

Package ‘nzffdr’

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

Version 1.0.0

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

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Depends R (>= 3.5.0)

Imports chron, curl, httr, jsonlite, stringr, utils, xml2

Suggests devtools, knitr, rmarkdown, roxygen2, testthat (>= 2.1.0)

Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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`nzffd_add`*Add River Environment Classification (REC) data to the NZFFD*

Description

Use the `nzreach` variable in the NZFFD to match NZFFD sample locations against the NZREACH code in the **River Environment Classification** (REC) database and attach corresponding REC data to the NZFFD dataframe.

Usage

```
nzffd_add(fishd)
```

Arguments

`fishd` A dataframe imported from the NZFFD using `nzffd_import`.

Details

Note that any row that has an `nzreach` value of 0, 9 or NA will not return any REC data. Also, this is the 2010 depreciated REC data (much of it is still relevant) not the latest (**REC2**) version. As it stands the NZFFD uses the `nzreach` variable to identify stream reaches, this variable has been superseded in REC2 with `Nzsegment` which makes cross referencing between NZFFD and REC2 difficult. In the future access to REC2 will be added.

This function requires an internet connection to query the REC database.

Value

A dataframe with the same number of rows as `fishd` but with 24 additional columns from the REC database added.

Examples

```
## Not run:  
  
df <- nzffd_add(nzffdr::nzffd_data)  
  
## End(Not run)
```

nzffd_clean	<i>Clean NZ freshwater Fish fishdatasets</i>
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Description

Clean up data imported from the NZ Freshwater Fish Database.

Usage

```
nzffd_clean(fishd)
```

Arguments

`fishd` A dataframe imported from the NZFFD using `nzffd_import`

Details

The first letter of all words in `catchname` and `locality` are capitalised and any non-alphanumeric characters are removed. `time` is converted to a standardised 24 hour format and nonsensical values converted to NA. `org` is converted to all lowercase and has non-alphanumeric characters removed. `map` is converted to lower case and has any non-three digit codes converted to NA. `catchname` codes are tidied following the suggested abbreviations (add URL), e.g. Cluth River, Clutha r and Clutha river all become Clutha R. Finally a new variable `form` is added which defines the sampled habitat type for each observation.

Value

A dataframe of the same dimensions as `fishd`, but cleaned.

Examples

```
## Not run:  
  
dat <- nzffd_clean(nzffdr::nzffd_data)  
  
## End(Not run)
```

`nzffd_data`*Sample dataframe of 200 rows of the NZFFD.*

Description

Sample dataframe of 200 rows of the NZFFD.

Usage

```
data(nzffd_data)
```

Format

A dataframe of 141708 rows and 22 variables:

card NZFFD card id

m month sampling occurred

y year sampling occurred

catchname catchment name

catch catchment number

locality sampling locality

time time sampling occurred

org 3 letter code identifying the organisation that carried out the sampling see vignette for code descriptions

map NZMS260 map tile code

east easting, in NZMG

north northing, in NZMG

altitude sample site altitude, in meters above sea level

penet distance to sea along the network, in meters

Source

NIWA

`nzffd_fill`*Add additional data to the NZFFD*

Description

Adds columns for family, genus, species and common names, the species threat classification status, whether the species is native or exotic. Also add missing values for the map and alt variables.

Usage

```
nzffd_fill(fishd, alt = TRUE, maps = TRUE)
```

Arguments

<code>fishd</code>	A dataframe imported from the NZFFD using <code>nzffd_import</code> .
<code>alt</code>	Should missing elevation data be added to the dataframe.
<code>maps</code>	Should missing map tiles be added to the dataframe.

Details

Altitude data is added by taking the site coordinates and pulling the relevant data from an 8m **DEM**. Note data taken from the DEM is suitable for cartographic visualisation only.

If `alt = TRUE` this function requires an internet connection to query the 8m DEM.

Value

A dataframe with the same number of rows as `fishd` but with seven additional columns added (`common_name`, `sci_name`, `family`, `genus`, `species`, `threat_class`, `native`).

Examples

```
## Not run:  
  
df <- nzffd_fill(nzffdr::nzffd_data)  
head(df)  
  
## End(Not run)
```

 nzffd_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 the **NZFFFD**, see their [help page](#) for details. To import the entire database leave all arguments blank.

Usage

```
nzffd_import(
  catchment = "",
  river = "",
  location = "",
  fish_method = "",
  species = "",
  starts = 1850,
  ends = 2100
)
```

Arguments

catchment	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 NZ.
river	river name. e.g. to get all records for the Clutha, river = "Clutha".
location	sampling locality. e.g. location = "Awakino". This only works when the location is included in the name of the waterway.
fish_method	fishing method used. There are 59 different possible options for fish_method, if you want to search for a specific fishing method look at the dataset ?nzffd_method to see a list of all possible options, you can then copy/paste from there (e.g. if we only wanted fish caught by lures use fish_meth = "Angling-Lure") don't set the arg if you want all fishing methods.
species	species of interest. There are 75 different possible options for species, use ?nzffd_species function to see a list of all possible options. You can search using either common or scientific names and can search for multiple species at once. e.g. to search for Black mudfish use species = "Black mudfish" or species = "Neochanna diversus" and to search for Black mudfish and Bluegill bully use species = c("Black mudfish", "Bluegill bully") etc.
starts	start year, 1850 at the earliest.
ends	end year.

Details

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

Data citation: Crow S (2017). New Zealand Freshwater Fish Database. Version 1.2. The National Institute of Water and Atmospheric Research (NIWA). Occurrence Dataset <https://doi.org/10.15468/ms5iqu>

Value

A dataframe consisting of 22 columns where each row is a record for an individual species. The number of rows will depend on search terms.

Examples

```
## Not run:  
  
df <- nzffd_import(nzffdr::nzffd_data)  
  
## End(Not run)
```

`nzffd_method`

Dataframe listing all fishing methods used in the NZFFD

Description

Dataframe listing the possible inputs for the `fish_method` argument of the `nzffd_import` function.

Usage

```
nzffd_method
```

Format

A dataframe of 59 rows and one variable:

method fishing method used

`nzffd_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: New Zealand Map Grid, EPSG:27200 (matching NZFFD observations). The map contains polygons for the three main island plus the Chatham Islands.

Usage`nzffd_nzmap`**Format**

A simple features dataframe with 4 rows and 3 columns:

name Island name

name_ascii Island name ascii characters

geometry Line geometry

Source

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

`nzffd_species`*Dataframe listing all species in the NZFFD*

Description

A dataframe listing the possible inputs for the species argument of the `nzffd_import` function. Either the scientific or common name can be used.

Usage`nzffd_species`**Format**

A dataframe of 75 rows and two variables:

sci Genus and species

common common name

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