Package ‘verbalisr’

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Type Package

Title Describe Pedigree Relationships in Words

Version 0.7.2

Description Describe in words the genealogical relationship between two members of a given pedigree, using the algorithm in Vigeland (2022) <doi:10.1186/s12859-022-04759-y>. 'verbalisr' is part of the 'pedsuite' collection of packages for pedigree analysis. For a demonstration of 'verbalisr', see the online app 'QuickPed' at <`https://magnusdv.shinyapps.io/quickped`>.

License GPL-3

URL `https://github.com/magnusdv/verbalisr`, `https://magnusdv.github.io/pedsuite/`

BugReports `https://github.com/magnusdv/verbalisr/issues`

Depends pedtools (>= 2.7.1), R (>= 4.1)

Imports ribd (>= 1.6.1)

Suggests testthat

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NeedsCompilation no

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Contents

`habsburg` *Habsburg pedigree.*

Description

A subset of the royal Habsburg family, showing the ancestry of (the infamously inbred) King Charles II of Spain.

Usage

```
habsburg
```

Format

A ped object containing a pedigree with 29 members.

Source

Adapted from `https://en.wikipedia.org/wiki/Habsburg_family_tree`

Examples

```
plot(habsburg, hatched = "Charles II", cex = 0.7)

verbalise(habsburg, ids = parents(habsburg, "Charles II"))
```

`print.pairrel` *Format and print relationship descriptions*

Description

This documents the options for formatting and printing the output of `verbalise()`.

Usage

```
## S3 method for class 'pairrel'
print(x, ...)

## S3 method for class 'pairrel'
format(
  x,
  cap = TRUE,
  simplify = FALSE,
  abbreviate = FALSE,
  collapse = NULL,
  includePaths = !simplify,
  ...
)
```

Arguments

`x`	An output of `verbalise()`.
`...`	Arguments passed on to `format.pairrel()`.
`cap`	A logical indicating if the first letter of each path description should be capitalised. By default TRUE.
`simplify`	A logical. If TRUE, the descriptions of lineal and avuncular relationships are simplified. Default: FALSE.
`abbreviate`	A logical. It TRUE, various abbreviations are applied to the descriptions, e.g. 'great-great-' -> 'gg-' and 'once removed' -> '1r'. Default: FALSE.
`collapse`	A single string, or NULL. If given, and the relationship has multiple descriptions, these are concatenated with `paste(..., collapse = collapse)`.
`includePaths`	A logical indicating if the complete paths should be included in the output. By default TRUE.

`verbalise` *Describe a pairwise relationship*

Description

The description includes all pedigree paths between the two individuals, indicating with brackets the topmost common ancestors in each path. See `print.pairrel()` for formatting options when printing the results.

Usage

```
verbalise(x, ids = leaves(x))
```

Arguments

`x`	A ped object, or a list of such.
`ids`	A vector containing the names of two pedigree members.

Value

An object of class `pairrel`. This is essentially a list of lists, containing many details about each path between the individuals. Most users will not interact with this list directly, but simply use the description provided by the `print()` method.

See Also

`print.pairrel()`.

Examples

```
# Example 1: Family quartet

x = nuclearPed(2)
verbalise(x, 1:2)
verbalise(x, 2:3)
verbalise(x, 3:4)

# Simplified output
verbalise(x, 2:3) |> print(simplify = TRUE)

# Example 2: Complicated cousin pedigree

y = doubleCousins(degree1 = 1, removal1 = 1, half1 = TRUE,
                  degree2 = 2, removal2 = 0, half2 = FALSE)
verbalise(y)

# Example 3: Full sib mating

z = fullSibMating(1)
verbalise(z)
verbalise(z, ids = c(1,5))
verbalise(z, ids = c(1,5)) |> print(simplify = TRUE)

# Example 4: Quad half first cousins

w = quadHalfFirstCousins()
verbalise(w)
```

Index