



UvA-DARE (Digital Academic Repository)

Towards global interoperability for supporting biodiversity research on Essential Biodiversity Variables (EBVs)

Kissling, W.D.; Hardisty, A.; García, E.A.; Santamaria, M.; De Leo, F.; Pesole, G.; Freyhof, J.; Manset, D.; Wissel, S.; Konijn, J.; Los, W.

Published in:
Biodiversity

DOI:
[10.1080/14888386.2015.1068709](https://doi.org/10.1080/14888386.2015.1068709)

[Link to publication](#)

Citation for published version (APA):

Kissling, W. D., Hardisty, A., García, E. A., Santamaria, M., De Leo, F., Pesole, G., Freyhof, J., Manset, D., Wissel, S., Konijn, J., & Los, W. (2015). Towards global interoperability for supporting biodiversity research on Essential Biodiversity Variables (EBVs). *Biodiversity*, 16(2-3), 99-107.
<https://doi.org/10.1080/14888386.2015.1068709>

General rights

It is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), other than for strictly personal, individual use, unless the work is under an open content license (like Creative Commons).

Disclaimer/Complaints regulations

If you believe that digital publication of certain material infringes any of your rights or (privacy) interests, please let the Library know, stating your reasons. In case of a legitimate complaint, the Library will make the material inaccessible and/or remove it from the website. Please Ask the Library: <https://uba.uva.nl/en/contact>, or a letter to: Library of the University of Amsterdam, Secretariat, Singel 425, 1012 WP Amsterdam, The Netherlands. You will be contacted as soon as possible.



Towards global interoperability for supporting biodiversity research on essential biodiversity variables (EBVs)

W. Daniel Kissling^{a*}, Alex Hardisty^b, Enrique Alonso García^c, Monica Santamaria^d, Francesca De Leo^d, Graziano Pesole^{d,e}, Jörg Freyhof^f, David Manset^g, Silvia Wissel^h, Jacco Konijn^h and Wouter Los^a

^a*Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam, Amsterdam, The Netherlands;*

^b*School of Computer Science & Informatics, Cardiff University, Cardiff, United Kingdom;* ^c*Councillor of State of the Kingdom of Spain and Honorary Researcher of the Franklin Institute of the University of Alcalá, Madrid, Spain;* ^d*Institute of Biomembranes and Bioenergetics-IBBE, National Research Council-CNR, Bari, Italy;* ^e*Department of Biosciences, Biotechnology and Biopharmaceutics, University of Bari, Bari, Italy;* ^f*Group on Earth Observations – Biodiversity Observation Network (GEO BON), German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Leipzig, Germany;* ^g*gnùbila France, Argonay, France;*

^h*Faculty of Science, University of Amsterdam, Amsterdam, The Netherlands*

(Received 10 April 2015; final version received 30 June 2015)

Essential biodiversity variables (EBVs) have been proposed by the Group on Earth Observations Biodiversity Observation Network (GEO BON) to identify a minimum set of essential measurements that are required for studying, monitoring and reporting biodiversity and ecosystem change. Despite the initial conceptualisation, however, the practical implementation of EBVs remains challenging. There is much discussion about the concept and implementation of EBVs: which variables are meaningful; which data are needed and available; at which spatial, temporal and topical scales can EBVs be calculated; and how sensitive are EBVs to variations in underlying data? To advance scientific progress in implementing EBVs we propose that both scientists and research infrastructure operators need to cooperate globally to serve and process the essential large datasets for calculating EBVs. We introduce GLOBIS-B (GLOBal Infrastructures for Supporting Biodiversity research), a global cooperation funded by the Horizon 2020 research and innovation framework programme of the European Commission. The main aim of GLOBIS-B is to bring together biodiversity scientists, global research infrastructure operators and legal interoperability experts to identify the research needs and infrastructure services underpinning the concept of EBVs. The project will facilitate the multi-lateral cooperation of biodiversity research infrastructures worldwide and identify the required primary data, analysis tools, methodologies and legal and technical bottlenecks to develop an agenda for research and infrastructure development to compute EBVs. This requires development of standards, protocols and workflows that are ‘self-documenting’ and openly shared to allow the discovery and analysis of data across large spatial extents and different temporal resolutions. The interoperability of existing biodiversity research infrastructures will be crucial for integrating the necessary biodiversity data to calculate EBVs, and to advance our ability to assess progress towards the Aichi targets for 2020 of the Convention on Biological Diversity (CBD).

Keywords: global change; global infrastructure cooperation; informatics; legal interoperability; user priorities; workflow development

Introduction

Global climate change, habitat loss, human appropriation of natural resources and the spread of pathogenic, exotic and domestic plants and animals are major challenges for humanity because these processes alter the functioning of ecosystems and their ability to provide human society with the goods and services needed to prosper (Cardinale et al. 2012; Naeem, Duffy, and Zavaleta 2012). The taxonomic, phylogenetic, genetic and functional diversity of nature therefore plays a crucial role for understanding and securing ecosystem processes and services, including food, biomaterials, biofuels, pollination, pest control, genetic resources, cultural values and many others. Yet, biodiversity is declining rapidly, with global and local extinctions and widespread population

declines. These declines are driven by many factors, including land use change, climate change and eutrophication. Most of these factors have been pushed beyond the ‘safe operating space’ for global societal development and tipping points may soon be reached (Steffen et al. 2015). The urgency of this matter is recognised by the Parties to the United Nations (UN) Convention on Biological Diversity (CBD) who have established the Aichi targets for 2020 (<http://www.cbd.int/sp/elements/default.shtml>). The 20 Aichi targets have the mission to take effective and urgent action to halt the loss of biodiversity to ensure resilient ecosystems that provide the essential services, thereby securing the planet’s variety of life and human well-being. Despite this clear mission, however, it remains unclear how specific variables or

*Corresponding author. Email: wdkissling@gmail.com

aggregated indicators of biodiversity and ecosystem change can be developed and applied globally to evaluate the accomplishment of the Aichi targets by 2020 (Geijzendorffer et al. [forthcoming](#); Mace et al. 2010; Metzger et al. 2013; Scholes et al. 2012; Tittensor et al. 2014).

The concept of essential biodiversity variables (EBVs) has been introduced by the Group on Earth Observations Biodiversity Observation Network (GEO BON) with the aim to identify key measurements that are required to study, report and manage biodiversity change (Pereira et al. 2013). EBVs are considered to provide a tractable and holistic approach to monitoring the state of biodiversity and are conceptually located between the primary data observations at the one end and the aggregated biodiversity indicators or final synthesis indices at the other end (Pereira et al. 2013). Hence, EBVs could form the basis of a comprehensive worldwide monitoring network (Schmeller et al. 2015) and might be crucial for the robust estimation and derivation of indicators to assess progress towards the Aichi targets (Geijzendorffer et al. [forthcoming](#); Pereira et al. 2013). A total of 22 EBVs have been proposed by GEO BON within six EBV classes (i.e. genetic composition, species populations, species traits, community composition, ecosystem functioning and ecosystem structure) (https://www.earthobservations.org/geobon_ebv.shtml). These EBVs cover multidimensional aspects of biodiversity, including genetic diversity of selected wild and domestic species, population abundances of representative species, three-dimensional habitat structures, nutrient retention rates in sensitive ecosystems and many others. EBVs further allow to facilitate the harmonisation of existing monitoring schemes and to guide the implementation of new monitoring schemes worldwide. However, a key question is how the multi-lateral cooperation of data collectors, data providers, monitoring schemes and biodiversity research infrastructures can be achieved at the global level to support the uniform implementation of EBVs.

Here, we introduce GLOBIS-B (GLOBAL Infrastructures for Supporting Biodiversity research), an EU-funded project supported by the Horizon 2020 research and innovation framework programme of the European Commission under the coordination and support action funding scheme (www.globis-b.eu). GLOBIS-B aims to facilitate and advance the global cooperation of world-class research infrastructures (e.g. from Australia, USA, Brazil, China, South Africa, Europe) with a focus on targeted services to address frontier research on quantifying and measuring EBVs. The project is centred around the required species-level biodiversity data and the collaboration among biodiversity research infrastructures (Figure 1). The project brings together top biodiversity scientists with global research infrastructure

operators and legal interoperability experts to address the research needs and infrastructure services underpinning the concept of EBVs. A key goal is to develop a research and infrastructure agenda for computing EBVs globally and to identify whether and how it is possible to calculate, analyse, visualise and interpret EBVs for any place, at any time, with any relevant data, and by any person. The project will organise several integrated scientific and technical workshops to identify (1) the required primary data, data standards, analysis tools, methodologies, etc., (2) legal and technical bottlenecks and (3) possibilities for enhancing the multi-lateral cooperation of research infrastructures and biodiversity scientists to support global research on EBVs. Here, we outline the major challenges for implementing EBVs globally as well as how GLOBIS-B aims to address them.

Major challenges for the global implementation of EBVs

The calculation of EBVs requires several components, including (1) the availability of biodiversity data at relevant spatial, temporal and topical scales; (2) appropriate analytical tools and services for calculating, analysing, visualising and interpreting EBVs; and (3) the interoperability of existing biodiversity research infrastructures for integrating biodiversity data and for continuously calculating EBVs on-demand (Geijzendorffer et al. [forthcoming](#); Hoffmann et al. 2014; Schmeller et al. 2015). First, biodiversity data for the calculation of EBVs need to become available and be discovered, e.g. from biodiversity and Earth observation realms and their data portals (Pereira et al. 2013). This includes remote sensing data (and derived products such as land cover maps), taxonomic backbone data (e.g. nomenclatorial data), genetic and genomics data (e.g. DNA barcodes), long-term observational data from monitoring programmes or biodiversity observatories (e.g. presence-absence, abundance, species interactions, etc.), specimen data from scientific collections and information on functional and ecological traits (Hobern et al. 2013; Hoffmann et al. 2014; Schmeller et al. 2015). Second, tools and services for EBV calculation, analysis, visualisation and interpretation are needed. This includes semantic approaches and ontologies for data integration and interoperability, methods for data presentation and data visualisation, scientific workflow systems for calculation, analysis and modelling and other ecoinformatics approaches such as up-scaling and down-scaling of biodiversity information and methods for modelling data collection processes (e.g. Azaele et al. 2015; De Giovanni et al. [Forthcoming](#); Hobern et al. 2013; Isaac et al. 2014; Jones et al. 2006; Kunin 1998; Mathew et al. 2014; Schmeller et al. 2015). Third, biodiversity information management has to be

enable the effective reuse of ecological data in a user-friendly manner (Veen et al. 2012). Prerequisites are standardisation of data, metadata and data sharing (e.g. data repositories); automation of analytical tools (e.g. automated processing pipelines); and appropriate software packages (Hardisty, Roberts, and The Biodiversity Informatics Community 2013; Vicario, Hardisty, and Haitas 2011). The other challenge is related to legal interoperability, conditional for the automatic processing of data as supported by ‘machine–machine’ interactions across political and institutional boundaries (Hosking, Gahegan, and Dobbie 2014). This is often difficult due to varying provenance of authorship and ownership of data and requires the identification of legal and policy bottlenecks. Comparing mutual agreements between research infrastructures and data providers may avoid potential problems with respect to sharing of data and resources, re-licensing of services and adoption of open/public access principles. Such topics are addressed internationally by the Research Data Alliance and its RDA-CODATA legal interoperability interest group (<https://rd-alliance.org/group/rdacodata-legal-interoperability-ig.html>), but issues specific to EBV-relevant biodiversity data need to be assessed separately.

How GLOBIS-B addresses these major challenges

The GLOBIS-B project aims to address these major challenges outlined above. In the following, the general structure, the scientific content and workshops and the expected impact and global outreach of GLOBIS-B will be outlined.

General structure of GLOBIS-B

GLOBIS-B will be built around six project partners and 12 biodiversity research infrastructures (Table 1). The six project partners cover expertise in ecology, biodiversity science, Earth observation systems, genomics, bioinformatics, cloud computing, workflow development and legal aspects. In addition, the 12 cooperating research infrastructures are focussing on data mobilisation and on knowledge production. They are located in Europe, the United States of America, China, South Africa, Australia and Brazil, and some have a global mission (e.g. GBIF, WDCM and GEO BON, see Table 1). Hence, the involved research infrastructures complement each other in terms of geographic scope and provided services (Figure 2). The objective of GLOBIS-B is to facilitate the multi-lateral cooperation among these research infrastructures with the aim to advance the implementation of EBVs. This includes to: (1) specify users’ requirements for extracting, handling, visualising and analysing the required biodiversity data; (2) identify where these research infrastructures can enhance existing capabilities

or develop new ones; (3) agree on realistic solutions for supporting user requirements so that the research infrastructures can offer targeted services to calculate selected EBVs; (4) draw up best practices for infrastructure support; and (5) address legal implications with respect to licensing, intellectual property rights, and sharing of resources.

To achieve this, GLOBIS-B is organised in five work packages (WPs) of which two (WP1 and WP5) are related to administrative issues and three (WP2–4) to the scientific and technical content (Figure 3). WP1 (coordination and management) is mainly responsible to ensure the project’s milestones; to link together the project components; and to maintain communication with the European Commission. WP2 (with focus on user requirements) is responsible to scientifically prepare and guide the planned workshops; to synthesise existing biodiversity research on EBVs; to summarise and publish workshop outputs; and to foster international cooperation of biodiversity scientists and research infrastructure operators. WP3 (data and technical services for infrastructure delivery) is responsible for the technical aspects of the workshop, i.e. those parts relevant for biodiversity informaticians and technologists of the cooperating research infrastructures; and for identifying common pertinent services that can support scientific work on EBVs (i.e. specification of end-to-end scientific workflows for preparing/calculating EBV values). WP4 (policy and legal aspects) mainly aims to analyse and evaluate legal interoperability issues that relate to the selected EBVs. Finally, WP5 (dissemination and workshop organisation) is the project’s prime outreach mechanism being responsible for the involvement of cooperating biodiversity research infrastructures, the practical organisation of the planned workshops and for informing relevant stakeholders and communities about the developing plans.

Scientific content and workshops of GLOBIS-B

The general scientific content of GLOBIS-B is centred on EBVs and the required biodiversity data and support from research infrastructures (Figure 1). Out of the many meanings of biodiversity – including biotic variation from the level of genes to ecosystems (Purvis and Hector 2000) as well as taxonomic, functional and phylogenetic aspects (Naem, Duffy, and Zavaleta 2012) – the GLOBIS-B project will mainly focus on the species level (Figure 1). This includes taking into account the above mentioned specificities in the case of microorganisms for which the species concept is not always tractable (Ahn, Chai, and Pan 2014; Caro-Quintero and Konstantinidis 2012). In particular, focus is put on data related to species distributions and abundances, species traits, and species interactions (Figure 1). This is justified because

Table 1. Project partners and supporting research infrastructures of the GLOBIS-B project. The listed supporting research infrastructures represent those that have agreed to contribute to the GLOBIS-B project.

Acronym	Organisation	Geographic scope	Website
<i>Project partners</i>			
UvA	University of Amsterdam (Institute for Biodiversity and Ecosystem Dynamics)	Netherlands	http://ibed.uva.nl/
CU	Cardiff University (School of Computer Science and Informatics)	UK	http://www.cs.cf.ac.uk/
GNUBILA	gnubila France	France	https://gnubila.fr/
CNR	Consiglio Nazionale delle Ricerche (Institute of Biomembranes and Bioenergetics)	Italy	http://www.cnr.it/sitocnr/home.html
FI-UAH	Universidad de Alcalá (Instituto Benjamin Franklin)	Spain	http://www.institutofranklin.net/
MLU	Martin-Luther-Universität Halle-Wittenberg (German Centre for Integrative Biodiversity Research i-Div)	Germany	http://www.idiv-biodiversity.de/idiv/research/geo-bon/
<i>Supporting research infrastructures</i>			
Atlas	Atlas of Living Australia	Australia	http://www.ala.org.au/
BC-CAS	Biodiversity Committee of the Chinese Academy of Sciences	China	http://www.kepingma.com/index.html
CRIA	Brazilian Reference Centre on Environmental Information	Brazil	http://www.cria.org.br/
DataONE	Data Observation Network for Earth	USA	http://www.dataone.org/
ELIXIR	European infrastructure for biological information	Europe	http://www.elixir-europe.org/
GBIF	Global Biodiversity Information Facility	Global	http://www.gbif.org/
GEO BON	Group on Earth Observations Biodiversity Observation Network	Global	http://www.geobon.org
GBoWS	Germplasm Bank of Wild Species at Kunming Institute of Botany	China	http://english.kib.cas.cn/
LifeWatch	European Infrastructure for Biodiversity and Ecosystem Research	Europe	http://lifewatch.eu/
NEON	National Ecological Observatory Network	USA	http://www.neoninc.org/
SANBI	South African National Biodiversity Institute	South Africa	http://www.sanbi.org/
WDCM	World Data Centre of Microorganisms at WFCC-MIRCEN	Global	http://www.wdcm.org/

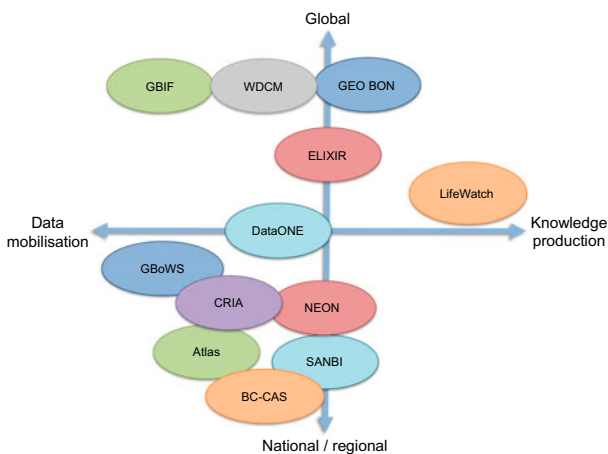


Figure 2. Characterisation of the biodiversity research infrastructures which cooperate in the GLOBIS-B project. Research infrastructures differ in their geographic scope (*y*-axis) and their focus on data mobilisation vs. knowledge production (*x*-axis). The figure is a modified and updated version from the roadmap document produced by the project CReATIVE-B (<http://creative-b.eu/documents>).

biodiversity is organised in complex networks of interacting species with different traits (e.g. pollinators and plants, predators and prey, etc.), and understanding and

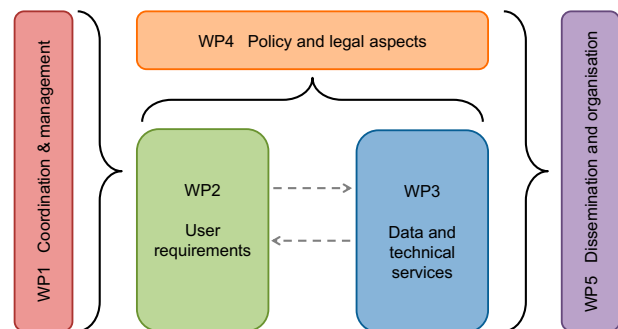


Figure 3. Graphical presentation of the GLOBIS-B work plan components consisting of five work packages (WP1–5). The work packages WP2–4 are responsible for the content of the workshops whereas WP1 and WP5 have mostly administrative tasks.

predicting these network dynamics remains one of the great challenges (e.g. Bascompte 2009; Blois et al. 2013; Kissling and Schleuning 2015; Lonsdorf et al. 2009). Although digital information on the spatial distribution of species (e.g. via GBIF, <http://www.gbif.org/>) is increasingly available, we still lack comprehensive, well-organised and easily accessible knowledge about species traits and species interactions. However, there are many ongoing efforts on collecting species traits

(e.g. Kattge et al. 2011; Kissling et al. 2014; Naeem and Bunker 2009), including comprehensive, open digital repositories such as TraitBank in the Encyclopedia of Life (<http://eol.org/info/516>). Similar efforts on open infrastructures for species interaction data have been started (Poelen, Simons, and Mungall 2014), but the limited availability of data for modelling species interactions across large spatial scales remains a challenge (e.g. Blois et al. 2013; Kissling et al. 2012; Morales-Castilla et al. 2015; Wisz et al. 2013). This lack of knowledge is severely constraining our ability to predict the consequences of climate change and other perturbations which impact biodiversity and human well-being.

The scientific content of GLOBIS-B will be addressed in four workshops focussing on three EBV topics (Figure 4). Workshop 1 and 2 will focus on species distributions and abundances (EBV class ‘Species populations’). This includes species distributional data (e.g. observations, point and transect counts, camera trapping, etc.) from monitoring programmes, systematic inventory schemes and citizen science initiatives (Schmeller et al. 2015). It also includes molecular biodiversity data (e.g. barcoding, meta-barcoding and metagenomic approaches based on next-generation sequencing technologies and bioinformatic data analysis) which increasingly allow species or strain identification at a high rate and accuracy, even in the most remote and extreme ecosystems (Gilbert and Dupont 2011; Kress et al. 2015; Shokralla et al. 2014; Simon and Daniel 2011). Workshop 3 will be centred on the EBV class

‘Species traits’ which can include phenology, plant functional traits, animal body mass, natal dispersal distances or migratory behaviour (Pereira et al. 2013). Finally, workshop 4 will focus on the EBV ‘Species interactions’ (EBV class ‘Community composition’) which can include changes in empirical estimates of interaction strengths (Berlow et al. 2004; Vazquez, Morris, and Jordano 2005; Wootton and Emmerson 2005) or more complex data from ecological networks (Ings et al. 2009). In addition, molecular methods could be potentially useful to measure biodiversity changes in predator–prey interactions (incl. invasive predators) and food webs (e.g. collecting and analysing data from guts and droppings), host–symbiont interactions (e.g. genetic, taxonomic and functional analysis of microorganisms which show symbiotic interactions in selected parts of the body or droppings of a host) or interactions among microorganisms (e.g. taxonomic and functional correlations among multiple symbionts in the same host species). Overall, the different EBVs were selected to represent different challenges, maturity levels and data availabilities. More specifically, the three types of data related to EBVs represent an increasing level of complexity for biodiversity monitoring and for developing the supporting research infrastructures, with potential implications for the legal interoperability at the supra-national and global scale.

The four workshops (Figure 4) will allow for an interaction between research needs and potential infrastructure service development. The key aim is to sort out how the global cooperation of research infrastructures can facilitate scientific work on improving knowledge and understanding of EBVs, as well as their applicability for assessing progress towards the Aichi targets for 2020 of the CBD. This starts with the options and problems to deliver biodiversity data at appropriate spatial and temporal scales for EBV calculation, and the associated provisions for research infrastructures to support the generation and calculation of EBVs. To achieve this goal, the workshops will bring together ecologists and biodiversity scientists, biodiversity informaticians and infrastructure operators and legal interoperability experts (Figure 4). This will allow to: (1) design and propose an international cooperation network to facilitate interoperable research infrastructures and harmonised observation systems supporting biodiversity monitoring and the measurement of EBVs; (2) identify initiatives, data portals and research infrastructures that aim at storing, disseminating and processing of EBV-relevant data on species populations, species traits, and species interactions; (3) identify missing data and services as well as possibilities for co-financing of existing research infrastructures; (4) identify challenges and limitations for sharing, reciprocal use, and openness of data; (5) develop recommendations and guidelines for the standardisation of EBV-relevant data collection and

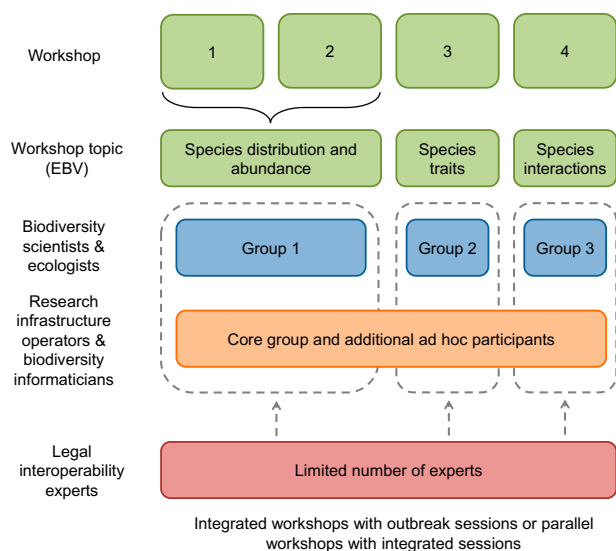


Figure 4. Overview of proposed workshops to discuss and develop the implementation of essential biodiversity variables (EBVs) among different participant groups (ecologists and biodiversity scientists, biodiversity informaticians and infrastructure operators and legal interoperability experts).

curation, and for the sharing of interoperable datasets; and (6) enhance existing capabilities and facilitate future development of cross-disciplinary computational tools and standardised protocols (workflows) for merging, disseminating, and sharing EBV-relevant data, and running calculations and analyses with it.

Impact and global outreach

The main expected impact of the GLOBIS-B project is an enhanced global infrastructure support for calculating EBVs and assessing progress towards the Aichi targets for 2020 of the CBD. More specifically, GLOBIS-B aims to contribute to the future agenda for biodiversity research by reaching out to three major target audiences. The first target audience is the international biodiversity research infrastructure community. GLOBIS-B benefits from the network of cooperating global research infrastructures (Table 1) as brought together by the preceding project ‘CREATIVE-B’ (<http://creative-b.eu/>). This ensures the outreach to major research infrastructure communities in the world, including their informatics specialists. The second target audience is the biodiversity scientific community. GLOBIS-B will invite key scientists with expert knowledge in the environmental sciences, ecology, biodiversity, monitoring and global change to ensure that biodiversity science is centrally positioned in the workshops. These participants can cover different domains (land, freshwater, marine) and various taxa (vertebrates, plants, invertebrates, microbes, etc.). The third target audience are major international policy bodies such as the CBD and IPBES. GLOBIS-B aims to directly approach these major global policy bodies and also reach out to more specific initiatives like the Research Data Alliance (RDA) and the International Conference on Research Infrastructures (ICRI). Additional links and collaborations will also be developed to other relevant projects (e.g. EU BON; <http://www.eubon.eu/>).

Conclusions

Above we presented the major components of GLOBIS-B, an ambitious project aiming to facilitate multi-lateral cooperation of biodiversity research infrastructures for advancing the implementation of EBVs worldwide. This global cooperation is meant to underpin the assessment of progress towards the Aichi targets for 2020 of the CBD. While there are many biodiversity data, monitoring programmes, and research infrastructures worldwide, there remain enormous challenges for the use, integration and processing of the relevant large data sets across institutional and national boundaries. The GLOBIS-B project aims to contribute to advance this field by

bringing together research infrastructure operators with a user community of top scientists to address the challenge of testing and calculating EBVs. This will ultimately allow us to better predict and monitor the ongoing and future changes that are happening in our biosphere.

Acknowledgements

The GLOBIS-B project has received funding from the European Union’s Horizon 2020 research and innovation programme under grant agreement No 654003. The work was also partly supported by the Molecular Biodiversity Laboratory of LifeWatch (Bari, Italy). WDK acknowledges a University of Amsterdam starting grant. We are grateful to Henrique Pereira and Bill Kunin for their support during the GLOBIS-B kick-off meeting at the University of Amsterdam in June 2015.

Disclosure statement

No potential conflict of interest was reported by the authors.

Funding

European Union Horizon 2020 research and innovation programme [Grant Number 654003].

References

- Ahn, T.-H., J. Chai, and C. Pan. 2014. “Sigma: strain-level Inference of Genomes from Metagenomic Analysis for Bio-surveillance.” *Bioinformatics* 31 (2): 170–177. doi:10.1093/bioinformatics/btu641.
- Azaele, S., A. Maritan, S. J. Cornell, S. Suweis, J. R. Banavar, D. Gabriel, and W. E. Kunin. 2015. “Towards a Unified Descriptive Theory for Spatial Ecology: Predicting Biodiversity Patterns across Spatial Scales.” *Methods in Ecology and Evolution* 6: 324–332. doi:10.1111/2041-210X.12319.
- Bascompte, J. 2009. “Disentangling the Web of Life.” *Science* 325 (5939): 416–419. doi:10.1126/science.1170749.
- Berlow, E. L., A. M. Neutel, J. E. Cohen, P. C. de Ruiter, B. Ebenman, M. Emmerson, J. W. Fox, et al. 2004. “Interaction Strengths in Food Webs: Issues and Opportunities.” *Journal of Animal Ecology* 73 (3): 585–598.
- Blois, J. L., P. L. Zarnetske, M. C. Fitzpatrick, and S. Finnegan. 2013. “Climate Change and the Past, Present, and Future of Biotic Interactions.” *Science* 341 (6145): 499–504. doi:10.1126/science.1237184.
- Cardinale, B. J., J. E. Duffy, A. Gonzalez, D. U. Hooper, C. Perrings, P. Venail, A. Narwani, et al. 2012. “Biodiversity Loss and Its Impact on Humanity.” *Nature* 486 (7401): 59–67.
- Caro-Quintero, A., and K. T. Konstantinidis. 2012. “Bacterial Species May Exist, Metagenomics Reveal.” *Environmental Microbiology* 14 (2): 347–355. doi:10.1111/j.1462-2920.2011.02668.x.
- Geijzendorffer, I. R., E. C. Regan, H. M. Pereira, L. Brotons, N. Brummitt, Y. Gavish, P. Haase, et al. Forthcoming. “Bridging the Gap between Biodiversity Data and Policy Reporting Needs: An Essential Biodiversity Variables

- Perspective.” *Journal of Applied Ecology*. doi:10.1111/1365-2664.12417.
- Gilbert, J. A., and C. L. Dupont. 2011. “Microbial Metagenomics: Beyond the Genome.” *Annual Review of Marine Science* 3 (1): 347–371. doi:10.1146/annurev-marine-120709-142811.
- De Giovanni, R., A. R. Williams, E. Vera Hernández, R. Kulawik, F. Q. Fernandez, and A. R. Hardisty. Forthcoming. “ENM Components: A New Set of Web Service-based Workflow Components for Ecological Niche Modelling.” *Ecography*. doi: 10.1111/ecog.01552.
- Hardisty, A., D. Roberts, and The Biodiversity Informatics Community. 2013. “A Decadal View of Biodiversity Informatics: Challenges and Priorities.” *BMC Ecology* 13 (1): 16.
- Hobern, D., A. Apostolico, E. Arnaud, J. C. Bello, D. Canhos, G. Dubois, D. Field, et al. 2013. *Global Biodiversity Informatics Outlook: delivering Biodiversity Knowledge in the Information Age*. Copenhagen, Denmark: GBIF Secretariat.
- Hoffmann, A., J. Penner, K. Vohland, W. Cramer, R. Doubleday, K. Henle, U. Kõljalg, et al. 2014. “Improved Access to Integrated Biodiversity Data for Science, Practice, and Policy – The European Biodiversity Observation Network (EU BON).” *Nature Conservation* 6: 49–65. doi:10.3897/natureconservation.6.6498.
- Hosking, R., M. Gahegan, and G. Dobbie. 2014. “An EScience Tool for Understanding Copyright in Data Driven Sciences.” 2014 *IEEE 10th International Conference on EScience* 1:145–152. doi: 10.1109/eScience.2014.37.
- Ings, T. C., J. M. Montoya, J. Bascompte, N. Blüthgen, L. Brown, C. F. Dormann, F. Edwards, et al. 2009. “Ecological Networks – Beyond Food Webs.” *Journal of Animal Ecology* 78 (1): 253–269. doi:10.1111/j.1365-2656.2008.01460.x.
- Isaac, N. J. B., A. J. van Strien, T. A. August, M. P. de Zeeuw, and D. B. Roy. 2014. “Statistics for Citizen Science: Extracting Signals of Change from Noisy Ecological Data.” *Methods in Ecology and Evolution* 5 (10): 1052–1060. doi:10.1111/2041-210X.12254.
- Jones, M. B., M. P. Schildhauer, O. J. Reichman, and S. Bowers. 2006. “The New Bioinformatics: Integrating Ecological Data from the Gene to the Biosphere.” *Annual Review of Ecology Evolution and Systematics* 37: 519–544. doi:10.1146/annurev.ecolsys.37.091305.110031.
- Kattge, J., S. Diaz, S. Lavorel, I. C. Prentice, P. Leadley, G. Bönisch, E. Garnier, et al. 2011. “Try – A Global Database of Plant Traits.” *Global Change Biology* 17 (9): 2905–2935. doi:10.1111/j.1365-2486.2011.02451.x.
- Kissling, W. D., and M. Schleuning. 2015. “Multispecies Interactions across Trophic Levels at Macroscales: Retrospective and Future Directions.” *Ecography* 38 (4): 346–357. doi:10.1111/ecog.00819.
- Kissling, W. D., C. F. Dormann, J. Groeneveld, T. Hickler, I. Kühn, G. J. McInerney, J. M. Montoya, et al. 2012. “Towards Novel Approaches to Modelling Biotic Interactions in Multispecies Assemblages at Large Spatial Extents.” *Journal of Biogeography* 39 (12): 2163–2178. doi:10.1111/j.1365-2699.2011.02663.x.
- Kissling, W. D., L. Dalby, C. Fløjgaard, J. Lenoir, B. Sandel, C. Sandom, K. Trøjelsgaard, and J.-C. Svenning. 2014. “Establishing Macroecological Trait Datasets: Digitalization, Extrapolation, and Validation of Diet Preferences in Terrestrial Mammals Worldwide.” *Ecology and Evolution* 4: 2913–2930. doi:10.1002/ece3.1136.
- Kress, W. J., C. García-Robledo, M. Uriarte, and D. L. Erickson. 2015. “DNA Barcodes for Ecology, Evolution, and Conservation.” *Trends in Ecology & Evolution* 30 (1): 25–35. doi:10.1016/j.tree.2014.10.008.
- Kunin, W. E. 1998. “Extrapolating Species Abundance across Spatial Scales.” *Science* 281 (5382): 1513–1515.
- Lonsdorf, E., C. Kremen, T. Ricketts, R. Winfree, N. Williams, and S. Greenleaf. 2009. “Modelling Pollination Services across Agricultural Landscapes.” *Annals of Botany* 103 (9): 1589–1600. doi:10.1093/aob/mcp069.
- Mace, G. M., W. Cramer, S. Díaz, D. P. Faith, A. Larigauderie, P. Le Prestre, M. Palmer, et al. 2010. “Biodiversity Targets after 2010.” *Current Opinion in Environmental Sustainability* 2 (1-2): 3–8. doi:10.1016/j.cosust.2010.03.003.
- Mathew, C., A. Güntsch, M. Obst, S. Vicario, R. Haines, A. Williams, Y. de Jong, and C. Goble. 2014. “A Semi-automated Workflow for Biodiversity Data Retrieval, Cleaning, and Quality Control.” *Biodiversity Data Journal* 2: e4221. doi:10.3897/BDJ.2.e4221.
- Metzger, M. J., D. J. Brus, R. G. H. Bunce, P. D. Carey, J. Gonçalves, J. P. Honrado, R. H. G. Jongman, A. Trabucco, and R. Zomer. 2013. “Environmental Stratifications as the Basis for National, European and Global Ecological Monitoring.” *Ecological Indicators* 33: 26–35. doi:10.1016/j.ecolind.2012.11.009.
- Morales-Castilla, I., M. G. Matias, D. Gravel, and M. B. Araújo. 2015. “Inferring Biotic Interactions from Proxies.” *Trends in Ecology & Evolution* 30 (6): 347–356. doi:10.1016/j.tree.2015.03.014.
- Naeem, S., and D. E. Bunker. 2009. “TraitNet: Furthering Biodiversity Research through the Curation, Discovery, and Sharing of Species Trait Data.” In *Biodiversity, Ecosystem Functioning, and Human Wellbeing: An Ecological and Economic Perspective*, edited by S. Naeem, D. E. Bunker, A. Hector, M. Loreau and Charles Perrings, 281–289. Oxford: Oxford University Press.
- Naeem, S., J. E. Duffy, and E. Zavaleta. 2012. “The Functions of Biological Diversity in an Age of Extinction.” *Science* 336 (6087): 1401–1406. doi:10.1126/science.1215855.
- Pereira, H. M., S. Ferrier, M. Walters, G. N. Geller, R. H. G. Jongman, R. J. Scholes, M. W. Bruford, et al. 2013. “Essential Biodiversity Variables.” *Science* 339 (6117): 277–278. doi:10.1126/science.1229931.
- Poelen, J. H., J. D. Simons, and C. J. Mungall. 2014. “Global Biotic Interactions: an Open Infrastructure to Share and Analyze Species-interaction Datasets.” *Ecological Informatics* 24: 148–159. doi:10.1016/j.ecoinf.2014.08.005.
- Purvis, A., and A. Hector. 2000. “Getting the Measure of Biodiversity.” *Nature* 405 (6783): 212–219.
- Schmeller, D. S., R. Julliard, P. J. Bellingham, M. Böhm, N. Brummitt, A. Chiarucci, D. Couvet, et al. 2015. “Towards a Global Terrestrial Species Monitoring Program.” *Journal*

- for *Nature Conservation* 25: 51–57. doi:10.1016/j.jnc.2015.03.003.
- Scholes, R. J., M. Walters, E. Turak, H. Saarenmaa, C. H. R. Heip, É. Ó. Tuama, D. P. Faith, et al. 2012. “Building a Global Observing System for Biodiversity.” *Current Opinion in Environmental Sustainability* 4 (1): 139–146. doi:10.1016/j.cosust.2011.12.005.
- Shokralla, S., J. F. Gibson, H. Nikbakht, D. H. Janzen, W. Hallwachs, and M. Hajibabaei. 2014. “Next-generation DNA Barcoding: Using Next-generation Sequencing to Enhance and Accelerate DNA Barcode Capture from Single Specimens.” *Molecular Ecology Resources* 14 (5): 892–901. doi:10.1111/1755-0998.12236.
- Simon, C., and R. Daniel. 2011. “Metagenomic Analyses: Past and Future Trends.” *Applied and Environmental Microbiology* 77 (4): 1153–1161. doi:10.1128/aem.02345-10.
- Steffen, W., K. Richardson, J. Rockström, S. E. Cornell, I. Fetzer, E. M. Bennett, R. Biggs, et al. 2015. “Planetary Boundaries: Guiding Human Development on a Changing Planet.” *Science* 347 (6223): 738. doi:10.1126/science.1259855.
- Tittensor, D. P., M. Walpole, S. L. L. Hill, D. G. Boyce, G. L. Britten, N. D. Burgess, S. H. M. Butchart, et al. 2014. “A Mid-term Analysis of Progress toward International Biodiversity Targets.” *Science* 346 (6206): 241–244. doi:10.1126/science.1257484.
- Vazquez, D. P., W. F. Morris, and P. Jordano. 2005. “Interaction Frequency as a Surrogate for the Total Effect of Animal Mutualists on Plants.” *Ecology Letters* 8 (10): 1088–1094. doi:10.1111/j.1461-0248.2005.00810.x.
- Veen, L. E., G. B. A. van Reenen, F. P. Sluiter, E. E. van Loon, and W. Bouten. 2012. “A Semantically Integrated, User-friendly Data Model for Species Observation Data.” *Ecological Informatics* 8: 1–9. doi:10.1016/j.ecoinf.2011.11.002.
- Vicario, S., A. Hardisty, and N. Haitas. 2011. “BioVeL: Biodiversity Virtual E-Laboratory.” 2011 17 (2): 5–6. doi:10.14806/ej.17.2.238.
- Wisz, M. S., J. Pottier, W. D. Kissling, L. Pellissier, J. Lenoir, C. F. Damgaard, C. F. Dormann, et al. 2013. “The Role of Biotic Interactions in Shaping Distributions and Realised Assemblages of Species: Implications for Species Distribution Modelling.” *Biological Reviews* 88 (1): 15–30. doi:10.1111/j.1469-185X.2012.00235.x.
- Wootton, J. T., and M. Emmerson. 2005. “Measurement of Interaction Strength in Nature.” *Annual Review of Ecology and Systematics* 36: 419–444. doi:10.1146/annurev.ecolsys.36.091704.175535.