



TaxonTableTools tutorial

Version 1.2.0

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TaxonTableTools tutorial

Tutorial data set will soon be available at:

- <https://github.com/TillMacher/TaxonTableTools>

Tutorial data:

- Macrozoobenthos kick-samples from 4 streams Germany
- DNA-metabarcoding data
 - Read table, produced with JAMP (<https://github.com/VascoElbrecht/JAMP>)
 - Taxonomy table, produced with BOLDigger (Buchner & Leese, in review)
- 12 samples
- 5 locations



Getting started with TTT



Install TaxonTableTools:

- <https://github.com/TillMacher/TaxonTableTools>

Installation short guide (see manual for more details):

- Install TaxonTableTools via pip:

```
$ pip3 install taxontabletools
```

- TaxonTableTools can then be started via:

```
$ python3 -m taxontabletools
```

- Updates can be installed via:

```
$ pip3 install --upgrade taxontabletools
```

Updates version 1.2.0



Major update:

- The identifier "IDs" was changed to "ID" in the TaXon table header!
 - Please adjust old TaXon tables accordingly!
 - Otherwise TTT will crash!

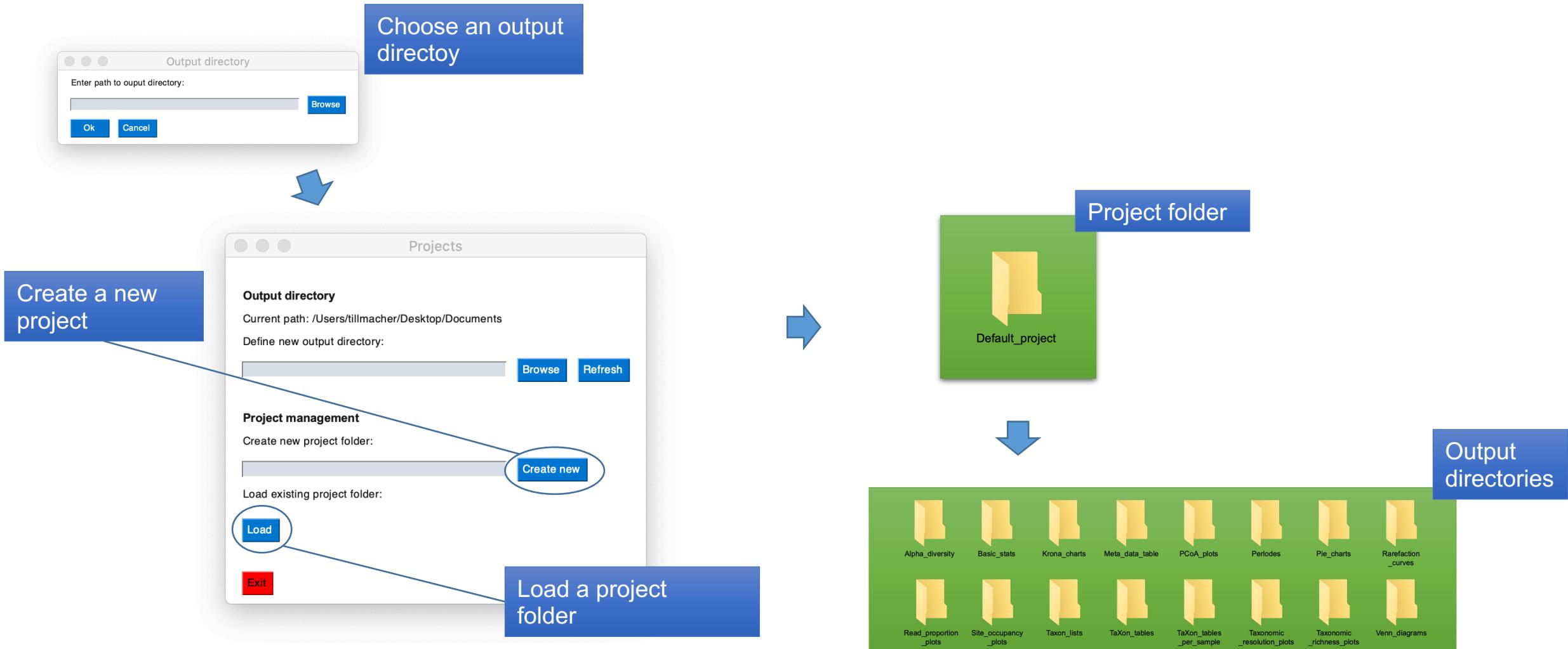
New features:

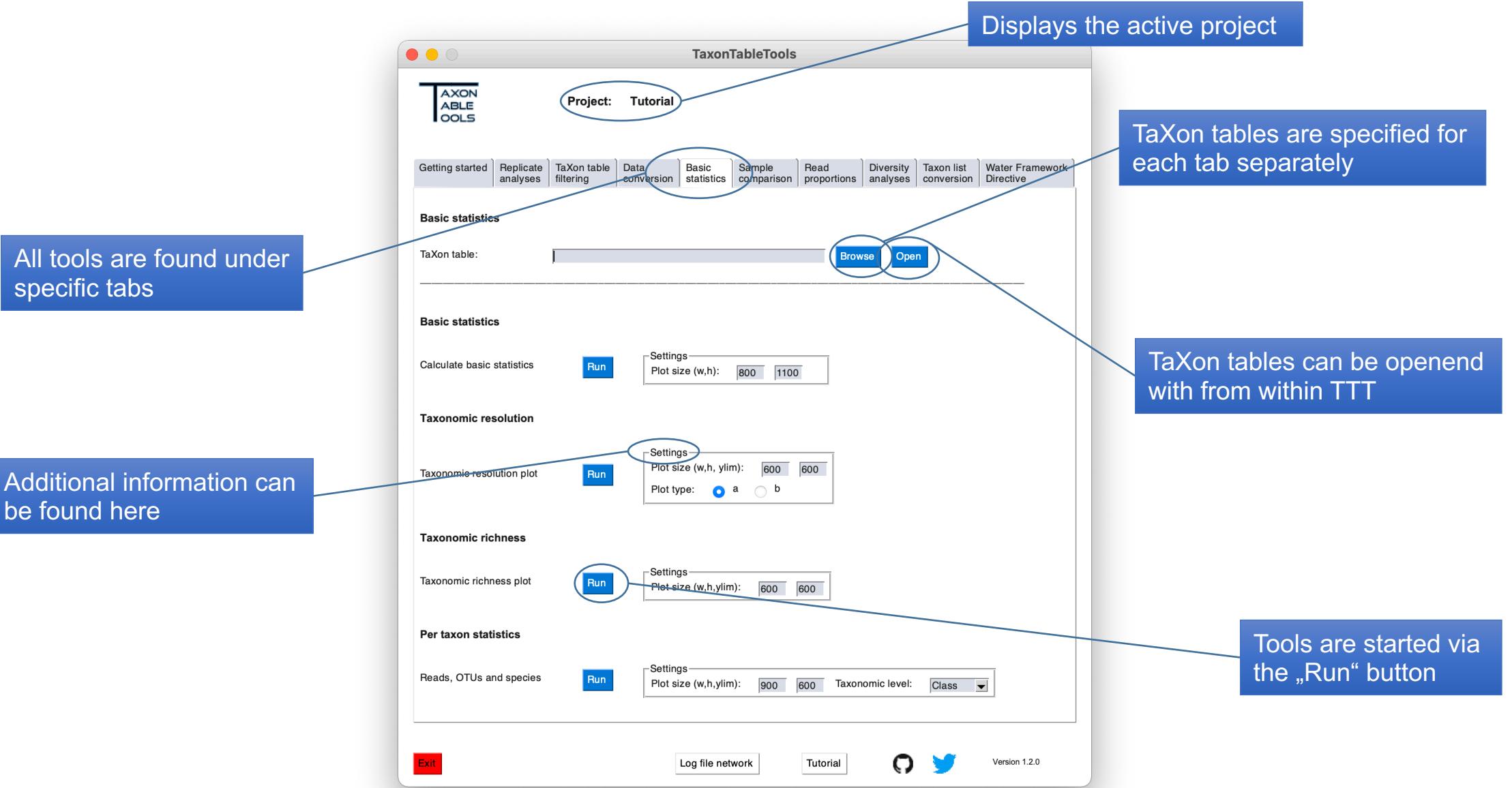
- Metadatables can now directly be adjusted from within TTT.
- Browsing TaXon tables will directly show the current project folder.
- The OTU prompt is more relaxed. Hash OTUs are accepted now.
- Qiime2 feature tables can now be converted to the TTT format.
- Additional options for customizing colors have been added.
- Font sizes can now be adjusted.
- Diversity and ordination analyses can now be performed on different taxonomic levels.
- Diversity and ordination analyses automatically transform data to boolean values.
Thus, also non presence/absence converted tables can be used.
- Moved various options to drop down menus.

Bug fixes:

- Fixed "shared OTUs" tool. More than 3 replicates are now supported.
- Changed x-axis value to read proportions in the per taxon analysis.
- Added missing package 'statsmodels' to installation.

Project management



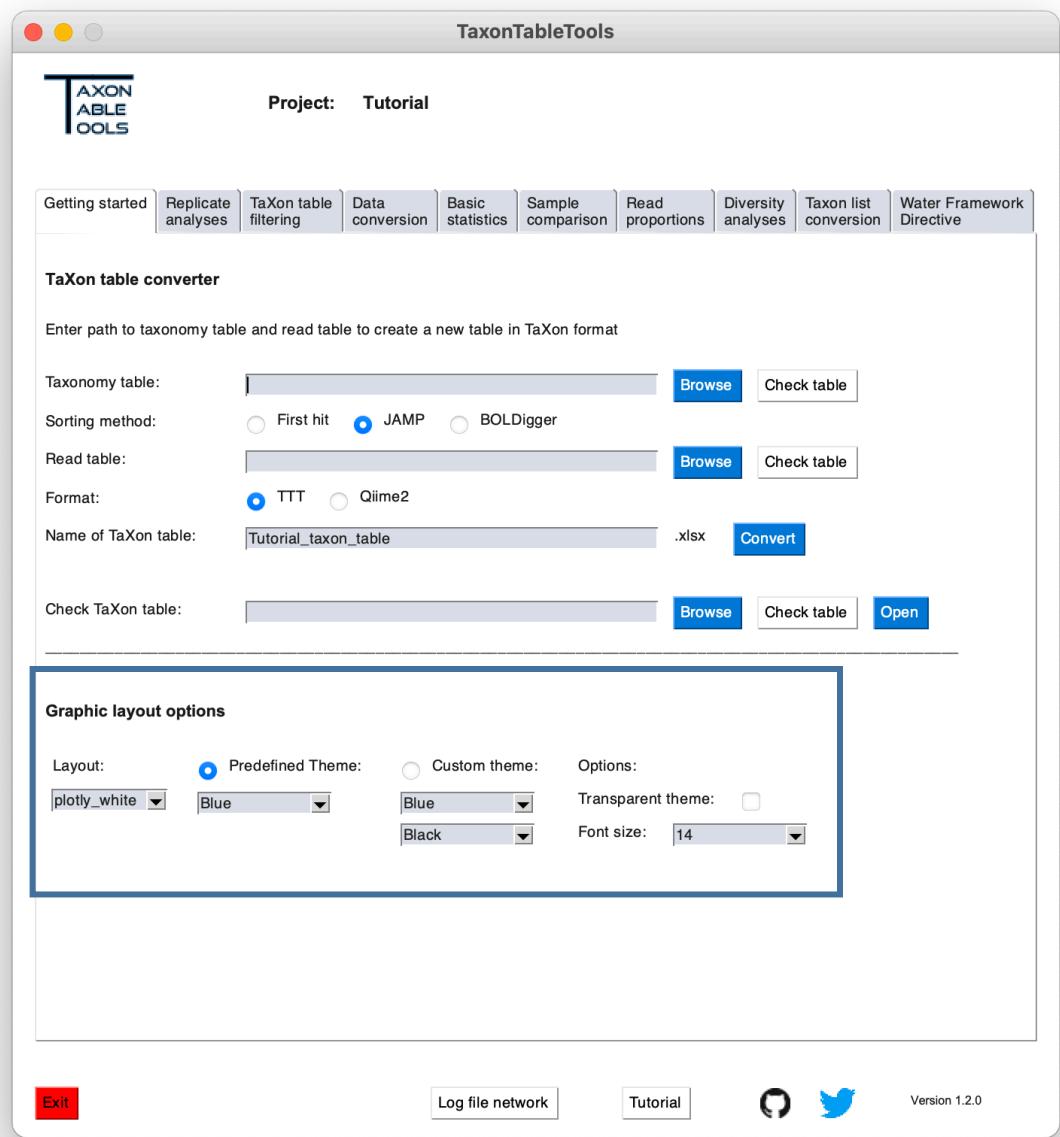


Individual styling

TTT allows the user to individualise the graphics layout

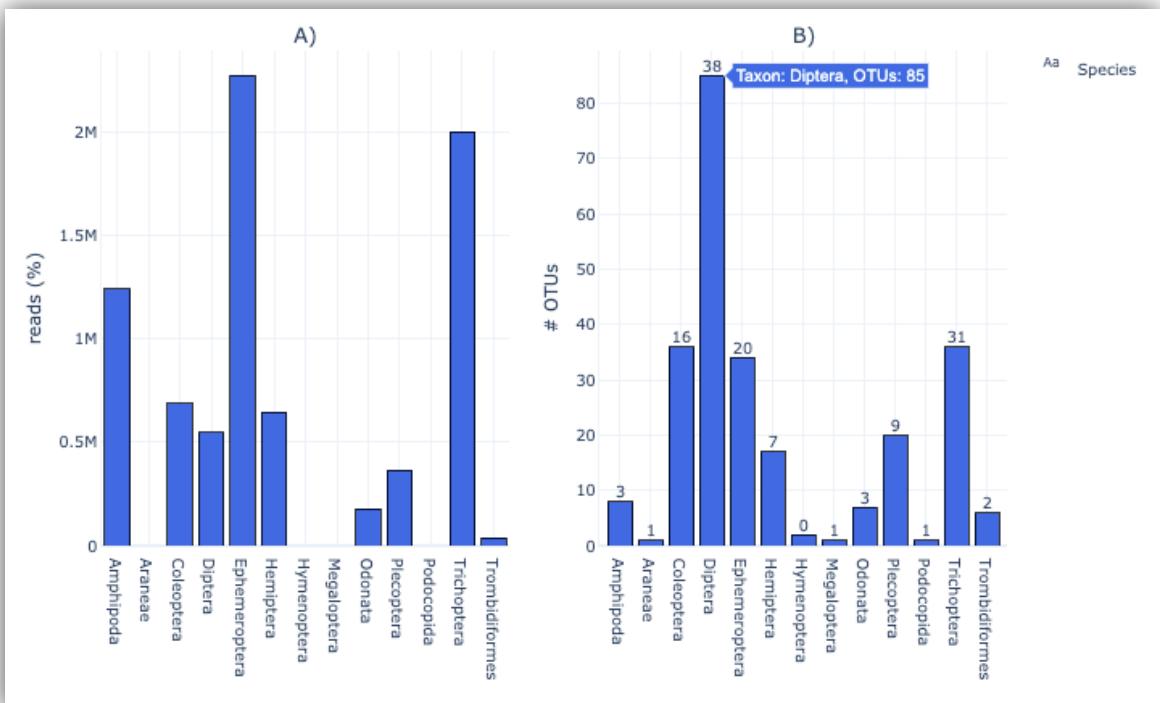
1. Choose a layout template
 - Several well known and widely used plot layouts are available such as “ggplot2” or “seaborn”
2. Choose a colour theme
 - Several pre-defined themes are available
 - Custom primary and secondary colours can be selected
3. Select transparency
 - This will return slightly transparent bars/scatters
4. Choose a font size (default is 14)

The layout options will be applied to every plot that is generated with TTT in this session

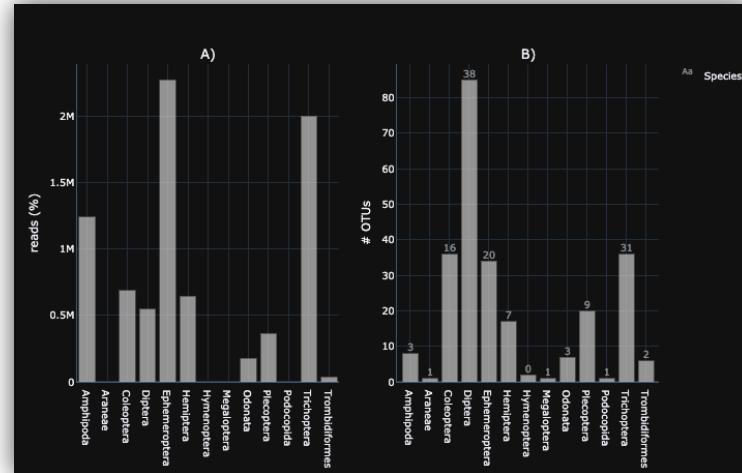


Individual styling

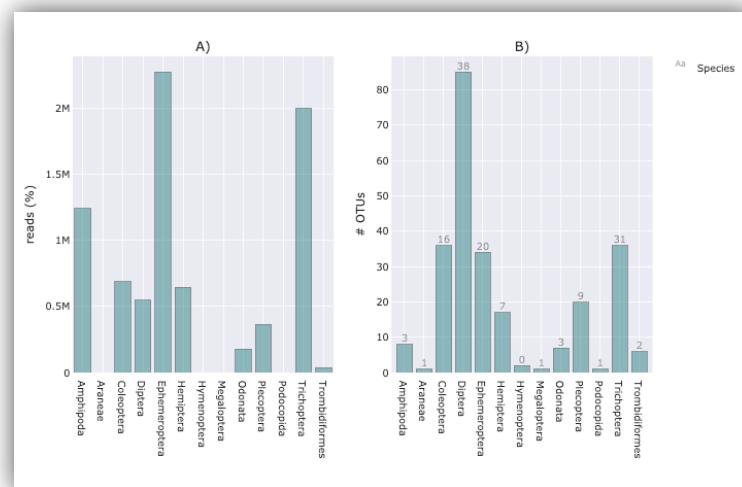
TTT standard



Plotly dark



Seaborn

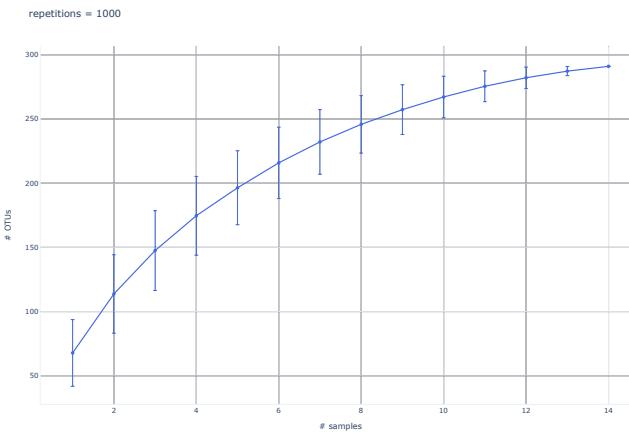


Plot formats

TTT exports plots into two different formats

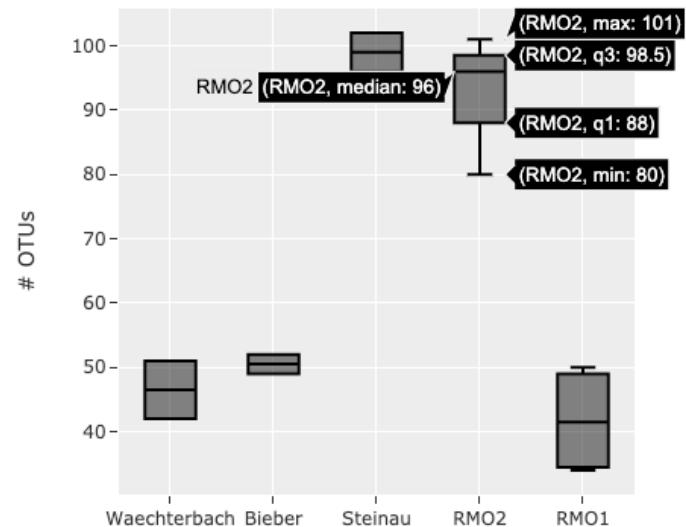
PDF

- Universal format for all kinds of graphics and documents
- These vector-based figures can be imported into any vector-editing software, such as Inkscape or Adobe Photoshop



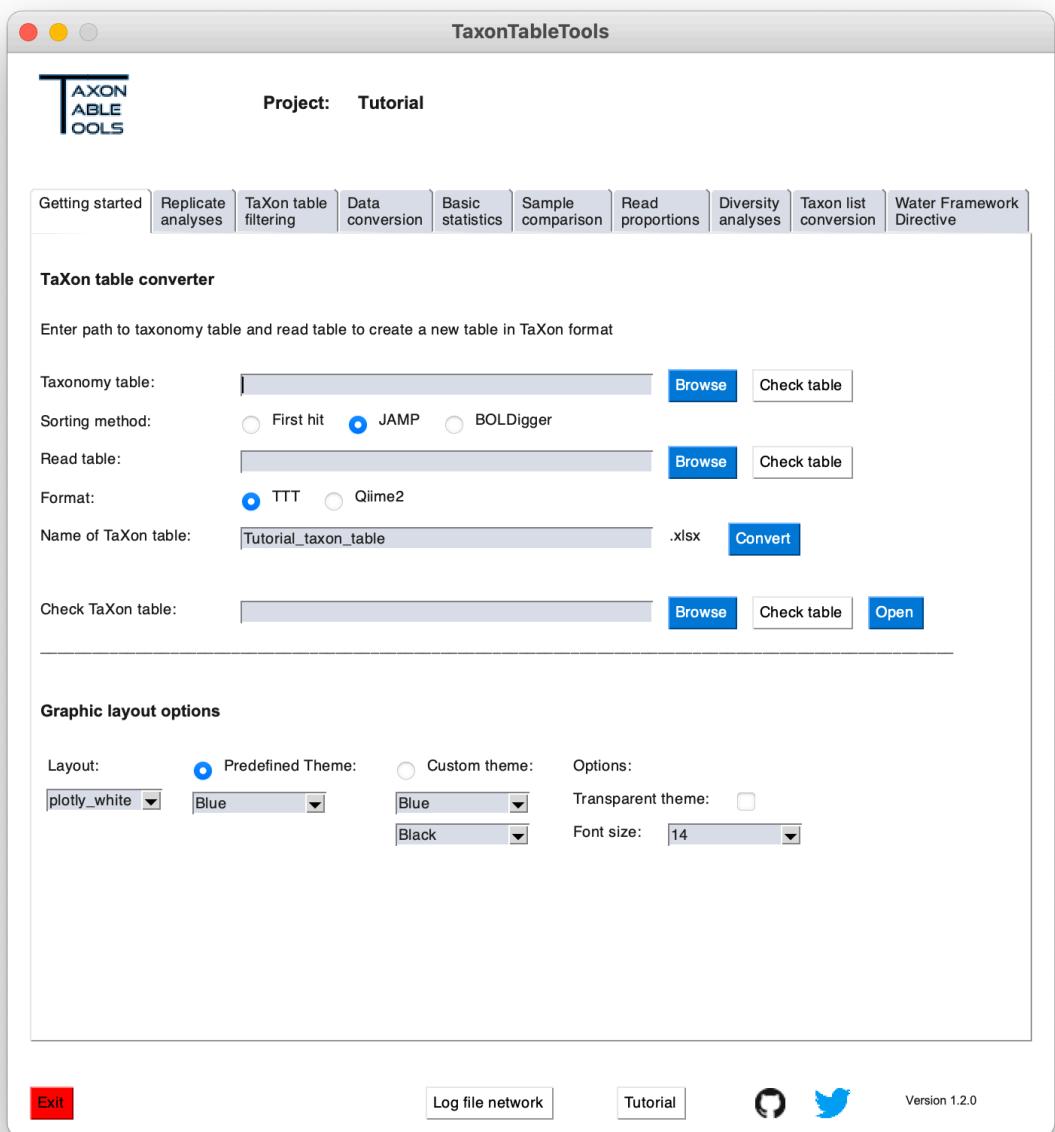
HTML

- This format can be read by any browser and is interactive
- The hovering-mode allows the user to explore the data presented within the plot



Getting started

- TaxonTableTools is based on two table formats
 - **Read table**, containing the read numbers of each OTU for each sample
 - **Taxonomy table**, containing the taxonomic assignment of each OTU
- These two tables are converted to one table, which is called “**TaXon table**”
- TaXon tables can also be manually created. If so, it is recommended to check the table for the correct format



Read table format – TTT

ID = column for OTU names

Sample names

Sequences = Sequence of each OTU

ID	Gelnhaus	Gelnha	NC_3	NC_1	NC_2 Sequences																										
OTU_1	0	0	73207	22730	54200	43835	89624	63425	80866	70832	26398	46747	56074	71498	0	0	86	0	23053	28499	21823	25719	22600	33354	18810	5350	0	0	75	55	21 GCGAATAAACATAATAAGAT
OTU_2	0	0	0	0	0	0	0	0	0	0	41041	57516	88458	99815	41	48	49	0	46993	52009	44050	51310	18689	29448	29758	8091	0	0	26	16	44 ACGTATAAAATAATATAAGAT
OTU_3	53646	15508	33964	10729	25656	19125	49195	32809	39980	34996	0	0	50	0	18291	24758	13192	31439	0	0	77	0	42	0	0	0	57249	19272	23	20	8 TCGTATAACACAACATAAGTT
OTU_4	0	0	0	0	0	0	0	0	0	0	27	0	0	0	6274	8381	4258	9421	35463	47156	31682	44662	38748	63461	34817	9647	0	0	2	5	24 ACGTATAAAATAATATAAGAT
OTU_5	0	0	11973	3177	11359	9177	73973	51333	65807	56794	0	0	0	0	10200	14540	10731	15357	0	0	109	0	86	0	0	0	0	0	13	17	12 TCGTATAAAATAATATAAGTT
OTU_6	39207	10829	21049	6366	18016	12879	0	0	0	86	131	408	453	31828	48688	24126	49884	2945	3774	2471	3074	5791	9285	6829	1676	37316	11656	29	0	0 GCGTATAAAATAATATAAGAT	
OTU_7	0	0	62378	20734	49093	38967	116063	77682	104454	91712	0	26	244	227	4333	6172	3193	7527	0	0	156	0	145	0	0	0	0	0	52	37	19 TCGTATAAAATAATATGAGTT
OTU_8	0	0	18676	6494	15541	11147	19816	13139	18987	17344	1538	2931	3681	4379	49129	72566	35137	84142	7007	9031	5739	8512	3644	6297	4722	938	0	0	17	7 0 CCGAATAAAATAATTAAAGAT	
OTU_9	17276	6379	8560	3516	11541	9605	7458	5876	6530	6368	0	0	40	0	27716	37258	18536	42260	0	0	0	0	95	173	158	75	33304	13444	17	1	2 CGAATAAAATACTAAAGATT
OTU_10	0	0	0	0	0	0	0	0	0	0	18072	29251	49125	58873	0	0	0	0	0	0	0	0	0	0	0	0	0	6	0	0 TCGTTAAACAATATGAGAT	
OTU_11	660	241	6079	1976	5030	3639	27135	20581	27303	24440	1755	2822	6554	6831	5757	7926	3241	7903	0	0	35	0	34	0	0	0	739	239	8	4	8 TCGAATAAAACAACATAAGAT
OTU_12	110	29	0	0	0	0	0	0	0	0	30	0	0	0	0	0	0	0	1521	2046	1327	1807	27058	41626	61287	16205	0	0	0	5	ACGGTTAAATAATTAAAGAT
OTU_13	39711	12454	0	0	0	0	0	0	0	0	0	0	0	0	559	721	248	591	0	0	0	0	0	0	0	0	0	1	0	0 TCGAATAAAATAATAAGAT	
OTU_14	34624	11075	0	0	0	0	0	0	0	0	0	0	0	0	36	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0 TCGAATAAAATAATAAGAT	
OTU_15	14166	4301	72605	24710	65920	52451	92	43	0	0	0	0	0	0	0	0	90	0	0	0	0	0	0	0	0	0	0	1	0	0 CCGTATAAAATAATATAAGAT	
OTU_16	0	0	0	0	0	0	0	0	0	0	804	1276	2033	2722	16843	25479	16320	29378	0	0	0	0	0	0	0	0	0	0	0 ACGTTTAAATAACATGAGAT		
OTU_17	79829	22784	1239	416	719	569	0	0	0	0	0	55	0	58	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0 CCGTATAAAATAACATAAGAT		
OTU_18	0	0	7618	2373	3736	2857	25430	17893	21917	19472	0	0	0	0	0	0	0	0	0	36	0	38	0	0	0	0	0	3	8 3 ACCAATAAAATAATAAGAT		
OTU_19	26395	7874	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0 TCGGTTAAATAACATAAGCT		
OTU_20	161	59	18638	6161	10551	7952	11237	8003	11984	10163	0	0	0	0	8912	12336	5971	14362	0	0	0	0	14	0	0	0	161	54	16	2	1 ACCAATAAAATAATATAAGAT

Read abundances

Read table format – Qiime2

Create a feature table (.tsv format) in qiime2 using:

```
$ qiime metadata tabulate  
$ qiime tools extract
```

Sample names

Sequence = Sequence
of each OTU

id	Gelnhausen_#q2:types	Gelnhausen_numeric	Gelnhausen_numeric	NC_3	NC_1	NC_2	Sequence										
	numeric	numeric	numeric	numeric	numeric	numeric	categorical										
OTU_1	0	0	73207	22730	54200	43835	89624	63425	80866	70832	26398	0	75	55	21	GCGAAATAAACATAAGATTTGACTTTACCCCTTCCCTAACACT	
OTU_2	0	0	0	0	0	0	0	0	0	0	41041	0	26	16	44	ACGTATAAATAATATAAGATTTGATTATTACCTCCCTCATTAACATT	
OTU_3	53646	15508	33964	10729	25656	19125	49195	32809	39980	34996	0	0	23	20	8	TCTGATAAACACATAAGTTGGTTATTGCCCTCTTAAACACT	
OTU_4	0	0	0	0	0	0	0	0	0	0	27	0	2	5	24	ACGTATAAATAATATAAGATTTGGCTTACCCCTCTTCTTACCTT	
OTU_5	0	0	11973	3177	11359	9177	73973	51333	65807	56794	0	0	13	17	12	TCGTATAAATAATATAAGATTTGATTATTGCCCTCGGCTTGACCTT	
OTU_6	39207	10829	21049	6366	18016	12879	0	0	0	0	86	0	29	0	0	0	CGGTATAAATAATATAAGATTTGACTACTTCTCTGCTTAAACACT
OTU_7	0	0	62378	20734	49093	38967	116063	77682	104454	91712	0	0	52	37	19	TCGTATAAATAATATGAGTTCTGGTTATTGCCACCTTCTTGACACT	
OTU_8	0	0	18676	6494	15541	11147	19816	13139	18987	17344	1538	0	17	7	0	CCGAATAATAATTAAAGATTTGATTCTCCCTCTTCTAGCTTC	
OTU_9	17276	6379	8560	3516	11541	9605	7458	5876	6530	6368	0	0	17	1	2	CGAATAATAATCTAAGATTTGATTTCACCCCTCTAATATTT	
OTU_10	0	0	0	0	0	0	0	0	0	0	18072	0	6	0	0	0	TCGTATAAACAATATGAGATTTGGTTATTGCCCTCTGCTTGCATT
OTU_11	660	241	6079	1976	5030	3639	27135	20581	27303	24440	1755	0	8	4	8	TCGAATAAACATAAGATTTGACTCTTCCCTCACTATCTC	
OTU_12	110	29	0	0	0	0	0	0	0	0	30	0	0	0	5	ACGGTTAAATAATTAAAGATTTGGCTTACCTATAGCTATGCTT	
OTU_13	39711	12454	0	0	0	0	0	0	0	0	0	0	1	0	0	0	TCGAATAATAATATAAGATTTGATTATTACCTCCGTATTAAATT
OTU_14	34624	11075	0	0	0	0	0	0	0	0	0	0	0	0	0	0	TCGAATAATAATATAAGATTTGATTATTACCTCCATATTAAATT
OTU_15	14166	4301	72605	24710	65920	52451	92	43	0	0	0	0	51	1	0	0	CCGTATAAATAATATAAGATTTGACTCTCCCTCCACTAAATCTA
OTU_16	0	0	0	0	0	0	0	0	0	0	804	0	1	0	0	0	ACGTTTAAATAACATGAGATTTGACTCTGCTTCCCTTAATTCT
OTU_17	79829	22784	1239	416	719	569	0	0	0	0	0	0	2	0	0	0	CCGTATAAATAACATAAGATTTGACTCTCCCACCCGACTAAATTT
OTU_18	0	0	7618	2373	3736	2857	25430	17893	21917	19472	0	0	3	8	3	ACGAATAATAATATAAGATTTGACTCTACCCCATCTTAACCTA	
OTU_19	26395	7874	0	0	0	0	0	0	0	0	0	0					
OTU_20	161	59	18638	6161	10551	7952	11237	8003	11984	10163	0	0					

id = column for
OTU names

Read abundances

Taxonomy table format

ID = column for OTU names

Taxonomic level column:
Phylum to Species

Species name should consist of
the genus name and epithet

ID	Phylum	Class	Order	Family	Genus	Species	Similarity	Status
OTU_1	Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus pulex	100	Published
OTU_2	Arthropoda	Insecta	Hemiptera	Aphelocheiridae	Aphelocheirus	Aphelocheirus aestivalis	100	Private
OTU_3	Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis rhodani	100	Published
OTU_4	Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus roeselii	100	Published
OTU_5	Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Ecdyonurus	Ecdyonurus torrentis	100	Private
OTU_6	Arthropoda	Insecta	Ephemeroptera	Ephemeridae	Ephemerida	Ephemerida danica	100	Published
OTU_7	Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis rhodani	99,74	Published
OTU_8	Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche pellucidula	100	Published
OTU_9	Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche siltalai	100	Published
OTU_10	Mollusca	Gastropoda	Littorinimorpha	Tateidae	Potamopyrgus	Potamopyrgus antipodarum	100	Published
OTU_11	Arthropoda	Insecta	Coleoptera	Elmidae	Limnius	Limnius volckmari	100	Private
OTU_12	Mollusca	Bivalvia	Venerida	Cyrenidae	Corbicula	Corbicula fluminea	100	Published
OTU_13	Arthropoda	Insecta	Trichoptera	Odontoceridae	Odontocerum	Odontocerum albicorne	100	Published
OTU_14	Arthropoda	Insecta	Trichoptera	Odontoceridae	Odontocerum	Odontocerum albicorne	100	Published
OTU_15	Arthropoda	Insecta	Trichoptera	Limnephilidae	Chaetopteryx	Chaetopteryx fusca	100	Published
OTU_16	Annelida	Clitellata	Haplotaxida	Lumbricidae	Eiseniella	Eiseniella tetraedra	100	Private
OTU_17	Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostoma	Sericostoma personatum	100	Published
Accepted sheet names:								
- JAMP hit								
- BOLDigger hit								
- First hit								

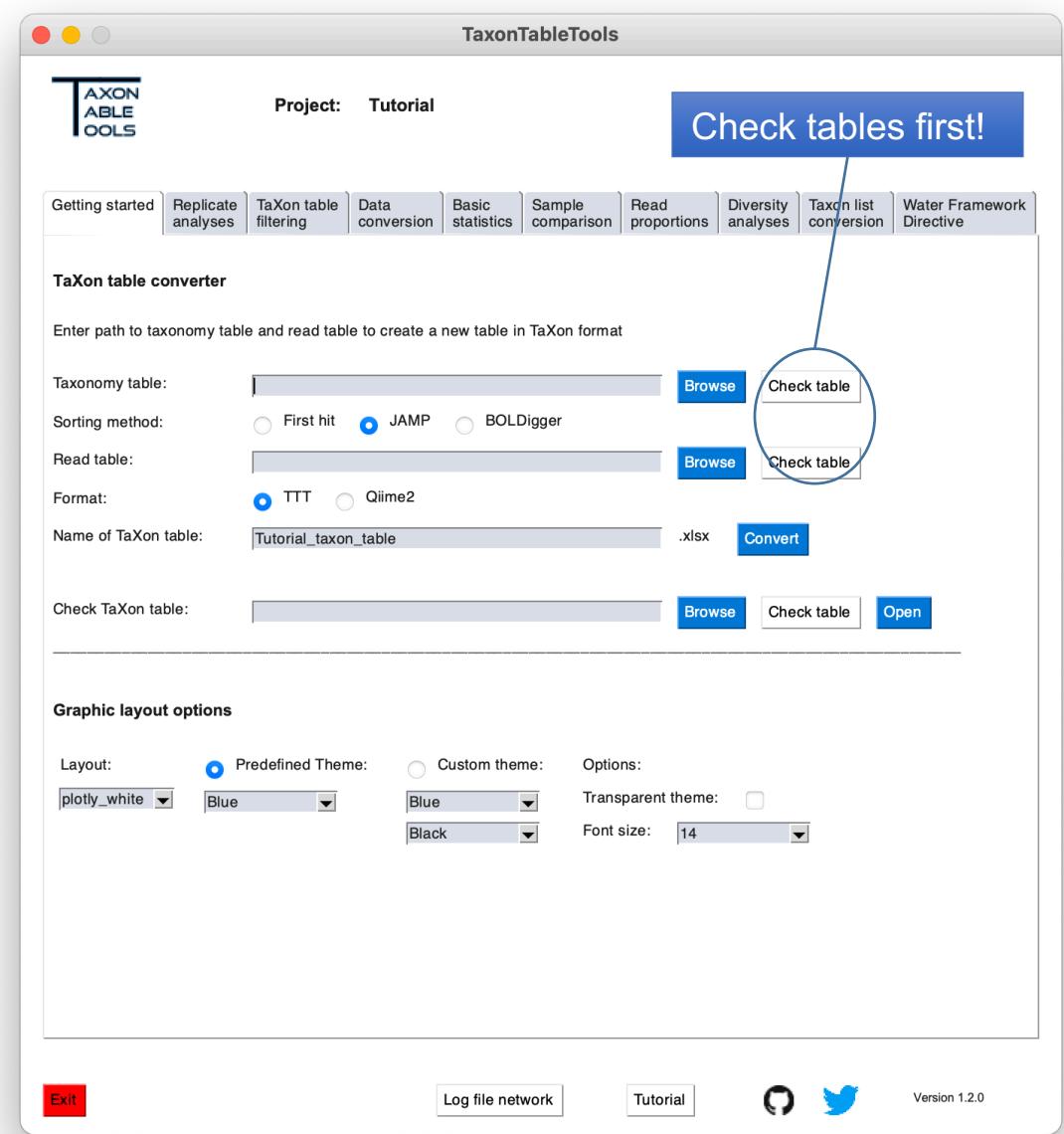
Database hit similarity

Database status

Getting started

TaXon table converter:

1. Browse both tables
2. Check the taxonomy table format
3. Check the read table format
4. Choose a name for the new TaXon table
 - For the tutorial: *TTT* (.xlsx)
5. Convert the tables



Replicate analysis

Load the TaXon table

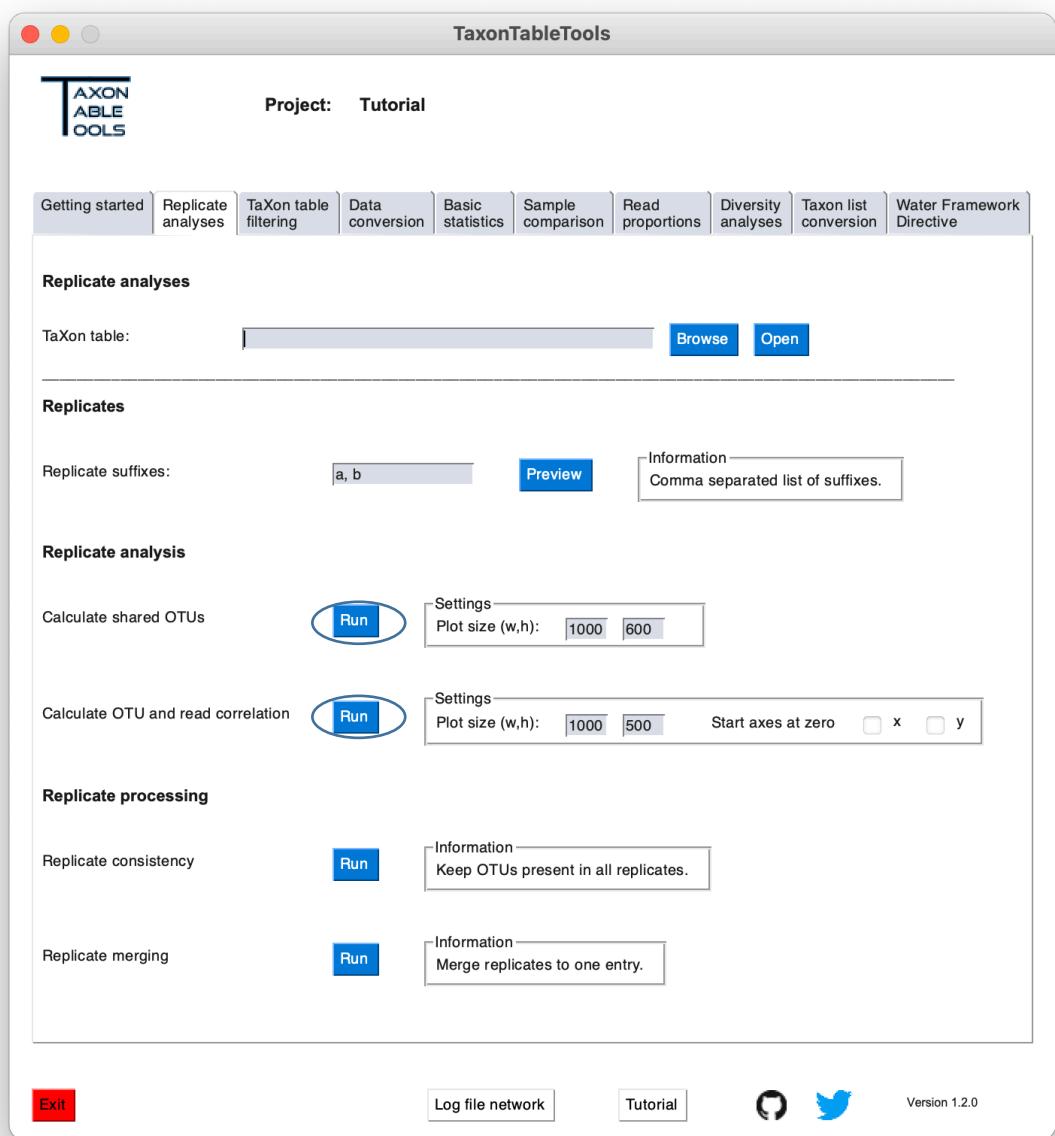
- First load the previously created raw TaXon table (*TTT.xlsx*) by clicking browse

Replicate input format

- Now type the replicate indicators (here: a, b)
- Press „Preview“ to show an example
- When merged the sample will be renamed to „_comb“

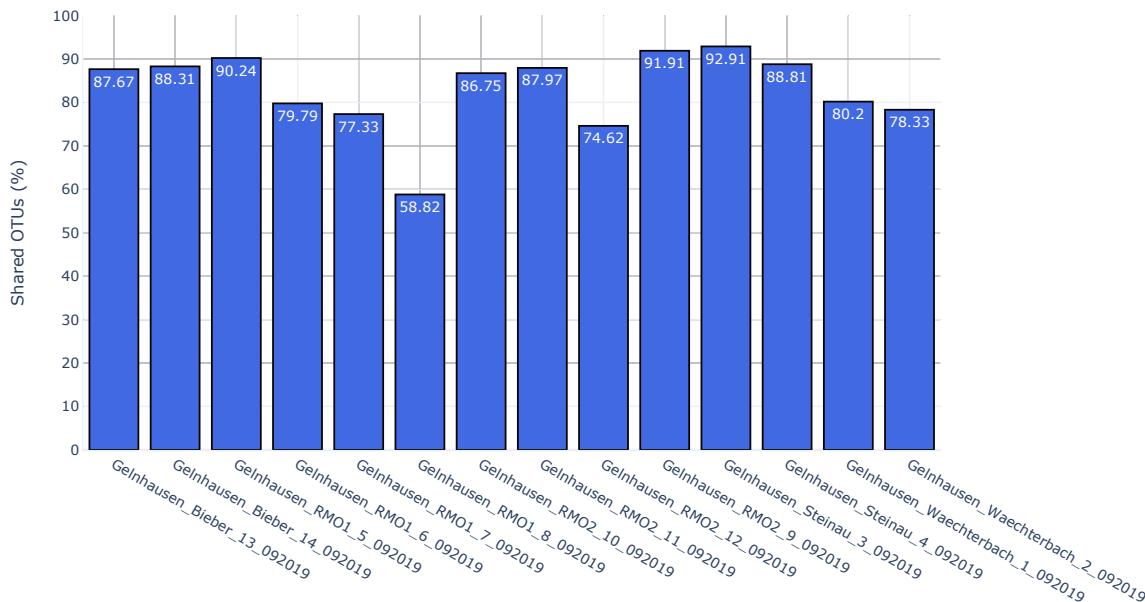
Replicate analysis

- Calculate the shared OTUs between samples
- Calculate the correlation of OTUs and reads between the replicates. This analysis is based on Spearman correlations

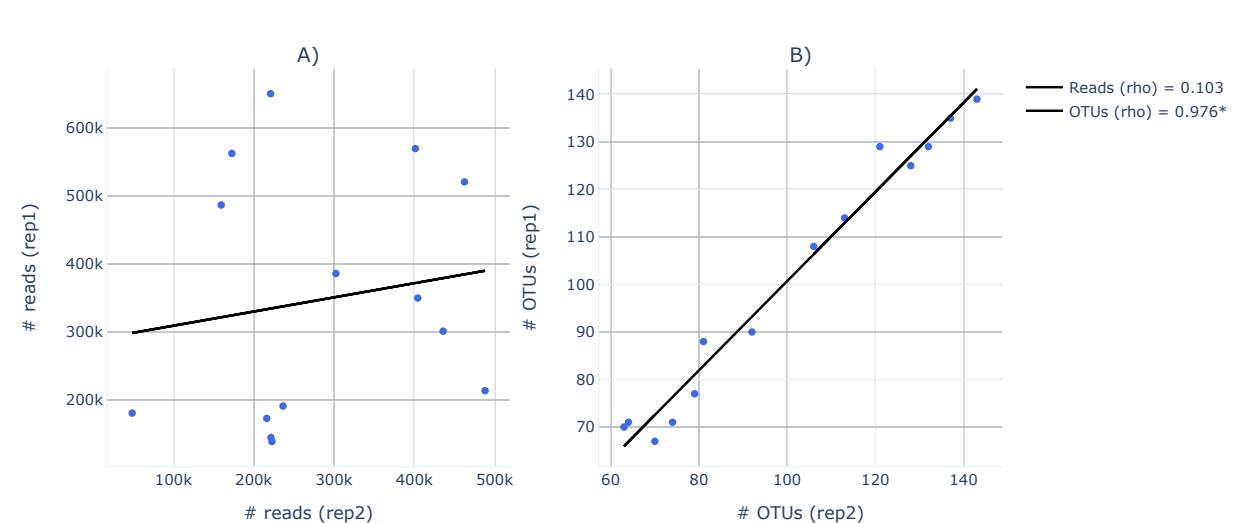


Replicate analysis

Shared OTUs between PCR replicates



Spearman correlation between PCR replicates



Replicate processing

Replicate consistency

- Now it is time to only keep OTUs that are present in both (PCR) replicates
- Run the replicate consistency module
- A new table named *TTT_cons.xlsx* was created

IDs	S1_a	S1_b
OTU_1	1230	2310
OTU_2	233	0
OTU_3	0	95



IDs	S1_a	S1_b
OTU_1	1230	2310
OTU_2	0	0
OTU_3	0	0

The screenshot shows the TaxonTableTools software window titled "TaxonTableTools". The "Project: Tutorial" tab is selected. In the top navigation bar, the "Replicate analyses" tab is highlighted. Below the tabs, there are several sections: "Replicate analyses" (with a "TaXon table:" input field and "Browse" and "Open" buttons), "Replicates" (with a "Replicate suffixes:" input field containing "a, b" and a "Preview" button), "Replicate analysis" (with "Calculate shared OTUs" and "Settings" for plot size w,h: 1000, 600), and "Replicate processing" (with "Replicate consistency" and "Replicate merging" sections, each having a "Run" button and an associated information box). At the bottom, there are "Exit", "Log file network", "Tutorial", social media icons for GitHub and Twitter, and the text "Version 1.2.0".

Replicate processing

Replicate merging

- Now load the previously created consistency filtered TaXon table (*TTT_cons.xlsx*)
- Reminder: Each module creates a new table! So, don't forget to always load the latest table**
- Now we want to merge both replicates of all samples
- A new table named *TTT_cons_derep.xlsx* was created

IDs	S1_a	S1_b
OTU_1	1230	2310
OTU_2	0	0
OTU_3	0	0



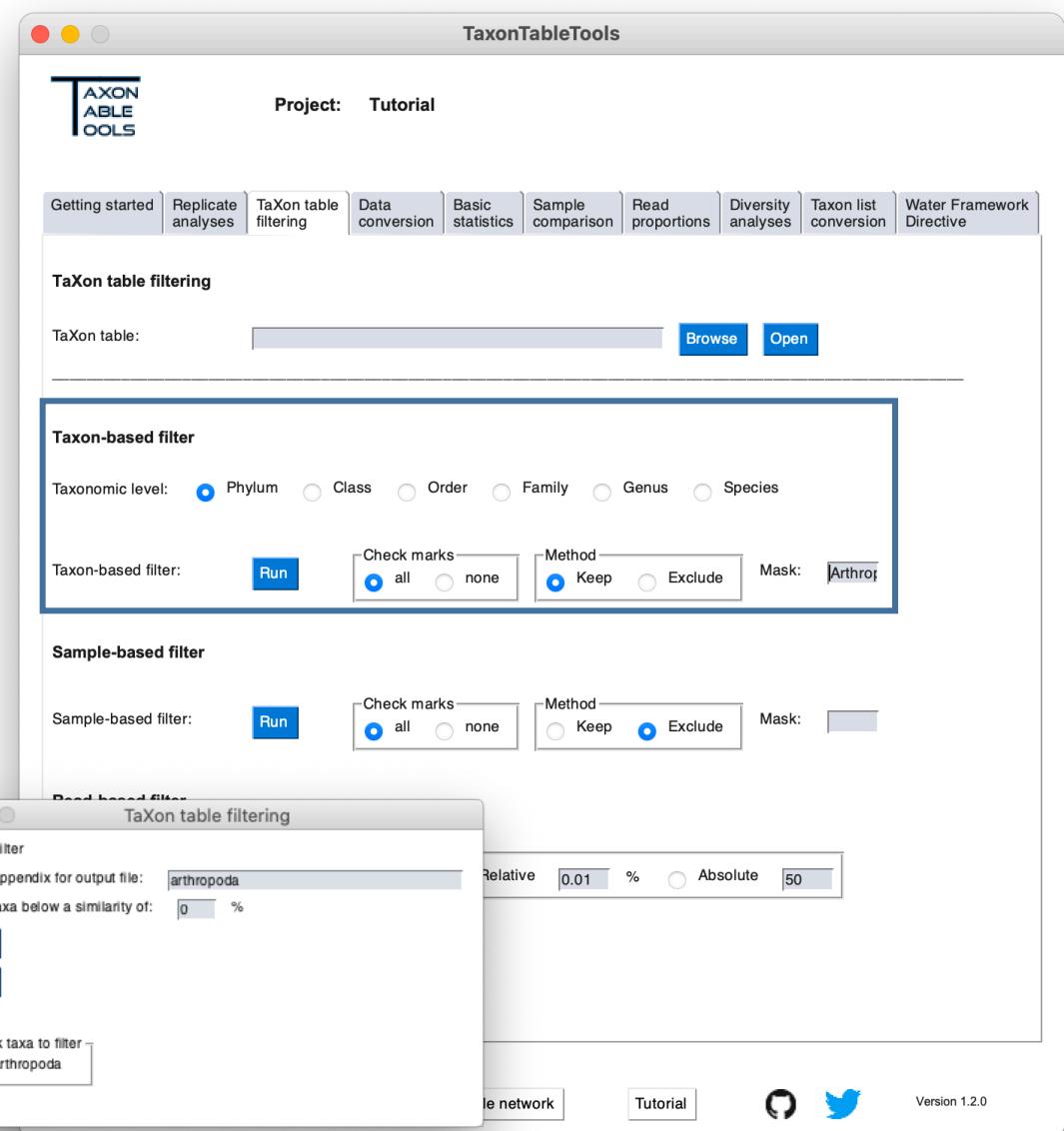
IDs	S1_comb
OTU_1	3540
OTU_2	0
OTU_3	0

The screenshot shows the TaxonTableTools software window with the title bar "TaxonTableTools" and "Project: Tutorial". The menu bar includes "Getting started", "Replicate analyses", "TaXon table filtering", "Data conversion", "Basic statistics", "Sample comparison", "Read proportions", "Diversity analyses", "Taxon list conversion", and "Water Framework Directive". The "Replicate analyses" tab is selected. The main area contains sections for "Replicates" and "Replicate analysis". In the "Replicates" section, there is a field for "Replicate suffixes" with "a, b" entered, and a "Preview" button. An information box says "Information - Comma separated list of suffixes.". In the "Replicate analysis" section, there are two buttons: "Calculate shared OTUs" with a "Run" button and a "Settings" box for "Plot size (w,h): 1000 600"; and "Calculate OTU and read correlation" with a "Run" button and a "Settings" box for "Plot size (w,h): 1000 500" and "Start axes at zero" checkboxes. Under "x" and "y", there are checkboxes. In the "Replicate processing" section, there are two buttons: "Replicate consistency" with a "Run" button and an information box "Information - Keep OTUs present in all replicates."; and "Replicate merging" with a "Run" button and an information box "Information - Merge replicates to one entry.". At the bottom, there are buttons for "Exit", "Log file network", "Tutorial", and social media links for GitHub and Twitter. The version is listed as "Version 1.2.0".

TaXon table filtering

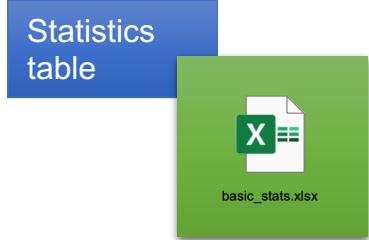
Taxon-based filter

- Since there are lots of non-target taxa present in this dataset, we want to focus on just the arthropods
- Therefore, load the latest TaXon table (*TTT_cons_derep.xlsx*)
- Set the marks to “Phylum”, “all” and “keep”
- Write “Arthropoda” in the mask field (case sensitive!)
- Click on Run and a new window will pop up
- Click Filter
- A new table named *TTT_cons_derep_arthropoda.xlsx* was created, which only includes Arthropoda hits



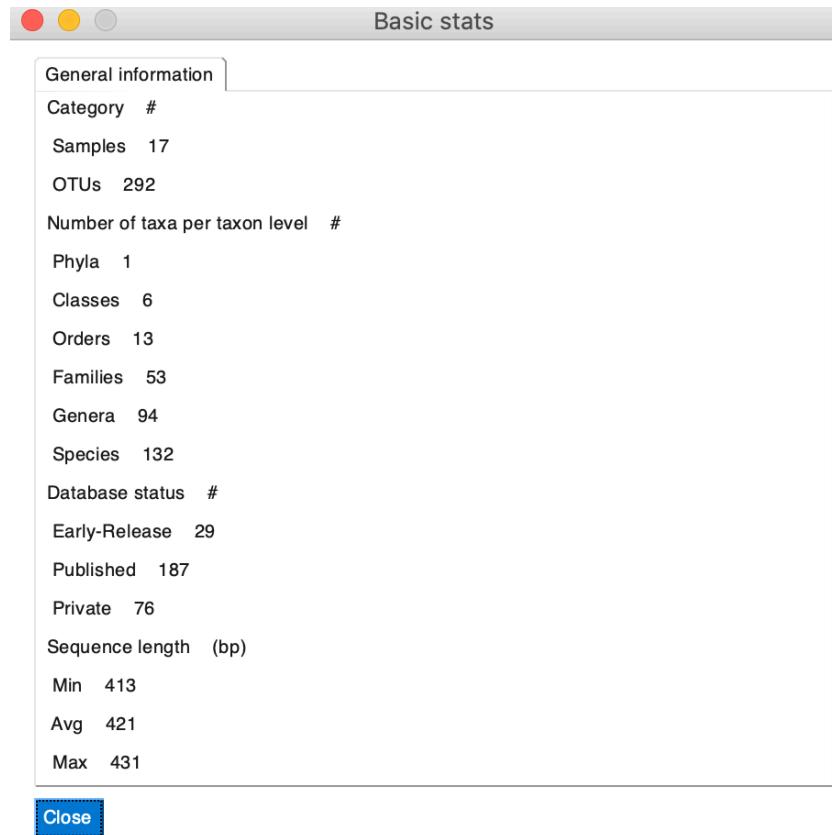
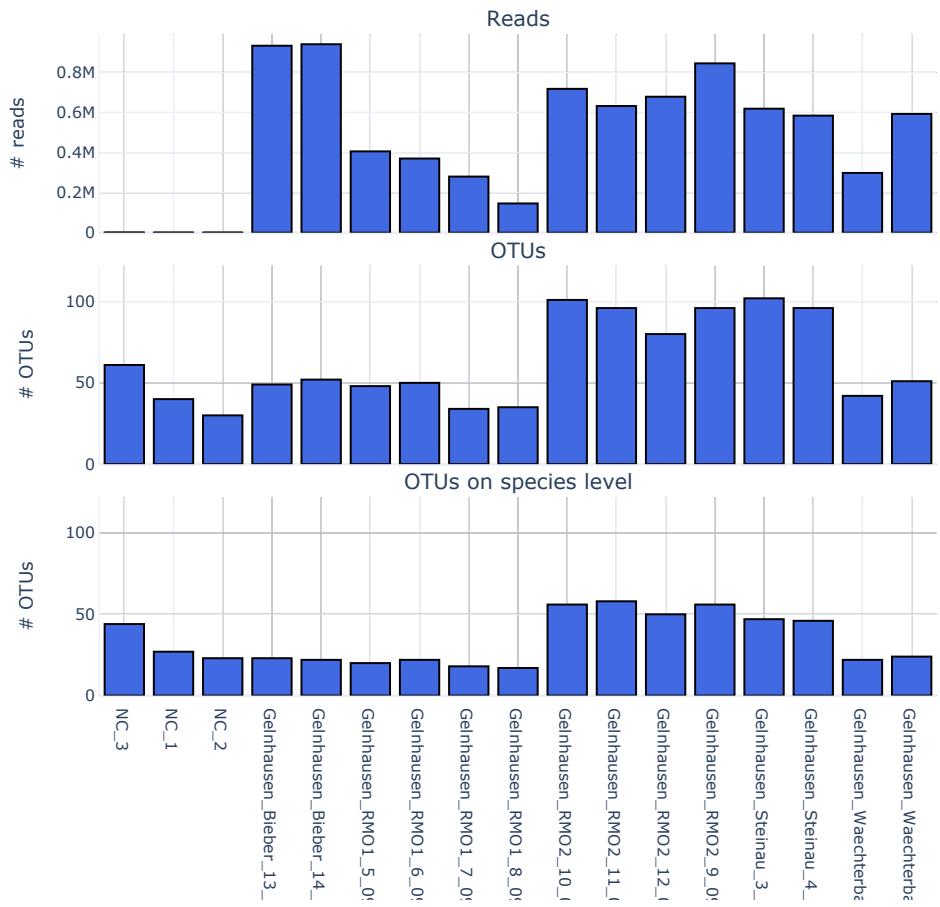
Basic statistics

- To get an overview of the data set we can calculate some basic statistics and plots
- Load the latest TaXon table (*TTT_... arthropoda.xlsx*) in the
- Click on Run
- Two windows will appear after each other:
 1. Three basic plots
 2. A table with useful statistics



The screenshot shows the TaxonTableTools software interface. At the top, there is a menu bar with 'Project: Tutorial' and several tabs: Getting started, Replicate analyses, Taxon table filtering, Data conversion, Basic statistics, Sample comparison, Read proportions, Diversity analyses, Taxon list conversion, and Water Framework Directive. Below the tabs, there are two main sections: 'Basic statistics' and 'Taxonomic resolution'. The 'Basic statistics' section contains a 'TaXon table:' input field with 'Browse' and 'Open' buttons, and a 'Run' button. The 'Taxonomic resolution' section contains a 'Taxonomic resolution plot' input field with a 'Run' button, and a 'Settings' panel for plot size (w,h) set to 800x1100. The 'Taxonomic richness' section contains a 'Taxonomic richness plot' input field with a 'Run' button, and a 'Settings' panel for plot size (w,h,ylim) set to 600x600. The 'Per taxon statistics' section contains a 'Reads, OTUs and species' input field with a 'Run' button, and a 'Settings' panel for plot size (w,h,ylim) set to 900x600 and a 'Taxonomic level' dropdown set to 'Class'. At the bottom, there are 'Exit', 'Log file network', 'Tutorial', and social media links for GitHub and Twitter, along with the text 'Version 1.2.0'.

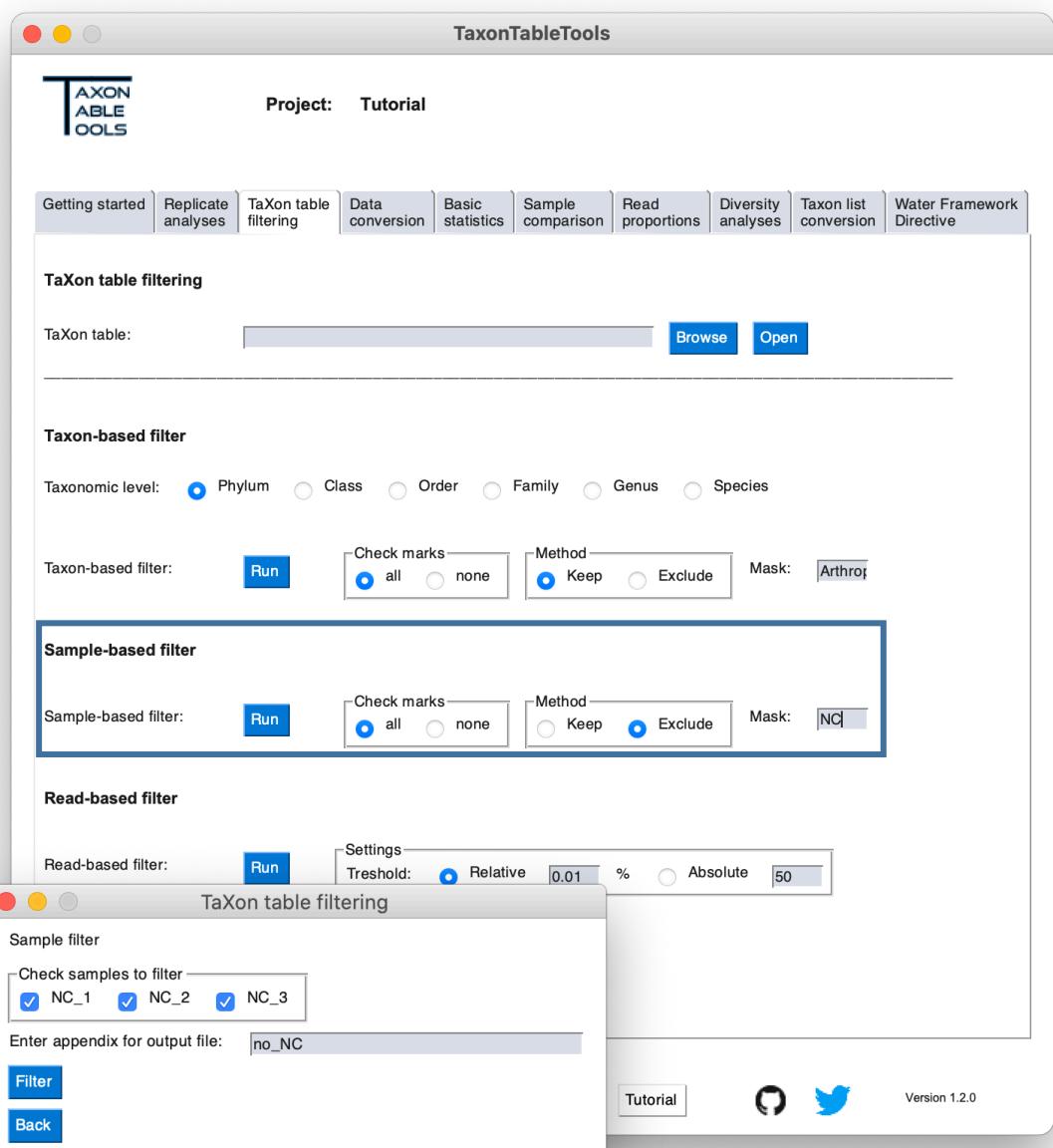
Basic statistics



TaXon table filtering

Sample-based filter

- Now we want to remove the negative controls from the data set
- Load the latest TaXon table (*TTT_..._arthropoda.xlsx*)
- Set the marks to “all” and “exclude”
- Write “NC” in the mask field (case sensitive!)
- Click on Run and a new window will pop up
- All three negative controls are check marked
- Enter a new appendix name (e.g.”no_NC“)
- Click Filter
- A new table named *TTT_cons_derep_arthropoda_no_NC.xlsx* was created



TaXon table filtering

But what if it's easier to filter my samples via Excel?

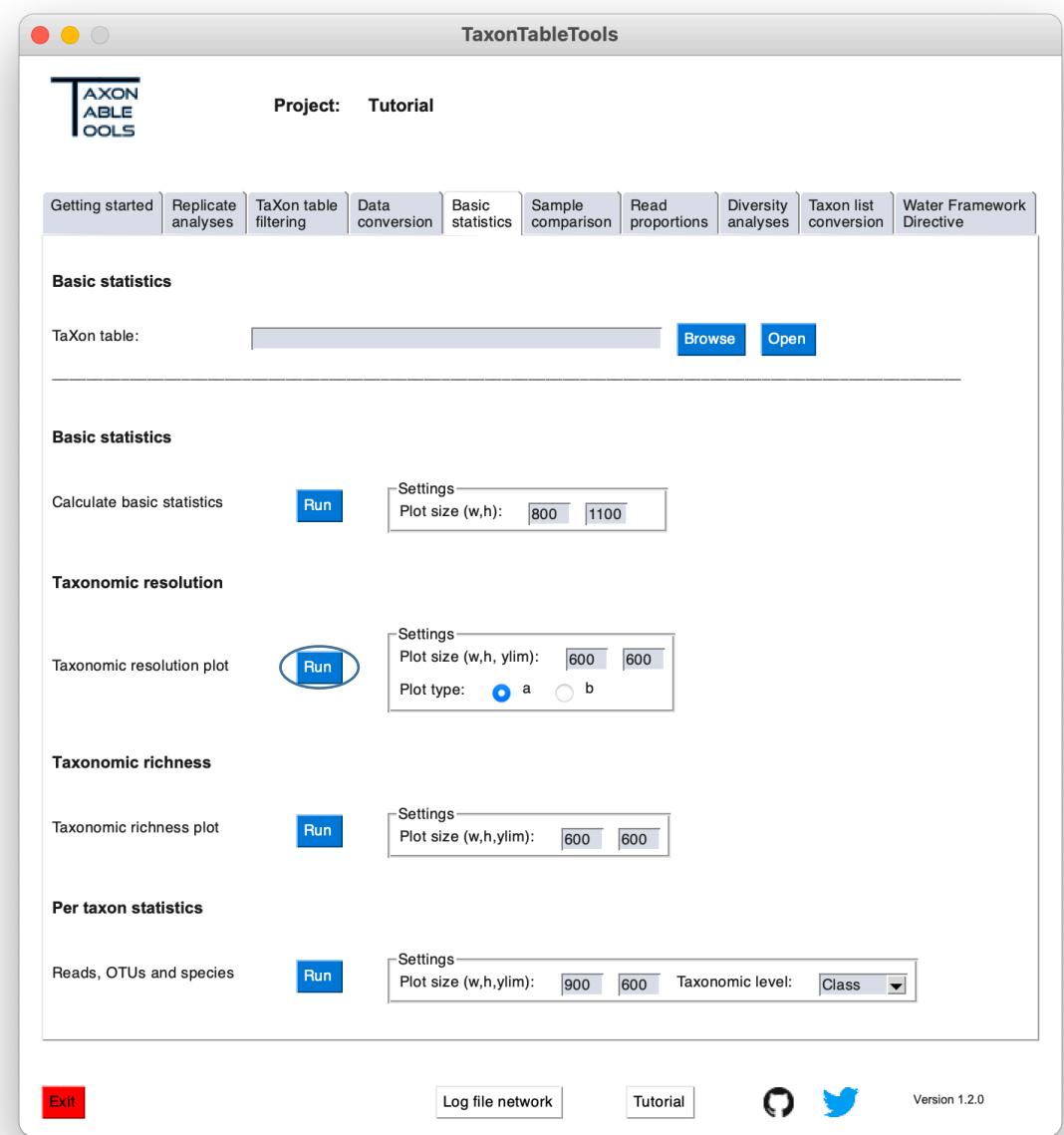
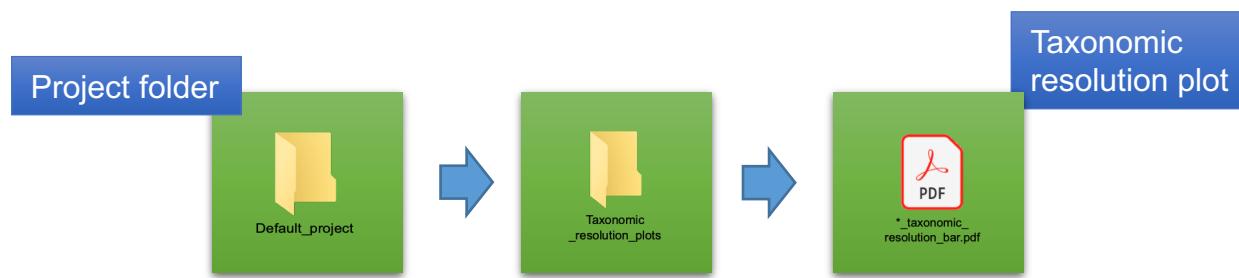
- This is also possible but can lead to biased analyses!
- Example:
 - Deleting samples by simply removing the column can lead to OTUs that are not present in the dataset anymore (i.e. 0 reads in all remaining samples)
 - The TaXon table format expects that if an OTU is present in the table, it is also represented by at least one sample!

Solution

- Prepare your TaXon table as desired
- Now use the „Check TaXon table“ function
- All OTUs that were only present in the deleted samples will be removed from the dataset

Taxonomic resolution

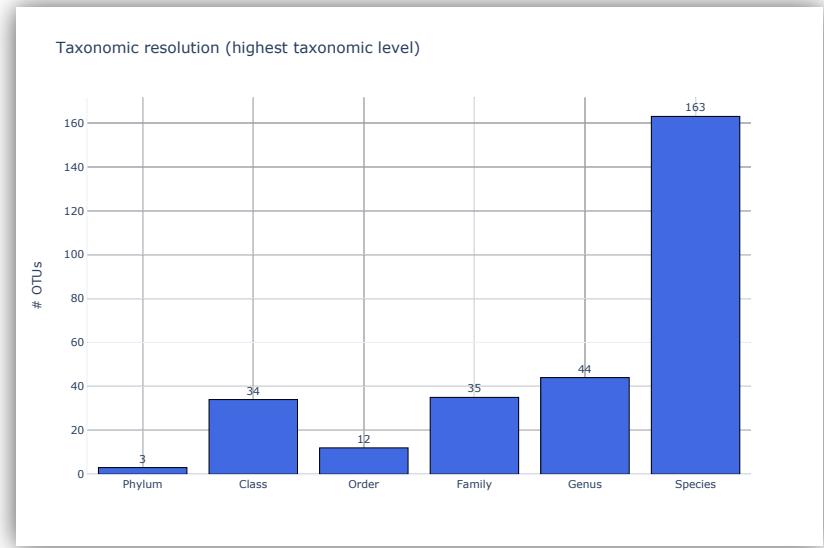
- Now we can check the taxonomic resolution of the data set
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Click on Run (repeat for plot type „b“)
- A new plot was created in the *Taxonomic_resolution_plots* folder



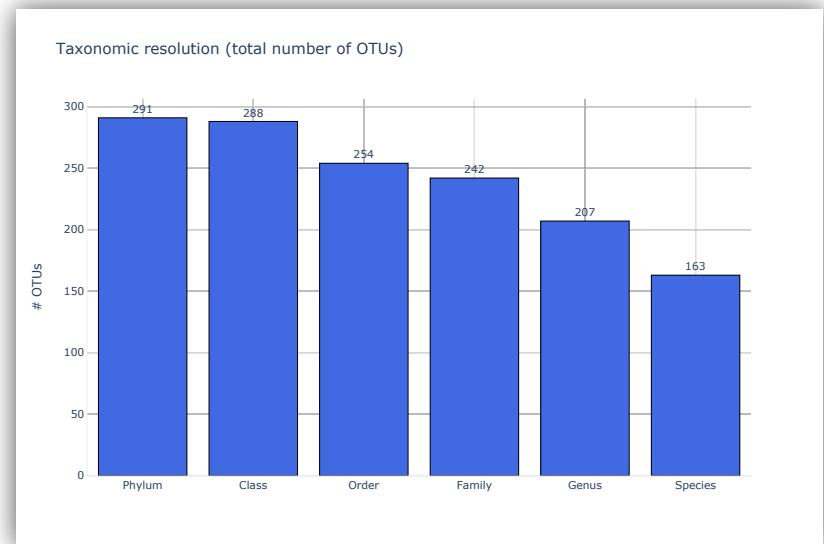
Taxonomic resolution

- Taxonomic resolution shows the highest level to which an OTU was identified
- In this case 3 OTUs could only be identified on phylum level
- Respectively 34 OTU were identified to class level
- And 163 were identified to species level

Plot a)

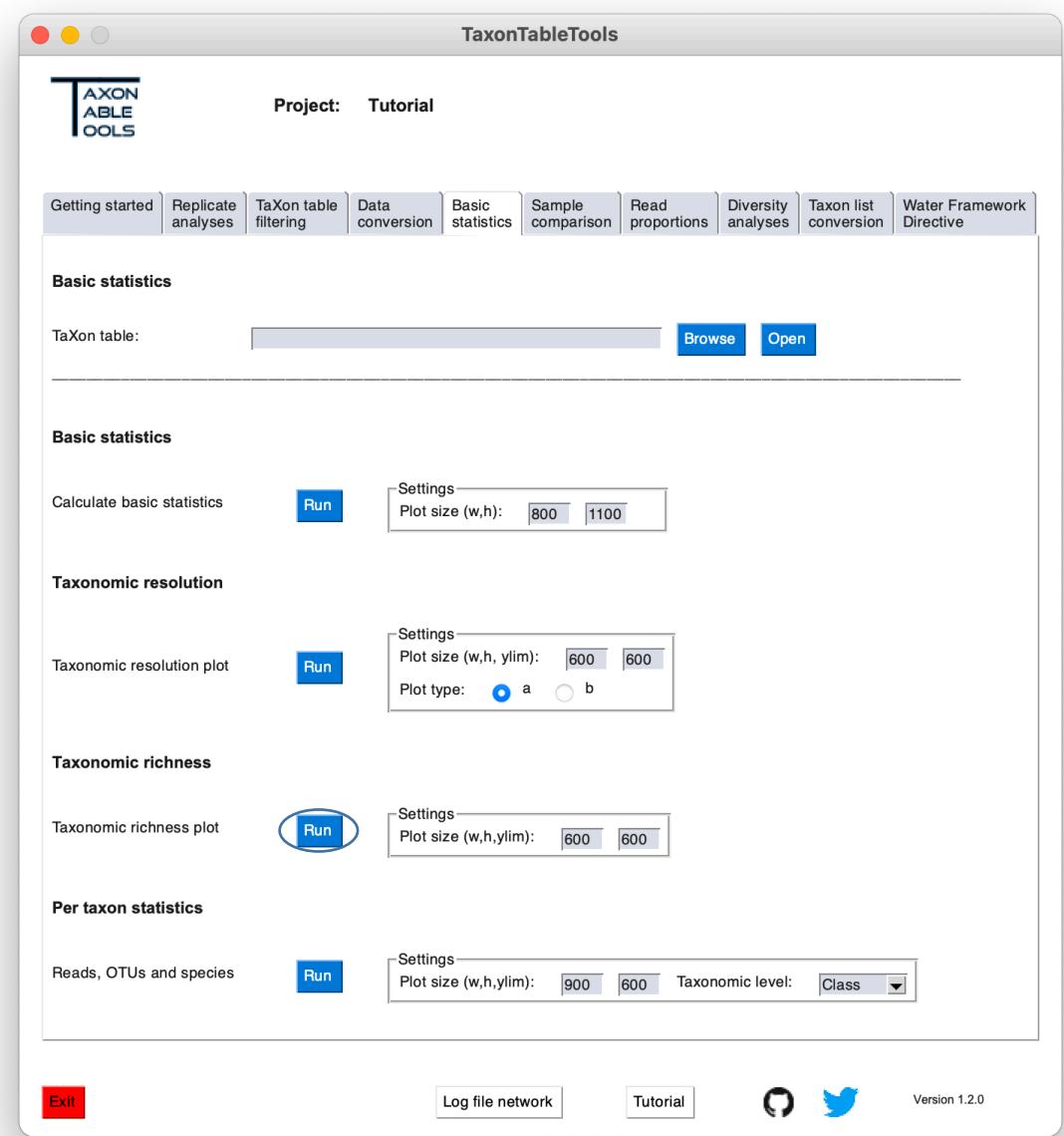
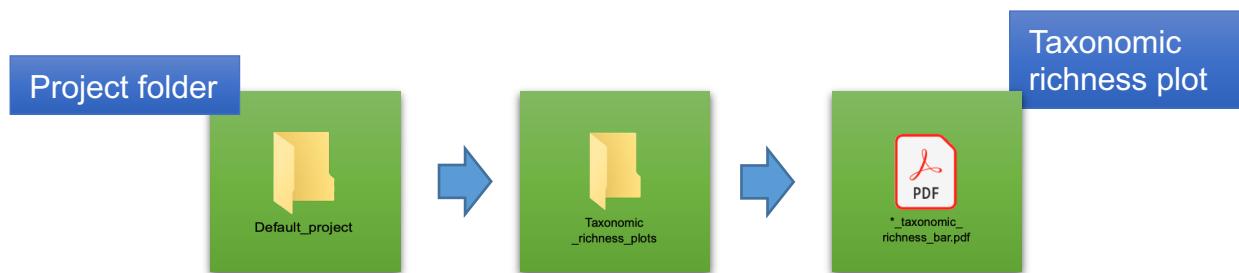


Plot b)



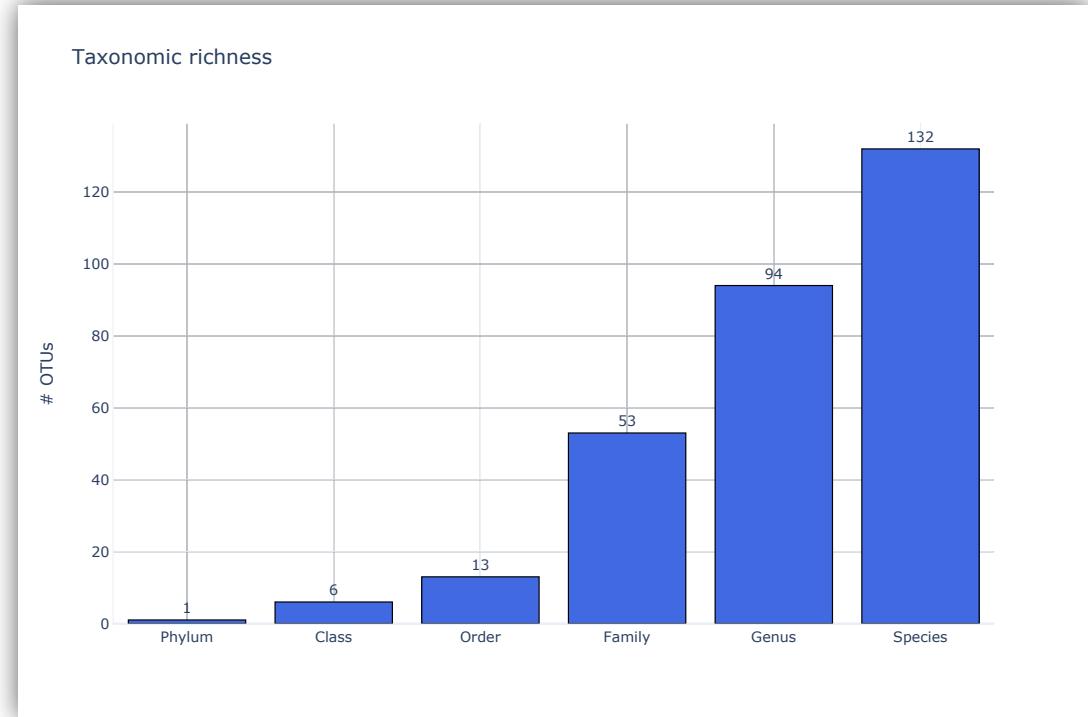
Taxonomic richness

- Now we can check how many taxa are present in the data set
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Click on Run
- A new plot was created in the *Taxonomic_richness_plots* folder



Taxonomic richness

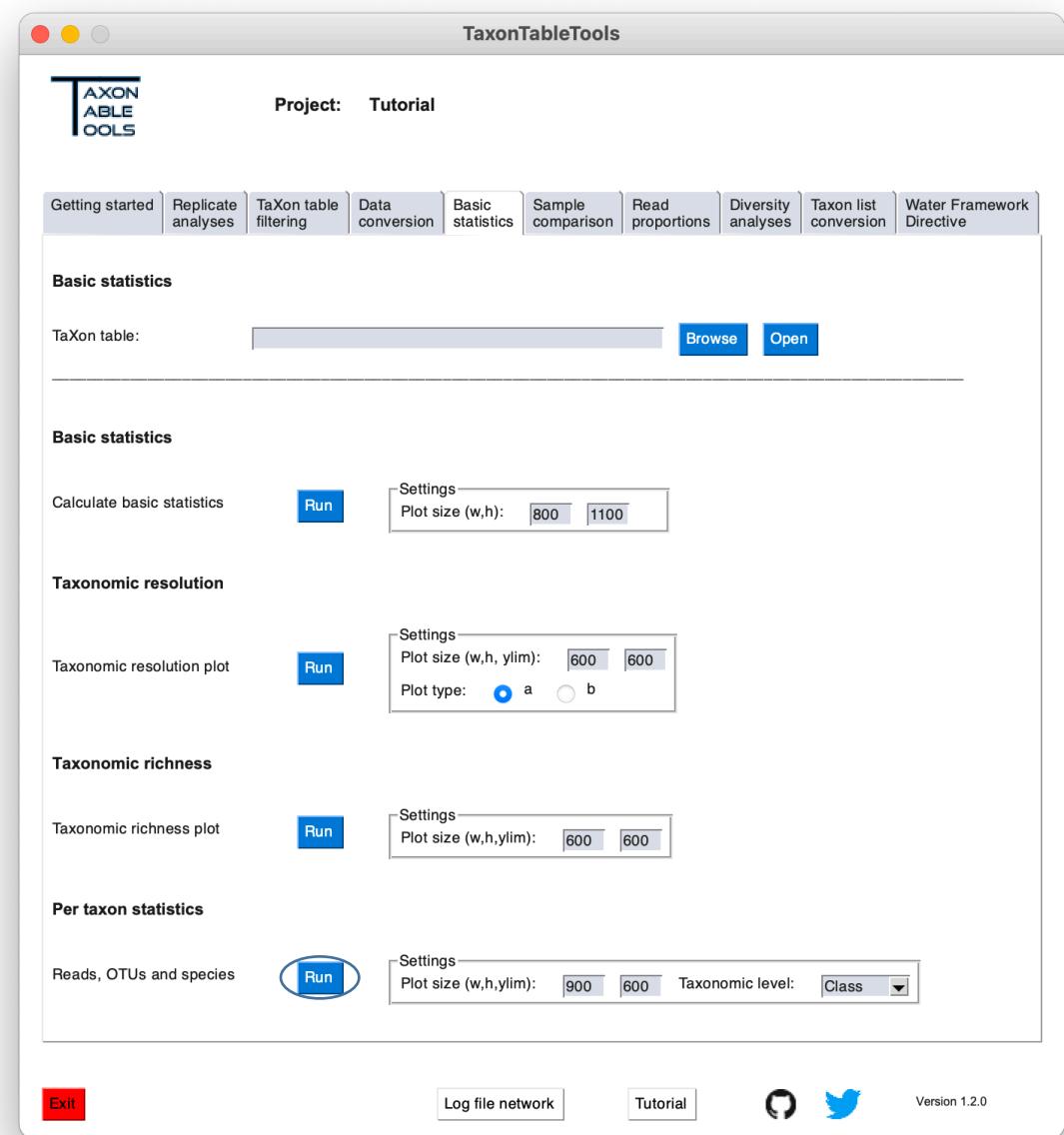
- Taxonomic richness shows the number of taxa for each taxonomic level
- In this case we only included the phylum „Arthropoda“ which results in one phylum
- Within the Arthropoda we found
 - 6 classes
 - 13 Orders
 - 53 Families
 - 94 Genera
 - 132 Species



Reads and OTUs per taxon

Next we should check which orders are present in the dataset

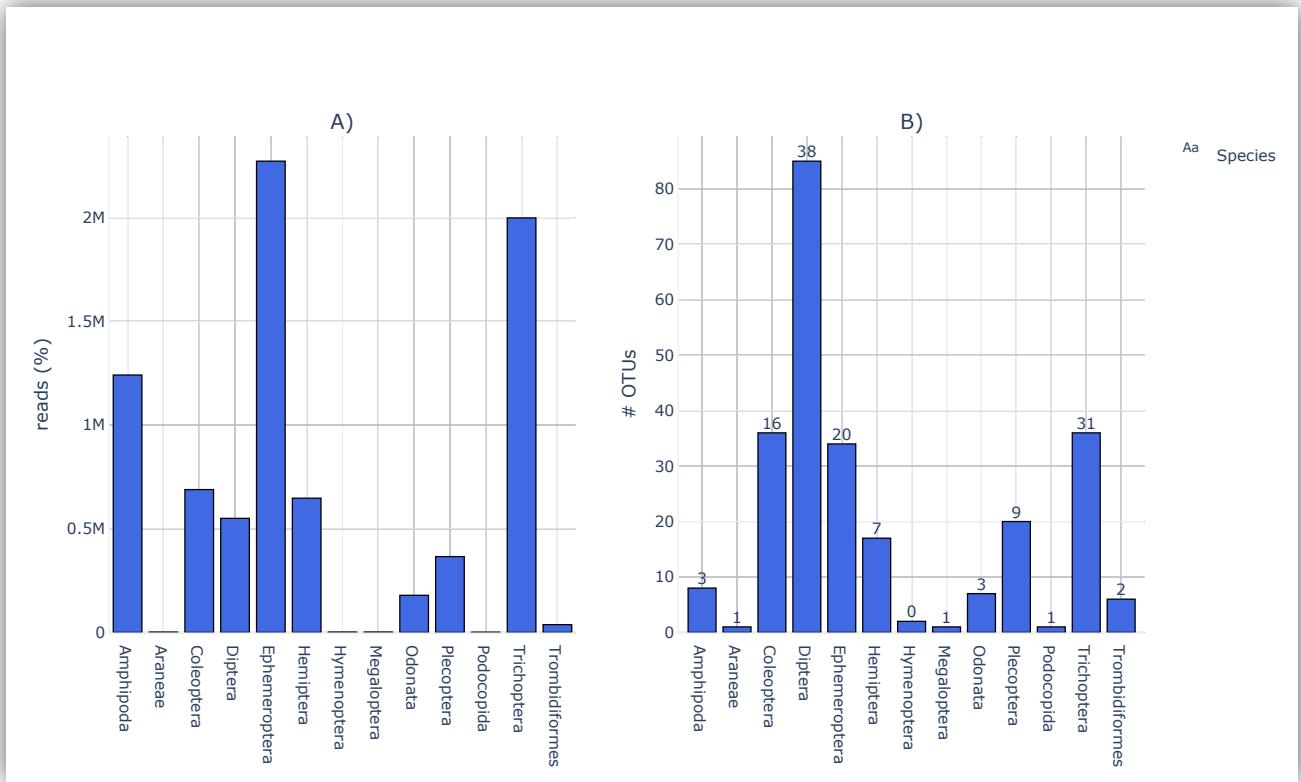
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Click on Run
- A new plot was created in the *Per_taxon_analysis* folder



Reads, OTUs and species per taxon

This plot shows the number of total reads, the number of OTUs and the number of species

- Note: This is the actual number of species.
NOT the number of OTUs on species level!
- Within the Arthropoda we can conclude that
 - Most reads belong to Ephemeroptera
 - Most OTUs were assigned to Diptera
 - Most species were found for Diptera



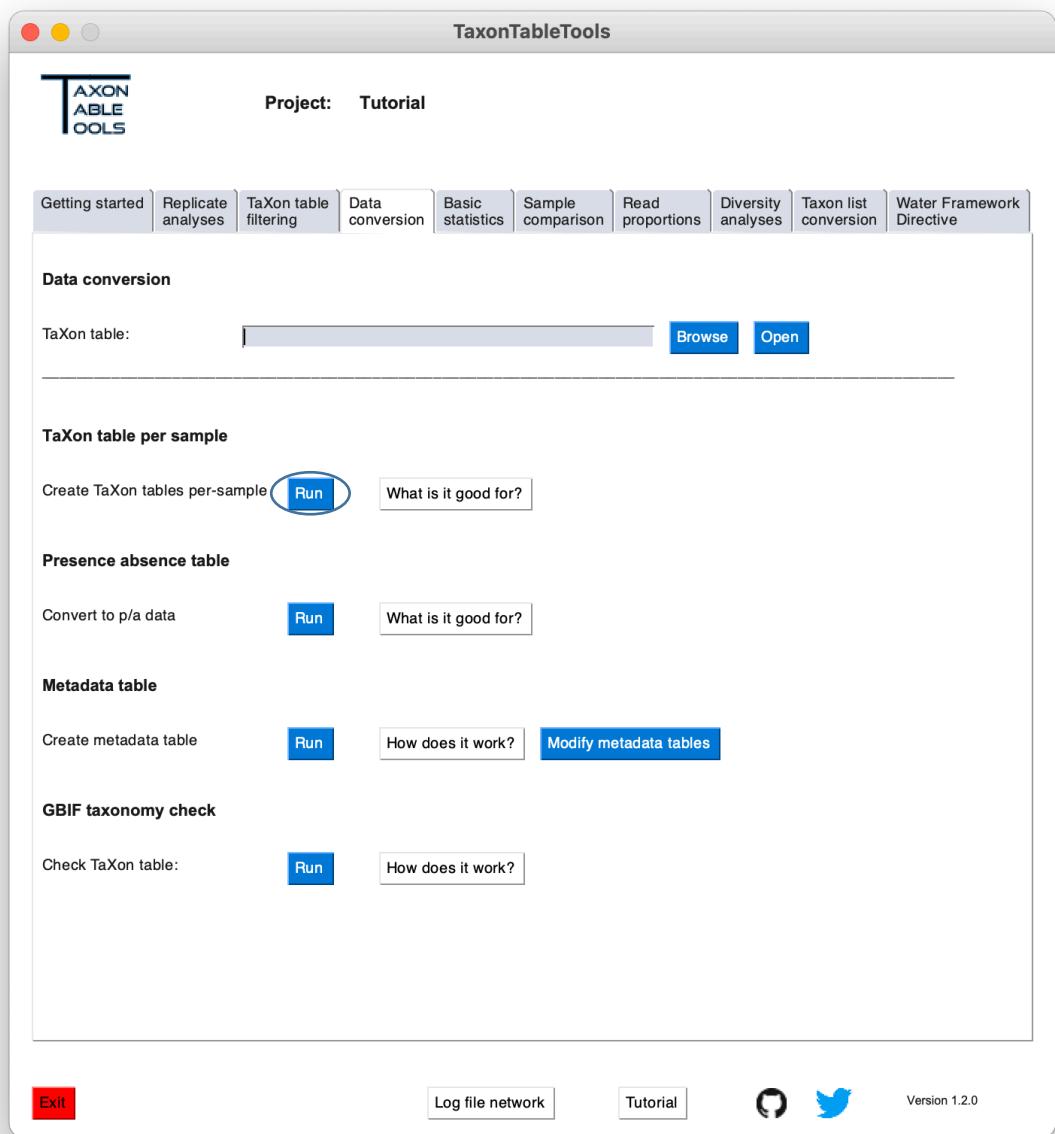
Creating sub sets

a. TaXon table per sample

- A first way to compare samples is to create individual TaXon tables
- To do so go to the **Data conversion tab** and use the TaXon table per sample tool
- This will create an individual table for each sample in a new folder
- We will use 3 of these to create venn diagrams

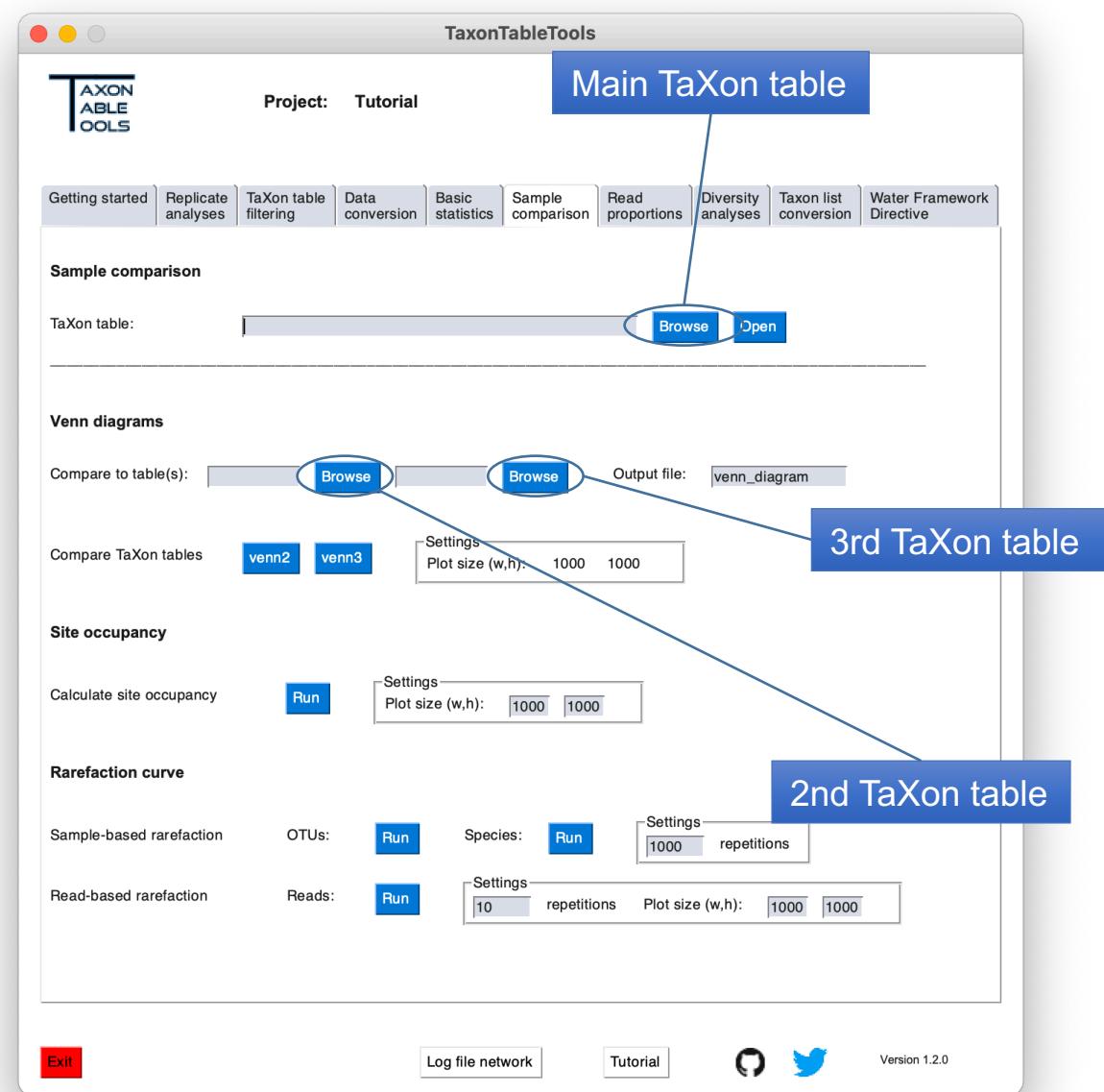
b. TaXon table subset

- Alternatively we can create subsets of the original table using the „sample-based filter“ tool



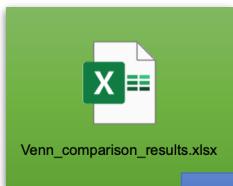
Venn diagrams

- The tables are ordered as follows:
 - Main TaXon table
 - Venn2 TaXon table
 - Venn3 TaXon table
- Venn2**
 - Load the main TaXon table (i.e. Bieber_13)
 - Load the second TaXon table (i.e. RMO1_5)
 - Press venn2
- Venn3**
 - Load the main TaXon table
 - Load the second TaXon table
 - Load the third TaXon table (i.e. Waechterbach_2)
 - Press venn3

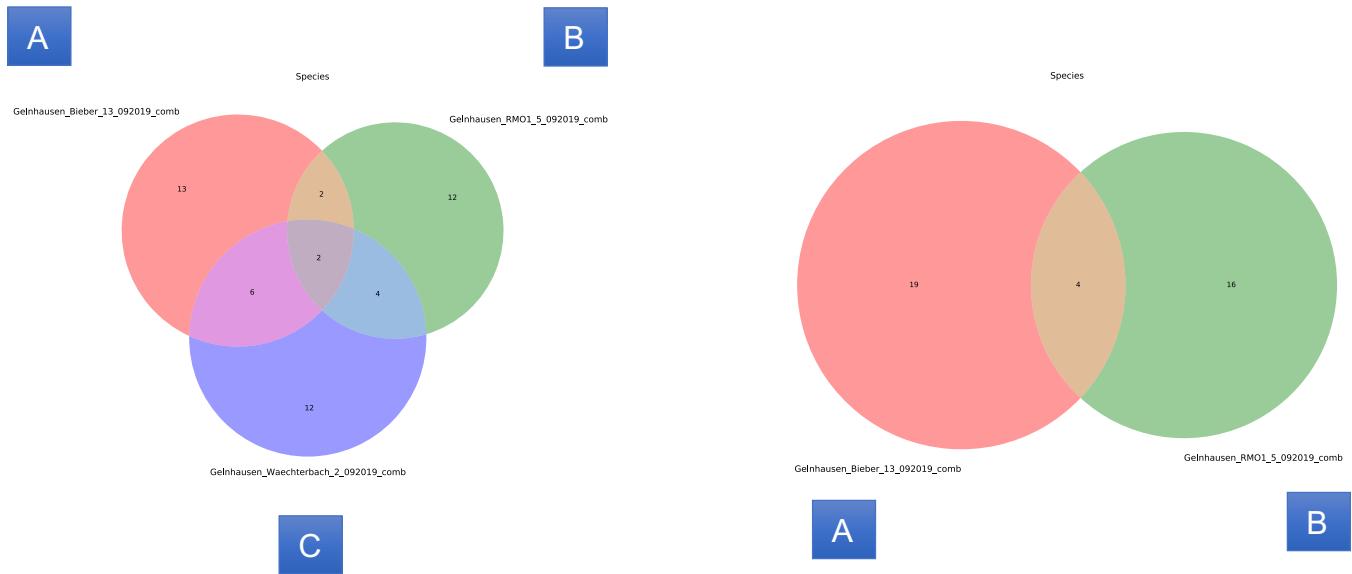


Venn diagrams

- 6 new plots will be created (from phylum to species level)
- Additionally the results will be saved to a new table named „Venn_comparison_results“
- It is recommended to adjust the venn diagrams in e.g. Inkscape



Venn diagram table

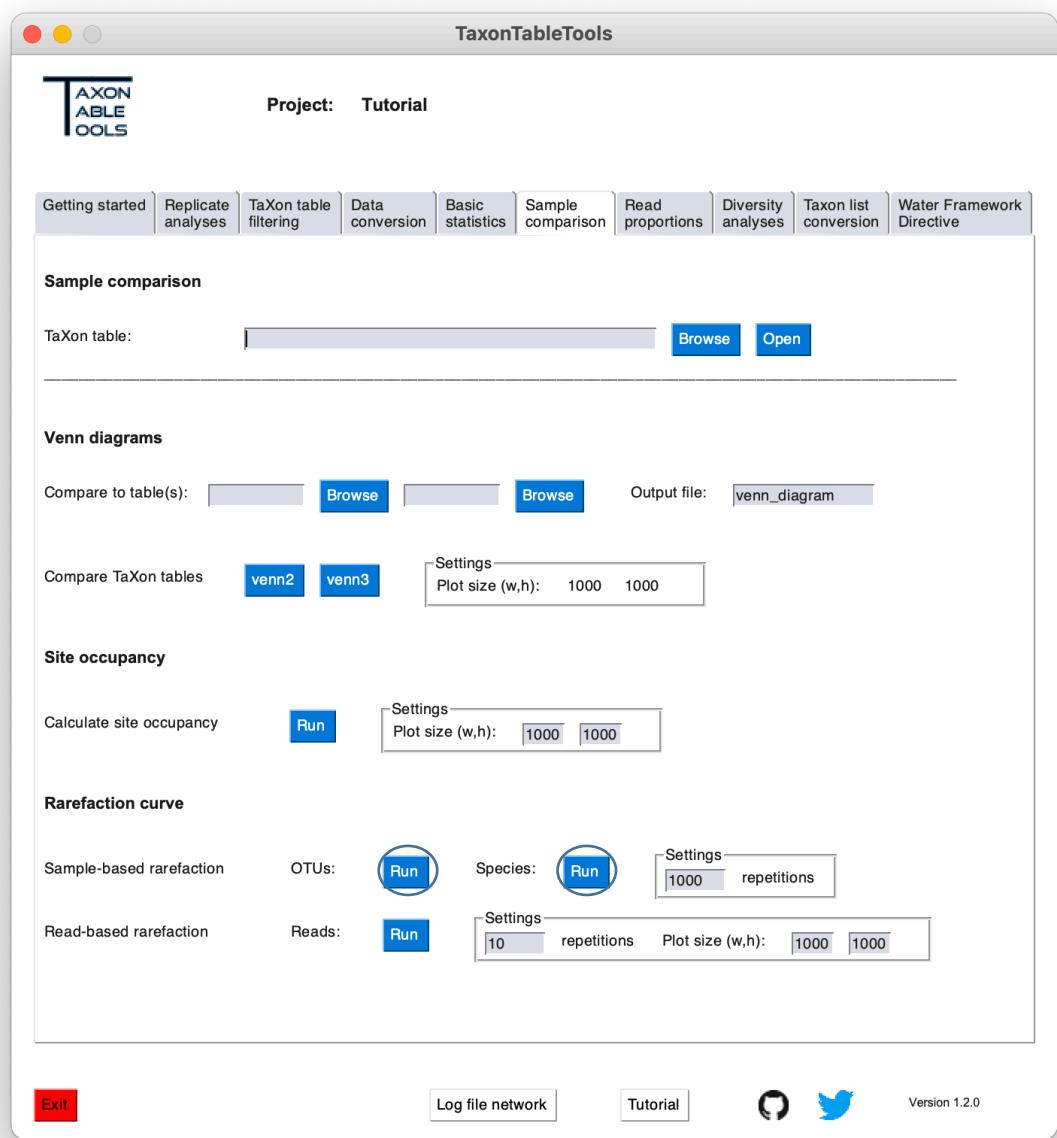
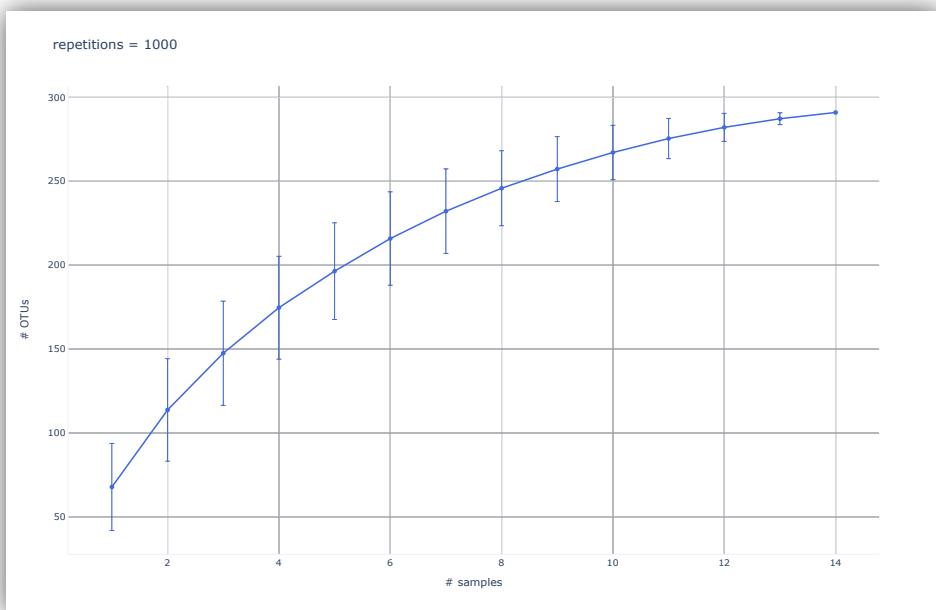


Species_a_only	Species_b_only	Species_c_only	Species_shared_all	Species_shared_a_b	Species_shared_a_c	Species_shared_b_c
Hydraena fosterorum	Simulium erythrocephalum	Baetis vardarensis	Gammarus pulex	Oulimnius tuberculatus	Esolus parallelepipedus	Aphelocheirus aestivalis
Rhithrogena semicolorata	Tanytarsus brundini	Heptagenia sulphurea	Hydropsyche pellucida	Orectochilus villosus	Elmis maugetii	Dicranota sp.
Hydraena riparia	Baetis vernus	Halesus tessellatus			Baetis rhodani	Baetis fuscatus
Chaetopteryx fusca	Polydipidium aegyptium	Atherix ibis			Limnius volckmari	Ephemera danica
Rhyacophila rubra	Ephemerella ignita	Lepidostoma hirtum			Elmis rioloides	
Rheotanytarsus distinctissimus	Heptagenia flava	Halesus digitatus			Hydraena gracilis	
Oreodytes sanmarkii	Goera pilosa	Polycentropus flavomaculatus				
Tvetenia verralli	Cricotopus vierriensis	Habroleptoides confusa				
Elmis aenea	Prodiamesa olivacea	Lebertia porosa				
Dicranota pavida	Psychomyia pusilla	Leuctra geniculata				
Hydropsyche siltalai	Gammarus roeselii	Leuctra fusca				
Ecdyonurus torrentis	Tipula sp. XJB	Linyphia hortensis				
Baetis scambus						

Sample-based rarefaction

Test the species richness from the results of sampling

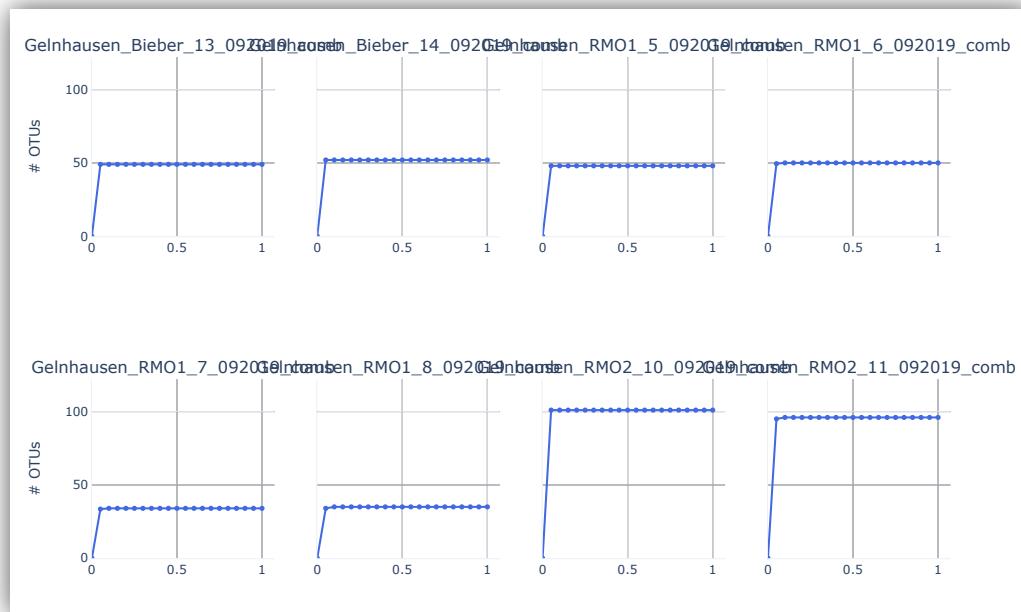
- Load the latest TaXon table (*TTT_cons_derep_arthropoda_no_NC.xlsx*)
- Enter the number of repetitions (e.g. 1000)
- Click on Run to test on either species or OTU level



Read-based rarefaction

Test the effect of sequencing depth

- Load the latest TaXon table (*TTT_cons_derep_arthropoda_no_NC.xlsx*)
- Enter the number of repetitions (e.g. 2 for test purposes)
- Click on Run



The screenshot shows the TaxonTableTools software interface. The main title bar says "TaxonTableTools". Below it, the "Project: Tutorial" is selected. A navigation bar includes links for "Getting started", "Replicate analyses", "TaXon table filtering", "Data conversion", "Basic statistics", "Sample comparison", "Read proportions", "Diversity analyses", "Taxon list conversion", and "Water Framework Directive". The "Sample comparison" section is active, showing fields for "TaXon table" with "Browse" and "Open" buttons. Below this, the "Venn diagrams" section shows fields for "Compare to table(s)" with "Browse" buttons and an "Output file" field set to "venn_diagram". Under "Compare TaXon tables", there are buttons for "venn2" and "venn3", and a "Settings" box for "Plot size (w,h): 1000 1000". The "Site occupancy" section includes a "Calculate site occupancy" button and a "Run" button, with a "Settings" box for "Plot size (w,h): 1000 1000". The "Rarefaction curve" section contains two parts: "Sample-based rarefaction" (with "OTUs:" and "Species:" buttons) and "Read-based rarefaction" (with "Reads:" and "Run" buttons). Both have "Settings" boxes for "repetitions" (set to 1000) and "Plot size (w,h): 1000 1000". At the bottom are "Exit", "Log file network", "Tutorial", social media icons for GitHub and Twitter, and the text "Version 1.2.0".

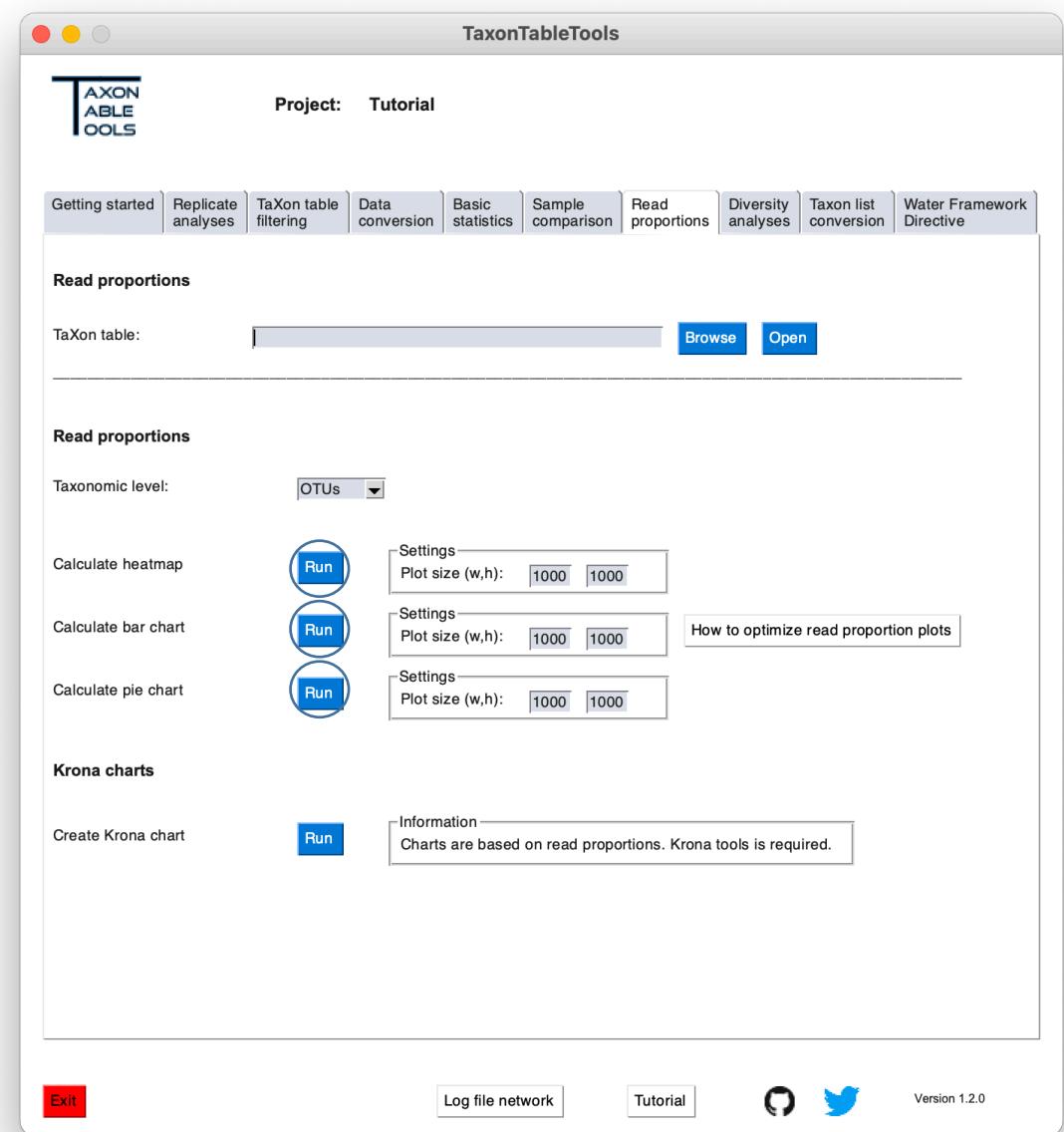
Read proportions

Read proportions per taxon for each sample

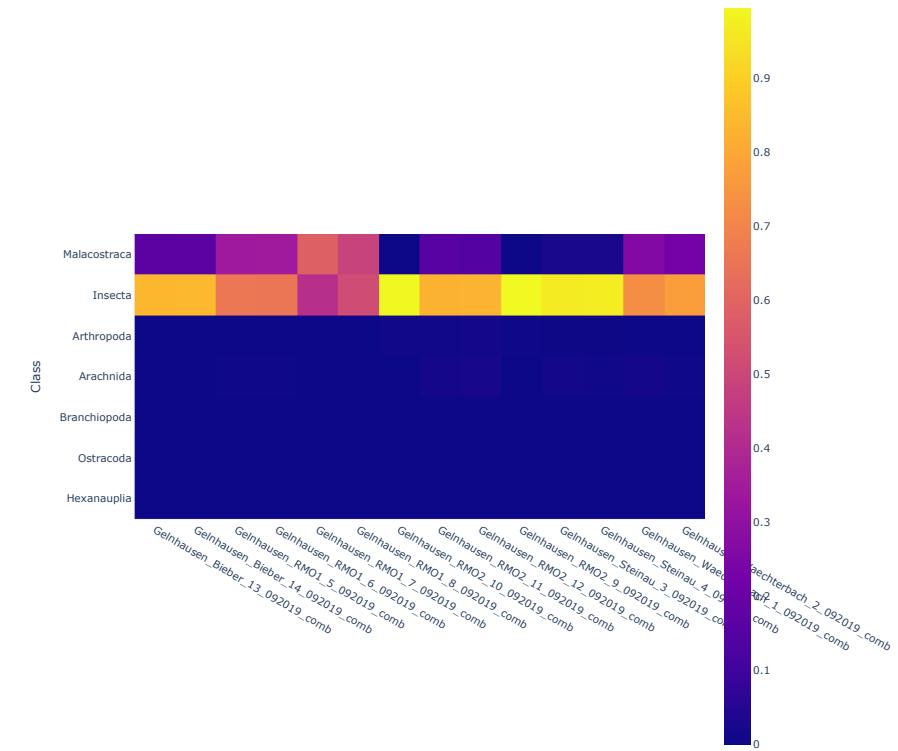
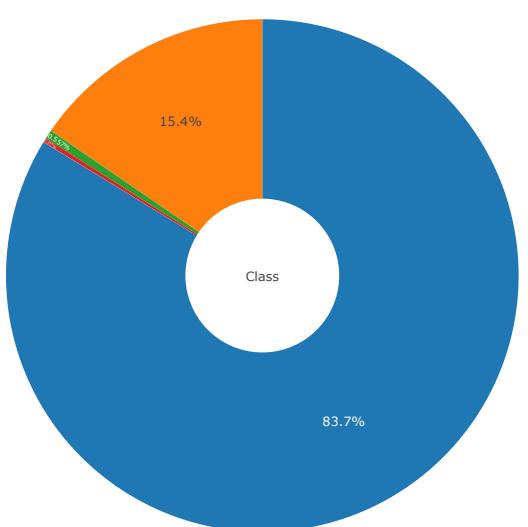
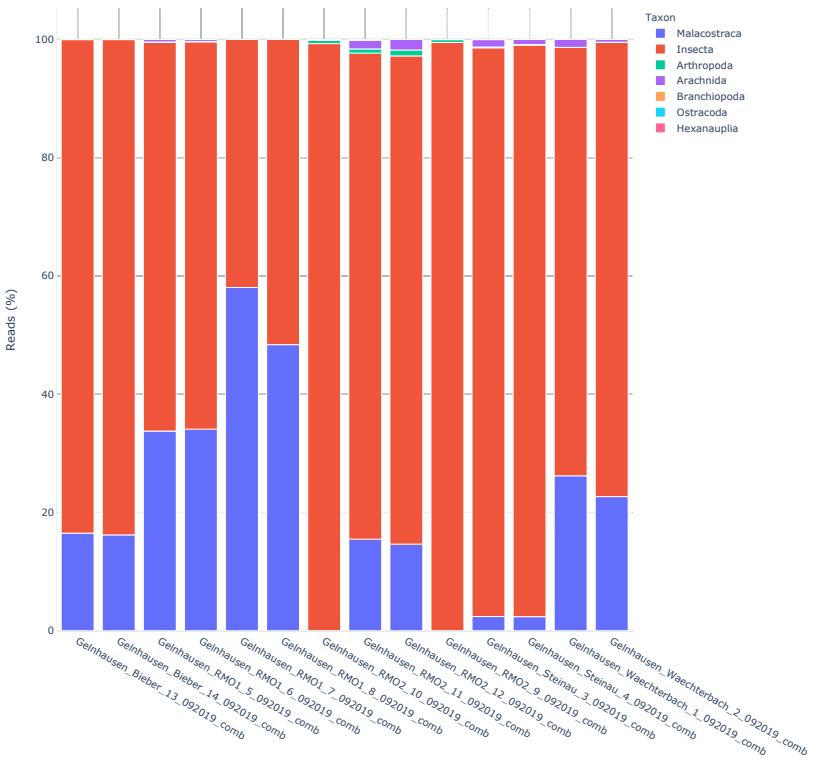
- Load the latest TaXon table (*TTT_cons_derep_arthropoda_no_NC.xlsx*)
- Check the taxonomic level for which to calculate the read proportions (i.e. family)
- Choose to either display the OTU as „best hit“ or as „nan“
- Click on Run

Optimize your plots by a priori filtering!

- OTUs that do not have a hit on the respective level will be set back to their last present taxonomic level
- To create clearer plots it is e.g. useful to filter for certain taxonomic groups and keep only hit on e.g. species level



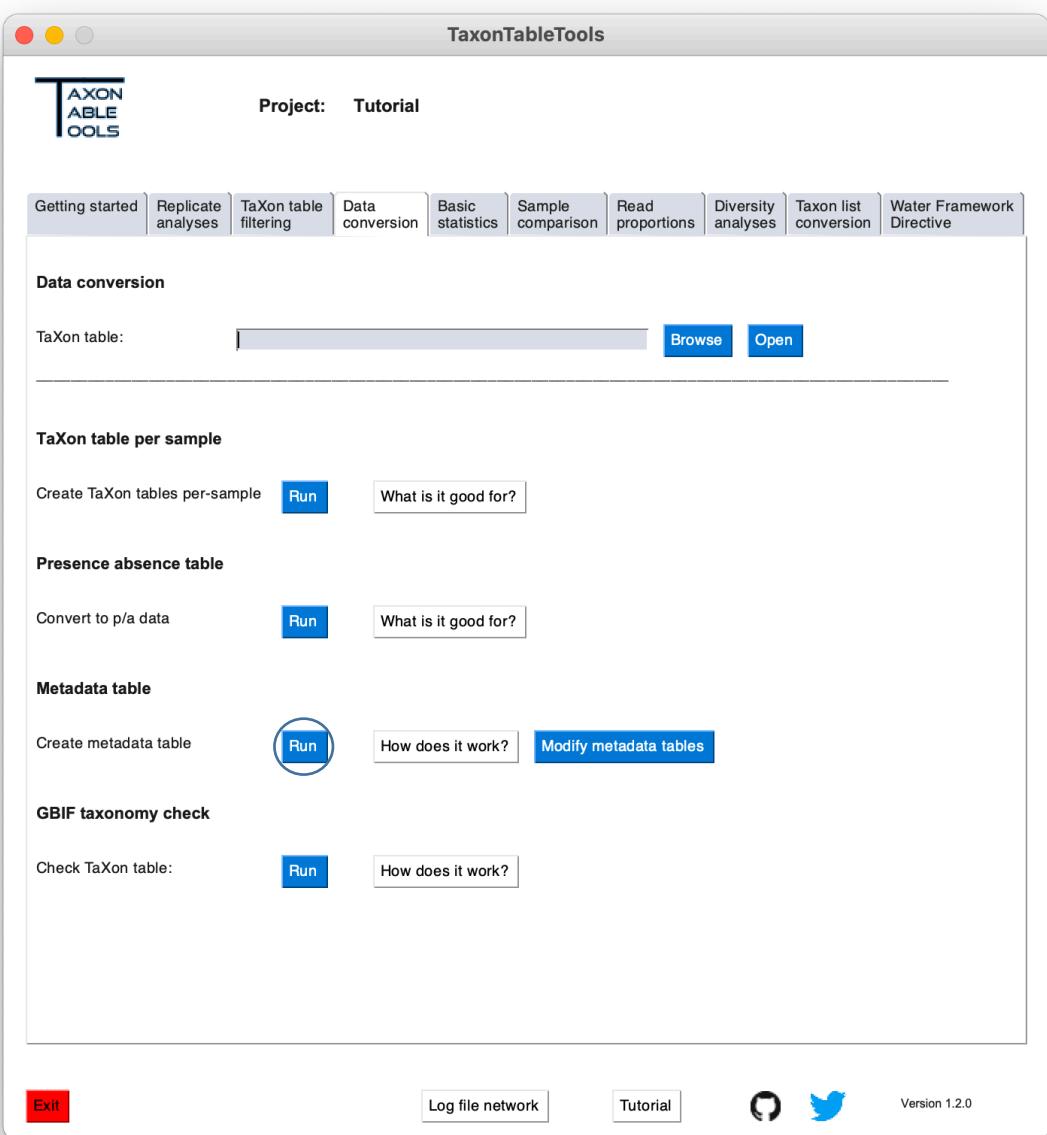
Read proportions



Metadata

Creating a new metadata table

- Go to the **Data conversion** tab
- Load the latest TaXon table (*TTT_cons_derep_arthropoda_no_NC.xlsx*)
- For more information click on „How does it work?“
- To create a new metadata table for the currently active file, click on Run
- You don't have to load the table separately when tools require it, as they will be automatically loaded. So do not change the name of the file
- ***The metadata table requires user-input outside from TTT!***
- ***New: Metadata tables can now be openend from within TTT***



Metadata table

Adjusting the metadata table

- Open the metadata table with e.g. Excel or directly from TTT
- The first column holds the sample names
 - Never change the names of the samples, as they must be equivalent to the respective TaXon table file
 - You can re-arrange the order of the samples for a better sorting
- Now adjust the metadata for each sample and rename the column headers according to your data
- The column header will show up in TTT and can be used to select the metadata to test on

Samples	1	2	3	4	5
Gelnhausen_Bieber_13_092019_comb	Gelnhausen	Bieber	13	092019	comb
Gelnhausen_Bieber_14_092019_comb	Gelnhausen	Bieber	14	092019	comb
Gelnhausen_RMO1_5_092019_comb	Gelnhausen	RMO1	5	092019	comb
Gelnhausen_RMO1_6_092019_comb	Gelnhausen	RMO1	6	092019	comb
Gelnhausen_RMO1_7_092019_comb	Gelnhausen	RMO1	7	092019	comb
Gelnhausen_RMO1_8_092019_comb	Gelnhausen	RMO1	8	092019	comb
Gelnhausen_RMO2_10_092019_comb	Gelnhausen	RMO2	10	092019	comb
Gelnhausen_RMO2_11_092019_comb	Gelnhausen	RMO2	11	092019	comb
Gelnhausen_RMO2_12_092019_comb	Gelnhausen	RMO2	12	092019	comb
Gelnhausen_RMO2_9_092019_comb	Gelnhausen	RMO2	9	092019	comb
Gelnhausen_Steinau_3_092019_comb	Gelnhausen	Steinau	3	092019	comb
Gelnhausen_Steinau_4_092019_comb	Gelnhausen	Steinau	4	092019	comb
Gelnhausen_Waechterbach_1_092019_comb	Gelnhausen	Waechterbach	1	092019	comb
Gelnhausen_Waechterbach_2_092019_comb	Gelnhausen	Waechterbach	2	092019	comb

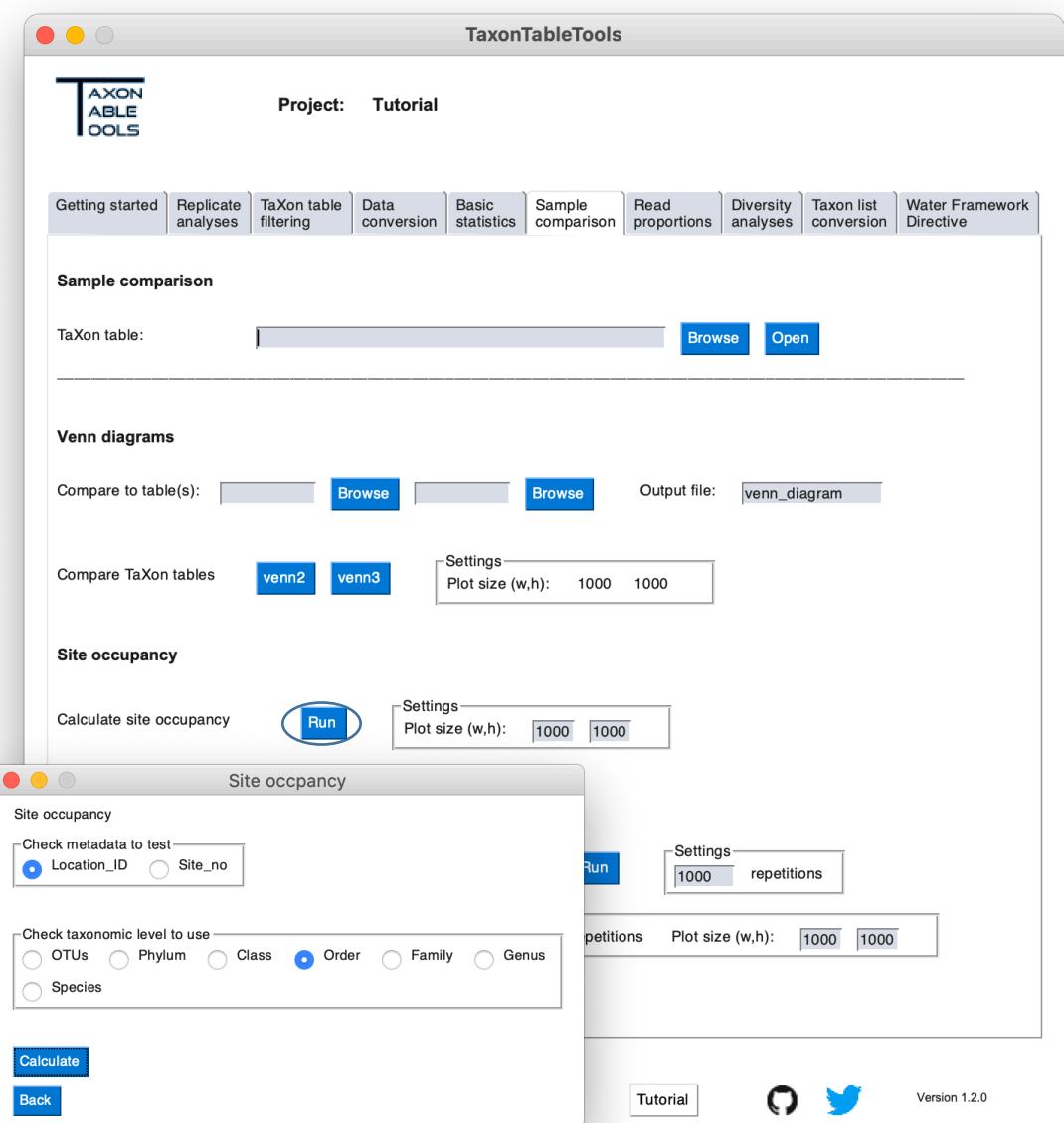


Samples	Location_ID	Site_No
Gelnhausen_Bieber_13_092019_comb	Bieber	13
Gelnhausen_Bieber_14_092019_comb	Bieber	14
Gelnhausen_RMO1_5_092019_comb	RMO1	5
Gelnhausen_RMO1_6_092019_comb	RMO1	6
Gelnhausen_RMO1_7_092019_comb	RMO1	7
Gelnhausen_RMO1_8_092019_comb	RMO1	8
Gelnhausen_RMO2_10_092019_comb	RMO2	10
Gelnhausen_RMO2_11_092019_comb	RMO2	11
Gelnhausen_RMO2_12_092019_comb	RMO2	12
Gelnhausen_RMO2_9_092019_comb	RMO2	9
Gelnhausen_Steinau_3_092019_comb	Steinau	3
Gelnhausen_Steinau_4_092019_comb	Steinau	4
Gelnhausen_Waechterbach_1_092019_comb	Waechterbach	1
Gelnhausen_Waechterbach_2_092019_comb	Waechterbach	2

Name of the metadata

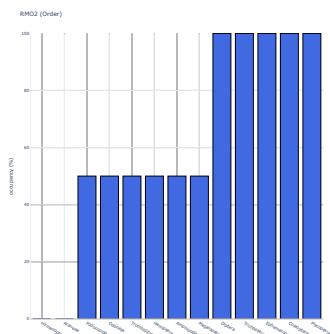
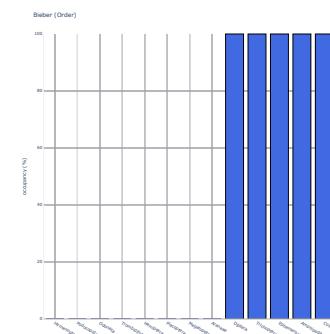
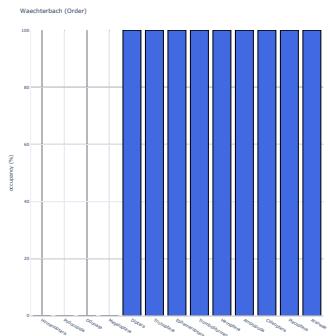
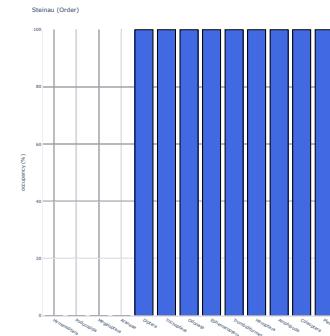
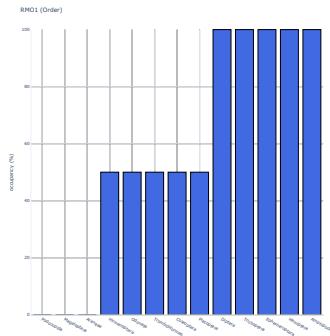
Site occupancy

- Load the latest TaXon table (*TTT_cons_derep_arthropoda_no_NC.xlsx*) in the **Analysis #3 tab**
- Remember: This TaXon table now has an according metadata table
- A new window will pop up and ask for additional information
 - In this case we choose the „Location_ID“ as metadata and „Order“ as taxonomic level
- The site occupancy will be calculated and the last (!) plot will be shown and all (!) plots will be saved



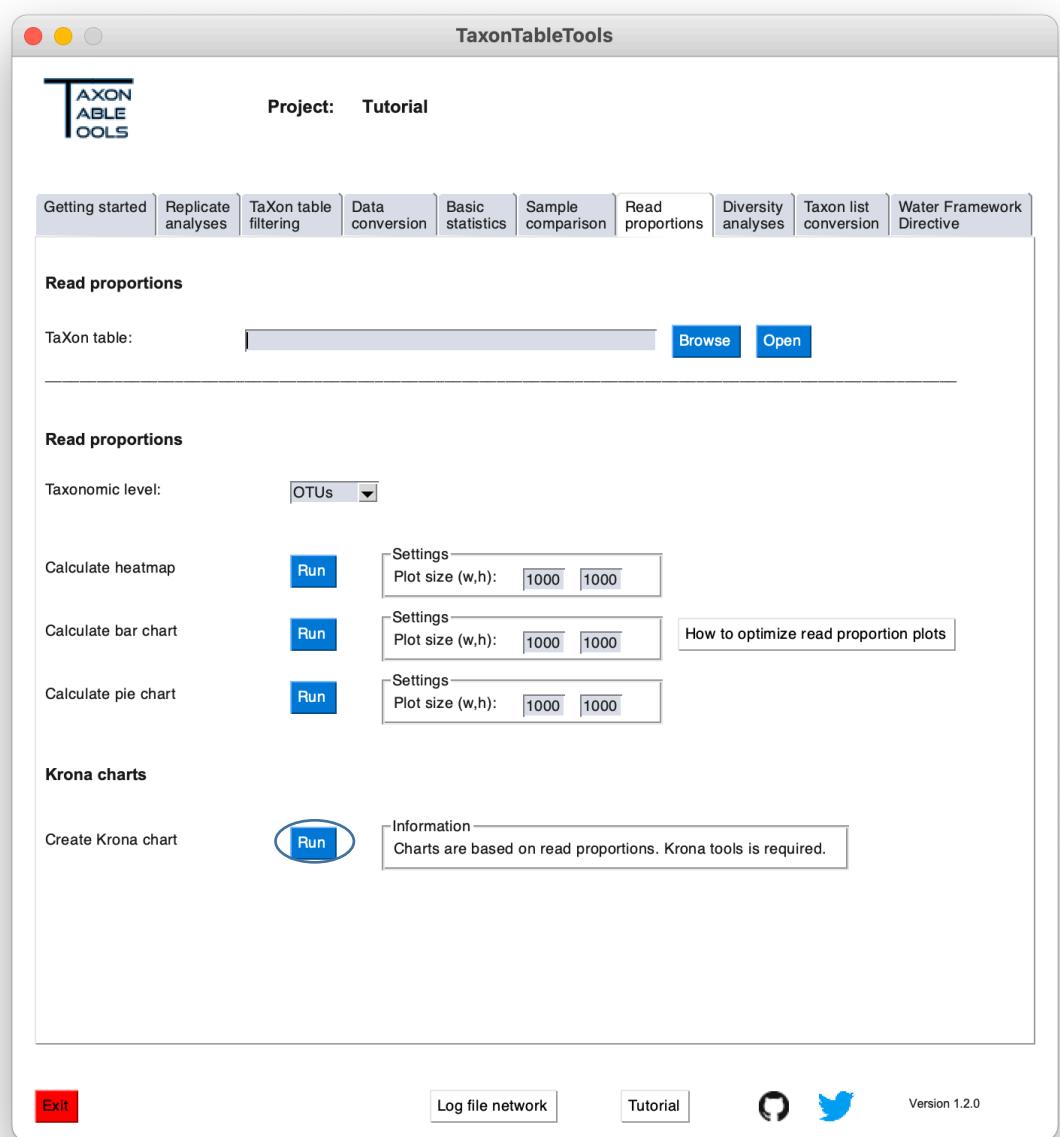
Site occupancy

- Each metadata (here: sampling site) was saved as an individual plot
- The x-axis shows the occupancy, ranging from 0 (present in none of the samples) to 100 (present in all of the samples)
- Note: despite its name, this tool is not limited to calculate the occupancy of a sampling site, but rather the taxon occupancy of any given metadata

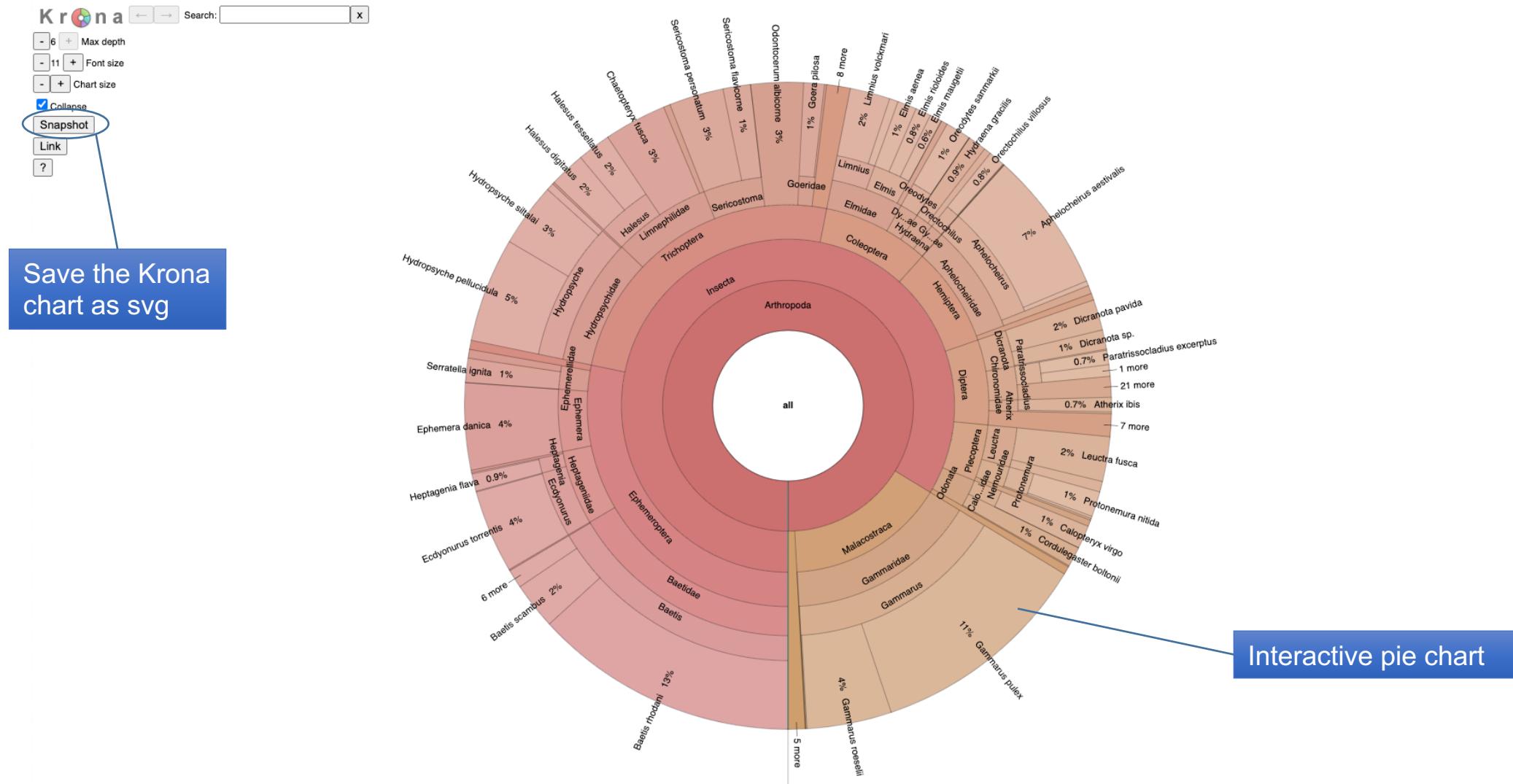


Krona charts

- Note: Krona tools is currently not available for Windows
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Click on Run
- The newly created Krona chart will be saved as html file
- The illustrated proportions are relative read abundances
- Open the file with any Browser (e.g. Chrome or Firefox)
- This interactive chart allows the user to zoom in to specific taxonomic level

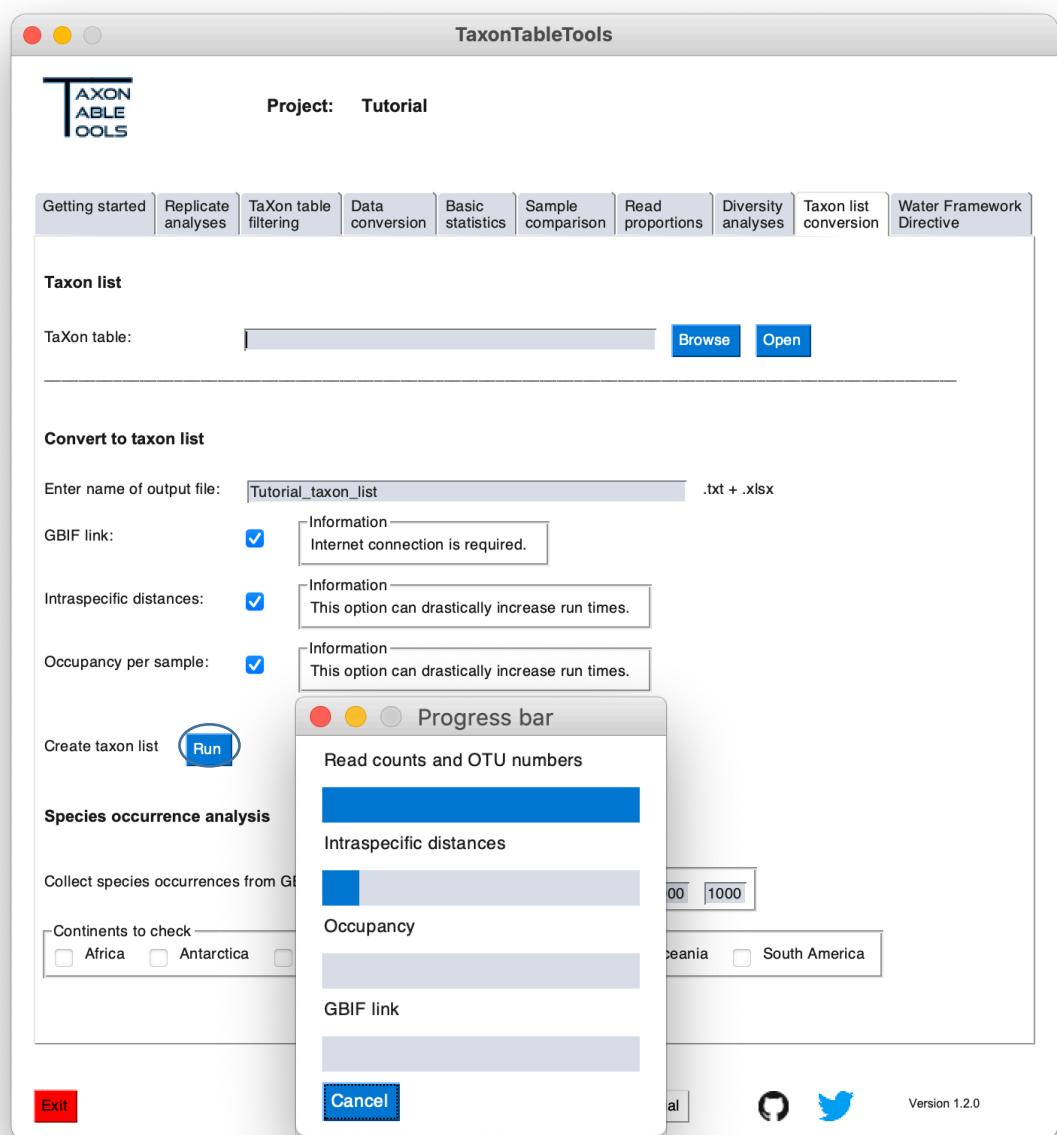


Krona charts



Taxon list

- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Enter the name of the output file
- Leave the all check mark
 - This requires internet connection
- Click on Run
- A new taxon list will be created that includes
 - All present taxa
 - Read counts (absolute, relative)
 - Occupancy across samples
 - Genetic distance for species level hits with multiple OTUs
 - GBIF link to the species



Taxon list

Taxon list statistics

Link to the gbif database

Phylum	Class	Order	Family	Genus	Species	reads	OTUs	occupancy	dist max	dist min	dist avg	gbif
Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus pulex	894888	2	0,71	3,09	3,09	3,09	https://www.gbif.org/species/2219853
Arthropoda	Insecta	Hemiptera	Aphelocheiridae	Aphelocheirus	Aphelocheirus aestivalis	567267	1	0,5				https://www.gbif.org/species/4485511
Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis rhodani	1062588	2	0,64	13,3	13,3	13,3	https://www.gbif.org/species/4481106
Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus roeselii	340348	3	0,43	9,26	3,09	6,97	https://www.gbif.org/species/5864277
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Ecdyonurus	Ecdyonurus torrentis	334421	1	0,43				https://www.gbif.org/species/4481477
Arthropoda	Insecta	Ephemeroptera	Ephemeridae	Ephemeria	Ephemeria danica	348767	1	0,86				https://www.gbif.org/species/5716472
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche pellucidula	420537	1	0,86				https://www.gbif.org/species/5054150
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche siltalai	256128	1	0,71				https://www.gbif.org/species/5054160
Arthropoda	Insecta	Coleoptera	Elmidae	Limnius	Limnius volckmari	160851	1	0,71				https://www.gbif.org/species/4427719
Arthropoda	Insecta	Trichoptera	Odontoceridae	Odontocerum	Odontocerum albicorne	210463	2	0,29	3,8	3,8	3,8	https://www.gbif.org/species/1437449
Arthropoda	Insecta	Trichoptera	Limnephilidae	Chaetopteryx	Chaetopteryx fusca	251747	1	0,36				https://www.gbif.org/species/1442278
Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostoma	Sericostoma personatum	218930	2	0,29	3,8	3,8	3,8	https://www.gbif.org/species/5053104
Arthropoda	Insecta	Coleoptera	Dytiscidae	Oreodytes	Oreodytes sanmarkii	102208	2	0,29	3,33	3,33	3,33	https://www.gbif.org/species/1038118
Arthropoda	Insecta	Odonata	Cordulegastridae	Cordulegaster	Cordulegaster boltonii	80464	1	0,14				https://www.gbif.org/species/1421161
Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis scambus	188247	4	0,57	4,04	2,61	3,44	https://www.gbif.org/species/4481160
Arthropoda	Insecta	Coleoptera	Elmidae	Elmis	Elmis aenea	76848	1	0,57				https://www.gbif.org/species/4427707
Arthropoda	Insecta	Diptera	Pediciidae	Dicranota	Dicranota pavida	123630	1	0,29				https://www.gbif.org/species/1510411
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptagenia	Heptagenia flava	69636	1	0,14				https://www.gbif.org/species/4481427
Arthropoda	Insecta	Trichoptera	Limnephilidae	Halesus	Halesus digitatus	143908	1	0,14				https://www.gbif.org/species/1441931
Arthropoda	Insecta	Trichoptera	Limnephilidae	Halesus	Halesus tessellatus	134187	1	0,29				https://www.gbif.org/species/119642498
Arthropoda	Insecta	Trichoptera	Goeridae	Goera	Goera pilosa	82978	1	0,14				https://www.gbif.org/species/1441388
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctra	Leuctra fusca	179718	2	0,71	2,85	2,85	2,85	https://www.gbif.org/species/2001954
Arthropoda	Insecta	Odonata	Calopterygidae	Calopteryx	Calopteryx virgo	93328	1	0,29				https://www.gbif.org/species/1427037
Arthropoda	Insecta	Coleoptera	Hydraenidae	Hydraena	Hydraena gracilis	74092	1	0,71				https://www.gbif.org/species/5748088
Arthropoda	Insecta	Diptera	Chironomidae	Paratrichocladius	nan	46912	1	0,29				
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Serratella	Serratella ignita	97111	1	0,14				https://www.gbif.org/species/4481256
Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostoma	Sericostoma flavicorne	110244	1	0,43				https://www.gbif.org/species/5053131
Arthropoda	Insecta	Coleoptera	Elmidae	Limnius	Limnius perrisi	34261	1	0,14				https://www.gbif.org/species/4427727
Arthropoda	Insecta	Trichoptera	Rhyacophilidae	Rhyacophila	Rhyacophila nubila	47439	1	0,43				https://www.gbif.org/species/1433809
Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis vernus	39676	2	0,43	5,46	5,46	5,46	https://www.gbif.org/species/4481086
Arthropoda	Insecta	Coleoptera	Elmidae	Elmis	Elmis riolooides	62192	3	0,71	4,28	3,09	3,49	https://www.gbif.org/species/4427709
Arthropoda	Insecta	Diptera	Pediciidae	Dicranota	Dicranota sp.	77673	4	0,86	7,13	3,33	5,9	

Taxonomic information

Taxon list

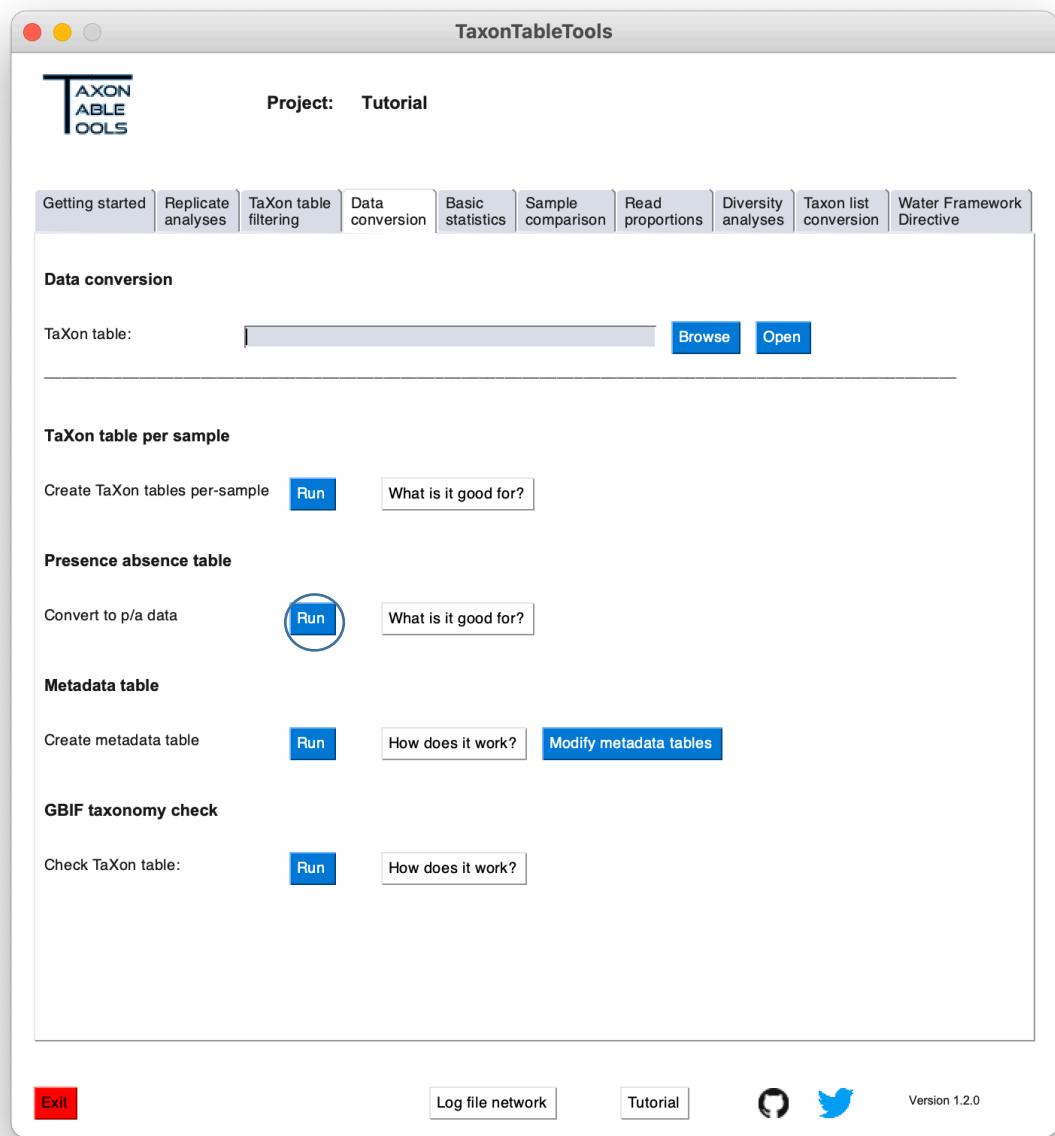
Intraspecific distances

- Intraspecific distances are calculated for species that were assigned to more than one OTU
- Three values are calculated:
 - Dist max = maximum genetic distance between OTUs
 - Dist min = minimum genetic distance between OTUs
 - Dis avg = average genetic distance between OTUs
- Large intraspecific distances can indicate:
 - Highly diverse species / cryptic species
 - Wrong taxonomic assignments
- Small intraspecific distances can indicate:
 - Overclustering

Species	reads	OTUs	occupancy	dist max	dist min	dist avg	
Gammarus pulex	894888	2	0,71	3,09	3,09	3,09	https://ww
Aphelocheirus aestivalis	567267	1	0,5				https://ww
Baetis rhodani	1062588	2	0,64	13,3	13,3	13,3	https://ww
Gammarus roeselii	340348	3	0,43	9,26	3,09	6,97	https://ww
Ecdyonurus torrentis	334421	1	0,43				https://ww
Ephemera danica	348767	1	0,86				https://ww
Hydropsyche pellucidula	420537	1	0,86				https://ww
Hydropsyche siltalai	256128	1	0,71				https://ww
Limnius volckmari	160851	1	0,71				https://ww
Odontocerum albicorne	210463	2	0,29	3,8	3,8	3,8	https://ww
Chaetopteryx fusca	251747	1	0,36				https://ww
Sericostoma personatum	218930	2	0,29	3,8	3,8	3,8	https://ww
Oreodytes sanmarkii	102208	2	0,29	3,33	3,33	3,33	https://ww
Cordulegaster boltonii	80464	1	0,14				https://ww
Baetis scambus	188247	4	0,57	4,04	2,61	3,44	https://ww
Elmis aenea	76848	1	0,57				https://ww
Dicranota pavida	123630	1	0,29				https://ww
Heptagenia flava	69636	1	0,14				https://ww
Halesus digitatus	143908	1	0,14				https://ww
Halesus tessellatus	134187	1	0,29				https://ww
Goera pilosa	82978	1	0,14				https://ww
Leuctra fusca	179718	2	0,71	2,85	2,85	2,85	https://ww
Calopteryx virgo	93328	1	0,29				https://ww
Hydraena gracilis	74092	1	0,71				https://ww
nan	46912	1	0,29				https://ww
Serratella ignita	97111	1	0,14				https://ww
Sericostoma flavicorne	110244	1	0,43				https://ww
Limnius perrisi	34261	1	0,14				https://ww
Rhyacophila nubila	47439	1	0,43				https://ww
Baetis vernus	39676	2	0,43	5,46	5,46	5,46	https://ww
Elmis rioloides	62192	3	0,71	4,28	3,09	3,49	https://ww
Dicranota sp.	77673	4	0,86	7,13	3,33	5,9	

Presence / absence data

- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*) in the **Data conversion** tab
- Convert the table to presence / absence data
- Note: This will create a new table and thus also a new meta data table is required
- You can either copy the previous meta data table and add the „_pa“ suffix to the file name or use the TTT module (but then you'll need to again adjust the meta data table)
- *Note: It is not required to convert the TaXon tables to presence/absence data for diversity and ordination analyses anymore! This will be done automatically.*

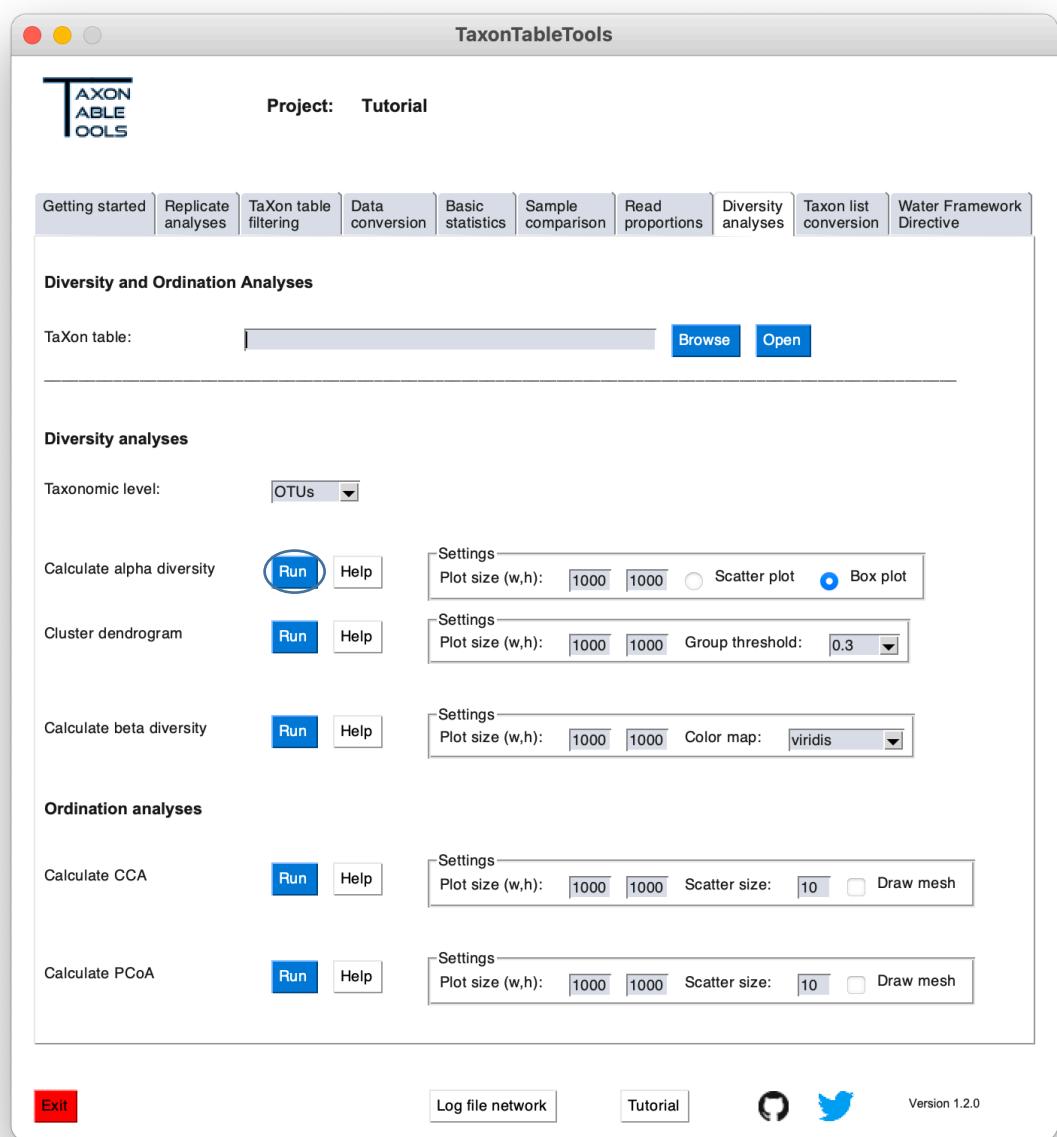


Diversity analyses

- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Note: The diversity analyses require a **TaXon table with a respective meta data table**
- **Taxonomic levels for diversity and ordination analyses can now be changed!**

Alpha diversity

- The ***Alpha diversity is measured as taxon richness***
- Choose a meta data to test (e.g. Location_ID)
- This will plot the number of OTUs per sample
- Create a scatter plot and a boxplot

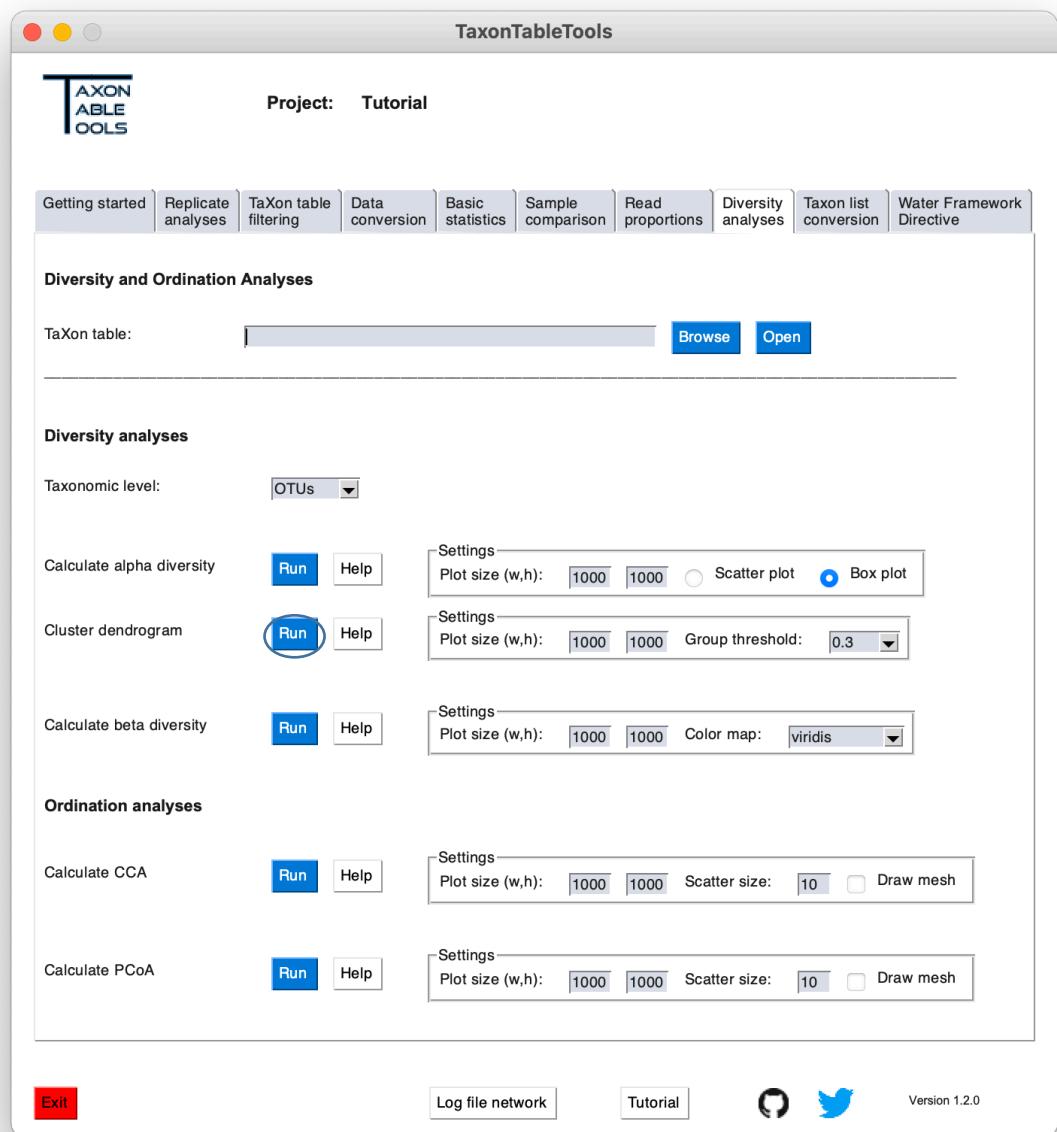


Diversity analyses

- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)

Cluster dendrogram

- This will calculate a cluster dendrogram, based on Jaccard distances of the samples
- The colour threshold for groupings can be adjusted

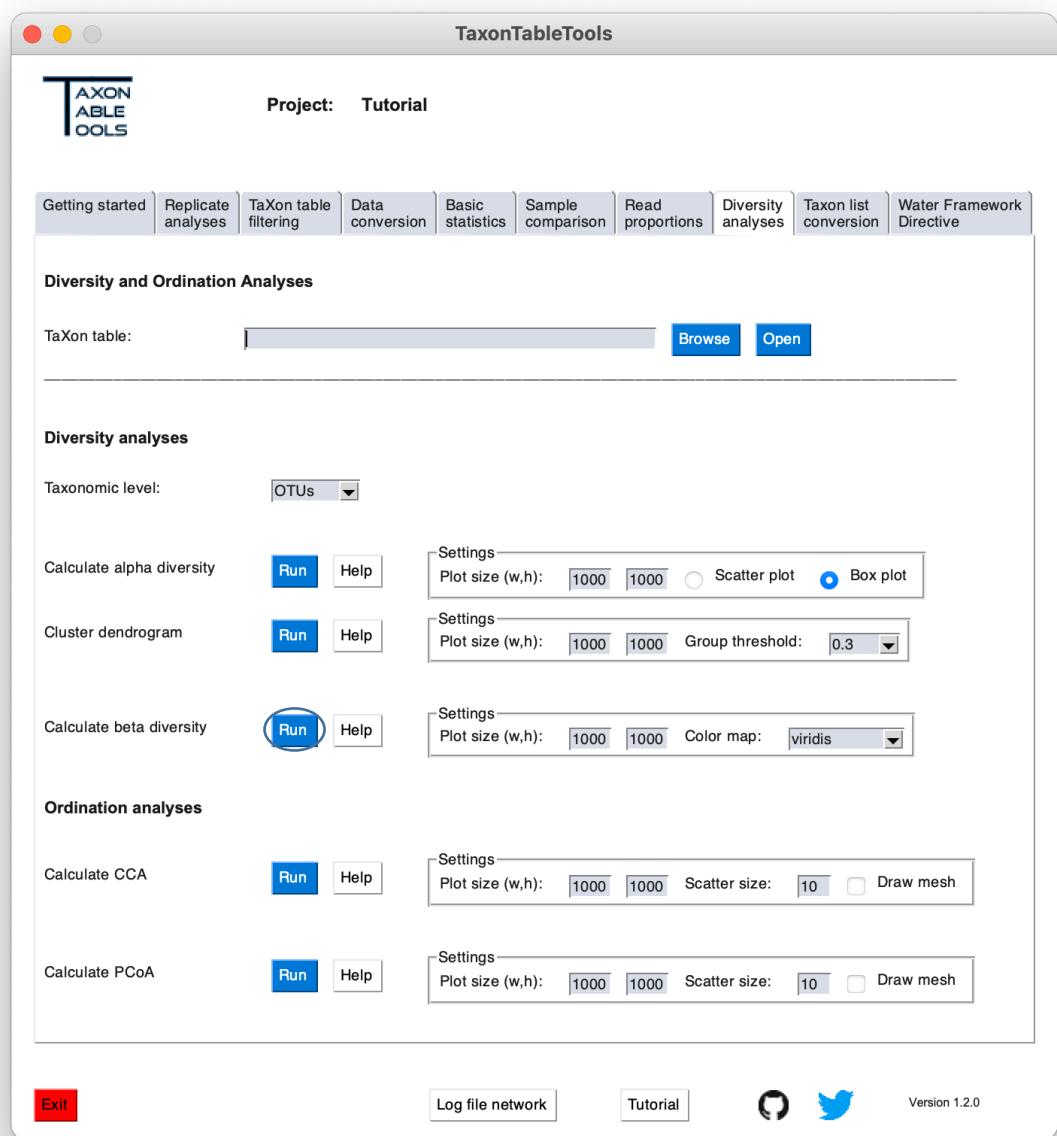


Diversity analyses

- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)

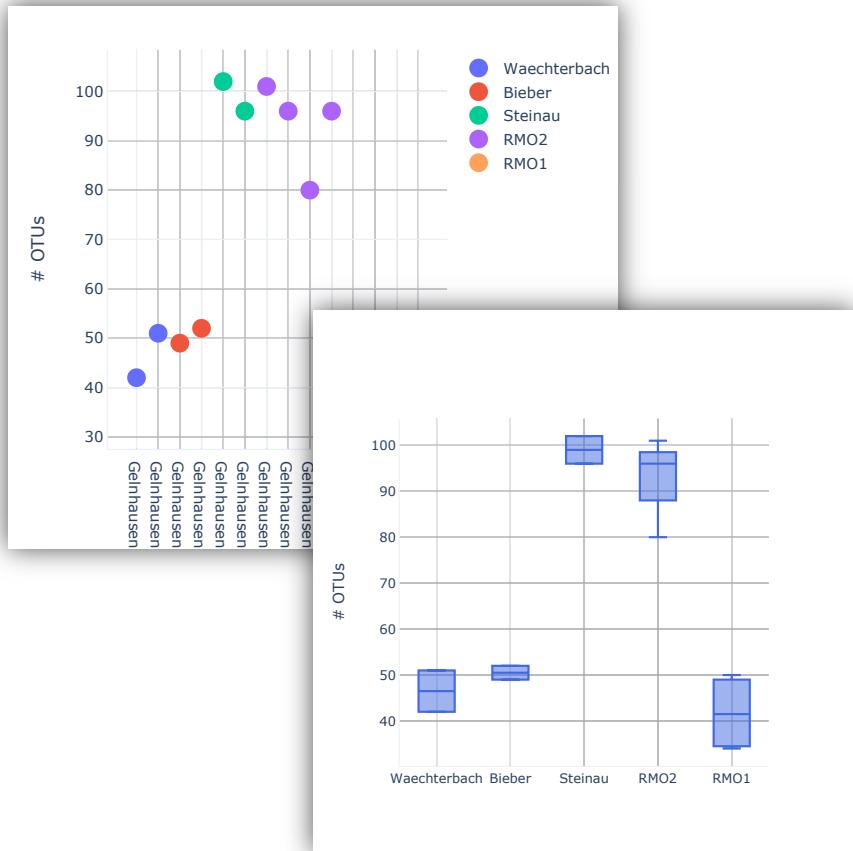
Beta diversity

- Choose a meta data to test (e.g. Location_ID)
- This will calculate **Jaccard distances** and perform an ANOSIM
- The colour of the plot can be adjusted with colourmaps

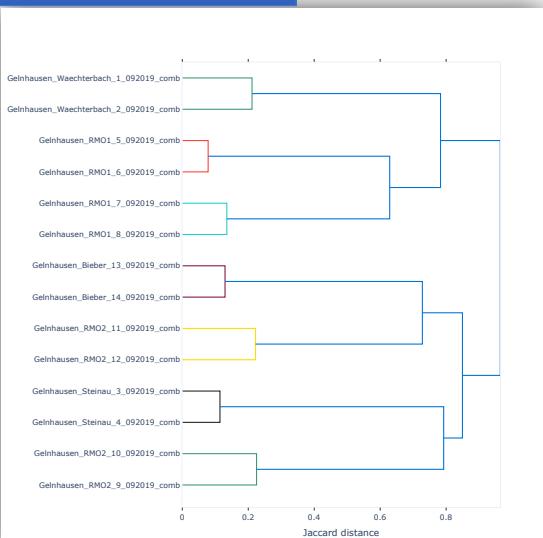


Diversity analyses

Alpha diversity



Beta diversity



Anosim (Location_ID) R = 0.90088 p = 0.001

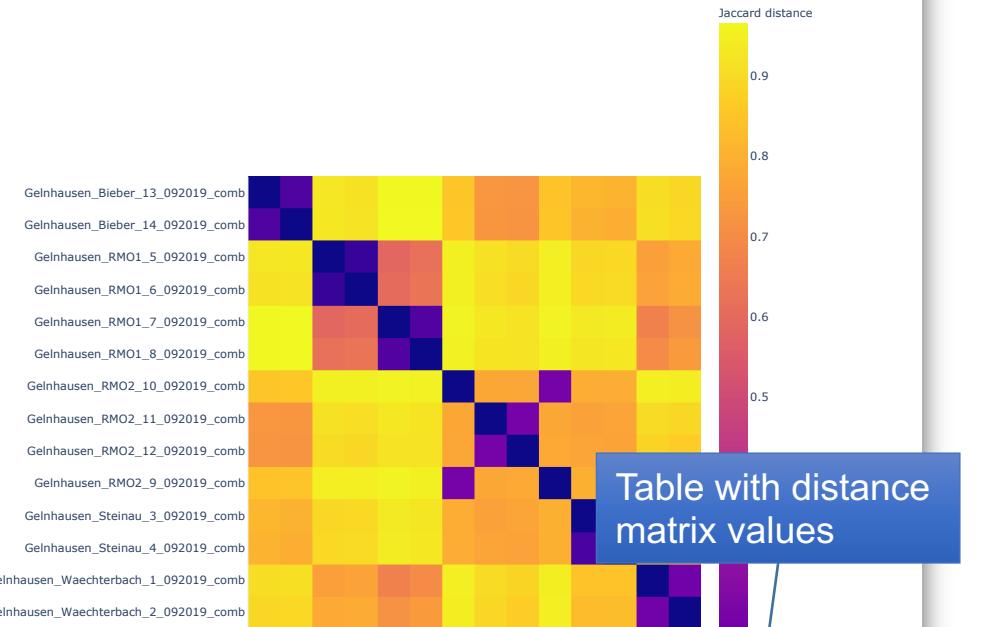
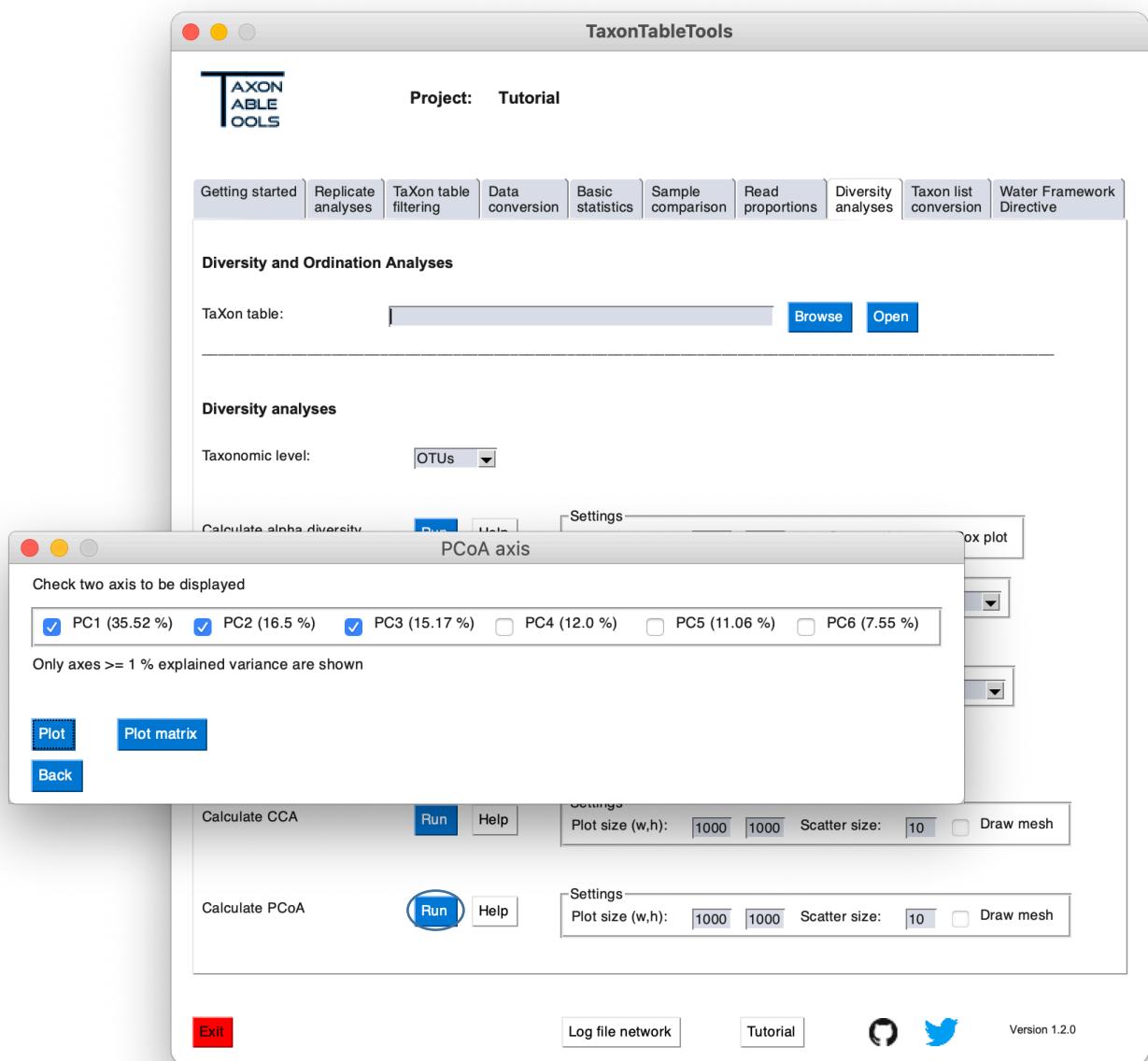


Table with distance matrix values

	Gelnhausen_Bieber_13_092019_comb	Gelnhausen_Bieber_14_092019_comb	RMO1_5_092019_comb	RMO1_6_092019_comb	RMO1_7_092019_comb	RMO1_8_092019_comb	RMO2_10_092019_comb	RMO2_11_092019_comb	RMO2_12_092019_comb	RMO2_9_092019_comb	Steinau_3_092019_comb	Steinau_4_092019_comb	Waechterbach_1_092019_comb	Waechterbach_2_092019_comb
Gelnhausen_Bieber_13_092019_comb	0	0,12963	0,92222	0,912088	0,9625	0,962963	0,846154	0,72807	0,722772	0,84,0,811024	0,80,0,1653	0,903614	0,888889	
Gelnhausen_Bieber_14_092019_comb	0,12963	0	0,924731	0,914894	0,963855	0,964286	0,849624	0,724138	0,718447	0,84375	0,796875	0,786885	0,906977	
Gelnhausen_RMO1_5_092019_comb	0,92222	0,924731	0	0,078431	0,586207	0,616667	0,943262	0,909091	0,896552	0,941176	0,888889	0,892308	0,75,0,777778	
Gelnhausen_RMO1_6_092019_comb	0,912088	0,914894	0,078431	0	0,6	0,629032	0,944056	0,902256	0,888889	0,942029	0,890511	0,893939	0,756757	
Gelnhausen_RMO1_7_092019_comb	0,9625	0,963855	0,586207	0,6	0	0,135135	0,953488	0,92562	0,914286	0,951613	0,929134	0,934426	0,666667	
Gelnhausen_RMO1_8_092019_comb	0,962963	0,964286	0,616667	0,629032	0,135135	0	0,945736	0,917355	0,915094	0,943548	0,92126	0,92623	0,694915	
Gelnhausen_RMO2_10_092019_comb	0,846154	0,849624	0,943262	0,944056	0,953488	0,945736	0	0,76875	0,768707	0,225225	0,784431	0,783951	0,940741	
Gelnhausen_RMO2_11_092019_comb	0,72807	0,724138	0,909091	0,902256	0,92562	0,917355	0,76875	0	0,222222	0,769231	0,754717	0,76129	0,896	
Gelnhausen_RMO2_12_092019_comb	0,722772	0,718447	0,896552	0,888889	0,914286	0,915094	0,768707	0,222222	0	0,777778	0,761905	0,760563	0,880734	
Gelnhausen_RMO2_9_092019_comb	0,84	0,84375	0,941176	0,942029	0,951613	0,943548	0,225225	0,769231	0,777778	0	0,792683	0,792453	0,938462	
Gelnhausen_Steinau_3_092019_comb	0,811024	0,796875	0,888889	0,890511	0,929134	0,92126	0,784431	0,754717	0,76129	0	0,114286	0,83871	0,823077	
Gelnhausen_Steinau_4_092019_comb	0,801653	0,786885	0,892308	0,893939	0,934426	0,92623	0,783951	0,76129	0,760563	0,792453	0,114286	0	0,840336	
Gelnhausen_Waechterbach_1_092019_comb	0,903614	0,906977	0,75	0,756757	0,666667	0,694915	0,940741	0,896	0,880734	0,938462	0,83871	0,840336	0,211538	
Gelnhausen_Waechterbach_2_092019_comb	0,888889	0,892473	0,777778	0,783133	0,712121	0,735294	0,937063	0,886364	0,86087	0,942446	0,823077	0,824	0,211538	

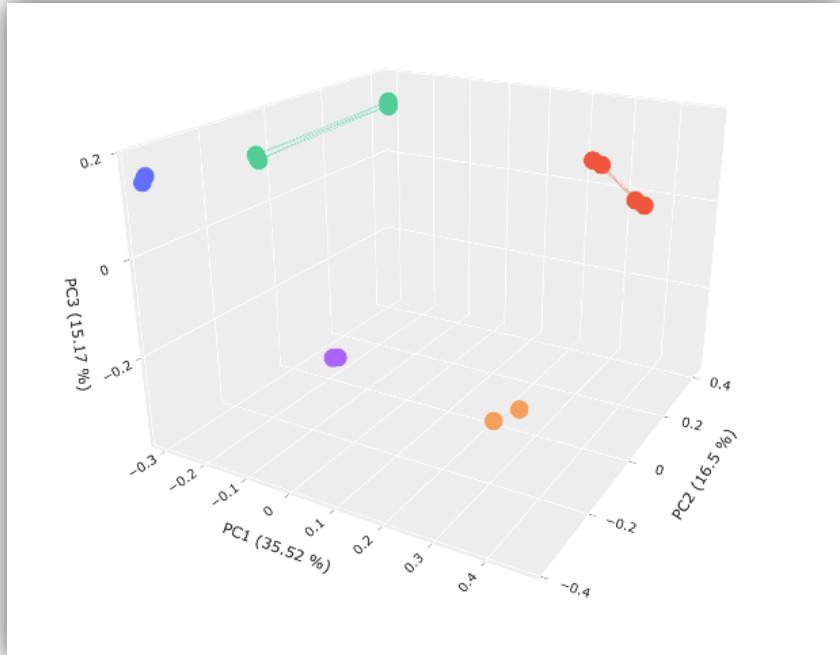
Ordination analyses

- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Perform a PCoA analysis
 - Choose a meta data to test (e.g. Location_ID)
 - This will plot the number of OTUs per sample
- Three options are available
 - Choosing 2 axes will create a 2D plot
 - Choosing 3 axes will create a 3D plot
 - The plot matrix option will create a matrix of the 4 first axes

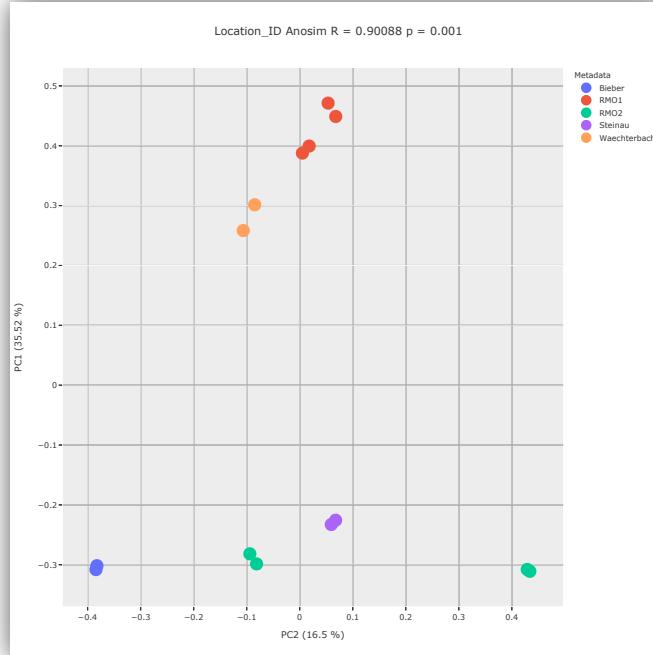


Ordination analyses

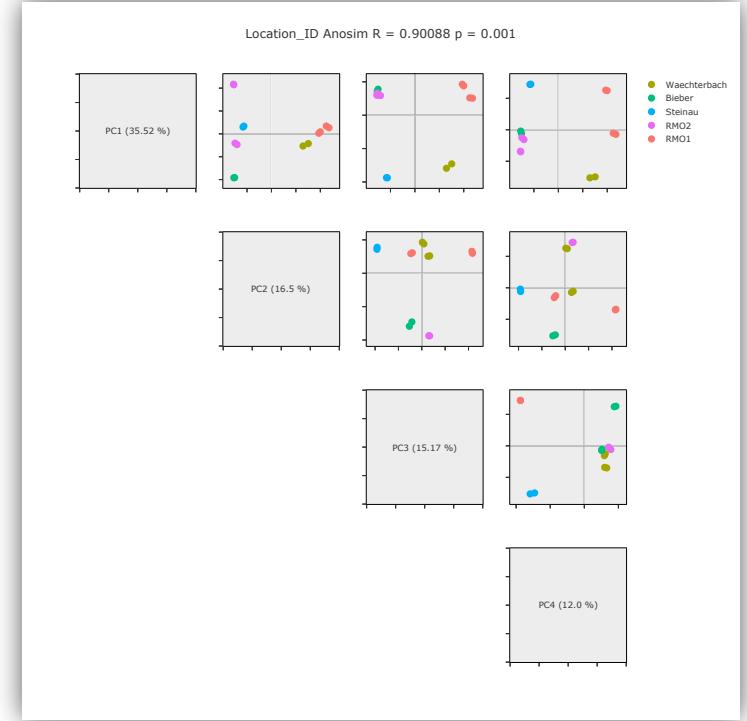
PCoA 3d plot



PCoA 2d plot



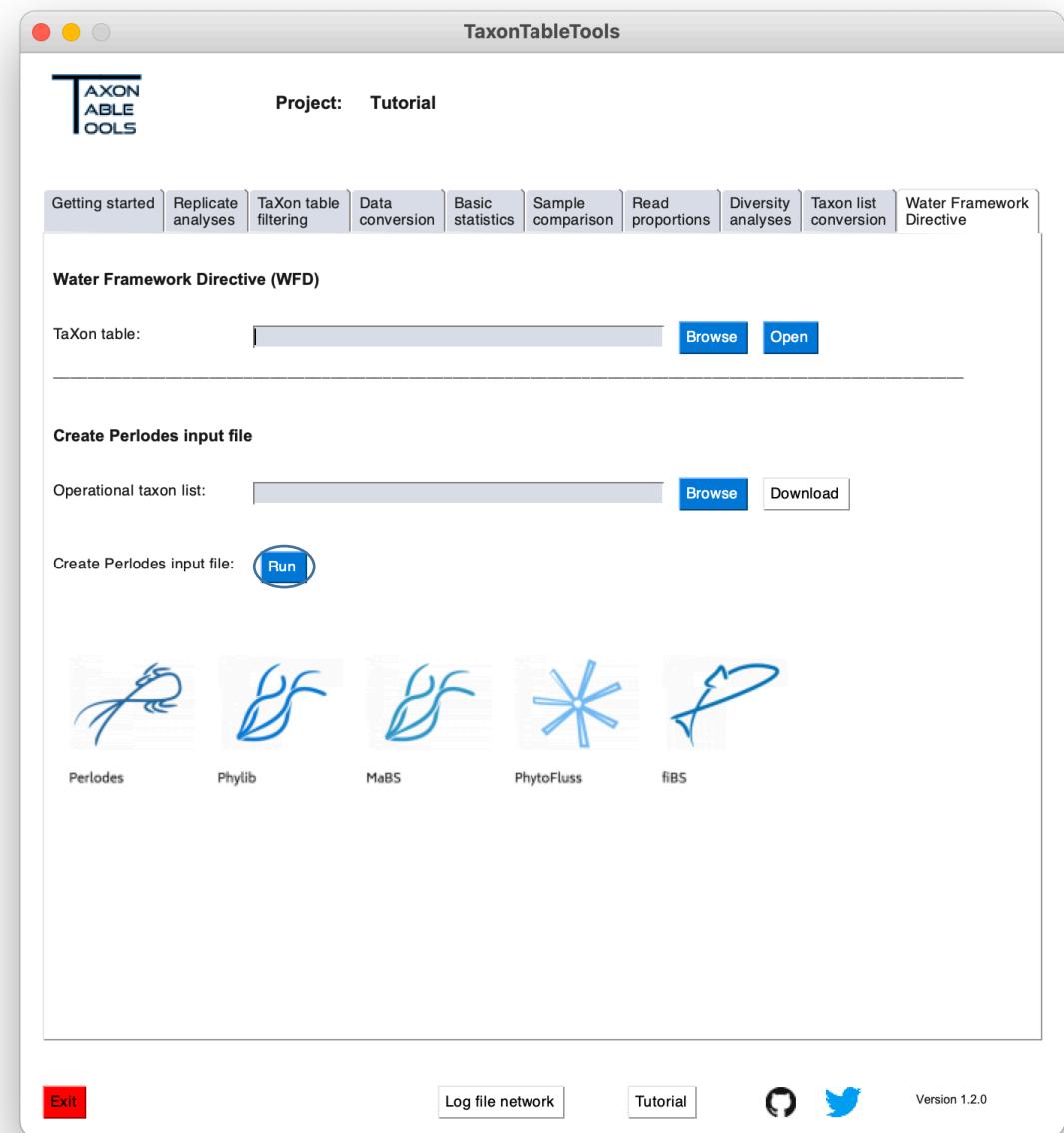
PCoA matrix plot



Water Framework Directive

TTT offer a conversion tool for the ecological quality assessment of streams according to the Water Framework Directive

- ***This is currently beta***
 - Only macrozoobenthos data can be converted for now
 - The conversion is based on the German evaluation program
 - Future versions will include more conversions
-
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
 - Download the latest operational taxon list
 - Convert the TaXon table to the perlodes format



Water Framework Directive

The operational taxon list is used as reference to assign the WFD specific ID to each species present in the dataset

Two tables are created:

- A conversion history table to check for potential errors
- A perlodes input-ready table for quality assessment evaluations

A	B	C	D	E	F	G	I	J
Gruppe	Familie	DV-Nr.	Taxonname (Bundesstaatliste)	ID-Art	Taxonname (Perlodes-Datenbank)	zu verwendende Bestimmungsliteratur	Anmerkungen	
Operationelle Taxalliste								
5	PORIFERA							
6	[Kl] Poriferidae	1014	Spongidae	8846	Spongidae Gen. sp.			
7						Holstein (1995), Bröch (1928)		
8	HYDROZOA							
9	[Kl] Hydrozoa	5892	Hydrozoa	9247	Hydrozoa Gen. sp.	Bröch (1928) nur relevant für Typ 2 & 3 Gewässer		
10	Cladidae	5289	Cordylophora caspia	4743	Cordylophora caspia	häufigste Art		
11	TURBELLARIA							
12						Reynoldson & Young (2000) plus Ergänzung Pauls (2004)		
13	[Kl] Turbellaria	3736	Turbellaria	8181	Turbellaria Gen. sp.	Die Bestimmung der Turbellaria sollte am lebenden Tier vorgenommen werden. Durch die Konserverierung in Alkohol verändert sich die Form deutlich. Durch Kontraktion oder Auflösen des Gewebes die Kopfform. Die Bestimmung erfolgt im Gelände nach Reynoldson & Young (2000) inklusive der Ergänzungen von Pauls (2004) zu Dugesiacephala und Dendrocoelium romanoianum.		
14	Dendrocoelidae	1320	Bellidiscula punctata	11361	Bellidiscula punctata	für unvollständige oder schlecht konservierte Exemplare		
15		1265	Dendrocoelum sp.	982	Dendrocoelum sp.	für unvollständige oder schlecht konservierte Exemplare		
16	1007	Dendrocoelum lacteum	4911	Dendrocoelum lacteum				
17		1243	Dendrocoelium romanoianum	9189	Dendrocoelium romanoianum			
18	Dugesidae	1946	Dugesia	5021	Dugesia sp.	Pauls (2004)		
19		1011	Dugesia gonocephala	5018	Dugesia gonocephala	für unvollständige oder schlecht konservierte Exemplare		
20		1177	Dugesia lugubris / polychaeta	9745	Dugesia lugubris / polychaeta	Pauls (2004)		
21		1104	Dugesia lugubris	5193	Dugesia lugubris	Nachweis aus Nordamerika, Irwinkella weit verbreitet		
22	Planariaidae	1046	Crenobia alpina	4771	Crenobia alpina	Quellen und Quellbäche		
23		1262	Phagocotyle	13646	Phagocotyle sp.			
24		1200	Platycephalus	6150	Platycephalus			
25		1371	Polydora	7744	Polydora sp.	für unvollständige oder schlecht konservierte Exemplare		
26		1016	Polydora felina	6463	Polydora felina	Quellen, Quellbäche, Bachoberläufe		
27		1222	Polydora nigra / fumosa	13866	Polydora nigra/fumosa			
28	GASTROPODA							
29						Göller & Meier-Brook (2003), Göller (2002)		
30	[Kl] Acochlididae	1095	Acrolochus lacustris	4205	Acrolochus lacustris	Siedlungsschwerpunkt im Stillgewässer		
31	Assimineidae	1202	Assiminea granaria	14464	Assiminea granaria	Brackwasser		
32		1112	Bithynia	4461	Bithynia sp.	nur für juvenile Tiere		
33		1398	Bithynia leachii	416	Bithynia leachii			
34		1009	Bithynia tentaculata	4462	Bithynia tentaculata			
35		1917	Bithynia triserialis	16772	Bithynia triserialis	Insbesondere die adulten sind leicht von B. leachii zu trennen. Vorher Untertar von B. leachii		
36		1564	Bithynia truncata	918	Bithynia truncata	für juv. Qualitäten und Quellbäche, kalkmeidend		
37		1067	Bythotrephidae	4513	Bythotrephidae			
38		1991	Bythotrephes	8808	Bythotrephes sp.			
39		1235	Bythotrephes cederstroemi	1235	Bythotrephes cederstroemi	Brackwasser		
40		1070	Lithoglyphus nativitatis	5896	Lithoglyphus nativitatis			
41		1200	Marionopsis schultzi	5847	Marionopsis schultzi			
42		8551	Monotropus aciculatus	8551	Monotropus aciculatus	zumindest Brackwasserarten - Nitrogen		
43	Anmerkungen							
44	Operationelle Taxalliste							

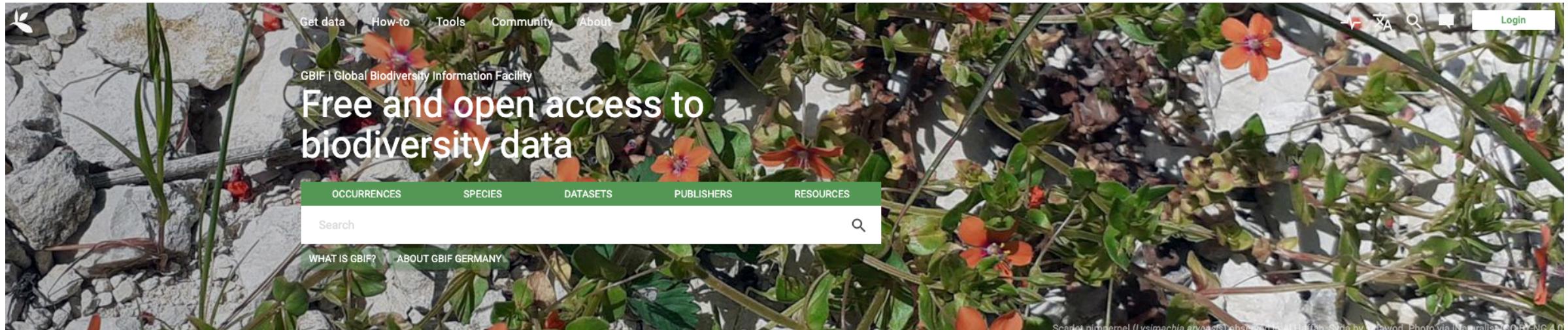


A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	I
ID_ART	TAXON_NAME	leber_13	leber_14	RM01_5	RM01_6	RM01_7	RM02_8	RM02_9	RM02_10	RM02_11	RM02_12	RM02_13	Steinau_3	Steinau_4	chterbach
2	Goera illosa	0	0	1	1	0	0	0	0	0	0	0	0	0	0
3	Limonia iliae Gen. sp.	1	1	0	0	0	0	0	0	0	0	0	0	0	0
4	Silo piceus	0	0	0	0	0	0	0	0	0	0	1	1	0	0
5	Baetis vardenensis	0	0	0	0	0	0	0	0	0	0	0	0	0	1
6	Silo pallipes	0	0	0	0	0	0	0	1	1	0	0	0	0	0
7	Aphelocheirus aestivalis	0	0	1	1	1	0	0	0	0	0	1	0	1	1
8	Ephemera danica	0	0	1	1	1	1	1	1	1	1	1	1	1	1
9	Cheumatopsyche lepidia	0	0	0	0	0	0	0	0	0	0	1	1	0	0
10	Caenis sp.	0	0	0	0	0	0	0	0	0	1	0	0	0	0
11	Heptagenia sulphurea	0	0	0	0	0	0	0	0	0	0	0	0	0	1
12	Leuctra geniculata	0	0	0	0	0	0	0	0	0	0	1	1	1	1
13	Ecdyonurus pullex	0	0	0	0	0	0	0	0	1	0	0	0	0	0
14	Aplochorema volckmarii	1	1	0	0	0	0	1	1	1	1	1	1	1	1
15	Baetis rhodani	0	0	0	0	0	0	0	0	0	0	1	1	0	0
16	Rhyacophila nubila	1	1	0	0	0	0	1	0	0	0	1	1	0	0
17	Rhyacophila semicolorata-Gr.	1	1	0	0	0	0	1	1	0	1	1	1	0	0
18	Sialis fuliginosa	1	0	0	0	0	0	0	1	1	1	1	0	0	0
19	Sialis fuliginosa	0	0	0	0	0	0	0	1	0	0	0	0	0	0
20	Torleya major	0	0	0	0	0	0	0	0	1	0	0	1	0	0

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P
ID_ART	TAXON_NAME	leber_13	leber_14	RM01_5	RM01_6	RM01_7	RM02_8	RM02_9	RM02_10	RM02_11	RM02_12	RM02_13	Steinau_3	Steinau_4	chterbach
2	Goera illosa	0	0	1	1	0	0	0	0	0	0	0	0	0	0
3	Limonia iliae Gen. sp.	1	1	0	0	0	0	0	0	0	0	0	0	0	0
4	Silo piceus	0	0	0	0	0	0	0	0	0	0	0	1	1	0
5	Baetis vardenensis	0	0	0	0	0	0	0	0	0	0	0	0	0	1
6	Aphelocheirus aestivalis	0	0	1	1	1	0	0	0	0	0	0	1	1	1
7	Ephemera danica	0	0	1	1	1	1	1	1	1	1	1	1	1	1
8	Cheumatopsyche lepidia	0	0	0	0	0	0	0	0	0	0	0	1	1	0
10	Caenis sp.	0	0	0	0	0	0	0	0	0	0	0	0	0	0
11	Heptagenia sulphurea	0	0	0	0	0	0	0	0	0	0	0	0	0	1
12	Leuctra geniculata	0	0	0	0	0	0	0	0	0	0	0	1	1	1
13	Ecdyonurus pullex	0	0	0	0	0	0	0	0	1	0	0	0	0	0
14	Aplochorema volckmarii	1	1	0	0	0	0	1	1	1	1	1	1	1	1
15	Baetis rhodani	0	0	0	0	0	0	0	0	0	0	0	1	1	0
16	Rhyacophila nubila	1	1	0	0	0	0	1	0	0	0	0	1	1	0
17	Rhyacophila semicolorata-Gr.	1	1	0	0	0	0	1	1	0	1	0	1	1	0
18	Sialis fuliginosa	1	0	0	0	0	0	0	1	1	1	1	1	0	0
19	Sialis fuliginosa	0	0	0	0	0	0	0	1	0	0	1	0	0	0
20	Torleya major	0	0	0	0	0	0	0	0	1	0	0	1	1	0

New in version 1.1: GBIF API-based tools

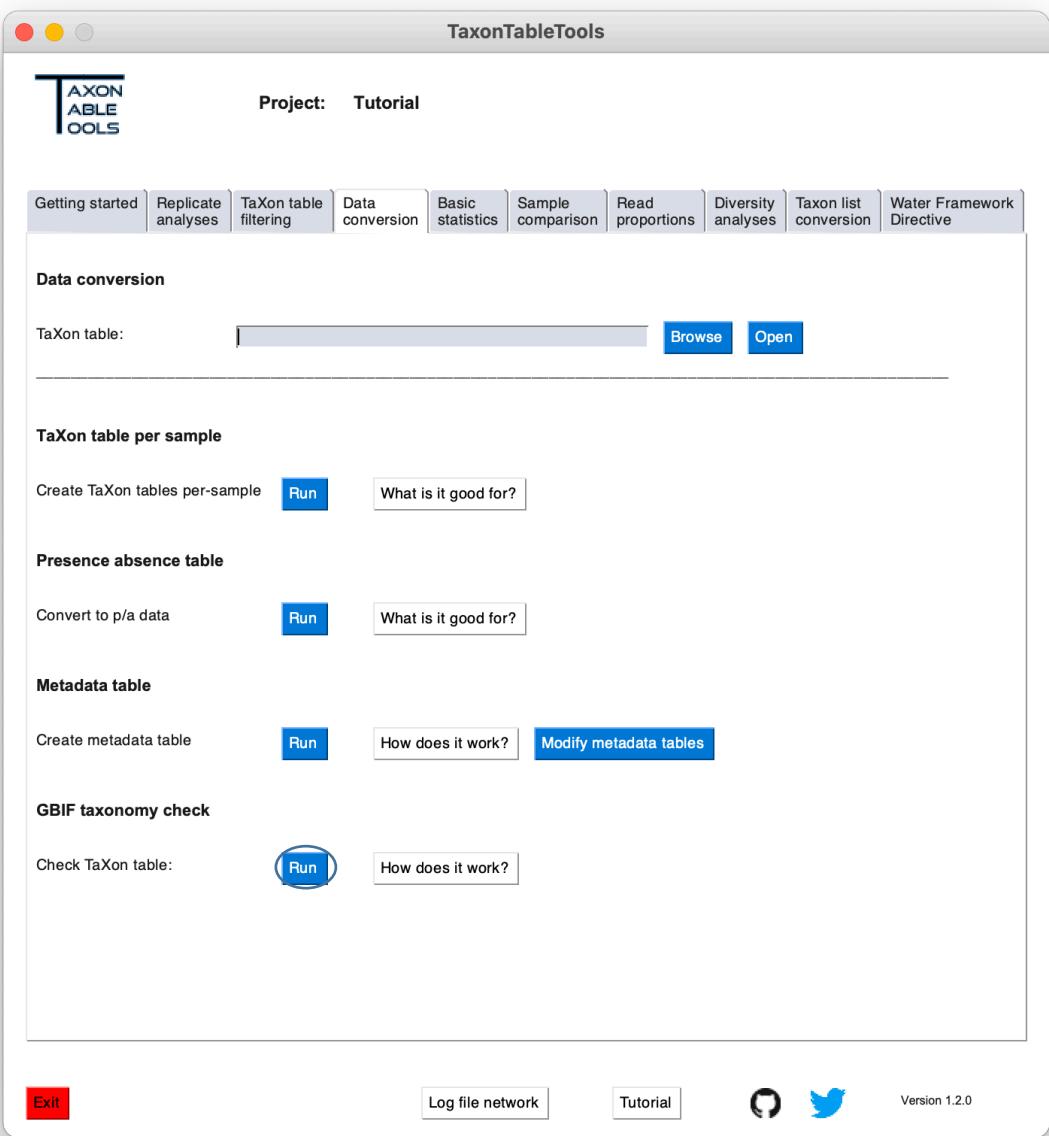
The GBIF (Global Biodiversity Information Facility) database offers several useful functions to download information on taxonomic data



GBIF taxonomy check

GBIF offers the correction for spelling mistakes and for synonyms of taxonomic datasets

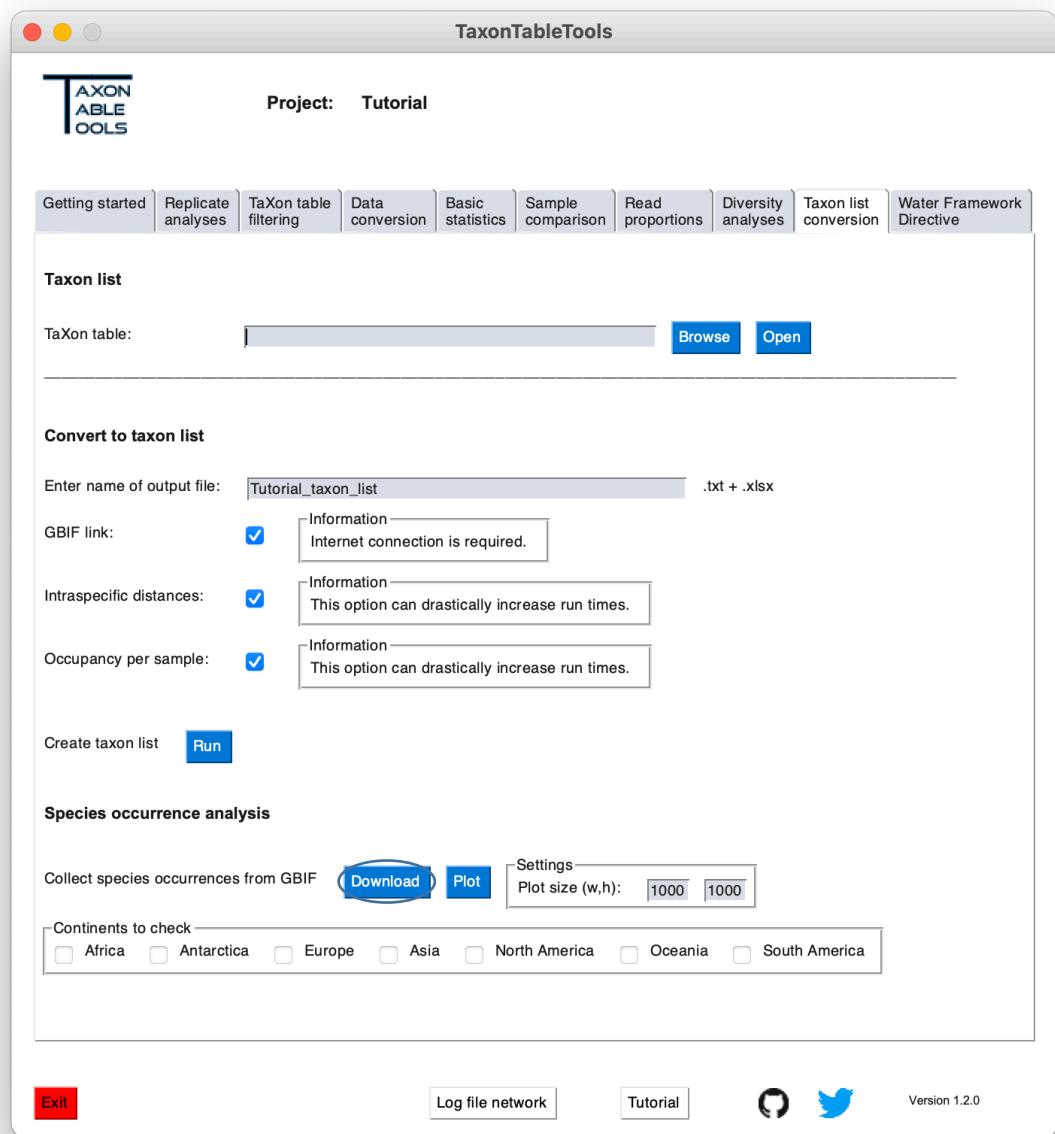
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC.xlsx*)
- Run the GBIF taxonomy check
- Two tables will be created:
 - A new, corrected TaXon table
 - A log file where each correction can be tracked
- Warning: Always check the GBIF log file for possible mistakes
- For some groups information on specific taxonomic levels is not available and will be left blank



GBIF species occurrence

GBIF offers the assessment of occurrence data for species

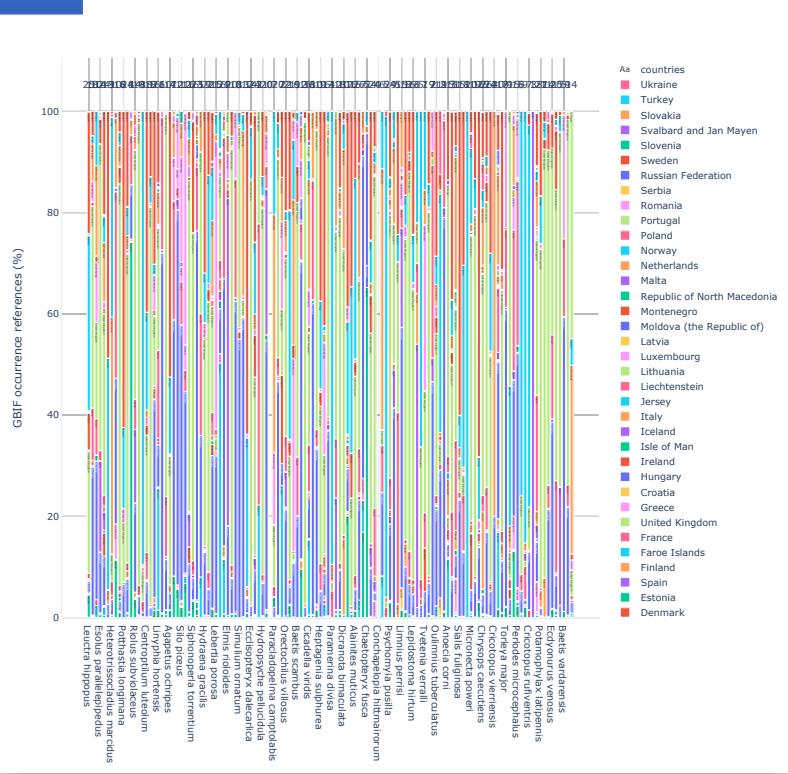
- Load the latest TaXon table (*TTT_cons_derep_arthropods_no_NC_gbif.xlsx*)
- Run the GBIF occurrence analysis
- Check mark Europe for this example
- This will roughly take 17 minutes
- The relative number of species reference in the GBIF database is plotted
- This allows to quickly assess the dataset for the species distributions
- Furthermore, potential bias can be quickly detected when species do not occur in the sampled region



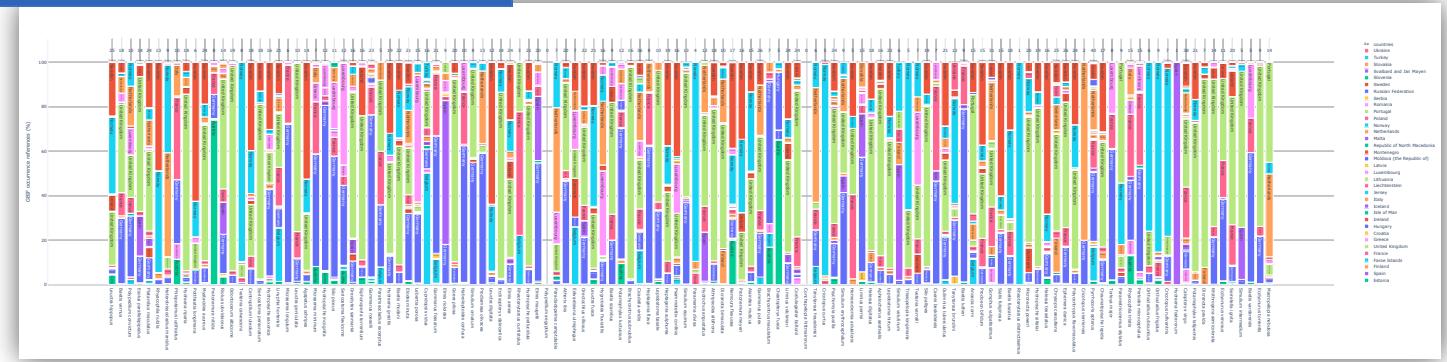
GBIF species occurrence

Use the plot function to plot the occurrence data again, with adjusted width and height!

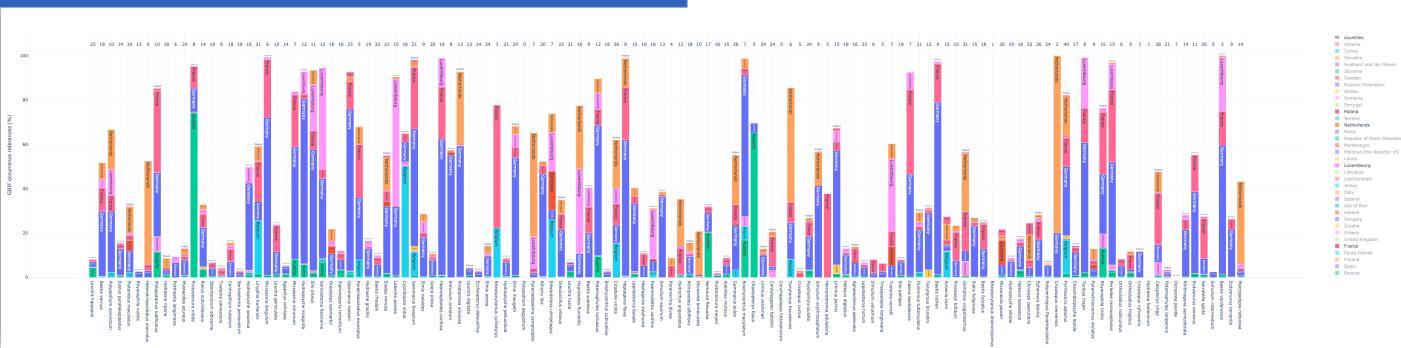
Raw



Re-plotted with adjusted size



Only Germany and surrounding countries



GBIF species occurrence

Both the absolute and relative occurrence reference numbers are written to an excel sheet

Relative values

Absolute values

TTT log file

TTT tracks each module that was run and writes the user history to a log file

- Based on the log table a log network can be created to visualise the usage history

Log table

A	B	C
task	input	output
2 taXon table converter	tutorial_taxonomy_table.xlsx + tutorial_read_table.xlsx	Tutorial_taxon_table.xlsx
3 taXon table converter	tutorial_taxonomy_table.xlsx + tutorial_read_table.xlsx	TTT.xlsx
4 replicate analysis	TTT.xlsx	Gelnhausen_Waechterbach_2_092019
5 replicate correlation analysis	TTT.xlsx	TTT_reportr_OUTUS.pdf
6 replicate consistency	TTT.xlsx	TTT.xlsx
7 replicate merging	TTT_cons.xlsx	TTT_cons.xlsx
8 taxon filter	TTT_cons_derep.xlsx	TTT_cons_derep.xlsx
9 basic stats	TTT_cons_derep_arthropoda.xlsx	TTT_cons_derep_arthropoda_basic_stats
10 sample filter	TTT_cons_derep_arthropoda.xlsx	TTT_cons_derep_arthropoda_no_NC.xlsx
11 taxonomic resolution	TTT_cons_derep_arthropoda_no_NC.xlsx	TTT_cons_derep_arthropoda_no_NC_taxonomic_resolution_a.pdf
12 taxonomic resolution	TTT_cons_derep_arthropoda_no_NC.xlsx	plot a
13 taxonomic resolution	TTT_cons_derep_arthropoda_no_NC.xlsx	TTT_cons_derep_arthropoda_no_NC_taxonomic_resolution_b.pdf
14 taxonomic resolution	TTT_cons_derep_arthropoda_no_NC.xlsx	plot b
15 taxonomic resolution	TTT_cons_derep_arthropoda_no_NC.xlsx	2020-12-04 19:18:34.412425 analysis

Log network

