

Package ‘verbalisr’

August 19, 2023

Type Package

Title Describe Pedigree Relationships in Words

Version 0.5.1

Description Describe in words the genealogical relationship between two members of a given pedigree. 'verbalisr' is part of the 'ped suite' collection of packages for pedigree analysis. For a demonstration of 'verbalisr', see the online app 'QuickPed' at <https://magnusdv.shinyapps.io/quickped>.

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

BugReports <https://github.com/magnusdv/verbalisr/issues>

Depends pedtools (>= 2.2.0), R (>= 4.1)

Imports ribd (>= 1.5.0)

Suggests testthat

Encoding UTF-8

Language en-GB

LazyData true

RoxygenNote 7.2.3

NeedsCompilation no

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format.pairrel	<i>Format relationship description</i>
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Description

This is the main formatting function called by `print.pairrel()`.

Usage

```
## S3 method for class 'pairrel'
format(x, cap = TRUE, includePaths = TRUE, ...)
```

Arguments

x	An output of <code>verbalise()</code> .
cap	A logical indicating if the first letter of each path description should be capitalised. By default TRUE.
includePaths	A logical indicating if the complete paths should be included in the output. By default TRUE.
...	Not used.

habsburg	<i>Habsburg pedigree.</i>
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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, margin = c(1,1,1,1))
verbalise(habsburg, ids = parents(habsburg, "Charles II"))
```

verbalise	<i>Describe a pairwise relationship</i>
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Description

The description includes all pedigree paths between the two individuals, indicating with brackets the topmost common ancestors in each path.

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, where each inner list describes a single path.

Examples

```
# Example 1: Family quartet
x = nuclearPed(2)
verbalise(x, 1:2)
verbalise(x, 2:3)
verbalise(x, 3:4)

# 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))  
  
# Example 4: Quad half first cousins  
  
w = quadHalfFirstCousins()  
verbalise(w)
```

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