

Package ‘verbalisr’

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Type Package

Title Describe Pedigree Relationships in Words

Version 0.4.0

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 (>= 1.1.0), R (>= 4.1)

Imports ribd (>= 1.3.1)

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

Language en-GB

RoxygenNote 7.1.2

LazyData true

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)
```

verbalisr

verbalisr: Describe pedigree relationships in words

Description

Describe the genealogical relationship between two members of a given pedigree. `verbalisr` is part of the *ped suite* collection of packages for pedigree analysis.

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