

Package: teethr (via r-universe)

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Title Working with dental data

Version 0.0.0.9000

Description A package to facilitate working with dental data and calculation of dental indices that are commonly used in dental anthropology.

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calculus_index	<i>Calculate calculus index</i>
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Description

Convenience function to calculate dental calculus index directly from a dental_longer() output.

Usage

```
calculus_index(.data, ..., .score = score, .method = c("simple", "greene2005"))
```

Arguments

- .data Data frame in long format, with one tooth surface per row, and one calculus score per surface.
- ... can be used to add arguments to [group_by](#). By default .add = T.
- .score numeric. Calculus score for each surface. Defaults to 'score' as provided by [dental_longer](#).
- .method string. Using .method = "greene2005" will apply dental_filter() and add quadrant to grouping variables (according to Greene et al. (2005)). .method = "simple" (default) just takes user input and no filter.

Details

Calculate the calculus index for each quadrant of an individual based on the method outlined in Greene et al. (2005). The original method calculates a score for each quadrant of the dentition, so it is recommended to group by quadrant, either in the function or using [group_by](#) above in a pipe (see examples).

Value

The default returns a data frame with the supplied groups and calculations for number of surfaces scored, number of teeth scored, sum of scores, and the calculus index.

Source

Greene, T.R., Kuba, C.L., Irish, J.D. 2005. Quantifying calculus: A suggested new approach for recording an important indicator of diet and dental health. [doi:10.1016/j.jchb.2005.02.002](https://doi.org/10.1016/j.jchb.2005.02.002)

Examples

```

library(dplyr)
mb11_calculus_long <- mb11_calculus %>%
  dental_longer(-id, names_sep = "_") %>%
  dental_join()
# example adding groups before call to function
mb11_calculus_long %>%
  group_by(id, quadrant) %>%
  calculus_index()

# example adding groups in call to function
mb11_calculus_long %>%
  calculus_index(id, quadrant)

# example of the Greene et al. 2005 method
mb11_calculus_long %>%
  calculus_index(.method = "greene2005")

```

count_caries

*Convert caries scores to lesion counts***Description**

Convert caries scores to lesion counts

Usage

```

count_caries(
  data,
  caries = score,
  no_lesion = NULL,
  lesion_sep = NULL,
  unobs = NA,
  method = c("location", "standards", "count")
)

```

Arguments

data	data frame containing caries scores
caries	column containing caries scores
no_lesion	value used to indicate no caries lesions
lesion_sep	string. character used to separate multiple lesions.
unobs	value used to indicate unobservable
method	string. what method was used to score caries lesions.

dental-indices	<i>Calculate a dental index or ratio</i>
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Description

Calculate a dental index, such as a calculus index, or ratio, such as caries ratio.

Usage

```
dental_index(data, score = score)
```

```
dental_ratio(data, count = count)
```

Arguments

data	long format data frame with tooth position information and either lesion counts or scores.
score	Scores of a dental lesion (e.g. caries counts or dental calculus score).
count	Counts of a dental lesion (e.g. caries counts or dental calculus score).

Details

Function to calculate the index or ratio of dental diseases. `dental_ratio()` is just a wrapper for `dental_index()` where the output column 'index' is changed to 'count', and 'score_sum' to 'ratio'.

Value

Returns a data frame containing the grouping variable(s), the number of teeth per group, the lesion count or sum of scores, and the calculated index or ratio.

Functions

- `dental_index()`: calculate dental disease index
- `dental_ratio()`: calculate dental disease ratio

Examples

```
library(dplyr)
library(tidyr)
# dental calculus index
mb11_calculus %>%
  dental_longer(-id, names_sep = "_") %>%
  dental_join() %>%
  group_by(class) %>% # calculate index per tooth class
  dental_index()
```

dental_arcade_mapping	<i>Dental arcade mapping data</i>
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Description

Used to map each tooth to `geom_sf()` to create a dental plot.

Usage

```
dental_arcade_mapping
```

Format

`dental_arcade_mapping`:

A data frame with 32 rows and 2 columns:

tooth string. Tooth with text notation.

geometry sfc. Simple feature geometry list-column for mapping teeth to `geom_sf()`. ...

Source

https://github.com/ZandraFagernas/dental_arcade/blob/v0.1/dental_arcade_empty_mapping.jpg

dental_filter	<i>Dentition filter</i>
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Description

Checks if the data frame satisfies the criterion that minimally, each surface must be scorable on at least one side of the dentition to obtain the index, then filters out groups that don't satisfy.

Usage

```
dental_filter(data, score = score)
```

Arguments

data long format data frame with tooth position information and either lesion counts or scores.

score Scores of a dental lesion (e.g. caries counts or dental calculus score).

Value

Returns a filtered data frame and a warning if any rows were removed.

dental_join	<i>Produce detailed tooth position information from tooth notation</i>
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Description

Produce detailed tooth position information from tooth notation

Usage

```
dental_join(data, by = tooth, notation = c("FDI", "standards", "text"), ...)
```

Arguments

data	A data frame containing a column with a unique identifier and one column per tooth or tooth surface.
by	string. name of column containing the tooth notation.
notation	string. Which notation convention is used to name the columns with dental scores. Options are "FDI", "standards", "text". See the <code>tooth_notation</code> object for more details.
...	supply additional arguments to <code>left_join()</code>

Value

Returns the original data frame along with detailed information about the tooth including, region (maxilla, mandible), position (anterior, posterior), side, class (incisor, canine, etc.), type, (first incisor, second molar, etc.), and quadrant.

Examples

```
mb11_caries %>%
  dental_longer(-id) %>%
  dental_join()
```

dental_longer	<i>Convert a data frame containing dental scores to long format and add tooth position variables.</i>
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Description

This function is a wrapper for `pivot_longer()` that converts a wide format data frame to a long format with tooth names in a `tooth` column (and `surface`, if applicable) and the score in a `score` column. It also attaches additional columns with information about the type of tooth and the position of the tooth in the mouth (`type`, `class`, `region`, etc.).

Usage

```
dental_longer(data, cols, ...)
```

Arguments

- data A data frame containing a column with a unique identifier and one column per tooth or tooth surface.
- cols Which columns to pivot into longer format. These should be the columns containing the scores for each tooth/surface.
- ... additional arguments passed on to [pivot_longer](#).

Details

If there are multiple columns per tooth, i.e., if teeth were scored per surface and variables are named something like `_`, `names_sep = "_"` (or whatever character was used to separate tooth number from tooth surface) should be passed to `pivot_longer` via `...`. If no such separator was used, use instead `names_pattern = <regex>`. See [pivot_longer](#) for more details.

Value

Returns a longer data frame with one row per tooth or tooth surface, with columns for tooth number, region (maxilla, mandible), position (anterior, posterior), side, class (incisor, canine, etc.), type, and quadrant.

Examples

```
# pivot calculus scores per surface (all columns except id)
# 't' prefix needs to be removed from column names
mb11_calculus %>%
  dental_longer(-id, names_sep = "_")

# pivot caries scores per tooth
mb11_caries %>%
  dental_longer(-id)
```

dental_recode	<i>Recode tooth notation</i>
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Description

Function to switch between tooth notations.

Usage

```
dental_recode(data, col, from, to)
```

Arguments

<code>data</code>	A data frame to convert
<code>col</code>	the column to convert. Must contain a tooth notation (e.g., FDI, standards).
<code>from</code>	string. the tooth notation of the original data.
<code>to</code>	string. The tooth notation you wish to convert to.

<code>mb11_calculus</code>	<i>Middenbeemster dental calculus data</i>
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Description

Dental calculus scores collected from Middenbeemster (MB11), a rural 19th century archaeological site in the Netherlands.

Usage

```
mb11_calculus
```

Format

```
mb11_calculus:
```

A data frame with 41 rows and 97 columns:

id Skeletal ID

t11:t48_buc/lin/ipx Calculus score per tooth surface. Variable naming: t<tooth number (FDI notation)>_. buc = buccal; lin = lingual, ipx = interproximal ...

Source

<https://doi.org/10.5281/zenodo.7649151>

<code>mb11_caries</code>	<i>Middenbeemster dental caries data</i>
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Description

Dental caries lesions collected from Middenbeemster (MB11), a rural 19th century archaeological site in the Netherlands.

Usage

```
mb11_caries
```

Format

mb11_carries:

A data frame with 41 rows and 33 columns:

id Skeletal ID

t11:t48 Caries lesion location(s) per tooth. Multiple scores separated by ';'. Variable naming: t<tooth number (FDI notation)>. mes = mesial, dis = distal, buc = buccal; lin = lingual, occ = occlusal, root = root, crown = large lesion of indeterminate origin ...

Source

<https://doi.org/10.5281/zenodo.7649151>

mb11_demography

Middenbeemster sample demographics

Description

Age and sex of the individuals with dental calculus scored in mb11_calculus.

Usage

mb11_demography

Format

mb11_demography:

A data frame with 41 rows and 97 columns:

id Skeletal ID

age Age category of the individual. eya = early young adult (18-24); lya = late young adult (25-34); ma = middle adult (35-49); old = old adult (50+).

sex Biological sex of individual estimated using osteological methods. f = female; pf = probable female; pm = probable male; m = male. ...

Source

<https://doi.org/10.5281/zenodo.7649151>

tooth_notation	<i>Common naming schemes in dental anthropology</i>
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Description

Used to convert between tooth naming conventions that are common in dental anthropology.

Usage

tooth_notation

Format

tooth_notation:

A data frame with 32 rows and 9 columns:

FDI Fédération dentaire internationale naming convention

standards Standards naming (Buikstra and Ubelaker 1994)

text Text naming: [UL][LR][ICPM][1-3] = upper/lower; left/right; incisor/canine/premolar/molar; tooth type (1-4). Example: Upper left lateral incisor = ULI2

region if the tooth is from the maxilla or mandible

position if the tooth is anterior or posterior

side if the tooth is from the left or right side

class if the tooth is incisor, canine, premolar, or molar

type if the tooth is central/lateral incisor, canine, first/second premolar, or first/second/third molar

quadrant Which quadrant of the mouth the tooth is from. Upper/lower anterior/posterior. ...

Source

Buikstra, J. E., & Ubelaker, D. H. (1994). Standards for data collection from human skeletal remains. Arkansas Archaeological Survey Research Series No. 44. Fayetteville: Arkansas Archaeological Survey.

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