

An Introduction to the taxize package

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October 14, 2012

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	TODO: Introduction to package, explanation of function names,...	

1 Phylomatic

1.1 Fetch a phylogenetic tree from Phylomatic

```
require(taxize)

## Loading required package: taxize
## Loading required package: rentrez
## Loading required package: RCurl
## Loading required package: bitops
## Loading required package: XML
## Loading required package: ritis

mytree <- "asteraceae/bidens/bidens_cernua\nasteraceae/madia/madia_exigua\nasteraceae/helian
```

1.1.1 Return a tree in the phylo object format

```
phylomatic_tree(mytree, "TRUE", "GET", "xml", "TRUE")

##
## Phylogenetic tree with 3 tips and 2 internal nodes.
##
## Tip labels:
```

```
## [1] "bidens_cernua"      "madia_exigua"      "helianthus_annuus"
## Node labels:
## [1] "euphyllophyte" ""
##
## Rooted; includes branch lengths.
```

1.1.2 Return a tree in the phylo object format, using POST method

```
phylomatic_tree(mytree, "TRUE", "POST", "xml", "TRUE")

##
## Phylogenetic tree with 3 tips and 2 internal nodes.
##
## Tip labels:
## [1] "bidens_cernua"      "madia_exigua"      "helianthus_annuus"
## Node labels:
## [1] "euphyllophyte" ""
##
## Rooted; includes branch lengths.
```

1.1.3 Return tree in newick format

```
phylomatic_tree(mytree, "TRUE", "GET", "new", "FALSE")

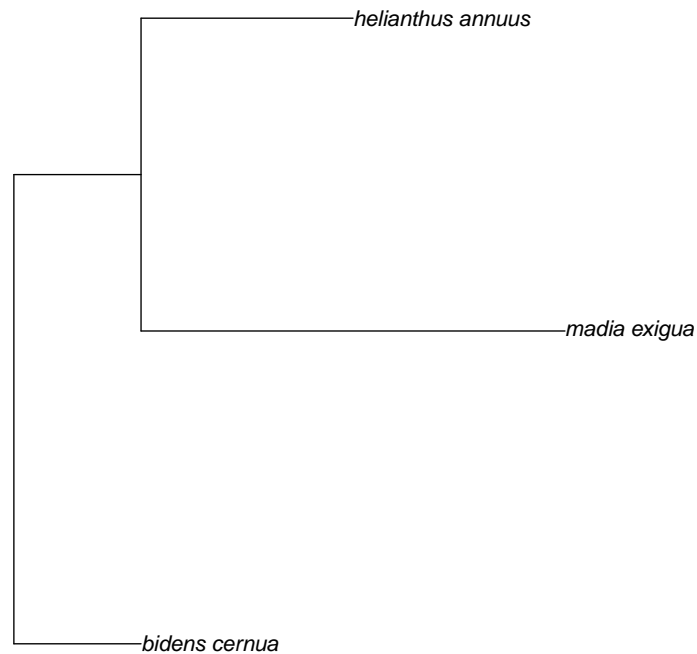
## [1] "(bidens_cernua:3.000000,(madia_exigua:10.000000,helianthus_annuus:5.000000):3.000000)"
```

1.2 Get a tree in newick format, read using ape::read.tree, and plot

```
tree <- phylomatic_tree(mytree, "TRUE", "POST", "new", "FALSE")
require(ape)

## Loading required package: ape

treephylo <- read.tree(text = tree)
plot(treephylo)
```



2 Integrated Taxonomic Information Service (ITIS)

2.1 Search by term and search type

Note: TSN stands for Taxonomic Serial Number

```
doc <- itis_get_xml("dolphin", "comname", "name")
doc <- itis_get_xml("grizzly bear", "comnameend", "name")
doc <- itis_get_xml("ursidae", "itistermssciname", "name")
```

2.2 Take advantage of default arguments, spaces accepted, and display data.frame output

```
doc <- itis_get_xml("Plethodon")
head(itis_parse(doc))

##               sci      com      tsn
## 1 Monophyllus plethodon 180073 180073
## 2           Plethodon 173648 173648
## 3       Plethodon aeneus 208328 208328
## 4 Plethodon ainsworthi 668315 668315
## 5       Plethodon albagula 208278 208278
## 6       Plethodon amplus 668316 668316
```

2.3 Show higher taxonomy for a given TSN

```
classification(685566, ID = "tsn")

## [[1]]
##      rank      taxon      tsn
## 1  Kingdom    Animalia 685566
## 2   Phylum   Chordata 202423
## 3 Subphylum Vertebrata 158852
## 4   Class     Amphibia 331030
## 5   Order     Caudata 173420
## 6   Family    Plethodontidae 173584
## 7 Subfamily  Plethodontinae 173631
## 8   Genus     Plethodon 550197
## 9   Species  Plethodon asupak 173648
```

2.4 Get a TSN from a species name

```
tsn <- get_tsn(searchterm = "Quercus_douglasii", searchtype = "sciname")

##
## Retrieving data for species ' Quercus_douglasii '

# use classification with get_tsn together:
classification(tsn)

## $`1`
##      rank      taxon      tsn
## 1  Kingdom    Plantae 19322
## 2  Subkingdom Viridaeplantae 202422
## 3  Infrakingdom Streptophyta 846492
```

```
## 4      Division      Tracheophyta 846494
## 5      Subdivision   Spermatophytina 846496
## 6      Infradivision   Angiospermae 846504
## 7      Class         Magnoliopsida 846505
## 8      Superorder     Rosanae      18063
## 9      Order          Fagales      846548
## 10     Family         Fagaceae     19273
## 11     Genus          Quercus      19275
## 12     Species       Quercus douglasii 19276
```

3 NCBI Taxonomy Browser

3.1 Get Unique Identifier

```
uids <- get_uid(c("Chironomus riparius", "Chaetopteryx"))
```

3.2 Retrieve classification for give UID

```
cl <- classification(uids)
cl

## [[1]]
##           ScientificName      Rank      UID
## 1      cellular organisms    no rank  131567
## 2           Eukaryota superkingdom   2759
## 3       Opisthokonta      no rank  33154
## 4           Metazoa      kingdom  33208
## 5       Eumetazoa      no rank   6072
## 6       Bilateria      no rank  33213
## 7       Coelomata      no rank  33316
## 8       Protostomia      no rank  33317
## 9       Ecdysozoa      no rank 1206794
## 10      Panarthropoda      no rank   88770
## 11       Arthropoda      phylum   6656
## 12      Mandibulata      no rank  197563
## 13      Pancrustacea      no rank  197562
## 14       Hexapoda      superclass   6960
## 15       Insecta      class    50557
## 16      Dicondylia      no rank   85512
## 17      Pterygota      no rank   7496
## 18      Neoptera      subclass  33340
```

```

## 19      Endopterygota   infraclass  33392
## 20      Diptera        order       7147
## 21      Nematocera     suborder  7148
## 22      Culicimorpha   infraorder 43786
## 23      Chironomoidea  superfamily 41828
## 24      Chironomidae   family     7149
## 25      Chironominae   subfamily  54970
## 26      Chironomini    tribe      72530
## 27      Chironomus     genus      7150
## 28 Chironomus incertae sedis   no rank 1165752
##
## [[2]]
##      ScientificName      Rank      UID
## 1  cellular organisms    no rank  131567
## 2      Eukaryota superkingdom    2759
## 3      Opisthokonta      no rank  33154
## 4      Metazoa          kingdom  33208
## 5      Eumetazoa        no rank   6072
## 6      Bilateria        no rank  33213
## 7      Coelomata        no rank  33316
## 8      Protostomia      no rank  33317
## 9      Ecdysozoa        no rank 1206794
## 10     Panarthropoda     no rank  88770
## 11     Arthropoda       phylum  6656
## 12     Mandibulata      no rank  197563
## 13     Pancrustacea     no rank  197562
## 14     Hexapoda         superclass  6960
## 15     Insecta          class    50557
## 16     Dicondylia       no rank  85512
## 17     Pterygota       no rank   7496
## 18     Neoptera         subclass 33340
## 19     Endopterygota    infraclass 33392
## 20     Amphiesmenoptera superorder  85604
## 21     Trichoptera      order     30263
## 22     Integripalpia    suborder  93875
## 23     Limnephiloidea   superfamily 41033
## 24     Limnephilidae    family    50645
## 25     Limnephilinae    subfamily 177669
## 26     Chaetopterygini  tribe     492564

```

4 Using ITIS and Phylomatic together

4.1 Use ITIS and `itis_get_phymat_format` to format a string for each species to be submitted to Phylomatic

```
require(plyr)

## Loading required package: plyr

dat <- lapply(list("36616", "19322", "183327"), itis_get_phymat_format, format = "rsubmit")
dat

## [1] "asteraceae%2Fhelianthus%2Fhelianthus_annuus"
## [2] "fagaceae%2Fquercus%2Fquercus_douglasii"
## [3] "pinaceae%2Fpinus%2Fpinus_contorta"

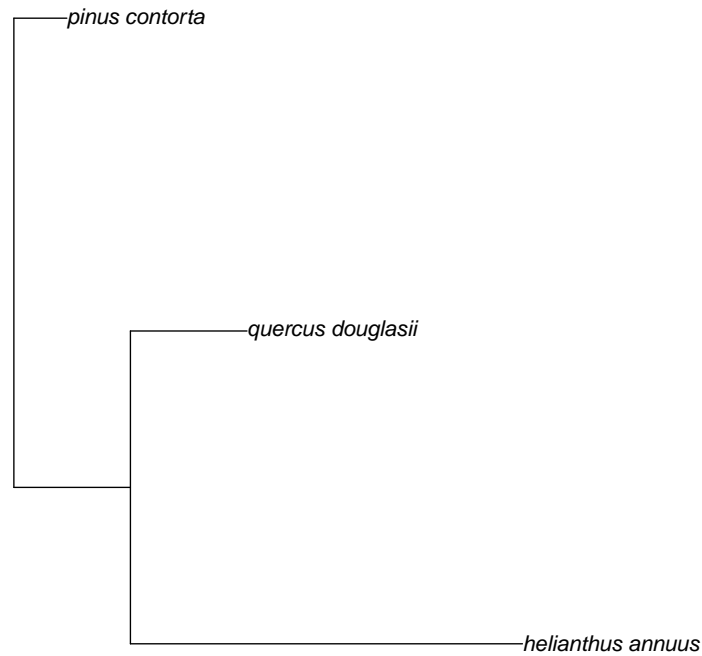
dat_mine <- paste(dat, collapse = "%OD%0A") # collapse and replace \n's
dat_mine

## [1] "asteraceae%2Fhelianthus%2Fhelianthus_annuus%OD%0Afagaceae%2Fquercus%2Fquercus_douglasii%OD%0Apinaceae%2Fpinus%2Fpinus_contorta"

tree <- phylomatic_tree(dat_mine, "FALSE", "GET", "new", "TRUE")
tree

##
## Phylogenetic tree with 3 tips and 2 internal nodes.
##
## Tip labels:
## [1] "helianthus_annuus" "quercus_douglasii" "pinus_contorta"
## Node labels:
## [1] "euphyllophyte" ""
##
## Rooted; includes branch lengths.

plot(tree)
```

4.2 A somewhat realistic workflow

4.2.1 User's species list

```
splist <- c("annona cherimola", "annona muricata", "shorea robusta", "pandanus patina",  
            "durio zibethinus")
```

4.2.2 Get TSN code for each species

```
tsns <- get_tsn(splist, "sciname")  
##  
## Retrieving data for species ' annona cherimola '
```

```
## Retrieving data for species 'annona muricata '
## Retrieving data for species 'shorea robusta '
## Retrieving data for species 'pandanus patina '
## Retrieving data for species 'durio zibethinus '

tsns

## [1] "506198" "18098" "506787" "507376" "506099"
## attr(,"class")
## [1] "tsn"
```

4.2.3 Get Phylomatic formatted strings for each species

```
dat <- laply(tsns, itis_get_phymat_format, format = "rsubmit")
dat

## [1] "annonaceae%2Fannona%2Fannona_cherimola"
## [2] "annonaceae%2Fannona%2Fannona_muricata"
## [3] "dipterocarpaceae%2Fshorea%2Fshorea_robusta"
## [4] "pandanaceae%2Fpandanus%2Fpandanus_patina"
## [5] "malvaceae%2Fdurio%2Fdurio_zibethinus"
```

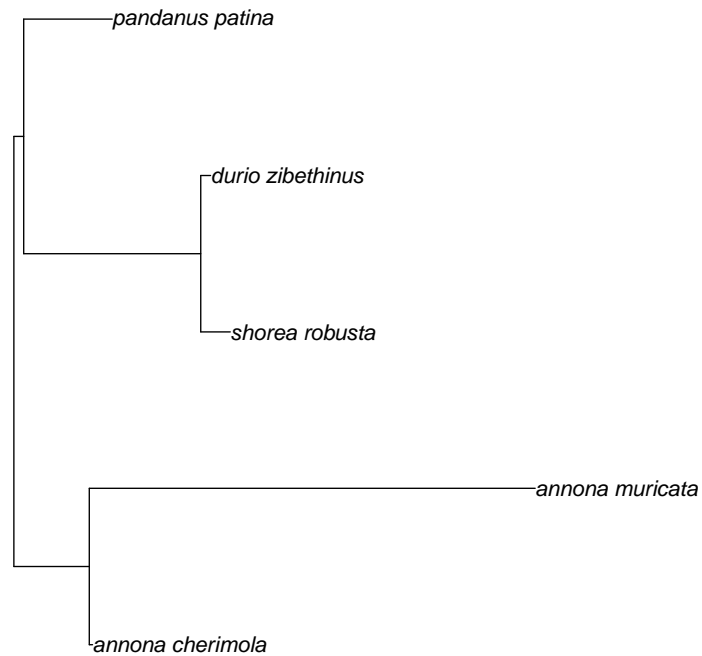
4.2.4 Send strings to Phylomatic and return newick tree

```
tree <- phylomatic_tree(dat, "TRUE", "GET", "new", "TRUE")
tree

##
## Phylogenetic tree with 5 tips and 4 internal nodes.
##
## Tip labels:
## [1] "annona_cherimola" "annona_muricata" "shorea_robusta"
## [4] "durio_zibethinus" "pandanus_patina"
## Node labels:
## [1] "euphyllophyte" "annona" "poales_to_asterales"
## [4] ""
##
## Rooted; includes branch lengths.
```

4.2.5 Plot tree, etc.

```
plot(tree)
```



5 Taxonomic Name Resolution Service

5.1 Name matching using the TNRS

```
iplant_tnrsmatch("best", taxnames = c("helianthus annuus", "acacia", "saltea"),
  output = "names") # just best names
```

Hitting the TNRS API and matching names...

##	AcceptedName	MatchFam	MatchGenus	MatchScore	Accept?
## 1	Helianthus annuus	Asteraceae	Helianthus	1	No opinion
## 2	Acacia	Fabaceae	Acacia	1	No opinion

```
## 3                               Saltera          0.93 No opinion
##      SubmittedNames
## 1 helianthus annuus
## 2          acacia
## 3          saltea
```

6 Global Names Resolver (GNR)

6.1 Get just id's and names of sources in a data.frame

```
tail(gnr_datasources(todf = TRUE))

##      id                               title
## 82 164                               BioLib.cz
## 83 165 Tropicos - Missouri Botanical Garden
## 84 166                               nlbif
## 85 167 The International Plant Names Index
## 86 168                               Index to Organism Names
## 87 169                               uBio NameBank
```

6.2 Give me the id for EOL (Encyclopedia of Life)

```
out <- gnr_datasources(todf = TRUE)
out[out$title == "EOL", "id"]

## [1] 12
```

6.3 Fuzzy search for sources with the word "zoo"

```
out <- gnr_datasources(todf = TRUE)
outdf <- out[agrep("zoo", out$title, ignore.case = TRUE), ]
outdf[1:2, ]

##      id          title
## 20 100 Mushroom Observer
## 25 105          ZooKeys
```

6.4 Resolve some names

6.4.1 Search for *Helianthus annuus* and *Homo sapiens*, return a data.frame

```
gnr_resolve(names = c("Helianthus annuus", "Homo sapiens"), returndf = TRUE)[1:2,
  ]
```

	data_source_id	submitted_name	name_string	score	title
## 1	4	Helianthus annuus	Helianthus annuus	0.988	NCBI
## 3	10	Helianthus annuus	Helianthus annuus	0.988	Freebase

6.4.2 Search for the same species, with only using data source 12 (i.e., EOL)

```
gnr_resolve(names = c("Helianthus annuus", "Homo sapiens"), data_source_ids = "12",
  returndf = TRUE)
```

	data_source_id	submitted_name	name_string	score	title
## 1	12	Helianthus annuus	Helianthus annuus	0.988	EOL
## 2	12	Homo sapiens	Homo sapiens	0.988	EOL

7 Tropicos

```
head(tp_getacceptednames(id = 25503923))
```

<http://services.tropicos.org/Name/25503923/AcceptedNames?apikey=e63f602b-f212-4c53-964c-5>

	variable	value	category
## 1	NameId	25503923	Synonym
## 2	ScientificName	Aira pumila	Synonym
## 3	ScientificNameWithAuthors	Aira pumila Pursh	Synonym
## 4	Family	Poaceae	Synonym
## 5	NameId	25509881	Accepted
## 6	ScientificName	Poa annua	Accepted

```
head(tp_getsynonyms(id = 25509881))
```

<http://services.tropicos.org/Name/25509881/Synonyms?apikey=e63f602b-f212-4c53-964c-94e70>

	variable	value	category
## 1	NameId	25503923	Synonym
## 2	ScientificName	Aira pumila	Synonym

```
## 3 ScientificNameWithAuthors Aira pumila Pursh Synonym
## 4 Family Poaceae Synonym
## 5 NameId 25509881 Accepted
## 6 ScientificName Poa annua Accepted
```

8 uBio

8.1 Search uBio using the namebank_search API method

```
ubio_namebank(searchName = "elephant", sci = 1, vern = 0)

## Error: object of type 'externalptr' is not subsettable

head(ubio_namebank(searchName = "Helianthus annuus", sci = 1, vern = 0)[, -c(2,
3)])

## Error: object of type 'externalptr' is not subsettable

out <- lapply(list("Helianthus debilis", "Astragalus aduncus"), function(x) ubio_namebank(sci = 1, vern = 0))

## Error: object of type 'externalptr' is not subsettable

head(out[[2]][, -c(2, 3)]) # just Astragalus aduncus output

## Error: incorrect number of dimensions
```

9 IUCN Red List

9.1 Query the Red List API

```
ia <- iucn_summary(c("Panthera uncia", "Lynx lynx"))
```

9.2 Extract status

```
lapply(ia, function(x) x$status)

## [1] "EN" "LC"
```

9.3 Extract Distribution

```
ia[["Panthera uncia"]]$distr  
## [1] "Afghanistan"      "Bhutan"           "China"  
## [4] "India"             "Kazakhstan"       "Kyrgyzstan"  
## [7] "Mongolia"          "Nepal"            "Pakistan"  
## [10] "Russian Federation" "Tajikistan"       "Uzbekistan"
```