

UniProt.ws: A package for retrieving data from the UniProt web service

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1 Configuring `uniport.ws`

The *UniProt.ws* package provides a `select` interface to the UniProt web service.

```
suppressPackageStartupMessages({  
  library(UniProt.ws)  
})  
up <- UniProt.ws(taxId=9606)
```

If you already know about the `select` interface, you can immediately learn about the various methods for this object by just looking at its help page.

```
help("UniProt.ws")
```

When you load the *UniProt.ws* package, it creates a `UniProt.ws` object. If you look at the object you will see some helpful information about it.

```
up  
  
## UniProt.ws interface object:  
## Taxonomy ID: 9606  
## Species name: Homo sapiens (Human)  
## List species with 'availableUniprotSpecies()'
```

By default, you can see that the `UniProt.ws` object is set to retrieve records from *Homo sapiens*. But you can change that of course. In order to change it, you first need to look up the appropriate taxonomy ID for the species that you are interested in. Uniprot provides support for over 20 thousand species, so there are a few to choose from! In order to make this easier, we have provided the helper function `availableUniprotSpecies` which will list all the supported species along with their taxonomy ids. When you call the `availableUniprotSpecies` function, it's recommended that you make use of the `pattern` argument to limit your queries like this:

```
availableUniprotSpecies(pattern="musculus")  
  
##      kingdom Taxon Node  Official (scientific) name  
## ANTMS      E      520121    Anthocoris musculus  
## ANTMU      E      208057    Anthoscopus musculus  
## APOMU      E      238007      Apomys musculus  
## BAIMU      E      213557    Baiomys musculus  
## BALMU      E        9771    Balaenoptera musculus  
## BLEMU      E      197864    Blepharisma musculus
```

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```
## MOUSE      E      10090      Mus musculus
## MUSMB      E      35531      Mus musculus bactrianus
## MUSMC      E      10091      Mus musculus castaneus
## MUSMM      E      57486      Mus musculus molossinus
## POVM1      V      1891730 Mus musculus polyomavirus 1
```

Once you have learned the taxonomy ID for the species of interest, you can then change the taxonomy id for the `UniProt.ws` object using `taxId` setter or by calling the constructor for `UniProt.ws`

```
mouseUp <- UniProt.ws(10090)
mouseUp

## UniProt.ws interface object:
## Taxonomy ID: 10090
## Species name: Mus musculus (Mouse)
## List species with 'availableUniprotSpecies()'
```

As you can see the species is different for the `mouseUp` new object.

2 Using UniProt.ws

Once you are satisfied that you have an `uniprot.ws` that is using the appropriate organisms, you can make use of the standard set of methods in a `select` interface. Specifically: `columns`, `keytypes`, `keys` and `select`.

You will probably notice that there are a large number of columns that can be retrieved.

```
head(keytypes(up))

## [1] "Allergome"      "ArachnoServer" "Araport"      "BioCyc"
## [5] "BioGRID"       "BioMuta"
```

And most (but not all) of these fields can also be used as keytypes.

```
head(columns(up))

## [1] "absorption"      "accession"
## [3] "annotation_score" "cc_activity_regulation"
## [5] "cc_allergen"     "cc_alternative_products"
```

If necessary you can also look up the keys of a given type. But please be warned that the web service is slow at this particular kind of lookup. So if you really want to do this kind of operation you are probably going to want to save the result to your R session.

```
egs <- keys(up, "GeneID")
```

Finally, you can loop up whatever combinations of columns, keytypes and keys that you need when using `select`.

Note. 'ENTREZ_GENE' is now 'GeneID'

```
keys <- c("1", "2")
columns <- c("xref_pdb", "xref_hgnc", "sequence")
```

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```
kt <- "GeneID"
res <- select(up, keys, columns, kt)
res

## From Entry PDB
## 1 1 P04217 <NA>
## 2 1 V9HWD8 <NA>
## 3 2 P01023 1BV8;2P9R;6TAV;707L;707M;707N;707O;707P;707Q;707R;707S;
## HGNC
## 1 HGNC:5;
## 2 <NA>
## 3 HGNC:7;
##
## 1
## 2
## 3 MGKNKLLHPSLVLLLLVLLPTDASVSGKPQYMLVPSLLHTETTEKGCVLLSYLNETVTVSASLESVRGNRSLFTDLEAENDVLHCVAFVAVPKSSSNEEVMFL
```

sessionInfo()

```
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## R version 4.2.2 (2022-10-31 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows Server x64 (build 20348)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=C
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## attached base packages:
## [1] stats graphics grDevices utils datasets methods base
##
## other attached packages:
## [1] UniProt.ws_2.38.1 BiocGenerics_0.44.0 RSQLite_2.2.19
##
## loaded via a namespace (and not attached):
## [1] KEGGREST_1.38.0 progress_1.2.2 tidyselect_1.2.0
## [4] xfun_0.35 purrr_0.3.5 vctrs_0.5.1
## [7] rjsoncons_1.0.0 generics_0.1.3 htmltools_0.5.4
## [10] stats4_4.2.2 BiocFileCache_2.6.0 yaml_2.3.6
## [13] utf8_1.2.2 blob_1.2.3 rlang_1.0.6
## [16] pillar_1.8.1 withr_2.5.0 glue_1.6.2
## [19] DBI_1.1.3 rappdirs_0.3.3 bit64_4.0.5
## [22] dbplyr_2.2.1 GenomeInfoDbData_1.2.9 lifecycle_1.0.3
## [25] stringr_1.5.0 zlibbioc_1.44.0 Biostrings_2.66.0
```

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```
## [28] memoise_2.0.1      evaluate_0.19      Biobase_2.58.0
## [31] knitr_1.41         IRanges_2.32.0    fastmap_1.1.0
## [34] GenomeInfoDb_1.34.4 curl_4.3.3        AnnotationDbi_1.60.0
## [37] fansi_1.0.3        highr_0.9         Rcpp_1.0.9
## [40] filelock_1.0.2     BiocManager_1.30.19 cachem_1.0.6
## [43] S4Vectors_0.36.1  jsonlite_1.8.4    XVector_0.38.0
## [46] bit_4.0.5          BiocStyle_2.26.0  hms_1.1.2
## [49] png_0.1-8          digest_0.6.31     stringi_1.7.8
## [52] dplyr_1.0.10       cli_3.4.1         tools_4.2.2
## [55] bitops_1.0-7       magrittr_2.0.3    tibble_3.1.8
## [58] RCurl_1.98-1.9     httpcache_1.2.0   BiocBaseUtils_1.0.0
## [61] crayon_1.5.2       pkgconfig_2.0.3   ellipsis_0.3.2
## [64] prettyunits_1.1.1  assertthat_0.2.1  rmarkdown_2.19
## [67] httr_1.4.4         R6_2.5.1          compiler_4.2.2
```