Package 'filterNHP'

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Type Package

Title Non-Human Primate Search Filters

Version 0.1.2

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Description Generate search filters to query scientific bibliographic sources, such as PubMed and Web of Science, for non-human primate related publications.

License AGPL (>= 3)

Encoding UTF-8

Depends R (>= 3.5.0)

RoxygenNote 7.1.2

Suggests testthat, knitr, rmarkdown

Imports data.tree (>= 1.0.0), shiny, shinyWidgets, shinyjs, shinyBS, rclipboard

Config/testthat/edition 3

NeedsCompilation no

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R topics documented:

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filter_nhp   *Format non-human primate search terms for use in databases*

Description

Function will return search terms for all taxa below the specified taxonomic level. Search terms for humans are always omitted, even if they are part of that taxonomic group.

Usage

```
filter_nhp(
  source = "PubMed",
  taxa = "nonhuman_primates",
  omit = NULL,
  simplify = TRUE
)
```

Arguments

source	A string indicating which bibliographic source search terms should be formatted for. Current options are "PubMed" (default), "PsycInfo" or "WebOfScience".
taxa	A character vector of primate taxa. If taxa = "nonhuman_primates" (default), function will return search terms for all non-human primates. Use get_nhp_taxa to print a list of valid taxa.
omit	An optional character vector of primate taxonomic groups that occur within taxa to omit from the search terms. This is useful for example when you need search terms for all species of one family except one genus.
simplify	Logical. Should printed output be simplified?

Details

If simplify = TRUE (default), then function will print search terms to the console that can be directly copy-pasted into the relevant bibliographic source as is. However, the object returned is NULL. If simplify = FALSE, then function returns a character vector of length == 1. This may be useful if the user wants to assign the output to an r object for further manipulation.

Value

NULL or a string of search terms that are associated with the specified taxa, formatted for use in the specified bibliographic source.

Examples

```
filter_nhp(source = "PsycInfo", taxa = "papio")
filter_nhp(source = "PsycInfo", taxa = "hominidae")
filter_nhp(source = "PubMed", taxa = "cercopithecidae", omit = c("papio", "macaca"))
filter_nhp(source = "PubMed", taxa = "platyrrhini", omit = "aotus")
```

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get_nhp_taxa   *Get taxonomic terms for non-human primates*

Description

Get taxonomic terms for non-human primates

Usage

```
get_nhp_taxa(level = "all")
```

Arguments

level   Specify which level to get taxonomic terms for. Defaults to "all". Other options are "suborder", "infraorder", "parvorder", "superfamily", "family", "subfamily", "tribe" or "genus".

Value

A named list with taxonomic terms for each level.

Examples

```
get_nhp_taxa("genus")
```

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run_filter_nhp_app   *Run filter_nhp() shiny app*

Description

Runs a user-friendly shiny app that calls on 'filter_nhp()'.

Usage

```
run_filter_nhp_app()
```

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