Package 'pedsuite'

January 7, 2022

Title Easy Installation of the 'ped suite' Packages for Pedigree Analysis

Version 1.1.0

Description The 'ped suite' is a collection of packages for pedigree analysis, covering applications in forensic genetics, medical genetics and more. A detailed presentation of the 'ped suite' is given in the book 'Pedigree Analysis in R' (Vigeland, 2021, ISBN: 9780128244302).

License GPL (>= 3)

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

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

Depends forrel, pedprobr, pedtools, ribd, verbalisr

Imports pedmut, dvir, ibdsim2, paramlink2, pedbuildr, segregatr

Suggests knitr, rmarkdown

VignetteBuilder knitr

Encoding UTF-8

Language en-GB

RoxygenNote 7.1.2

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-01-07 13:12:42 UTC

R topics documented:

`pedsuite` *pedsuite: A collection of packages for pedigree analysis in R*

Description

This meta-package makes it easy to install and load the **ped suite** packages for pedigree analysis in R, covering applications in forensic genetics, medical genetics and others. A detailed presentation of the **ped suite** is given in the book *Pedigree Analysis in R* (Vigeland, 2021, ISBN: 9780128244302).

Core packages

At the centre of the **ped suite** we find the package **pedtools**, on which all the others depend. In addition, several packages contain basic features often needed in many types of analysis. These are the *core* packages:

- pedtools: Creating and working with pedigrees and marker data
- verbalisr: Textual descriptions of pedigree relationships
- ribd: Pedigree-based relatedness coefficients
- pedprobr: Marker probabilities and pedigree likelihoods
- forrel: Forensic pedigree analysis and relatedness analysis

Specialised packages

The following packages are devoted to special applications. They must be loaded separately, e.g., `library(ibdsim2)`.

- dvir: Disaster victim identification
- ibdsim2: Simulation of identity-by-descent sharing by family members
- paramlink2: Parametric linkage analysis
- pedbuildr: Reconstructing pedigrees from marker data
- pedmut: Mutation models for pedigree likelihood computations
- segregatr: Segregation analysis for clinical variant interpretation

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