Package ‘verbalisr’

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>.
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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Imports ribd (>= 1.3.1)
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**R topics documented:**

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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**

`habsburg`

**Format**

A `ped` object containing a pedigree with 29 members.
verbalise

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"))

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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
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

\[ z \equiv \text{fullSibMating}(1) \]

verbalise(z)
verbalise(z, ids = c(1,5))

# Example 4: Quad half first cousins

\[ w \equiv \text{quadHalfFirstCousins}() \]

verbalise(w)

---

**verbalisr**

**verbalisr**: Describe pedigree relationships in words

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**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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