

# Material- and Datenfluss innerhalb des German Barcode of Life Projektes

- DWB im BMBF-Verbundprojekt GBOL -



## **Für die Öffentlichkeit:**

- Schnelle und sichere Identifizierung von Arten
- Leichter Zugang zu Sequenz und Biodiversitäts Daten
- Aktuelle Verbreitungskarten von Arten in Deutschland

## **Für die GBOL-Experten:**

- Welches GBOL-Institut nimmt mein Sammlungsmaterial?
- Wo kann ich Daten eingeben?
- Ich habe Bilder, wo kann ich diese hochladen?
- Was passiert mit meinen Daten?

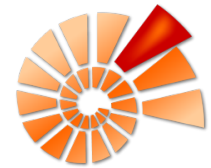
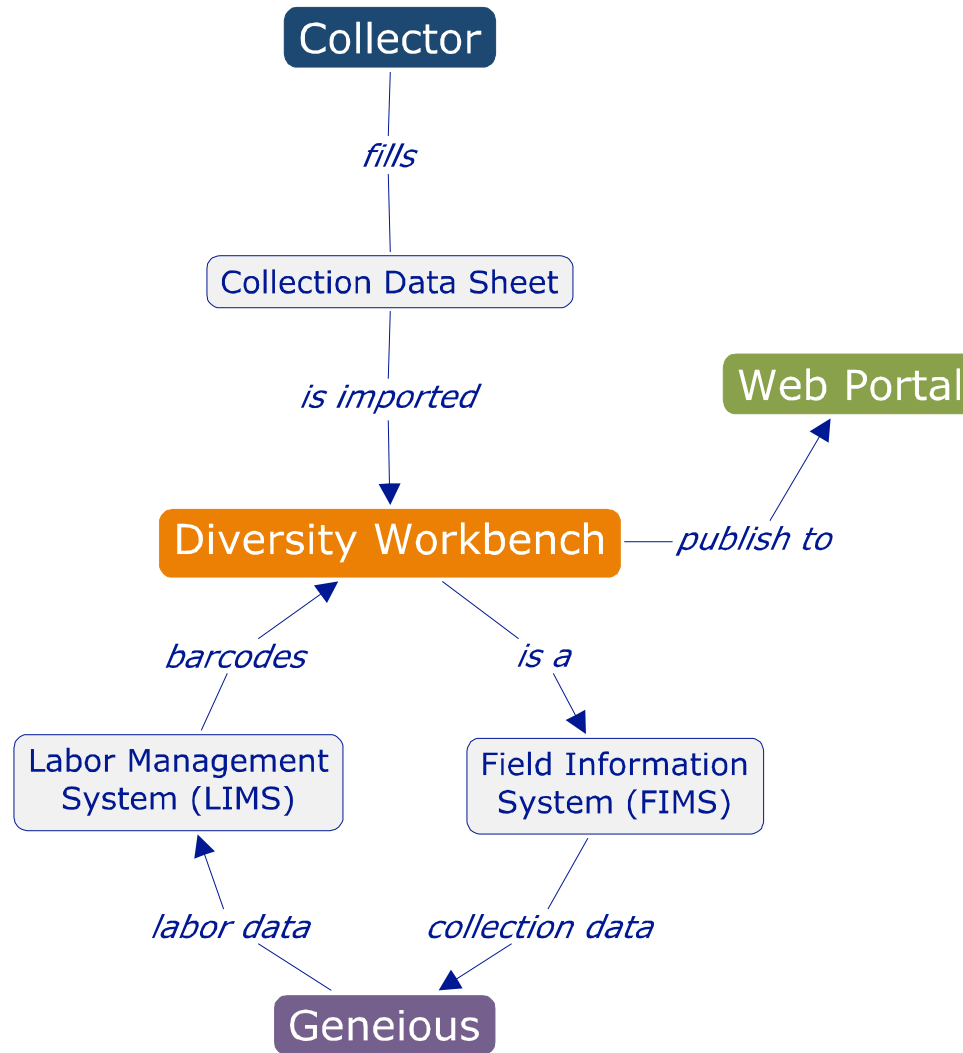
## **GBOL-Institutionen:**

- Verwaltung der Taxonomischen Experten
- Speichern der Feld- und Labordaten
- Monitoring des Sammelfortschritts
- Verbreitung und Veröffentlichung der Daten

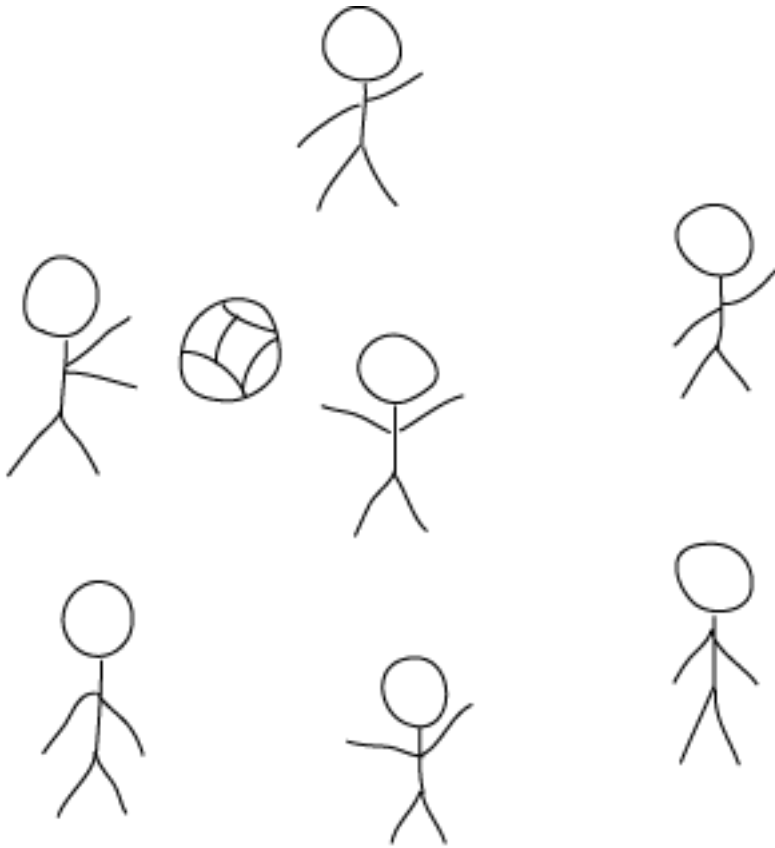
## **Anforderung an die Qualität:**

- Alle Arten sind bestimmt
- Alle Sammelorte Georeferenziert
- Für jeden DNA Barcode: Verbindung zum Belegmaterial mit allen zugehörigen Daten
- Langzeitverfügbarkeit

# Datenfluss – ein Überblick



# Mitspieler



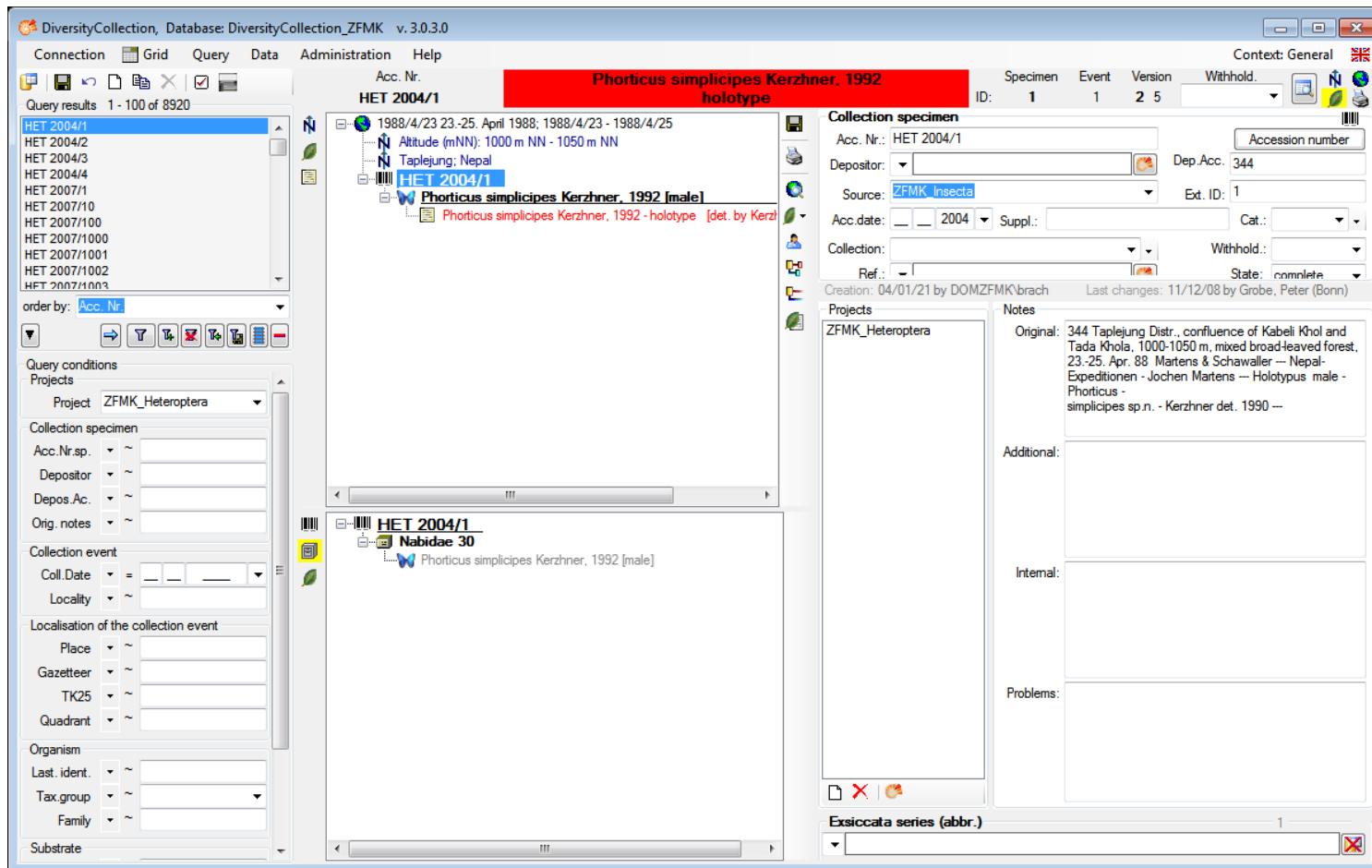


The screenshot shows the website's layout with a green and white color scheme. At the top left is the GBOL logo. The main header features a large image of a lizard with the text 'Deutschlands Fauna und Flora in einer einzigartigen genetischen Bibliothek.' Below this is a navigation menu with items: 'Das Projekt', 'DNA-Barcoding', 'Das Team', 'Mitmachen!', 'News & Publikationen', 'Links', 'Fundstellen', 'Kontakt', and 'Experten-Bereich' (highlighted in purple). A central banner reads 'Biodiversität – jede Art zählt!' and 'Was wäre, wenn wir jedes Tier, jeden Pilz und jede Pflanze exakt und schnell identifizieren könnten?' with an arrow pointing to 'Infos zum Projekt!'. Below the banner are three columns: 'Das Projekt' (with a moss image), 'DNA Barcoding' (with a blue insect image), and 'Das Team' (with a red fruit image). On the right, a 'Machen Sie mit...' section includes 'Registrieren!' (with a 'Registrieren Sie sich noch heute als Sammler...' button), 'Anmelden' (with a 'Sie sind schon registriert? Loggen Sie sich ein...' button), and 'Newsletter' (with a 'Bleiben Sie stets aktuell informiert!' button).

- Registrierung
- Bestellung Material
- Hochladen von  
Feldinformationen
- Eingabe von  
Feldinformationen
- Nutzerverwaltung
- Übersicht Aktivität/Fundorte



The screenshot shows the website's layout. At the top left is the GBOL logo. The main header features a large image of a lizard with the text 'Deutschlands Fauna und Flora in einer einzigartigen genetischen Bibliothek.' Below this is a navigation menu with items: 'Das Projekt', 'DNA-Barcoding', 'Das Team', 'Mitmachen!', 'News & Publikationen', 'Links', 'Fundstellen', 'Kontakt', and 'Experten-Bereich'. A central banner reads 'Biodiversität – jede Art zählt!' with the question 'Was wäre, wenn wir jedes Tier, jeden Pilz und jede Pflanze exakt und schnell identifizieren könnten?' and a link 'Infos zum Projekt!'. Below the banner are three columns: 'Das Projekt' (describing the inventory and genetic characterization of German fauna and flora), 'DNA Barcoding' (explaining short DNA segments as unique barcodes for species identification), and 'Das Team' (listing museums and research institutions). On the right, a sidebar titled 'Machen Sie mit...' contains buttons for 'Registrieren!', 'Anmelden', and 'Newsletter'.

DiversityCollection, Database: DiversityCollection\_ZFMK v. 3.0.3.0

Connection Grid Query Data Administration Help

Context: General

Acc. Nr. **HET 2004/1** **Phorticus simplicipes Kerzhner, 1992 holotype** Specimen ID: 1 Event 1 Version 2 5 Withhold.

1988/4/23 23.-25. April 1988; 1988/4/23 - 1988/4/25

Altitude (mNN): 1000 m NN - 1050 m NN

Taplejung; Nepal

**HET 2004/1**

Phorticus simplicipes Kerzhner, 1992 [male]

Phorticus simplicipes Kerzhner, 1992 - holotype [det. by Kerz]

Collection specimen

Acc. Nr.: HET 2004/1 Accession number

Depositor: Dep. Acc.: 344

Source: ZFMK\_Insecta Ext. ID: 1

Acc. date: 2004 Suppl.: Cat.:

Collection: Withhold.:

Ref.: State: nmmla

Creation: 04/01/21 by DOMZFMK/brach Last changes: 11/12/08 by Grobe, Peter (Bonn)

Projects

ZFMK\_Heteroptera

Notes

Original: 344 Taplejung Distr., confluence of Kabeli Khol and Tada Khol, 1000-1050 m, mixed broad-leaved forest, 23.-25. Apr. 88 Martens & Schawaller - Nepal-Expeditionen - Jochen Martens - Holotypus male - Phorticus - simplicipes sp.n. - Kerzhner det. 1990 --

Additional:

Internal:

Problems:

Exsiccata series (abbr.) 1

Query results 1 - 100 of 8920

HET 2004/1

HET 2004/2

HET 2004/3

HET 2004/4

HET 2007/1

HET 2007/10

HET 2007/100

HET 2007/1000

HET 2007/1001

HET 2007/1002

HET 2007/1003

order by: Acc. Nr.

Query conditions

Projects

Project ZFMK\_Heteroptera

Collection specimen

Acc. Nr. sp. ~

Depositor ~

Depos. Ac. ~

Orig. notes ~

Collection event

Coll. Date =

Locality ~

Localisation of the collection event

Place ~

Gazetteer ~

TK25 ~

Quadrant ~

Organism

Last. ident. ~

Tax. group ~

Family ~

Substrate

HET 2004/1

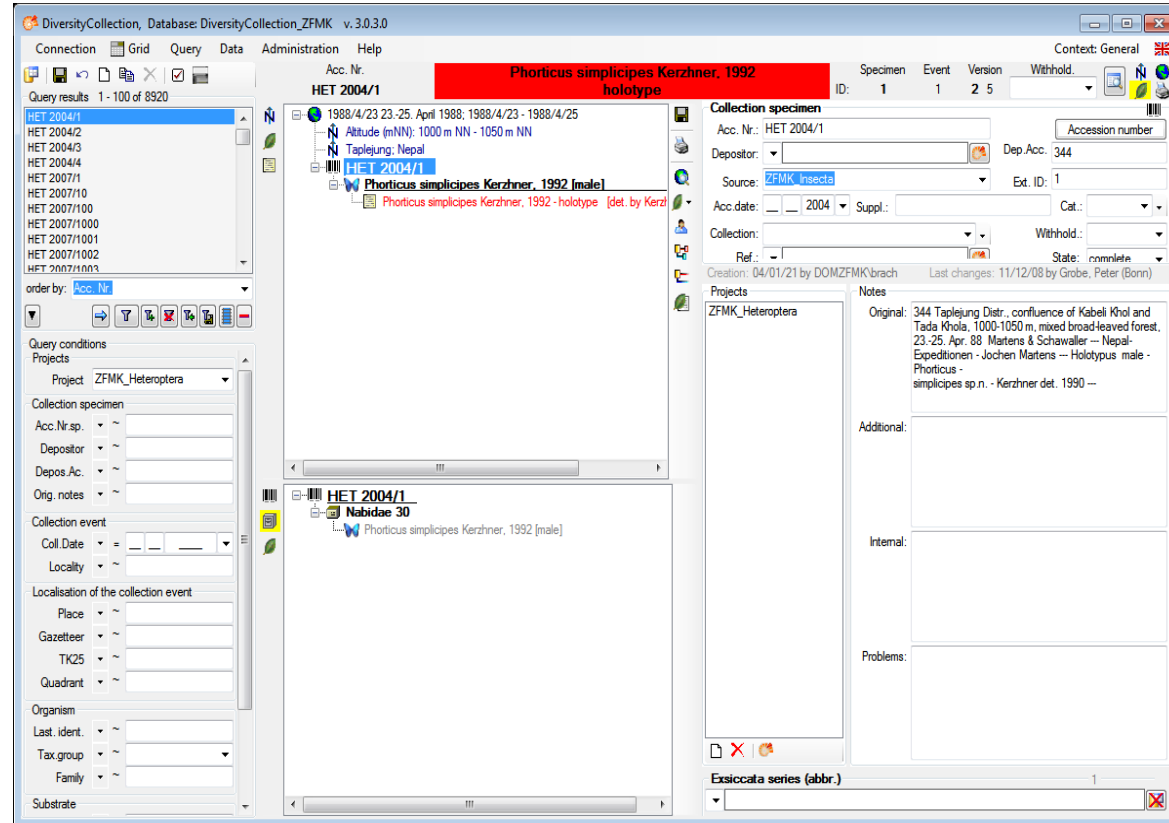
Nabidae 30

Phorticus simplicipes Kerzhner, 1992 [male]





- Feldinformationssystem
- Speichern und Verwalten aller Feld-, Sammlungs- und Laborergebnisse
- Bereitstellung von Taxonomischen Listen



The screenshot displays the DiversityWorkbench interface for specimen management. The main window shows a tree view of collection events and specimens. The selected specimen is *Phorticus simplicipes Kerzhner, 1992* (holotype), accession number HET 2004/1. The interface includes a menu bar (Connection, Grid, Query, Data, Administration, Help), a toolbar, and a sidebar with query conditions. The specimen details panel on the right shows fields for accession number, depositor, source, collection date, and notes. The notes field contains detailed collection information: "Original: 344 Taplejung Distr., confluence of Kabei Khol and Tada Khol, 1000-1050 m, mixed broad-leaved forest. 23.-25. Apr. 88 Martens & Schawaller - Nepal-Expeditionen - Jochen Martens - Phorticus - Phorticus - simplicipes sp.n. - Kerzhner det. 1990 -".

# Labordaten-Verwaltung

## Bioinformatics Software Platform

### Geneious



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### Superior visualization

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gfp gene  
2,200  
2,400  
gfp CDS  
2,600  
SV40 polyA signal

Monkey  
Baboon  
Mangabey  
Orangutan  
Gorilla  
Chimpanzee  
Human  
Lemur

Sandprouse  
Spoonbill  
ibis  
Chicken  
Cattle  
Ostrich  
Warbler  
Sparrow  
Catbird  
Sparling  
Sea Turtle



- Labor-Information-Management-System (*LIMS*)
- Alle Daten über
  - DNA-Extraktion
  - PCR
  - Rohsequenzen
  - DNA-Barcodes



# Multimedia-Verwaltung

## Morphological Description Database

### Morph·D·Base



feedback

Taxonomy
Browse Content
New/Edit Content
Home



## Morph·D·Base

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Start Purpose of MDB History of MDB Imprint & Copyright



**Random Images**

**MDB Stats**

User: 128	<b>Media:</b>
Groups: 11	Total: 500
<b>Specimen:</b>	Publicly accessible: 178
Total: 272	
Publicly accessible: 104	



**In the News**

Kamp, T. van de; Vagovic, P.; Baumbach, T.; Riedel, A. (2011): A Biological Screw in a Beetle's Leg. *Science* 333(6038):52-52.  
doi:10.1126/science.1204245.  
Direct Links: [www.morphdbase.de?A\\_Riedel\\_20110523-M-3.1](http://www.morphdbase.de?A_Riedel_20110523-M-3.1),  
[www.morphdbase.de?A\\_Riedel\\_20110523-M-4.1](http://www.morphdbase.de?A_Riedel_20110523-M-4.1)

Vogt, L.; Grobe, P. (2010): Morph-D-Base - Eine online Datenbank für morphologische Daten und Metadaten. *GFBS Newsletter* 24:29-34.  
 Open access

Vogt, L.; Bartolomaeus, T.; Giribet, G. (2010): The linguistic problem of morphology: structure versus homology and the standardization of morphological data. *Cladistics* 26(3):301-325.

Vogt, L. (2009): The future role of bio-ontologies for developing a general data standard in biology: chance and challenge for zoo-morphology. *Zoornorphology* 128(3):201-217.

Vogt, L. (2008): Learning from Linnaeus: towards developing the foundation for a general structure concept for morphology. *Zootaxa* 1950:123-152.  
 Open access

Ziegler, A. (2008): Non-invasive imaging and 3D visualization techniques for the study of sea urchin internal anatomy. Dissertation, Freie Universität Berlin.  
[www.diss.fu-berlin.de/diss/receive/FUDISS\\_thesis\\_000000006510](http://www.diss.fu-berlin.de/diss/receive/FUDISS_thesis_000000006510)

**News and updates**

1. Feb. 2013 [-]

**2nd Annual Meeting BioSyst.EU 2013 Global systematics!**  
*Morph-D-Base* will be presented during the Software Bazar in on Thursday, Feb. 21th 2013 at the 2nd Annual Meeting BioSyst.EU 2013 Global systematics!  
[Link to meetings website](#)

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14. Feb. 2012 [-]

**Annual Meeting of the Gesellschaft für Biologische Systematik, February 23-25, 2012, at the ZFMK, Bonn, Germany**  
The matrix module of *Morph-D-Base* will be introduced in the Workshop "*Morph-D-Base*: Data Repository, Collaboration Platform, Image Annotator, and Character Matrix Module for Morphological Data" at the 13th annual meeting of the GFBS.  
The workshop is scheduled on Saturday, Feb. 25th, 8:30h, at "Museum school, main building 2. floor" at the Zoologisches Forschungsmuseum Alexander Koenig.  
**The workshop will be divided into the following sections:**

- A brief introduction, which will give an overview of the interface and the general idea and motivation for the *Morph-D-Base* Project.
- In a "hands on" section, the participants can use own material to upload and edit content into the database, annotate it, and share it with other participants.
- In the last part, the matrix module will be introduced and used by the participants. Participants will learn how to build a morphological character matrix from scratch and how to link individual matrix cells to other contents from *Morph-D-Base*, thereby providing a detailed documentation of relevant data and metadata for each matrix cell.
- We will conclude with an outlook on future developments for *Morph-D-Base*.

[Link to meetings website](#)

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29. Jun. 2011 [-]

**Morph-D-Base Version 3.0 Beta online**  
The new version 3.0 Beta is now online and adds a *character matrix editor* module to *Morph-D-Base*. The matrix editor allows the collaborative generation of phylogenetic character matrices, in which each cell can be linked to relevant specimen, media, literature, and taxon entries within *Morph-D-Base*. Many features for managing and **collaborative editing** of matrices are implemented: e.g., **live editing** with dynamic update of the user interface of all user logged into the same matrix, color labeling of cells/rows/columns, schedule-notification, change tracking, progress markers.  
In the next minor version the *import/export* of NEXUS and NeXML files will be available. It will also be possible to *specify class-subclass and part-whole relations* between entire characters, which can be used to preclude inconsistent combinations of certain character state combinations in absent/present coding. And, of course, many more features are planned to be included in the future. Besides some minor improvements we made the following two changes to *Morph-D-Base* since *Version 2.7*:

Found a bug?
Morph-D-Base Ver. 3.0 Beta - © 2004-2011 The Morph-D-Base Project - [info@morphdbase.de](mailto:info@morphdbase.de)
Last updated: 17.02.2013

# Speicherung von Bildern

Morphological Description Database

Morph·D·Base



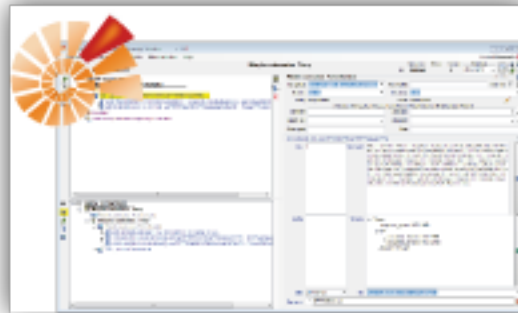

The screenshot shows the Morph-D-Base website interface. At the top, there is a navigation menu with 'Start', 'Purpose of MDB', 'History of MDB', and 'Imprint & Copyright'. A login section includes fields for 'Username' and 'Password', with 'Login' and 'Register' buttons. The main content area is divided into several sections:

- Random Images:** Displays three small images of biological specimens.
- MDB Stats:** Shows statistics: User: 128, Groups: 11, Specimen: Total: 272, Publicly accessible: 104. It also includes a 'Media' section with Total: 500 and Publicly accessible: 178.
- News and updates:** Contains several news items:
  - 1. Feb. 2013:** 2nd Annual Meeting BioSyst.EU 2013 Global systematics! Morph-D-Base will be presented during the Software Bazar on Thursday, Feb. 21st 2013 at the 2nd Annual Meeting BioSyst.EU 2013 Global systematics! Link to meetings website
  - 14. Feb. 2012:** Annual Meeting of the Gesellschaft für Biologische Systematik, February 23-25, 2012, at the ZFMK, Bonn, Germany. The matrix module of Morph-D-Base will be introduced in the Workshop Character Matrix Module for Morphological Data\* at the 13th annual meeting of the GBS. The workshop is scheduled on Saturday, Feb. 25th, 8:30h, at "Museum school, February 23-25, 2012, at the ZFMK, Bonn, Germany". A brief introduction, which will give an overview of the interface and the general idea and motivation for the Morph-D-Base Project.
    - In a "hands on" section, the participants can use own material to upload and edit content into the database, annotate it, and share it with other participants.
    - In the last part, the matrix module will be introduced and used by the participants. Participants will learn how to build a morphological character matrix from scratch and how to link individual matrix cells to their contents and metadata for each matrix cell.
    - We will conclude with an outlook on future developments for Morph-D-Base. Link to meetings website
  - 29. Jun. 2011:** Morph-D-Base Version 3.0 Beta online. The new version 3.0 Beta is now online and adds a character matrix editor module to Morph-D-Base. The matrix editor allows the collaborative generation of phylogenetic character matrices, in which each cell can be linked to relevant specimen, media, literature, and taxon entries within Morph-D-Base. Many features for managing and collaborative editing of matrices are implemented: e.g., live editing with dynamic update of the user interface of all user logged into the same matrix, color labeling of cells/rows/columns, schedule-between entire characters, which can be used to preclude inconsistent combinations of certain character state combinations in absent/present coding. Besides some minor improvements we made the following two changes to Morph-D-Base since version 2.3.
- In the News:** Lists recent publications:
  - Kamp, T. van de; Vagovic, P.; Baumbach, T.; Riedel, A. (2011): A Biological Screw in a Beetle's Leg. Science 333(6038):52-52. doi:10.1126/science.1204245. Direct Links: www.morphbase.de/A\_Riedel\_20110523-M-3-1, www.morphbase.de/A\_Riedel\_20110523-M-4-1
  - Vogt, L.; Grobe, P. (2010): Morph-D-Base - Eine online Datenbank für morphologische Daten und Metadaten. GBS Newsletter 24:29-34. Open access
  - Vogt, L.; Bartolomeus, T.; Giribet, G. (2010): The linguistic problem of morphology: structure versus homology and the standardization of morphological data. Cladistics 26(3):301-325.
  - Vogt, L. (2009): The future role of bio-ontologies for developing a general data standard in biology: chance and challenge for zoo-morphology. Zoo-morphology 128(3):201-217.
  - Vogt, L. (2009): Learning from Linnaeus: towards developing the foundation for a general structure concept for morphology. Zootaxa 1950:123-152. Open access
  - Ziegler, A. (2008): Non-invasive imaging and 3D visualization techniques for the study of sea urchin internal anatomy. Dissertation, Freie Universität Berlin. www.diss.fu-berlin.de/diss/ceive/FUDISS\_thesis\_000000006510

- Speicherung und Archivierung
- Alle Arten von Multimedia-Dateien
- Für GBOL:
  - Bilder von Sammlungsobjekten
  - Habitatansichten

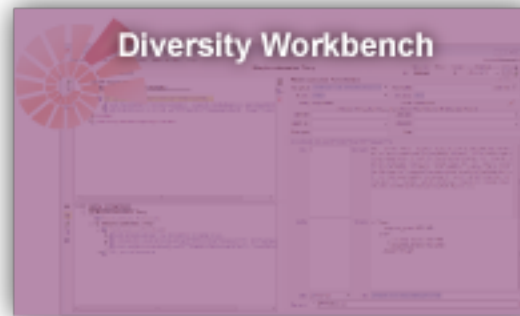


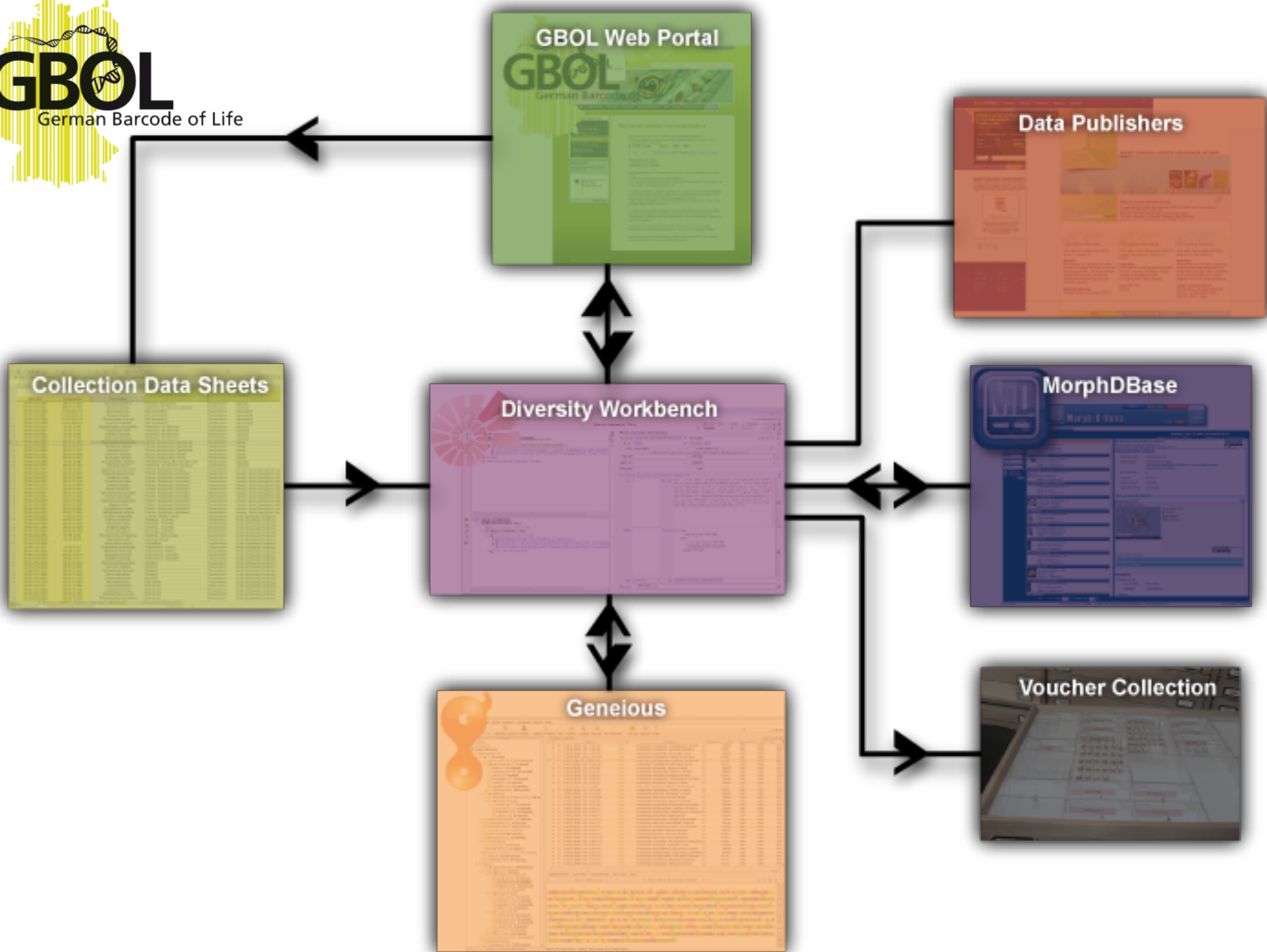
A screenshot of a data table from the GBOL database. The table has multiple columns with headers in German, including "Species", "Barcode", "Accession", and "Date". The rows contain detailed information for various species, with some cells highlighted in yellow and purple.



A screenshot of a data table from the GBOL database, showing a large number of rows. The table has multiple columns with headers in German, including "Species", "Barcode", "Accession", and "Date". The rows contain detailed information for various species, with some cells highlighted in green and yellow.

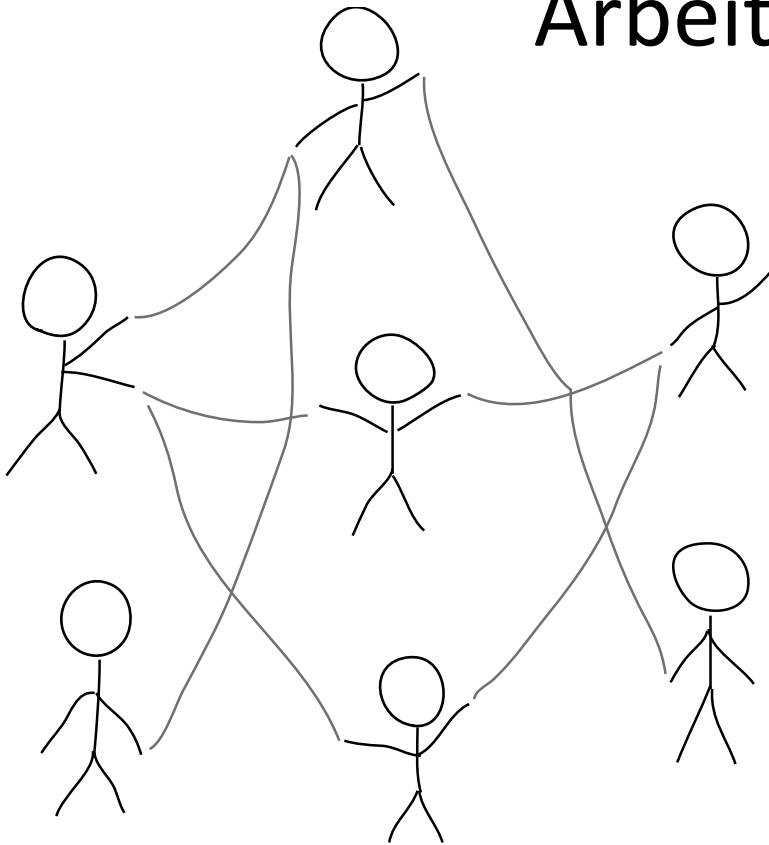








# Arbeitsablauf und Datenfluss



# Bestellung von Material

- GBOL-Experte bestellt Material
  - Art der Sammelröhrchen
  - Anzahl
  - Taxonomische Gruppe

## Versandmaterial anfordern

### Ihre Adresse

Herr Dr. Peter Grobe  
Zoologisches Forschungsmuseum Alexander Koenig  
Adenauer Allee 160  
53113 Bonn  
Deutschland

**Bitte überprüfen Sie Ihre Adresse. Sollte sie fehlerhaft sein, korrigieren Sie bitte Ihre Daten in [Ihrem Nutzerprofil](#).**

### Art der Sammelröhrchen \*

2ml Röhrchen

### Anzahl der gewünschten Sammelröhrchen \*

95

Bitte wählen Sie aus, wie viele Sammelröhrchen Sie benötigen. Geben Sie bitte immer nur Individuen einer einzigen Art in ein Gefäß; bei Tieren in 96% Ethanol (weitere Hinweise in den Sammelinfos).

### Taxonomische Gruppe \*

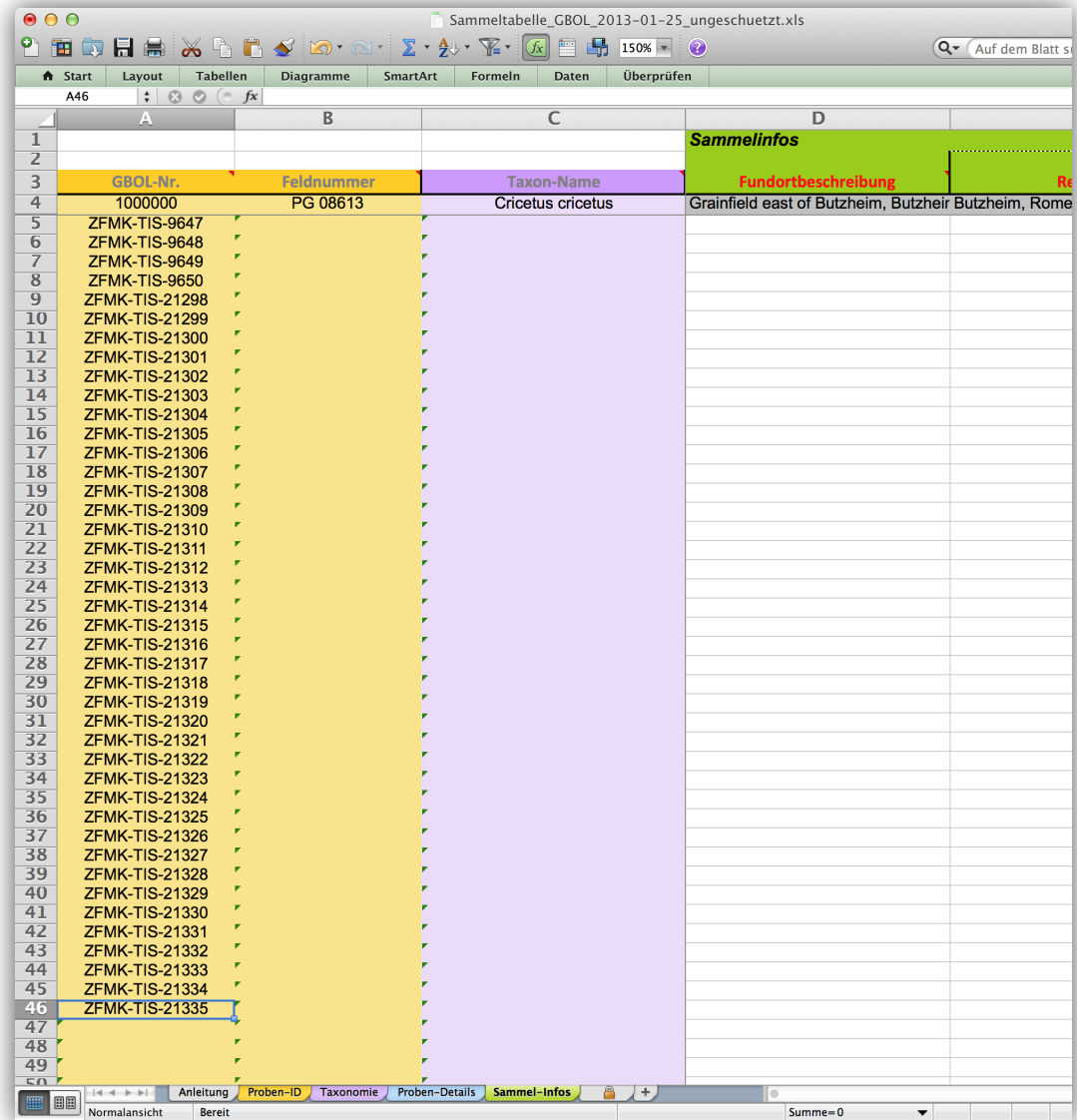
Arachnida, Zoologisches Forschungsmuseum Alexander Koenig (ZFMK) (Björn Rulik)

Bitte geben Sie an, für welches Taxon Sie Sammelröhrchen benötigen und von welchem Institut Sie diese bestellen möchten.

Absenden

# Bestellung von Material

- GBOL-System generiert Leereinträge in der Sammlungsdatenbank
- Herunterladen der GBOL-Sammeltabelle



Sammeltabelle\_GBOL\_2013-01-25\_ungeschuetzt.xls

	A	B	C	D
				<b>Sammelinfos</b>
	<b>GBOL-Nr.</b>	<b>Feldnummer</b>	<b>Taxon-Name</b>	<b>Fundortbeschreibung</b>
4	1000000	PG 08613	Cricetus cricetus	Grainfield east of Butzheim, Butzheir Butzheim, Rome
5	ZFMK-TIS-9647			
6	ZFMK-TIS-9648			
7	ZFMK-TIS-9649			
8	ZFMK-TIS-9650			
9	ZFMK-TIS-21298			
10	ZFMK-TIS-21299			
11	ZFMK-TIS-21300			
12	ZFMK-TIS-21301			
13	ZFMK-TIS-21302			
14	ZFMK-TIS-21303			
15	ZFMK-TIS-21304			
16	ZFMK-TIS-21305			
17	ZFMK-TIS-21306			
18	ZFMK-TIS-21307			
19	ZFMK-TIS-21308			
20	ZFMK-TIS-21309			
21	ZFMK-TIS-21310			
22	ZFMK-TIS-21311			
23	ZFMK-TIS-21312			
24	ZFMK-TIS-21313			
25	ZFMK-TIS-21314			
26	ZFMK-TIS-21315			
27	ZFMK-TIS-21316			
28	ZFMK-TIS-21317			
29	ZFMK-TIS-21318			
30	ZFMK-TIS-21319			
31	ZFMK-TIS-21320			
32	ZFMK-TIS-21321			
33	ZFMK-TIS-21322			
34	ZFMK-TIS-21323			
35	ZFMK-TIS-21324			
36	ZFMK-TIS-21325			
37	ZFMK-TIS-21326			
38	ZFMK-TIS-21327			
39	ZFMK-TIS-21328			
40	ZFMK-TIS-21329			
41	ZFMK-TIS-21330			
42	ZFMK-TIS-21331			
43	ZFMK-TIS-21332			
44	ZFMK-TIS-21333			
45	ZFMK-TIS-21334			
46	ZFMK-TIS-21335			
47				
48				
49				
50				

Normalansicht Bereit Summe=0

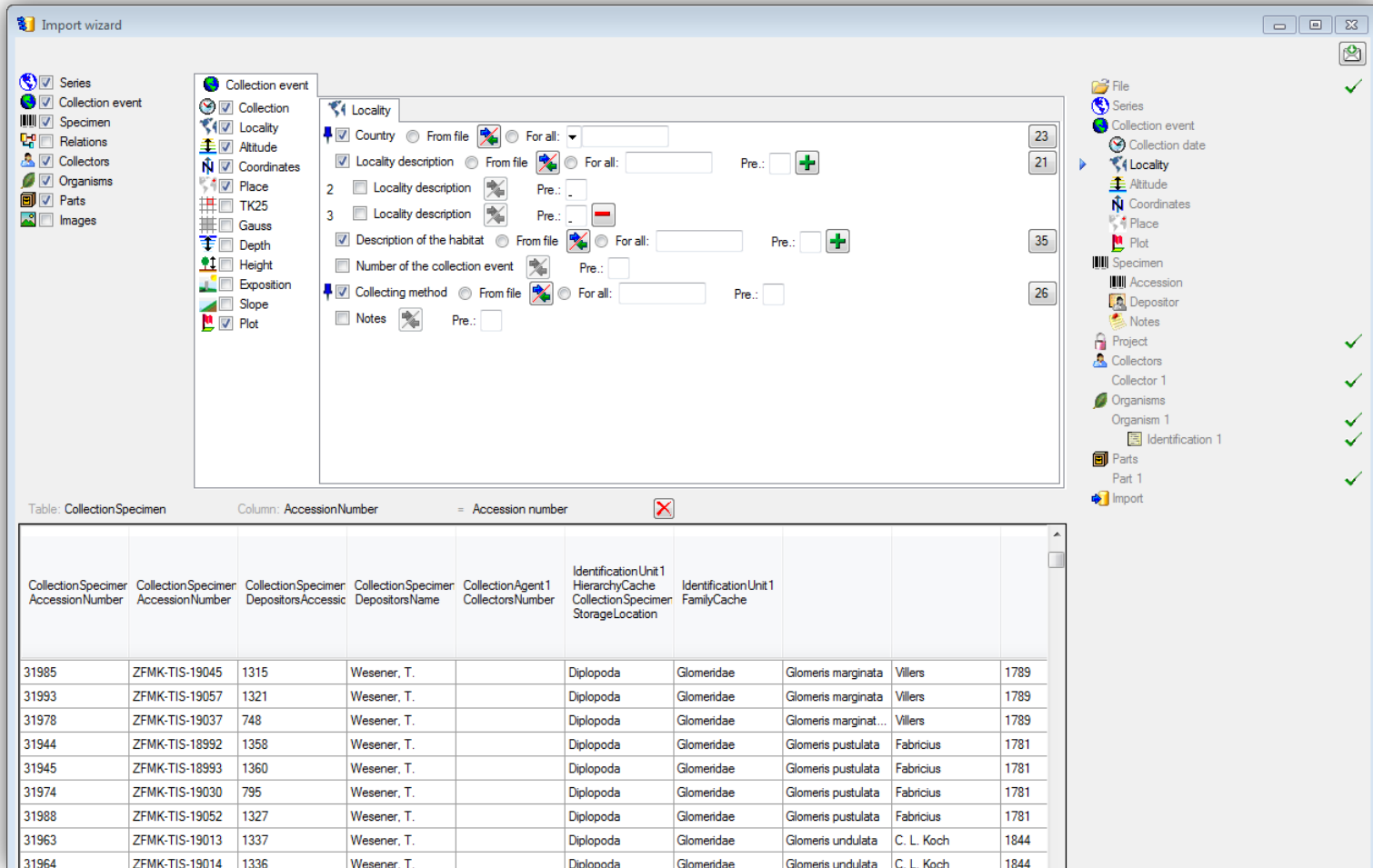
# Dateneingabe

- Dateneingabe-Möglichkeiten
  - Sammelliste
  - Hochladen in die Sammlungsdatenbank per ImportWizard
  - DiversityWebEditor
- Senden der Belege an den zuständigen Taxonkoordinator in einem der GBOL Institute
- (SMNG, SMNK, SMNS, ZFMK, ZSM, etc.)





## DiversityWorkbench Import Wizard Ver. I + II



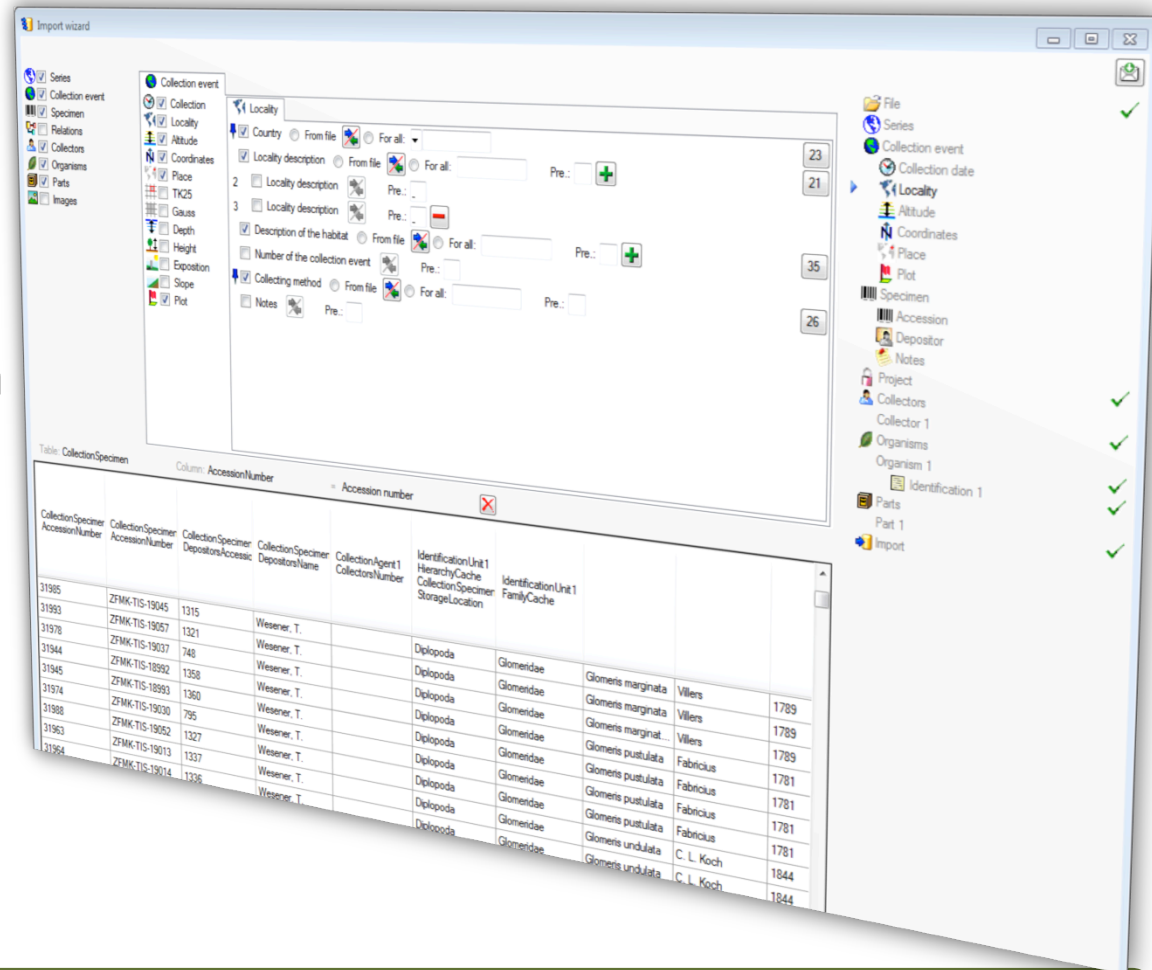
The screenshot shows the 'Import wizard' window with the 'Collection event' tab selected. The 'Locality' section is expanded, showing options for 'Country', 'Locality description', 'Description of the habitat', 'Number of the collection event', 'Collecting method', and 'Notes'. Each option has a 'Pre.' field and a 'For all' dropdown menu. The 'Table: CollectionSpecimen' is displayed below the configuration window, showing a list of specimens with their accession numbers and associated data.

CollectionSpecimen AccessionNumber	CollectionSpecimen AccessionNumber	CollectionSpecimen DepositorsAccessic	CollectionSpecimen DepositorsName	CollectionAgent 1 CollectorsNumber	IdentificationUnit1 HierarchyCache CollectionSpecimen StorageLocation	IdentificationUnit1 FamilyCache			
31985	ZFMK-TIS-19045	1315	Wesener, T.		Diplopoda	Glomeridae	Glomeris marginata	Villers	1789
31993	ZFMK-TIS-19057	1321	Wesener, T.		Diplopoda	Glomeridae	Glomeris marginata	Villers	1789
31978	ZFMK-TIS-19037	748	Wesener, T.		Diplopoda	Glomeridae	Glomeris marginat...	Villers	1789
31944	ZFMK-TIS-18992	1358	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata	Fabricius	1781
31945	ZFMK-TIS-18993	1360	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata	Fabricius	1781
31974	ZFMK-TIS-19030	795	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata	Fabricius	1781
31988	ZFMK-TIS-19052	1327	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata	Fabricius	1781
31963	ZFMK-TIS-19013	1337	Wesener, T.		Diplopoda	Glomeridae	Glomeris undulata	C. L. Koch	1844
31964	ZFMK-TIS-19014	1336	Wesener, T.		Diplopoda	Glomeridae	Glomeris undulata	C. L. Koch	1844



## DiversityWorkbench Import Wizard

- Import der Daten aus Sammelliste
- Stellen alle Feld- und Taxondaten zur weiteren Nutzung zur Verfügung

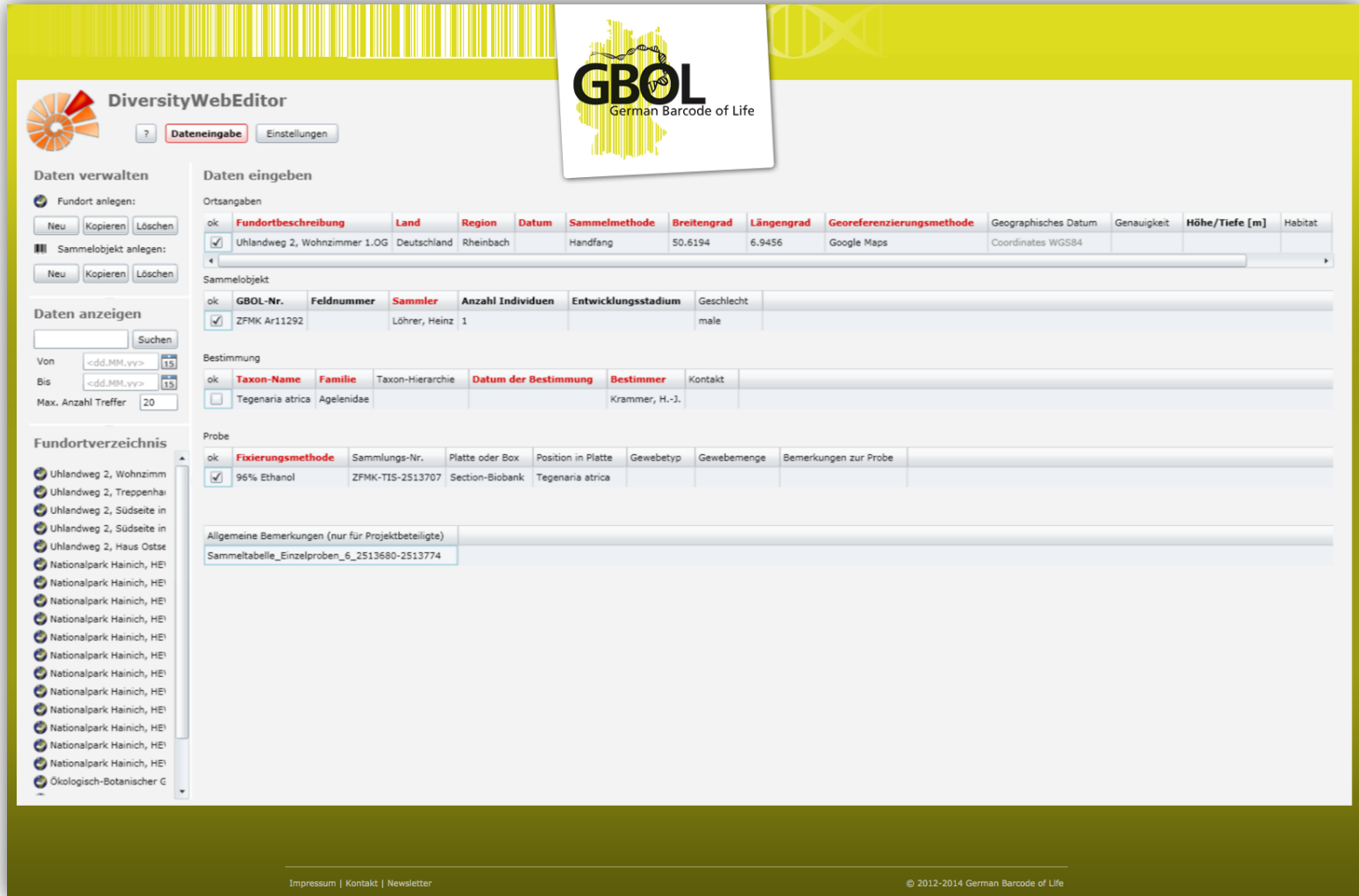


The screenshot shows the 'Import wizard' window. On the left, a sidebar lists various data fields to be imported, such as 'Series', 'Collection event', 'Specimen', 'Locality', 'Altitude', etc. The main area displays a table of 'CollectionSpecimen' with columns for 'AccessionNumber', 'Depositor/Accession', 'Depositor/Name', 'CollectionAgent1', 'Collectors/Number', 'IdentificationUnit1', and 'FamilyCache'. The table contains several rows of specimen data.

CollectionSpecimen AccessionNumber	CollectionSpecimen AccessionNumber	CollectionSpecimen Depositor/Accession	CollectionSpecimen Depositor/Name	CollectionAgent1 Collectors/Number	IdentificationUnit1 HierarchyCache CollectionSpecimen Storage/Location	IdentificationUnit1 FamilyCache	
31985	ZFMK-TIS-19045	1315	Wesener, T.				
31983	ZFMK-TIS-19057	1321	Wesener, T.		Diplopoda	Glomeridae	
31978	ZFMK-TIS-19037	748	Wesener, T.		Diplopoda	Glomeridae	Glomeris marginata Villers 1789
31944	ZFMK-TIS-18992	1358	Wesener, T.		Diplopoda	Glomeridae	Glomeris marginata Villers 1789
31945	ZFMK-TIS-18993	1360	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata Fabricius 1781
31974	ZFMK-TIS-19030	795	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata Fabricius 1781
31988	ZFMK-TIS-19052	1327	Wesener, T.		Diplopoda	Glomeridae	Glomeris pustulata Fabricius 1781
31963	ZFMK-TIS-19013	1337	Wesener, T.		Diplopoda	Glomeridae	Glomeris undulata C. L. Koch 1844
31984	ZFMK-TIS-19014	1336	Wesener, T.		Diplopoda	Glomeridae	Glomeris undulata C. L. Koch 1844



<https://dwb.snsb.info/DiversityWebEditor/>



The screenshot shows the DiversityWebEditor web interface. At the top, there is a navigation bar with the GBOL logo and a 'Dateneingabe' button. The main content area is divided into several sections:

- Daten verwalten:** Includes buttons for 'Fundort anlegen', 'Sammelobjekt anlegen', and 'Daten anzeigen'.
- Daten eingeben:** Contains a form for entering data, including a table for 'Ortsangaben' and 'Sammelobjekt'.
- Daten anzeigen:** Includes a search bar and date selection fields.
- Fundortverzeichnis:** A list of collection sites with checkboxes for selection.
- Bestimmung:** A table for taxonomic determination.
- Probe:** A table for specimen details.
- Allgemeine Bemerkungen:** A text area for general remarks.

At the bottom of the interface, there is a footer with 'Impressum | Kontakt | Newsletter' and '© 2012-2014 German Barcode of Life'.



Eingabe von Felddaten direkt über das Web Portal

- Entwickelt hier (W. Reichert)
- Synchronisierung der Daten zwischen dem GBOL Web Portal und der Sammlungsdatenbank
- Integriert in das GBOL Web Portal, in Kürze freigeschaltet



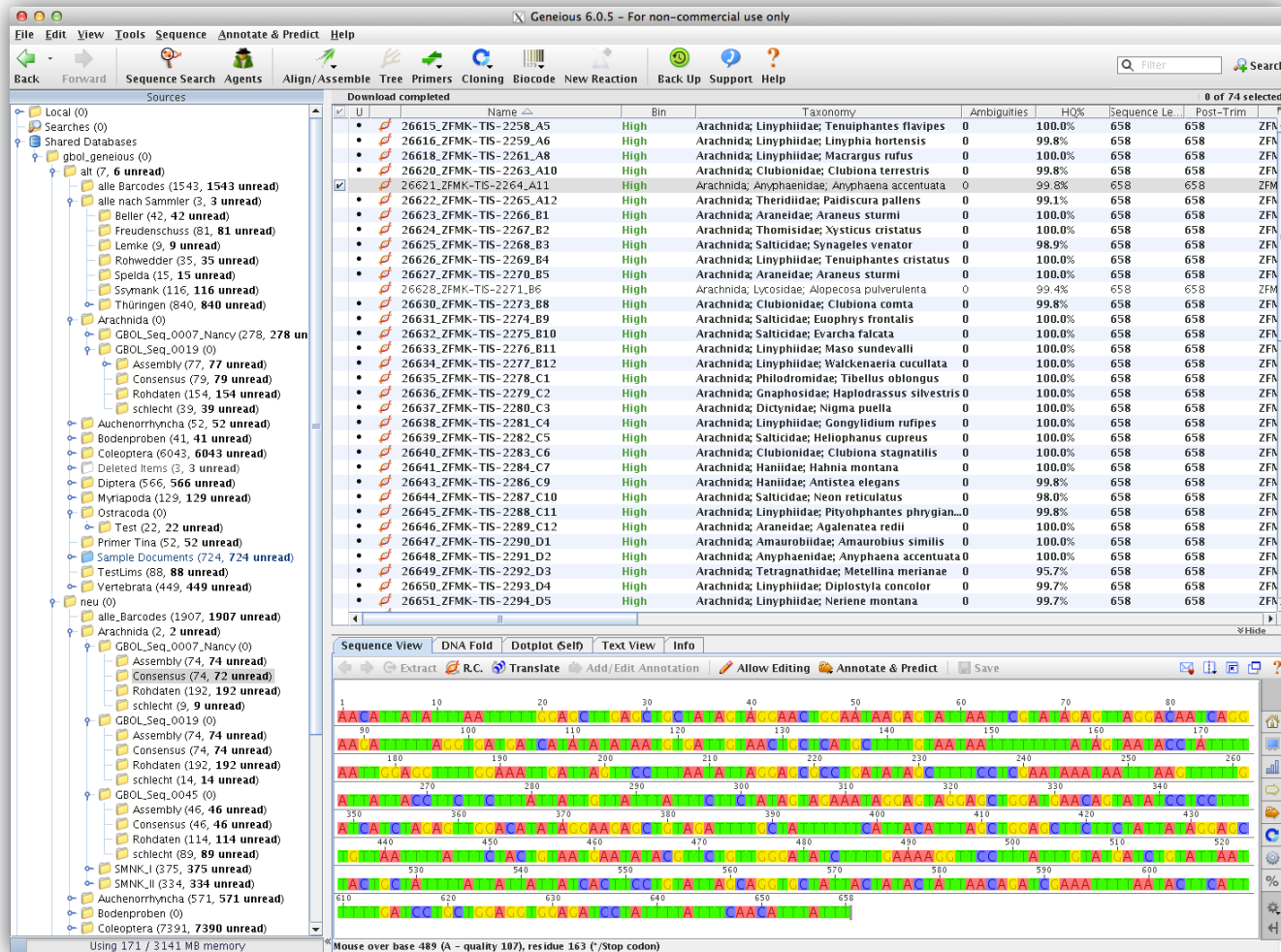
The screenshot shows the DiversityWebEditor interface. At the top, there is a header with the GBOL logo and navigation buttons for 'Dateneingabe' and 'Einstellungen'. The main content area is divided into several sections:

- Daten verwalten:** Includes buttons for 'Fundort anlegen', 'Sammlungsobjekt anlegen', and 'Daten anzeigen'.
- Daten eingeben:** A form for entering specimen data with fields for 'Fundortbeschreibung', 'Land', 'Region', 'Datum', 'Sammelmethode', 'Breitengrad', 'Längengrad', 'Georeferenzierungsmethode', and 'Geographische Koordinaten W'. Below this is a table for 'Sammelobjekt' with columns for 'GBOL-Nr.', 'Feldnummer', 'Sammler', 'Anzahl Individuen', 'Entwicklungsstadium', and 'Geschlecht'. A 'Bestimmung' section follows with fields for 'Taxon-Name', 'Familie', 'Taxon-Hierarchie', 'Datum der Bestimmung', 'Bestimmer', and 'Kontakt'.
- Fundortverzeichnis:** A list of collection sites on the left side of the interface.
- Probe:** A section for specimen details with fields for 'Fixierungsmethode', 'Sammlungs-Nr.', 'Platte oder Box', 'Position in Platte', 'Gewebetyp', 'Gewebemenge', and 'Bemerkungen zur Probe'.
- Allgemeine Bemerkungen:** A text area for general notes, with a 'Sammetabelle\_Einzelproben\_8\_2512680-2512774' link.



# Erzeugung des DNA Barcodes

## Geneious – Labor Management System (LIMS)

The screenshot displays the Geneious 6.0.5 interface. The top menu bar includes File, Edit, View, Tools, Sequence, Annotate & Predict, and Help. Below the menu is a toolbar with icons for various functions like Back, Forward, Sequence Search, Agents, Align/Assemble, Tree, Primers, Cloning, Biocode, New Reaction, Back Up, Support, and Help. A search bar is located on the right side of the toolbar.

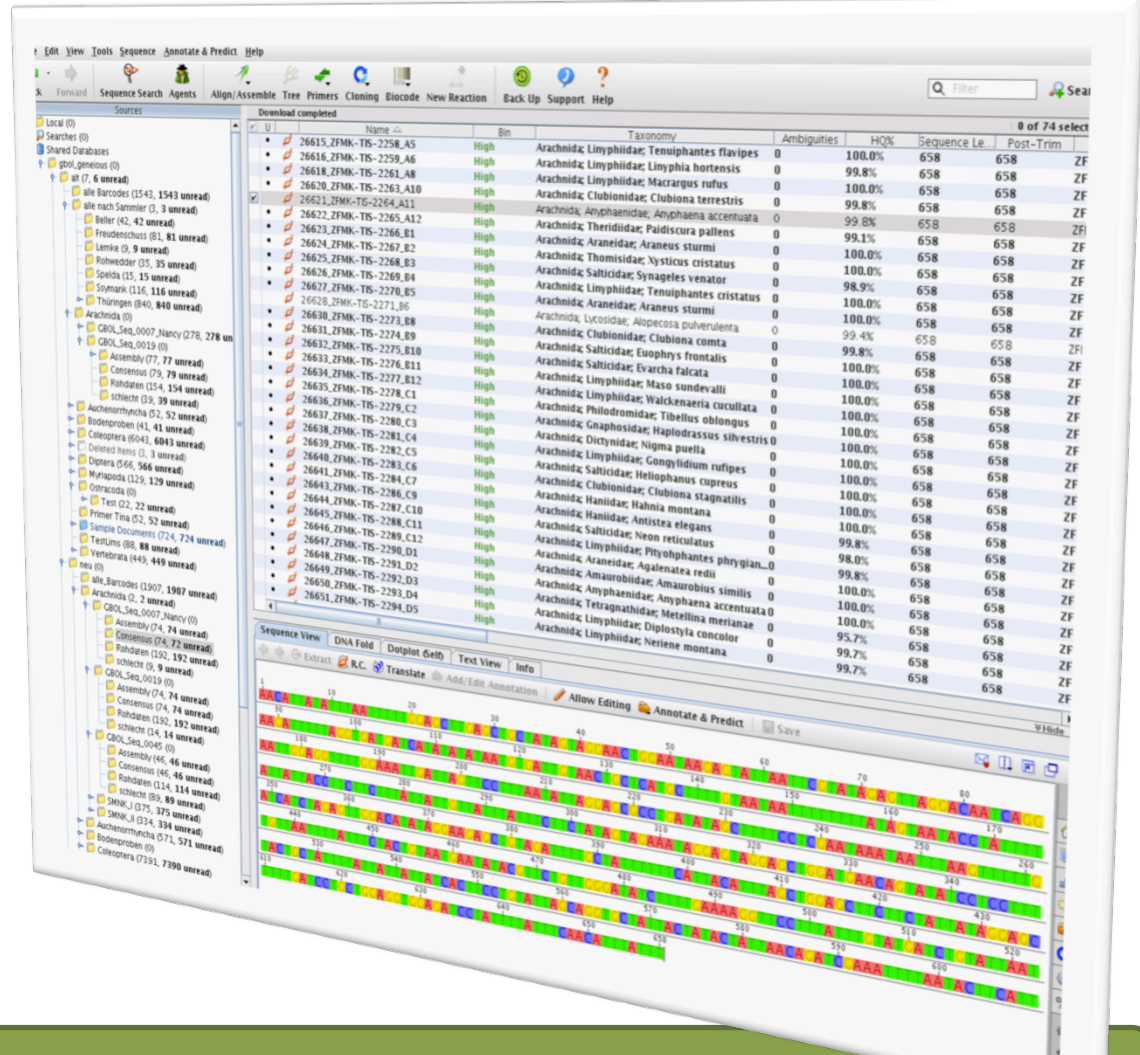
The main window is divided into two panes. The left pane shows a hierarchical tree view of sources, including Local (0), Searches (0), Shared Databases, and gbol\_geneious (0). The right pane displays a list of sequences with columns for Name, Bin, Taxonomy, Ambiguities, HQ%, Sequence Le., and Post-Trim. The list shows various species such as *Tenuiphantes flavipes*, *Linyphia hortensis*, *Macrargus rufus*, *Clubiona terrestris*, *Anyphaena accentuata*, *Paidiscura pallens*, *Araneus sturmi*, *Xysticus cristatus*, *Synageles venator*, *Tenuiphantes cristatus*, *Araneus sturmi*, *Lyxosidae*, *Alopecosa pulverulenta*, *Clubiona comta*, *Euoophys frontalis*, *Evarcha falcata*, *Maso sundevalli*, *Walckenaeria cucullata*, *Tibellus oblongus*, *Gnaphosidae*, *Haplodrassus silvestris*, *Dictynidae*, *Nigma puella*, *Gongyldium rufipes*, *Heliophanus cupreus*, *Clubionidae*, *Clubiona stagnatilis*, *Hahnina montana*, *Antistea elegans*, *Neon reticulatus*, *Pityohphantes phrygian...*, *Araneidae*, *Agalenatea redii*, *Amaurobiidae*, *Amaurobius similis*, *Anyphaenidae*, *Anyphaena accentuata*, *Tetragnathidae*, *Metellina merianae*, *Diplostyla concolor*, and *Nerine montana*.

The bottom pane shows a detailed sequence view for a selected sequence. The sequence is displayed as a horizontal bar with nucleotide bases (A, C, G, T) and their corresponding quality scores. The sequence starts with AACAATAA and ends with AAGAAATA. The quality scores are shown as numbers above the bases. The interface also includes buttons for Extract, R.C., Translate, Add/Edit Annotation, Allow Editing, Annotate & Predict, and Save.



### Labor

- DNA-Extraktion
- PCR
- DNA-Sequenzierung (BGI, Macrogen)
- Rohsequenzen
- DNA-Barcodes

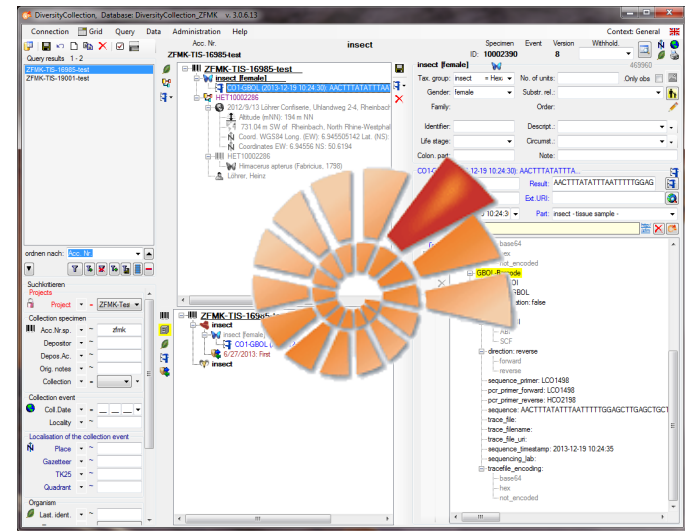
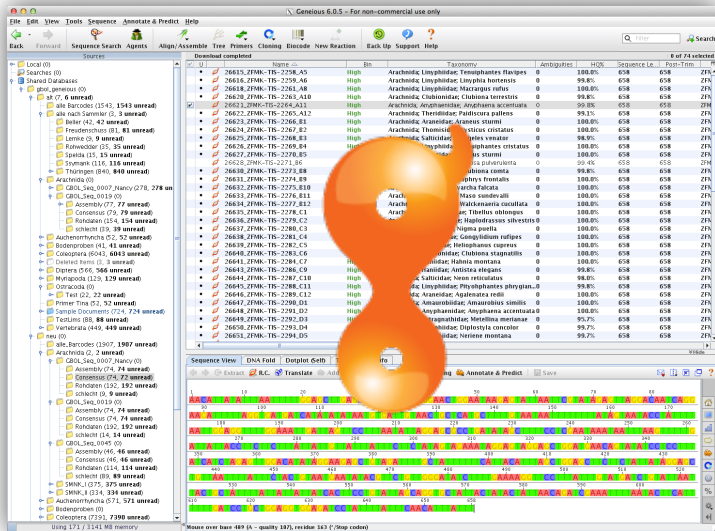


The screenshot displays the Geneious LIMS interface. The top menu includes 'Edit', 'View', 'Tools', 'Sequence', 'Annotate & Predict', and 'Help'. Below the menu is a toolbar with icons for various functions like 'Forward', 'Sequence Search', 'Agents', 'Align/Assemble', 'Tree', 'Primers', 'Cloning', 'Barcode', 'New Reaction', 'Back Up', 'Support', and 'Help'. The main window is divided into several panes:

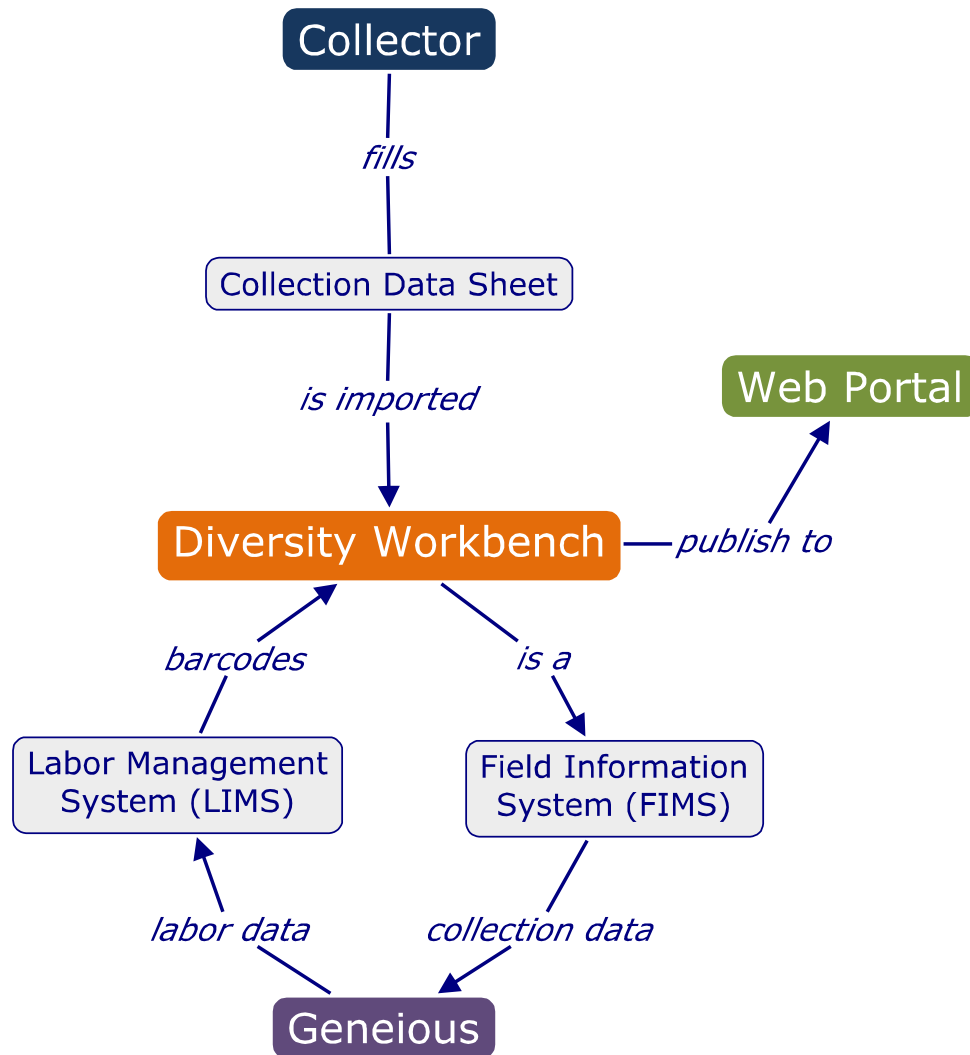
- Sources:** A tree view on the left showing project folders like 'Local (0)', 'Shared Databases', and 'not geneious (0)'. It lists various sample folders such as 'alle Barcodes (1543, 1543 unread)', 'Beller (42, 42 unread)', 'Freudenstich (81, 81 unread)', etc.
- Table:** A central table listing individual sequences. Columns include 'Name', 'Bin', 'Taxonomy', 'Ambiguities', 'HQs', 'Sequence Le.', and 'Post-Trim'. The table shows a list of sequences with their corresponding taxonomic classifications and quality metrics.
- Sequence View:** A bottom pane showing a detailed view of a sequence alignment. It includes a 'DNA Fold' view, a 'Dotplot (6x6)', and 'Text View'. The sequence is displayed with a color-coded alignment and a 'Sequence Logo' below it.

# Verknüpfung von Feld-, Taxon und Barcodes

- Geneious (*LIMS*) ist mit der Sammlungsdatenbank (*FIMS*) verknüpft:
- *LIMS* liest *FIMS*-Daten
- Generierung des Barcodes (im Labor)
- *LIMS* übergibt Barcode an die Sammlungsdatenbank



# Datenfluss



## Fundstellen



Impressum | Kontakt | Newsletter **Angemeldet: Dr. Peter Grobe**

**GBOL**  
German Barcode of Life

Deutschlands Fauna und Flora in einer einzigartigen genetischen Bibliothek.

Das Projekt | DNA-Barcoding | Das Team | Mitmachen! | News & Publikationen | Links | **Fundstellen** | Kontakt | Experten-Bereich

### Fundstellen

--> Suche:  Kategorie:

**Taxa**

Ampel-Legende:  
Anzahl **bekannte** / **vorhandene** / **barcode** Arten

- + Plants (1633/0/0)
- **Animalia (3256/420/245)** →
- + **Vertebrata (779/148/94)** →
- + **Arachnida (694/30/20)** →
- + **Citellata (288/4/0)** →
- + **Chilopoda (62/22/12)** →
- + **Diplopoda (135/98/32)** →
- + Bryozoa (16/0/0)
- + Annelida (6/0/0)
- + **Arthropoda (304/106/82)** →
- + **Chordata (24/1/0)** →
- + **Mollusca (22/2/1)** →
- + **Plathelminthes (5/2/0)** →



Suchergebnisse

Anzahl gefundene Individuen: 160

Taxon-Name	Land	Datum	Sex	Entwicklungsstadium	Taxonomie
<i>Cricetus cricetus</i>	Deutschland	02.12.2013		Juvenile	Chordata » Mammalia » Cricetus » Cricetidae » Rodentia » Animalia » Vertebrata
<i>Cricetus cricetus</i>	Deutschland	02.12.2013			Chordata » Mammalia » Cricetus »

Impressum | Kontakt | Newsletter © 2012-2014 German Barcode of Life

## Fundstellen

- Suche nach Arten, Fundorten, Sammler, ...
- Sperrung sensibler Daten für Öffentlichkeit
- Taxon-Browser mit Ampel
- Darstellung auf Karte
- Herunterladen der Ergebnisliste

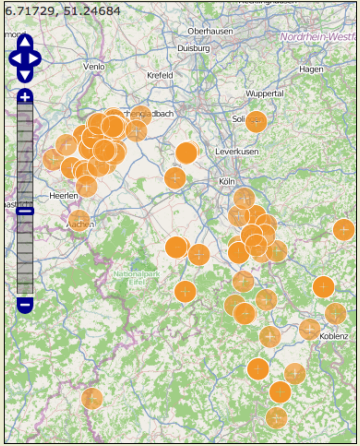
### Fundstellen

--> Suche:  Kategorie:  Suchen

**Taxa**

Ampel-Legende:  
Anzahl **bekannt** / **vorhandene** / **barcode** Arten

- + Plants (1633/0/0)
- Animalia (3256/420/245) →
- + Vertebrata (779/148/94) →
- + Arachnida (694/30/20) →
- + Clitellata (288/4/0) →
- + Chilopoda (62/22/12) →
- + Diplopoda (135/98/32) →
- + Bryozoa (16/0/0)
- + Annelida (6/0/0)
- + Arthropoda (304/106/82) →
- + Chordata (24/1/0) →
- + Mollusca (22/2/1) →
- + Plathelminthes (5/2/0) →



**Suchergebnisse**

Anzahl gefundene Individuen: 160

Taxon-Name	Land	Datum	Sex	Entwicklungsstadium	Taxonomie
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<i>Cricetus cricetus</i>	Deutschland	02.12.2013			Chordata » Mammalia » Cricetus »

[Excel Export](#)

# Datenverzahnung

Eindeutige ID über den gesamten Arbeits- und Datenfluss

11	ZFMK-TIS-2261	29.04.12-03	Macrargus rufus
12	ZFMK-TIS-2262	29.04.12-03	Neriere clathrata
13	ZFMK-TIS-2263	29.04.12-03	Clubiona terrestris
14	ZFMK-TIS-2264	29.04.12-473	Anyphaena accentuata
15	ZFMK-TIS-2265	29.04.12-473	Paidiscura pallens
16	ZFMK-TIS-2266	29.04.12-473	Araneus sturmi

Sammeltabelle

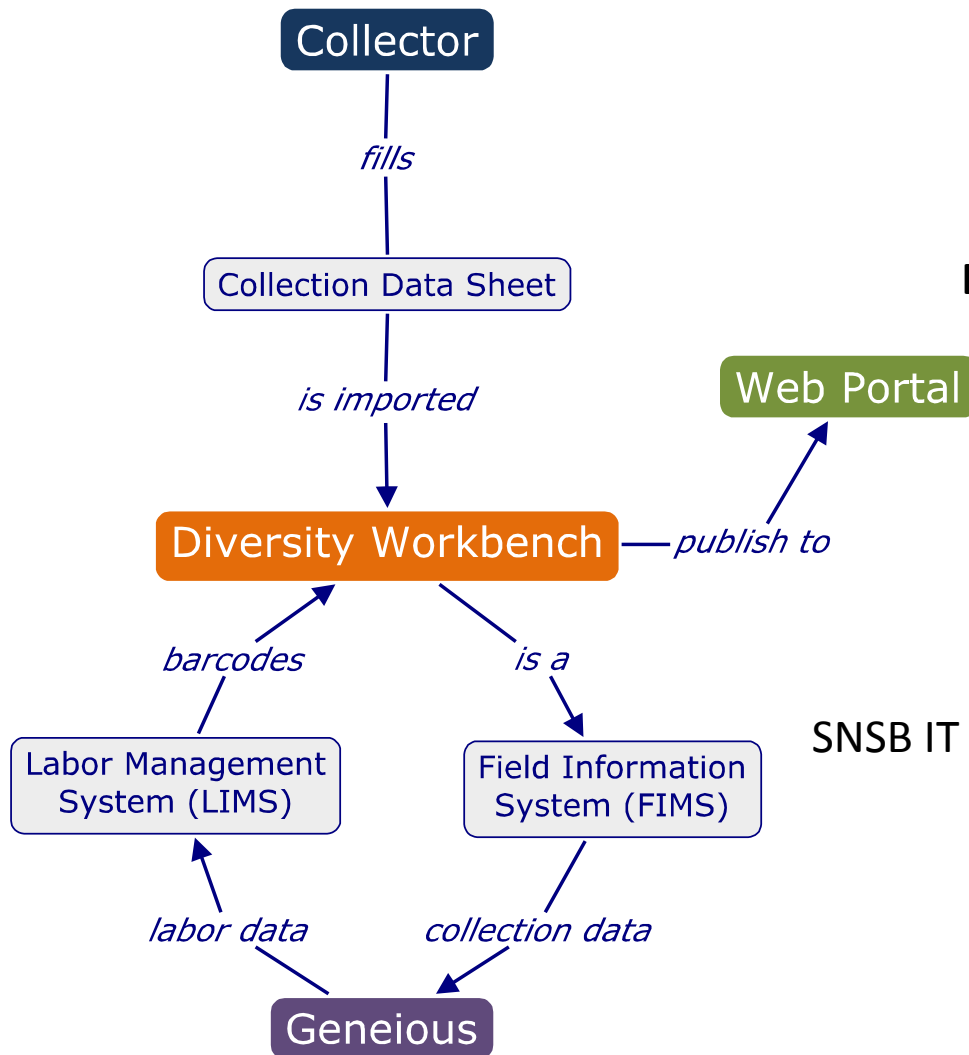
DiversityWorkbench

•	26618_ZFMK-TIS-2261_A8	High	Arachnida; Linyphiidae; Macrargus rufus	0
•	26620_ZFMK-TIS-2263_A10	High	Arachnida; Clubionidae; Clubiona terrestris	0
<input checked="" type="checkbox"/>	26622_ZFMK-TIS-2264_A11	High	Arachnida; Anyphaenidae; Anyphaena accentuata	0
•	26622_ZFMK-TIS-2265_A12	High	Arachnida; Theridiidae; Paidiscura pallens	0
•	26623_ZFMK-TIS-2266_B1	High	Arachnida; Araneidae; Araneus sturmi	0

Laborverwaltung Geneious

Multimedia-Verwaltung Morph·D·Base

# Vielen Dank!



## Dank an:

Stefanie Pietsch (Koordination)  
Jonas Astrin (DNA-Barcodes)  
Björn Rulik (Taxon-Koordination)  
Karl-Heinz Klameth (Programmierung)  
Laura von der Mark (TA)  
Jana Thormann (TA)  
Data in transit & TEDSoft (Webportal)  
SNSB IT Center München (Diversity Workbench)