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WORLDFLORA

User Guide for Graphical User Interface

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1. Introduction

This document provides a worked example with the [RcmdrPlugin.WorldFlora](#) package of standardizing plant names with a downloaded copy of the Taxonomic Backbone data set of [World Flora Online](#). *RcmdrPlugin.WorldFlora* provides a graphical user interface (GUI) that is integrated in the [R Commander](#) GUI for the [WorldFlora](#) package

The suggested citation of the World Flora Online (WFO) is:

WFO ([Year]): World Flora Online. Version [Year].[Month]. Published on the Internet;
<http://www.worldfloraonline.org>. Accessed on: [Date]"

A manuscript describing the *WorldFlora* package has been accepted for Applications in Plant Sciences. Once published, this article will be the suggested citation for using *WorldFlora* and *RcmdrPlugin.WorldFlora*.

A pre-print of the manuscript is available here:

Kindt R. 2020. WorldFlora: An R package for exact and fuzzy matching of plant names against the World Flora Online Taxonomic Backbone data.

<https://www.biorxiv.org/content/10.1101/2020.02.02.930719v1>

The worked example is a list of 636 gymnosperms that was downloaded from the [World Economic Plants in GRIN-Global](#), obtained on 28-JUN-2020 with the query of:

```
family/altfamily = 'gymnosperms' & native country = 'all countries' & economic uses: economic  
classes = 'All'
```

2. Installation

The recommended installation is to install the packages in the following sequence.

First fully install the R Commander

```
install.packages("Rcmdr", dependencies=TRUE)
```

Note that the R language is case sensitive, so `Install.Packages` will not work!

Launch the R Commander and then also install other packages that are suggested:

```
library(Rcmdr)
```

In case that you encounter any problems, check the [R Commander installation notes](#).

Next install the *WorldFlora* package

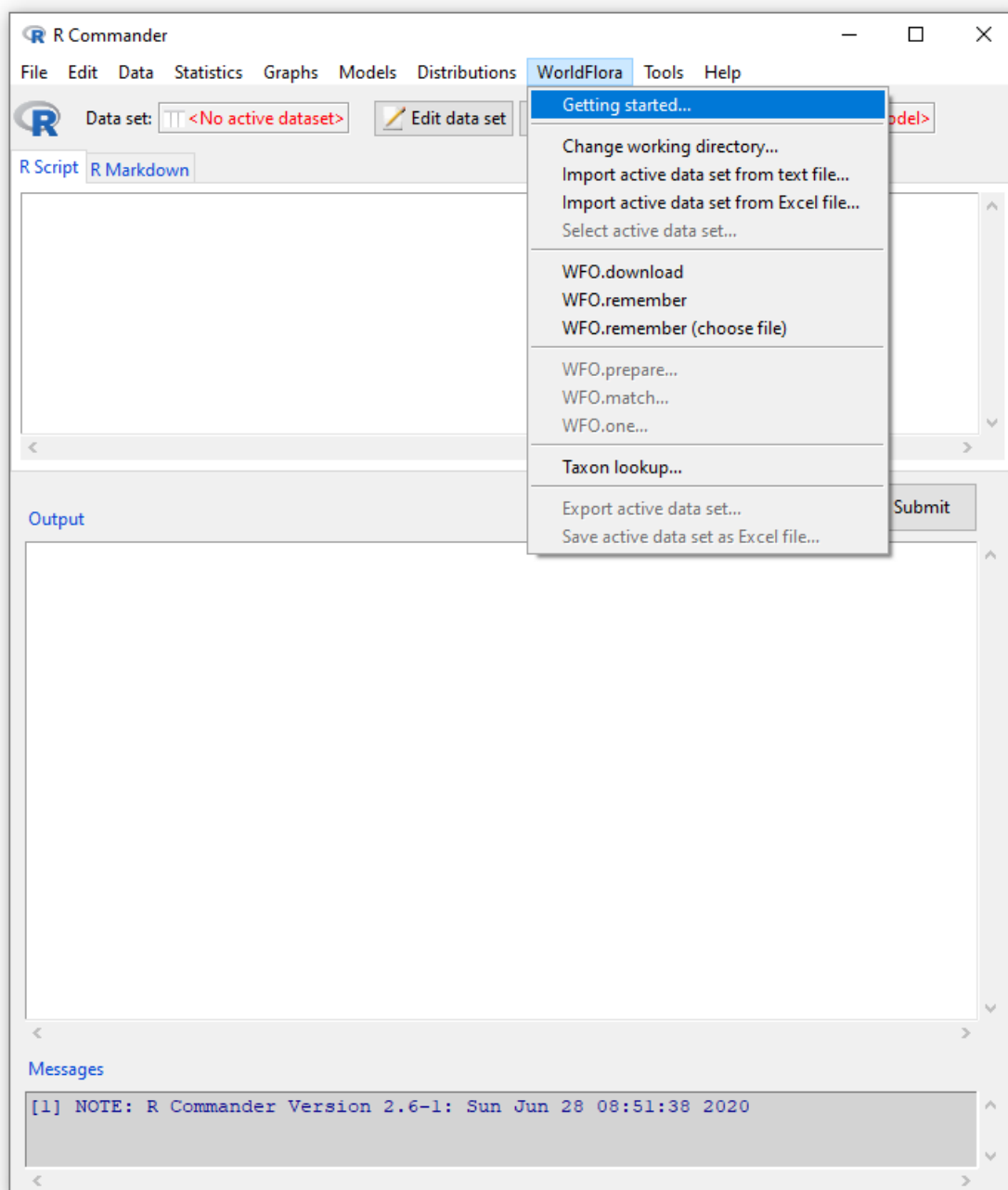
```
install.packages("WorldFlora", dependencies=TRUE)
```

Finally install the *RcmdrPlugin.WorldFlora* package

```
install.packages("RcmdrPlugin.WorldFlora", dependencies=TRUE)
```

Possibly you need to terminate the R session at this point, then launch R again.

Figure 2.1. The WorldFlora Graphical User Interface is integrated in the R Commander



It should now be possible to launch the Graphical User Interface through following command

```
library(RcmdrPlugin.WorldFlora)
```

Note that after installations, the Graphical User Interface (Figure 2.1) can be immediately launched with the command directly above.

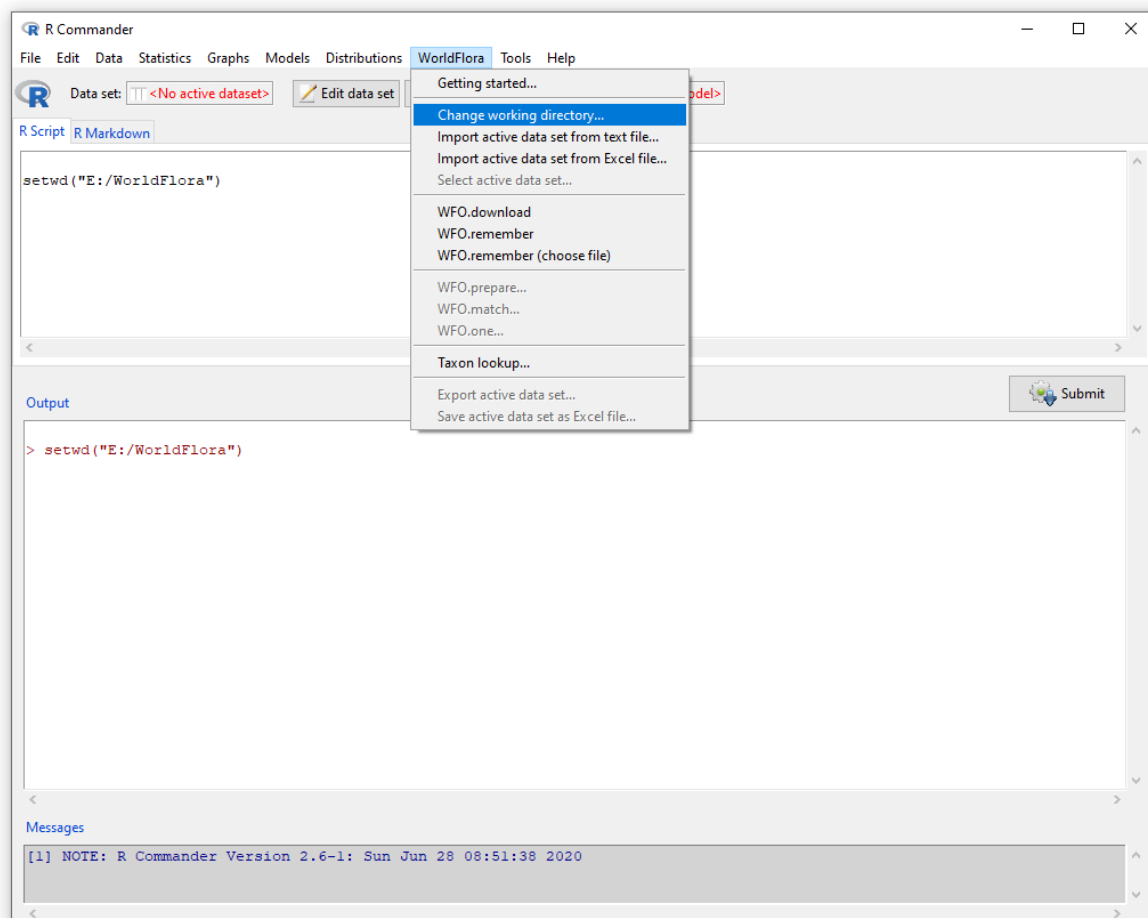
3. Change the working directory

Change the working directory. This is the default folder where R will import and save data. It will be folder where the WFO taxonomic backbone will be downloaded to (Section 4).

The result of selecting the menu option of: WorldFlora > Change working directory... will be that a script for changing the working directory (`setwd("E:/WorldFlora")`) will be included in the script window and that outputs will be shown in the Output window (unless R Commander options are changed; see the [introductory manual for the R Commander](#)).

Note that it is possible to directly provide or modify scripts in the R Script window. These scripts will be executed after highlighting them and then clicking on the Submit button (a button on the bottom right of the R Script window). It is also possible to copy the script to the R GUI and the executed from the R GUI, as recommended in some of the following sections.

Figure 3.1. Change the working directory.



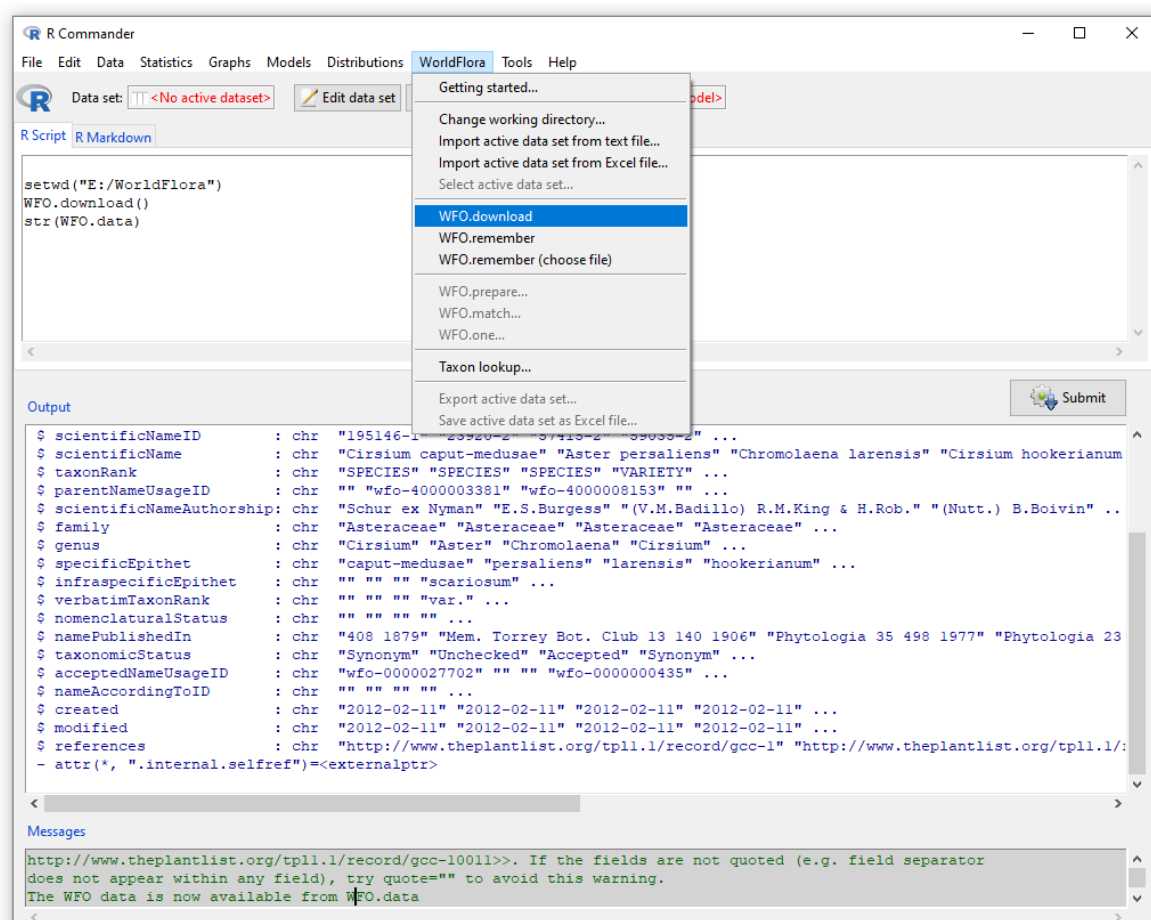
4. Download or remember the World Flora Online taxonomic backbone

When using the package the first time, you need to download the WFO taxonomic backbone first. This can be done through the menu option of `WFO.download` (Figure 4.1). The taxonomic backbone will be unzipped as 'classification.txt' into the working directory. After download, the file will be loaded into R as data set **WFO.data**. Please be patient when this data is loading as this will take some time for the over 1,300,000 observations for 19 variables.

A next that you use the package, use menu option of `WFO.remember`, which will download the **WFO.data** from the location where it was downloaded to earlier.

In case that you wanted to change the location of the 'classification.txt' data set, use menu option of `WFO.remember` (choose file) to provide the changed location.

Figure 4.1. Menu option of `WFO.download` will save a copy of the WFO taxonomic backbone into the working directory.



Once the WFO.data was loaded, you can now directly match a single taxon through the menu option of Taxon lookup... (Figure 4.2).

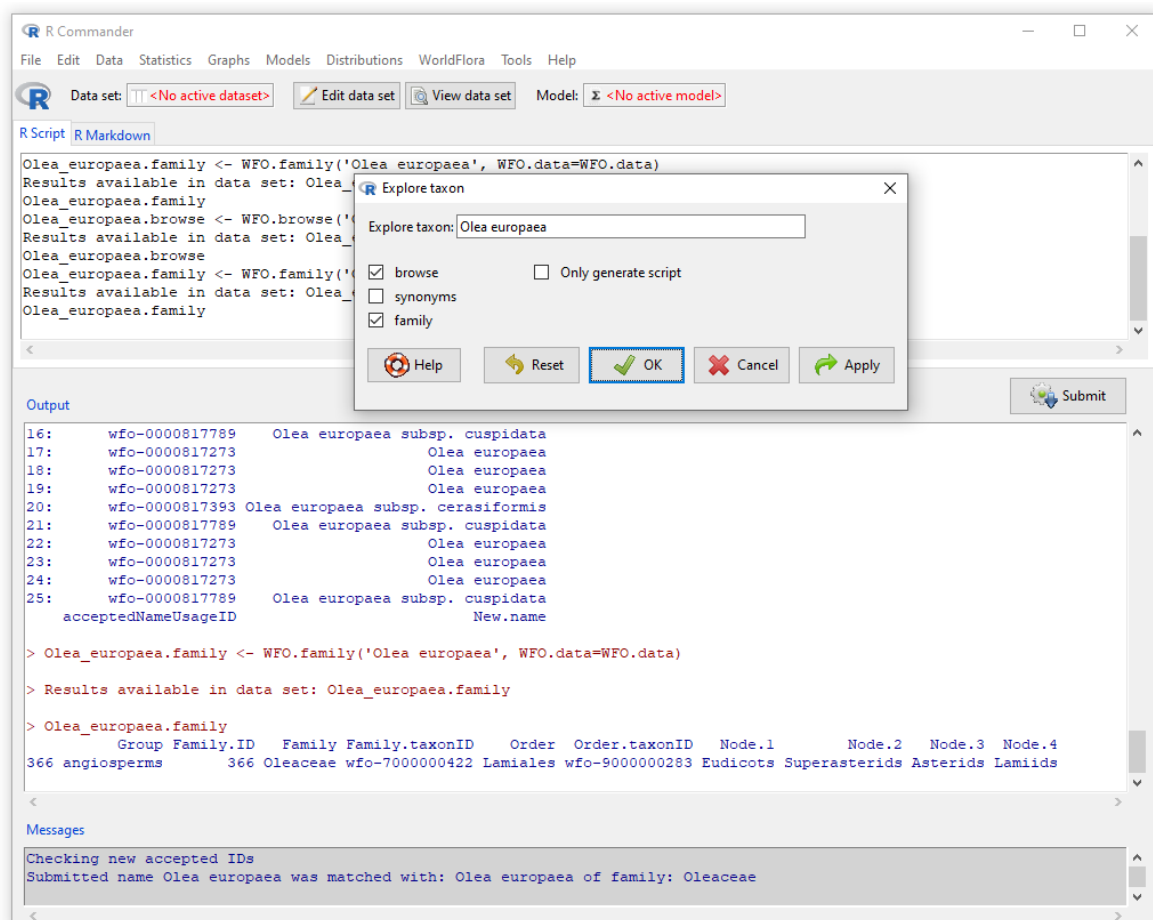
The options of the interface refer to 3 *WorldFlora* functions:

- WFO.browse gives a list of all taxa at the next taxonomic level (in the example given here, a list of forms, subspecies and varieties of species *Olea europaea*)
- WFO.synonyms gives a list of all synonyms and the accepted name
- WFO.family gives information at higher taxonomic levels (including family and order)

More details about the functions can be obtained through the Help button (bottom left of the interface).

The option in the interface of 'only generate script' has the effect that only the script will be shown on the R Script window, but that this script will not be executed. This feature allows to copy and paste the script directly into the R GUI (not the R Commander GUI). This may be desired to see messages directly displayed in the main output, something that may be preferred for the WFO.match and WFO.one functions as well (next sections).

Figure 4.2. For a single taxon, you can match with WFO data through the menu option of Taxon lookup.



5. Import the data set with plant names to be checked

The R Commander provides various methods of importing data that are available from the menu option of Data > Import data.

Two of the options are also available from the *WorldFlora* menu:

- Import active data set from text file...
- Import active data set from Excel file...

When importing the data, it is important that characters are not converted to factors, especially if you want to check a large number of plant names (Figure 5.1).

As our worked example, we import the 636 names of gymnosperms from GRIN-global (see introduction).

Figure 5.1. Importing the data from Excel. Uncheck the box to Convert character data to factors.

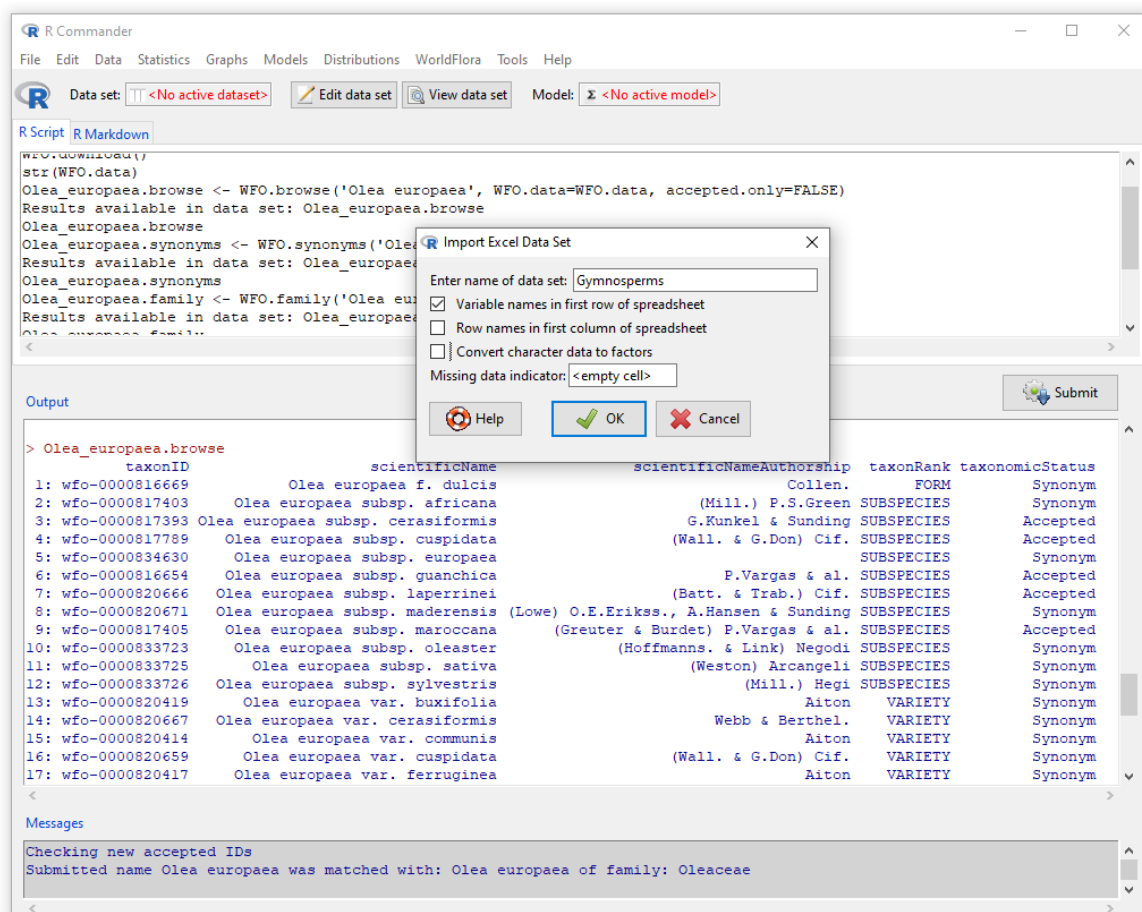
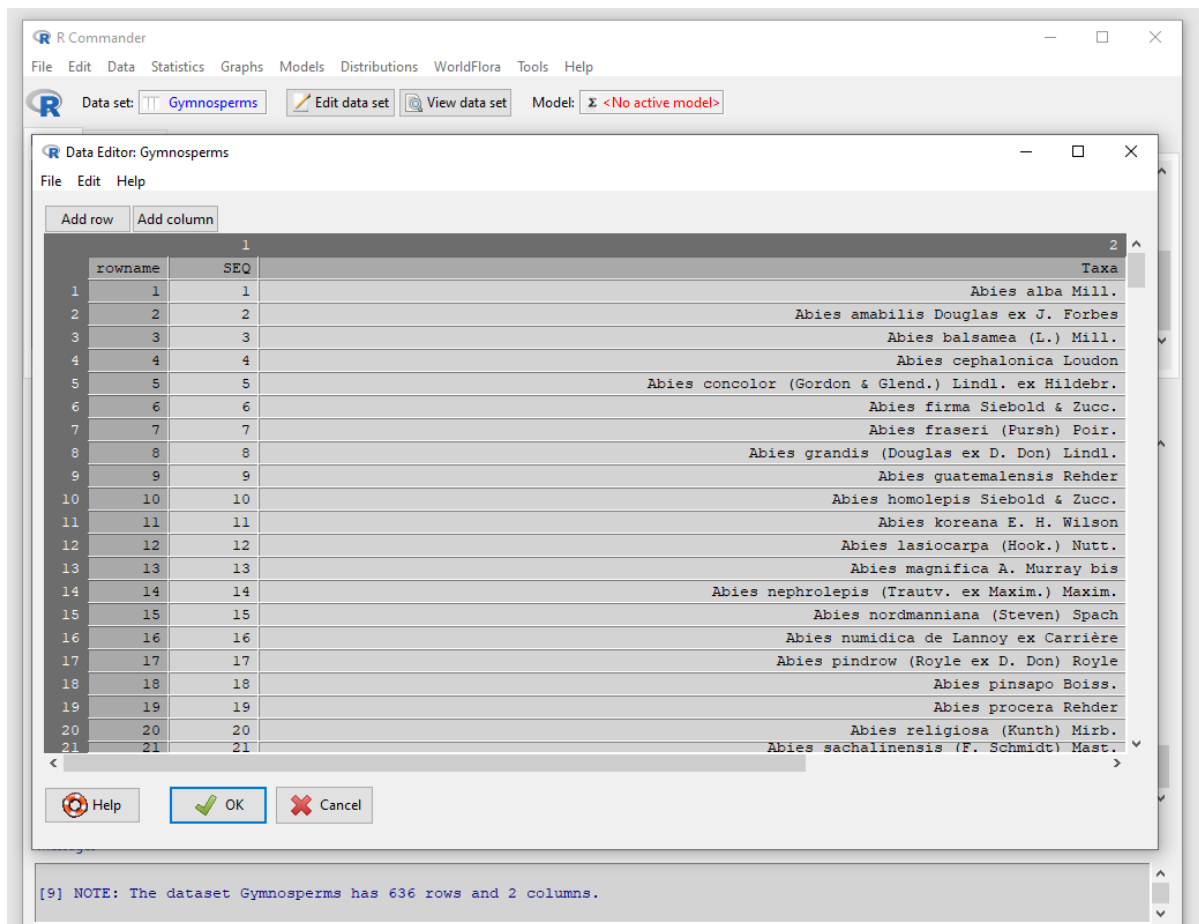


Figure 5.2. After importing the data, it becomes the active data set of the R Commander. You can then view the data from the 'Edit data set' options.



6. Prepare the data set

The main functions of the *WorldFlora* package (`WFO.match` and `WFO.one`) assume that the naming authority is not part of the plant name. In our working example, the authority is given together with the plant name. Therefore, we need to split the names into two different fields, one for the taxonomic name and another one for the naming authority.

The menu option of `WFO.prepare` attempts to make this split (Figure 6.1). Check the help function for the various options refer to, such as the ‘punctuation.flag’ that flags that submitted plant names contain punctuation characters such as ! " # \$ % & ' () * + , - . / : ; < = > ? @ [] ^ _ ` { | } and ~.

As the function may generate a large number of messages, you may prefer to only generate the script from the menu interface and then paste this script in the main R GUI (Figure 6.2).

The function will result in a new data set (‘XXX.prep’) that will have attempted the desired split (Figure 6.3). This new data set will now become the active data set, that can be exported.

Figure 6.1. Menu option of `WFO.prepare` will attempt to split names into the botanical name and the naming authority.

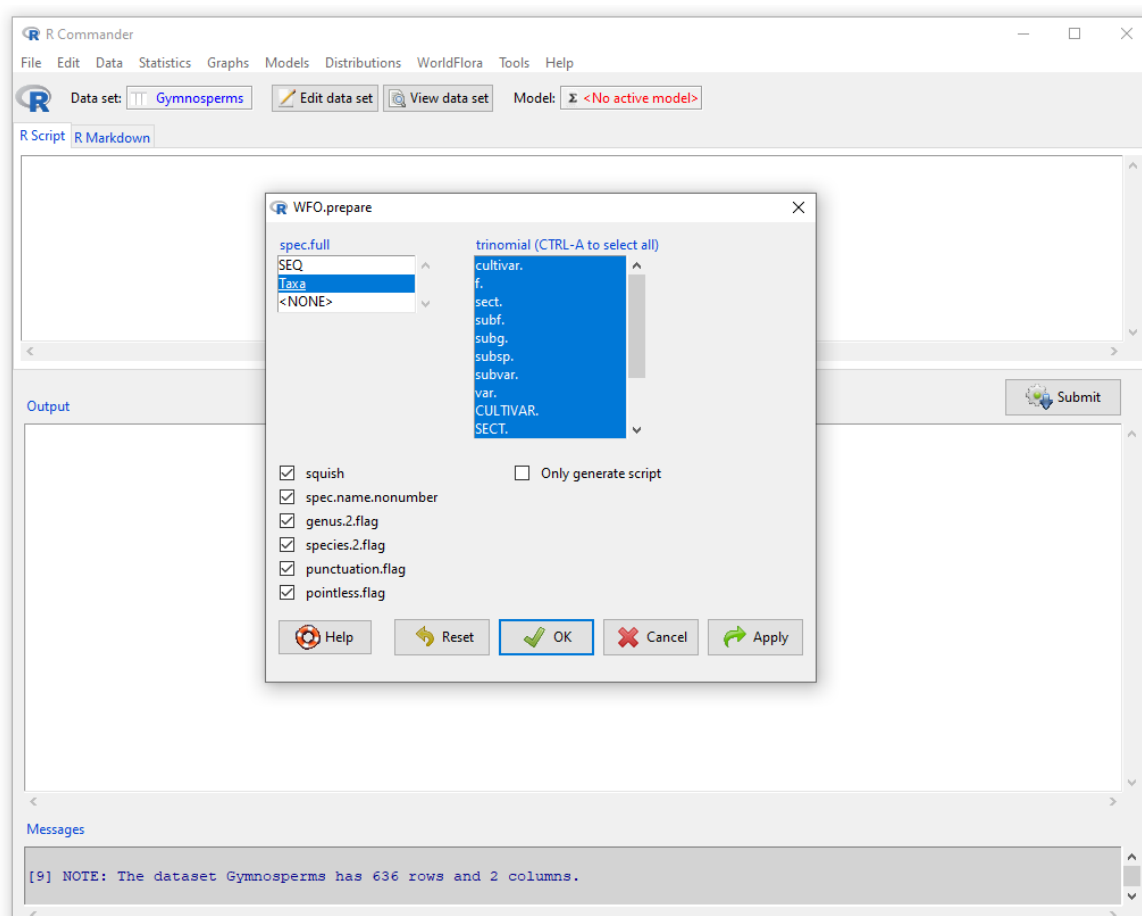


Figure 6.2. Copying the script from the R Commander to the R GUI makes it easier to see the messages.

```
R Console (64-bit)
File Edit Misc Packages Windows Help

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> library(RcmdrPlugin.WorldFlora)
Loading required package: WorldFlora
WorldFlora 1.6: Use function WFO.match to check plant names;
First you need to download and unzip the World Flora Online taxonomic backbone from
www.worldfloraonline.org/downloadData;
Use functions WFO.download and WFO.reload to download and reload the backbone data.
Registered S3 methods overwritten by 'lme4':
  method      from
  cooks.distance.influence.merMod car
  influence.merMod car
  dfbeta.influence.merMod car
  dfbetas.influence.merMod car
> Gymnosperms.prep <- WFO.prepare(Gymnosperms, spec.full='Taxa', squish=TRUE, spec.name.nonnumber=TRUE,
+ genus.2.flag=TRUE, species.2.flag=TRUE, punctuation.flag=TRUE, pointless.flag=TRUE, trinomial=c('cultivar.', 'f.',
+ 'sect.', 'subf.', 'subg.', 'subsp.', 'subvar.', 'var.', 'CULTIVAR.', 'SECT.', 'SUBF.', 'SUBG.', 'SUBSP.',
+ 'SUBVAR.', 'VAR.'), verbose=TRUE, counter=1000)
```

```
R Console (64-bit)
File Edit Misc Packages Windows Help

Punctuation mark detected for: Cycas lane-poolei
Subpattern without punctuation mark (' pl') detected for: Cycas platyphylla
Subpattern without punctuation mark (' sp') detected for: Cycas spherica
Removed sub.patterns from Cycas spp. resulting in: Cycas
Subpattern without punctuation mark (' sp') detected for: Dioon spinulosum
Removed sub.patterns from Dioon spp. resulting in: Dioon
Punctuation mark detected for: Encephalartos eugene-maraisii
Punctuation mark detected for: Encephalartos friderici-guilielmi
Removed sub.patterns from Encephalartos spp. resulting in: Encephalartos
Punctuation mark detected for: Juniperus wallichiana f. &
Punctuation mark detected for: Larix gmelinii var. principis-rupprechtii
Warning in WFO.prepare(Gymnosperms, spec.full = "Taxa", squish = TRUE, spec.name.nonnumber = TRUE, :
  No trinomial epithet provided for Larix griffithii Hook. f.
Punctuation mark detected for: Larix *marschlinsi
Subpattern without punctuation mark (' pl') detected for: Libocedrus plumosa
Punctuation mark detected for: Macrozamia pauli-guilielmi
Subpattern without punctuation mark (' pl') detected for: Macrozamia platyrachis
Subpattern without punctuation mark (' pl') detected for: Macrozamia plurinervia
Subpattern without punctuation mark (' sp') detected for: Macrozamia spiralis
Warning in WFO.prepare(Gymnosperms, spec.full = "Taxa", squish = TRUE, spec.name.nonnumber = TRUE, :
  No trinomial epithet provided for Phyllocladus aspleniifolius (Labill.) Hook. f.
Warning in WFO.prepare(Gymnosperms, spec.full = "Taxa", squish = TRUE, spec.name.nonnumber = TRUE, :
  Two trinomial epithets provided for Taxus chinensis var. mairei (Lemée & H. Lév.) W. C. Cheng & L. K. Fu (=Taxus walli$
Punctuation mark detected for: Taxus *media
Subpattern without punctuation mark (' pl') detected for: Thuja plicata
Removed sub.patterns from Unident-Cycadaceae spp. resulting in: Unident-Cycadaceae
Punctuation mark detected for: Unident-Cycadaceae
Removed sub.patterns from Unident-Zamiaceae spp. resulting in: Unident-Zamiaceae
Punctuation mark detected for: Unident-Zamiaceae
Warning in WFO.prepare(Gymnosperms, spec.full = "Taxa", squish = TRUE, spec.name.nonnumber = TRUE, :
  No trinomial epithet provided for Welwitschia mirabilis Hook. f.
Warning in WFO.prepare(Gymnosperms, spec.full = "Taxa", squish = TRUE, spec.name.nonnumber = TRUE, :
  No trinomial epithet provided for Zamia furfuracea L. f.
Subpattern without punctuation mark (' gen') detected for: Zamia gentryi
Warning in WFO.prepare(Gymnosperms, spec.full = "Taxa", squish = TRUE, spec.name.nonnumber = TRUE, :
  No trinomial epithet provided for Zamia integrifolia L. f.
Subpattern without punctuation mark (' sp') detected for: Zamia spartea
Removed sub.patterns from Zamia spp. resulting in: Zamia
> |
```

Figure 6.3. The result of function *WFO.prepare* with separate columns for the botanical name (spec.name) and the naming authority (Authorship) added to the submitted data set.

	A	B	C	D	E	F	G	H	I	J	K
1	SEQ	Taxa	spec.name	Authorship	genus.nch	genus.2	species.n	species.2	punctuati	pointless	
2	1	Abies alba Mill.	Abies alba	Mill.	5		4				
3	2	Abies amabilis Douglas ex J. Forbes	Abies amabilis	Douglas ex J. Forbes	5		8				
4	3	Abies balsamea (L.) Mill.	Abies balsamea	(L.) Mill.	5		8				
5	4	Abies cephalonica Loudon	Abies cephalonica	Loudon	5		11				
6	5	Abies concolor (Gordon & Glend.) Lindl	Abies concolor	(Gordon & Glend.) Lindl. ex Hil	5		8				
7	6	Abies firma Siebold & Zucc.	Abies firma	Siebold & Zucc.	5		5				
8	7	Abies fraseri (Pursh) Poir.	Abies fraseri	(Pursh) Poir.	5		7				
9	8	Abies grandis (Douglas ex D. Don) Lindl	Abies grandis	(Douglas ex D. Don) Lindl.	5		7				
10	9	Abies guatemalensis Rehder	Abies guatemalensis	Rehder	5		13				
11	10	Abies homolepis Siebold & Zucc.	Abies homolepis	Siebold & Zucc.	5		9				
12	11	Abies koreana E. H. Wilson	Abies koreana	E. H. Wilson	5		7				
13	12	Abies lasiocarpa (Hook.) Nutt.	Abies lasiocarpa	(Hook.) Nutt.	5		10				
14	13	Abies magnifica A. Murray bis	Abies magnifica	A. Murray bis	5		9				
15	14	Abies nephrolepis (Trautv. ex Maxim.)	Abies nephrolepis	(Trautv. ex Maxim.) Maxim.	5		11				
16	15	Abies nordmanniana (Steven) Spach	Abies nordmanniana	(Steven) Spach	5		12				
17	16	Abies numidica de Lannoy ex Carrière	Abies numidica	de Lannoy ex Carrière	5		8				
18	17	Abies pindrow (Royle ex D. Don) Royle	Abies pindrow	(Royle ex D. Don) Royle	5		7				
19	18	Abies pinsapo Boiss.	Abies pinsapo	Boiss.	5		7				
20	19	Abies procera Rehder	Abies procera	Rehder	5		7				
21	20	Abies religiosa (Kunth) Mirb.	Abies religiosa	(Kunth) Mirb.	5		9				
22	21	Abies sachalinensis (F. Schmidt) Mast.	Abies sachalinensis	(F. Schmidt) Mast.	5		13				
23	22	Abies sibirica Ledeb.	Abies sibirica	Ledeb.	5		8				
24	23	Abies spectabilis (D. Don) Mirb.	Abies spectabilis	(D. Don) Mirb.	5		11			TRUE	
25	24	Abies veitchii Lindl.	Abies veitchii	Lindl.	5		8				
26	25	Afrocarpus falcatus (Thunb.) C. N. Page	Afrocarpus falcatus	(Thunb.) C. N. Page	10		8				
27	26	Afrocarpus gracillor (Pilg.) C. N. Page	Afrocarpus gracillor	(Pilg.) C. N. Page	10		9				
28	27	Afrocarpus mannii (Hook. f.) C. N. Page	Afrocarpus mannii	(Hook. f.) C. N. Page	10		6				

In a spreadsheet, data can now be sorted by the various flagging fields.

Sorting by the column of **punctuation** selects the taxa shown in Table 6.1. Based on a manual inspection of these fields, we changed the names for some of the plants (Table 6.2). After making these changes, we pasted the columns of **spec.name** and **Authorship** into our original data set and then re-imported the data as active data set Gymnosperm2.

Table 6.1. Records flagged by the **punctuation** column

Taxa	spec.name	Authorship
Cupressus ×leylandii A. B. Jacks. & Dallim.	Cupressus ×leylandii	A. B. Jacks. & Dallim.
Cycas lane-poolei C. A. Gardner	Cycas lane-poolei	C. A. Gardner
Encephalartos eugene-maraisii I. Verd.	Encephalartos eugene-maraisii	I. Verd.
Encephalartos friderici-guilielmi Lehm.	Encephalartos friderici-guilielmi	Lehm.
Juniperus wallichiana Hook. f. & Thomson ex Brandis	Juniperus wallichiana f. &	Thomson ex Brandis
Larix gmelinii var. principis-rupprechtii (Mayr) Pilg.	Larix gmelinii var. principis-rupprechtii	(Mayr) Pilg.
Larix ×marschlinsi Coaz	Larix ×marschlinsi	Coaz
Macrozamia pauli-guilielmi W. Hill & F. Muell.	Macrozamia pauli-guilielmi	W. Hill & F. Muell.
Taxus ×media Rehder	Taxus ×media	Rehder
Unident-Cycadaceae spp.	Unident-Cycadaceae	
Unident-Zamiaceae spp.	Unident-Zamiaceae	

Table 6.2. Manual changes made in records flagged by the **punctuation** column

spec.name	Authorship
Cupressus ×leylandii	A. B. Jacks. & Dallim.
Cycas lane-poolei	C. A. Gardner
Encephalartos eugene-maraisii	I. Verd.
Encephalartos friderici-guilielmi	Lehm.
Juniperus wallichiana	Hook. f. & Thomson ex Brandis
Larix gmelinii var. principis-rupprechtii	(Mayr) Pilg.
Larix ×marschlinsi	Coaz
Macrozamia pauli-guilielmi	W. Hill & F. Muell.
Taxus ×media	Rehder
Cycadaceae	
Zamiaceae	

7. Check for matching names

The menu option of `WFO.match` brings up a menu interface for the `WFO.match` function of *WorldFlora* (Figure 7.1). Note that this menu interface uses the active data set, which may have to be selected anew after importing data.

The Authorship field is optional and `<NONE>` should be selected when this data is not available (or when a user prefers not to calculate the Levenshtein distance to the Authorship).

When using the GUI only to generate the script and then copying into the main R GUI, it is easier to read through the messages (Figure 7.2).

Note that the checks will take a while if many fuzzy matches are explored, so please be patient.

Figure 7.1. Menu interface for the `WFO.match` function.

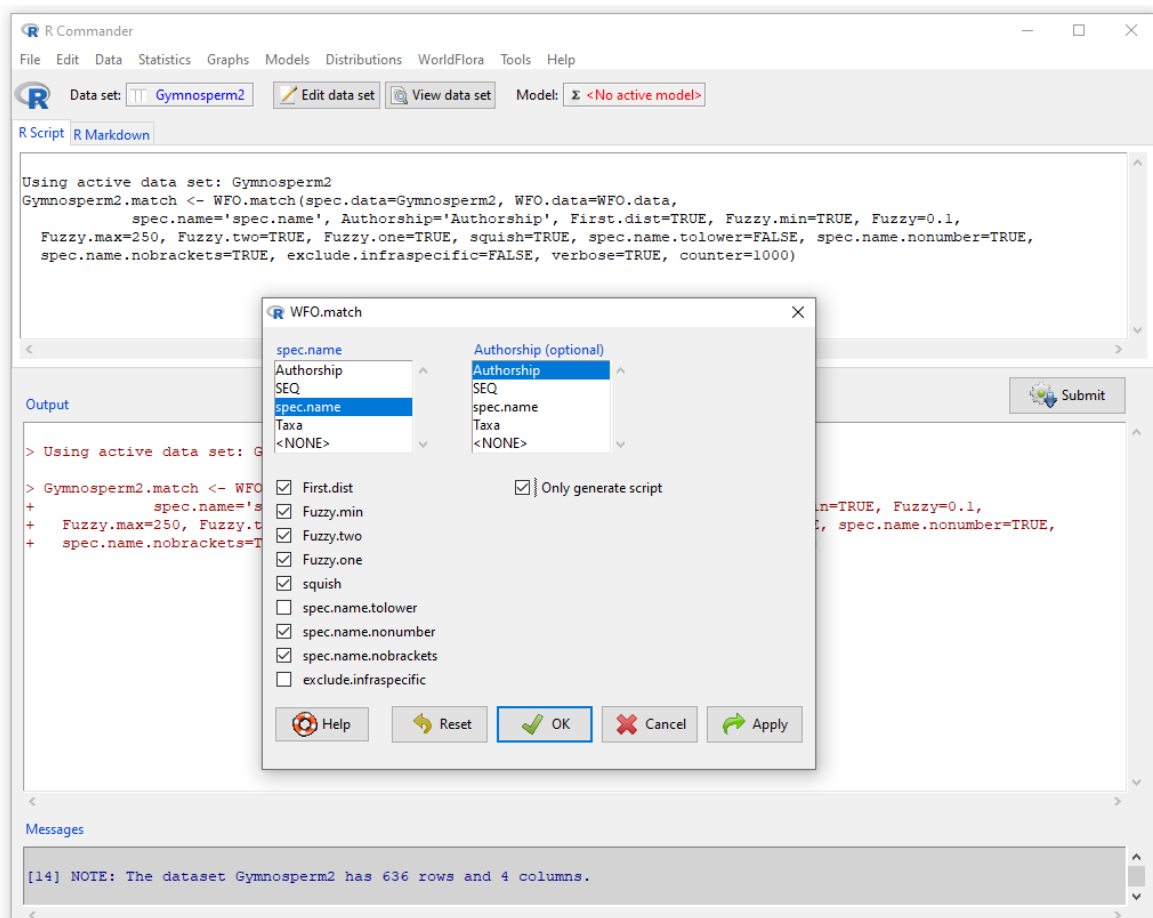
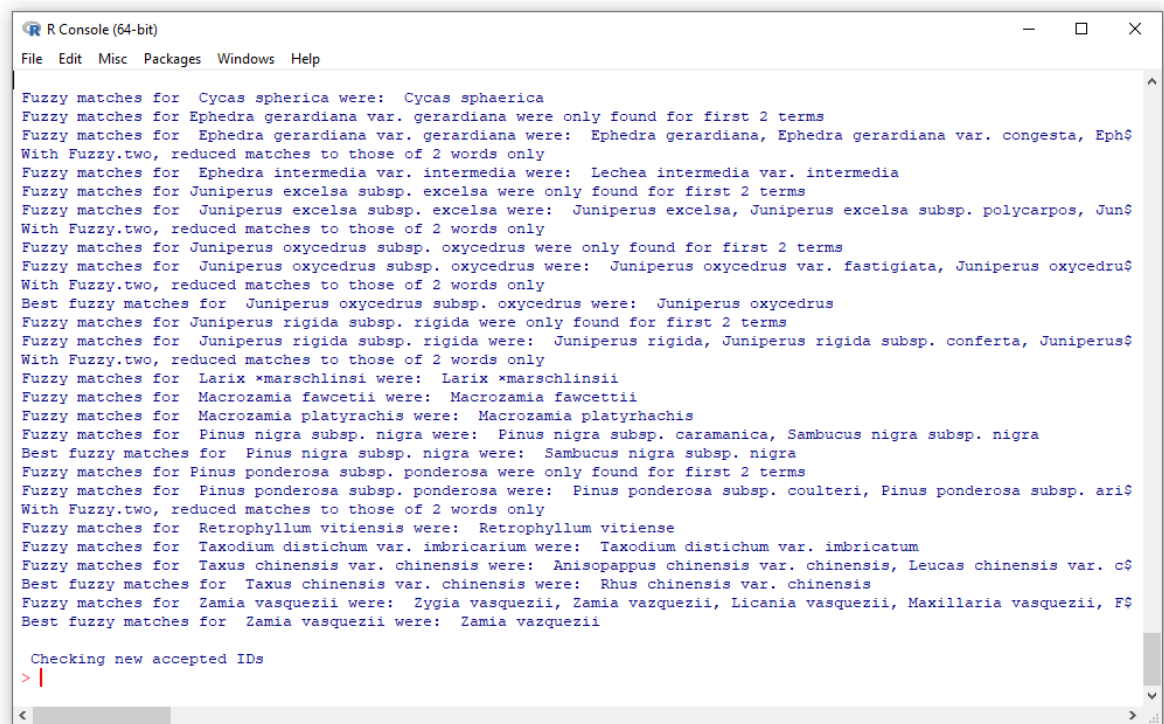


Figure 7.2. Messages when copying the script in the main R GUI.



```
R Console (64-bit)
File Edit Misc Packages Windows Help

Fuzzy matches for Cycas sphaerica were: Cycas sphaerica
Fuzzy matches for Ephedra gerardiana var. gerardiana were only found for first 2 terms
Fuzzy matches for Ephedra gerardiana var. gerardiana were: Ephedra gerardiana, Ephedra gerardiana var. congesta, Eph$
With Fuzzy.two, reduced matches to those of 2 words only
Fuzzy matches for Ephedra intermedia var. intermedia were: Lechea intermedia var. intermedia
Fuzzy matches for Juniperus excelsa subsp. excelsa were only found for first 2 terms
Fuzzy matches for Juniperus excelsa subsp. excelsa were: Juniperus excelsa, Juniperus excelsa subsp. polycarpus, Jun$
With Fuzzy.two, reduced matches to those of 2 words only
Fuzzy matches for Juniperus oxycedrus subsp. oxycedrus were only found for first 2 terms
Fuzzy matches for Juniperus oxycedrus subsp. oxycedrus were: Juniperus oxycedrus var. fastigiata, Juniperus oxycedru$
With Fuzzy.two, reduced matches to those of 2 words only
Best fuzzy matches for Juniperus oxycedrus subsp. oxycedrus were: Juniperus oxycedrus
Fuzzy matches for Juniperus rigida subsp. rigida were only found for first 2 terms
Fuzzy matches for Juniperus rigida subsp. rigida were: Juniperus rigida, Juniperus rigida subsp. conferta, Juniperus$
With Fuzzy.two, reduced matches to those of 2 words only
Fuzzy matches for Larix marschlinii were: Larix marschlinii
Fuzzy matches for Macrozamia fawcettii were: Macrozamia fawcettii
Fuzzy matches for Macrozamia platyrhachis were: Macrozamia platyrhachis
Fuzzy matches for Pinus nigra subsp. nigra were: Pinus nigra subsp. caramanica, Sambucus nigra subsp. nigra
Best fuzzy matches for Pinus nigra subsp. nigra were: Sambucus nigra subsp. nigra
Fuzzy matches for Pinus ponderosa subsp. ponderosa were only found for first 2 terms
Fuzzy matches for Pinus ponderosa subsp. ponderosa were: Pinus ponderosa subsp. coulteri, Pinus ponderosa subsp. ari$
With Fuzzy.two, reduced matches to those of 2 words only
Fuzzy matches for Retrophyllum vitiense were: Retrophyllum vitiense
Fuzzy matches for Taxodium distichum var. imbricarium were: Taxodium distichum var. imbricatum
Fuzzy matches for Taxus chinensis var. chinensis were: Anisopappus chinensis var. chinensis, Leucas chinensis var. c$
Best fuzzy matches for Taxus chinensis var. chinensis were: Rhus chinensis var. chinensis
Fuzzy matches for Zamia vasquezii were: Zygia vasquezii, Zamia vazquezii, Licania vasquezii, Maxillaria vasquezii, F$
Best fuzzy matches for Zamia vasquezii were: Zamia vazquezii

Checking new accepted IDs
> |
```


8. Check for the best single match

Function *WFO.one* reduces the number of matches to one for each submitted plant name. It operates on the results from *WFO.match*, so make sure that these results are in the active data set (Figure 8.1). Once again it is possible to use the interface to generate the script only and then copy in the R GUI (Figure 8.2).

Figure 8.1. Menu interface for the *WFO.match* function.

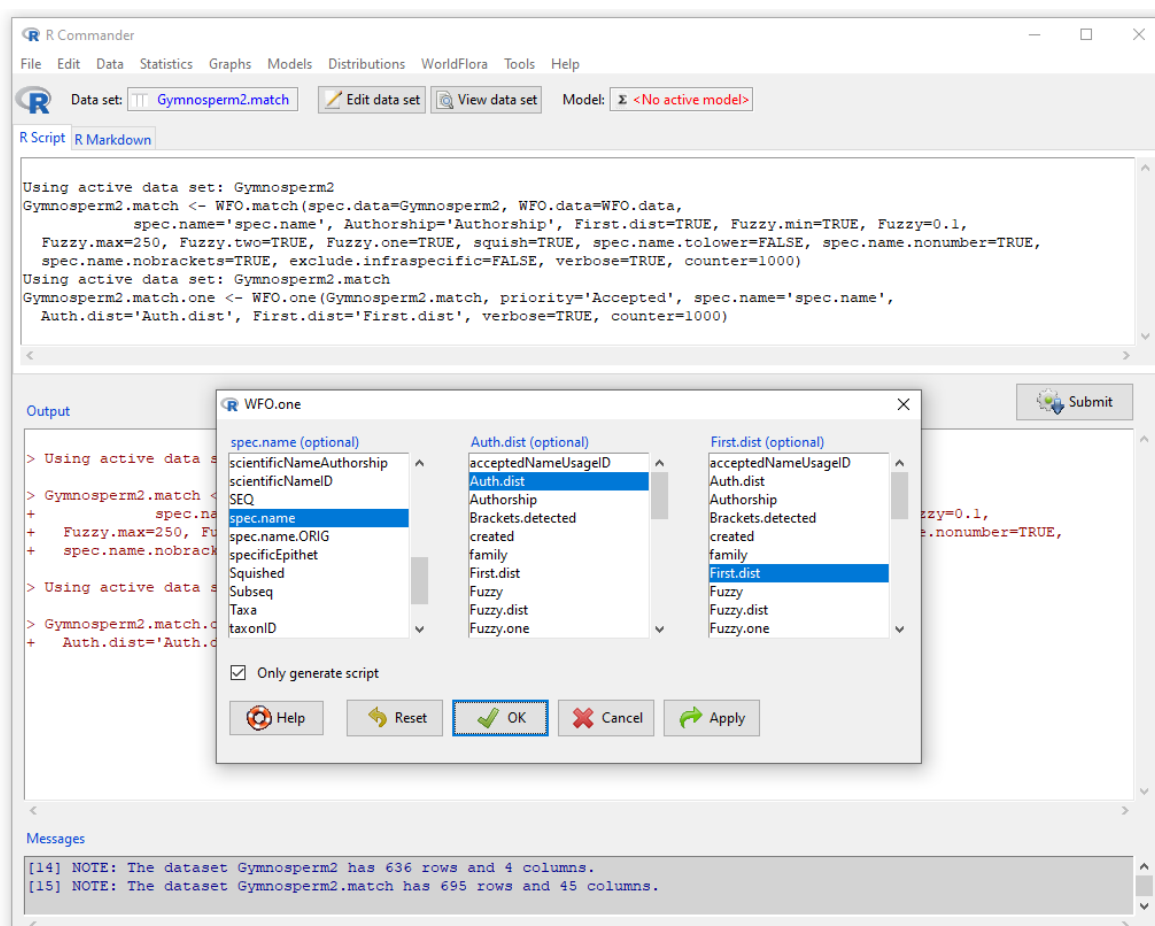


Figure 8.2. Messages when copying the script in the main R GUI.

```

R Console (64-bit)
File Edit Misc Packages Windows Help

Found unique best Authorship match case for record # 469
Different candidates for original record # 473, including Pinus montezumae
Found unique best Authorship match case for record # 473
Different candidates for original record # 477, including Pinus muricata
Found unique best Authorship match case for record # 477
Different candidates for original record # 478, including Picea mariana
Found unique non-synonym case for record # 478
Different candidates for original record # 482, including Pinus occidentalis
Found unique best Authorship match case for record # 482
Different candidates for original record # 492, including Pinus ponderosa var. scopulorum
Smallest ID candidates for 492 were: Pinus ponderosa var. scopulorum, Pinus ponderosa var. scopulorum
Selected record with smallest ID for record # 492
Different candidates for original record # 493, including Pinus montezumae
Found unique best Authorship match case for record # 493
Different candidates for original record # 498, including Pinus resinosa
Found unique best Authorship match case for record # 498
Different candidates for original record # 499, including Pinus rigida
Found unique best Authorship match case for record # 499
Different candidates for original record # 503, including Abies sibirica
Found unique best Authorship match case for record # 503
Different candidates for original record # 508, including Pinus kesiya var. langbianensis
Found unique best Authorship match case for record # 508
Different candidates for original record # 520, including Nageia wallichiana
Found unique best Authorship match case for record # 520
Different candidates for original record # 547, including Cephalotaxus harringtonii
Found unique best Authorship match case for record # 547
Different candidates for original record # 593, including Zamia fischeri
Found unique best Authorship match case for record # 593
Different candidates for original record # 622, including Zamia pygmaea
Found unique best Authorship match case for record # 622
>
> |

```

After executing the script, the results become the active data set. This data set can now be exported and cross-checked. With our Gymnosperm data set, there were no exact matches at the genus level for three taxa as shown by the variable of **First.dist** (Table 8.1). The submitted names were matched with different genera with an exact match at infrageneric levels in these cases. In a typical work flow, a user may want to check next for matches at the species level (such as matches for *Pinus nigra*) for these three cases by removing the infraspecific parts.

For our example with the Gymnosperms data set, from the full list of submitted names, one can immediately confirm that *Ephedra intermedia* and *Pinus nigra* are accepted names, as these were among submitted species names. In checking the submitted names, it also becomes obvious that the submitted taxon name of ‘*Taxus chinensis* (Pilg.) Rehder (= *Taxus wallichiana* var. *chinensis* (Pilg.) Florin)’ was split erroneously into ‘*Taxus chinensis* var. *chinensis*’ and ‘(Pilg.) Florin)’ (this is a consequence from *WFO.prepare* working on the assumption that ‘var.’ is followed by the infraspecific name and that the section before ‘var.’ consists of the genus and species names and their naming authorities). A subsequent check among the submitted names can then confirm that *Taxus wallichiana* var. *chinensis* is an accepted name.

Table 8.1. The three records with a **First.dist** larger than 0.

Submitted	First.dist	scientificName	Old.status	Old.name
<i>Pinus nigra</i> subsp. <i>nigra</i>	6	<i>Sambucus nigra</i>	Synonym	<i>Sambucus nigra</i> subsp. <i>nigra</i>
<i>Ephedra intermedia</i> var. <i>intermedia</i>	5	<i>Lechea intermedia</i>	Synonym	<i>Lechea intermedia</i> var. <i>intermedia</i>
<i>Taxus chinensis</i> var. <i>chinensis</i>	3	<i>Rhus chinensis</i>	Synonym	<i>Rhus chinensis</i> var. <i>chinensis</i>

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