

Package ‘pedsuite’

October 14, 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).

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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

Author Magnus Dehli Vigeland [aut, cre]
(<https://orcid.org/0000-0002-9134-4962>),
Thore Egeland [aut] (<https://orcid.org/0000-0002-3465-8885>)

Maintainer Magnus Dehli Vigeland <m.d.vigeland@medisin.uio.no>

Repository CRAN

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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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