



# TaxonTableTools tutorial

Version 1.0

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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
```

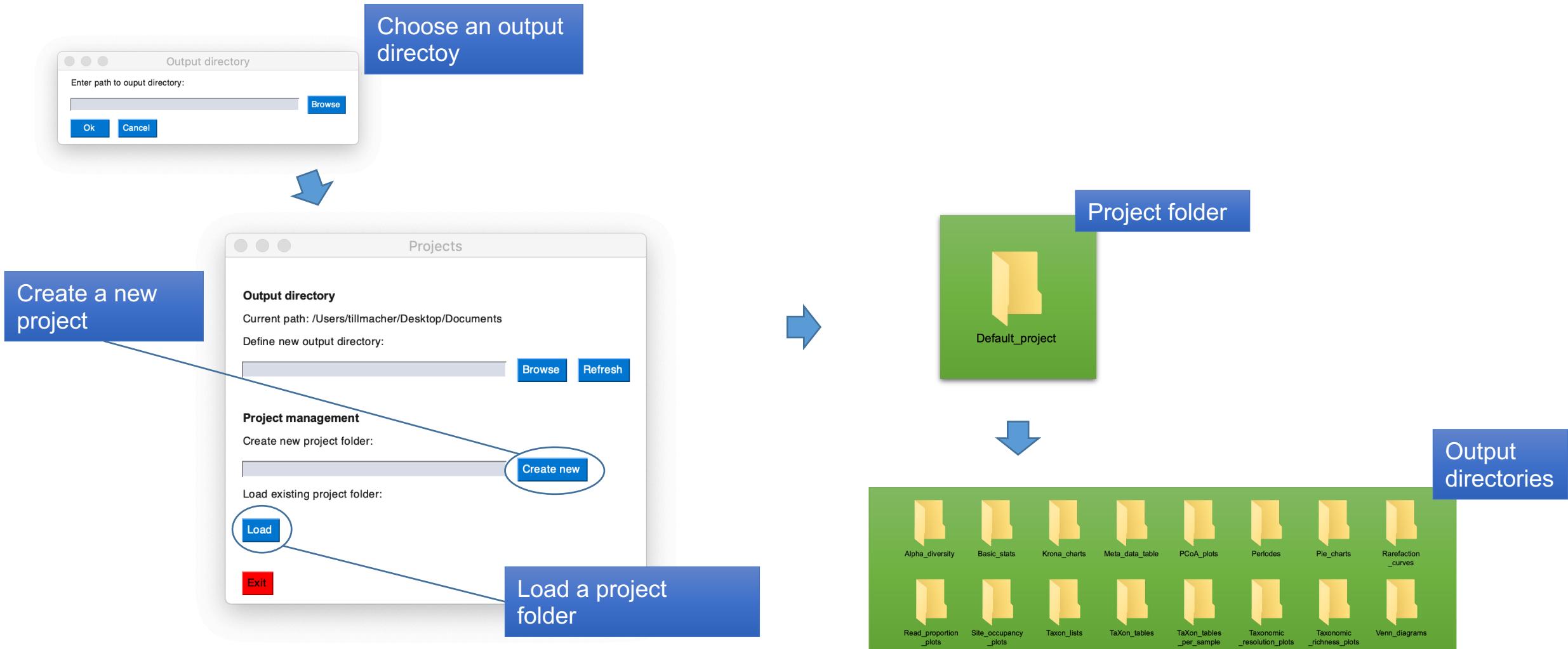
- TaxonTableTools can then be started via:

```
$ python3 -m taxontabletools
```

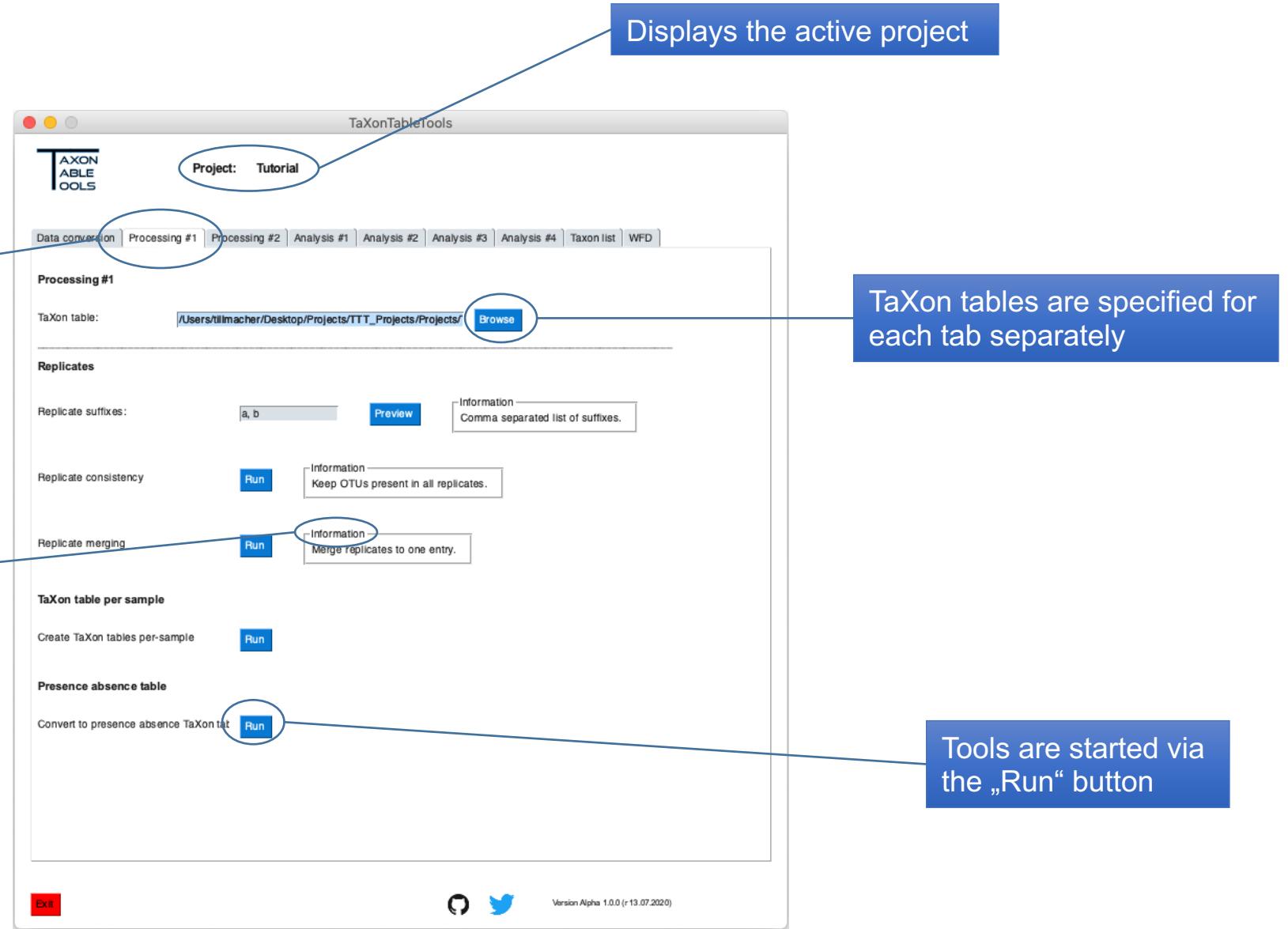
- Updates can be installed via:

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

# Project management



All tools are found under specific tabs



Additional information can be found here

# Read table format

IDs = column for  
OTU names

## Sample names

Sequences = Sequence  
of each OTU

## Read abundances



# Taxonomy table format

IDs = column for OTU names

Taxonomic level column:  
Phylum to Species

Species name should consist of  
the genus name and epithet

A	B	C	D	E	F	G	H	I
IDs	Phylum	Class	Order	Family	Genus	Species	Similarity	Status
2	OTU_1	Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus pulex	100
3	OTU_2	Arthropoda	Insecta	Hemiptera	Aphelocheiridae	Aphelocheirus	Aphelocherrus aestivalis	100
4	OTU_3	Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis rhodani	100
5	OTU_4	Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus roeselii	100
6	OTU_5	Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Ecdyonurus	Ecdyonurus torrentis	100
7	OTU_6	Arthropoda	Insecta	Ephemeroptera	Ephemeridae	Ephemerina	Ephemerina danica	100
8	OTU_7	Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis rhodani	99,74
9	OTU_8	Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche pellucidula	100
10	OTU_9	Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche siltalai	100
11	OTU_10	Mollusca	Gastropoda	Littorinimorpha	Tateidae	Potamopyrgus	Potamopyrgus antipodarum	100
12	OTU_11	Arthropoda	Insecta	Coleoptera	Elmidae	Limnus	Limnus volckmari	100
13	OTU_12	Mollusca	Bivalvia	Venerida	Cyrenidae	Corbicula	Corbicula fluminea	100
14	OTU_13	Arthropoda	Insecta	Trichoptera	Odontoceridae	Odontocerum	Odontocerum albicorne	100
15	OTU_14	Arthropoda	Insecta	Trichoptera	Odontoceridae	Odontocerum	Odontocerum albicorne	100
16	OTU_15	Arthropoda	Insecta	Trichoptera	Limnephilidae	Chaetopteryx	Chaetopteryx fusca	100
17	OTU_16	Annelida	Clitellata	Haplotaxida	Lumbricidae	Eiseniella	Eiseniella tetraedra	100
18	OTU_17	Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostoma	Sericostoma personatum	100
19	OTU_18	Arthropoda	Insecta	Coleoptera	Dytiscidae	Oreodytes	Oreodytes sanmarkii	100
20	OTU_19	Arthropoda	Insecta	Odonata	Cordulegastridae	Cordulegaster	Cordulegaster boltonii	100
21	OTU_20	Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis scambus	100

Database hit similarity

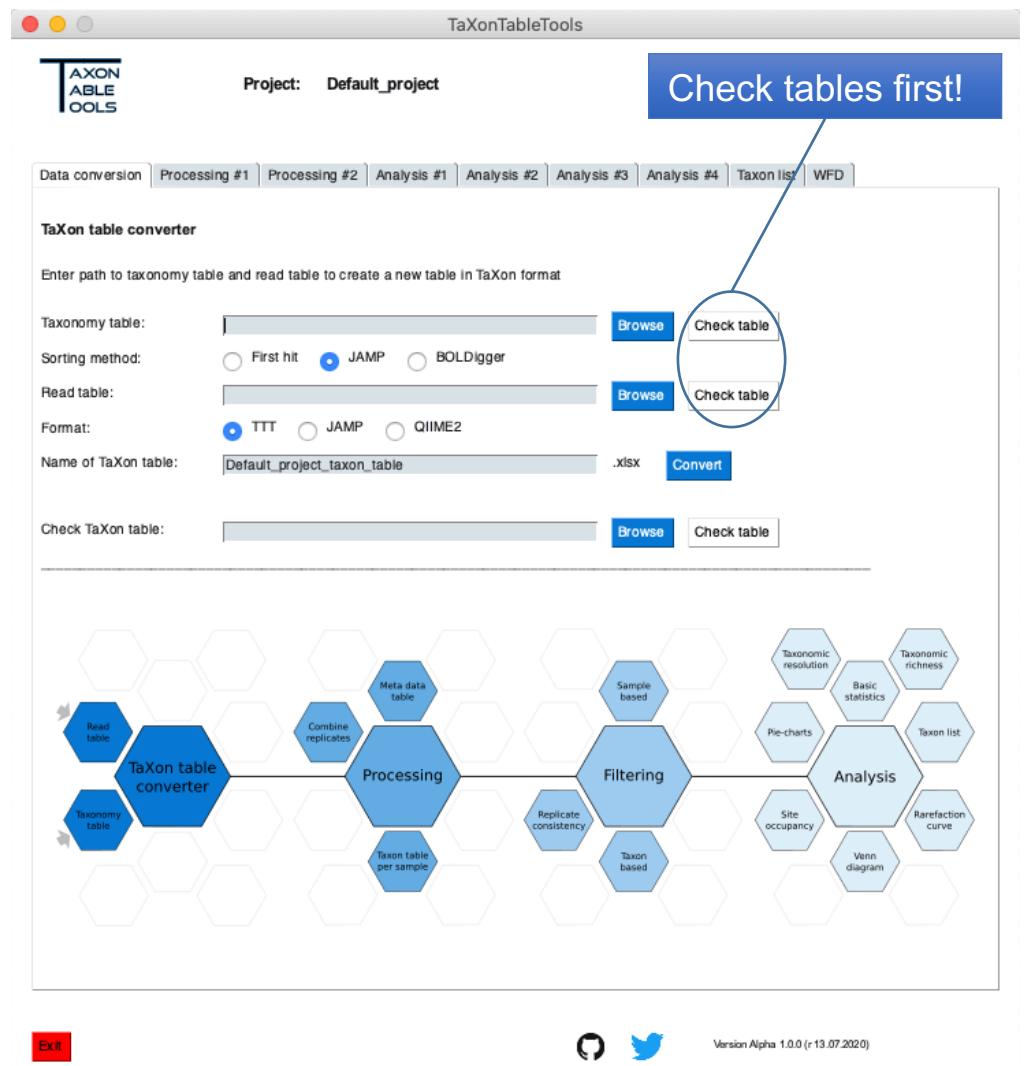
Database status

# Data conversion

## 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

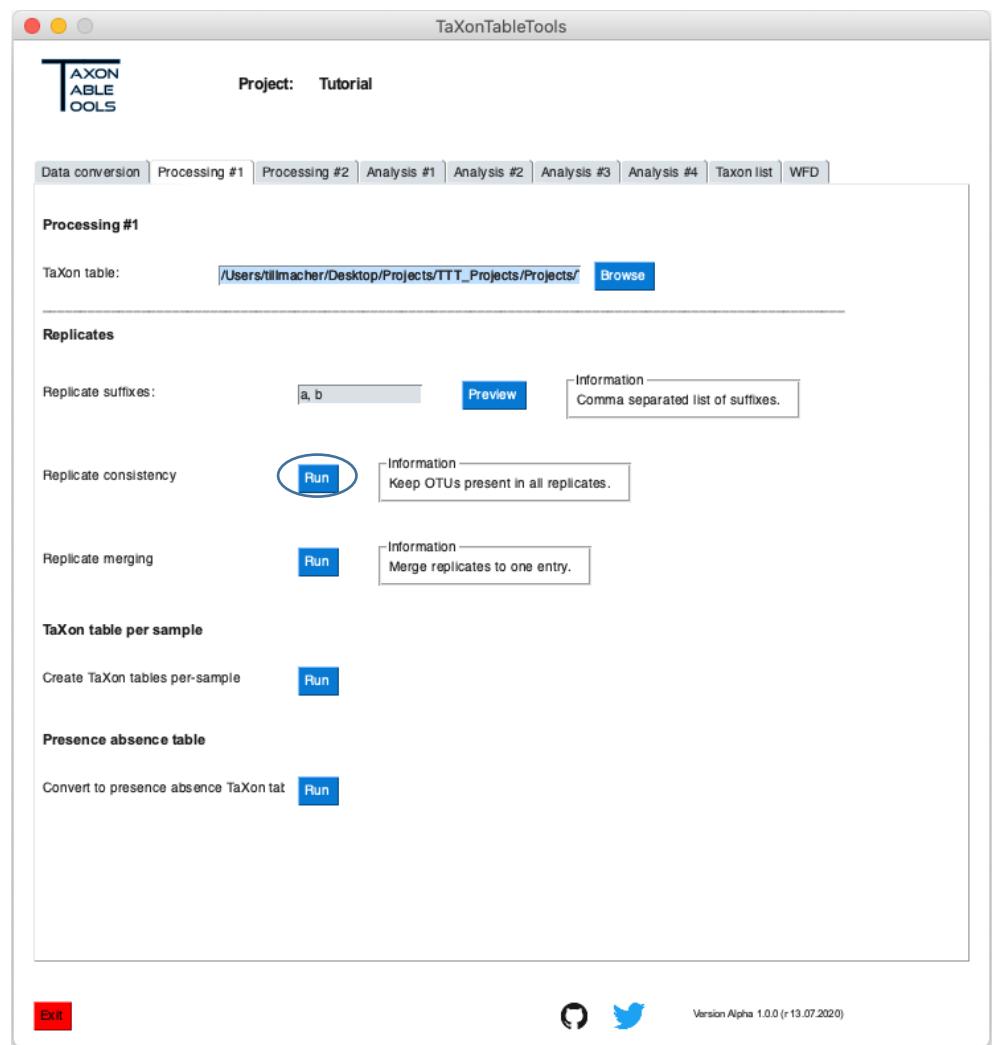
Optionally: Check a manually created TaXon table



# Preparing the TaXon table

## Replicate consistency

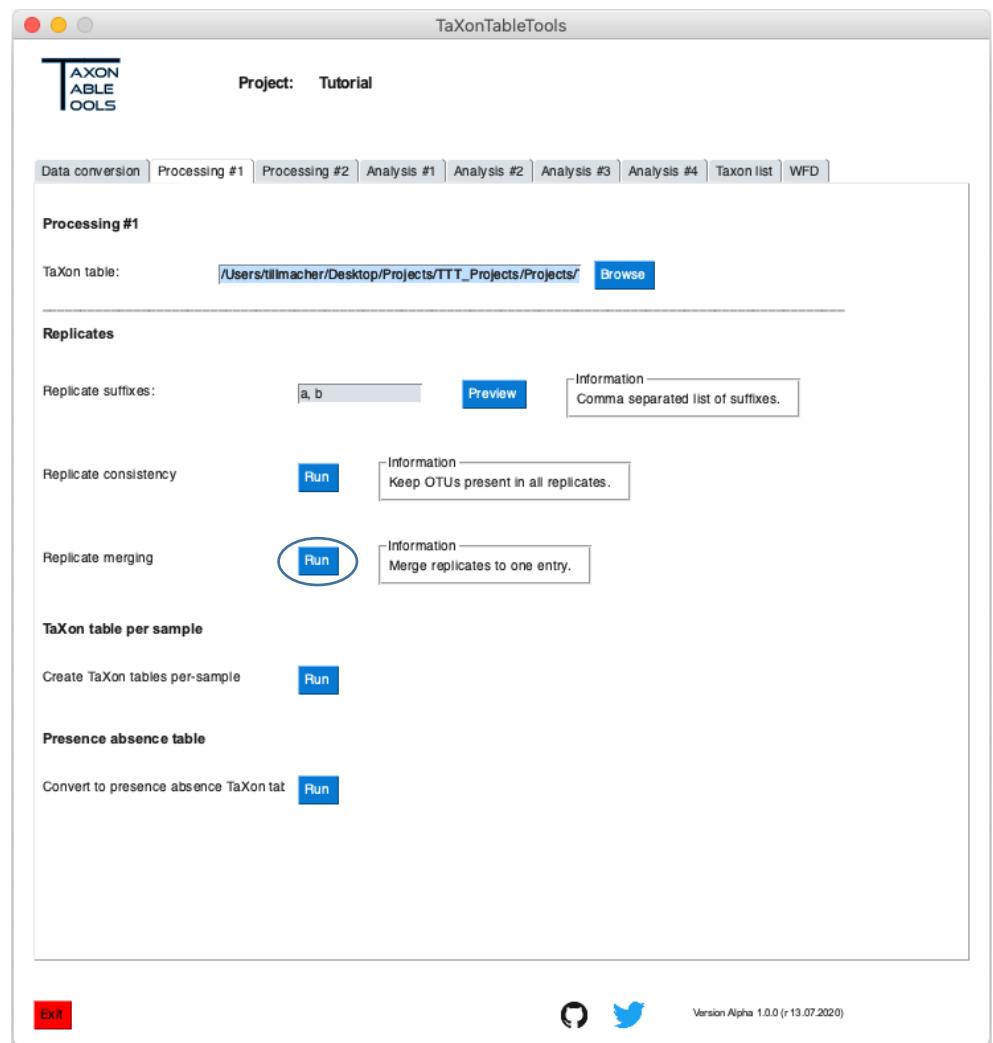
- First load the previously created raw TaXon table (*TTT.xlsx*)
- Now type the replicate indicators: a, b
- Press „Preview“ to show an example
- When merged the sample will be renamed to „\_comb“
- First we want to use the replicate consistency tool:
  - To remove all OTUs that are not present in both samples click the run Run button
  - A new table named *TTT\_cons.xlsx* was created
- When looking at the tables, all OTUs that were not consistent in all samples were set to a read abundance of zero



# Preparing the TaXon table

## Replicate merging

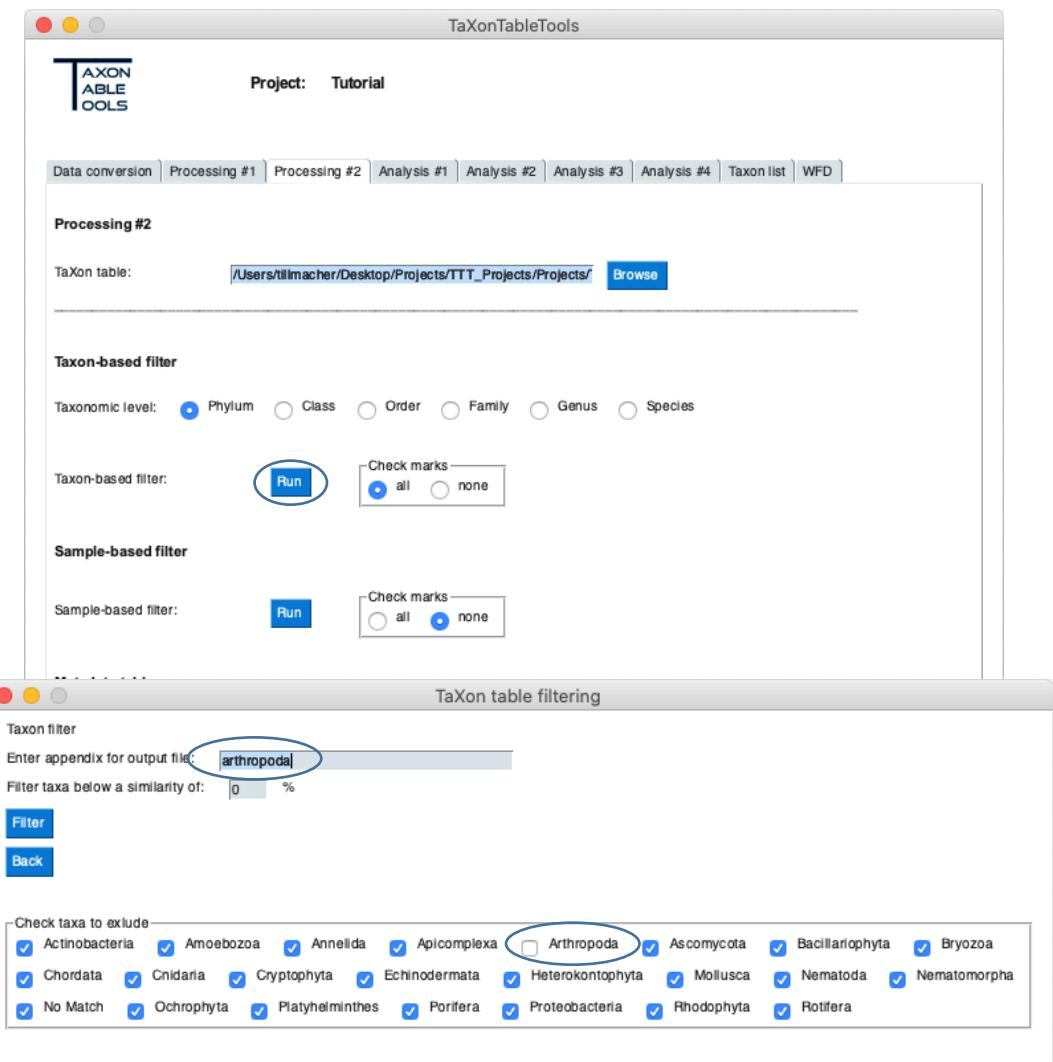
- Now load the previously created consistency filtered TaXon table (*TTT\_cons.xlsx*) in the **Processing #1** tab
- Reminder: Each module creates a new table! So don't forget to always load the latest table**
- Now we want to merge both replicates of all samples
- A new table named *TTT\_cons\_derep.xlsx* was created
- In this case there were no replicates found for „NC“, which are the negative controls. This will be printed in the console



# TaXon table filtering

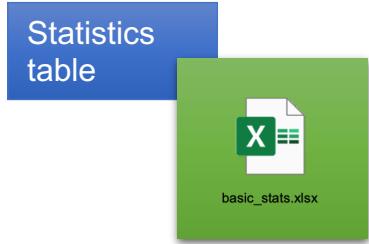
## Taxon-based filter

- 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*) in the **Processing #2 tab**
- Set the marks to „Phylum“ and „all“
- Click on Run and a new window will pop up
- Remove the check mark from „Arthropoda“, enter a new appendix name (e.g. „arthropoda“)
- Click Filter
- A new table named *TTT\_cons\_derep\_arthropoda.xlsx* was created

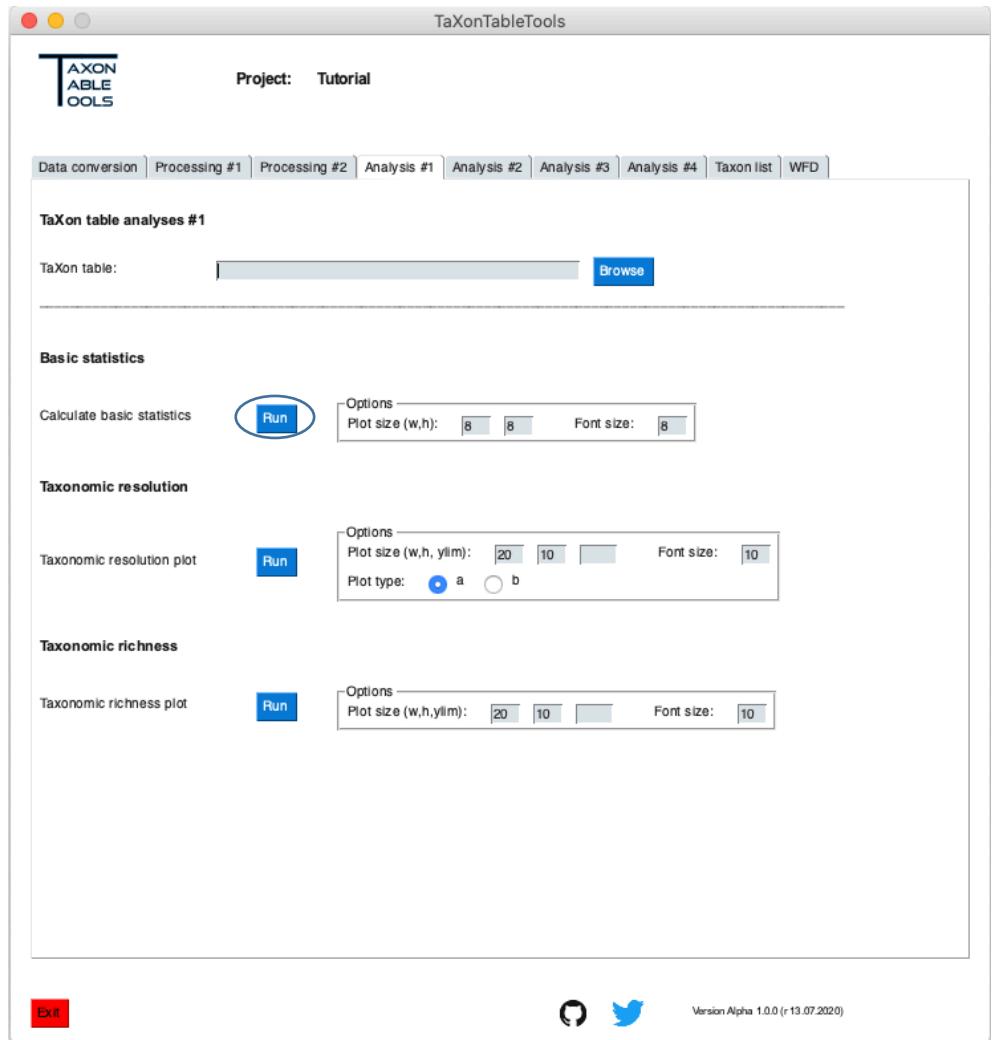


# Basic statistics

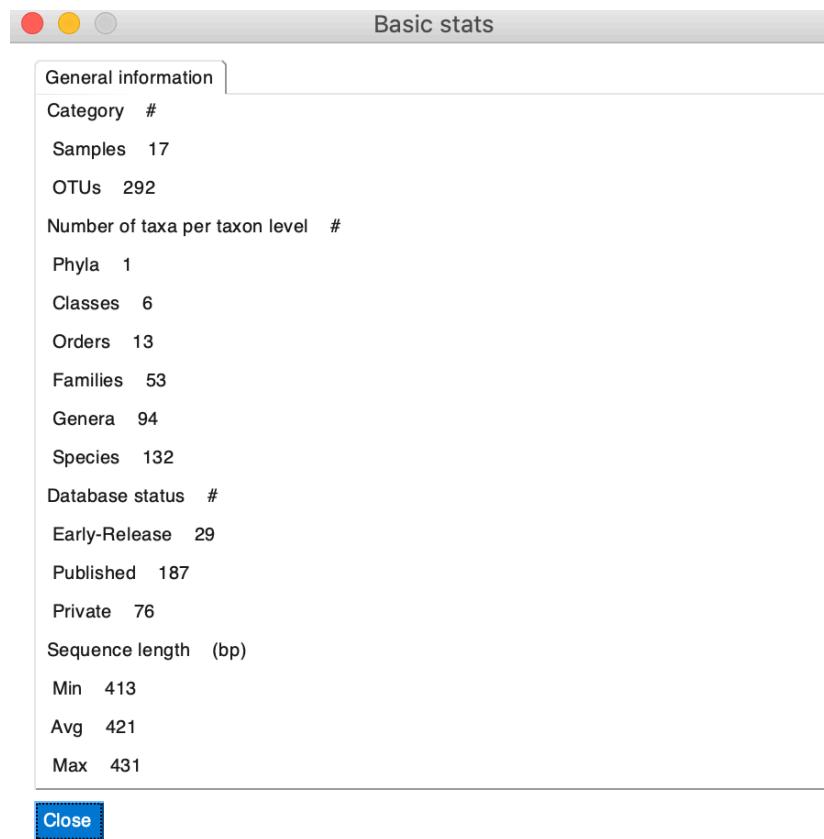
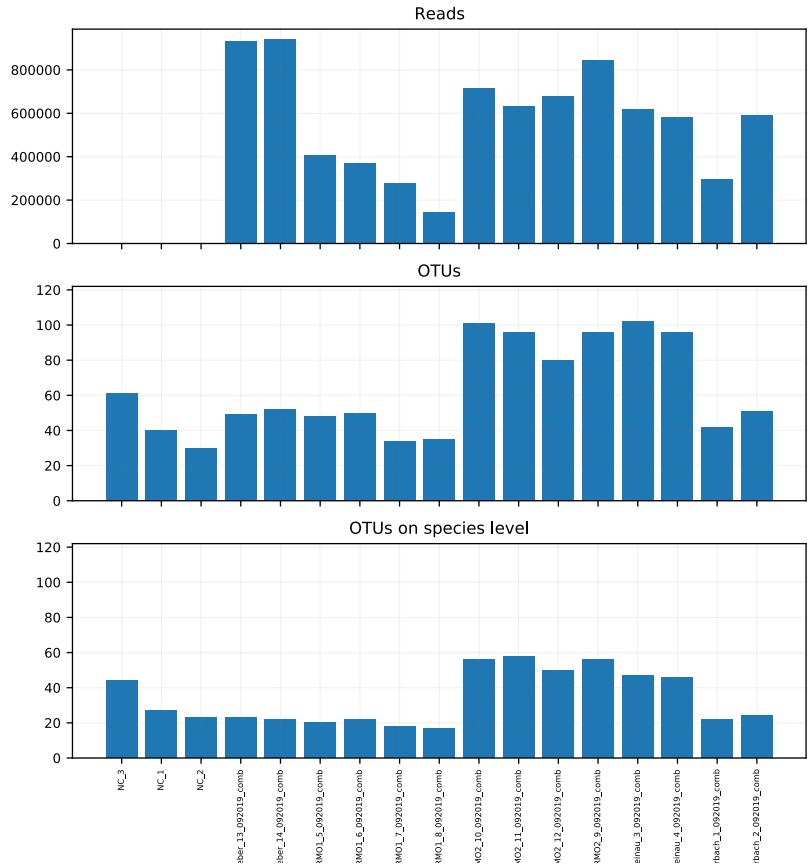
- To get an overview of the data set we can calculate some basic statistics and plots
- Load the latest TaXon table (*TTT\_... arthropoda.xlsx*) in the **Analysis #1 tab**
- Click on Run
- Two windows will appear after each other:
  1. Three basic plots
  2. A table with useful statistics



D	E	F	G	H
Sample	avg reads	total reads	n OTUs	n Species
Gelnhausen_Bieber_13_092019_comb	1604	466651	49	23
Gelnhausen_Bieber_14_092019_comb	1616	470354	52	22
Gelnhausen_RMO1_5_092019_comb	697	202958	48	20
Gelnhausen_RMO1_6_092019_comb	636	185120,5	50	22
Gelnhausen_RMO1_7_092019_comb	481	140084,5	34	18
Gelnhausen_RMO1_8_092019_comb	251	72992,5	35	17
Gelnhausen_RMO2_10_092019_comb	1234	359008	101	56
Gelnhausen_RMO2_11_092019_comb	1086	316136,5	96	58
Gelnhausen_RMO2_12_092019_comb	1166	339359	80	50
Gelnhausen_RMO2_9_092019_comb	1452	422607,5	96	56
Gelnhausen_Steinau_3_092019_comb	1064	309528	102	47
Gelnhausen_Steinau_4_092019_comb	1004	292194	96	46
Gelnhausen_Waechterbach_1_092019_comb	513	149179	42	22
Gelnhausen_Waechterbach_2_092019_comb	1019	296444,5	51	24
Total reads		4022617		



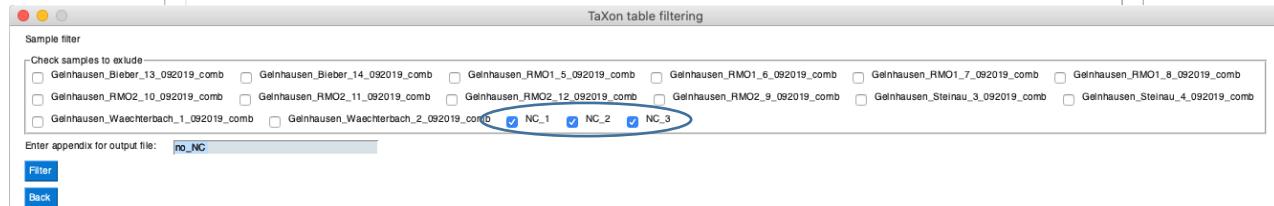
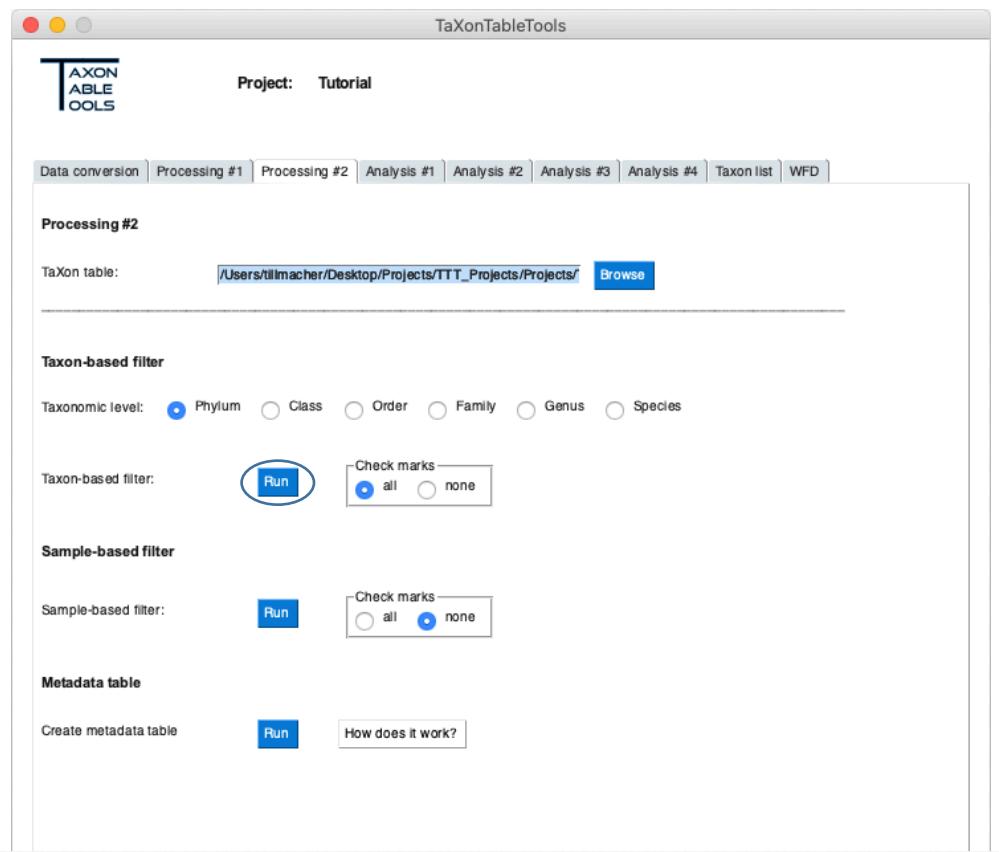
# Basic statistics



# TaXon table filtering

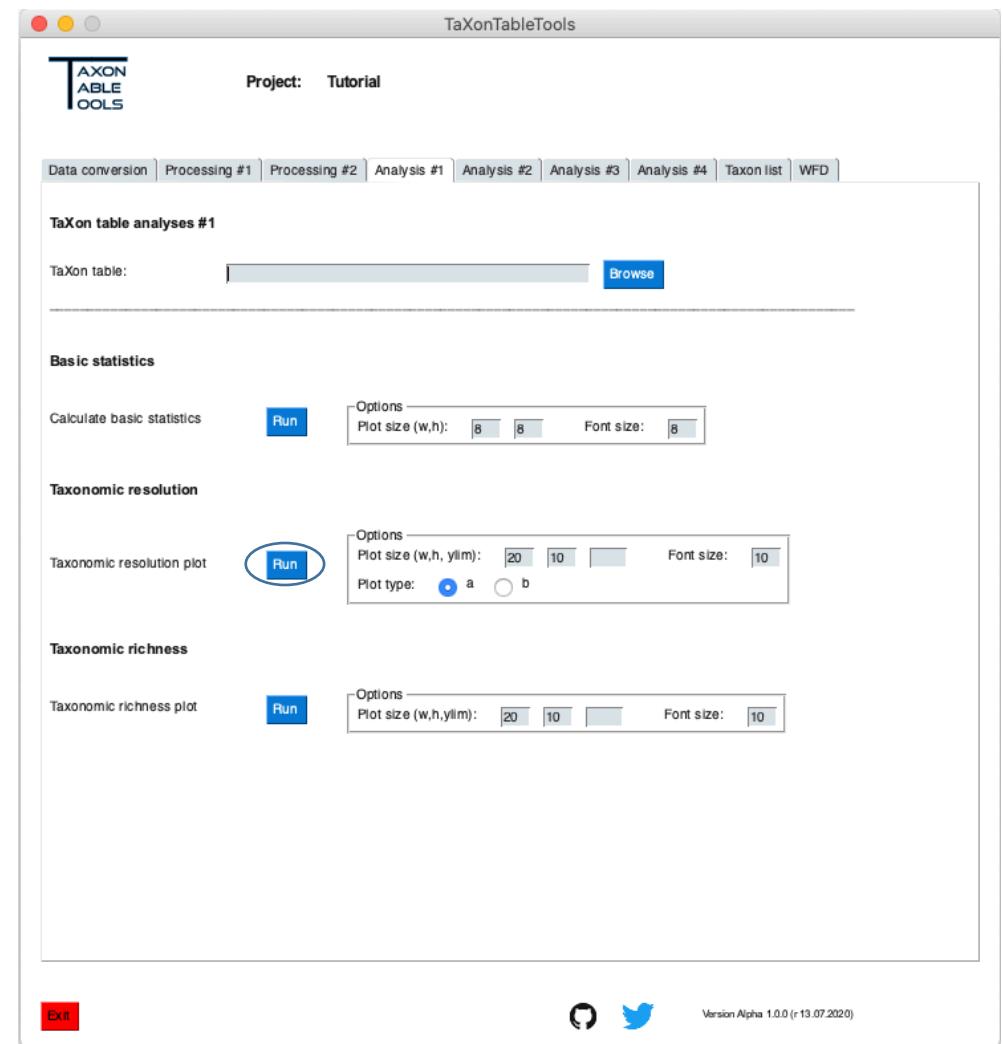
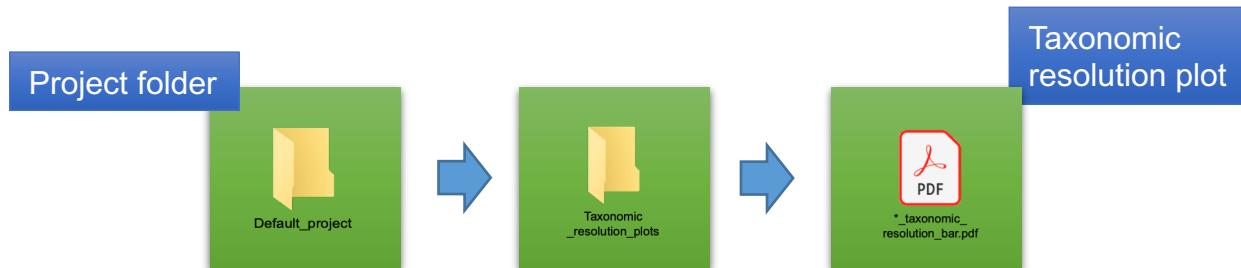
## Sample-based filter

- Now we want to remove the negative controls from the data set
- Load the latest TaXon table (*TTT\_...\_arthropoda.xlsx*) in the **Processing #2** tab
- Set the check marks option to „none“
- Click on Run and a new window will pop up
- Check all three negative controls and enter a new appendix name (e.g. „no\_NC“)
- Click Filter
- A new table named *TTT\_cons\_derep\_arthropoda\_no\_NC.xlsx* was created



# Taxonomic resolution

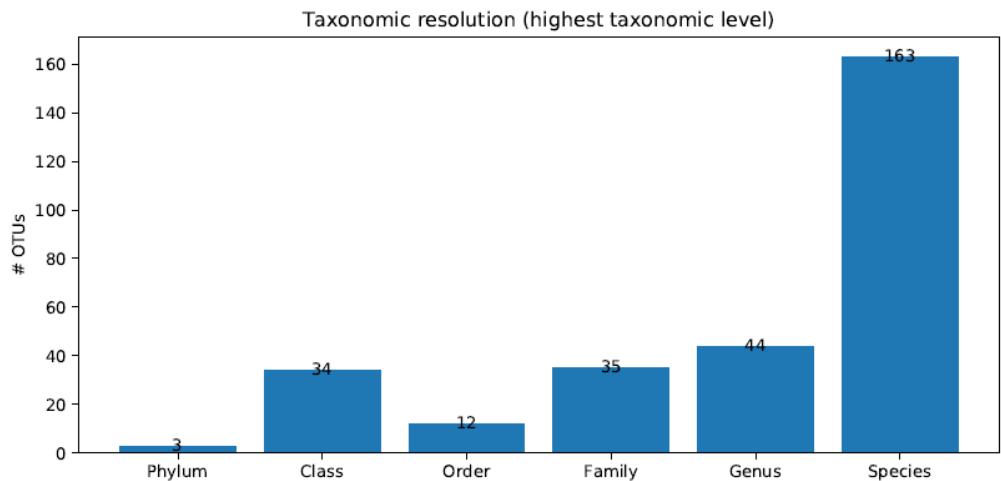
- Now we can check how many taxa we have in the data set
- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC.xlsx*)
- We want the plot to be a square-like bar plot, so adjust the plot width to 10 / 10
- Click on Run (repeat for plot type „b“)
- A plot preview will pop up. If you are happy with the visuals, click „save“
- A new plot was created in the *Taxonomic\_resolution\_plots* folder



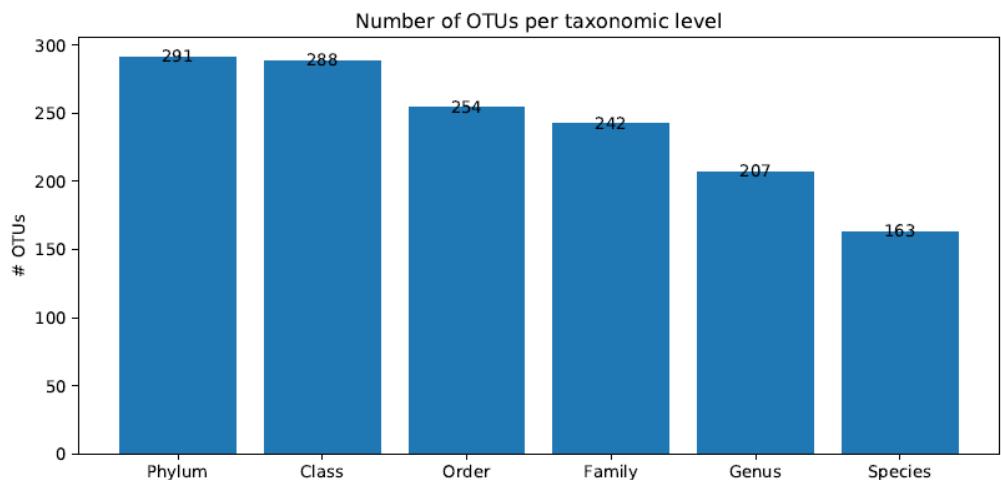
# Taxonomic resolution

- 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 OTUs were identified to Class level
- The plot type b) shows the number of OTUs that were identified in the specific level
- Here, 291 OTUs were identified on Phylum level
- And e.g. 207 OTUs were identified in species level

Type a)

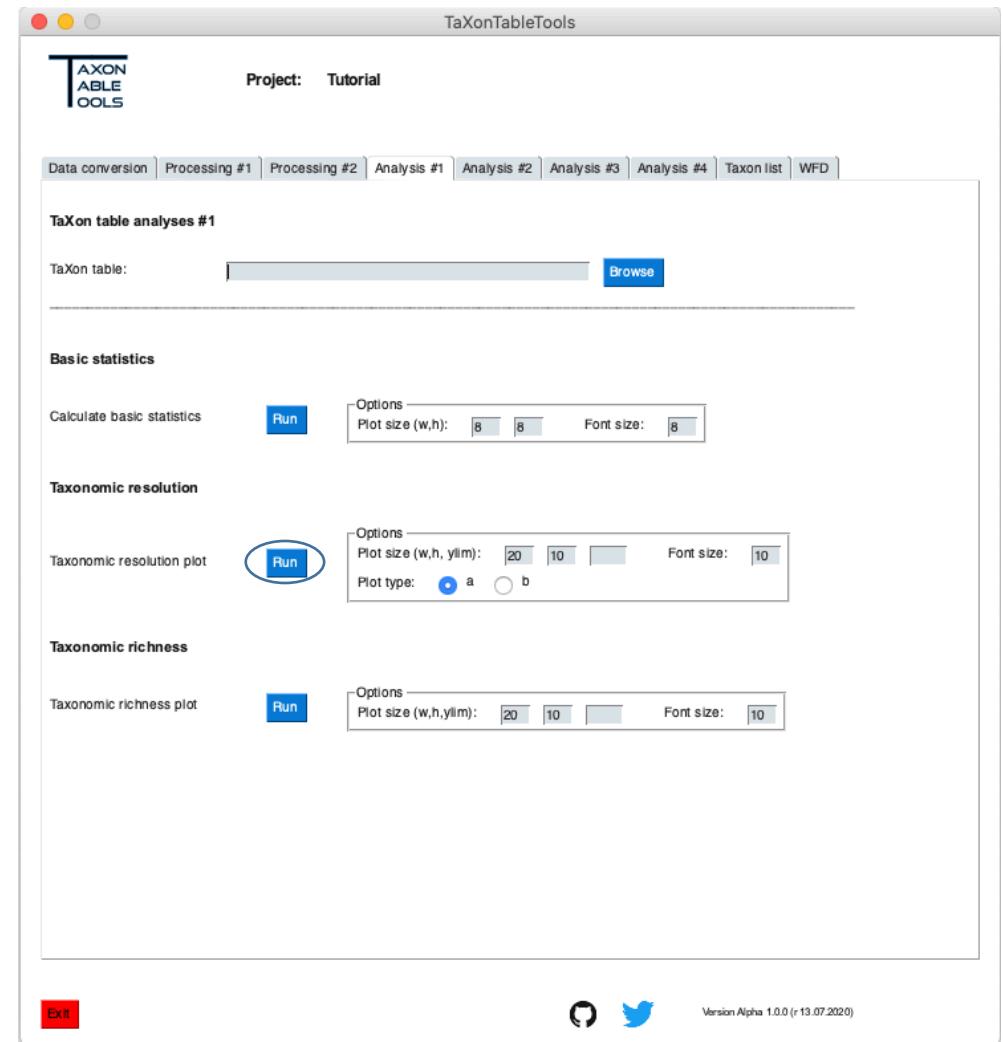
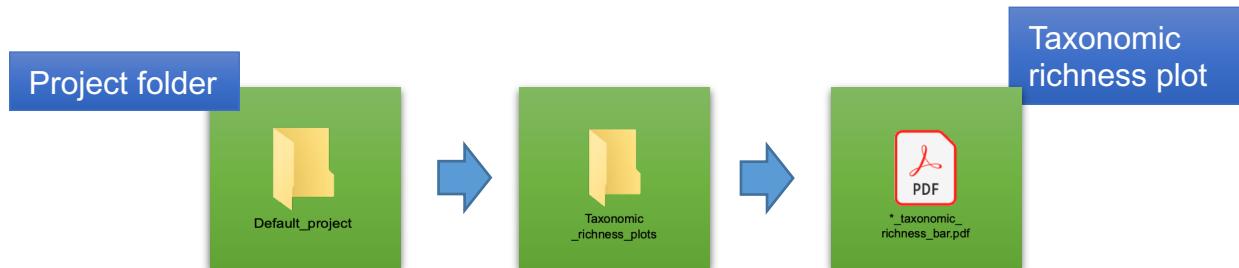


Type b)



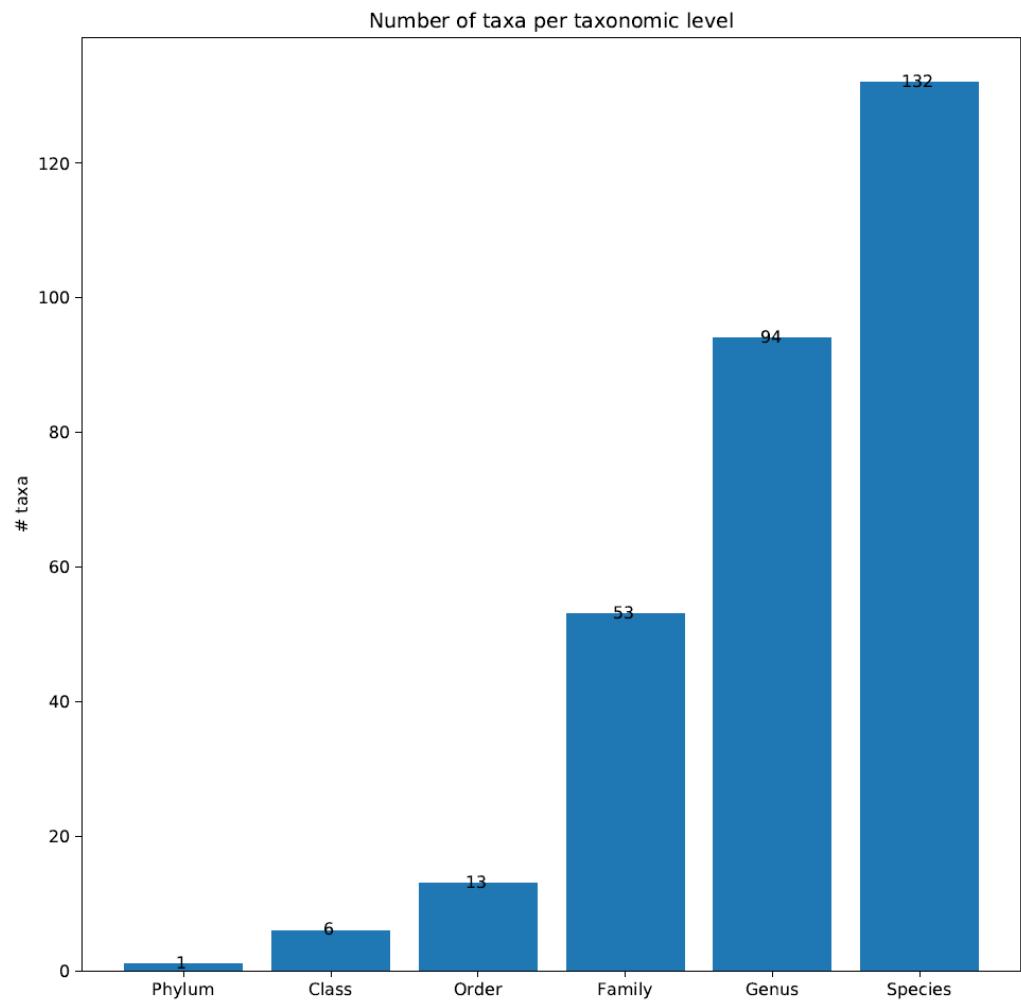
# Taxonomic richness

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC.xlsx*)
- Again, we want the plot to be a square-like bar plot, so adjust the plot width from 20 to 10
- Click on Run
- A plot preview will pop up. If you are happy with the visuals, click „save“
- A new plot was created in the *Taxonomic\_richness\_plots* folder



# Taxonomic richness

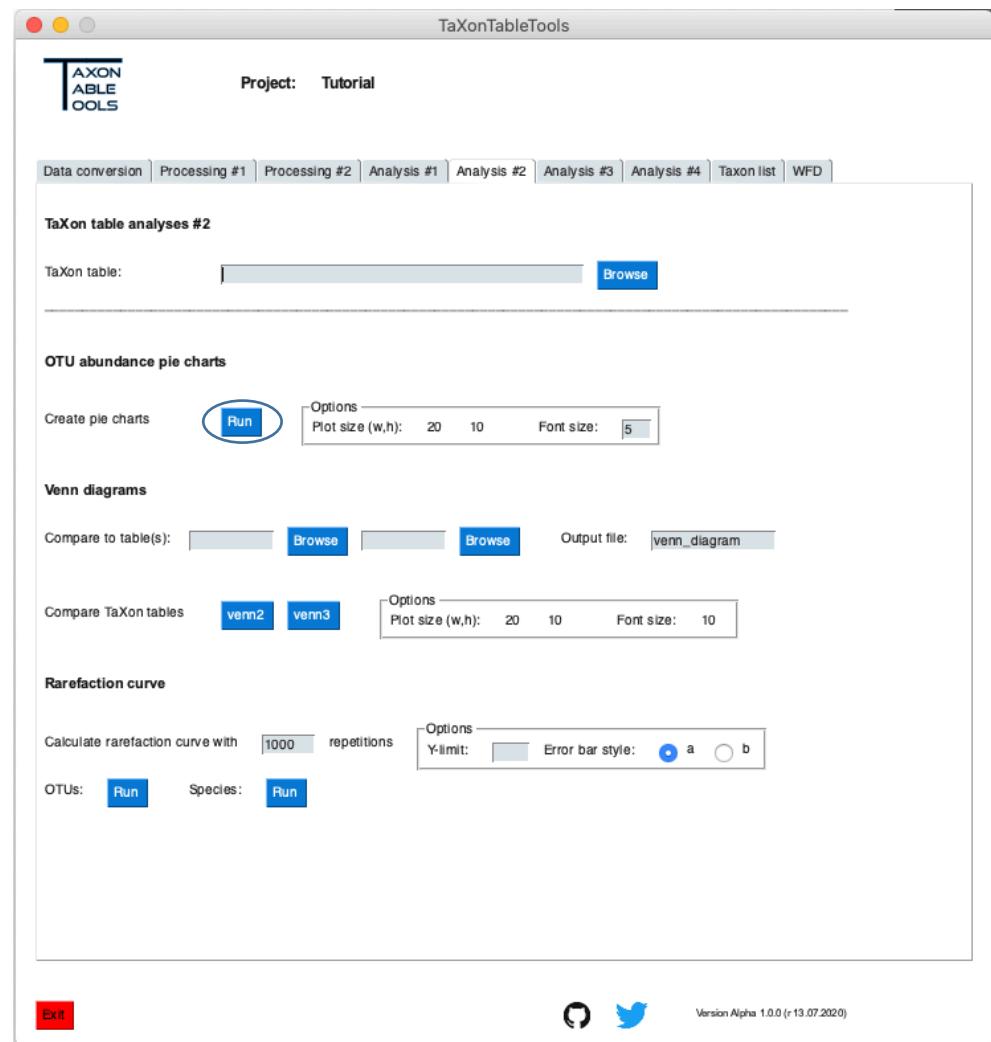
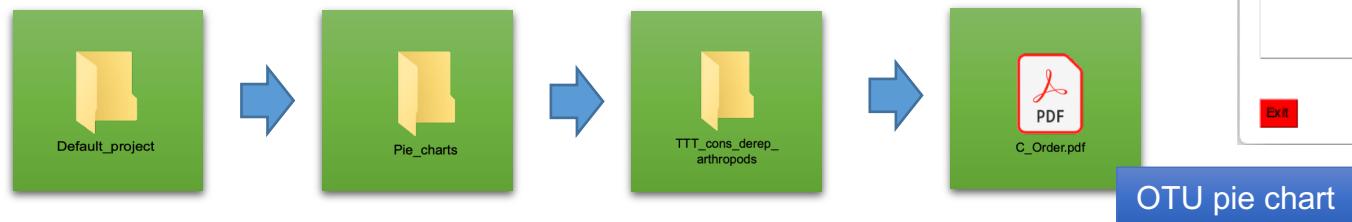
- Taxonomic richness shows the number of taxa for each taxonomic level
- In this case we only included the phylum „Arthropoda“ which results in one phylum
- Within the Arthropoda we found
  - 6 classes
  - 13 Orders
  - 53 Families
  - 94 Genera
  - 132 Species



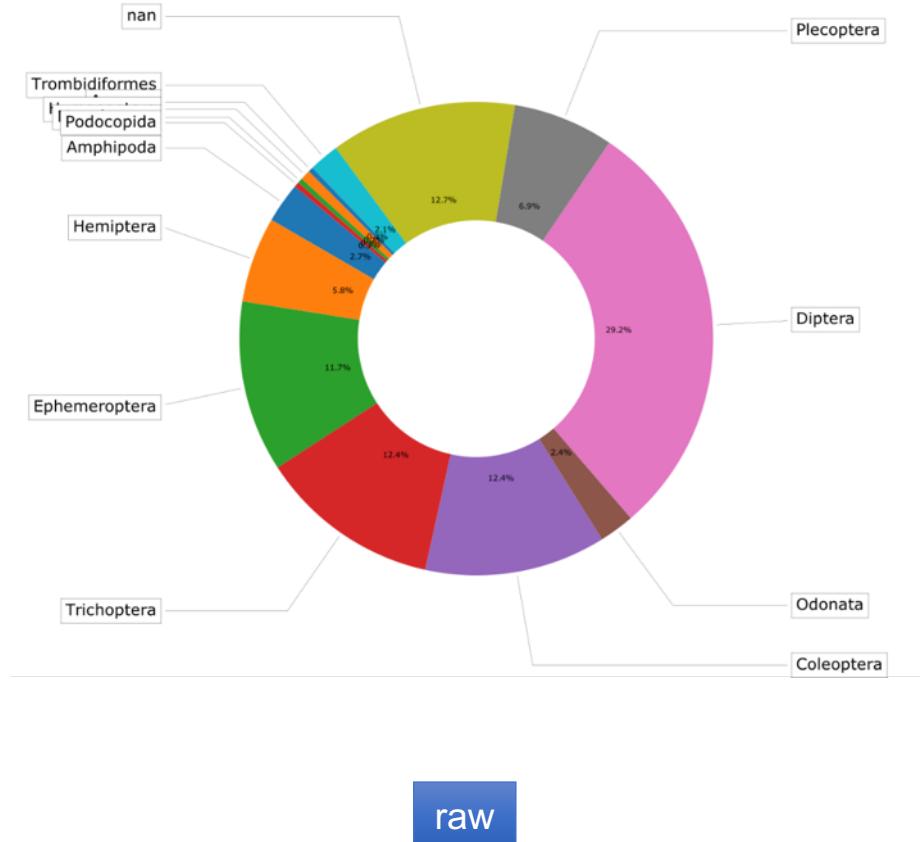
# OTU abundance

## Pie charts

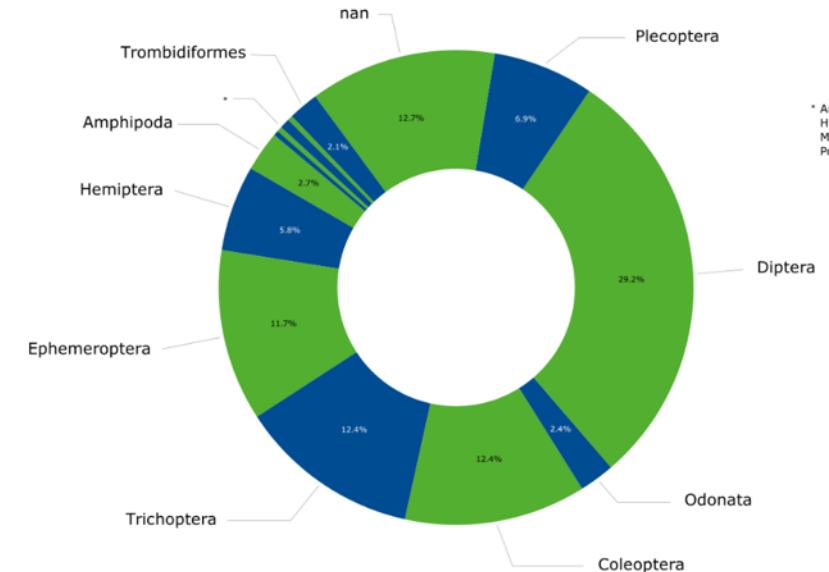
- Load the latest TaXon table (*TTT\_cons\_derep\_arthropoda\_no\_NC.xlsx*) in the **Analysis #2 tab**
- In this case we set the font size to 10
- Click on Run
- This will calculate 6 different pie charts, from phylum to species level
- The plots illustrate the relative number of OTUs for this sample set (not read proportions!)
- Now we can adjust the raw plot with any vector manipulation program



# OTU abundance - Orders



raw



adjusted

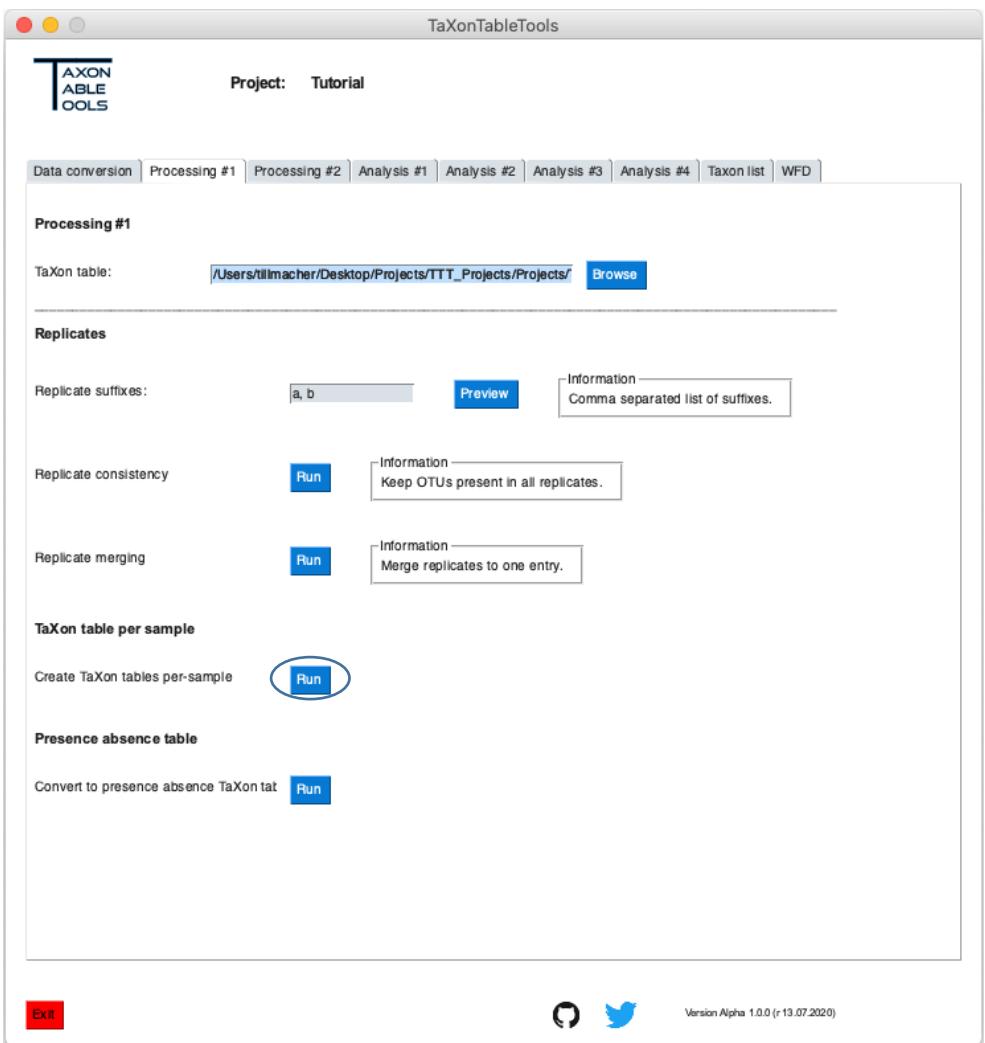
# Creating sub sets

## a. TaXon table per sample

- A first way to compare samples is to create individual TaXon tables
- To do so go to the **Processing #1 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

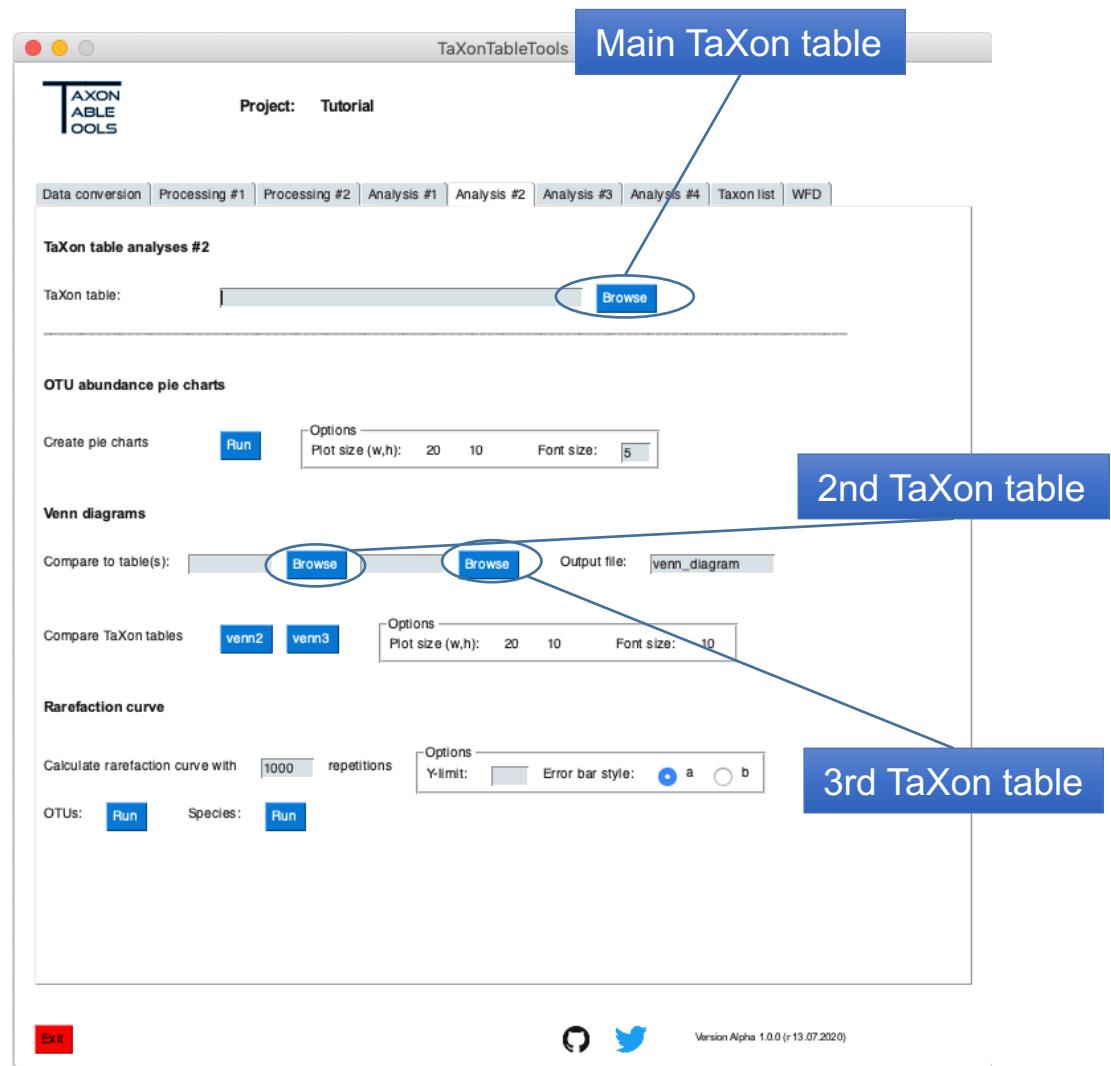
## b. TaXon table subset

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



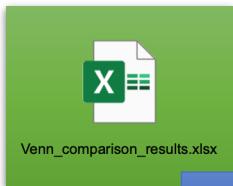
# Venn diagrams

- 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

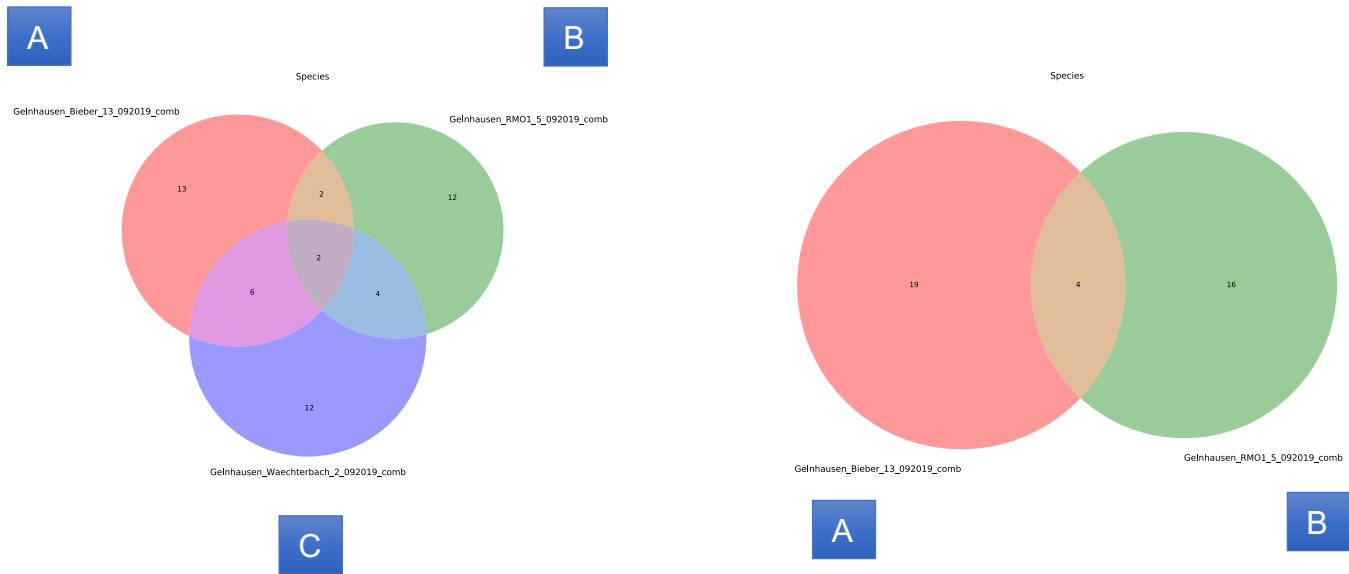


# Venn diagrams

- 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

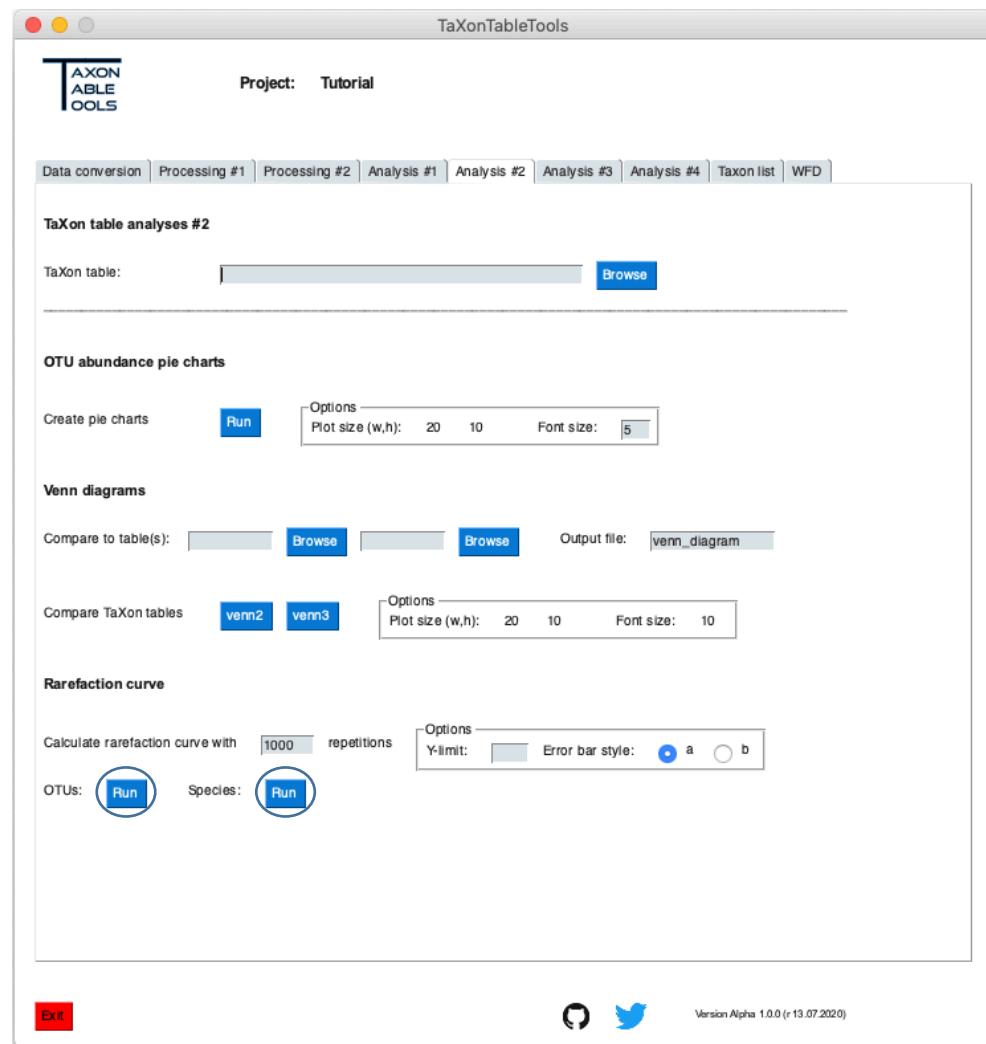
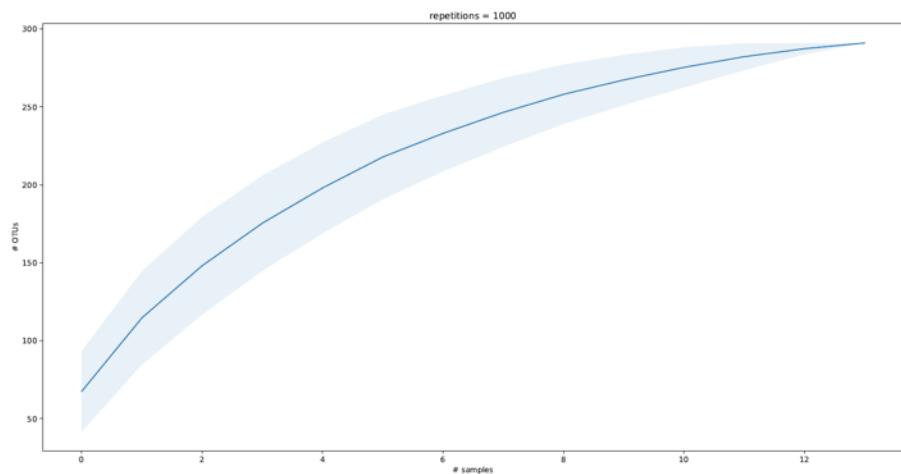


Species_a_only	Species_b_only	Species_c_only	Species_shared_all	Species_shared_a_b	Species_shared_a_c	Species_shared_b_c
Hydraena fosterorum	Simulium erythrocephalum	Baetis vardarensis	Gammarus pulex	Oulimnius tuberculatus	Esolus parallelepipedus	Aphelocheirus aestivalis
Rhithrogena semicolorata	Tanytarsus brundini	Heptagenia sulphurea	Hydropsyche pellucidula	Orectochilus villosus	Elmis maugetii	Dicranota sp.
Hydraena riparia	Baetis vernus	Halesus tessellatus			Baetis rhodani	Baetis fuscatus
Chaetopteryx fusca	Polyphemidium aegyptium	Atherix ibis			Limnius volckmari	Ephemera danica
Rhyacophilus nobilis	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						

# Rarefaction curve

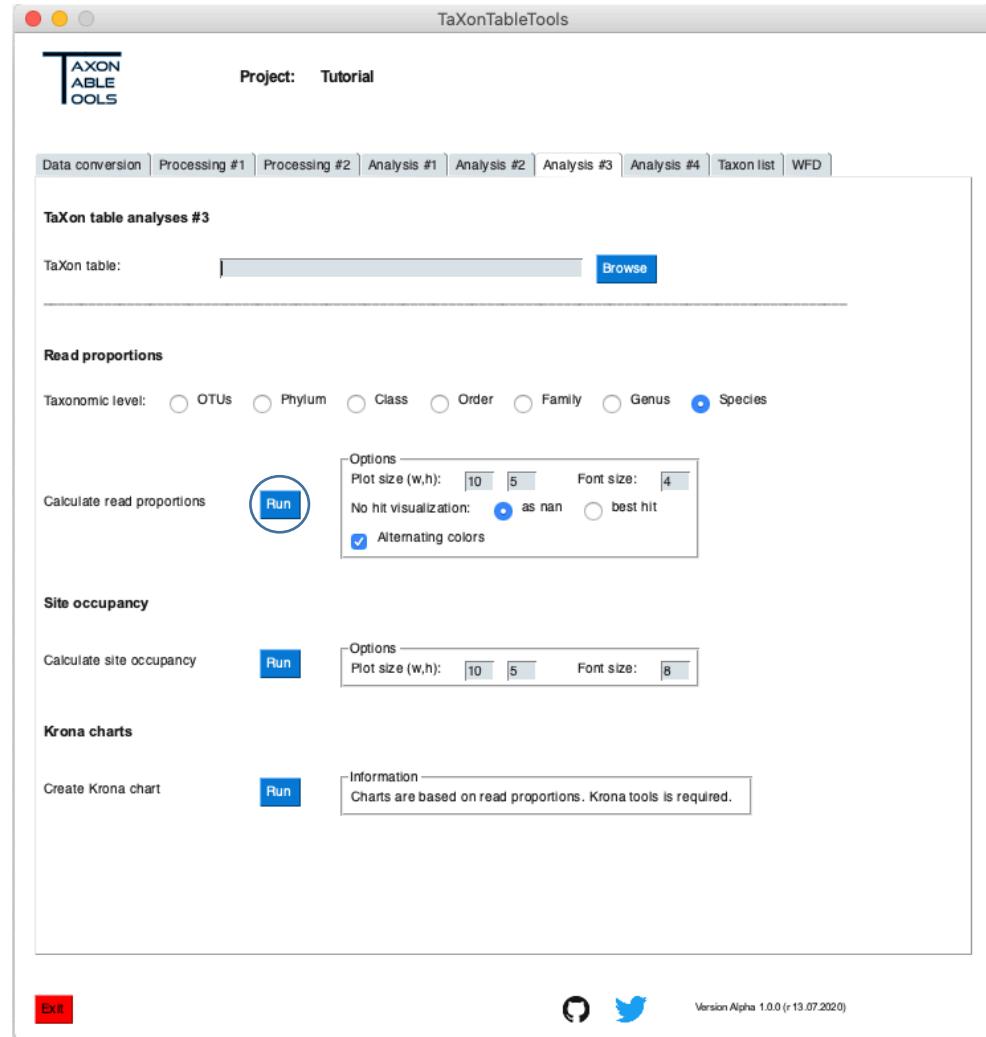
## Species richness from the results of sampling

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropoda\_no\_NC.xlsx*)
- Enter the number of repetitions (e.g. 1000) and choose the error bar style
- Click on Run to test on either species or OTU level

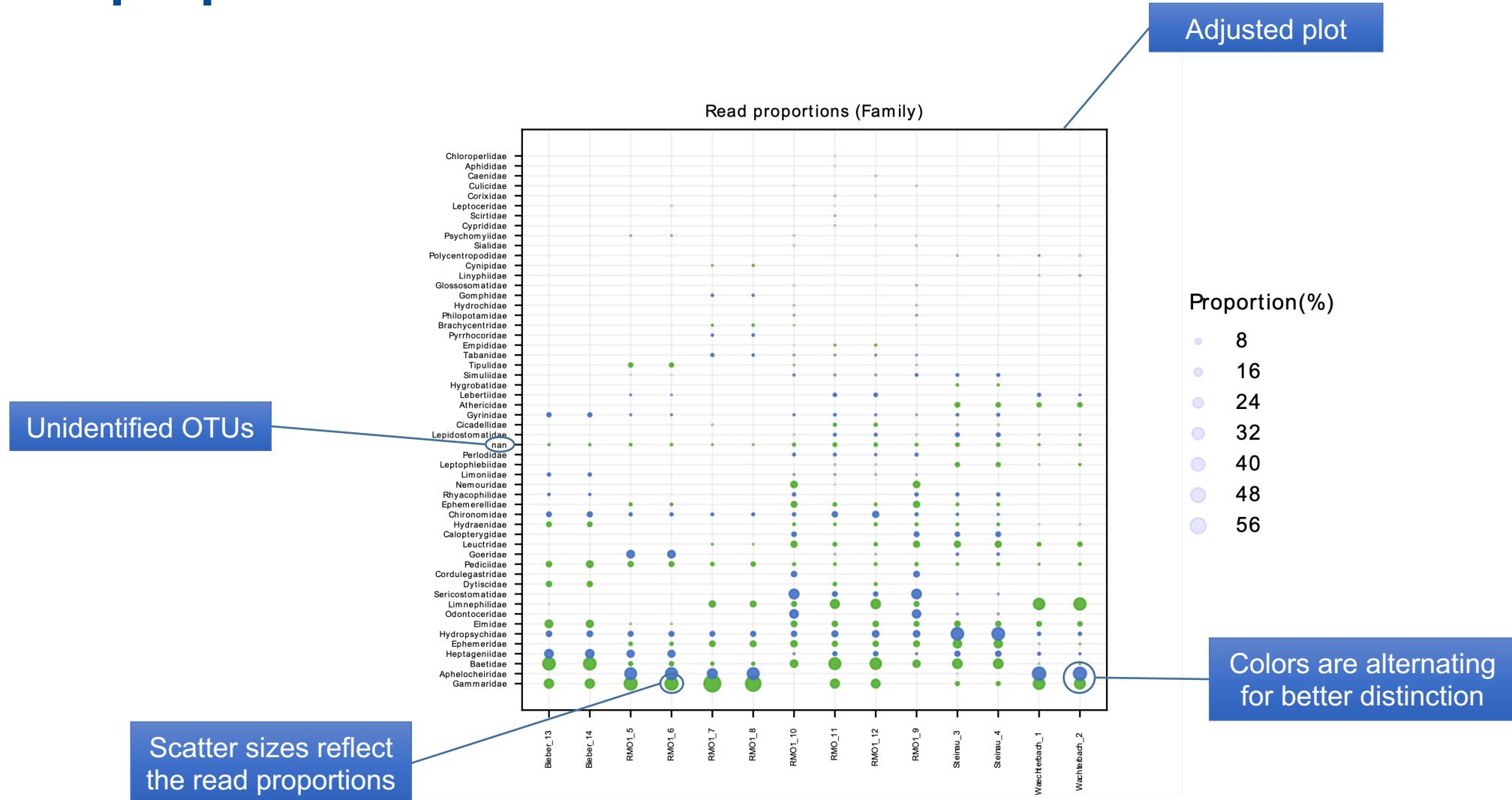


# Read proportions

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropoda\_no\_NC.xlsx*) in the **Analysis #3 tab**
- Check the taxonomic level for which to calculate the read proportions (i.e. family)
- Adjust the plot size and font size (i.e. 5,5,4)
- Choose to either display the OTU as „best hit“ or as „nan“
  - Best hit = Choose the highest available level
  - Nan = Combine all OTUs that don't have taxonomy information on the chosen level
- Click on Run
- Here, it is often useful to check the preview until you are happy with the plot visualization



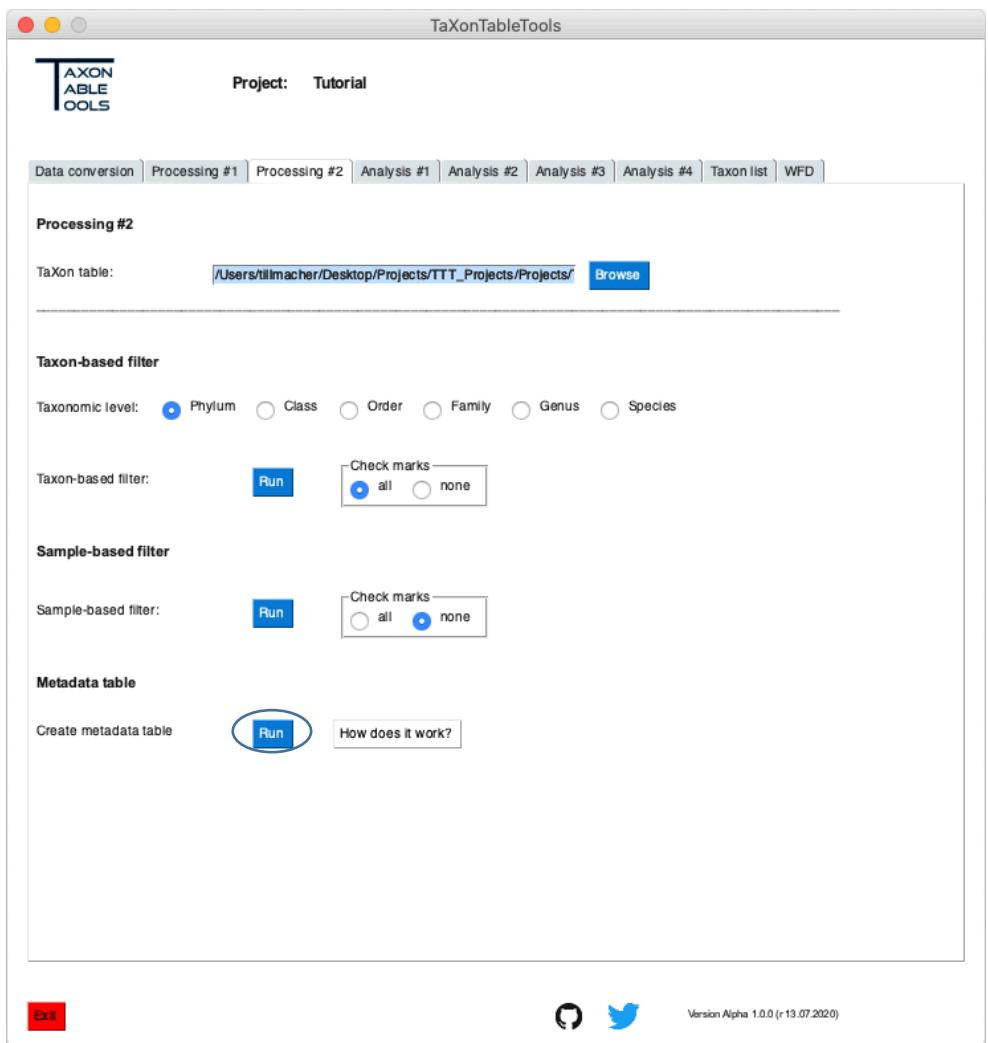
# Read proportions



# Metadata table

## Creating a new metadata table

- Go to the **Processing #2 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 new metadata table is now ready to be adjusted



# Metadata table

## Adjusting the metadata table

- Open the metadata table with e.g. Excel
- 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
- The table can hold as columns (=metadata), as the user defines
- The standard information is collected from the sample name („\_“ as separator)
- Now rename the metadata accordingly and delete not-required columns

Name of the metadata

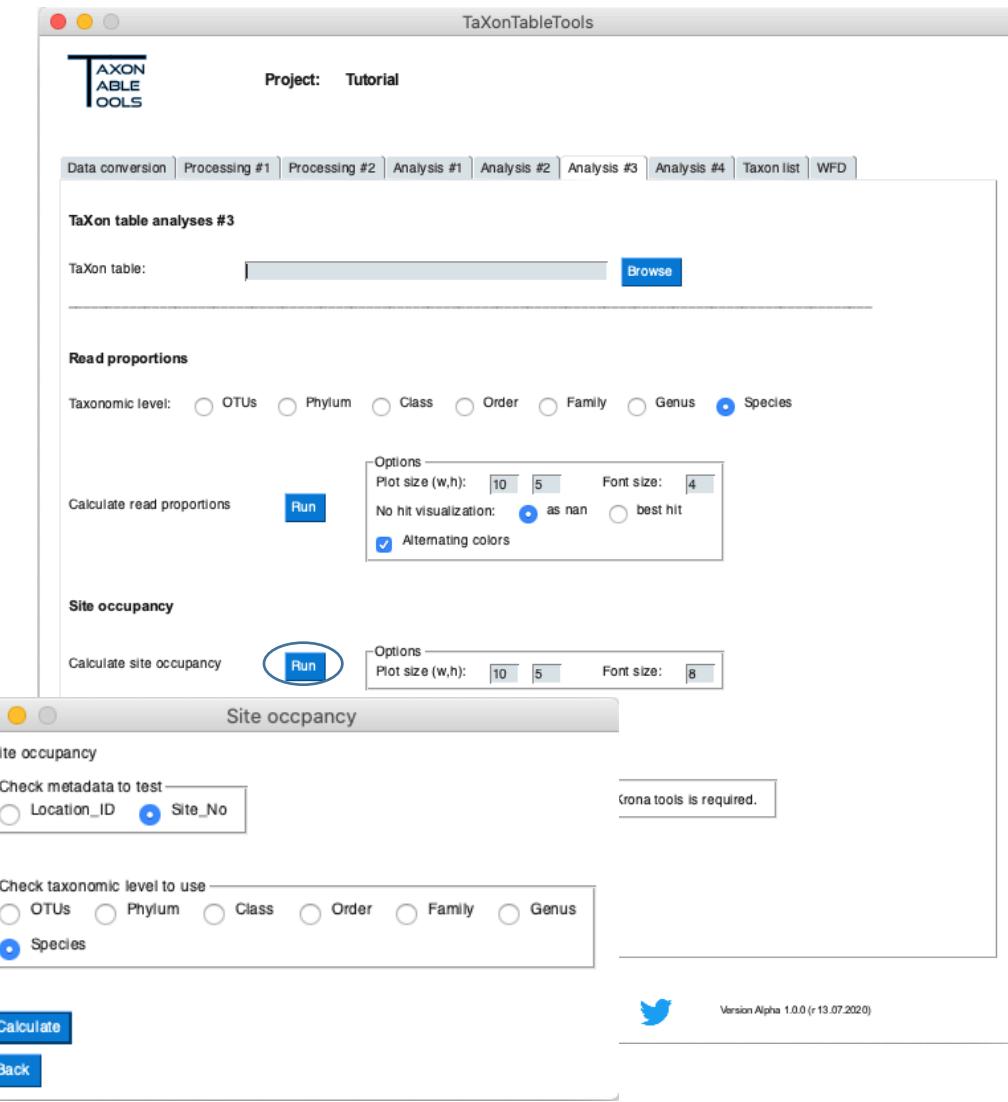
Samples	1	2	3	4	5
Gelnhausen_Bieber_13_092019_comb	Gelnhausen	Bieber	13	092019	comb
Gelnhausen_Bieber_14_092019_comb	Gelnhausen	Bieber	14	092019	comb
Gelnhausen_RMO1_5_092019_comb	Gelnhausen	RMO1	5	092019	comb
Gelnhausen_RMO1_6_092019_comb	Gelnhausen	RMO1	6	092019	comb
Gelnhausen_RMO1_7_092019_comb	Gelnhausen	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

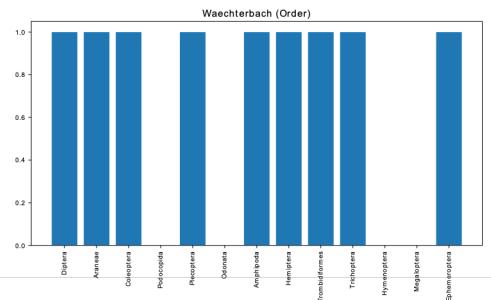
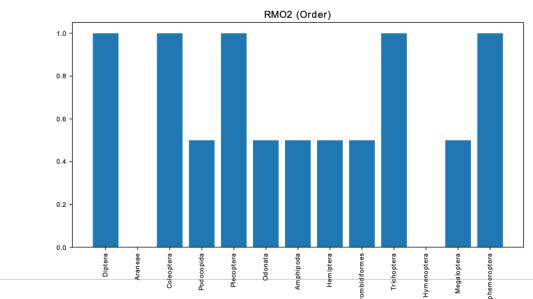
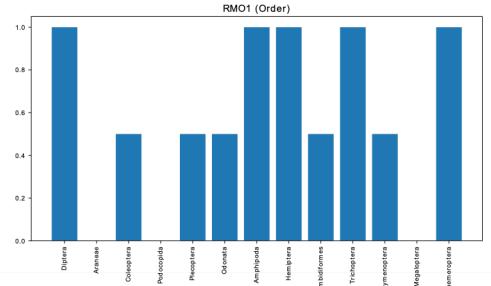
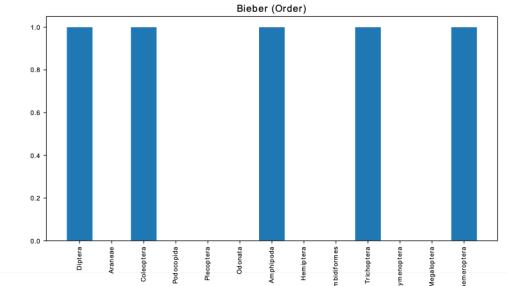
# Site occupancy

- 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



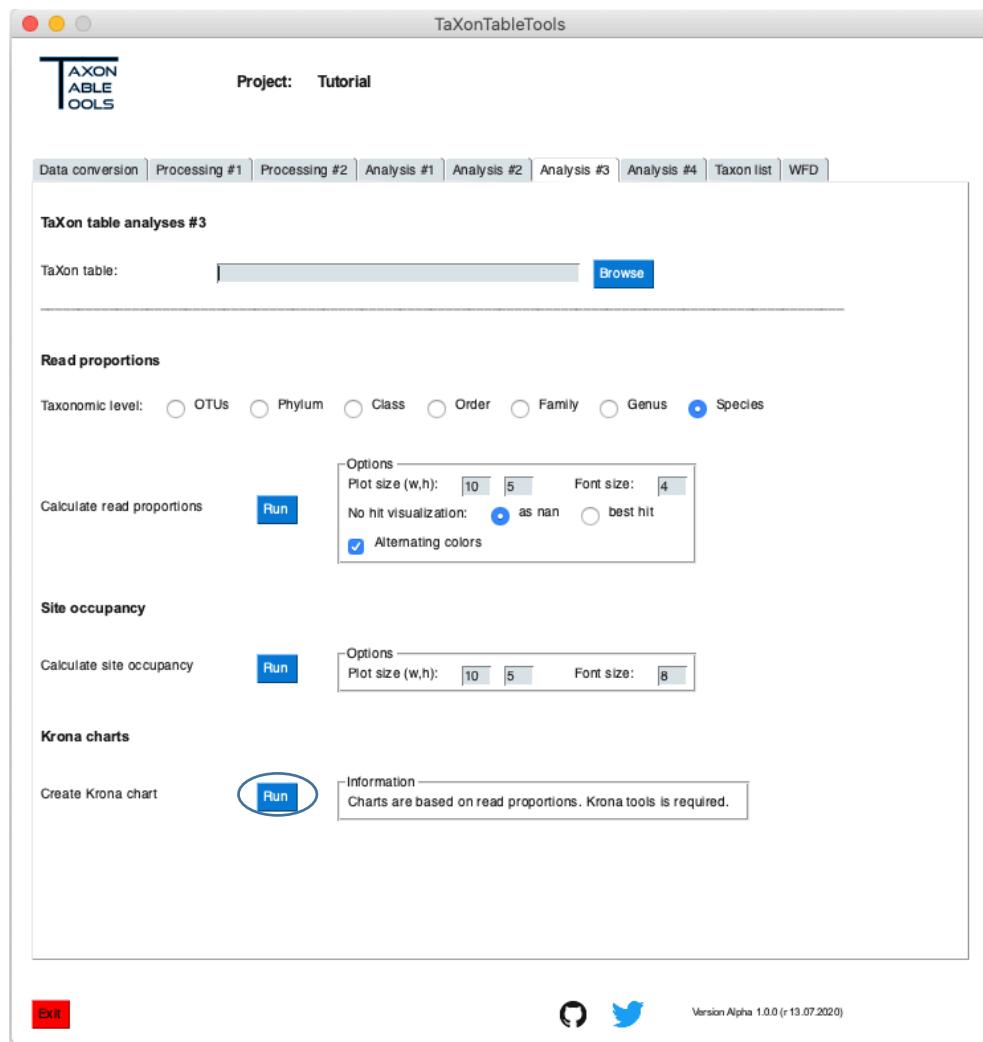
# Site occupancy

- 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 1 (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

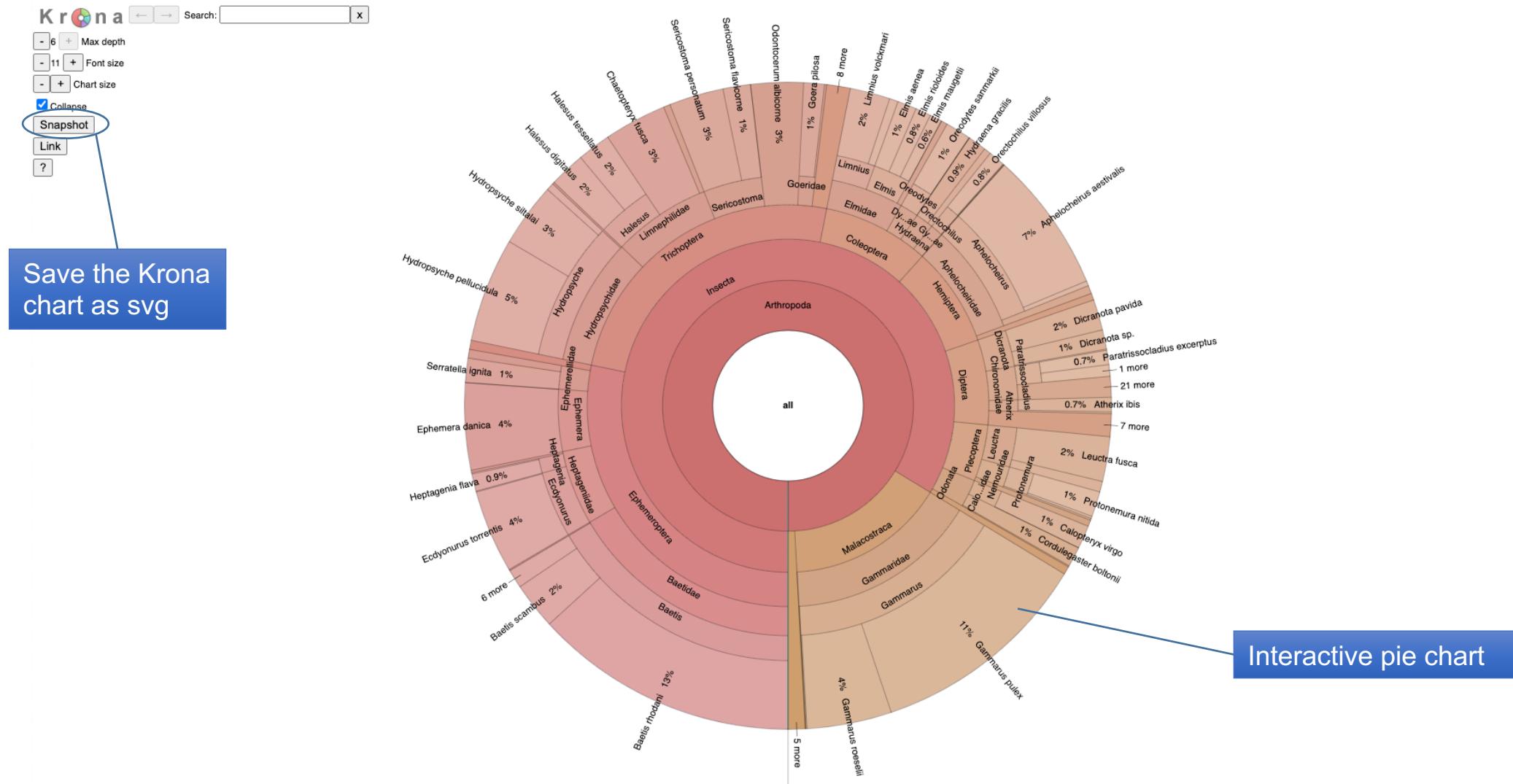


# Krona charts

- 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

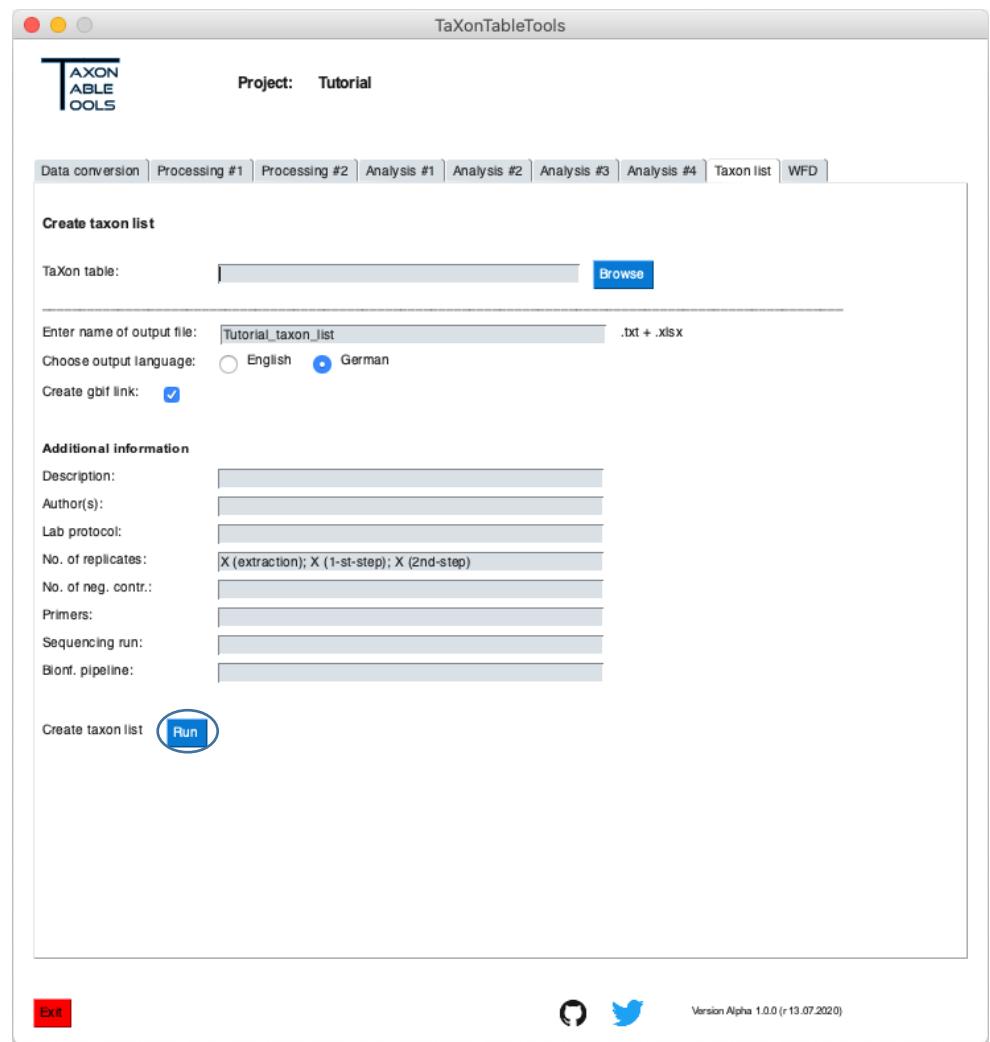


# Krona charts



# Taxon list

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC.xlsx*)
- Enter the name of the output file
- Choose language
- Leave the GBIF link check mark
  - This requires an active internet connection
  - For all species-level identified OTUs, a link to the respective GBIF site will be created
- Enter the additional information as needed (can also be left blank)
- Click on Run

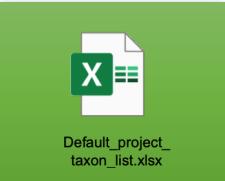


# Taxon list

Link to the gbif database

Taxon list statistics

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	<a href="https://www.gbif.org/species/2219853">https://www.gbif.org/species/2219853</a>
Arthropoda	Insecta	Hemiptera	Aphelocheiridae	Aphelocheirus	Aphelocheirus aestivalis	567267	1	0,5				<a href="https://www.gbif.org/species/4485511">https://www.gbif.org/species/4485511</a>
Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis rhodani	1062588	2	0,64	13,3	13,3	13,3	<a href="https://www.gbif.org/species/4481106">https://www.gbif.org/species/4481106</a>
Arthropoda	Malacostraca	Amphipoda	Gammaridae	Gammarus	Gammarus roeselii	340348	3	0,43	9,26	3,09	6,97	<a href="https://www.gbif.org/species/5864277">https://www.gbif.org/species/5864277</a>
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Ecdyonurus	Ecdyonurus torrentis	334421	1	0,43				<a href="https://www.gbif.org/species/4481477">https://www.gbif.org/species/4481477</a>
Arthropoda	Insecta	Ephemeroptera	Ephemeridae	Ephemerina	Ephemerina danica	348767	1	0,86				<a href="https://www.gbif.org/species/5716472">https://www.gbif.org/species/5716472</a>
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche pollucidula	420537	1	0,86				<a href="https://www.gbif.org/species/5054150">https://www.gbif.org/species/5054150</a>
Arthropoda	Insecta	Trichoptera	Hydropsychidae	Hydropsyche	Hydropsyche sitalai	256128	1	0,71				<a href="https://www.gbif.org/species/5054160">https://www.gbif.org/species/5054160</a>
Arthropoda	Insecta	Coleoptera	Elmidae	Limnius	Limnius volckmari	160851	1	0,71				<a href="https://www.gbif.org/species/4427719">https://www.gbif.org/species/4427719</a>
Arthropoda	Insecta	Trichoptera	Odontoceridae	Odontocerum	Odontocerum albicorne	210463	2	0,29	3,8	3,8	3,8	<a href="https://www.gbif.org/species/1437449">https://www.gbif.org/species/1437449</a>
Arthropoda	Insecta	Trichoptera	Limnephilidae	Chaetopteryx	Chaetopteryx fusca	251747	1	0,36				<a href="https://www.gbif.org/species/1442278">https://www.gbif.org/species/1442278</a>
Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostoma	Sericostoma personatum	218930	2	0,29	3,8	3,8	3,8	<a href="https://www.gbif.org/species/5053104">https://www.gbif.org/species/5053104</a>
Arthropoda	Insecta	Coleoptera	Dytiscidae	Oreodytes	Oreodytes sammarkii	102208	2	0,29	3,33	3,33	3,33	<a href="https://www.gbif.org/species/1038118">https://www.gbif.org/species/1038118</a>
Arthropoda	Insecta	Odonata	Cordulegastridae	Cordulegaster	Cordulegaster boltonii	80464	1	0,14				<a href="https://www.gbif.org/species/1421161">https://www.gbif.org/species/1421161</a>
Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis scambus	188247	4	0,57	4,04	2,61	3,44	<a href="https://www.gbif.org/species/4481160">https://www.gbif.org/species/4481160</a>
Arthropoda	Insecta	Coleoptera	Elmidae	Elmis	Elmis aenea	76848	1	0,57				<a href="https://www.gbif.org/species/1427707">https://www.gbif.org/species/1427707</a>
Arthropoda	Insecta	Diptera	Pediciidae	Dicranota	Dicranota pavida	123630	1	0,29				<a href="https://www.gbif.org/species/1510411">https://www.gbif.org/species/1510411</a>
Arthropoda	Insecta	Ephemeroptera	Heptageniidae	Heptagenia	Heptagenia flava	69636	1	0,14				<a href="https://www.gbif.org/species/4481427">https://www.gbif.org/species/4481427</a>
Arthropoda	Insecta	Trichoptera	Limnephilidae	Halesus	Halesus digitatus	143908	1	0,14				<a href="https://www.gbif.org/species/1441931">https://www.gbif.org/species/1441931</a>
Arthropoda	Insecta	Trichoptera	Limnephilidae	Halesus	Halesus tessellatus	134187	1	0,29				<a href="https://www.gbif.org/species/119642498">https://www.gbif.org/species/119642498</a>
Arthropoda	Insecta	Trichoptera	Goeridae	Goera	Goera pilosa	82978	1	0,14				<a href="https://www.gbif.org/species/1441388">https://www.gbif.org/species/1441388</a>
Arthropoda	Insecta	Plecoptera	Leuctridae	Leuctra	Leuctra fusca	179718	2	0,71	2,85	2,85	2,85	<a href="https://www.gbif.org/species/2001954">https://www.gbif.org/species/2001954</a>
Arthropoda	Insecta	Odonata	Calopterygidae	Calopteryx	Calopteryx virgo	93328	1	0,29				<a href="https://www.gbif.org/species/1427037">https://www.gbif.org/species/1427037</a>
Arthropoda	Insecta	Coleoptera	Hydraenidae	Hydraena	Hydraena gracilis	74092	1	0,71				<a href="https://www.gbif.org/species/5748088">https://www.gbif.org/species/5748088</a>
Arthropoda	Insecta	Diptera	Chironomidae	Paratrichoscladius	nan	46912	1	0,29				
Arthropoda	Insecta	Ephemeroptera	Ephemerellidae	Serratella	Serratella ignita	97111	1	0,14				<a href="https://www.gbif.org/species/4481256">https://www.gbif.org/species/4481256</a>
Arthropoda	Insecta	Trichoptera	Sericostomatidae	Sericostoma	Sericostoma flavicorne	110244	1	0,43				<a href="https://www.gbif.org/species/5053131">https://www.gbif.org/species/5053131</a>
Arthropoda	Insecta	Coleoptera	Elmidae	Limnius	Limnius perrisi	34261	1	0,14				<a href="https://www.gbif.org/species/4427727">https://www.gbif.org/species/4427727</a>
Arthropoda	Insecta	Trichoptera	Rhyacophilidae	Rhyacophila	Rhyacophila rubila	474349	1	0,43				<a href="https://www.gbif.org/species/1433809">https://www.gbif.org/species/1433809</a>
Arthropoda	Insecta	Ephemeroptera	Baetidae	Baetis	Baetis vernus	39676	2	0,43	5,46	5,46	5,46	<a href="https://www.gbif.org/species/4481086">https://www.gbif.org/species/4481086</a>
Arthropoda	Insecta	Coleoptera	Elmidae	Elmis	Elmis rioloides	62192	3	0,71	4,28	3,09	3,49	<a href="https://www.gbif.org/species/4427709">https://www.gbif.org/species/4427709</a>
Arthropoda	Insecta	Diptera	Pediciidae	Dicranota	Dicranota sp.	77673	4	0,86	7,13	3,33	5,9	



Taxon list (2020-04-29)

Data sheet:

Project(s): Gelnhausen

Water ID(s): Bieber, RM01, RM02, Steinau, Waechterbach

Sample site(s): 1, 10, 11, 12, 13, 14, 2, 3, 4, 5, 6, 7, 8, 9

Description: TTT Tutorial test data

Author(s): TM

Lab protocol: Tutorial

No. of replicates: 2

No. of negative controls: 3

Primers: BF2, BR2

Sequencing run: MiSeq 25 bp

Bionf. pipeline: JAMP

Taxon Table Tools: Version 1.0 (r28.04.2020)



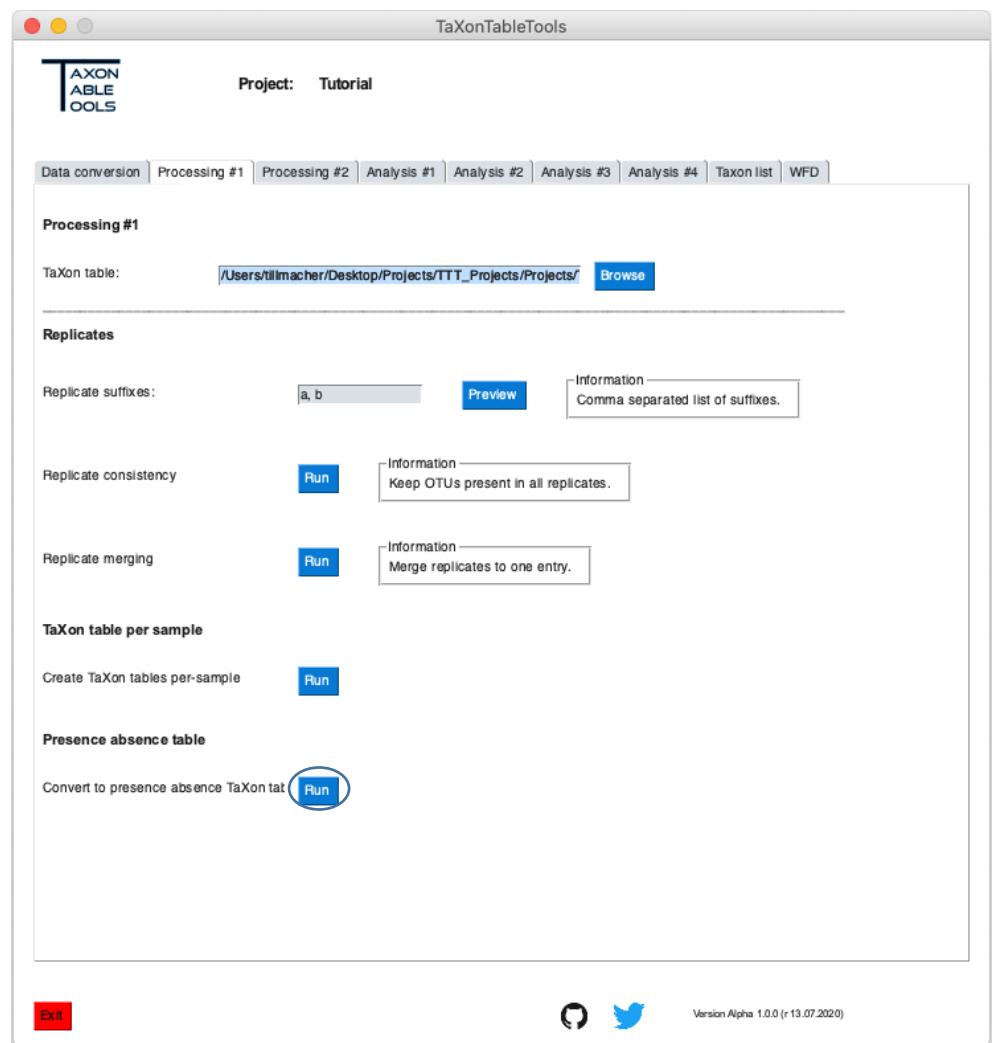
Taxonomic information

Excel-Sheet: Projects\Default\_project\Taxon\_lists\Default\_project\_taxon\_list.xlsx

Location of the taxon list

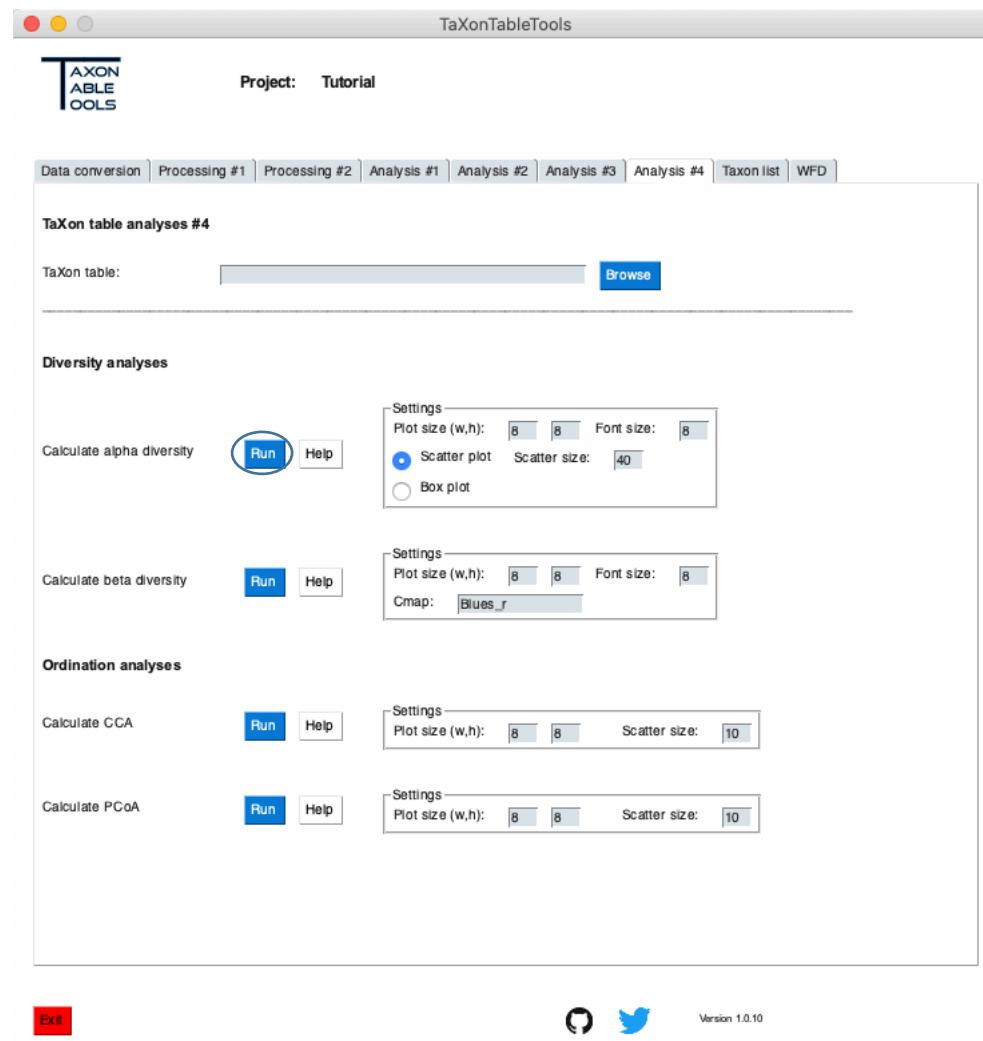
# Presence / absence data

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC.xlsx*) in the **Processing #1** 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)



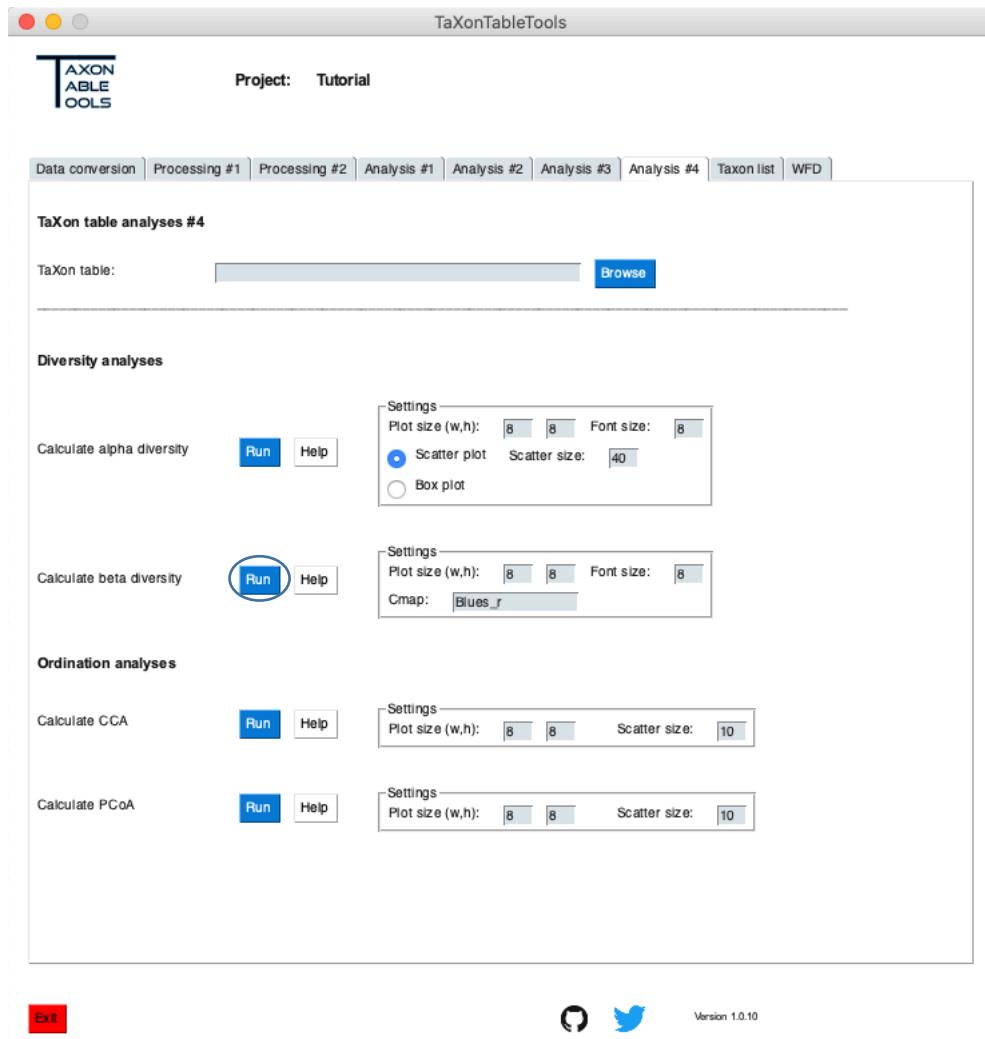
# Diversity analyses

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC\_pa.xlsx*) in the **Analysis #4** tab
- Note: the diversity analyses require **presence absence data** and a **meta data table**
- Calculate the Alpha diversity
  - 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



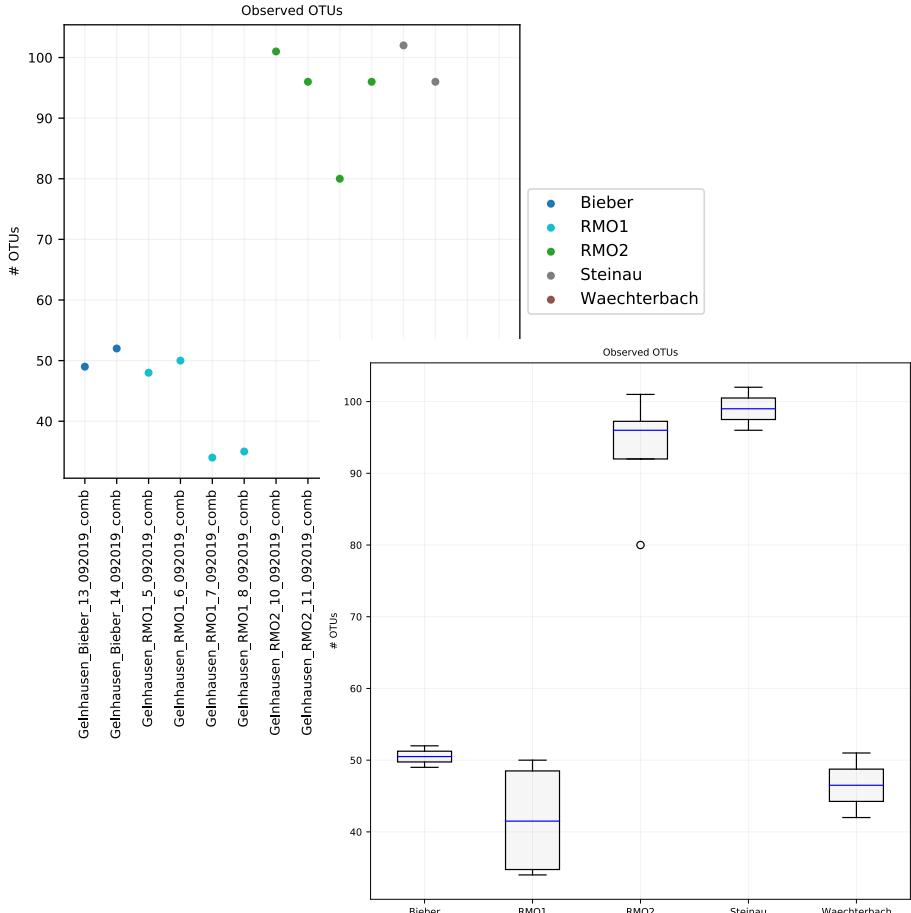
# Diversity analyses

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC\_pa.xlsx*) in the **Analysis #4** tab
- Note: the diversity analyses require **presence absence data** and a **meta data table**
- Calculate the 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 colormaps, Find further information about colormaps here:  
<https://matplotlib.org/3.1.0/tutorials/colors/colormaps.html>

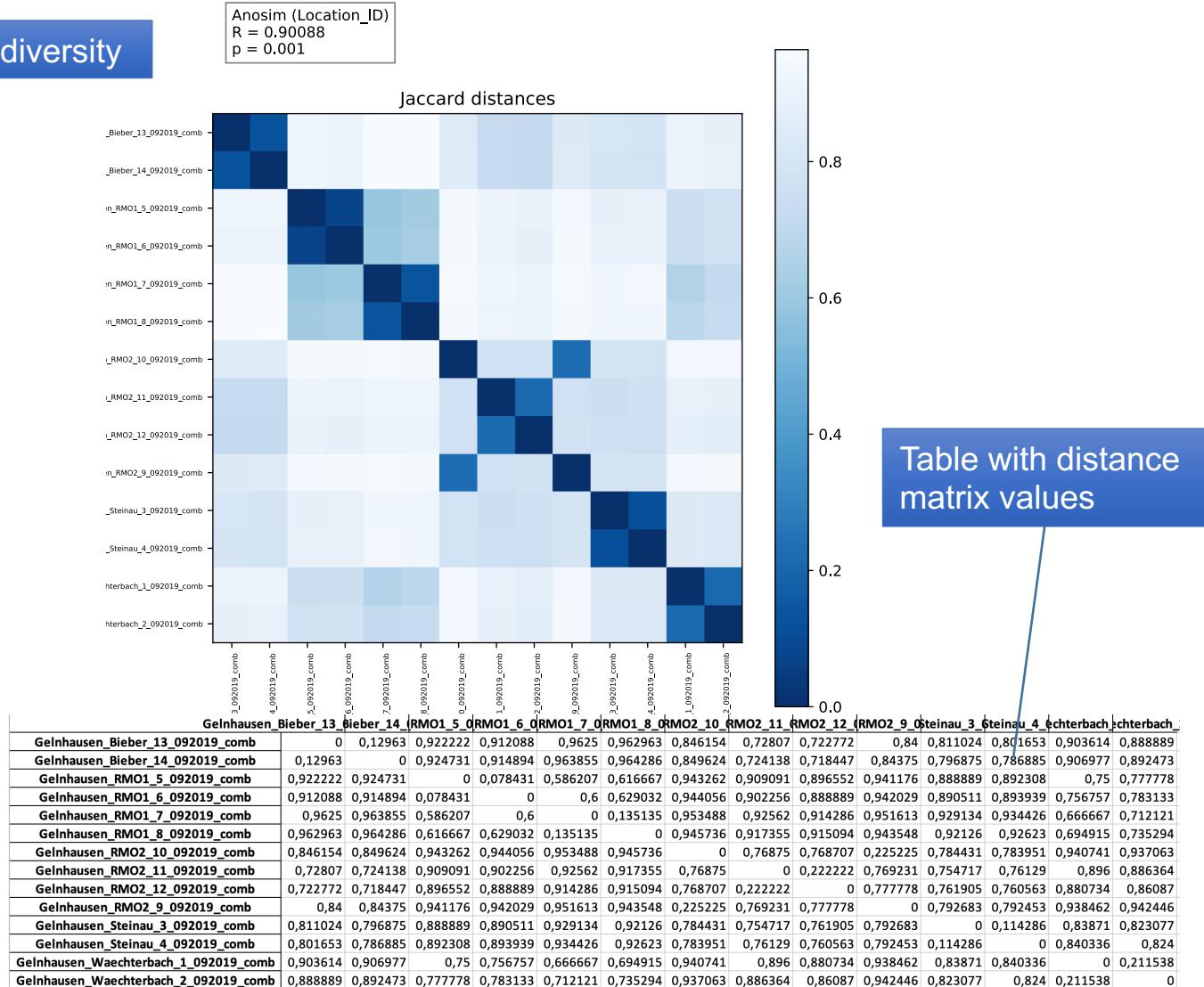


# Diversity analyses

## Alpha diversity

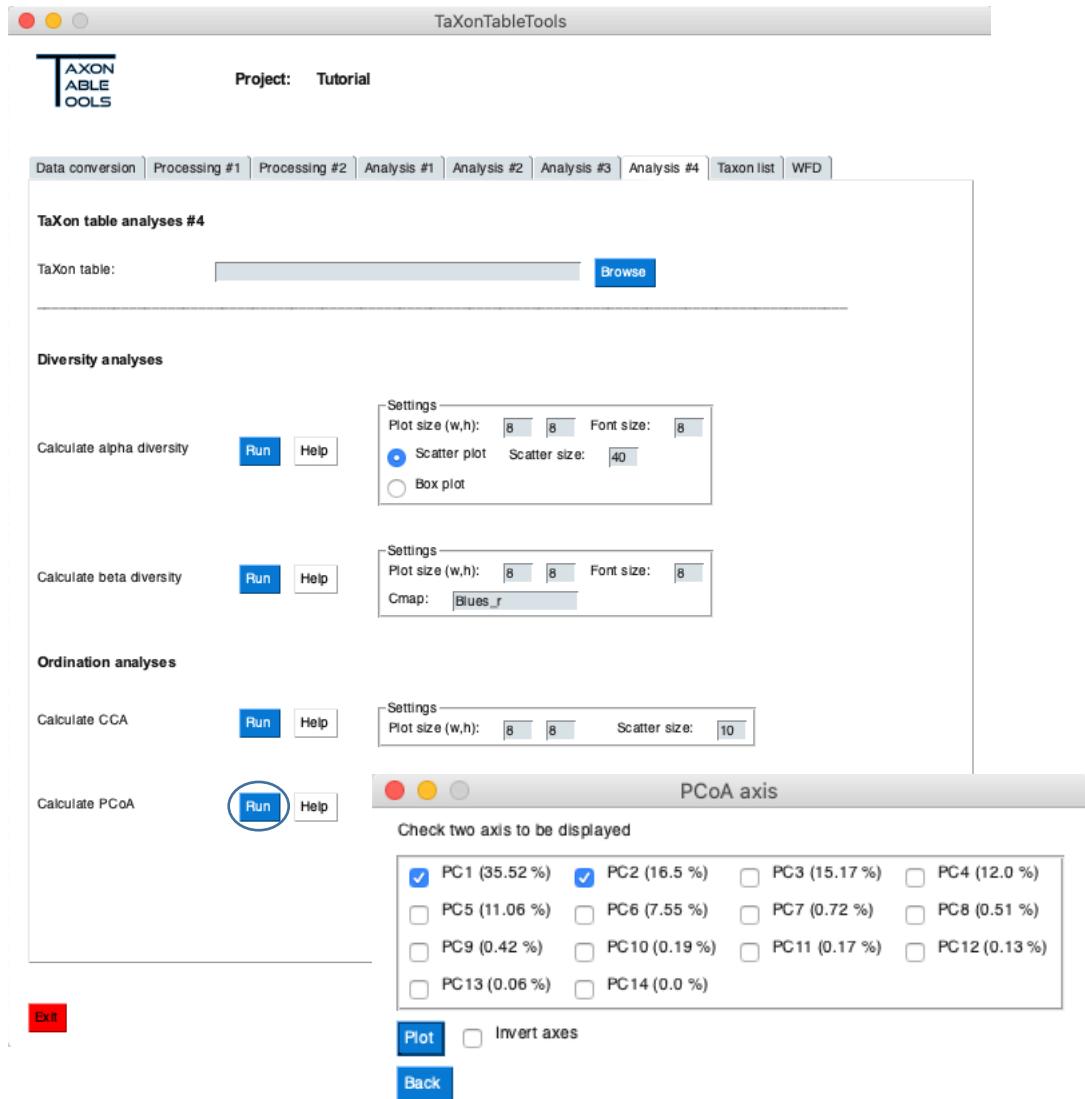


## Beta diversity



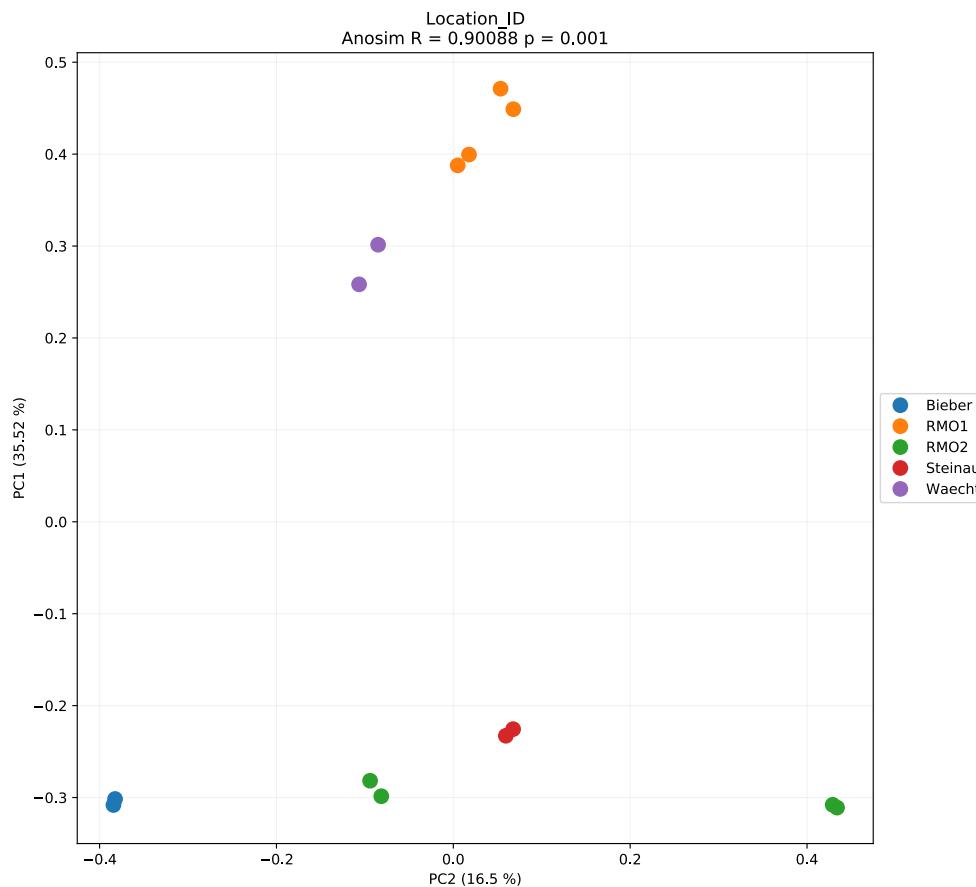
# Ordination analyses

- Load the latest TaXon table (*TTT\_cons\_derep\_arthropods\_no\_NC.xlsx*) in the **Analysis #4** tab
- All ordination analyses require **presence absence data and a meta data table**
- Perform a PCoA analysis
  - Choose a meta data to test (e.g. Location\_ID)
  - This will plot the number of OTUs per sample



# Ordination analyses

PCoA plot



PCoA eigenvalues

	PC2	PC1
Gelnhausen_Bieber_13_092019_comb	-0,382521235	-0,301574442
Gelnhausen_Bieber_14_092019_comb	-0,384360491	-0,308087991
Gelnhausen_RMO1_5_092019_comb	0,017748437	0,399525345
Gelnhausen_RMO1_6_092019_comb	0,004968135	0,387732975
Gelnhausen_RMO1_7_092019_comb	0,053435089	0,471212002
Gelnhausen_RMO1_8_092019_comb	0,067866178	0,448881819
Gelnhausen_RMO2_10_092019_comb	0,433944613	-0,310941484
Gelnhausen_RMO2_11_092019_comb	-0,081423665	-0,298542015
Gelnhausen_RMO2_12_092019_comb	-0,094108371	-0,281702159
Gelnhausen_RMO2_9_092019_comb	0,429013996	-0,307874185
Gelnhausen_Steinau_3_092019_comb	0,067618717	-0,225576871
Gelnhausen_Steinau_4_092019_comb	0,05941049	-0,232795733
Gelnhausen_Waechterbach_1_092019_comb	-0,085042599	0,301433247
Gelnhausen_Waechterbach_2_092019_comb	-0,106549295	0,258309491