

Package ‘KLINK’

April 5, 2024

Title Kinship Analysis with Linked Markers

Version 0.7.3

Description A 'shiny' application for forensic kinship testing, based on the 'pedsuite' R packages. 'KLINK' is closely aligned with the (non-R) software 'Familias' and 'FamLink', but offers several unique features, including visualisations and automated report generation. The calculation of likelihood ratios supports pairs of linked markers, and all common mutation models.

License GPL (>= 3)

URL <https://github.com/magnusdv/KLINK>

BugReports <https://github.com/magnusdv/KLINK/issues>

Depends R (>= 4.1)

Imports forrel (>= 1.6.0), gt (>= 0.9.0), openxlsx, pedFamilias, pedmut (>= 0.7.1), pedprobr (>= 0.9.3), pedtools (>= 2.6.0), shiny (>= 1.7.4), shinydashboard, verbalisr, zip

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launchApp	<i>Launch KLINK</i>
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Description

This launches the KLINK app. runKLINK() is a synonym for launchApp().

Usage

```
launchApp()
```

```
runKLINK()
```

Value

No return value, called for side effects.

Examples

```
## Not run:
launchApp()

## End(Not run)
```

LINKAGEMAP	<i>Built-in linkage map</i>
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Description

A genetic map including 9 pairs of linked STR markers.

Usage

```
LINKAGEMAP
```

Format

A data frame with 18 rows and 5 columns.

linkedLR	<i>LR with pairwise linked markers</i>
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Description

This function does the main LR calculations of the KLINK app.

Usage

```
linkedLR(pedigrees, linkageMap, markerData = NULL, mapfun = "Kosambi")
```

Arguments

pedigrees	A list of two pedigrees.
linkageMap	A data frame with columns including Pair, Marker, Chrom, PosCM
markerData	A data frame, normally extracted automatically from pedigrees.
mapfun	Name of the map function to be used; either "Haldane" or "Kosambi" (default)

Value

A data frame with detailed LR results.

Examples

```
library(forrel)

ped1 = nuclearPed(fa = "AF", child = "CH") |>
  profileSim(markers = NorwegianFrequencies)

ped2 = singletons(c("AF", "CH")) |>
  transferMarkers(from = ped1, to = _)

pedigrees = list(ped1, ped2)

linkedLR(pedigrees, LINKAGEMAP)
```

loadFamFile	<i>Load .fam file</i>
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Description

Load .fam file

Usage

```
loadFamFile(path, fallbackModel = "equal", withParams = FALSE)
```

Arguments

- path The path to a .fam file.
- fallbackModel The name of a mutation model; passed on to `pedFamilies::readFam()`.
- withParams A logical indicating if the Families parameters should be included in the output. (See `pedFamilies::readFam()`.)

Value

A list of two ped objects.

Examples

```
fam = system.file("extdata/halfsib-test.fam", package = "KLINK")
peds = loadFamFile(fam)
pedtools::plotPedList(peds)
```

markerSummary	<i>Generate table of marker data</i>
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Description

Generate table of marker data

Usage

```
markerSummary(pedigrees, linkageMap = NULL)
```

Arguments

- pedigrees A list of 2 pedigrees.
- linkageMap A data frame.

Value

A data frame.

Examples

```
markerSummary(paternity)
```

paternity	<i>Dataset for a paternity case</i>
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Description

A list of two pedigrees forming the hypotheses in a paternity case: H1 (AF is the father of CH) and H2 (unrelated). AF and CH are genotyped with 11 markers, with allele frequencies from `forrel::NorwegianFrequencies`.

Usage

```
paternity
```

Format

A list of two pedigrees, named H1 and H2.

Examples

```
pedtools::plotPedList(paternity, marker = "SE33")
forrel::kinshipLR(paternity)
```

writeResult	<i>Write data and results to Excel</i>
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Description

This function produces an Excel document containing the genotype data and various LR tables.

Usage

```
writeResult(
  resultTable,
  pedigrees,
  linkageMap,
  markerData,
  outfile,
  notes = NULL,
  fam = NULL
)
```

Arguments

resultTable	A data frame.
pedigrees	A list of two ped objects.
linkageMap	A data frame.
markerData	A data frame.
outfile	The output file name.
notes	A character vector.
fam	The name of the input .fam file.

Examples

```
# Built-in dataset `paternity`
peds = paternity
map = LINKAGEMAP
mdata = markerSummary(peds, map)

# Result table
LRtab = linkedLR(pedigrees = peds, linkageMap = map, markerData = mdata)

# Write to excel
tmp = paste0(tempfile(), ".xlsx")
writeResult(LRtab,
            pedigrees = peds,
            linkageMap = map,
            markerData = mdata,
            outfile = tmp)

# openxlsx::openXL(tmp)
```

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