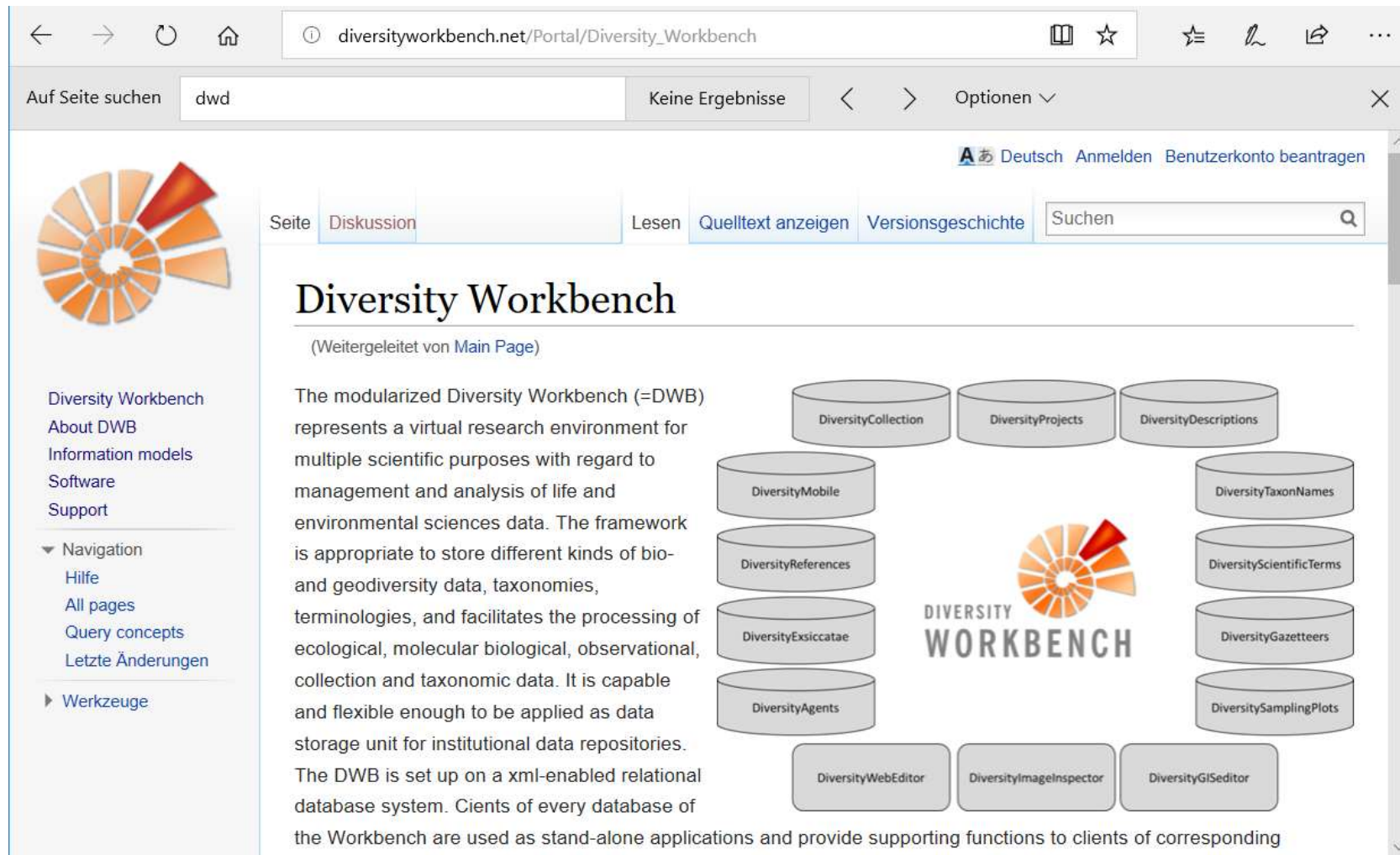


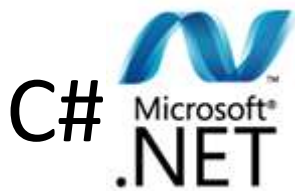
Introduction to *DiversityDescriptions*

Anton Link

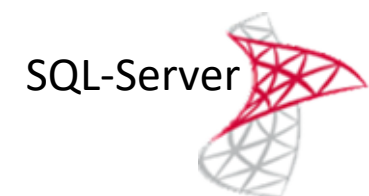


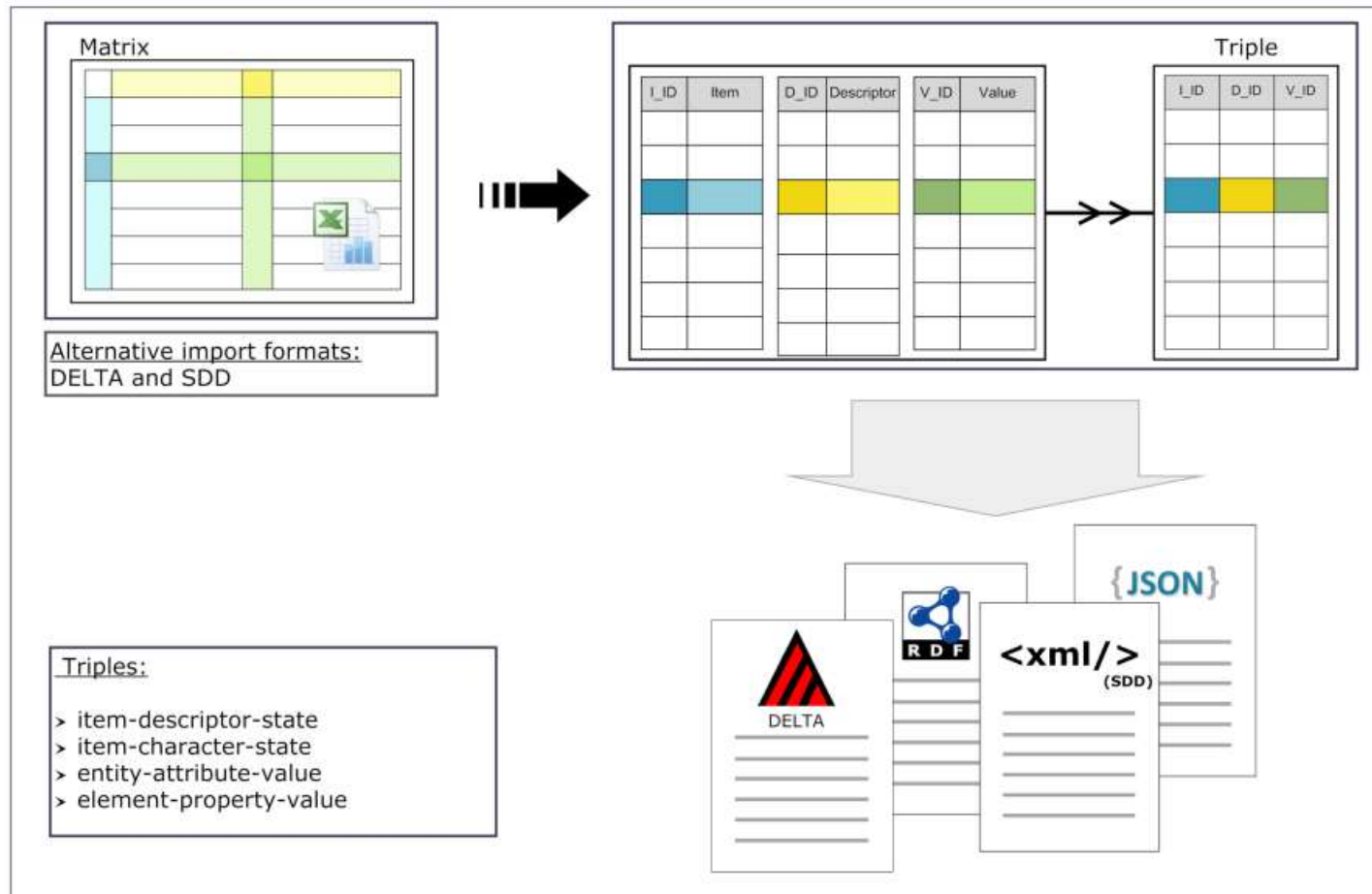
The screenshot shows a web browser window with the URL `diversityworkbench.net/Portal/Diversity_Workbench`. The page features a search bar with the text "Auf Seite suchen" and "dwd", and a status message "Keine Ergebnisse". The main content area displays the "Diversity Workbench" title and a description: "The modularized Diversity Workbench (=DWB) represents a virtual research environment for multiple scientific purposes with regard to management and analysis of life and environmental sciences data. The framework is appropriate to store different kinds of bio- and geodiversity data, taxonomies, terminologies, and facilitates the processing of ecological, molecular biological, observational, collection and taxonomic data. It is capable and flexible enough to be applied as data storage unit for institutional data repositories. The DWB is set up on a xml-enabled relational database system. Clients of every database of the Workbench are used as stand-alone applications and provide supporting functions to clients of corresponding".

Surrounding the central text is a diagram of the system architecture, consisting of several database cylinders and application boxes. The top row includes `DiversityCollection`, `DiversityProjects`, and `DiversityDescriptions`. The middle row includes `DiversityMobile`, `DiversityReferences`, and `DiversityExsiccatae`. The bottom row includes `DiversityAgents`, `DiversityWebEditor`, `DiversityImageInspector`, and `DiversityGISeditor`. On the right side, there are additional cylinders for `DiversityTaxonNames`, `DiversityScientificTerms`, `DiversityGazetteers`, and `DiversitySamplingPlots`. The central logo "DIVERSITY WORKBENCH" is also visible.



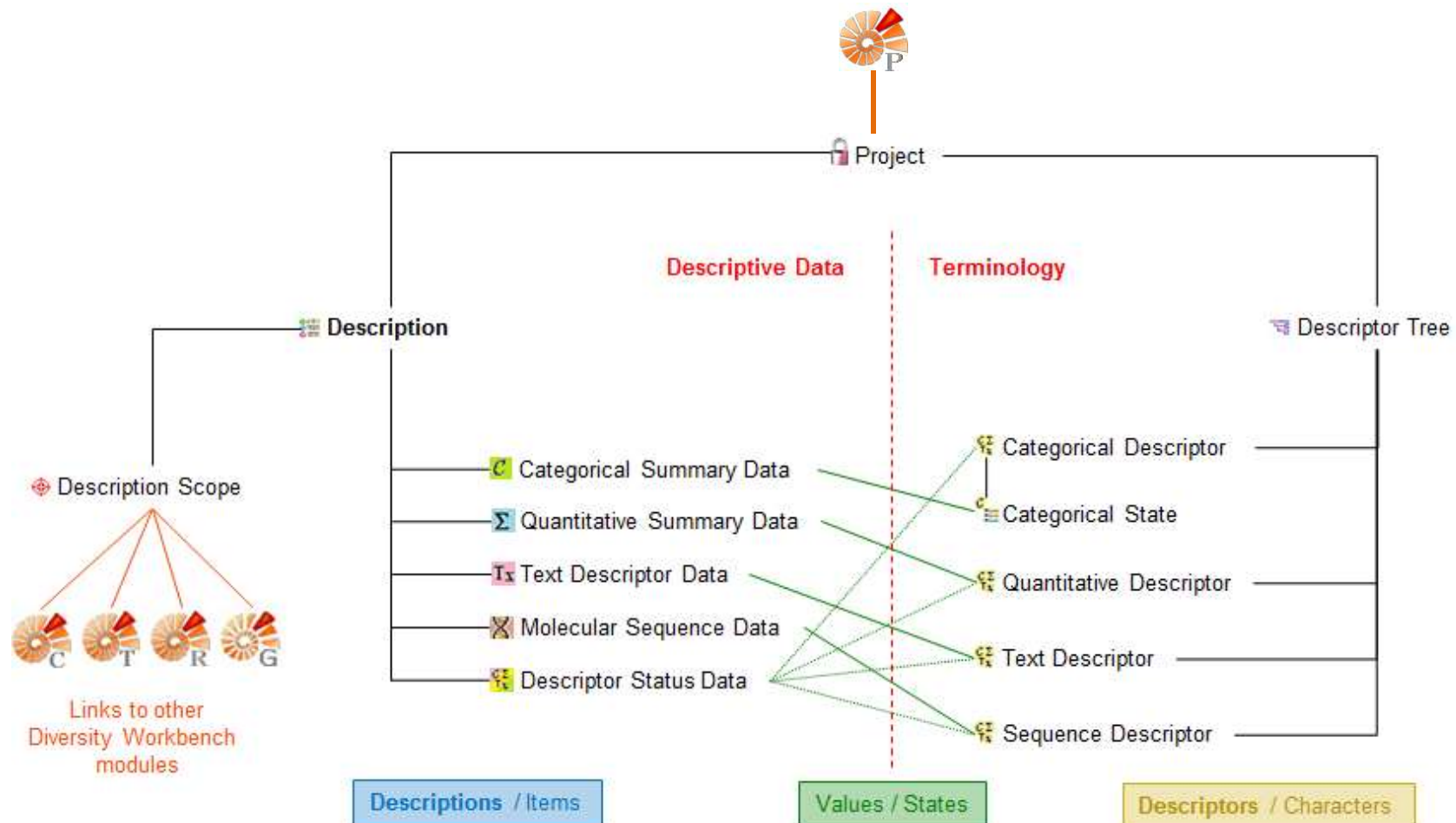
Open Source
20 years of development





- Typical spreadsheet structure: A column for each property, a line for each item
- Triple state structure:
Descriptor defines properties, **Item** holds item data, **Value** keeps descriptor value

Simplified data model with links to other Diversity Workbench modules



DiversityDescriptions, Database: DiversityDescriptions_Import v. 3.0.2.3

Connection Edit Grid Query Data Administration Help

Abierhiza tomentosa + Abies

Suchergebnisse 1 - 100 von 554

Description: Abierhiza tomentosa + Abies ID: 585930

Main attributes Descriptor view Continuous view Resource links Sample data

Details:

Description scopes

Scope type	Scope value
Taxon name	Abierhiza tomentosa + Abies
Reference	Haug I, Weber R, Oberwinkler

Suchkriterien

Search criteria: ID, Title, Details, Project (Deemy)

Description resource

Descriptor

Project

- BactDescDSMZ
- BFLheilpflanzendesc
- Biomass
- Biomass as description
- Biomass as sample
- Copy of Deemy
- Copy of MycoPhylogenyNet
- Deemy
- DescriptionList (2)
- Encarsia
- Fagales_Gallen_Minien
- Import DFL TA

Edit descriptions

Main description attributes

DiversityDescriptions, Database: DiversityDescriptions_Import v. 3.0.2.3

Connection Edit Grid Query Data Administration Help

Abierhiza tomentosa + Abies

Suchergebnisse 1 - 100 von 554

Description: Abierhiza tomentosa + Abies ID: 585930

Main attributes Descriptor view Continuous view Resource links Sample data

Summary data

- literature references: Haug I, Weber R, Oberwinkler F, Tschern J (1994) The mycorrhizal system of Abies
- morphology mycorrhizal system ramification presence-type: monopodial-pinnate
- morphology mycorrhizal system ramification presence-type: absent
- morphology unramification: yellow, white
- morphology unramification: visible
- morphology unramification: smooth, not smooth
- morphology rhizome: $\mu = 3$
- morphology sclerotia: absent
- anatomy entire mycorrhizal system: absent
- anatomy mantle matrix presence: present
- anatomy mantle matrix location: middle mantle layer

Categorical states

x	No.	State	Modifier	Frequency	Notes
<input type="checkbox"/>	1	absent			
<input type="checkbox"/>	2	monopodial-pinnate			
<input type="checkbox"/>	3	monopodial-pyramidal			
<input type="checkbox"/>	4	dichotomous			
<input type="checkbox"/>	5	irregularly pinnate, d...			
<input type="checkbox"/>	6	coralloid			
<input type="checkbox"/>	7	tubercle-like			
<input type="checkbox"/>	8	braid-like			

Media view

Site collection model: OrSet

Status data

x	ID	Status	Notes
<input checked="" type="checkbox"/>	!	To be checked	
<input type="checkbox"/>	o	Not to be recorded	
<input type="checkbox"/>	-	Not applicable	
<input type="checkbox"/>	?	Data unavailable	
<input type="checkbox"/>	#	Not interpretable	
<input type="checkbox"/>	\$	Data withheld	
<input type="checkbox"/>	0	Missing data	

Descriptor tree:

- Categorical Descriptor
- Text Descriptor
- Quantitative Descriptor
- Sequence Descriptor

Edit descriptions

Resource view of a state

Three main tasks of the descriptor trees

1. Assignment of descriptors to project

The screenshot shows the DiversityDescriptions software interface. The main window displays a project named 'LIASlight' with ID 111. The 'Descriptor tree' tab is active, showing a hierarchical tree structure. The root node is 'LIASlight', which is highlighted with a red box. Below it, several categories are listed, including 'Data record', 'References', 'Taxonomy', 'Occurrence', 'Ecology', 'Chemistry', and 'Thallus'. The 'Thallus' category is expanded, showing a list of descriptors such as 'thallus <growth habit>', 'thallus <compartmentation>', and various morphological and surface descriptors. A red box highlights the 'thallus <growth habit>' descriptor, and a red arrow points from the 'LIASlight' root node to this descriptor, illustrating the assignment of descriptors to the project.

Three main tasks of the descriptor trees

The screenshot shows the 'DiversityDescriptions' software interface. The main window displays a 'Descriptor tree' for the project 'LIASlight'. The tree structure includes categories like 'Data record', 'References', 'Taxonomy', 'Occurrence', 'Ecology', 'Chemistry', and 'Thallus'. A specific node, '[th] morphol substructures (eg areoles, lobes, branches)', is highlighted with a red box. To the right of the tree, there are three panels for configuration: 'Recommended statistical measure', 'Recommended modifier', and 'Recommended frequency'. A red box highlights the 'Recommended statistical measure' panel, which has several options checked, including 'Lower range limit (legacy data stat. meth. unknown)', 'Upper range limit (legacy data stat. meth. unknown)', 'Central or typical value (legacy data stat. meth. unknown)', 'Minimum value', 'Maximum value', and 'Mean (= average)'. The 'Recommended modifier' panel shows 'uncertain' checked. The 'Recommended frequency' panel shows 'mostly' checked. The interface also includes a search bar, a menu bar, and a sidebar with search criteria.

1. Assignment of descriptors to project
2. Assignment of allowed statistical measures, modifier and frequency values to descriptors

Three main tasks of the descriptor trees

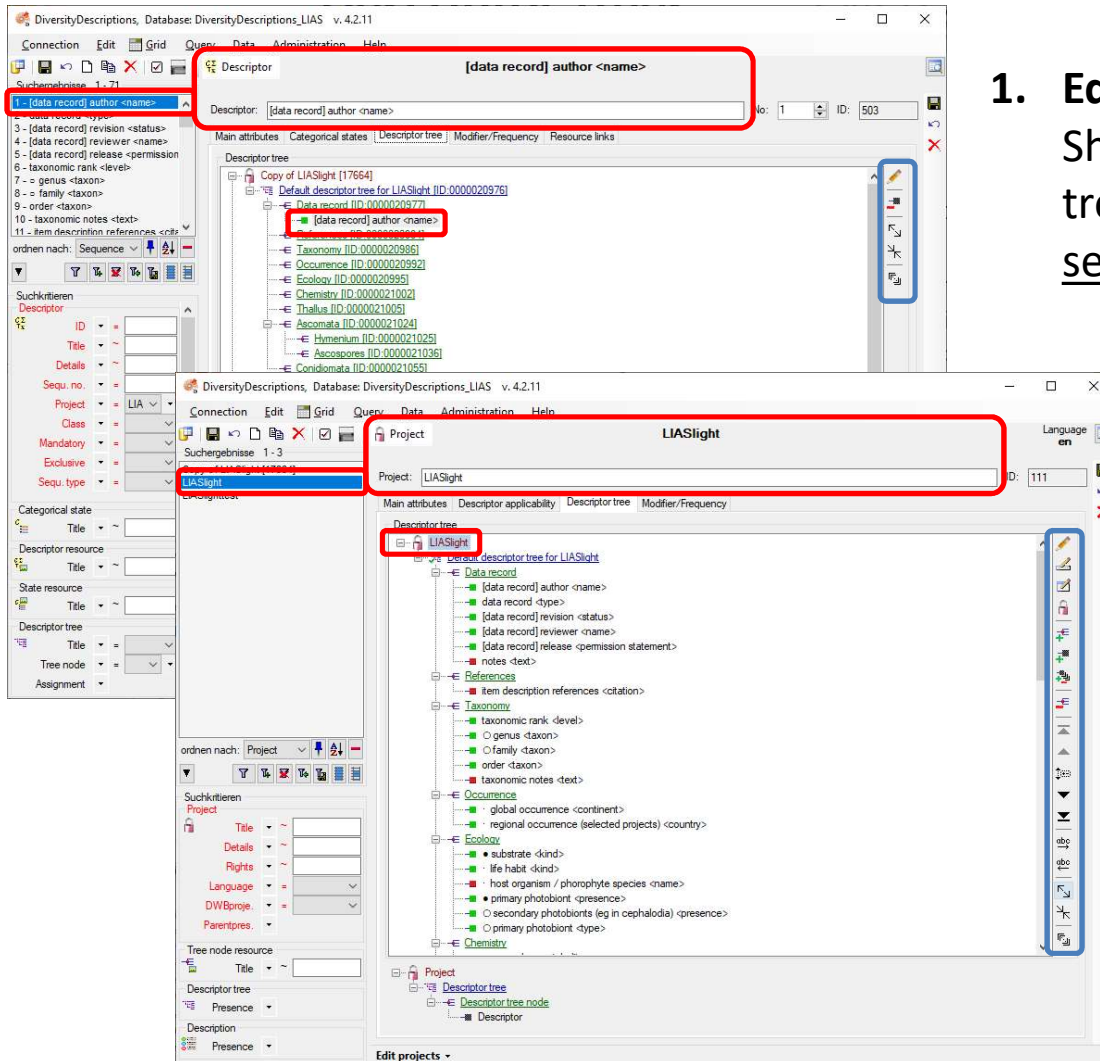
The screenshot shows the DiversityDescriptions software interface. The main window displays a descriptor tree for the project 'LIASlight'. The tree is structured as follows:

- LIASlight
 - Default descriptor tree for LIASlight
 - Data record
 - References
 - Taxonomy
 - Occurrence
 - Ecology
 - Chemistry
 - secondary metabolites <presence>
 - secondary metabolites <compound>
 - Triletes
 - Ascomata
 - Hymenium
 - [ascm, if apoth] margin excipular photobionts <presence, abundance>
 - [ascm, if apoth] subhymenial layers, hypothecium: [if perith] basal excipulum <colour (in H₂O)>
 - [ascm] paraphyses/-oids <presence>
 - [ascm] paraphyses/-oid cells width
 - [ascm] paraphyses/-oid apical cells width
 - [ascm] epihymenium, epithecium <colour (in H₂O)>
 - asci <dehiscence major type>
 - [asc] tholus <development>
 - [asc] tholus amyloidity (iodine reaction) <presence>
 - [asc] tholus amyloidity pattern <type>
 - Ascospores
 - ascospores <number per ascus>
 - [asp] shape <kind>
 - [asp] length
 - [asp] width

The 'Hymenium' and 'Ascospores' nodes are highlighted by a red oval in the screenshot. The interface also shows a search results pane on the left, a menu bar at the top, and various toolbars.

1. Assignment of descriptors to project
2. Assignment of allowed statistical measures, modifier and frequency values to descriptors
3. Structured grouping and selection of descriptors

Why is the control for descriptor trees available at two different places?



The image displays two screenshots of the Diversity Workbench software interface, illustrating the control for descriptor trees available at two different places.

1. Edit descriptors: Shows all projects and descriptor trees in the database where the selected descriptor is inserted.

2. Edit projects: Shows all descriptors of the selected project.

In **Edit projects** many powerful features for organizing descriptor trees are available.

File conversion

Tab separated lists

CollectionSpecimenID	Accession number	Taxon
CollectionSpecimenID	CollectionSpecimen	IdentificationUnit
CollectionSpecimenID	AccessionNumber	LastIdentificationCache
TO	TZ	

Import

CollectionSpecimenID	Accession number	Taxon
CollectionSpecimen	CollectionSpecimen	IdentificationUnit
CollectionSpecimenID	AccessionNumber	LastIdentificationCache
TO	TZ	

Export

XML file check

Import wizard

Matrix wizard

CSV export

List export

Questionnaires

DiversityDescriptions

DELTA import

SDD import

Cache database

Structured export

SDD import

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Deemy.xml

File tree

- Project: Deemy
 - Metadata
 - Descriptor trees
 - Descriptions
 - Alnihiza atroverucosa + Alnus
 - Alnihiza cana + Alnus
 - Alnihiza cremicolor + Alnus
 - Alnihiza cystidiobrunnea + Alnus
 - Alnihiza lilacina + Alnus
 - Alnihiza suffusa + Alnus
 - Alnihiza texta + Alnus
 - Alnihiza violacea + Alnus

Analysis settings

Default language: en

Import settings

Workbench project: Tutorial

Accept comma as decimal separator:

Create default descriptor tree:

Import trees for "natural language description":

Import trees without "role":

Analyse data

Descriptors

Descriptor trees

Descriptions

Abierhiza fascicularis + Abies

TextChar

literature references

Content

Haug I, Weber R, Oberwinkler F, Tschen J (1994) The mycorrhizal status of Taiwanese trees and the description of some ectomycorrhizal types. Trees 8: 237-

remarks public notes

Content

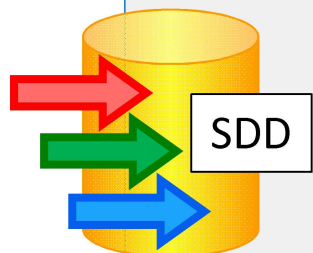
Mycorrhizal ends velvety; cells of middle mantle layers in plan view angular; mantle in ultrastructure with no matrix material in the middle region, hyphal walls inte

Quantitative

Start import

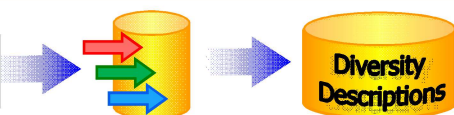
Import to database: DiversityDescriptions_Import

Analysis success



Source data

Accession	Species	Collector	Date	Locality	Notes
...



Import Delta

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Import\LiasLight

Encoding: Auto

Delta import

File tree | Advanced settings

- 初级共生藻 <存在>
- 第二共生藻 (例如在衣藻中) <存在>
- [03] - 绿藻门 - 桔色藻属, 桔色藻类
- 注释 - 衣藻
- Desc
- Manc
- Incompatible states
- Descriptions
- A
- <DALI-ID=1997; RLL-ID=23493>
- 15/6

Analysis settings

Default language: en - Englisch

Import settings

No update

To project

Create default descriptor tree

Analyse data

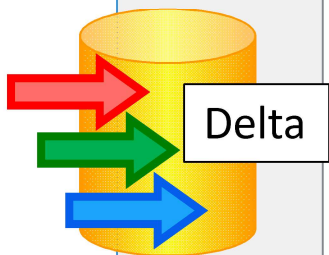
Absconditella celata Döbbele & Poelt

- Categorical
 - 属
 - 科
 - 全球分布
 - 基物
 - State
 - [06] - 土壤, 粘土, 腐殖土, 草坪, 碎石, 枯叶
 - [05] - 树木 - 枯木, 活木
 - 地衣体
 - [地衣体] 上表面
 - State
 - 绿色的 (浅绿色的)
 - 灰 (浅灰) 绿色的

Start import

Import to database: DiversityDescriptions_Import

Analysis error



Source data



Matrix wizard


- Simplified import of terminology and description items in one step
- Additional import wizards for descriptors, descriptions, resources
- Provides connection to conventional import wizards

Schedule for matrix import of tab-separated text files into DiversityDescri

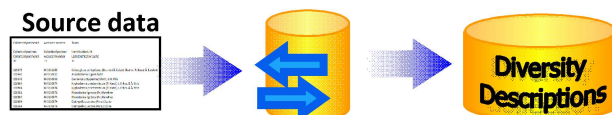
Target within DiversityDescriptions: **Description**

Encoding: ANSI

Type	0	1	2	3	4
	Categorical	Text	Categorical	Categorical	Quantitative
▶ 1	CSP	date	functional group	sublocation	biomass
2	CSP01	2008-05-15 00:0...	woody	NE_c	4.827
3	CSP01	2008-05-15 00:0...	woody	NW_c	28,20200000000...
4	CSP01	2008-05-15 00:0...	woody	SE_c	1.035
5	CSP01	2008-05-15 00:0...	woody	SW_c	2.561
6	CSP01	2008-05-15 00:0...	climber	NE_c	0
7	CSP01	2008-05-15 00:0...	climber	NW_c	4.539
8	CSP01	2008-05-15 00:0...	climber	SE_c	1.148
9	CSP01	2008-05-15 00:0...	climber	SW_c	0.078
10	CSP01	2008-05-15 00:0...	monocotyl herbs	NE_c	2.295
11	CSP01	2008-05-15 00:0...	monocotyl herbs	NW_c	0



Matrix
Wizard



Data export

File name: D:\Subversion\Projekte\DiversityDescriptions\bin\Debug\Export\DiversityDescriptions_Import_BactDescDSMZ

Export project: **BactDescDSMZ**

- Inclusion of data from other DWB module possible (e.g. DiversityProjects)
- Selection of export language for multilingual databases
- Individual options for each export format available

Options:

- Export withheld data
- Hide withheld descriptor
- Read external data
- Check strings for illegal characters
- Include resources

Write EML

- EML settings
- Generate file **eML**

Write Delta

- Compatible
- Delta settings
- Generate file **Delta**

Write SDD

- Compatible
- SDD settings
- Generate file **SDD**

Export from database: **DiversityDescriptions_Import** Analysis success



Matrix wizard

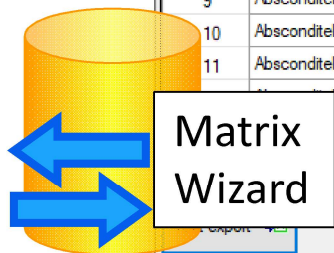
- Simplified export of terminology and description items
- Generates mapping data and import schema for re-import
- Provides state selection by text or ordinal numbers
- Allows easy re-import of modified data with Matrix Import Wizard

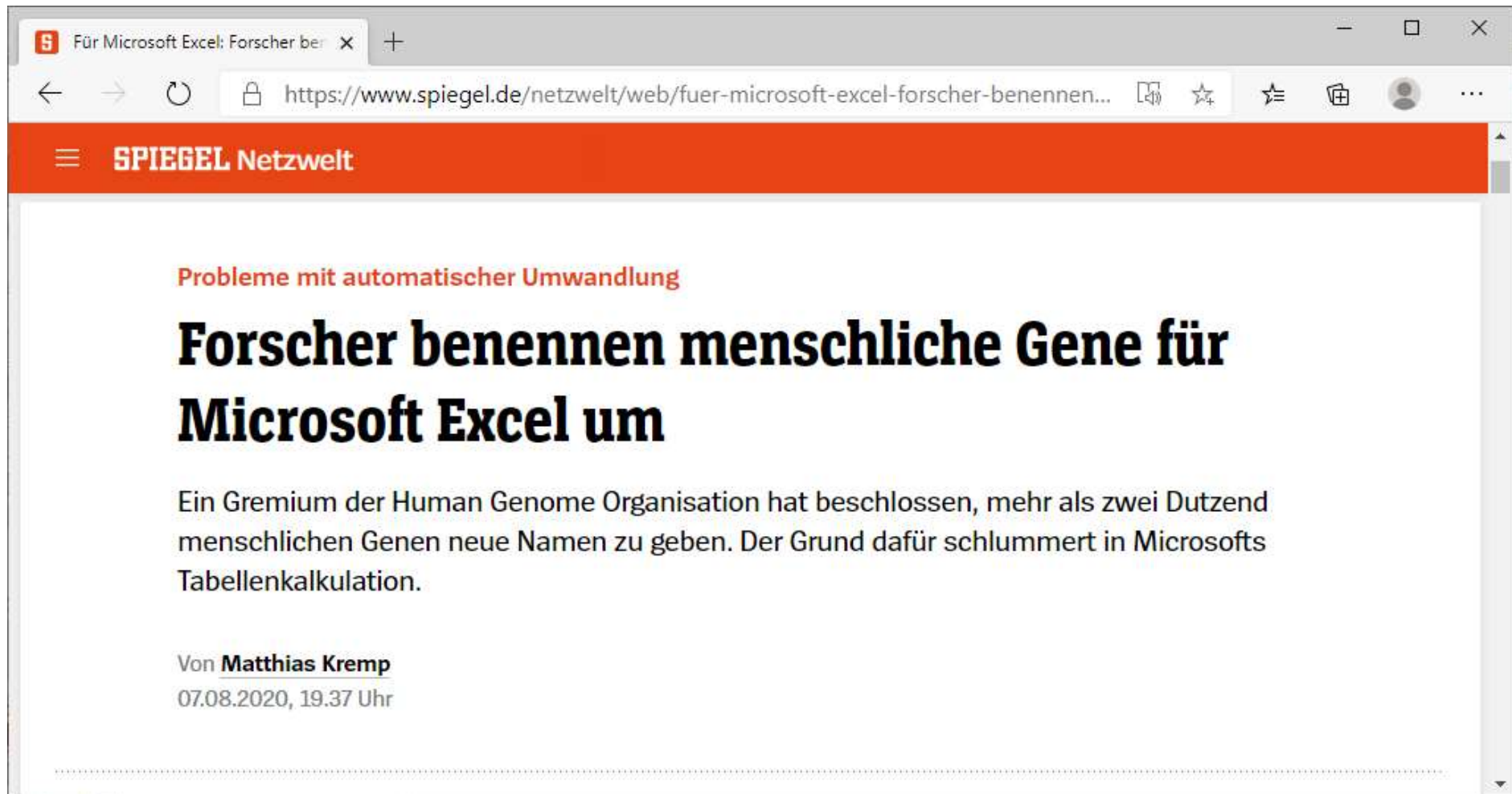
		[data record] aut...	data record <type>	[data record] revi...	[data record] revi...	[data record] rele...	taxonomic rank <l...	genus <taxon>	of
		503	510	516	520	526	529	535	163
4	Absconditella am...	12561	7	2	1	2	2	2	125
5	Absconditella an...	16341	7	2	1	2	2	2	125
6	Absconditella ant...	15460	7	2	1	2	2	2	125
7	Absconditella cel...	12261	3	2	1	2	2	2	125
8	Absconditella del...	10099	4	2	2	5	2	2	125
9	Absconditella du...	17088	6	2	1	2	2	2	125
10	Absconditella fos...	17089	6	2	1	2	2	2	125
11	Absconditella lign...	12464	2	2	2	2, 5	2	2	125
	la pa...	7440	3	2	2	5	2	2	125
	la sph...	7441	4	2	2	5	2	2	125
	stufi	7442	4	2	2	5	2	2	125

Export from database: DiversityDescriptions_LIAS

Export aborted

Start export





Für Microsoft Excel: Forscher be... x +

← → ↻ 🔒 <https://www.spiegel.de/netzwelt/web/fuer-microsoft-excel-forscher-benennen...> 📄 ☆ ⌘ 👤 ...

☰ **SPIEGEL** Netzwelt

Probleme mit automatischer Umwandlung

Forscher benennen menschliche Gene für Microsoft Excel um

Ein Gremium der Human Genome Organisation hat beschlossen, mehr als zwei Dutzend menschlichen Genen neue Namen zu geben. Der Grund dafür schlummert in Microsofts Tabellenkalkulation.

Von **Matthias Kremp**
07.08.2020, 19.37 Uhr

- Beware of automatic conversions!
- Prefer text type for columns when opening the tab-separated text files!

