Webinar 2

Resolving Nomenclature: Making Appropriate Taxonomic Choices

Session Summary Webinar 1

- **Advances in biodiversity science**, combined with emerging technologies and the ability to handle "big data" **have greatly improved** and expanded our capability to explore biodiversity in an unprecedented fashion. We can now **link data** from growing repositories (**trees**, **occurrences**, **traits**) **and computational tools/approaches to integrate evolution and ecology at broad scale**. This new synthesis is reshaping views of ecology/evolution with important conservation implications.

- **Scaling biogeographic analyses** from a small number of species or genera to explore patterns of evolution and diversity for thousands or tens of thousands of taxa on continental and global scales **requires software tools that automate and parallelize computational tasks to make analyses practically feasible, efficient, with reasonable timelines**.

Allen et al.. 2019. Biodiversity synthesis across the green branches of the tree of life. *Nature Plants* 5:11-13.

Goals

Learn why and how to treat nomenclatural data that will be used in multiple biodiversity analysis

Learning Objectives

Biological Objectives:

- ✓ **Introduce the reasoning for making nomenclatural decisions.**

Technological Objectives :

- ✓ **Introduce technological tools available for making nomenclatural decisions.**

Webinar organization

1. Exploring Concepts: why ensuring nomenclature is an important first step in this workflow!
2. Demonstrations: manual and automated ways of properly treating nomenclature decisions
3. Exercises: practice automated ways of treating nomenclature
4. Session Summary, Q&A and Discussion

Exploring Concepts

Why do we have to make nomenclatural decisions?

Ensure taxa names are ready for integration on a large scale!

Names must be…

- ✓ **accepted**
- ✓ **unique**
- ✓ **consistent**

Demonstration: Manual

Demonstration: showing manual ways of properly treating nomenclature decisions:

a) **Useful for smaller datasets,**

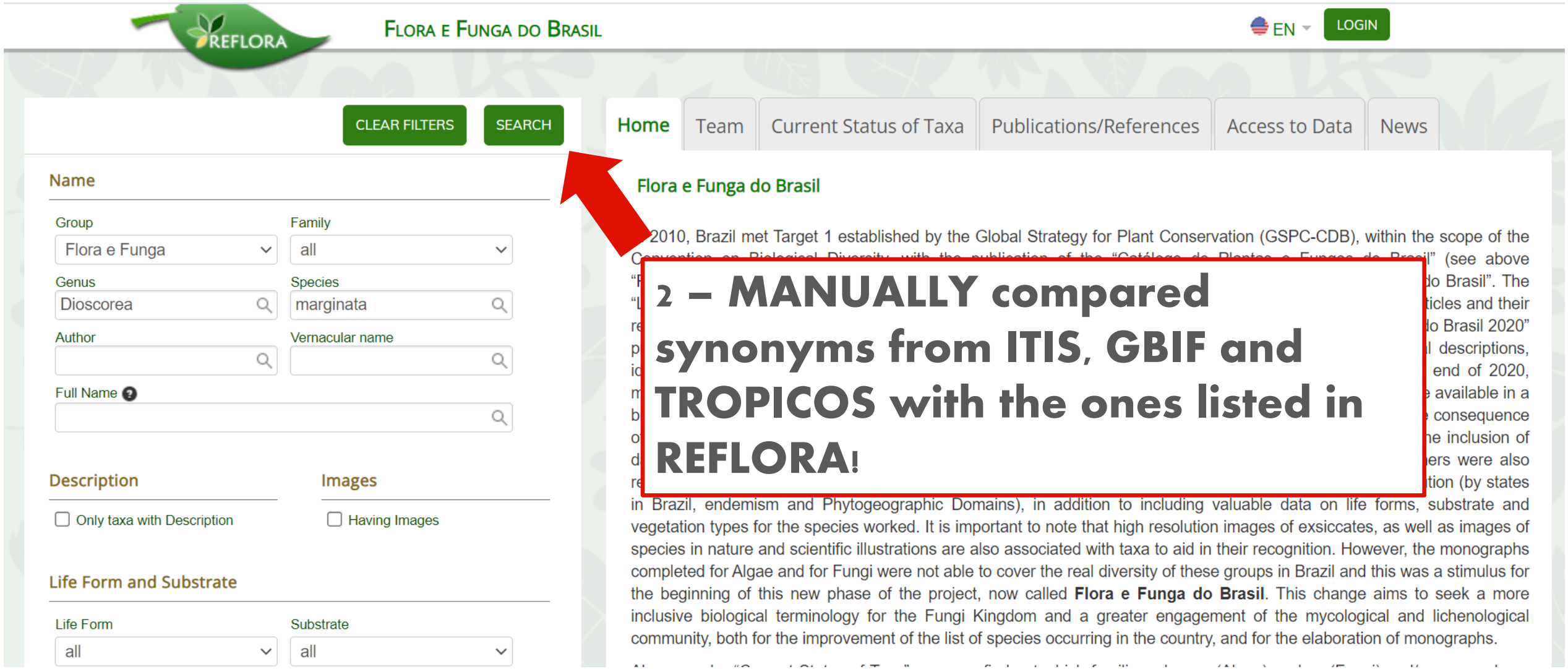
b) **Tool to subset large datasets and verify procedures**

Demonstration: Manual

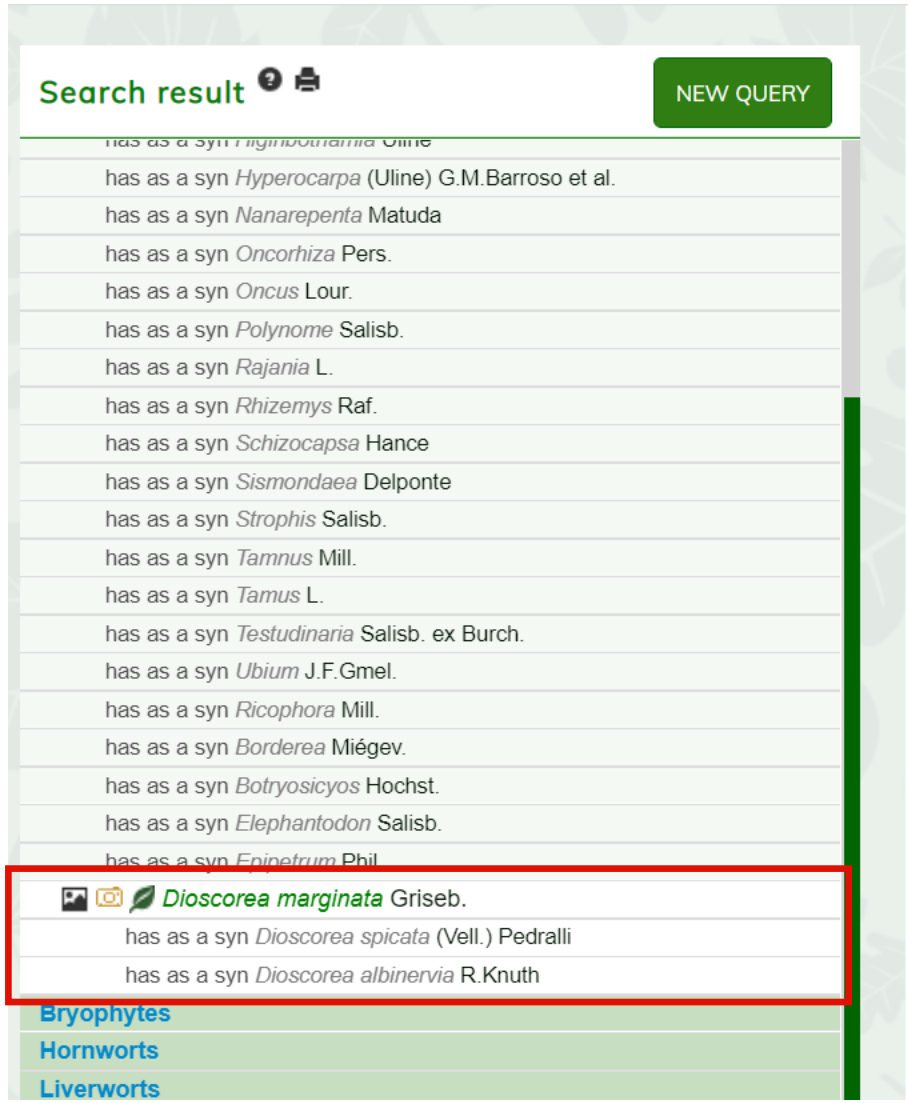
1615	1614	Dioscorea marginata	Dioscorea albinervia, Dioscorea cynanchifolia
1616	1615	Dioscorea sincorensis	NA
1617	1616	Dioscorea stenophylla	Dioscorea stenophylla paucinervis
1618	1617	Diospyros sericea	Diospyros praetermissa, Diospyros vestita, Maba sericea, Ebenus sericea
1619	1618	Diplococcium dendrocalami	NA
1620	1619	Diplopterys hypericifolia	Banisteria hypericifolia, Banisteria rigida, Banisteriopsis hypericifolia
1621	1620	Diplusodon adpressipilus	NA
1622	1621	Diplusodon aggregatifolius	NA
1623	1622	Diplusodon alatus	NA
1624	1623	Diplusodon appendiculosus	NA
1625	1624	Diplusodon argenteus	NA
1626	1625	Diplusodon argyrophyllus	NA
1627	1626	Diplusodon bahiensis	NA
1628	1627	Diplusodon bradei	NA
1629	1628	Diplusodon buxifolius	Diplusodon buxifolius naudinii, Diplusodon vaccinifolius, Friedlandia buxifolia, Friedlandia vaccinifolia
1630	1629	Diplusodon canastrensis	NA
1631	1630	Diplusodon candollei	Diplusodon candollei
1632	1631	Diplusodon ciliiflorus	NA
1633	1632	Diplusodon cordifolius	NA
1634	1633	Diplusodon decussatus	NA

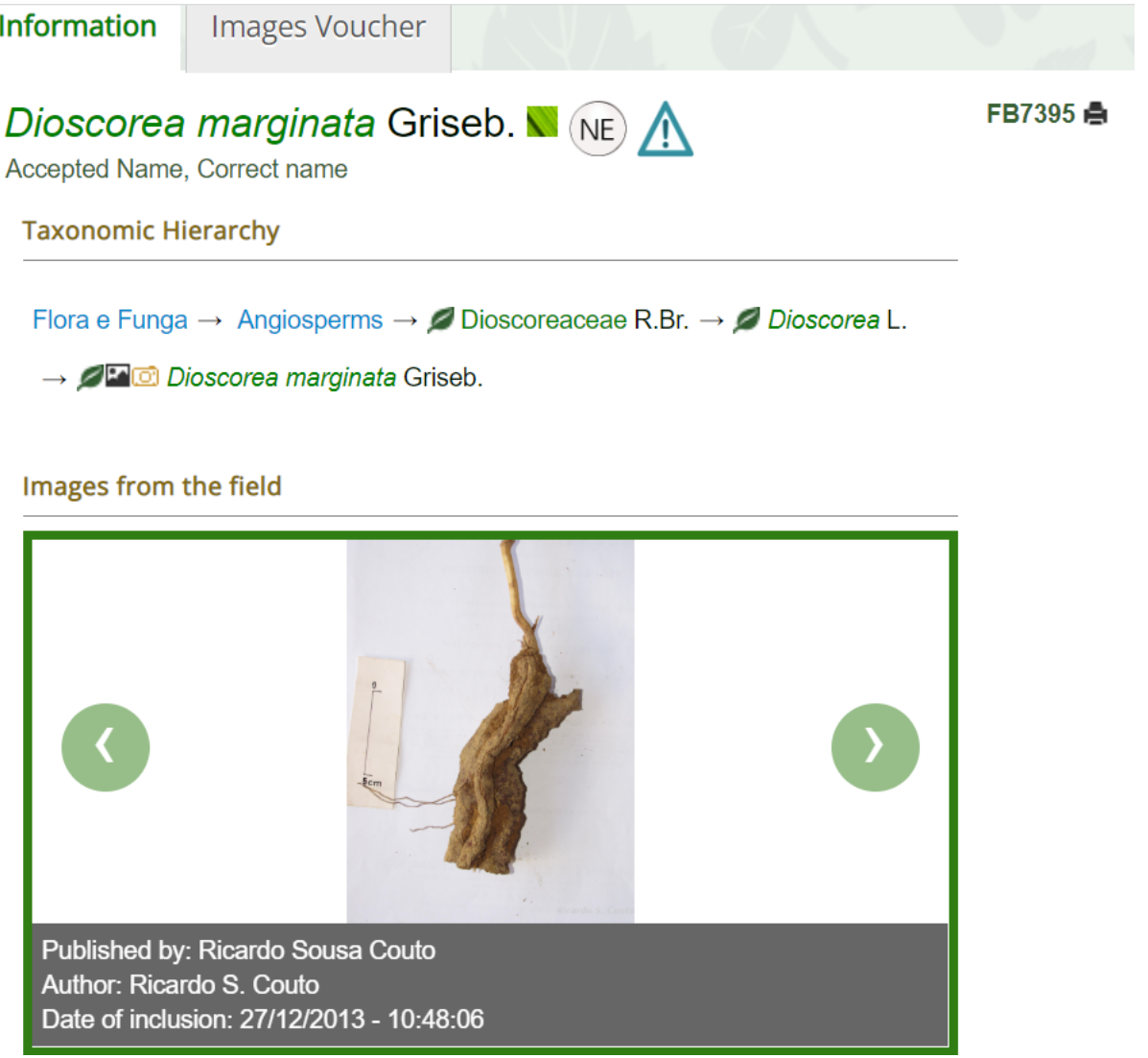
1 – Downloaded lists with accepted names (from REFLORA) and synonyms from ITIS, GBIF and TROPICOS

Demonstration: Manual



Demonstration: Manual





Demonstration: Manual

1482	Accepted	Angiosperms	1614	Dioscorea marginata	Dioscorea albinervia, Dioscorea cynanchifolia, Dioscorea spicata
1483	Accepted	Angiosperms	1615	Dioscorea sincorensis	NA
1484	Accepted	Angiosperms	1616	Dioscorea stenophylla	Dioscorea stenophylla var. paucinervis
1485	Accepted	Angiosperms	1617	Diospyros sericea	Diospyros praetermissa, Diospyros vestita, Maba sericea, Ebenus sericea
1486	Accepted	Angiosperms	1619	Diplopterys hypericifolia	Banisteria hypericifolia, Banisteria rigida, Banisteriopsis hypericifolia
1487	Accepted	Angiosperms	1620	Diplusodon adpressipilus	NA
1488	Accepted	Angiosperms	1621	Diplusodon aggregatifolius	NA
1489	Accepted	Angiosperms	1622	Diplusodon alatus	NA
1490	Accepted	Angiosperms	1623	Diplusodon appendiculosus	NA
1491	Accepted	Angiosperms	1624	Diplusodon argenteus	NA
1492	Accepted	Angiosperms	1625	Diplusodon argyrophyllus	NA
1493	Accepted	Angiosperms	1626	Diplusodon bahiensis	NA
1494	Accepted	Angiosperms	1627	Diplusodon bradei	NA, Diplusodon rupestris
1495	Accepted	Angiosperms	1628	Diplusodon buxifolius	Diplusodon buxifolius naudinii, Diplusodon vaccinifolius, Friedlandia buxifolia, Friedlandia vaccinifolia
1496	Accepted	Angiosperms	1629	Diplusodon canastrensis	NA
1497	Accepted	Angiosperms	1630	Diplusodon candollei	NA
1498	Accepted	Angiosperms	1631	Diplusodon ciliiflorus	NA, Diplusodon psammophilus
1499	Accepted	Angiosperms	1632	Diplusodon cordifolius	NA
1500	Accepted	Angiosperms	1633	Diplusodon decussatus	NA
1501	Accepted	Angiosperms	1634	Diplusodon epilobioides	Friedlandia epilobioides
1502	Accepted	Angiosperms	1635	Diplusodon ericoides	NA
1503	Accepted	Angiosperms	1636	Diplusodon fastigiatus	NA
1504	Accepted	Angiosperms	1637	Diplusodon glaucescens	Friedlandia glaucescens, Friedlandia nummularifolia

No synonyms listed under any of the databases!

Demonstration: Manual

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1503	Accepted	Angiosperms	1636	Diplusodon fastigiatus	NA
1504	Accepted	Angiosperms	1637	Diplusodon glaucescens	Friedlandia glaucescens, Friedlandia nummularifolia

Synonyms listed ONLY in REFLORA!

Demonstration: Manual

1482	Accepted	Angiosperms	1614	Dioscorea marginata	Dioscorea albinervia, Dioscorea cynanchifolia, Dioscorea spicata
1483	Accepted	Angiosperms	1615	Dioscorea sincorensis	NA
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Synonyms NOT listed in REFLORA!

Demonstration: Manual

Original list, synonyms compiled from ITIS, TROPICOS and GBIF

Dioscorea marginata	Dioscorea albinervia, Dioscorea cynanchifolia

Dioscorea marginata	Dioscorea albinervia, Dioscorea cynanchifolia, Dioscorea spicata

Synonym listed in both REFLORA and compiled list

Synonym NOT listed in REFLORA!

Synonym listed ONLY in REFLORA!

Time to Exercise!

What happens when there is a large dataset?

Should we manually check 40,000 records?

We use BiotaPhy tools to automate nomenclatural decision making!

Time to Exercise!

Let's put the automated framework developed by BiotaPhy to test!

How to resolve a species list name:

3 steps:

- ✓ **Data Preparation**
- ✓ **Run Tutorial**
- ✓ **Inspect Output**

Input: species list

Input: Wrangler configuration file

Input: Script parameter file

Data Preparation: species list

Data preparation

Input: species list

Use an existing or prepare a new species list, a text file with one name per line. This file is specified in the script parameter file described below.

1. The tutorial example species list is heuchera.txt.
2. Some resources:
    1. World Flora Online, WFO
    2. Query GBIF, i.e. heuchera query

```
1   Heuchera nana (A. Gray) Rydb.
2   Heuchera alpina (S. Watson) Blank.
3   Heuchera versicolor Greene
4   Heuchera sitgreavesei Rydb.
5   Heuchera townsendii Rydb.
6   Heuchera racemosa S.Watson
7   Heuchera mexicana W. Schaffn. ex Rydb.
8   Heuchera amoena Rosend. & Butters & Lakela
9   Heuchera divaricata Fisch. ex Ser.
10  Heuchera drummondii G.Nicholson
11  Heuchera x easthamii Calder & Savile
12  Heuchera flabellifolia Rydb.
13  Heuchera foliosa Rahn.
14  Heuchera gracilis Rydb.
```

Data Preparation: species list

Data preparation

Input: species list

Use an existing or prepare a new specie
in the script parameter file described be

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2. Some resources:
    1. World Flora Online, WFO
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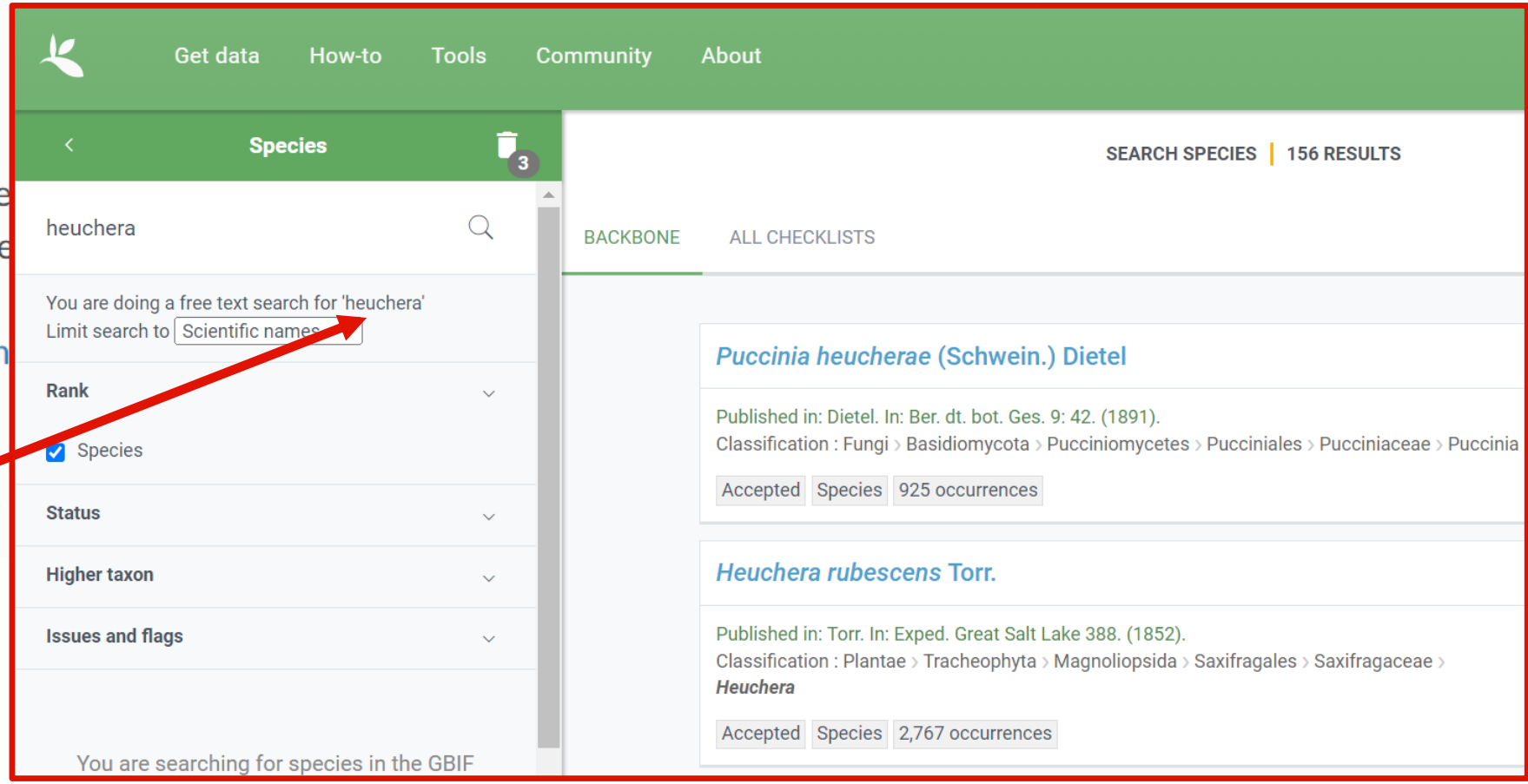


Data Preparation: wrangler file

Input: Wrangler configuration file

A data wrangler configuration is a file containing a JSON list of zero or more wranglers - each performs a different operation, and each has its own parameters. More information on file format, available wrangler types, and the required and/or optional parameters for each are at Species List: Wrangling.

Species List Wrangler Types

Wrangler types that perform different operations when dealing with species lists! You add the name of the corresponding wrangler after the parameter: "*wrangler_type*"

Data Preparation: wrangler file

Species List Wrangler Types

AcceptedNameSpeciesListWrangler

- optional
  - name_map (str or dict): A dictionary or filename containing a dictionary of original name to accepted name. Defaults to None, but either this or name_resolver **must be** provided.
  - name_resolver (str or Method): Use this method for getting new accepted names. If set to 'gbif' or 'otol', use GBIF or OTOL name resolution respectively. Defaults to None, but either this or name_map must be provided.
  - out_map_filename (str): Output for name-mapping between original and accepted names. This file is then acceptable for use as a **name-map** input for subsequent name wrangling. Defaults to None.
  - map_write_interval (int): Interval at which to write records to disk. Used to ensure that if something fails, all is not lost. Defaults to 100.
  - out_map_format (str): Type of file format for out_map_filename, defaults to "json".

IntersectionSpeciesListWrangler

- required
  - species_list (str): Filename containing species list to intersect

MatchMatrixSpeciesListWrangler

- required
  - matrix (str): Filename containing matrix to match

MatchTreeSpeciesListWrangler

- required
  - tree (str): Filename containing tree to match

UnionSpeciesListWrangler

- required
  - species_list (str): Filename containing species list to join

Data Preparation: wrangler file

main ▾ tutorials / data / wranglers / splist_wranglers_gbif.json

Go to file ···

zzeppozz doc ✓ Latest commit 5e23b7c 5 days ago History

1 contributor

9 lines (9 sloc) | 247 Bytes Raw Blame

```
1  [
2      {
3          "wrangler_type": "AcceptedNameSpeciesListWrangler",
4          "name_resolver": "gbif",
5          "out_map_filename": "/volumes/output/heuchera_name_map.json",
6          "map_write_interval": 100,
7          "out_map_format": "json"
8      }
9  ]
```

Specifies how to get the accepted names

Output: name map where original names inputted are connected to the accepted names retrieved!

Data Preparation: script file

Input: Script parameter file

A JSON parameter file is required for this command. The tutorial parameter file is wrangle_species_list_gbif.json. These are the required and optional parameters:

Required:

- **in_species_list_filename**: Input filename containing species list, described in the section above. The tutorial example species list is heuchera.txt.
- **wrangler_configuration_file**: species list wrangler configuration file, described in the previous input section. The tutorial example wrangler configuration contains one wrangler, the AcceptedNameSpeciesListWrangler, and is in splist_wranglers_gbif.json
- **out_species_list_filename**: output filename for resolved species list.

Optional

- **log_filename**: Output filename to write logging data
- **log_console**: 'true' to write log to console
- **report_filename**: output filename with data modifications made by wranglers

```
1  Heuchera nana (A. Gray) Rydb.
2  Heuchera alpina (S. Watson) Blank.
3  Heuchera versicolor Greene
4  Heuchera sitgreavesei Rydb.
5  Heuchera townsendii Rydb.
6  Heuchera racemosa S.Watson
7  Heuchera mexicana W. Schaffn. ex Rydb.
8  Heuchera amoena Rosend. & Butters & Lakela
9  Heuchera divaricata Fisch. ex Ser.
10 Heuchera drummondii G.Nicholson
```

The file we just saw in the previous slide!

??????

Data Preparation: script file

main ▾ tutorials / data / config / wrangle_species_list_gbif.json

Go to file ···

zzeppozz testing ✓ Latest commit 12b731e 22 hours ago History

1 contributor

8 lines (8 sloc) | 383 Bytes Raw Blame

```
{
  "log_filename": "/volumes/output/wrangle_species_list1.log",
  "log_console": true,
  "report_filename": "/volumes/output/wrangle_species_list1_rpt.json",
  "in_species_list_filename": "/volumes/data/input/heuchera.txt",
  "wrangler_configuration_file": "/volumes/data/config/splist_wranglers_gbif.json",
  "out_species_list_filename": "/volumes/output/heuchera_accepted1.txt"
}
```

Optional parameters

Required parameters

Especially important to help visualize what is happening and to make sure code is running smoothly! **Optional, BUT HIGHLY RECOMMENDED!**

Let's run this tutorial!

Hands-on: Run tutorial with 'gbif' service

Initiate the process with the following:

```
./run_tutorial.sh wrangle_species_list data/config/wrangle_species_list_gbif.json
```

Goal: produce a file with resolved species names (ONLY ACCEPTED NAMES)

Windows users will run with: run_tutorial.bat

Remember, you will RUN this code in the terminal or in the command prompt for Windows!

Let's look at the output!

Output

This process outputs files configured in the script parameter file:

2. If *report_filename* is specified in the script parameter file, a summary of name resolutions, like wrangle_species_list_gbif.log
3. If *log_filename* is specified in the script parameter file, a report like wrangle_species_list_gbif.rpt containing a summary of the processing.

3. If *log_console* is specified in the script parameter file, logs will be written to the command prompt during execution.
4. an output species list named in the out_species_list_filename, like heuchera_wrangled.txt containing the modified species list, one name per line.

The process produces one additional file configured in the wrangler configuration file:

- An *out_map_filename* containing a name-map from the AcceptedNameSpeciesListWrangler. The name-map is a JSON file with pairs of names - the original name to the accepted name according to the specified authority. This name-map is suitable to use for input when resolving another dataset containing a subset of the same original names. A sample output name-map is splist_wrangle_gbif.namemap.

SECONDARY OUTPUT

PRIMARY OUTPUT

Let's look at the output!

While it runs let's look at... SECONDARY OUTPUT

main | tutorials / data / easy_bake / wrangle_species_list_gbif.log | Go to file | ...

zzeppozz tutorial data ✓ Latest commit e696d1f 7 minutes ago History

1 contributor

135 lines (135 sloc) | 16.1 KB | Raw | Blame

```
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera richardsonii R. Br. to Heuchera richardsonii
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera americana L. to Heuchera americana
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera x easthamii Calder & Savile to Heuchera easthamii
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Elmera racemosa (S.Watson) Rydb. to Elmera racemosa
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera halstedii Rydb. to Heuchera halstedii
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera macrophylla Lodd. ex G.Don to Heuchera macrophylla
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera flabellifolia Rydb. to Heuchera flabellifolia
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera macrorhiza Small to Heuchera villosa
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera merriamii Eastw. to Heuchera merriamii
09 Sep 2022 15:26 DEBUG    AcceptedNameSpeciesListWrangler: Resolved Heuchera novamexicana Wheelock to Heuchera novamexicana
```

Logging of the process!

Let's look at the output!

While it runs let's look at... SECONDARY OUTPUT

main | tutorials / data / easy_bake / wrangle_species_list_gbif.rpt | Go to file | ...

zzeppozz test, rename inputs, outputs ✓ Latest commit 6aee525 6 days ago History

1 contributor

8 lines (8 sloc) | 142 Bytes | Raw | Blame

```
1  [
2      {
3          "name": "AcceptedNameSpeciesListWrangler",
4          "version": "1.0",
5          "unresolved": 4,
6          "duplicates": 41
7      }
8  ]
```

Summary of the process!

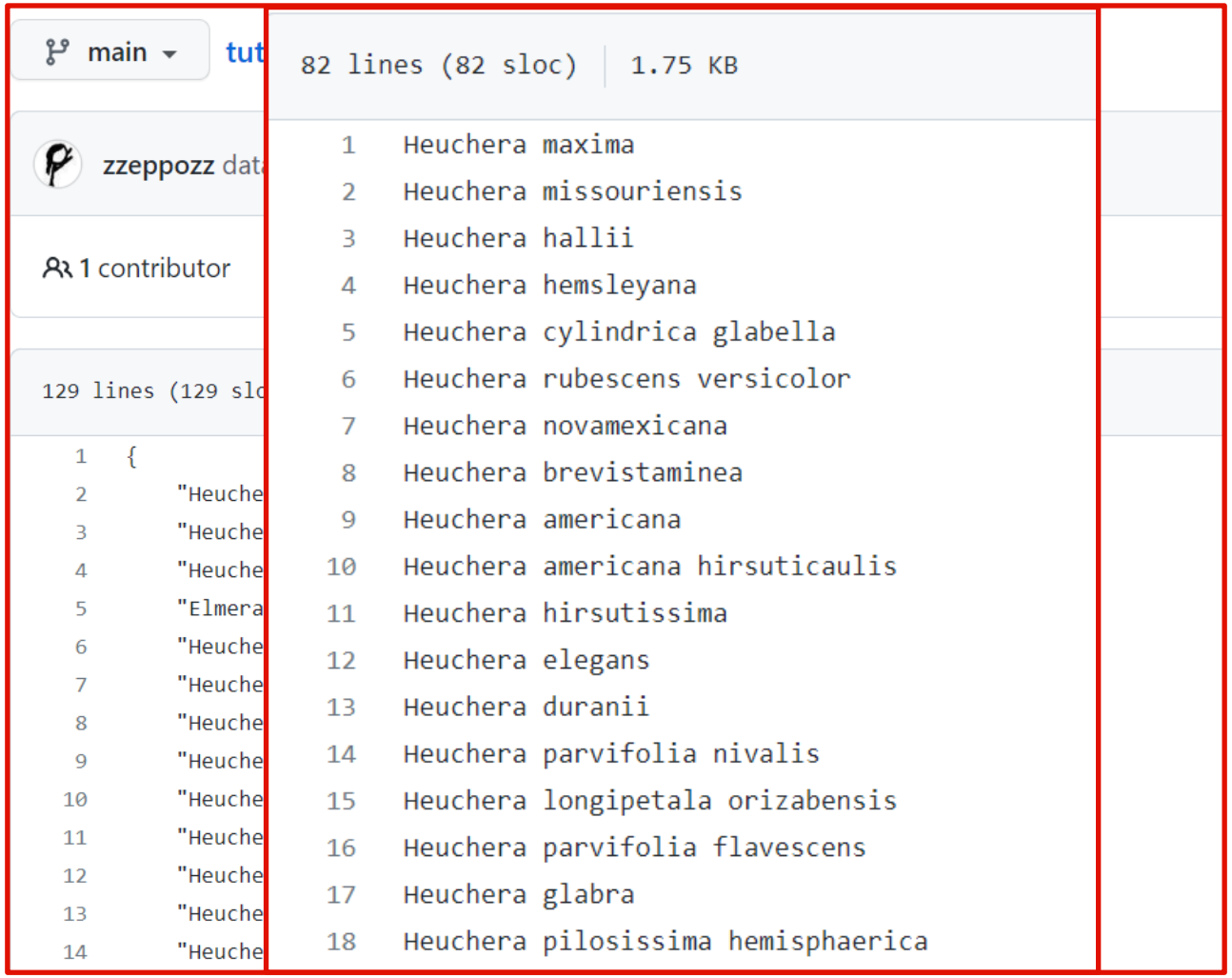
Let's look at the output!

While it runs let's look at...

PRIMARY OUTPUT

Goal: produce a file with resolved species names (ONLY ACCEPTED NAMES)

By product: NAME-MAP connecting original and accepted names using GBIF! !



Session Summary, Q&A and Discussion

1. Species list must contain: ACCEPTED, UNIQUE and CONSISTENT names!
2. Manual ways of treating nomenclature: useful for small datasets and to subset large datasets.
3. Automated ways of treating nomenclature: useful for large datasets.
4. BiotaPhy framework is a great toolkit for automated pathway!

Any questions??

Please, use the link to the Jamboard to write your question!