Package 'nzffdr'

November 8, 2022

Title Import, Clean and Update Data from the New Zealand Freshwater
Fish Database

Version 2.1.0

Description Access the New Zealand Freshwater Fish Database from R and a few func-
tions to clean the data once in R.

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Depends R (>= 4.0.0)

Imports curl, httr, rlang, stringi, tidyr, utils, xml2

Suggests devtools, knitr, rmarkdown, roxygen2,

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URL

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R topics documented:

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nzffdr_add_dates *Add dates to a NZFFD dataset*

Description

Add year, month and day columns to a NZFFD dataset.

Usage

```
nzffdr_add_dates(fishd)
```

Arguments

fishd a dataframe imported from the NZFFD using nzffdr_import(), which contains the column "eventDate"

Details

Adds year, month and day columns to a NZFFD dataset, based on values in the "eventDate" column.

Value

a NZFFD dataframe, with year, month and day columns added.

Examples

```
nzffdr_add_dates(nzffdr::nzffdr_data)
```

---

nzffdr_clean *Clean NZ Freshwater Fish Datasets*

Description

Clean up data imported from the NZ Freshwater Fish Database.

Usage

```
nzffdr_clean(fishd)
```

Arguments

fishd a dataframe imported from the NZFFD using nzffdr_import()

Details

Cleans up a few inconsistencies in the NZFFD data returned from `nzffd_import()`. Column types are checked and converted to, integer, numeric or character. Empty cells are filled with NA, variable 'catchmentName' entries are standardised (e.g. Clutha r, Clutha River and Clutha R all become Clutha R) and, any empty columns are removed.

Value

A cleaned NZFFD dataframe.

Examples

```
nzffdr_clean(nzffdr::nzffdr_data)
```

---

nzffdr_data   *Sample NZFFD data.*

Description

Sample NZFFD data.

Usage

```
data(nzffdr_data)
```

Format

A dataframe of 200 rows and 67 variables.

Source

[NIWA](#)

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nzffdr_get_table   *Get NZFFD search terms*

Description

Lists of possible argument options for function nzffdr_import().

Usage

```
nzffdr_get_table(x = c("fish_method", "institution", "taxon"))
```

Arguments

x   one of "fish_method", "institution" or "taxon", depending on which argument
                        values are wanted.

Details

Returns the possible argument values for arguments: fish_method, institution and taxon, used in the
function nzffdr_import().

This function requires an internet connection to query NIWA's database.

Value

A dataframe or character string of argument options.

Examples

```
## Not run:

dat <- nzffdr_get_table("taxon")


## End(Not run)
```

---

  nzffdr_import   *Import NZ Freshwater Fish datasets.*

Description

Import data from the NZ Freshwater Fish Database. Enter search terms as arguments as you would
in the NZFFD and import directly into R. You can search using all the same query options which
are used for in the [NZFFFD](#), see their [info page](#) for details. To import the entire database leave all
arguments as default.

Usage

```
nzffdr_import(
  institution = "",
  catchment_num = "",
  catchment_name = "",
  water_body = "",
  fish_method = "",
  taxon = "",
  starts = "",
  ends = "",
  download_format = "all"
)
```

Arguments

`institution`	institution that collected the data. Use the `nzffdr_get_table("institution")` function to see a list of all possible options, or don't set the arg if you want all institutions in the database.
`catchment_num`	catchment number. A 6 digit number unique to the reach of interest. You can search using the individual number (e.g. `catchment = "702.500"`), or for all rivers in a catchment you can use the wildcard search term (e.g. `catchment = "702%"`), or don't set the arg if you want all catchments in the database.
`catchment_name`	catchment name. e.g. `catchment_name = "Hinds R"`. Case sensitive. Don't set the arg if you want all catchments in the database.
`water_body`	water body name. e.g. to get all records for Limestone Creek, `water_body = "Limestone Creek"`. Don't set the arg if you want all water bodies in the database.
`fish_method`	fishing method used. Use the `nzffdr_get_table("fish_method")` function to see a list of all possible options. If you only want fish caught be lures use `fish_meth = "Angling - Lure"`, don't set the arg if you want all fishing methods in the database.
`taxon`	taxon of interest. Use the `nzffdr_get_table("taxon")` function to see a list of all possible options. You can search using either common or scientific names and can search for multiple taxon at once, e.g. to search for Black mudfish use `taxon = "Black mudfish"` or `taxon = "Neochanna diversus"` and to search for Black mudfish and Bluegill bully use `taxon = c("Black mudfish", "Bluegill bully")` etc.
`starts`	start year. Don't set the arg if you want all records in the database.
`ends`	end year. Don't set the arg if you want all records in the database.
`download_format`	
	use "all" or "essential" to download either, all variables (67 columns), which now includes some River Environment Classification data, or just essential data (23 columns).

Details

This function requires an internet connection to query NIWA's database.

Data citation: Stoffels R (2022). New Zealand Freshwater Fish Database (extended). The National Institute of Water and Atmospheric Research (NIWA). Sampling event dataset https://doi.org/10.15468/jbpw92

Value

A dataframe where each row is a NZFFD record.

Examples

```
## Not run:
# import entire NZFFD
dat <- nzffdr_import()

## End(Not run)
```

---

nzffdr_ind_lengths   *Fish length to tidy long format*

Description

Converts individual fish length measures from multiple entries in a single cell to tidy long format.

Usage

```
nzffdr_ind_lengths(fishd)
```

Arguments

fishd   an NZFFD dataframe returned from nzffdr_import(). Must contain the columns
                   "nzffdRecordNumber", "taxonName" and "indLengths".

Value

A dataframe with three columns,"nzffdRecordNumber", "taxonName" and "indLengths".

Examples

```
nzffdr_ind_lengths(nzffdr::nzffdr_data)
```

---

nzffdr_nzmap   *Simple features map of New Zealand*

Description

A simple features map of New Zealand. A simplified version of the 1:150k NZ map outline available
from Land Information New Zealand. CRS: NZ Transverse Mercator (NZTM: EPSG 2193).

Usage

```
nzffdr_nzmap
```

Format

A simple features dataframe with 4 rows and 2 columns:

island Island name

geometry Line geometry

Source

<https://data.linz.govt.nz>

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nzffdr_razzle_dazzle   *Wrapper for multiple nzffdr functions*

Description

Wraps multiple nzffdr functions allowing, importing, cleaning and adding of new information all in one step.

Usage

```
nzffdr_razzle_dazzle()
```

Details

Wraps: [nzffdr_import()], [nzffdr_clean()], [nzffdr_add_date()], [nzffdr_taxon_threat()], [nzffdr_widen_habitat()] and runs the lot in one go, returning a downloaded and cleaned NZFFD dataset.

This function requires an internet connection to query the NZFFD

Value

An NZFFD dataframe which has been cleaned and had date, taxonomic and threat classification status data added.

Examples

```
## Not run:
dat <- nzffdr_razzle_dazzle()

## End(Not run)
```

---

nzffdr_taxon_threat   *Add taxonomic and threat status data*

Description

Adds additional common and scientific names, and threat classification status information.

Usage

```
nzffdr_taxon_threat(fishd)
```

Arguments

fishd   A dataframe imported from the NZFFD using nzffd_import

Details

Adds additional taxonomic data ("commonMaoriName", "alternativeNames", "species", "genus", "family", "order", "class", "phylum") and NZ Threat Classification Status information ("category", "status", "taxonomicStatus", "bioStatus"). See NZTCS for details regarding the NZTCS variables.

Value

An NZFFD dataframe, with 12 additional columns.

Examples

```
nzffdr_taxon_threat(nzffdr::nzffdr_data)
```

---

nzffdr_widen_habitat   *Converts habitat variables to tidy wide format*

Description

Converts habitat variables to tidy wide format columns and appends to original dataframe. Warning, with large (>100k rows) datasets this function slow (~30 seconds).

Usage

```
nzffdr_widen_habitat(
  fishd,
  cols_to_expand = c("habitatFlowPercent", "habitatInstreamCoverPresent",
    "habitatRiparianVegPercent", "habitatSubstratePercent")
)
```

Arguments

fishd	an NZFFD dataframe returned from nzffdr_import.
cols_to_expand	the habitat columns to expand, can be any combination of "habitatFlowPercent", "habitatInstreamCoverPresent", "habitatRiparianVegPercent", "habitatSubstratePercent".

Value

An NZFFD dataframe with added wide format columns for each of the selected habitat columns.

Examples

```
nzffdr_widen_habitat(nzffdr::nzffdr_data)
```

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