence (Breitschwerdt, Jandt & Bruelheide, 2015) or niche overlap (Broennimann et al., 2012). In addition, emerging tools such as Markov networks can be used to infer strengths of interspecific interactions (Harris, 2016). When investigating community assembly rules, the same information can be used to derive species pools for specific vegetation types (de Bello et al., 2016; Lewis, Szava-Kovats & Pärtel, 2016; Karger et al., 2016). Moreover, the co-occurrence data from sPlot can be used to address fundamental patterns and drivers of plant invasions better than information on large geographic entities (e.g. van Kleunen et al., 2015) alone could.

2.) sPlot ~~provides diversity information at a very fine grain, i.e. within plant communities (alpha diversity). These~~ data can be aggregated ~~at broader scales for complementing grid-cell inventory data (**Figure 1**). Aggregation is also possible~~ across all types of plots, by grid cells, ecoregions, environment, or even vegetation type or formation. Furthermore, replicated plots within grid cells, ecoregions, or any other subdivision of environmental conditions or vegetation types allow users to derive measures of compositional differences between plant communities within grid cells (= beta diversity; **Table 1**). Thus, the community data are an important complement to regional-scale species occurrence data (e.g. Kreft & Jetz, 2007; Enquist et al., 2016).

3.) sPlot data provide information on the proportion of species in communities. When combined with functional trait information, relative abundance of species allows calculation of community abundance-weighted mean trait values (Bruelheide et al. 2018~~**Table 1**~~). ~~These values may differ considerably from non-weighted means calculated at the grid cell level, depending on the degree to which trait values of abundant species deviate from those of less abundant species and how strongly different communities in a~~

~~grid cell differ in their community mean values (**Figure 1**).~~ Information on the relative contribution of species to a community-aggregated trait value is particularly necessary when traits are used as proxies for vegetation functions and processes, allowing to test, among other things, the mass ratio hypothesis (Grime, 1998; Garnier et al., 2004) and to assess the role of divergent traits (Díaz et al., 2007; Kröber et al., 2015).

4.) Plant species within plots can be linked to traits that predict interactions with organisms from other trophic groups, both belowground (mycorrhizae, soil decomposers) and aboveground (herbivores and pollinators). This will allow to link vegetation plot information to ecosystem processes and services such as pest control, pollination and nutrient cycling (e.g. de Bello et al., 2010).

Despite the large amount of available data and its potential suitability for global research, a number of limitations must be considered by future users of sPlot, such as i) biases towards certain regions and communities, ii) near-complete lack of plots with complete vascular plant species composition for certain regions (e.g. the wet tropics), iii) identification or sampling errors by the surveyors and incomplete records because the detection of some species may be precluded in certain seasons by their phenology, iv) taxonomic uncertainty particularly in the tropics, v) strongly varying plot sizes employed in different studies and regions, vi) lack of trait measures at the plot level. For example, ~~trends~~ patterns of diversity components are typically affected by grain size. This means that using sPlot data for such studies ~~with sPlot data~~ either requires filtering for plots with identical or at least similar size or accounting for the plot-size effects in the statistical model ~~can only be explored by adjusting plot area, as different plots size may affect the results~~. In addition, ~~links to phylogenetic or~~analyses of functional diversity with sPlot data is limited by the absence of~~t~~ trait data for a (small~~er~~) portion of the species and by the l~~through databases is limited by the l~~ack of plot-specific trait measures. ~~Therefore, corrections for bias must be undertaken in studies using sPlot and~~Furthermore, the non-random and geographically and ecologically very unequal distribution of the plots contained in sPlot call for stratified resampling~~ of plots has to be applied~~ to balance records of different environments (e.g. stratified by climate, **Figure 2**) or physiognomic formations (**Figure 4**). Users of sPlot need to be aware of these and other limitations ~~by careful study of the sPlot documentations~~ and to find correct ~~ion of~~ potential biases for their specific research question.

6. CONCLUSION

~~In summary,~~ sPlot is a unique global database of plant community records sampled with ~~comparable~~ relatively similar methods widely used in vegetation ecology. The integration of co-occurrence data into a unified database that can be directly linked to environmental, functional and phylogenetic information, makes sPlot an unprecedented and essential tool for analyzing global plant diversity, the structure of plant communities and the co-occurrence of plant species. The compatibility of this consolidated database with other global databases, e.g. via a joint taxonomic backbone with TRY and the Global Naturalized Alien Flora (GloNAF; van Kleunen et al., 2015) (via taxon names), or via standardized geo-reference with databases of environmental information such as CHELSA, WorldClim or SoilGrids (Bruelheide et al. 2018), facilitates data integration and creates new research opportunities. The adaptive management of the database employed by the sPlot consortium allows regular incorporation of new data, resulting in a dynamic platform for storing and analyzing the most comprehensive compilation of plant community data worldwide.

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DATA ACCESSIBILITY

The data contained in sPlot (the vegetation-plot data complemented by species phylogeny and environmental information) are available by request, through contacting any of the consortium members for submitting a paper proposal. The proposals should follow the Governance and Data Property Rules of the sPlot Working Group, which are available on the sPlot website (www.idiv.de/sPlot). After acceptance, the respective data will be provided. In addition to the plot data, CWMs and CWVs of 18 plant traits are available for every plot.

SUPPORTING INFORMATION

Additional Supporting Information may be found online in the supporting information tab for this article.

Appendix S1 Additional references, attributions and disclaimers for datasets included in sPlot 2.1

Appendix S2 Data associated to the vegetation plot records stored in sPlot 2.1

Appendix S3 Details on the workflow for setting up plot definitions in sPlot 2.1

Appendix S4 Biome classification created for sPlot 2.1

Appendix S5 Zip file of the biome classification of Appendix S4 containing the shapefile (Geospatial vector data for geographic information system (GIS) software) and accompanying accessory files (database, projection etc.).

Appendix S6~~5~~ Trait information in sPlot 2.1

Appendix S7~~6~~ Phylogenetic information in sPlot 2.1

Appendix S8~~7~~ Gap-filled trait information

Appendix S9~~8~~ Global patterns of community-weighted variances

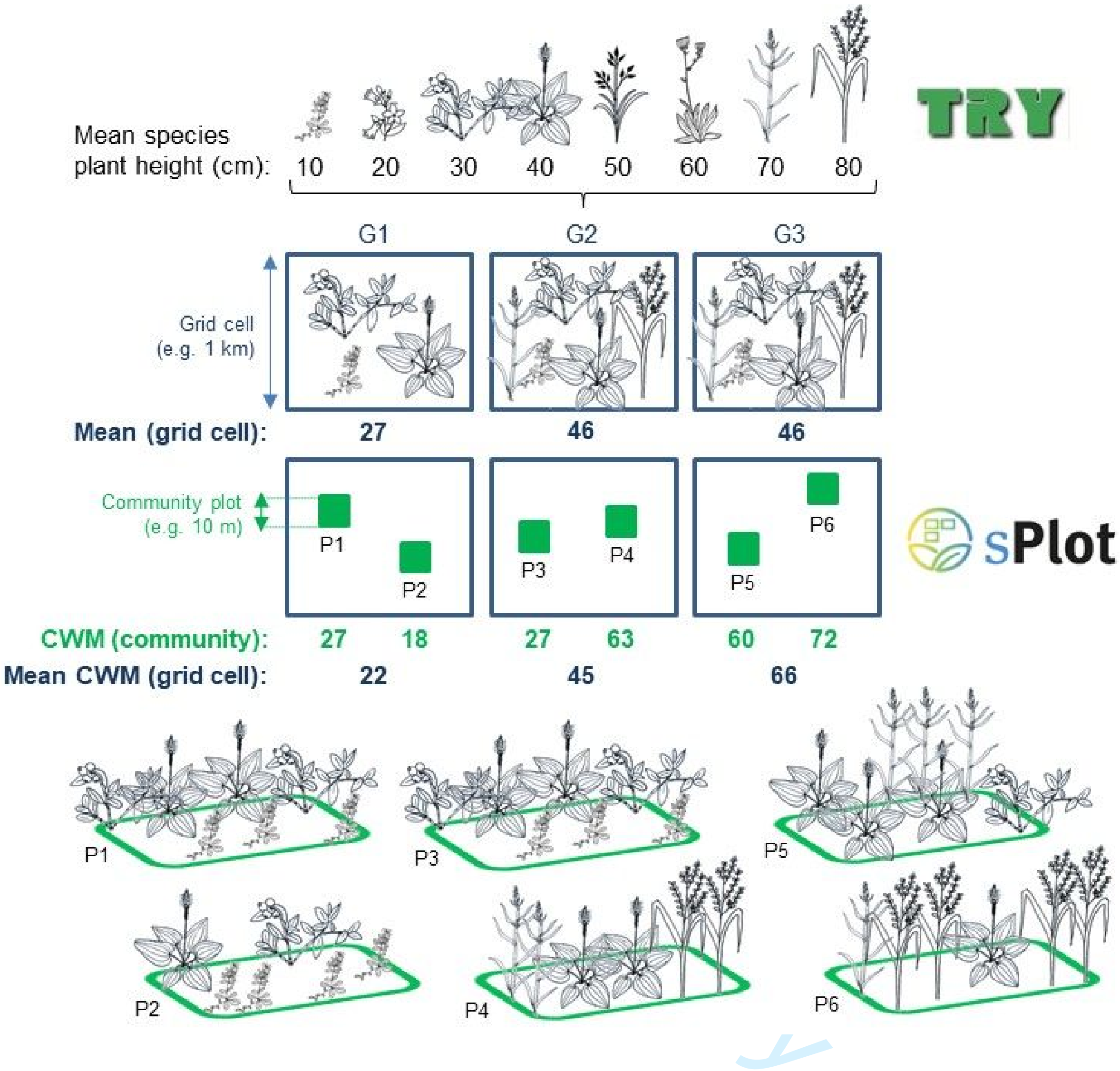
Mean species plant height (cm):
10
20
30
40
50
60
70
80
TRY
G1
G2
G3
Grid cell (e.g. 1 km)
Mean (grid cell):
27
46
46
Community plot (e.g. 10 m)
P1
P2
P3
P4
P5
P6
sPlot
CWM (community):
27
18
27
63
60
72
Mean CWM (grid cell):
22
45
66
P1
P3
P5
P2
P4
P6

Figure 1. Conceptual figure visualizing how functional composition (in this case plant height) differs between calculations based on mean traits for grid cells and community data sampled in vegetation plots. Occurrence data (e.g. from distribution atlases, GBIF, etc.) can be used to calculate mean trait values in grid cells G1–G3. However, community weighted means (CWMs) of traits differ across local plots (P1–P6), while the mean values of CWMs in the grid cells differ from the unweighted values calculated in the grid cells. This example is simplified by showing few species and few plots. In reality, differences are generally more pronounced.

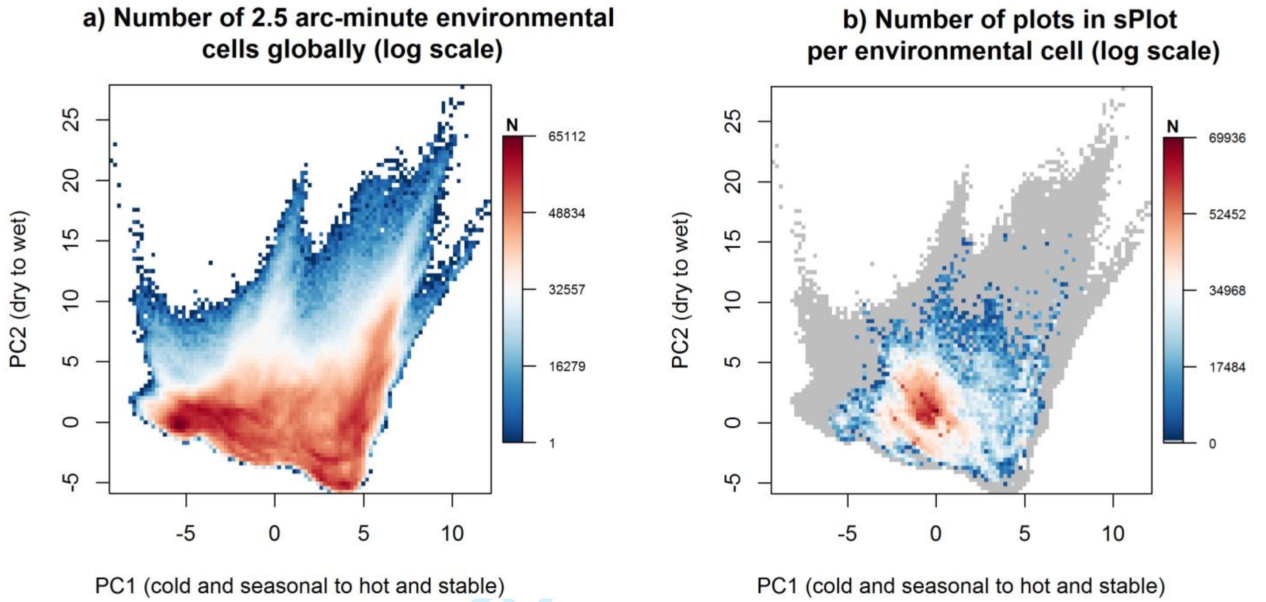

Figure 2. Distribution of vegetation plots from sPlot 2.1 in the global environmental space. Comparison of the distribution of all terrestrial 2.5 arc-minute cells (a) and plots in sPlot 2.1 (b) in the principal component analysis (PCA) space defined on 30 environmental (climate and soil) variables. The PCA space was divided into a 100 × 100 regular grid. For each element of this grid, the graphs show the number of 2.5 arc-minute cells (a) and plots (b), respectively. Colors refer to the logarithm of number of plots, with the legend showing untransformed number of plots. The first and second PCA axis explained 48.6% and 27.3% of the total variance**.**

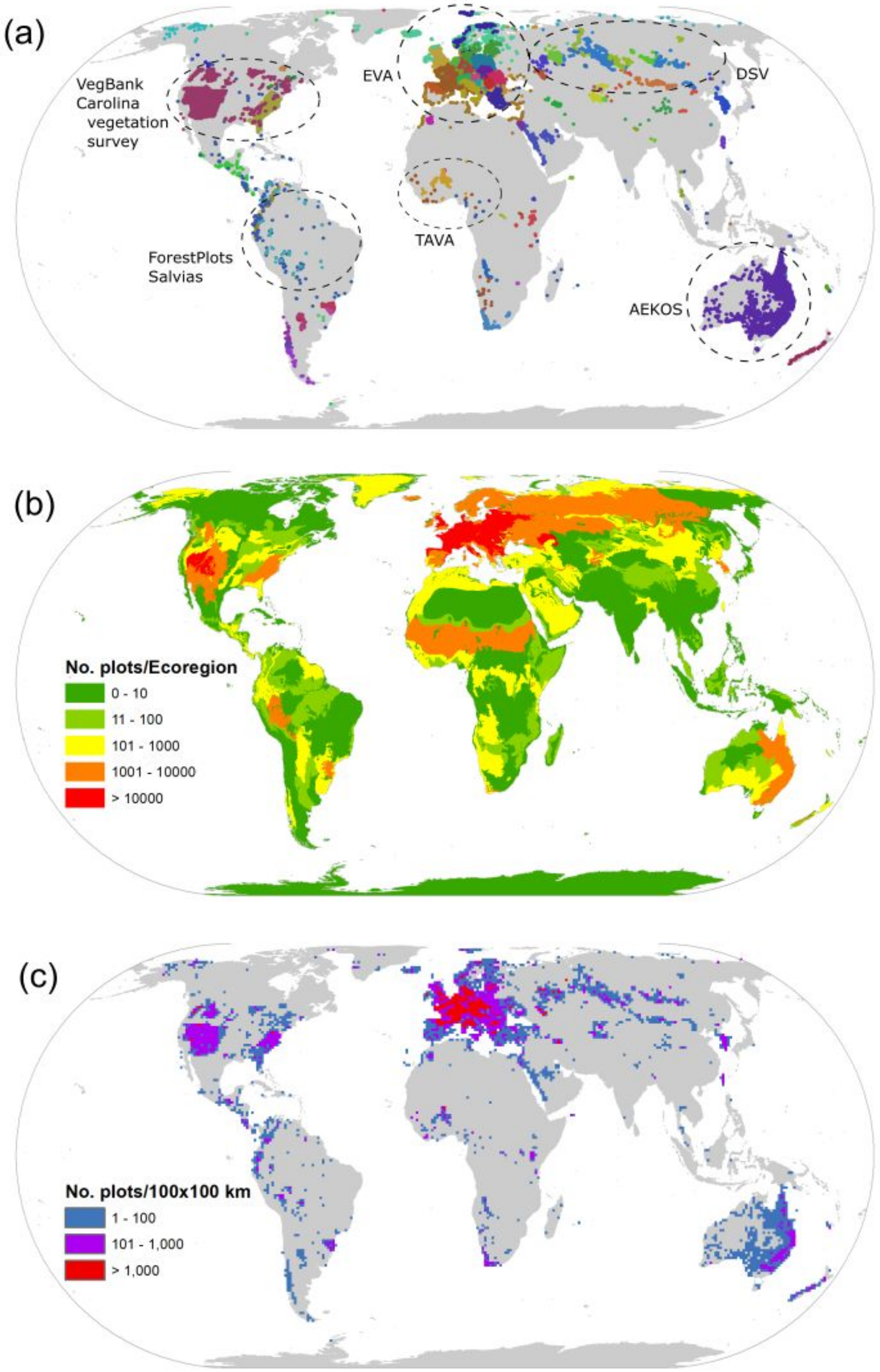

Figure 3. Global coverage of sPlot 2.1; (a) contributing databases identified by different colours with indication of the two data aggregators (EVA, TAVA) and a few particularly large individual databases; (b) available plot numbers per WWF Ecoregion; and (c) available plot density in grid cells of 100 km × 100 km.

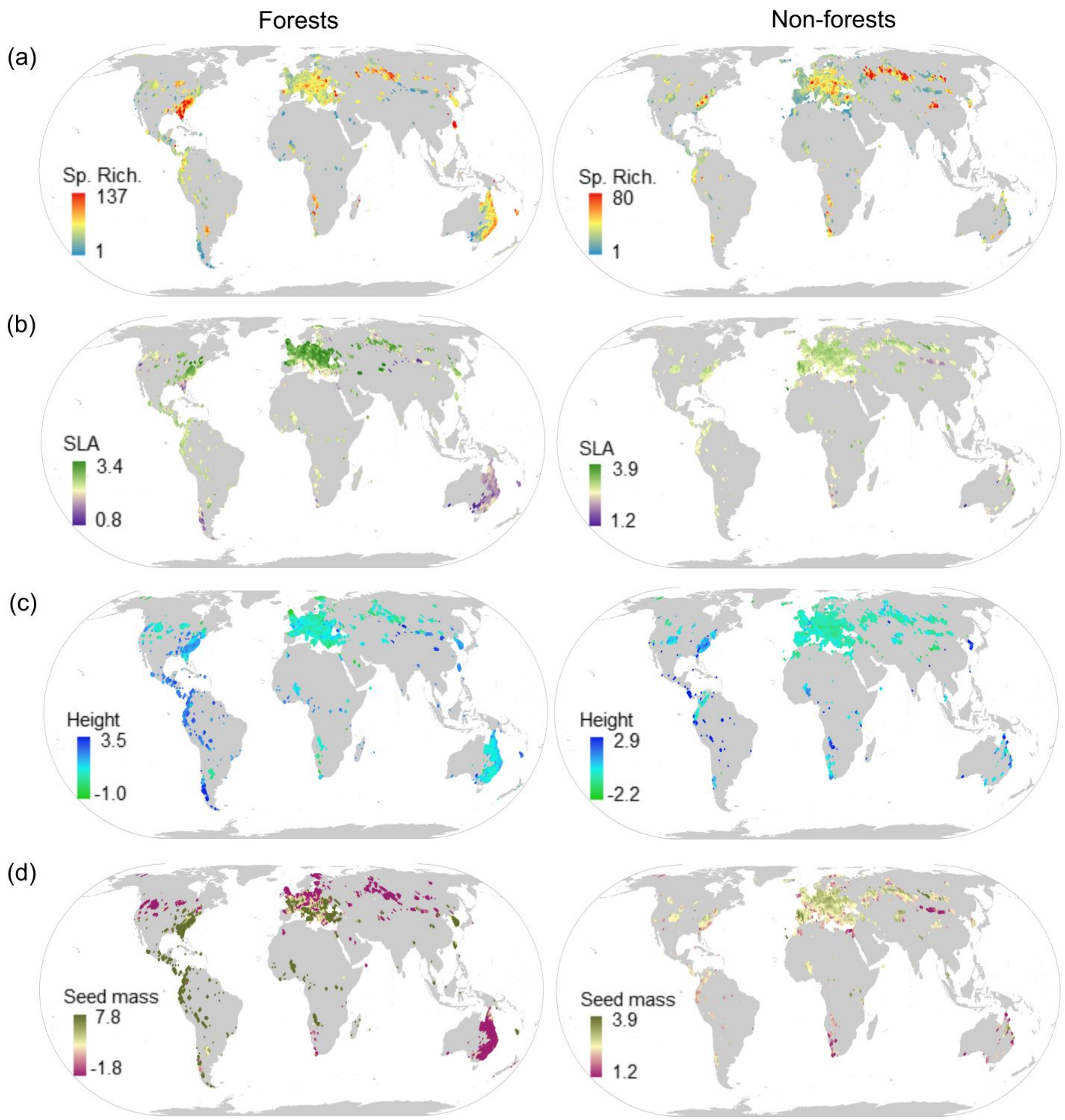

Figure 4. Examples of global community-level patterns that can be derived from (a) sPlot alone and (b–d) sPlot combined with TRY, here shown as raw data averaged by 1-degree grid cells. There are only a very few cells (142 out of 2633) comprising only a single plot. For the maps, only plots with full vascular species composition and spatial accuracy < 5 km were used. They are based on 148,474 and 218,051 plots for forests and non-forests respectively. Note that these maps are not corrected for biases caused by the facts that not all community types were

recorded in all grid cells and that plot sizes as well as the fraction of species with available trait data varied spatially. Maps show patterns of (a) fine-grain alpha diversity, expressed as vascular plant species richness (only plots with plot sizes of 100–1000 m² for forests and 5–100 m² for non-forests); (b) community-weighted means (CWMs) for $\log_e$-transformed trait values of specific leaf area (SLA, m^2 kg^{-1}), (c) plant height (m) and (d) seed mass (mg).

~~**Appendix 1.** References to datasets included in sPlot 2.1.~~

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Table 1. Types of information provided by single vegetation plots, vegetation plots aggregated within grid cells (or other geographic units) and single species occurrence records aggregated within grid cells. The three levels are illustrated in Figure 1.

Information ~~on~~from...	Single vegetation plots	Set of vegetation plots aggregated within grid cells	Grid-cell data from floristic inventories
T~~t~~o derive information on the …	Plot level	Grid cell level	Grid cell level
Type of occurrence	Co-occurrence, occurrence by vegetation type	Occurrence by vegetation type	Occurrence
Community assembly rules	Yes (co-occurrence is a prerequisite for species interactions)	No	No
Absences	Yes (for the target plant group in a study)	No (except for ~~extraordinarily~~ intensive sampling schemes)	Depending on sampling intensity
Floristic composition …	… of the local community	… of the species pools of vegetation types	… of the total set of species
Diversity	α	β, γ	γ
~~l~~Species abundance	Local cover-abundance	Mean cover-abundance and frequency by vegetation type	Occurrence only
Combination with traits	Functional composition of the local community (traits unweighted or weighted by cover: CWM, CWV)	Functional composition of the species pool (unweighted or weighted)	Functional composition of the total set of species (unweighted only)
Environmental filtering …	… at the local level	… at the regional level	… at the regional level

Table 2. Plot datasets included in sPlot 2.1. GIVD ID refers to the ID in the Global Index of Vegetation-Plot Databases (http://www.givd.info), which manages the metadata for sPlot and provides updated online descriptions of these databases; * after the GIVD ID indicates that the respective database description is currently not visible on the GIVD website. Datasets contributed in harmonized format from a continental data aggregator (“collective database” according to the sPlot Rules) are listed under its name. ~~The references are included in Appendix 1, while f~~Further references, attributions and disclaimers for particular datasets are found Appendix S1.

GIVD ID	Database name	# of plots in sPlot 2.1	Custodian	Deputy custodian	Reference
[Aggregator]	**European Vegetation Archive (EVA)**	**950,001**	**Milan Chytrý**	**Ilona Knollová**	**Chytrý et al. (2016)**
00-00-004	Vegetation Database of Eurasian Tundra	1,132	Risto Virtanen		
00-RU-001	Vegetation Database Forest of Southern Ural	1,102	Vassiliy Martynenko		
00-RU-003	Database Meadows and Steppes of Southern Ural	2,354	Sergey Yamalov	Mariya Lebedeva	
00-TR-001	Forest Vegetation Database of Turkey - FVDT	919	Ali Kavgacı		
00-TR-002*	Non-forest Vegetation Database of Turkey	3,018	Deniz Işık	Didem Ambarlı	
AS-TR-002	Vegetation Database of Oak Communities in Turkey	1,181	Emin Uğurlu		
EU-00-002	Nordic-Baltic Grassland Vegetation Database (NBGVD)	7,675	Jürgen Dengler	Łukasz Kozub	Dengler & Rūsiņa (2012)
EU-00-011	Vegetation-Plot Database of the University of the Basque Country (BIOVEG)	18,441	Idoia Biurrun	Itziar García-Mijangos	Biurrun et al. (2012)
EU-00-013	Balkan Dry Grasslands Database	7,683	Kiril Vassilev	Armin Macanović	Vassilev et al. (2012)
EU-00-016	Mediterranean Ammophiletea Database	7,359	Corrado Marcenò	Borja Jiménez-Alfaro	Marcenò & Jiménez-Alfaro (2017)
EU-00-017	European Coastal Vegetation Database	4,624	John Janssen		
EU-00-018	The Nordic Vegetation Database	5,477	Jonathan Lenoir	Jens-Christian Svenning	Lenoir et al. (2013)
EU-00-019	Balkan Vegetation Database	9,118	Kiril Vassilev	Hristo Pedashenko	Vassilev et al. (2016)
EU-00-020	WetVegEurope	14,111	Flavia Landucci		Landucci et al. (2015)
EU-00-022	European Mire Vegetation Database	10,147	Tomáš Peterka	Martin Jiroušek	Peterka et al. (2015)
EU-AL-001	Vegetation Database of Albania	290	Michele De Sanctis	Giuliano Fanelli	De Sanctis et al. (2017)
EU-AT-001	Austrian Vegetation Database	34,458	Wolfgang Willner	Christian Berg	Willner et al. (2012)
EU-BE-002	INBOVEG	25,665	Els De Bie		
EU-BG-001	Bulgarian Vegetation Database	5,254	Iva Apostolova	Desislava	Apostolova et al. (2012)

				Sopotlieva	
EU-CH-005	Swiss Forest Vegetation Database	14,193	Thomas Wohlgemuth		Wohlgemuth (2012)
EU-CZ-001	Czech National Phytosociological Database	104,697	Milan Chytrý	Dana Holubová	Chytrý & Rafajová (2003)
EU-DE-001	VegMV	53,822	Florian Jansen	Christian Berg	Jansen et al. (2012)
EU-DE-013	VegetWeb Germany	23,078	Jörg Ewald		Ewald et al. (2012)
EU-DE-014	German Vegetation Reference Database (GVRD)	30,840	Ute Jandt	Helge Bruelheide	Jandt & Bruelheide (2012)
EU-DK-002	National Vegetation Database of Denmark	24,264	Jesper Erenskjold Moeslund	Rasmus Ejrnæs	
EU-ES-001	Iberian and Macaronesian Vegetation Information System (SIVIM) Wetlands	6,560	Aaron Pérez-Haase	Xavier Font	
EU-FR-003	SOPHY	209,864	Henry Brisse	Patrice De Ruffray	Brisse et al. (1995)
EU-GB-001	UK National Vegetation Classification Database	28,533	John S. Rodwell		
EU-GR-001	KRITI	292	Erwin Bergmeier		
EU-GR-005	Hellenic Natura 2000 Vegetation Database (HelNatVeg)	5,168	Panayotis Dimopoulos	Ioannis Tsiripidis	Dimopoulos & Tsiripidis (2012)
EU-GR-006	Hellenic Woodland Database	3,199	Georgios Fotiadis	Ioannis Tsiripidis	Fotiadis et al. (2012)
EU-HR-001	Phytosociological Database of Non-Forest Vegetation in Croatia	5,057	Zvjezdana Stančić		Stančić (2012)
EU-HR-002	Croatian Vegetation Database	8,734	Željko Škvorc	Daniel Krstonošić	
EU-HU-003	CoenoDat Hungarian Phytosociological Database	8,505	János Csiky	Zoltán Botta-Dukát	Lájer et al. (2008)
EU-IT-001	VegItaly	15,332	Roberto Venanzoni	Flavia Landucci	Landucci et al. (2012)
EU-IT-010	Italian National Vegetation Database (BVN/ISPRA)	3,562	Laura Casella	Pierangela Angelini	Casella et al. (2012)
EU-IT-011	Vegetation-Plot Database Sapienza University of Rome (VPD-Sapienza)	12,780	Emiliano Agrillo	Fabio Attorre	Agrillo et al. (2017)
EU-LT-001	Lithuanian Vegetation Database	7,821	Valerijus Rašomavičius	Domas Uogintas	
EU-LV-001	Semi-natural Grassland Vegetation Database of Latvia	5,594	Solvita Rūsiņa		Rūsiņa (2012)
EU-MK-001	Vegetation Database of the Republic of Macedonia	1,417	Renata Ćušterevska		
EU-NL-001	Dutch National Vegetation Database	102,327	Joop H.J. Schaminée	Stephan M. Hennekens	Schaminée et al. (2006)
EU-PL-001	Polish Vegetation Database	22,229	Zygmunt Kącki	Grzegorz Swacha	Kącki & Śliwiński (2012)
EU-RO-007	Romanian Forest Database	6,017	Adrian Indreica	Pavel Dan Turtureanu	Indreica et al. (2017)
EU-RO-008	Romanian Grassland Database	1,921	Eszter Ruprecht	Kiril Vassilev	Vassilev et al. (2018)
EU-RS-002	Vegetation Database Grassland Vegetation of Serbia	5,587	Svetlana Aćić	Zora Dajić Stevanović	Aćić et al. (2012)
EU-RU-002	Lower Volga Valley Phytosociological Database	14,853	Valentin Golub	Viktoria Bondareva	Golub et al. (2012)
EU-RU-003	Vegetation Database of the Volga and the Ural Rivers Basins	1,516	Tatiana Lysenko		Lysenko et al. (2012)
EU-RU-011	Vegetation Database of Tatarstan	7,471	Vadim Prokhorov	Maria Kozhevnikova	Prokhorov et al. (2017)
EU-SI-001	Vegetation Database of Slovenia	10,986	Urban Šilc	Filip Küzmič	Šilc (2012)
EU-SK-001	Slovak Vegetation Database	36,405	Milan Valachovič	Jozef Šibík	Šibík (2012)

EU-UA-001	Ukrainian Grasslands Database	4,043	Anna Kuzemko	Yulia Vashenyak	Kuzemko (2012)
EU-UA-006	Vegetation Database of Ukraine and Adjacent Parts of Russia	3,326	Viktor Onyshchenko	Vitaliy Kolomiychuk	
[Aggregator]	**Tropical African Vegetation Archive (TAVA)**	**6,677**	**Marco Schmidt**	**Stefan Dressler**	**Janßen et al. (2011)**
AF-00-001	West African Vegetation Database	3,129	Marco Schmidt	Georg Zizka	Schmidt et al. (2012)
AF-00-008	PANAF Vegetation Database	2,469	Hjalmar Kühl	TeneKwetche Sop	
AF-BF-001	Sahel Vegetation Database	1,079	Jonas V. Müller	Marco Schmidt	Müller (2003)
	Other databases	**164,566**			
00-00-001	RAINFOR data managed by ForestPlots.net	1,827	Oliver L. Phillips	Aurora Levesley	Lopez-Gonzalez et al. (2011)
00-00-003	SALVIAS	4,883	Brian Enquist	Brad Boyle	
00-00-005	Tundra Vegetation Plots (TundraPlot)	577	Anne D. Bjorkman	Sarah Elmendorf	Elmendorf et al. (2012)
00-RU-002	Database of Masaryk University`s Vegetation Research in Siberia	1,547	Milan Chytrý		Chytrý (2012)
AF-00-003	BIOTA Southern Africa Biodiversity Observatories Vegetation Database	1,666	Norbert Jürgens	Gerhard Muche	Muche et al. (2012)
AF-00-006	SWEA-Dataveg	2,704	Miguel Alvarez	Michael Curran	
AF-00-009	Vegetation Database of the Okavango Basin	590	Rasmus Revermann	Manfred Finckh	Revermann et al. (2016)
AF-CD-001	Forest Database of Central Congo Basin	292	Elizabeth Kearsley	Hans Verbeeck	Kearsley et al. (2013)
AF-ET-001	Vegetation Database of Ethiopia	74	Desalegn Wana	Anke Jentsch	Wana & Beierkuhnlein (2011)
AF-MA-001	Vegetation Database of Southern Morocco	1,337	Manfred Finckh		Finckh (2012)
AF-ZA-003*	SynBioSys Fynbos Vegetation Database	3,810	John Janssen		
AF-ZW-001*	Vegetation Database of Zimbabwe	36	Cyrus Samimi		Samimi (2003)
AS-00-001	Korean Forest Database	4,885	Tomáš Černý	Petr Petřík	Černý et al. (2015)
AS-00-003	Vegetation of Middle Asia	1,381	Arkadiusz Nowak	Marcin Nobis	Nowak et al. (2017)
AS-00-004	Rice Field Vegetation Database	179	Arkadiusz Nowak		
AS-BD-001	Tropical Forest Dataset of Bangladesh	211	Mohammed A.S. Arfin Khan	Fahmida Sultana	
AS-CN-001	China Forest-Steppe Ecotone Database	148	Hongyan Liu	Fengjun Zhao	Liu et al. (2000)
AS-CN-002	Tibet-PaDeMoS Grazing Transect	146	Karsten Wesche		Wang et al. (2017)
AS-CN-003*	Vegetation Database of the BEF China Project	27	Helge Bruelheide		Bruelheide et al. (2011)
AS-CN-004*	Vegetation Database of the Northern Mountains in China	485	Zhiyao Tang		
AS-CN-005*	Database Steppe Vegetation of Xinjiang	129	Kohei Suzuki		
AS-EG-001	Vegetation Database of Sinai in Egypt	926	Mohamed Z. Hatim		Hatim (2012)
AS-ID-001	Sulawesi Vegetation Database	24	Michael Kessler		
AS-IR-001	Vegetation Database of Iran	2,335	Jalil Noroozi	Parastoo Mahdavi	
AS-KG-001	Vegetation Database of South-Western Kyrgyzstan	452	Peter Borchardt	Udo Schickhoff	Borchardt & Schickhoff (2012)
AS-KZ-001	Database of Meadow Vegetation in the NW Tian Shan Mountains	94	Viktoria Wagner		Wagner (2009)
AS-MN-001	Southern Gobi Protected Areas	1,516	Henrik von	Karsten Wesche	von Wehrden et al.

	Database		Wehrden		(2009)
AS-RU-001	Wetland Vegetation Database of Baikal Siberia (WETBS)	2,381	Victor Chepinoga		Chepinoga (2012)
AS-RU-002	Database of Siberian Vegetation (DSV)	9,116	Andrey Korolyuk	Andrei Zverev	
AS-RU-004	Database of the University of Münster - Biodiversity and Ecosystem Research Group's Vegetation Research in Western Siberia and Kazakhstan	445	Norbert Hölzel	Wanja Mathar	
AS-SA-001*	Vegetation Database of Saudi Arabia	919	Mohamed Abd El-Rouf Mousa El-Sheikh		
AS-TJ-001	Eastern Pamirs	282	Kim André Vanselow		Vanselow (2016)
AS-TW-001	National Vegetation Database of Taiwan	930	Ching-Feng Li	Chang-Fu Hsieh	
AS-YE-001	Socotra Vegetation Database	396	Michele De Sanctis	Fabio Attorre	De Sanctis & Attorre (2012)
AU-AU-002	TERN AEKOS	21,261	Anita Smyth	Ben Sparrow	Turner et al (2017)
AU-NC-001	New Caledonian Plant Inventory and Permanent Plot Network (NC-PIPPN)	201	Jérôme Munzinger	Philippe Birnbaum	Ibanez et al. (2014)
AU-NZ-001	New Zealand National Vegetation Databank	1,895	Susan Wiser		Wiser et al. (2001)
AU-PG-001	Forest Plots from Papua New Guinea	63	Timothy Whitfeld	George Weiblen	Whitfeld et al. (2014)
NA-00-002	Tree Biodiversity Network (BIOTREE-NET)	1,757	Luis Cayuela		Cayuela et al. (2012)
NA-CA-003	Database of Timberline Vegetation in NW North America	110	Viktoria Wagner	Toby Spribille	agner et al. (2014)
NA-CA-004	Understory of Sugar Maple Dominated Stands in Quebec and Ontario (Canada)	156	Isabelle Aubin		Aubin et al. (2007)
NA-CA-005*	Boreal Forest of Canada	89	Yves Bergeron	Louis De Grandpré	
NA-GL-001	Vegetation Database of Greenland	664	Birgit Jedrzejek	Fred J.A. Daniëls	Sieg et al. (2006)
NA-US-002	VegBank	67,352	Robert K. Peet	Michael T. Lee	Peet et al. (2012a)
NA-US-006	Carolina Vegetation Survey Database	17,221	Robert K. Peet	Michael T. Lee	Peet et al. (2012b)
NA-US-014	Alaska-Arctic Vegetation Archive	1,363	Donald A. Walker	Amy Breen	Walker et al. (2016)
SA-00-002	VegPáramo	2,643	Gwendolyn Peyre	Xavier Font	Peyre et al. (2015)
SA-AR-002	Vegetation Database of Central Argentina	218	Marcelo R. Cabido	Alicia Acosta	
SA-BO-003	Bolivia Forest Plots	75	Michael Kessler	Sebastian Herzog	
SA-BR-002	Forest Inventory, State of Santa Catarina, Brazil (IFFSC Project)	1,669	Alexander Christian Vibrans	André Luis de Gasper	Vibrans et al. (2010)
SA-BR-003	Grasslands of Rio Grande do Sul, Brazil	320	Eduardo Vélez-Martin	Valério De Patta Pillar	
SA-BR-004	Grassland Database of Campos Sulinos	161	Gerhard E. Overbeck	Valério De Patta Pillar	
SA-CL-002	SSAForests_Plots_db	261	Alvaro G. Gutierrez		
SA-CL-003*	Chilean Park Transects - Fondecyt 1040528	165	Aníbal Pauchard	Alicia Marticorena	Pauchard et al. (2003)
SA-EC-001	Ecuador Forest Plot Database	172	Jürgen Homeier		

SUPPORTING INFORMATION TO THE PAPER

Bruelheide et al. sPlot – a new tool for global vegetation analyses. *Journal of Vegetation Science*.

APPENDIX S1: Additional references, attributions and disclaimers for datasets included in sPlot 2.1. The datasets are listed under their GIVD ID (see Table 2)

00-00-001:

A contribution of RAINFOR data managed by ForestPlots.net.

Lopez-Gonzalez, G., Lewis, S. L., Burkitt, M., Baker T. R. & Phillips, O. L. (2009). ForestPlots.net Database. www.forestplots.net. Date of extraction [15 November 2014].

AF-00-006:

Alvarez, M., Möseler, B. M., Josko, M. et al. (2012a). SWEA-Dataveg – vegetation of small wetlands in East Africa. *Biodiversity & Ecology*, 4, 294-295.

Alvarez, M., Becker, M., Böhme, B. et al. (2012b). Floristic classification of the vegetation in small wetlands of Kenya and Tanzania. *Biodiversity & Ecology*, 4, 63-76.

Alvarez, M. (2017). Classification of aquatic and semi-aquatic vegetation in two East African sites: Cocktail definitions and syntaxonomy. *Phytocoenologia*, 47, 345-364.

Alvarez, M. & Luebert, F. (2018). The taxlist package: managing plant taxonomic lists in R. *Biodiversity Data Journal*, in press.

Behn, K., Becker, M., Burghof, S. et al. (2018). Using vegetation attributes to rapidly assess degradation of East African wetlands. Ecological Indicators 89: 250-259.

Scherer, L., Curran, M. & Alvarez, M. (2017a). Expanding Kenya's protected areas under the Convention on Biological Diversity to maximize coverage of plant diversity. *Conservation Biology*, 31, 302-310.

Scherer, L., Curran, M. & Alvarez, M. (2017b). Staggering financial shortfalls to meet biodiversity targets in Kenya. *Atlas of Science*, February.

AF-00-009:

Revermann, R., Finckh, M., Stellmes, M., Strohbach, B., Frantz, D. & Oldeland, J. (2016). Linking land surface phenology and vegetation-plot databases to model terrestrial plant alpha diversity of the Okavango Basin. *Remote Sensing* 8, Article 370.

Revermann, R., Oldeland, J., Gonçalvess, F.M., Luther-Mosebach, J., Gomes, A.L., Jürgens, N. & Finckh, M. (2018). Dry tropical forests and woodlands of the Cubango Basin in southern Africa: A first classification and assessment of their woody species diversity. *Phytocoenologia*, 48. DOI: 10.1127/phyto/2017/0154.

Wallenfang, J., Finckh, M., Oldeland, J. & Revermann, R., 2015. Impact of shifting cultivation on dense tropical woodlands in southeast Angola. *Tropical Conservation Science*, 8, 863-892.

AU-AU-002:

Dengler, J., Jansen, F., Glöckler, F., Peet, R. K., De Cáceres, M., Chytrý, M., … TERN Eco-informatics (2015). A subset of ÆKOS Australian Vegetation sPlot Extraction (http://doi.org/10.4227/05/548530103BCAE). Obtained via Global Index of Vegetation-Plot Databases (http://www.givd.info/givd/faces/databases.xhtml) and TERN AEKOS Data Portal, rights owned by GIVD and The University of Adelaide.

AU-NZ-001:

Website: https://nvs.landcareresearch.co.nz/

Broadbent, H., Spencer, N. & Wiser, S. (2012). New Zealand National Vegetation Databank. *Biodiversity & Ecology*, 4, 318.

SUPPORTING INFORMATION TO THE PAPER

Bruelheide et al. sPlot – a new tool for global vegetation analyses. *Journal of Vegetation Science*.

EU-BE-002:

Website: http://www.inbo.be/en/inboveg

EU-RS-002:

Dajic Stevanovic, Z., Petrovic, M., Šilc, U. & Acic, S. (2012). Database of Halophytic Vegetation in Serbia. *Biodiversity & Ecolog*y, 4, 417-417.

EU-RU-003:

Golub, V.B., Sorokin, A.N., Ivakhnova, T.L., Starichkova, K.A., Nikolaychuk, L.F. & Bondareva. V.V. (2009). Geobotanicheskaya baza dannyh doliny Nizhnei Volgi [Geobotanical database of the Lower Volga valley]. *Izvestiya Samarskogo nauchnogo centra RAN*, 11, 577–582. (In Russian)

Sorokin, A., Golub, V., Ivakhnova, T., Starichkova, K., Nikolaychuk, L. & Bondareva, V. (2010). Lower Volga Valley Phytosociological Database. In: Dengler, J., Finckh, M. & Ewald, J. (eds.) *Book of Abstracts. 9th international Meeting on Vegetation Databases "Vegetation Databases and Climate Change". Hamburg, 24–26 February 2010*, pp. 91–91. BEE, University of Hamburg, Hamburg.

EU-SI-001

Šilc, U. (2006). Slovenian phytosociology in a database: state of the art, basic statistics and perspectives. *Hladnikia,* 19, 27–34.

NA-00-002:

Cayuela, L., Gálvez-Bravo, L., de Albuquerque, F. S., Golicher, D. J., González-Espinosa, M., Ramírez-Marcial, N., … Zamora, R. (2012). La Red Internacional de Inventarios Forestales (BIOTREE-NET) en Mesoamérica: avances, retos y perspectivas futuras. *Ecosistemas*, 21, 126–135.

SA-00-002:

Website: http://www.vegparamo.com/

SUPPORTING INFORMATION TO THE PAPER
Bruelheide et al. sPlot – a new tool for global vegetation analyses. *Journal of Vegetation Science*.

APPENDIX S2. Data associated to the vegetation plot records stored in sPlot 2.1

Table S2.1. List of variables, type of data, number of records for which the variable was recorded, range (min; max) for numeric values and description of the header data of plot records in sPlot 2.1. Ranges of cover values of strata only refer to records in which the stratum was present.

Variable	**Type**	**No. of records**	**Range**	**Description**
PlotObservationID	integer	1,121,244	1; 1121244	Identificator provided by Turboveg 3, unique for each plot
Country	character	1,119,575		Original country name in Turboveg 3
NAME2	character			Official name of country
ISO2	character			Two-letter ISO country code
Date of recording	Date	983,267	"1885-07-01"; "2015-02-03"	Date referring to the observation or to the publication from which it comes
Syntaxon	character	387,900		As provided by the source database
Relevé area (m^2)	numeric	725,845	0.01; 250000	Plot size
Altitude (m)	numeric	649,240	-32; 4070	As provided by the source database
Aspect (°)	numeric	348,192	0;360	Standardized in degrees in Turboveg 3
Slope (°)	numeric	439,312	0;99	Standardized in degrees in Turboveg 3
Cover total (%)	numeric	278,141	1;100	As provided by the source database
Cover tree layer (%)	numeric	140,661	0.5;100	As provided by the source database
Cover shrub layer (%)	numeric	161,046	0.1;100	As provided by the source database
Cover herb layer (%)	numeric	413,629	0.2;100	As provided by the source database
Cover moss layer (%)	numeric	182,242	1;100	As provided by the source database
Cover lichen layer (%)	numeric	3,754	1;99	As provided by the source database
Cover algae layer (%)	numeric	1,683	1;100	As provided by the source database
Cover litter layer (%)	numeric	38,869	1;100	As provided by the source database
Cover bare rock (%)	numeric	14,177	1;100	As provided by the source database

Height (highest) trees (m)	numeric	64,227	1;99	As provided by the source database
Height lowest trees (m)	numeric	4,819	0.8;95	As provided by the source database
Height (highest) shrubs (m)	numeric	44,357	0.1;10	As provided by the source database
Height lowest shrubs (m)	numeric	4,241	0.1;10	As provided by the source database
Aver. height (high) herbs (cm)	numeric	111,189	0.1;800	As provided by the source database
Aver. height lowest herbs (cm)	numeric	28,215	1;353	As provided by the source database
Max. height herbs (cm)	numeric	29,428	1;800	As provided by the source database
Mosses identified (y/n)	logical	376831	0;1	Inferred when not provided by the source database
Lichens identified (y/n)	logical	243,052	0;1	Inferred when not provided by the source database
Cover cryptogams (%)	numeric	7,350	1;100	As provided by the source database
Herbs identified (y/n)	logical	38,803	0;1	Inferred when not provided by the source database
Plants recorded	character	61,224		It shows which subset of plants was recorded. Possible entries are: "Complete vegetation (including non-terricolous taxa)"; "Complete vegetation"; "All vascular plants and bryophytes"; "All vascular plants and dominant cryptogams"; "All vascular plants"; "Woody plants >= 10 cm dbh"; "Woody plants >= 5 cm dbh", "Woody plants >= 10 cm dbh and dominant understory", "Only dominants"
Cover bare soil (%)	numeric	10,333	0.02;100	As provided by the source database
Longitude	numeric	1,120,686	-162.741; 179.590	Standardized to decimal degrees in Turboveg 3
Latitude	numeric	1,120,686	-64.78; 80.15	Standardized to decimal degrees in Turboveg 3
Location uncertainty (m)	numeric	1,120,425	1; 5032594	Assigned either by the source databases or by management in Turboveg 3, based on the number of decimal places of

				the given coordinates
Dataset	character	1,121,244		Name of the source database (short version) in Turboveg 3
is.forest	logical	504,567	0;1	Community corresponding to forest formation (standardized in sPlot)
is.non.forest	logical	1,105,180	0;1	Community corresponding to non-forest formation (standardized in sPlot)
EVA	integer	950,001	61000001; 112004950	Relational IDs for the plots provided by the European Vegetation Archive
ESY	character	949,967		EUNIS code assigned to EVA plots by Expert System
Naturalness	Integer	953,904	0;3	0 (unknown), 1 (natural), 2 (semi-natural), 3 (anthropogenic)
Forest	logical	850,108	0;1	Formation type (when existing in the data source)
Shrubland	logical	794,722	0;1	Formation type (when existing in the data source)
Grassland	logical	874,654	0;1	Formation type (when existing in the data source)
Sparse.vegetation	logical	763,759	0;1	Formation type (when existing in the data source)
Wetland	logical	813,383	0;1	Formation type (when existing in the data source)
Biome	character	1,120,686		sPlot biomes adapted from Schultz (2005) and Körner et al (2017)
BiomeID	Integer	1,120,686	1;10	Codes for biomes from 1 to 10
REALM	character	1,120,686		Biogeographical realm from WWF Ecoregions (Olson et al. 2001)
BIOME2		1120686		Biome code from WWF Ecoregions (Olson et al. 2001)
ECO_ID		1120686		Ecoregion code from WWF Ecoregions (Olson et al. 2001)
ECO_NAME	character			Ecoregion name from WWF Ecoregions (Olson et al. 2001)
CONTINENT	character			Assigned from ESRI layer
POINT_X	numeric			Longitude corrected to fit with coastlines and land
POINT_Y	numeric			Latitude corrected to fit with coastlines and land

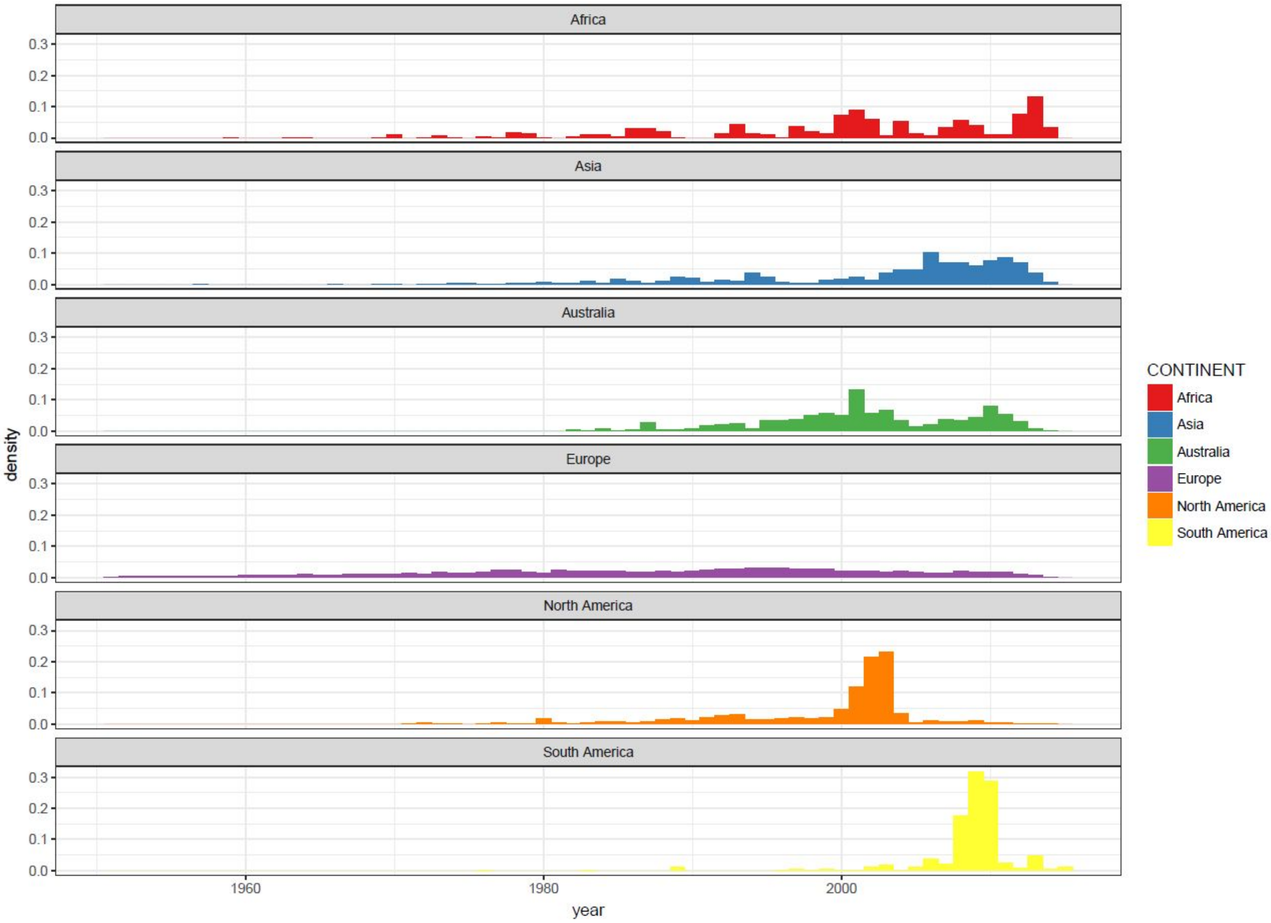

Fig. S2.1. Temporal distribution of vegetation plots stored in sPlot 2.1, divided per continent. Y axis (density) reflects the frequency of plots scaled from 0 to 1.

SUPPORTING INFORMATION TO THE PAPER

Bruelheide et al. sPlot – a new tool for global vegetation analyses. *Journal of Vegetation Science*.

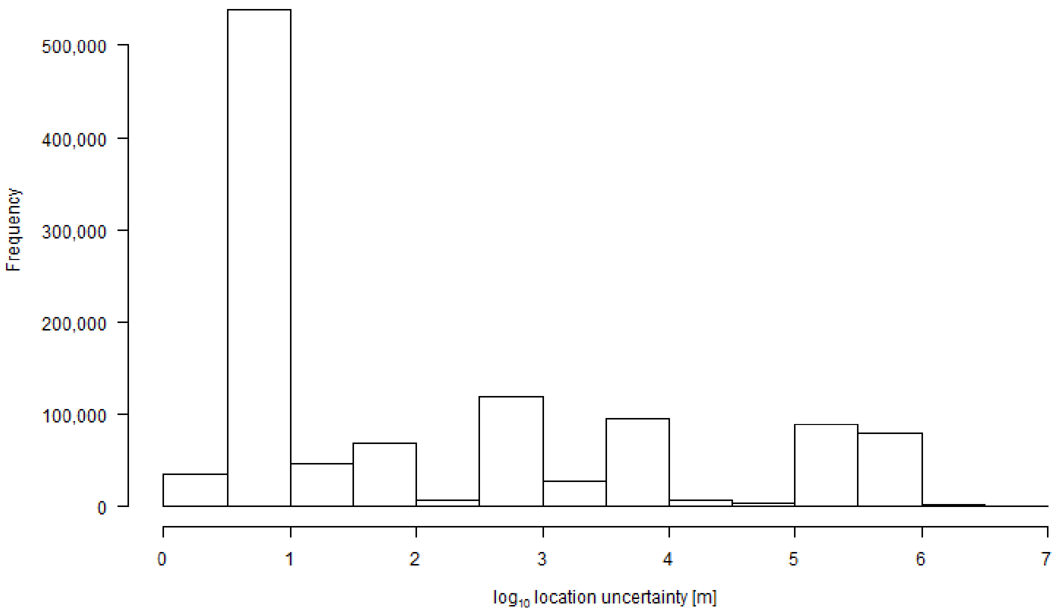

Fig. S2.2. Histogram of plot location uncertainty.

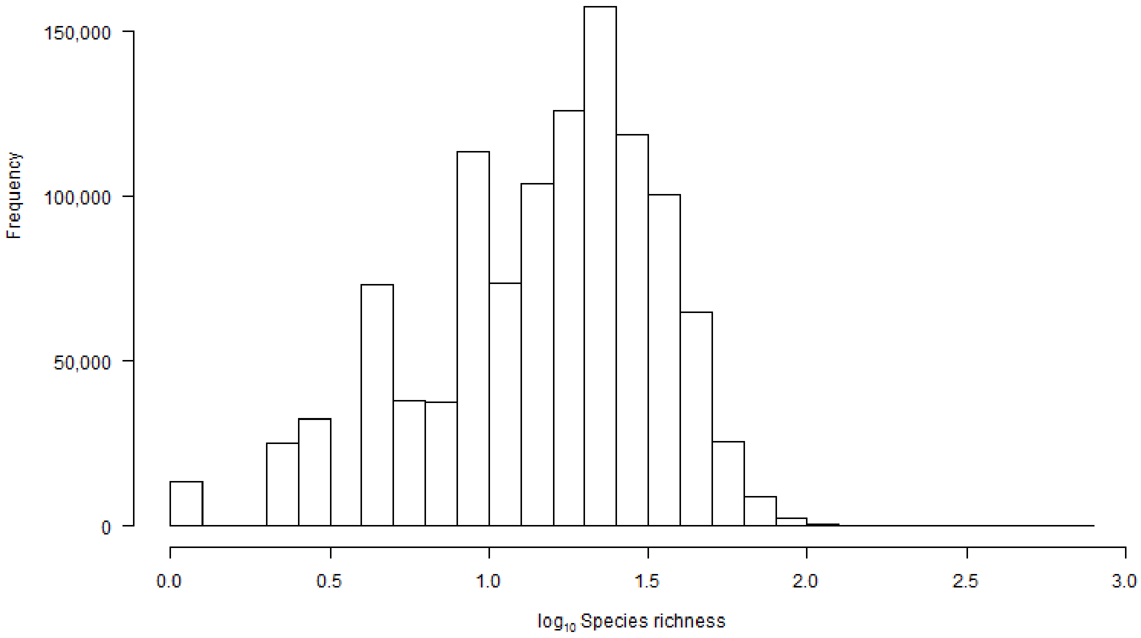

Fig. S2.3. Histogram of species richness. The most frequent richness class was between 20 and 25 species (i.e. between 10^1.3 and 10^1.4, respectively). Note that the graph shows raw richness, which has not been corrected for plot area.

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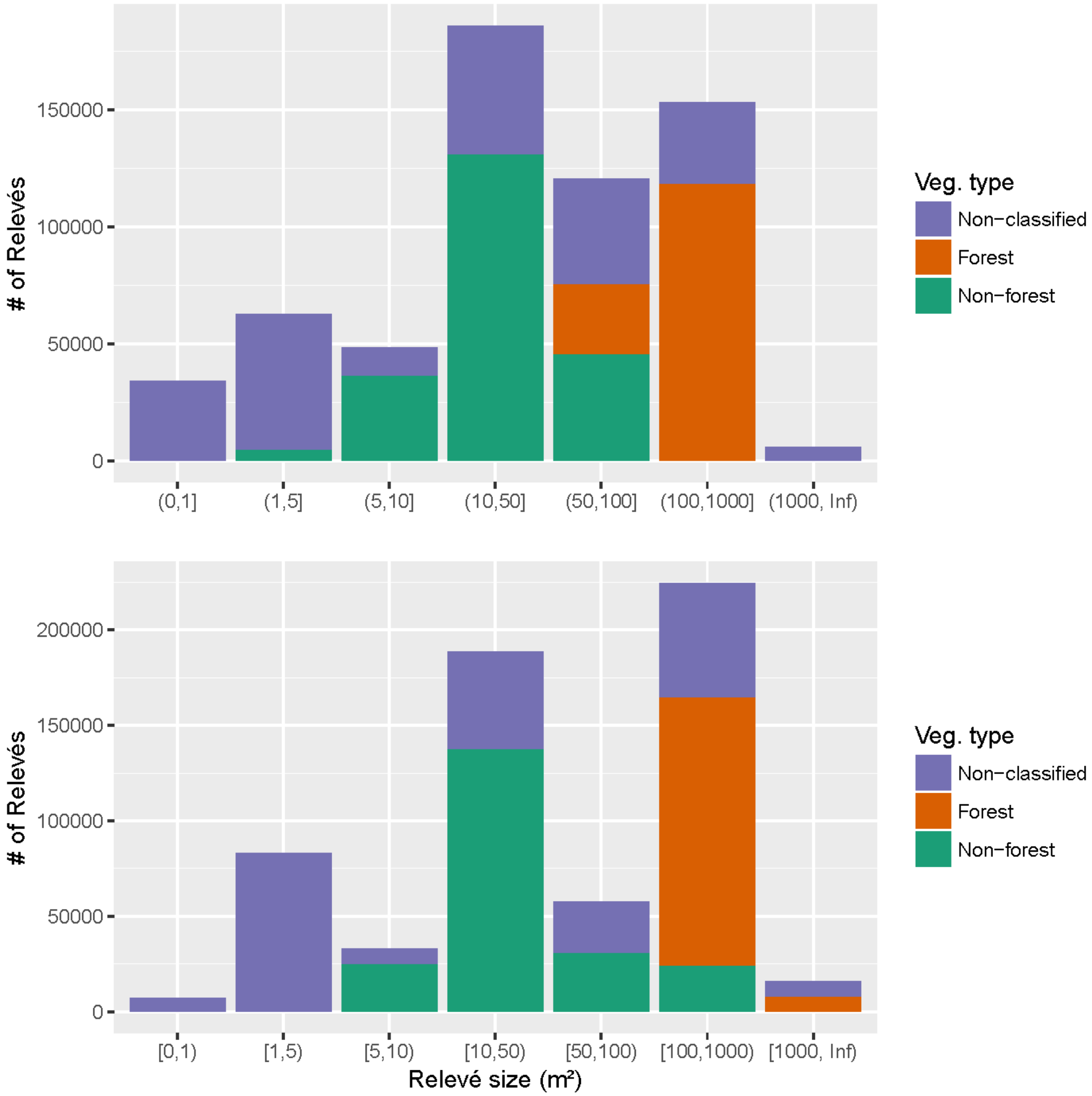

Fig. S2.4. Histogram of plot sizes, using breaks that either include the lower boundaries (top) or upper boundaries (bottom) in the size categories.

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APPENDIX S3. Details on the workflow for setting up plot definitions in sPlot 2.1

Definition of physiognomic formations

Plots that had information on vegetation type or layer-specific cover (ca. 20% of all plots) were broadly classified into communities that were tree-dominated (forests), shrub-dominated (shrublands), or lacked tree or shrub species (grasslands), sparsely vegetated types and wetlands or combinations thereof, using a 0/1 coding. For example, if forest = 1 and grassland = 1, this would code for a savanna-like vegetation. Note that the assignment procedure is ongoing and not all plots have been yet assigned to formations.

Table S3.2. Definitions and examples of the physiognomic formations used in sPlot. They are derived by the combination of five basic categories: Forest, Shrubland, Grassland, Sparse.vegetation and Wetland, each rated with 0/1. We use the terms tree for woody species > 5 m height and shrub for woody species of 0.5–5 m height. "x" means that either 0 or 1 are possible, resulting in different types.

Forest	Shrubland	Grassland	Sparse. vegetation	Wetland	Formation	Definition
1	0	0	0	0	Forest	Total cover >= 25%; tree cover >= 25%
1	1	0	0	0	Shrubland with some trees	Total cover >= 25%; tree cover 10 - <25%; shrub cover > herb cover
1	0	1	0	0	Savanna	Total cover >= 25%; tree cover 10 - <25%; herb cover > shrub cover
1	0	0	1	0	Scattered trees	Total cover < 25%; tree cover >0 - < 10%
0	1	0	0	0	Shrubland	Total cover >= 25%; no trees; shrub cover > herb cover or if smaller then shrub cover > 50%
0	1	1	0	0	Grassland with some shrubs or heathland	Total cover >= 25%; no trees; herb cover > shrub cover; also for heathlands!
0	1	0	1	0	Scattered shrubs	Total cover < 25%; no trees; shrub cover > herb cover
0	0	1	0	0	Grassland or herbland	Total cover >= 25%; no trees, shrubs < 10%
0	0	1	1	0	Open grassland or desert steppe	Total cover 10 - <25%; no trees, shrubs < 10%
0	0	0	1	0	Sparsely vegetated	Total cover <10%, no trees, no shrubs (e.g. rocks, screes, open sand dunes, deserts, nival vegetation)
0	0	0	0	1	Aquatic vegetation	Permanently water-covered
x	x	x	x	1	Semi-aquatic vegetation	Very wet or temporarily water-covered (e.g. flood plains, mires, springs, temporary pools, salt marshs, mangroves)
0	0	0	0	0	Not assigned yet	

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Definition of the degree of naturalness

We were able to assign the majority of plots to one of three levels of naturalness from 1 (natural), through 2 (semi-natural), to 3 (anthropogenic). Categories of naturalness and formations were approximately derived from information provided by the source databases to match the definitions in Table S4.3. Main pieces of information used were (a) vegetation height; (b) cover values per vegetation layer; (c) vernacular names of vegetation types; (d) phytosociological classifications in the large majority of European plots and some from other continents, and (e) land use information. Often the database as a whole already provided part of the information, e.g. when it only contained tropical forest plots or rice field plots. Note that the assignment procedure is ongoing and not all plots have been yet assigned to a degree of naturalness.

Table S3.3. Definition and examples of the categories of naturalness used in sPlot.

Code	Meaning	Definition	Examples
0	Not assessed	-	-
1	Natural or near-natural	Same formation as naturally occurring vegetation and species all or largely native, with low-intensity human land use, e.g. logging of timber or pasturing of steppes as long as it does not fundamentally change site conditions or structure and species composition of the vegetation.	Forests composed of native species; grasslands in regions where grasslands form the climax vegetation; various types of azonal vegetation (e.g. aquatic, bog, fen, coastal, rock, scree, alpine vegetation)
2	Semi-natural	Vegetation types that are more profoundly changed by humans, but with a species composition that still has many similarities with the natural vegetation and site conditions that are not fundamentally altered compared to natural conditions.	Forest plantations composed of non-native species; shrublands in the cultural landscape; mown or livestock-grazed secondary grasslands and heathlands in forest biomes.
3	Anthropogenic	Vegetation types that have very little in common with the natural vegetation on sites with profoundly altered site conditions and/or disturbance regimes.	Arable fields; ruderal vegetation; vegetation of anthropogenic structures; frequently mown and reseeded grasslands

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APPENDIX S4. Biome classification created for sPlot 2.1

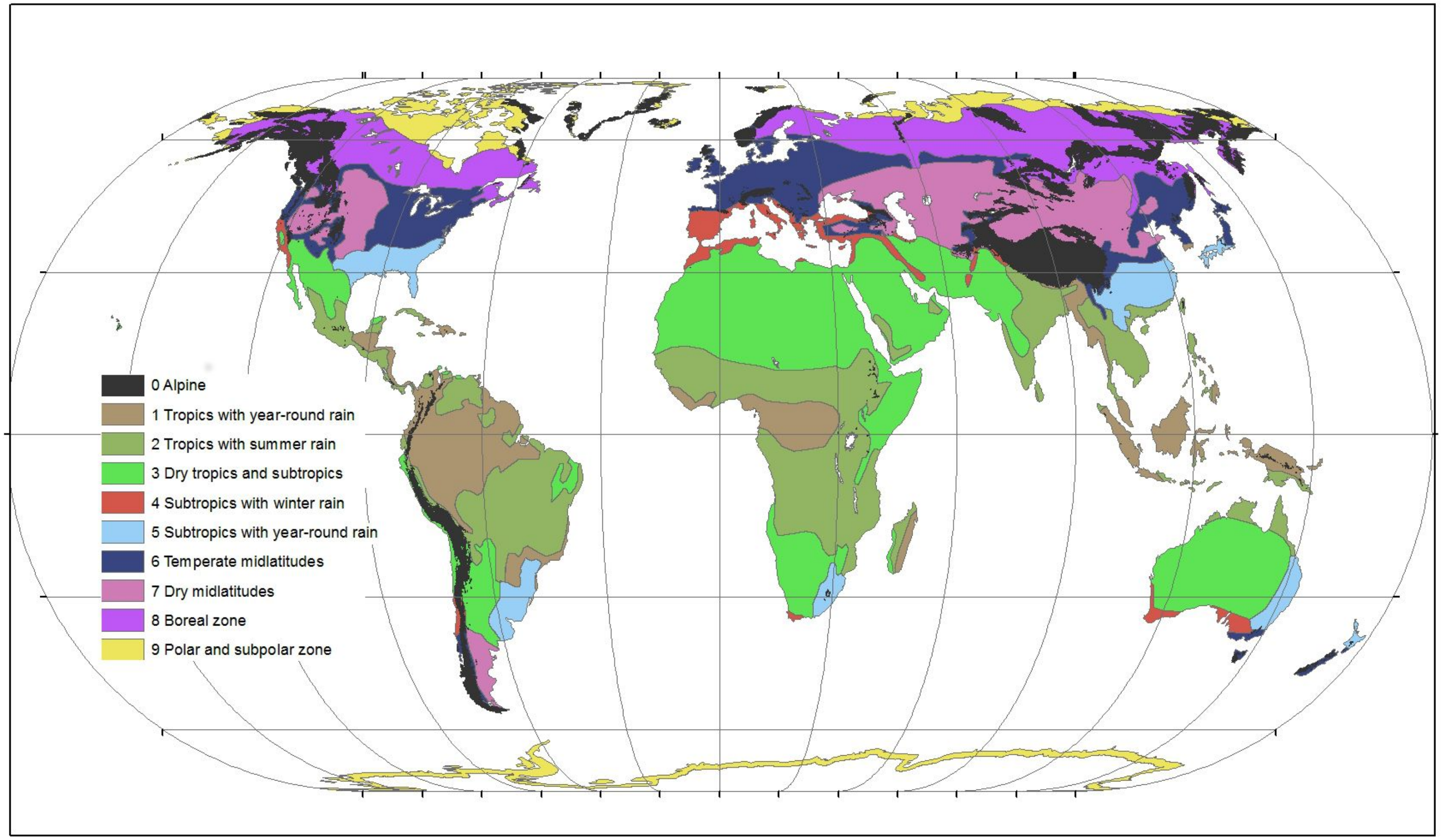

Figure S4.5. Biome classification based on the ecozones of Schultz (2005), with a further differentiation of an Alpine biome including major mountain regions according to Körner et al. (2017). The shapefile for the biomes is provided as Appendix S5.

References

Körner, C., Jetz, W., Paulsen, J., Payne, D., Rudmann-Maurer, K., & Spehn, E. M. (2017). A global inventory of mountains for bio-geographical applications. *Alpine Botany, 127,* 1–15.

Schultz, J. (2005). *The ecozones of the world* (2nd ed.) Berlin: Springer.

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APPENDIX S6. Trait information in sPlot 2.1

Table S6.4. List of traits, abbreviation of trait names, identifier in the Thesaurus Of Plant characteristics (TOP; Garnier et al., 2017) and mean values of community-weighted means (CWM) and community-weighted variances (CWV) calculated across 1,117,369 and 1,099,463 plots, respectively. All trait values refer to gap-filled trait values and were available for 26,632 out of the 54,519 taxa in sPlot (45.9%). Trait values were log-transformed prior to analysis. *Stem specific density* is stem dry mass per stem fresh volume, *specific leaf area* is leaf area per leaf dry mass, *leaf C*, *N* and *P* are leaf carbon, nitrogen and phosphorus content, respectively. *Leaf dry matter content* is leaf dry mass per leaf fresh mass, *leaf delta ^{15}N* is the leaf nitrogen isotope ratio, *stem conduit density* is the number of vessels (angiosperms) or tracheids (gymnosperms) per unit area in a cross section, *conduit element length* refers to both vessel elements and tracheids.

Trait	Abbreviation in sPlot dataset	TOP	Unit	Mean Log(CWM)	Mean Log(CWV)
Leaf area	LA	25	mm^2	6.130	1.565
Stem specific density	SSD	286	$g\ cm^{-3}$	-0.869	0.058
Specific leaf area	SLA	50	m^2kg^{-1}	2.850	0.150
Leaf C	LeafC	452	$mg\ g^{-1}$	6.116	0.002
Leaf N	LeafN	462	$mg\ g^{-1}$	3.038	0.063
Leaf P	LeafP	463	$mg\ g^{-1}$	0.535	0.117
Plant height	Plant.height	68	m	-0.315	1.259
Seed mass	Seed.mass	103	mg	0.407	2.784
Seed length	Seed.length	91	mm	1.069	0.365
Leaf dry matter content	LDMC	45	$g\ g^{-1}$	-1.294	0.130
Leaf N per area	LeafN.per.area	481	$g\ m^{-2}$	0.251	0.099
Leaf N:P ratio	Leaf.N:P.ratio	-	$g\ g^{-1}$	2.444	0.081
Leaf $\delta^{15}N$	Leaf.delta15N	-	per million	0.521	0.455
Seed number per reproductive unit	Seed.num.rep.unit	-		6.179	5.156
Leaf fresh mass	Leaf.fresh.mass	35	g	-2.125	1.520
Stem conduit density	Stem.cond.dens	-	mm^{-2}	4.407	0.975
Dispersal unit length	Disp.unit.length	90	mm	1.225	0.451
Conduit element length	Cond.elem.length	-	µm	5.946	0.367

References

Garnier, E., Stahl, U., Laporte, M.-A., Kattge, J., Mougenot, I., Kühn, I., … Klotz, S. (2017). Towards a thesaurus of plant characteristics: an ecological contribution. *Journal of Ecology*, *105*, 298–309.

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APPENDIX S7. Phylogenetic information in sPlot 2.1

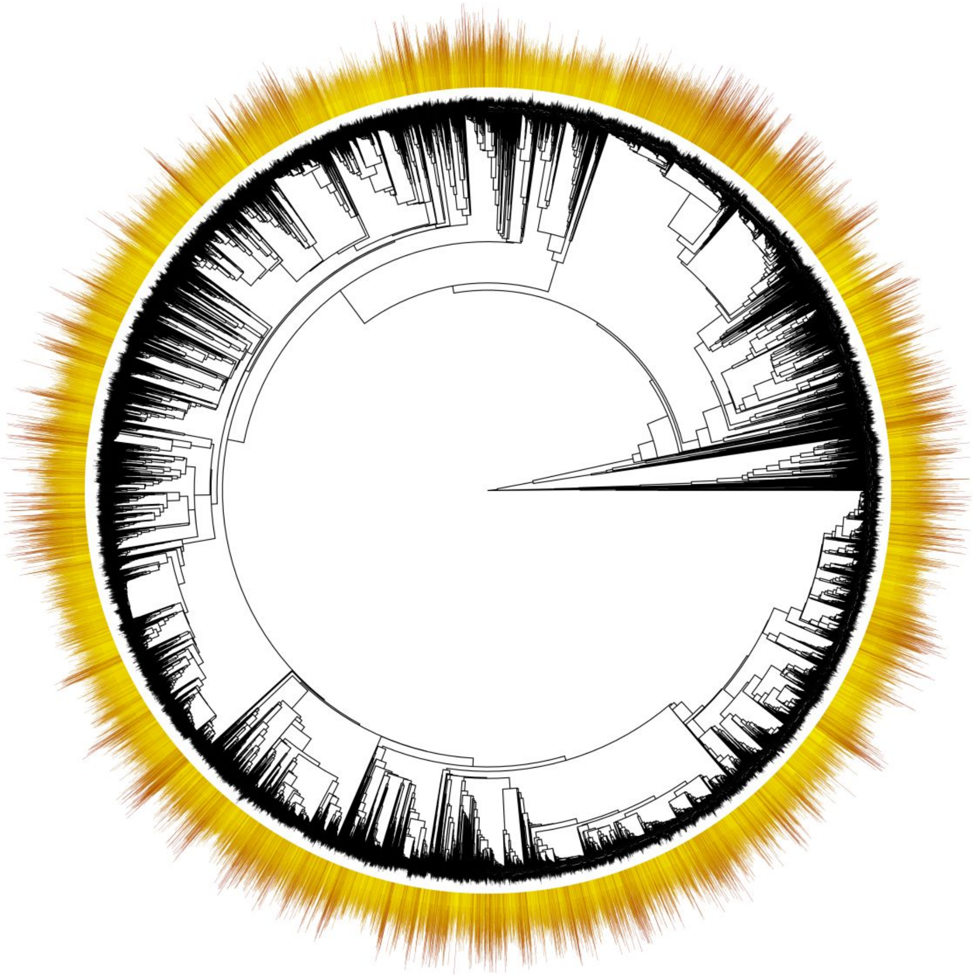

Fig. S7.6. Phylogenetic tree of 53,489 species sampled in the vegetation plots stored in sPlot 2.1. The length of the spikes show log frequency of species occurring in the database, ranging from 1 to 128,942 times (*Festuca rubra*). Colors of spikes rank from low (yellow) to high (redish) frequencies.

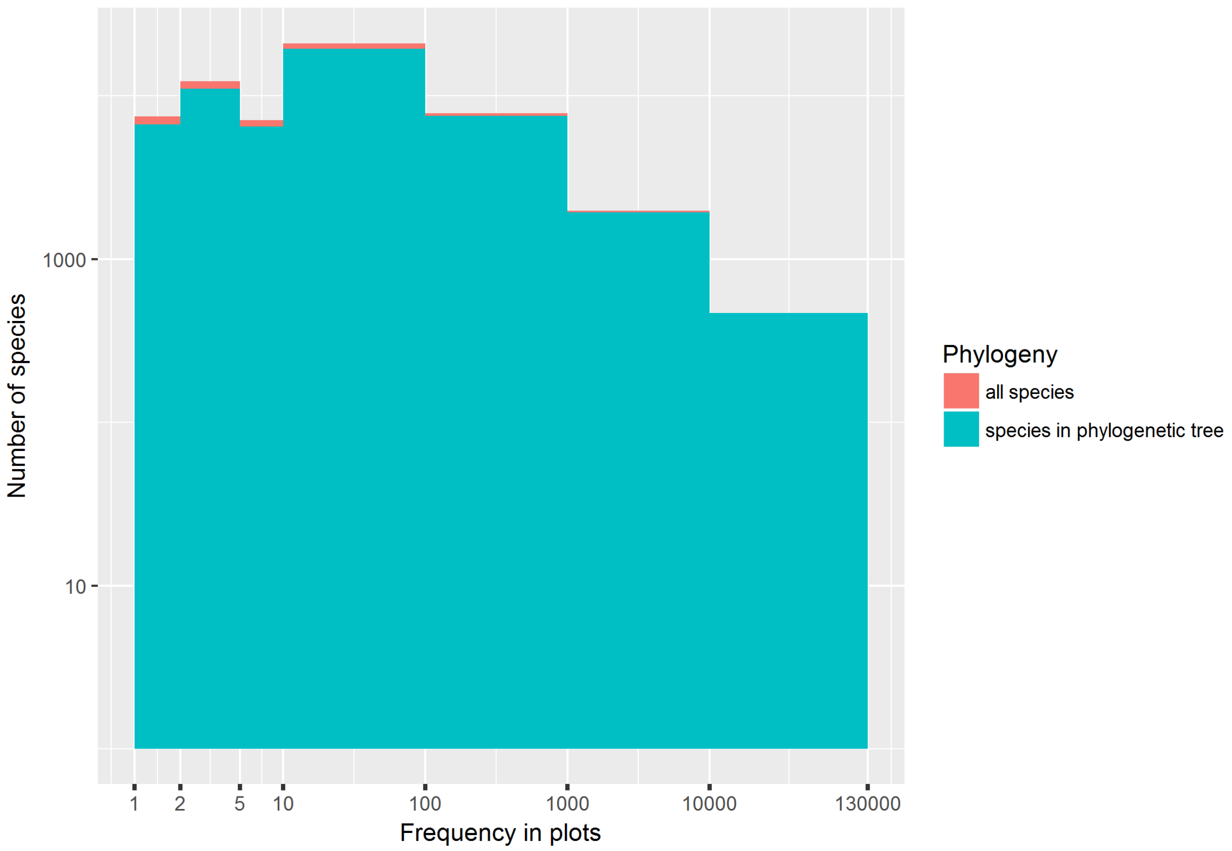

Fig. S7.7. Histogram of number of species by frequency classes in sPlot. Coverage of species included in the phylogeny was 89%, 90%, 91%, 92%, 96%, 99% and 100% of species that occurred with a frequency of 1; 2-5; 6-10; 11-100; 101-1,000; 1,001-10,000 and >10,000 in the plots.

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APPENDIX S8. Gap-filled trait information

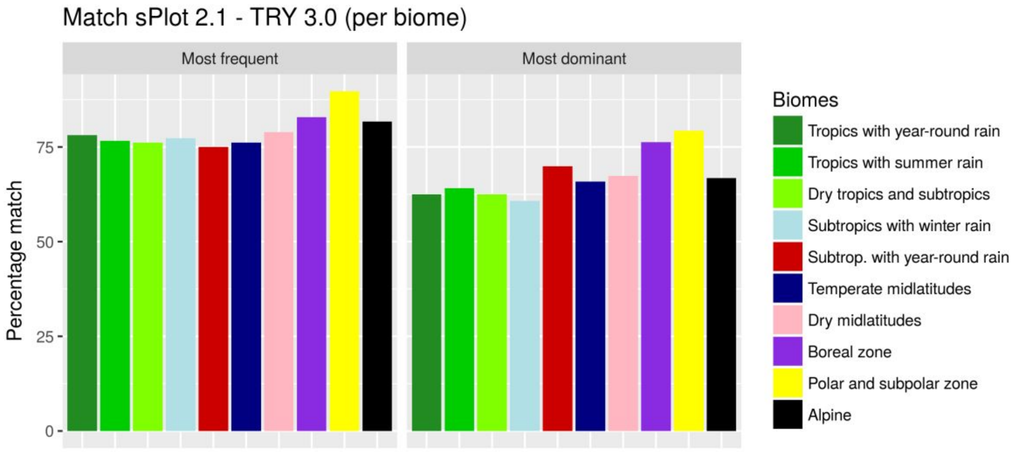

Fig. S8.8. Taxonomical match between sPlot 2.1 and TRY 3.0 per biome. The graphs show the percentages of the number of the 25% most frequent and 25% most dominant species in sPlot 2.1, for which gap-filled trait information was available in TRY 3.0.

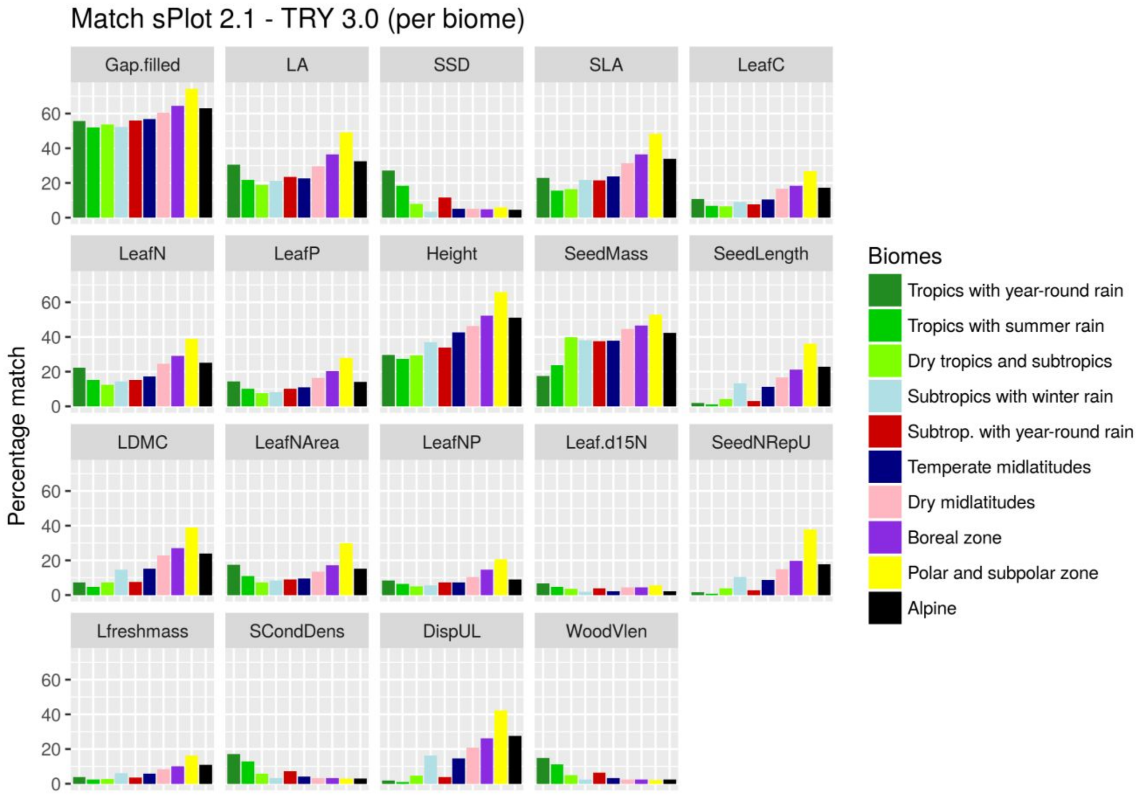

Fig. S8.9. Taxonomical match of gap-filled trait information between sPlot 2.1 and TRY 3.0 per biome and for the originally measured 18 traits selected from TRY. LA: Leaf area, SSD: Stem specific density, SLA: Specific leaf area, LeafC: Leaf C concentration, LeafN: Leaf N concentration, leafP: Leaf P concentration, Height: Plant height, , SeedMass: Seed mass, SeedLength: Seed length, LDMC: Leaf dry matter content, LeafNArea: Leaf N content per area, LeafNP: Leaf N:P ratio, Leaf-d15N: Leaf $\delta^{15}N$ concentration, SeedNRepU: Seed number per reproductive unit, Lfreshmass: Leaf fresh mass, SCondDens: Stem conduit density, DispUL: Dispersal unit length, WoodVlen: Conduit element length.

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APPENDIX S9. Global patterns of community-weighted variances

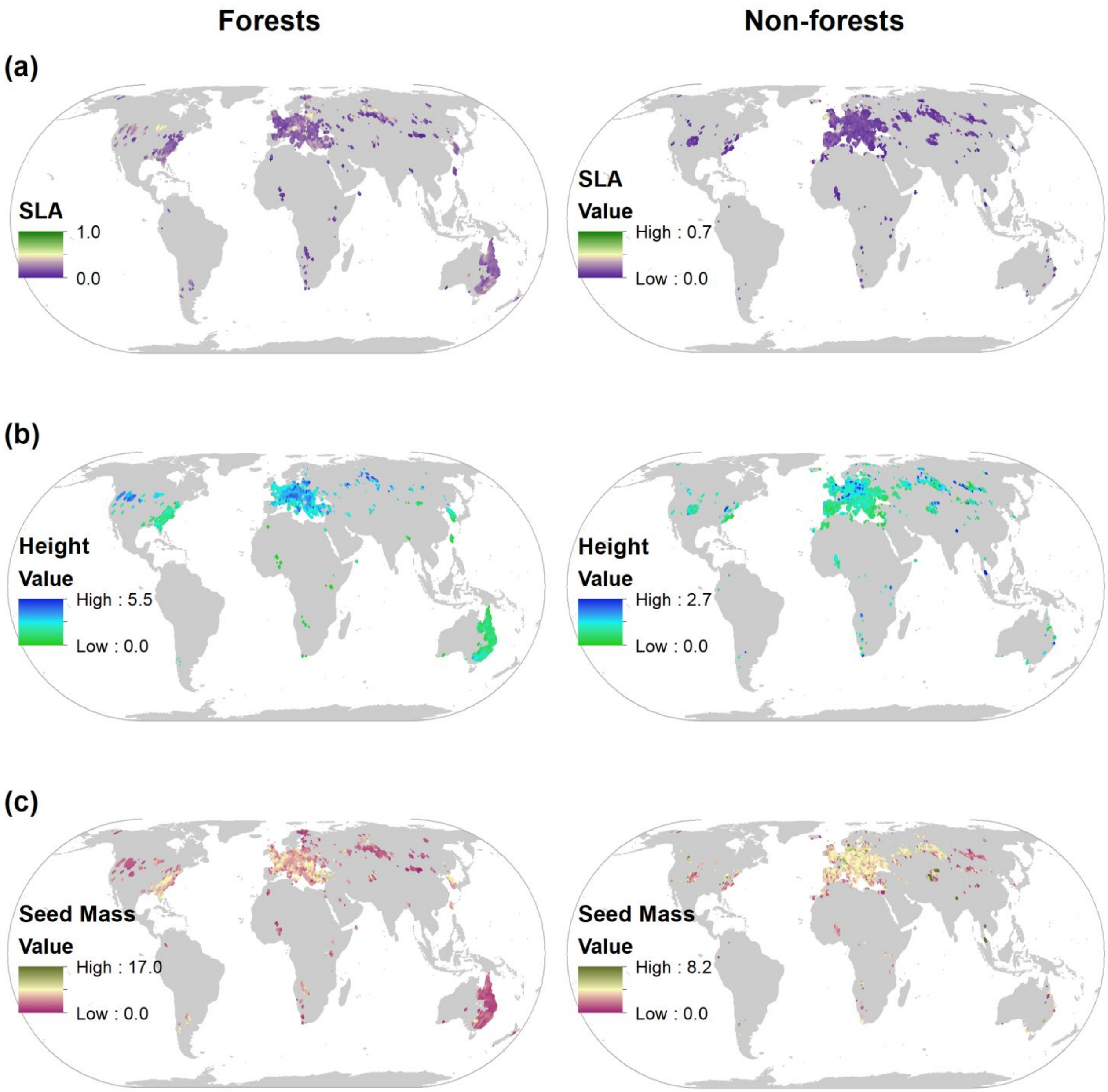

Fig. S9.10. (a) Community-weighted variances (CWVs) for $\log_e$-transformed trait values of specific leaf area (SLA, m^2 kg^{-1}), (b) plant height (m) and (c) seed mass (mg). CWV are averaged by grid cells of 1 degree.