Abstracts demonstrations and posters at Biodiversity Informatics Horizons 2013

Demonstrations

D1

Swedish LifeWatch Analysis portal

Wremp, A. M.

Following the guidelines and technical standards defined by LifeWatch, Sweden was the first country in Europe to begin constructing a national e-infrastructure for biodiversity data. The objective of the Swedish LifeWatch project is to make all major national biodiversity databases interoperable and accessible through standardized web services.

The coherent Analysis portal provides a single access point to all data connected to the infrastructure, together with a range of analytical services. The Analysis portal enables free access to a wide selection of biodiversity and environmental data based on taxonomical, ecological, temporal or spatial choice. Data can also be aggregated, analysed, visualized and downloaded according to preferences. This demonstration will focus on possibilities of the Swedish LifeWatch Analysis portal, but will also provide some insights into the Swedish Species Observation System and a new dynamic taxonomic backbone (Dyntaxa).

D2

The BioFresh Platform

Schmidt-Kloiber, A., Bremerich, V., De Wever, A., Freyhof, J., Jepson, P. & Tockner, K.

The BioFresh Platform serves as information hub for global freshwater biodiversity. It offers a collection of resources and tools to support better science, policy and management of freshwater life: (1) the BioFresh data portal, a single gateway for freshwater species occurrence data, (2) the BioFresh global freshwater biodiversity atlas, a constantly expanding collection of key maps related to freshwater biodiversity, (3) the BioFresh metadatabase, to discover all kind of data, their holders and access rights, (4) the BioFresh research and outreach area, offering scientists, policy makers, managers consultants and students a quick entry point to all kind of freshwater related information (important journals, publications, online learning resources, blog, discussion groups etc.). The use of all these different parts of the BioFresh Platform can be presented during the demo session.

D3

BioMaS: a comprehensive pipeline for Bioinformatic analysis of Metagenomic AmpliconS

Fosso, B., Santamaria, M., Marzano, M. & Pesole, G.

Researchers involved in advanced metagenomics projects need both powerful computational platforms and, in most case, robust bioinformatics know-how to suitably apply and combine tools for filtering, denoising and binning NGS data in order to obtain, finally, a consistent taxonomic classification. Unfortunately, in common practice, some of these steps are skipped or improperly carried out resulting in incorrect inferences. The fundamental purpose of BioMaS (Bioinformatic analysis of Metagenomic AmpliconS) is to provide the biomolecular researchers involved in taxonomic surveys of environmental microbial communities with a comprehensive workflow including all the fundamental steps for the NGS amplicon-based metagenomic analysis, by leading the data processing from raw sequences to final taxonomic identification. In its current version, BioMaS can be performed for the analysis of 454 and Illumina sequences from both bacterial and fungal environments.

D4

Encyclopedia of Life and TraitBank

Sims Parr, C.

After building its initial infrastructure for aggregating descriptive information on all living biodiversity, the Encyclopedia of Life (EOL, http://eol.org) is undergoing a major transformation in order to better serve scientific discovery. In a computer demonstration we show our progress on implementing for marine biodiversity use cases. We also share our vision for using TraitBank™ to manage trait data across the tree of life.

Initial attributes include but will likely not be limited to numeric data such as body size and longevity, controlled vocabularies such as habitat classifications, and relations such as ecological interactions among taxa. Data on a new "Data" tab on each EOL taxon page is sourced both from external providers and through direct addition to EOL. Core information is managed using Virtuoso, though some metadata will be handled in our existing relational database. We establish high-level integration via EOL's taxonomic names infrastructure and TDWG Species Profile Model terms, preserving (or in some cases, minting) low-level semantics and provenance for offline analysis and deep integration by users. These data will be subject to validation and curation. Users will eventually be able to search for and download all data relevant to topics such as reproduction or physical description, for all data using a particular EnvO habitat term (for example), or for data available for a collection of taxa.

The TraitBank effort will mobilize and add value to data archived in long-term repositories such as Dryad, to data papers in journals such as the Biodiversity Data Journal, and specimen and observation data from databases. We will leverage text mining and standardization efforts of several pilot projects such as Global Biotic Interactions (http://globalbioticinteractions.wordpress.com/) and ENVIRONMENTS (http://environments-eol.blogspot.com/).

We intend to work closely with European partners towards global Big Data initiatives in evolutionary and ecological science.

D5

EnvEurope Drupal Ecological Information System - making long-term ecological data available through the Internet

Kliment, T., Oggioni, A., Peterseil, J., Pugnetti A. & Carrara P.

The EnvEurope Drupal Ecological Information Management System (DEIMS) for managing metadata and sharing the data was developed in EnvEurope project based on the first official release of the Drupal metadata editor developed by US LTER. EnvEurope DEIMS currently consists of three main components:

1. Metadata editor: a web-based client interface to enter and manage metadata of three information resource types - datasets, persons and research sites.
2. Discovery client: provides several search profiles for datasets, persons, research sites and external resources normally used in the domain, e.g. Catalogue of Life, based on several search patterns ranging from simple full text search, glossary browsing to categorized faceted search.
3. Geo-Viewer: a map client that portrays boundaries and centroids of the research sites as Web Map Service (OGC-WMS) layers.

Sharing of the dataset metadata provided through the DEIMS is ensured in 2 ways to provide information for:

1. ILTER: periodic collecting of metadata records according to the EML schema, by Metacat to produce a data catalogue, which can be used by international or European initiatives (e.g. DataOne, GBIF) and projects (e.g. LifeWatch);
2. Spatial Data Infrastructure (INSPIRE): periodic harvesting of metadata into GeoNetwork catalogue, thus providing catalogue service for web (OGC-CSW), which can be invoked for metadata collection by remote clients, e.g. by INSPIRE Geoportal.

The EnvEurope DEIMS is being designed and implemented to provide an integrated environmental information management system and to bridge the gap between science and policy and to improve the scientific support to the EU environmental policy and conservation plans.

D6

The LifeWatch Alien Species Virtual Lab

Fiore, N., Basset, A. & Corriero G.

In order to provide a common point for researchers to access and sharing the data, the LifeWatch infrastructure includes a set of virtual labs. A virtual lab is an interoperable computing environment that allows a researcher to enter new data and use analytical tools. Furthermore, it also permits the collaboration with other researchers distributed across countries, time zones and disciplines in order to produce relevant information to respond to needs of the scientific community. The lab is also open to policy makers, entrepreneurs, students and any other interested citizens from different countries to contribute their own observations, know-how and opinions. The "**Alien Species Virtual Lab**" is a product of the Italian LifeWatch Network and the LifeWatch Service Centre Staff. The Virtual Lab is serving the Virtual Project '**Patterns of ecosystem fragility to alien and invasive species in Europe**'. It is an example of the kinds of scientific studies that biodiversity researchers would like to be able to undertake. The goal is to reach a list of capabilities in regard that topic to offer through LifeWatch portal for all those interested in alien species not only in Italy but worldwide. We collected, from the existing works given by the several universities and institutions involved in the development of the showcase, data about 11570 species from 314 different terrestrial and marine ecosystems.

The list of capabilities is as follows data interoperability; quality assurance process definition; metadata definition for the domain of interest; niche modeling techniques and tools; biological valuation maps.

D7

MyRice, Phyknome and J-Marine: Exemplars biodiversity databases developed using an integrated biodiversity content management system and real-time reporting on mobile app

Talkah, S., Amirah, A., Zulkifli, I., Bal, P., Shaiful Abdul Rahim, M., Shahir Shamsir, M. & Mohd Salleh, F.

Despite being one of the richest biodiversity countries in the world, Malaysia still lags significantly in the management of its biodiversity knowledge. We hope to spur adoption of mobile technologies using Sharkpad and AnnApp, a biodiversity data management system with an integrated mobile app which enables researchers to capture species occurrence in field, record and share data in real-time. Inspired by Scratchpads, we present exemplar databases MyRice, Phyknome and J-Marine as part of our effort to create the momentum urgently needed to take Malaysia abreast with global trends in biodiversity data management.

D8

ReFinder: Services to discover, format and convert bibliographic references

Penev, L., Biserkov, J., Ilieva, R, Georgiev T. & Stoev P.

The Bibliography of Life platform is developed within the FP7 project ViBRANT and consists of two components - RefBank (see D9) and ReFinder. ReFinder is designed to discover and download references from a wide range of open access online bibliographies, such as CrossRef, PubMed, Mendeley, Biodiversity Heritage Library (BHL), RefBank, Biostore, Bionames and others.

ReFinder provides an easy search function, based on a simple interface that collates the results from the search engines multiple queries for presentation to the user with the option to refine the results or submit a new search altogether. The searched references may be used for different purposes, e.g. conversion in some 600 citation styles and download into widely accepted bibliographic metadata standards (e.g., BibTex, MODS). The software is available through Bibliography of Life, as a standalone application at www.refinder.org, and will also be used as reference search backend for other tools, e.g., Scratchpads and Pensoft Writing Tool (PWT).

D9

RefBank: Services to store, deduplicate and parse bibliographic references

Sautter, G. & King, D.

The Bibliography of Life platform is developed within the EU FP7 project ViBRANT and consists of two components - RefBank and ReFinder (see D8). RefBank is a network of servers to store, deduplicate and parse bibliographic references.

RefBank provides a bibliographic reference service to users. This covers the basic services of loading and retrieving references, with search and formatting capabilities to assist in these tasks. Two key enhancements over other bibliographic services are:

1. the automatic deduplication of retrieved references to make reading the search results list easier for a user, and
2. the ability for a user to load plain text references, such as those a user might have accumulated in a Word document, into RefBank, which then automatically parses the reference into its components such as author, year, title, etc. to make later use of the reference much easier.

RefBank stored references may be used for different purposes, being available in a variety of citation styles and downloaded into widely accepted bibliographic metadata standards (e.g., BibTex, MODS).

RefBank is accessible as a standalone application, programmatically through an API, and is also integrated into Scratchpads.

The source code, with installation instructions, is available at https://git.scratchpads.eu/v/refbank.git.

D10

iMarine facilities for empowering biodiversity science

Coro, G., Ellenbroek, A. & Pagano, P.

This demo will cover:

* Exploiting the iMarine Biodiversity Research Environment to demonstrate the facilities the infrastructure offers to collect occurrence points and then analyze/project those points and access species taxon names from several data sources

* Exploiting the iMarine Scalable Data Mining environment for demonstrating the facilities that the infrastructure offers to perform analysis, mining and modeling of biogeographic data

* Exploiting the Ecological Modelling Research Environment to demonstrate the facilities that the infrastructure offers to discover, access, compare, and export geo-referenced products.

D11

CartoDB, an Open Source database on the cloud

CartoDB.com

We help people visualize and analyze geospatial data. CartoDB is a cloud based mapping, analysis and visualization engine that lets users build spatial applications for both mobile and the web. Major news organizations, research institutions, non-profits, and geospatial application developers throughout the world are already using the CartoDB platform. We'll demonstrate how easy it is to upload some data to create a new map, filter the data, add styling, and then make it shareable and embeddable.

Posters

P1

LifeWatch-WB : Geographic data services for biodiversity research

Radoux, J., Rousseau, C., De Maet, T. & Defourny, P.

The focus of the LifeWatch-WB team is to develop and make biodiversity data available on a regular basis, and more specifically data about habitats status and their dynamics. At this stage, two types of products have been developed. The first product is an integrated geographic database base on remote sensing data analysis and key abiotic factors. This dataset includes a delineation of potential habitats enriched with various attributes for flexible analysis. The beta version is available for Belgium based on Rapideye image at 5 m resolution, and should be extended to other European countries with the launch of the Sentinel-2 satellites. The second product is a set of biophysical variables extracted from long-term time series of Earth observation data. Information about snow, fires, vegetation and sunshine are provided at 500 m resolution. Web mapping, viewing and downloading services will allow an easy access to this pan-European information.

P2

Interoperability model between PLAZI and the EDIT CDM Platform

Agosti, D., Güntsch, A., Kelbert, P. & Sautter, G.

Plazi maintains a digital taxonomic literature repository to enable archiving of taxonomic treatments and EDIT Platform for Cybertaxonomy cover aspects of the taxonomic workflow, such as, taxonomic editing, publishing of edited data, data storage and exchange, collections and specimens, descriptions, fieldwork, literature and geography. In order to improve and fine-tune the quality of the marked-up treatments, interoperability model between PLAZI and the EDIT CDM Platform is an on-going process.

P3

Tracking biogeographical change from its footprints in botanical literature

Groom, Q., Eckert, S., Güntsch, A., Kelbert, P. & Sautter, G.

Hidden away in the vast corpus of botanical literature are data on the distributions of practically all described plants. Nevertheless, with the exception of a few rare species, it is extremely difficult to find accurate, global distribution maps. Furthermore, even though we know some species are expanding their range, while others are declining, we lack the data to quantify these changes. As a pilot project in pro-iBiosphere we are examine published floras to determine their value as a source of biogeographical information. Using the GoldenGATE Editor we are marking-up treatments and extracting data from as many sources as possible to create the best possible distribution maps of our model species.

P4

Biodiversity data use, modelling and organization: some research and development projects at CREAF

Marcer, A.

In this poster, we showcase some of the research and information system developments done at CREAF (Universitat Autònoma de Barcelona) on Biodiversity related issues. Biodiversity is one of the strategic areas of research at CREAF, funded by Catalan, Spanish and European grants. We show examples of conservation-related research such as methodologies to leverage information from biodiversity databases, to perform conservation assessments of endemic species and to monitor biodiversity protection over time through the use of information systems. We also give some examples of basic biogeographic research such as the modelling of natural spatial genetic variation of species. Finally, we exemplify our work on information systems developments by three projects, which deal with monitoring faunal species of conservation interest, invasive alien species in aquatic environments and geo-referencing biological specimens from natural history museums.

P5

A common, automated, pre-publication registration model for higher plants (International Plant Names Index, IPNI), fungi (Index Fungorum, MycoBank) and animals (ZooBank)

Penev, L., Georgiev, T., Stoev, P., Biserkov, J., Barker, C., Nicholson, N., Kirk, P., Paton, A., Robert, V. & Pyle R.

The process of post-publication recording and indexing of taxonomic and nomenclatural acts has a long tradition, in some cases dating as far back as the middle of 19th century (e.g. Index Kewensis, Zoological Record, etc.). The online publication of nomenclatural novelties brought into focus the concept of *pre-publication registration* and inclusion of the registries' persistent identifiers in the publications. This process has become mandatory in fungal and animal nomenclature due to the amendments to the biological Codes accepted recently. The pre-publication model is based on XML query/response model and includes various steps.

P6

BioVeL: Tools for modelling and predicting biodiversity

BioVel-consortium

Models and scenarios are essential to understand the complexity and intricacies of biodiversity. This knowledge is required to support the management and decision-making of the resources and services that biodiversity and ecosystems provide. Valid models use large amounts of data from various fields of research. BioVeL workflows make it easy to import data and create models. The results are in well-visualized formats like species distribution maps, population structure graphs or ecosystem service indicator charts. This poster highlights some recent work on a) ecological niche modelling of European forest insect pests in response to climate change; b) calculation of provisioning and regulating ecosystem service indicators at a West Hungarian arable/grassland/forest site; and c) the response in population growth rates as a result of deliberate vegetation disturbances for the Marsh Gentian, Gentiana pneumonanthe.

P7

Tailor made Web Portals for the Biodiversity Science Community in Belgium

Brosens, D., Heughebaert, A. & Segers, H.

The Belgian Biodiversity Platform continuously tries to engage scientists and biodiversity working groups in publishing their data on the Internet. One of the incentives is creating tailor made web portals on biodiversity data. The workflow, which results in the publication of the data and the creation of biodiversity portals can be an inspiration for others, as it includes: data cleaning & standardization, engaging existing communities, data paper publication and portal development. During the poster presentation we will showcase our two most recent portals, the Belgian IFBL checklists site on http://projects.biodiversity.be/ifbl and the online ants-atlas on www.formicidae-atlas.be.

P8

eMonocot - An online resource for monocot plants

Santarsiero, A., Clark, B., Kelly, J. & Godfray, C.

eMonocot is a resource covering the biodiversity, ecology, and evolution of monocot plants. Created and maintained by the global community of taxonomic experts, it represents the best information on these organisms online.

This content is enhanced using innovative tools that allow you to identify monocots, browse the current classification, and explore a wealth of information about these important plants.

P9

BioVeL: Tools for metagenomics and phylogenetics

BioVel-consortium

Current techniques to extract DNA and genomic sequences make it possible to study vast numbers of organisms. The fields of phylogenetics and metagenomics are quickly expanding, generating enormous amounts of data. BioVeL workflows allow for reliable and standardized processing of genetic sequencing data. BioVeL's workflows yield reliable and comparable results. This poster highlights some recent work on a) Exploration of a set of community traits in 53 metagenomic aquatic samples from the Global Ocean Sampling (GOS) expedition and b) What is the relationship between host and parasite biomas in the case of the relationship between larva of honey bees and varroa mites?

P10

Biodiversity information driving advances in Epidemiology and Climate Change: Two use cases from EUBrazilCC

Blanquer, I. & Brasileiro, F.

EUBrazil Cloud Connect (EUBrazilCC) is a European-Brazilian project focused on advancing on the use of cloud computing infrastructures for research.

Two of the three use cases of EUBrazilCC deal with biodiversity information. The first example aims at studying the distribution and genetic variability of the protozoa causing Leishmaniasis and its sandfly vectors.

The second example is on the study of the climate change based on the evolution and distribution of forest species.

P11

EU-Brazil Open Data and Cloud Computing e-Infrastructure for Biodiversity

EUBrazilOpenBio-consortium

EUBrazilOpenBio is a collaborative initiative addressing strategic barriers in biodiversity research by integrating open access data and user-friendly tools widely available in Brazil and Europe. EUBrazilOpenBio deploys a joint EU-Brazil cloud-based e-infrastructure that allows the sharing of hardware, software and data on-demand. Biodiversity scientists can use these open access resources and the applications developed by the project to conduct a wide range of conservation and research programmes.

The EUBrazilOpenBio e-Infrastructure development is being guided by two Use Cases. The first one focuses on comparing regional and global taxonomies, such as the regional List of Species of Brazilian Flora against the global Species2000/ITIS Catalogue of Life, helping taxonomists to manage differences between catalogues and in the taxonomic treatment of species. The second use case builds on work by organisations such as the Brazilian Virtual Herbarium of Flora and Fungi to facilitate the generation of niche models that predict the potential distribution of species under different environmental conditions.

P12

iDigBio: Engaging the public in digitization of a billion biodiversity research specimens

Mast, A., Dunckel, B. A., Nelson, G., Paul, D., MacFadden, B. J., Riccardi, G. & Page, L.

There are about a billion biodiversity research specimens in the U.S., only about 10% of which have been digitized (i.e., databased, imaged, and/or georeferenced). A goal of the biodiversity research community is to digitize most of the remaining specimens within a decade. To meet this ambitious goal requires increased collaboration, technological innovation, and broader engagement in digitization. Engaging the public in digitization, rather than simply hiring more digitizers, promises to both serve the digitizing institutions and further public understanding of science. We present a classification of public participation in digitization activities that emerged from an iDigBio workshop on the subject in September 2012, the results from experiments engaging the public in two of the main activities of digitization (label transcription and georeferencing), and an assessment of opportunities to engage K–16 students in digitization.

P13

Bibliography of Life: Comprehensive services for biodiversity bibliographic references

King, D. & Morse D. R.

The underlying principle of the Bibliography of Life is to provide taxonomists and others with a freely accessible bibliography covering the whole of life. Such a bibliography had been achieved for specific study areas within taxonomy, but not for "life" as a whole.

Now the EU FP7 ViBRANT project has progressed the Bibliography of Life and produced the two components needed to realize this concept - RefBank and ReFinder. RefBank is a network of servers to store, deduplicate and parse bibliographic references. ReFinder is designed to discover and download references from a wide range of open access online bibliographies, such as CrossRef, PubMed, Mendeley, Biodiversity Heritage Library (BHL), RefBank, Biostore, Bionames and others. Demonstrations of these two components are being run as part of BIH2013.

P14

Mobilising Freshwater Biodiversity Data

Schmidt-Kloiber, A., Bremerich, V., De Wever, A., Freyhof, J., Jepson, P. & Tockner, K.

Efforts of BioFresh to mobilise freshwater biodiversity data include (1) online publishing of metadata to make a dataset more visible to the public and to detect other freshwater datasets, (2) assistance to data holders to produce data papers in one of the new generation of data journals, (3) online publication of datasets on the BioFresh data portal and (4) featuring geographic results and maps in the BioFresh global freshwater biodiversity atlas. All these options contribute to the development of freshwater biodiversity science, they increase the visibility of a data holder and her/his dataset, therefore generating more recognition for the work that combining such datasets entails. As well as the benefits of reliable storage and archiving, contributors to the BioFresh publishing options are able to demonstrate a track-record in data publication. BioFresh provides full acknowledgment of contributors to the data portal and atlas and provides clear citation guidelines.

P15

agINFRA / Natural.Europe

agINFRA-consortium / Natural.Europe-consortium

agINFRA is an FP7- Integrated Infrastructure Initiative (I3), project co-funded by the EC. agINFRA will introduce the agricultural scientific communities into the vision of open and participatory data-intensive science. In particular, agINFRA aims to design and develop a scientific data infrastructure for agricultural sciences that will facilitate the development of policies and the deployment of services that will promote sharing of data among agricultural scientists and develop trust within and among their communities. agINFRA will remove existing obstacles concerning the open access to scientific information and data in agriculture, as well as improve the preparedness of agricultural scientific communities to face, manage and exploit the abundance of relevant data that is (or will be) available and can support agricultural research. Ultimately, agINFRA will demonstrate how a data infrastructure for agricultural scientific communities can be set up to facilitate data generation, provenance, quality assessment, certification, curation, annotation, navigation and management.

Natural Europe is a project co-funded by EC under the ICT-PSP programme which suggests a coordinated solution at European level in order to overcome such barriers, by connecting the digital collections of a number of European NHMs with Europeana, and studying the educational methods and deploy the necessary software tools that will allow museum educators to design innovative online pathways through the digital collections of NHMs. To this end, the federation of the Natural Europe digital libraries aims to facilitate: storage, search and retrieval of digital content that is related to Natural History; as well as search and retrieval of content objects related to educational objectives and curricula on Natural History, Environmental Education, and Biological Sciences.

P16

The Analysis portal – the heart of the Swedish LifeWatch initiative / S.O.S. – aiding biodiversity research and sustainable management

Wremp, A. M., Gärdenfors U. & Kindvall, O.

The Analysis portal – the heart of the Swedish LifeWatch initiative - The Swedish LifeWatch project was initiated in 2010 and will complete its construction phase in 2014. Following the guidelines and technical standards defined by LifeWatch, Sweden was the first country in Europe to begin constructing a national e-infrastructure for biodiversity data.

The main objective of Swedish LifeWatch is to make all major national biodiversity databases interoperable through standardized web services. The infrastructure will be based on systems architecture standardisation, enabling access to data providers from biodiversity and climate archives, observatories, as well as international databases. Implementing web services at all important primary databases means that data can easily be shown at or exported to other biodiversity initiatives, not the least LifeWatch and GBIF.

All data within the infrastructure will be easily accessible through one single access point: The Analysis portal. The portal enables free access to biodiversity and environmental data and will also offer a range of analytical and visualisation services.

The Analysis portal will provide an important tool for researchers, conservation biologists and policy makers, for frontline research and a better understanding and sustainable management of biodiversity and ecosystem services.

The project is largely financed by the Swedish Research Council and builds upon a network of national data centres and user communities for biodiversity research, such as universities, institutes and museums, including the Swedish GBIF node and the Swedish Species Observation System.

S.O.S. – aiding biodiversity research and sustainable management - One of the largest data providers within the Swedish LifeWatch infrastructure is the Swedish Species Observation System (http://www.artportalen.se). This Internet-based, freely accessible reporting system handles reports of geo-referenced species observations of all major organism groups from all environments, including terrestrial, freshwater and marine habitats.

The database has expanded exponentially since its launch in year 2000 and currently holds more than 37 million observations. Every day, year around, 10−15 000 new species observations are submitted. With the exception of a few sensitive species, all data is freely accessible to view and download.

The Species Observation System is used by scientists for storage of research data, by citizen scientists for sharing nature observations and by governmental agencies and county administrations for long-term storage of all publicly funded species observation data. The variety of users and data contributors, the large amount of observations and the fact that the system handles all major organism groups, makes it unique in a worldwide perspective.

A new more powerful and user friendly version of the system is being developed as a joint project between the Swedish Species Observation Centre and its Norwegian counterpart with funding from the Swedish Environmental Protection Agency and the Norwegian Ministry of Environment. The new version was partly launched this summer and will provide not only a new interface but also many new possibilities.

P17

EU BON - integrating biodiversity information for Europe

Häuser, C., Hoffmann, A., Penner, J. & Vohland, K.

The **EU BON** (Building the **Eu**ropean **B**iodiversity **O**bservation **N**etwork) project offers an innovative approach towards integration of biodiversity information systems from on-ground to remote sensing data, for addressing policy and information needs in a timely and customized manner. It will build on existing biodiversity data and observation systems, in particular GBIF, the emerging LifeWatch infrastructure, and national biodiversity data centers in Europe, as well as other environmental datasets. These current systems are mostly unbalanced in coverage and not yet integrated, limiting integrative analyses and implementation of environmental policies. A key feature of **EU BON** will be the delivery of relevant data - from on-ground observation and remote sensing - to various stakeholders and end users ranging from local to global levels. The project is implemented via a consortium of 30 partners from 18 countries, coordinated by the Museum für Naturkunde, Berlin, and is supported by the European Commission under the 7th Framework Programme (contract no. 308454). For further information, see: www.eubon.eu

P18

BioMaS: a comprehensive pipeline for Bioinformatic analysis of Metagenomic AmpliconS

Fosso, B., Santamaria, M., Marzano, M. & Pesole, G.

See D3

P19

Assembling High-Quality Biodiversity Data on a European Level – The EU BON Approach

Wetzel,F., Köljalg, U., Güntsch, A., Ronquist, F., de Jong, Y., Hoffmann, A. & Häuser C.

EU BON is an innovative approach to develop a European Network for Biodiversity Observation that covers integrated biodiversity information from various sources on a European level. One of the key factors for the success of such a portal and network are the available data sources that will also be the baseline for all other activities. Currently, more and more data on species and ecosystems at different levels is available. However, there is the need for data that meets high scientific quality standards, with an adequate coverage and standardized formats in order to answer most important questions related to biodiversity. One of the aims of the EU BON project is to assemble such high-quality information and to make this information available for the scientific community through a data portal. On the other hand, there are still gaps in the data and for many species data is scattered and sparse. Thus, another important field of work will be to find current gaps in European datasets, to identify priorities for filling these gaps, to homogenize and update "backbones" of relevant species datasets (like taxonomy or species distributions) and homogenize future monitoring approaches on a European scale.

P20

Indexing for Life: improving data flow for Catalogue of Life

Culham, A., Sitko, M., Roskov, Y., Matthias, R., Kunze, T., Didžiulis, V., Cheung, K., Addink, W., Döring, M., Cochrane, G., Riviėre, S., Robert, V., Bogdanowicz, W., Hilton-Taylor, C., Berendsohn, W., Güntsch, A., Jones, A., White, R., Bourgoin, T. & Schalk, P.

Whether you are looking for DNA sequences, distribution patterns or conservation status of your chosen species, the shared and interlinked catalogues of organism names in i4Life will help you to find the same plant, animal, fungus or micro-organism under the same name in each data portal.

The i4Life project is enabling a flow of names and taxonomic concepts between the Catalogue of Life, its supporting Global Species Databases and the internationally used Biodiversity Data Portals.

P22

MS.MONINA

Authors: Pernkopf, L. & Lang S.

Abstract: Satellite Earth observation (EO), complemented by in-situ observation networks, provides the means for regularly updated information on biodiversity and ecosystem dynamics on adaptable scales. The European Copernicus program fosters the development of EO-based information services for all societal realms of concern, including habitat and ecosystem monitoring. In the Copernicus project MS.MONINA, the EC Habitat Directive is addressed with geospatial information services designed to support (1) site managers in their monitoring obligations, as well as (2) member states in their state-wide reporting requirements. In addition, (3) an EU service is provided which enables ad-hoc analysis of biodiversity hot-spots and trans-boundary protected areas.