

The SNSB data pipelines for publishing occurrence data via GBIF are appropriate for human osteological collections

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SNSB IT Center



SNSB has a biodiversity informatics department and a number of recognized data repositories



contact imprint, privacy policy and accessibility disclaimer webmaster

About us

ABOUT US PEOPLE

SERVICES

WORKSHOPS

Based on about 20 years IT experience the SNSB IT Center was established in 2006. It is associated to the <u>Botanische Staatssammlung München</u> using its administrative and logistic infrastructure as well as its scientific and curatorial experience.

The in-house technical staff is administrating a server cluster using LINUX and MS Windows platforms with around 60 TByte storage units. The back up systems and archives of the regional computing center Leibniz-Rechenzentrum München are essential part of the storage concepts.

The SNSB IT Center is participating on several national and international initiatives within the field of biodiversity informatics, e. g. acting as a <u>GBIF data publisher</u> and <u>GFBio data center</u>, running a <u>BiNHum search portal for SNSB collections</u> (prototype) and providing a number of <u>services and products</u>, e.g. in connection with the Nationale Forschungsdateninfrastruktur (<u>NFDI</u>). It hosts data for <u>universitary and non-universitary research partner organisations</u>.

At the EU level the SNSB IT Center contributes significantly to the information science and technology concept development of the <u>CETAF consortium</u>, the design set up of the Distributed System of Scientific Collections (<u>DiSSCo</u>) and its German part <u>DiSSCo-D</u>. DiSSCo is a priority project on the Roadmap 2018 of the European Strategy Forum on Research Infrastructures (ESFRI) and will provide unified access to European Natural Science Collections. The SNSB are chairing training activities of the EU COST Action CA17106 – Mobilising Data, Policies and Experts in Scientific Collections (<u>MOBILISE</u>).

The SNSB IT Center offers the direct assignment of Digital Object Identifiers (DOIs) for research datasets published via GFBio services and data pipelines. For that we use DataCite services.

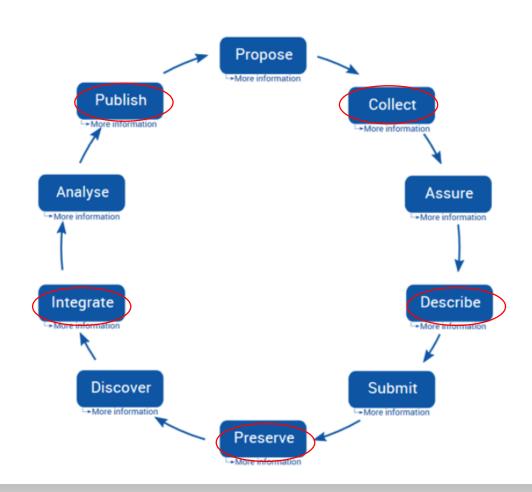




SNSB IT Center



 The core services for collection data are following the Data Life Cycle and are on the way to be certified.



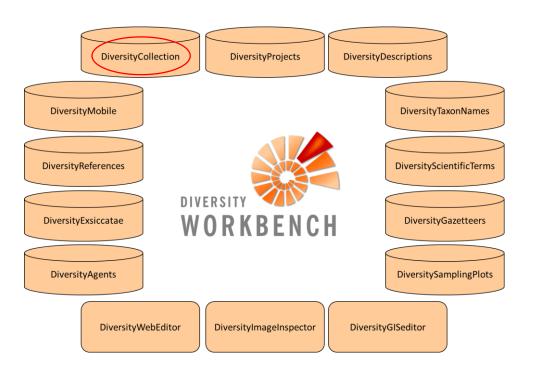


SNSB IT Center - DWB



- Data management of all repositories is done in own installations of DWB databases (www.diversityworkbench.net)
- Administration of 200 DWB accounts
- For collection and occurrence data: DiversityCollection

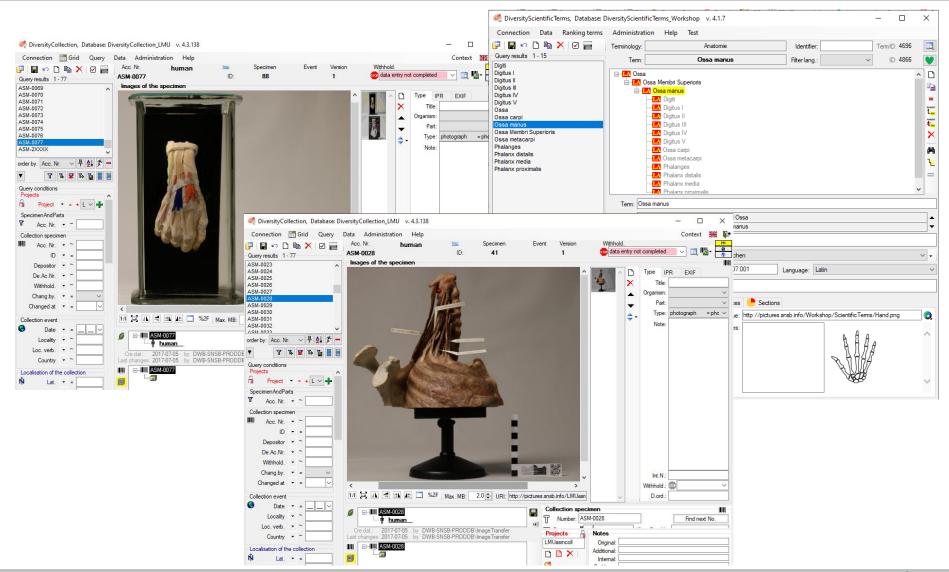






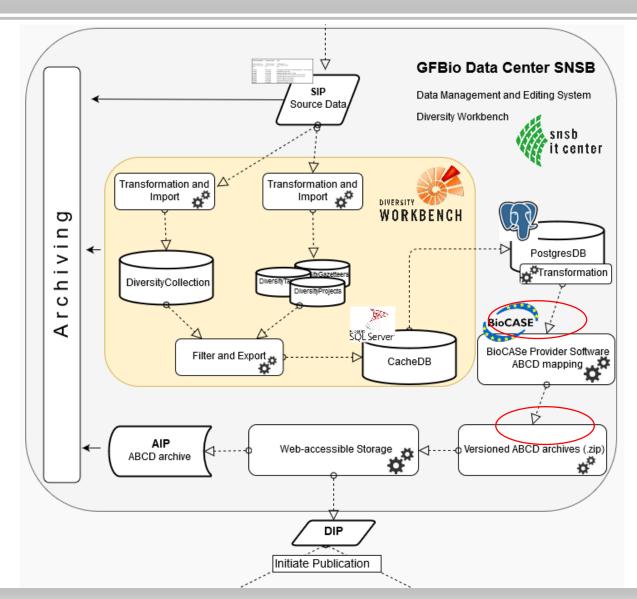
SNSB IT Center - DWB





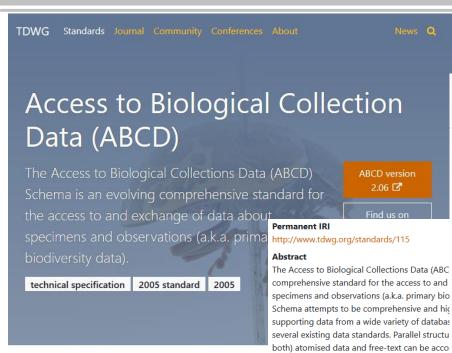
SNSB Data Pipelines





TDWG Standard ABCD





♠ / Standards / Access to Biological Collection Data (ABCD)

Header section

Title

Access to Biological Collection Data (ABCD) Schema

Date created

2005-09-16

Status

Current (2005) standard

Category

Technical specification

\equiv ABCD 3.0

... is here!

The ABCD 3.0 project was successfully completed on 2019-01-31. This site gives an overview about the outcomes.

What's new?

XMI Schema

We developed a new XML Schema. The changes we made were focused on element reuse, implementation of requests from the community and harmonization with the new ABCD 3.0 Ontology. A detailed documentation of all changes as well as an XPath Mapping can be found here.

ABCD Ontology

The ABCD Standard is now described as an XML Schema and an Ontology. This allows the access of the standard through semantic queries, encourages element reuse and serves as basis for future software and services in the area of semantic web. The XML Schema is linked to the Ontology via SAWSDL Annotations. An Introduction to the features of the ontology is available here.

between terms, ABCD is a step towards an onticollections.

Creator

Access to Biological Collections Data task grou Information Standards (TDWG)

and 2.06 are currently in use with the GBIF (Glc

Information Facility) and BioCASe (Biological C

for Europe) networks. Apart from the GBIF and

potential for the application of ABCD extends t in-house legacy data access (e.g. datasets from

shall not be converted and integrated into an i

be kept separately, though easily accessible). B

Bibliographic citation

Access to Biological Collections Data task group (2007) Access to Biological Collection Data (ABCD), Version 2.06. Biodiversity Information Standards (TDWG) http://www.tdwg.org/standards/115



SNSB BioCASe Pipeline



DWB data in BioCASe Provider Software:

BioCASe Provider Software 3.7.3

Start

Welcome to the BioCASe provider software entrance page. This is BPS version 3.7.3. Your BioCASe installation is up to date.

Documentation

debugging, and other useful

PyWrapper Wiki to find tutorials on installation. configuration, mapping,

Configure new datasources, general options, the querytool. statistics, etc.

Config Tool Utilities

Several other utilities useful when managing your data provider software.

Query Tool Ouerv this

datasource using a generic software that works with any database.

Report a Bug

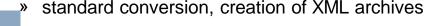
If you find a bug, please send us a short message.

DataSources

Each data source in a BioCASe service represent a database mar Darwin Core or ABCD). Click on its name to get more information

- AHGSwildbeescoll
- BCPtest
- BFLportal01coll
- BFLportal04coll • BFLtestcoll
- BIOTAlichencoll
- Blettaucoll
- BSMeryscoll
- BSMfungicoll
- BSMgrossebrcoll
- BSMlichenscoll
- BSMlichfungicoll
- BSMmicrofexscoll • BSMmyxmaincoll
- BSMneubert
- BSMschiefcoll
- BSMschnittler
- BSMvplantscoll
- BSMweinzierlcoll
- BSMwohlfcoll
- BSPGcoll
- BSPGpiscescoll
- DiversityIndexing_GBIFdoppelbaur
- GFBio201900216SNSB GFBio201900230SNSB
- GFBio201900284SNSB
- GFBio201900288SNSB
- GEBio202000316SNSB
- GFBio202000340SNSB
- GFBio202000341SNSB GFBio202000344SNSB
- GLMcoll
- GOETbrvocoll

- GOETvplantscoll
- HALcoll
- HYMIScoll
- IBFfungicoll
- IBFgallscoll IBFlichenscoll
- IBForthopteracoll
- IBFplantscoll
- JMEfossilcoll
- JMEpiscescoll
- JMRCfungicoll
- LEmvxcoll
- MBcoll
- Morphyllcoll MSBvplantscoll
- REGvplantscoll
- SAPMmammaliacoll
- SAPMpiscescoll
- SMNKfungicoll
- SMNKspidercoll
- SMNKspiderstudcoll
- SMNS-E-araneaecoll
- SMNS-Z-herpcoll
- TUBvplantscoll
- ZSMarthrovariacoll
- ZSMavstudiescoll
- ZSMbfbcoll
- ZSMpiscescoll



PyWrapper Manual Query Form

Home | Overview | Settings | DB connection | DB structure | Archiving & Filtered export | QueryForms | Help | Report a Bug

Debugging:	WARNING. Logs at /biocase/log system settings	
Wrapper:	http://biocase.snsb.info/wrapper/pywrapper.cgi?dsa=SAPMmammaliacoll	Reset
	Submit	

PLEASE ENTER SOME BIOCASE PROTOCOL XML

Replace form with templates for a:

ABCD scan, ABCD search, ABCD2 scan, ABCD2 search, ABCD2.1 scan, ABCD2.1 search earch, TCS 1.01 Scan, TCS 1.01 Search, SPICE-1 Scan , SPICE-1 Search , SPICE-2 Scan , SPICE-2 Search , SPICE-4 Search , SPICE-5 Search , GCP Passport 1.03 Scan, GCP Passport 1.03 Search, GCP Passport 1.04 Scan, GCP Passport 1.04 Search

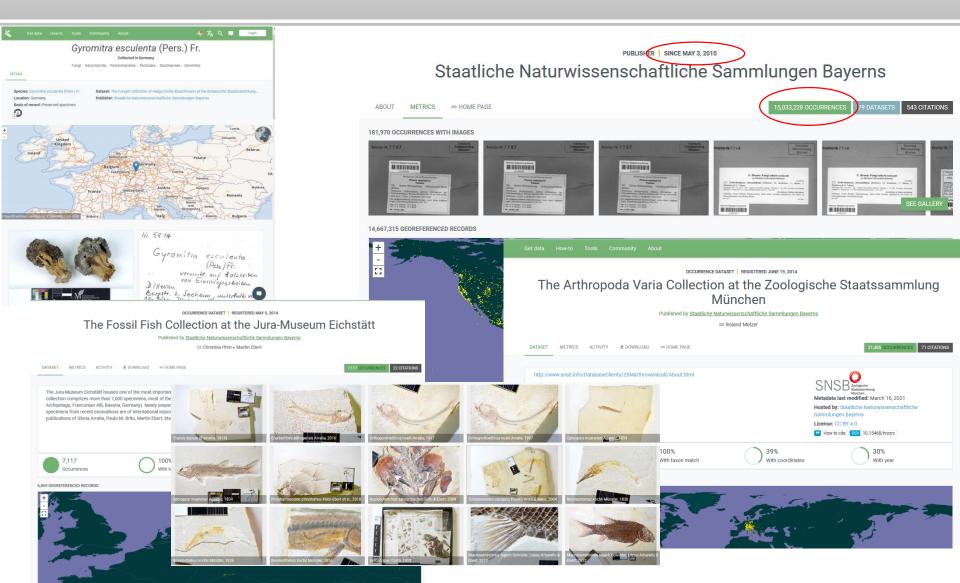


Imprint and Privacy Policy



SNSB: GBIF Data Publisher

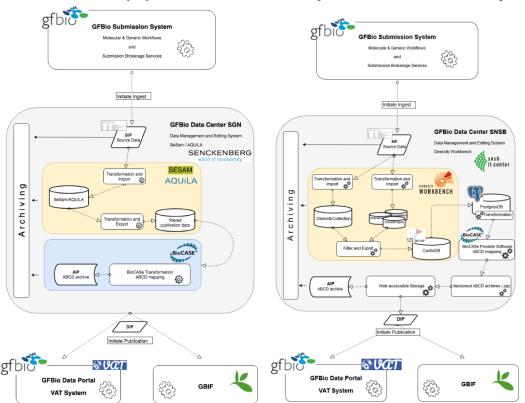




Benefit in Using ABCD



- ABCD structured data in national/international data portals, free for download
 - → GBIF, GFBio and NFDI4BioDiversity
- ABCD data pipelines at all major Natural History Collections in Germany





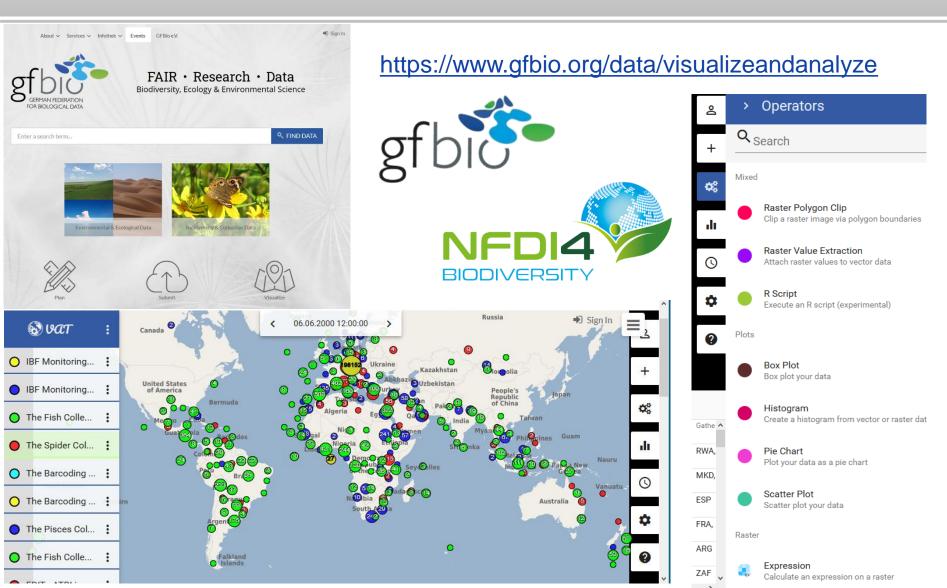






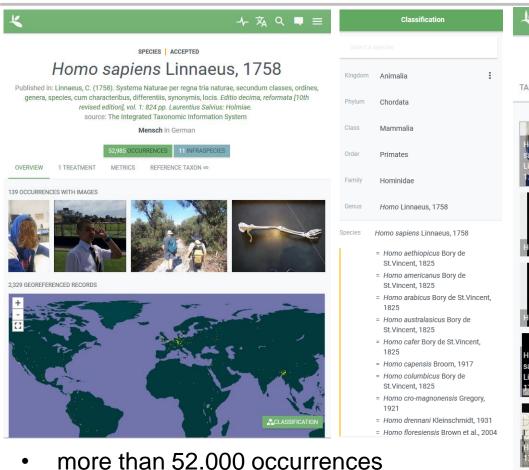
ABCD Data in GFBio and NFDI



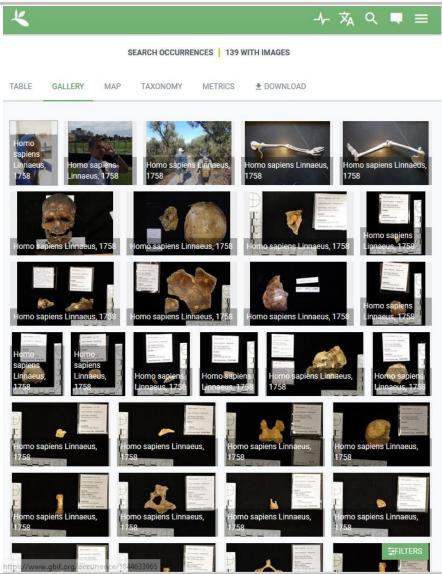


Anthropology Data in GBIF





 from major natural history collections, e.g. MfN-Berlin, NHM-London



Anthropology Data in GBIF





Species: Homo sapiens Linnaeus, 1758

Location: Europe > France Basis of record: Fossil specimen

Dataset: Natural History Museum (London) Colle

Publisher: Natural History Museum





Record license: http://creativeco.../licenses/by/4.0/

Rights holder: The Trustees of the Natural History Museum, London

Identifier: https://www.nhm.a.../contents/preview

Suggested attribution: "NHM-UK_PA_EM3978_1_M_1.jpg" - Homo sapiens Linnaeus, 1758 collected in France by The Trustees of the Natural History Museum, London (licensed under http://creativecommons.org/licenses/by/4.0/)





Title: NHM-UK_PA_EM3978_2_M_1.jpg

Suggested attribution: "NHM-UK_PA_EM3978_2_M_1.jpg" - Home Linnaeus, 1758 collected in France by The Trustees of the Natura Museum, London (licensed under http://creativecommons.org/lic

Occurrence



Record license: http://creativeco.../licenses/by/4.0/

Rights holder: The Trustees of the Natural History Museum, Lond Identifier: https://www.nhm.a.../contents/preview



Record			
Term	Interpreted	Original	Remarks
Dynamic properties	D_WGS84"], "created": 1380125005000, "donor- name": "F de Lastic", "associ- atdmediacount": 3, "determi- nationnames": "Homo sapiens Linnaeus, 1758", "subdepart-	Homo sapiens. Bruniquel Cave, France. Magdalenian period.", "gbifissue": ["GEODETIC_DATUM_ASSUME D_WGS84"], "created": 1380125005000, "donor- name": "F de Lastic", "associ- atedmediacount": 3, "determi- nationnames": "Homo sapiens	
Institution code	NHMUK Natural History Museum, London	NHMUK	Institution mat
Basis of record	Fossil specimen	FossilSpecimen	
Collection code	PAL	PAL	

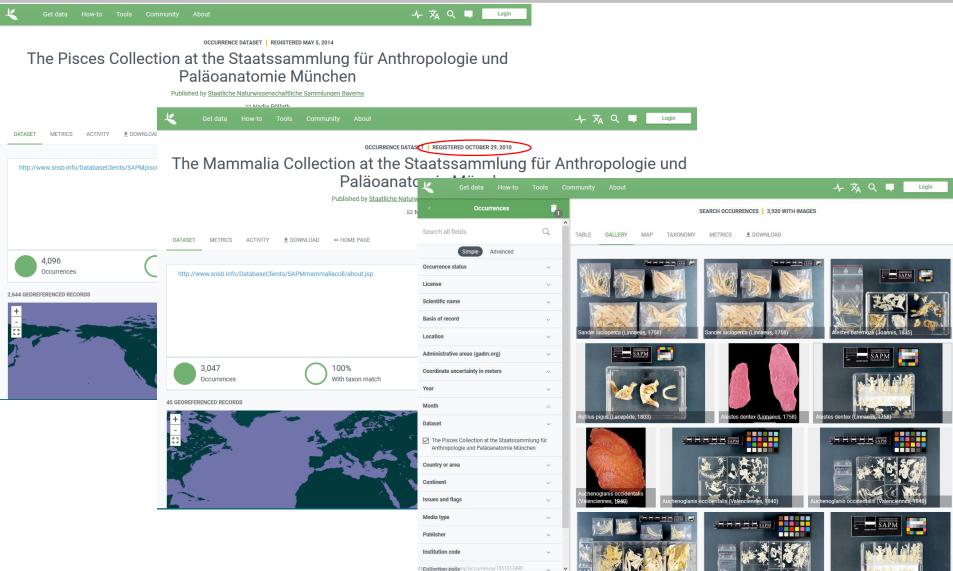
Term	Interpreted	Original	Remarks
Catalogue number	PA EM 3978	PA EM 3978	
Occurrence ID	f26a491c-b124-4341- afb4-58a666283c2a	f26a491c-b124-4341- afb4-58a666283c2a	
Occurrence status	PRESENT	present	
Other catalogue numbers	NHMUK:ecatalogue:2827575	NHMUK:ecatalogue:2827575	
Recorded by	F de Lastic	F de Lastic	

Event			
Term	Interpreted	Original	
Year	1863	1863	
Event date	1863-01-01T00:00:00)	



SNSB-SAPM Osteological Data in GBIF





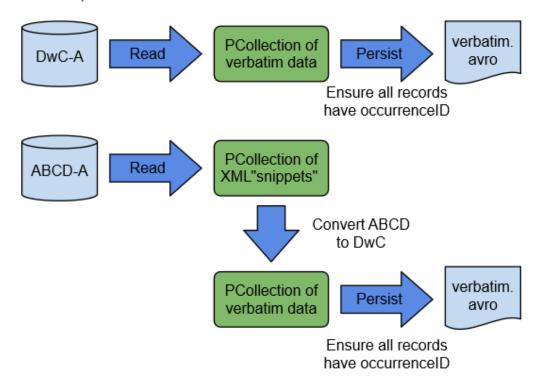
GBIF Pipelines for Ocurrence Data



⊘ Ingress

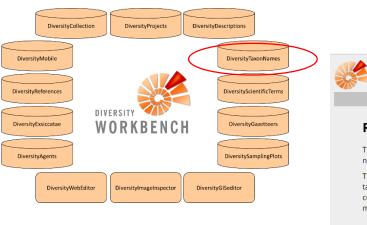
Ingress is from Darwin Core Archive (zip files of one or more delimited text files) or ABCD Archives (compressed XML) only[1]. During ingress data is converted from its native format and stored as Avro files containing Darwin Core compliant data.

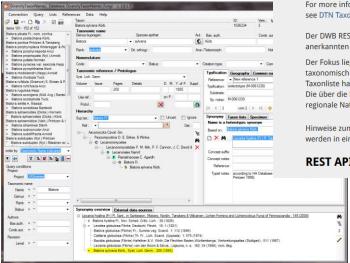
This is depicted below:



DWB Taxonomies









For more information please check How to use the DWB REST We see DTN Taxon Lists Services.

Der DWB REST Webservice for Taxon Lists ist Teil eines Netzwerke For further information and how to use this service please see the documentation.

Der Fokus liegt dabei zur Zeit auf domän-spezifischen Listen (Che taxonomisch oder floristisch bzw. faunistisch arbeitenden Experte Animalia Taxonliste hat ihre eigene Geschichte und Zielvorstellungen, wird Die über die REST API zugänglichen DiversityTaxonNames (DTN) D Taxon list of Annelida from Germany compiled in the context of the GBOL project regionale Naturschutzeinrichtungen und Umweltprojekte von Bec

Hinweise zum Einsatz der REST API finden sich unter How to use t werden in einer Übersicht angezeigt. Weitere Information zum In Taxon list of Araneae from Germany compiled in the context of the GBOL project

REST API Documentation

Regionalised and Domain-specific Taxon Lists

anerkannten Taxonnamen, Synonymen, Klassifikationen und deut Overview on Published Lists

TaxRef_GBOL_Annelida_DE

TaxRefCode: TaxRef_GBOL_Araneae_DE

· Höfer, Hubert, Dr.

Taxon list of Bryozoa from Germany compiled in the context of the GBOL project

TaxRefCode:

TaxRef_GBOL_Bryozoa_DE

Taxon list of Chilopoda from Germany compiled in the context of the GBOL project

TaxRefCode:

TaxRef GBOL Chilopoda DE

- · Spelda, Jörg, Dr.
- · Wesener, Thomas, Dr.



GBIF Pipelines for Checklist Data









DiversityTaxonNames Server

DwCAHowToGuide

Matt Blissett edited this page on 8 Feb · 58 revisions

Darwin Core Archives - How-to Guide

Version 2.1

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- · Registration of DwC-As with GBIF
- Annex: Preparing Your Data
 - o Required and recommended terms
 - Character Encoding
 - Data From a Database
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Installation type: Http installation

Hosted by: Staatliche Naturwissenschaftliche Sammlungen Bayerns

Registered: November 4, 2015

32 DATASETS

Taxon list of Araneae from Germany compiled in the context of the GBOL project

Checklist dataset

http://www.diversitymobile.net/wiki/About_%22Taxon_list_of_Araneae_from_Germany_compiled_in_the_context_of_the_GBOL_project%22

1,647 records

Taxon list of Hymenoptera from Germany compiled in the context of the GBOL project

Checklist dataset

http://www.diversitymobile.net/wiki/About_%22Taxon_list_of_Hymenoptera_from_Germany_compiled_in_the_context_of_the_GBOL_project%22

11,471 records

Taxon list of Orthoptera (Grashoppers) from Germany compiled at the SNSB

Checklist dataset

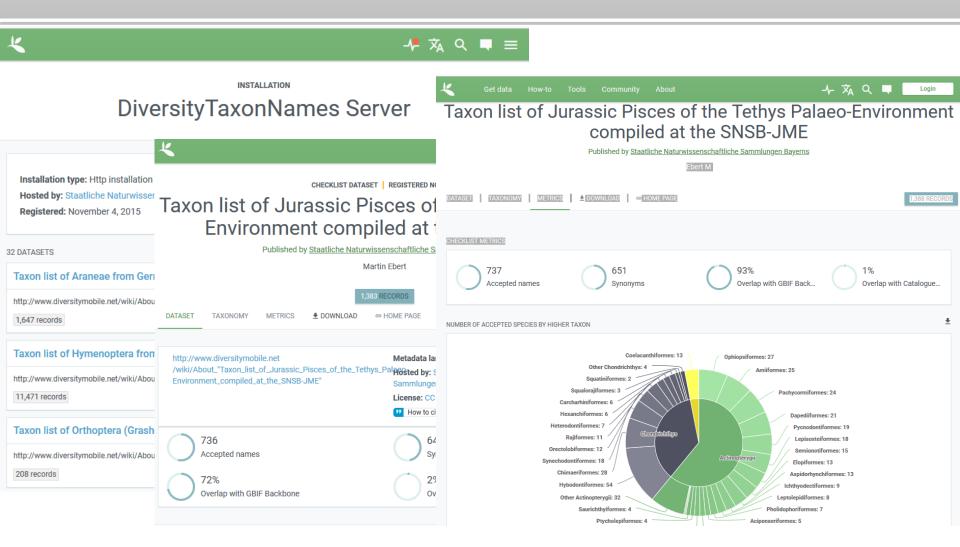
http://www.diversitymobile.net/wiki/About_the_%22Taxon_list_of_Orthoptera_(Grashoppers)_from_Germany_compiled_at_the_SNSB%22

208 records



DWB Taxonomies in GBIF





Description

http://www.diversitymobile.net/wiki/About_"Taxon_list_of_Jurassic_Pisces_of_the_Tethys_Palaeo-



.... become part of the GBIF Network





GBIF Tools

An index to tools brought to you be the Global Biodiversity Facility.

GBIF Excel Templates Darwin Core Archive Assistant Darwin Core Archive Validator Name Parser

GBIF Excel Templates

The GBIF Excel Templates are MS Excel spreadsheets that support biodiversity data entry in a standardized format. There is one template for each of the three classes of biodiversity data:

- 1. Checklist Data
- 2. Occurrence Data
- 3. Sampling Event Data

To publish the data through the GBIF network, upload the templates to the GBIF Integrated Publishing Toolkit (IPT). To enter dataset metadata, use the IPT's built-in metadata editor. If you require an account on an IPT, it is highly recommended that you save yourself time and money by requesting an account on a <u>trusted data hosting centre</u> located in your country. If you need assistance, please contact the <u>GBIF Helpdesk</u> for assistance.

Darwin Core Archive Assistant

The Darwin Core Archive Assistant is a web application that presents a simple interface for describing the data elements a data publisher wishes to serve to the GBIF network as basic text files and composes the appropriate XML descriptor file as defined in the Darwin Core Text Guidelines to accompany them. It communicates with the GBIF registry to provide an up-to-date listing of all relevant Darwin Core terms and available extensions and presents these in a simple checklist format.

The <u>Darwin Core</u> is a body of standards that include a set of terms relating to taxa and their occurrence in nature, and a set of practices regarding the use of these terms in the publication of biodiversity data and information. GBIF has adopted a text-based solution for using Darwin Core that both simplifies and extends the publication of species and species-occurrence data. This format is referred to as a Darwin Core Archive (DWCA) and provides a relatively non-technical option for publishing biodiversity data that does not require complicated installations of data publication software. Darwin Core Archives can be published via a simple web address or URL.

Darwin Core Archives support the publication of enriched data types that extend the core terms while retaining the relatively simple, text-based data format. These extensions, however, require the inclusion of an XML descriptor file (metaxml) that serves as a map to the different files and data elements in the archive. Many biologists and data managers find working with XML challenging while otherwise finding the technical threshold for producing Darwin Core Archives quite low.

Darwin Core Archive Validator

The validator is a tool to test Darwin Core Archives as specified in the <u>Darwin Core Text Guidelines</u>. Due to the simplicity of the archives GBIF encourages publishers to create them using simple custom scripts. Therefore the need arises to provide a testing framework for developers to make sure GBIF and others can read the information as expected.

The validator uses the official XML schema to validate the metaxml descriptor, but additionally it uses the <u>Darwin Core Archive Reader</u> java library to validate the content against the known extensions and terms registered within the GBIF network for sharing biodiversity data. GBIF runs a production and a development registry that keeps track of extensions, both of which are used by this validator.

GBIF recommends to bundle an <u>Ecological Markup Language</u> (EML) xml file with an archive. As EML is a rather large and complex schema GBIF has specified a <u>GBIF profile</u> that uses a subset of EML 2.1.1 and also declares specific additions to EML within the generic additional Metadata section of EML. Every valid GBIF profile document should therefore always be valid according to the official EML schema. The EML validation is done according to the official EML schema.



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