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>.
License GPL-3
URL https://github.com/magnusdv/verbalisr,
https://magnusdv.github.io/pedsuite/
BugReports https://github.com/magnusdv/verbalisr/issues
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## format.pairrel

Format relationship description

### Description

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

### Usage

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

### Arguments

- `x`: An output of `verbalise()`.
- `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

Habsburg pedigree.

### Description

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

### Usage

```r
habsburg
```

### Format

A ped object containing a pedigree with 29 members.

### Source

Adapted from [https://en.wikipedia.org/wiki/Habsburg_family_tree](https://en.wikipedia.org/wiki/Habsburg_family_tree)
Examples

```r
plot(habsburg, hatched = "Charles II", cex = 0.7, margin = c(1,1,1,1))

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

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**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.

**Usage**

```r
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**

```r
# 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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