Package 'ribd'

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Type Package

Title Pedigree-based Relatedness Coefficients

Version 1.5.0

Description Recursive algorithms for computing various relatedness coefficients, including pairwise kinship, kappa and identity coefficients. Both autosomal and X-linked coefficients are computed. Founders are allowed to be inbred, which enables construction of any given kappa coefficients, as described in Vigeland (2020) <doi:10.1007/s00285-020-01505-x>. In addition to the standard coefficients, 'ribd' also computes a range of lesser-known coefficients, including generalised kinship coefficients (Karigl (1981) <doi:10.1111/j.1469-1809.1981.tb00341.x>; Weeks and Lange (1988) <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1715269>), two-locus coefficients (Thompson (1988) <doi:10.1093/imammb/5.4.261>) and multi-person coefficients. This package is part of the 'ped suite', a collection of packages for pedigree analysis in R. Several methods of 'ribd' are featured in the online app 'QuickPed' available at <https://magnusdv.shinyapps.io/quickped>. See Vigeland (2022) <doi:10.1186/s12859-022-04759-y>.

License GPL-3

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

Depends pedtools, R (>= 3.5.0)

Imports glue, kinship2, slam

Suggests spelling, testthat

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R topics documented:

`coeffTable` *Table of pairwise relatedness coefficients*

Description

Creates a data frame containing various relatedness coefficients between all pairs of individuals in a given pedigree.

Usage

```
coeffTable(
  x,
  ids = labels(x),
  coeff = c("f", "phi", "deg", "kappa", "identity", "detailed"),
  self = FALSE,
  Xchrom = FALSE
)
```

Arguments

x	A pedigree in the form of a pedtools::ped object.
ids	A character (or coercible to character) containing ID labels of two or more pedigree members.
coeff	A character vector containing one or more of the keywords "f", "phi", "deg", "kappa", "identity", "detailed".
self	A logical indicating if self-relationships should be included. Default: FALSE.
Xchrom	A logical indicating if the coefficients should be autosomal (default) or X-chromosomal. If Xchrom = NA, both sets are included.

Details

Available coefficients (indicated in coeff) include:

- f: The inbreeding coefficient of each pair member. Columns: f1 and f2.
- phi: The kinship coefficient. Column: phi.
- deg: The degree of relationship, as computed by kin2deg. Column: deg
- kappa: The IBD coefficients computed by kappaIBD. (These are NA for pairs involving inbred individuals.) Columns: k0, k1, k2.
- identity: The 9 condensed identity coefficients of Jacquard, computed by identityCoefs(). Columns: D1, ..., D9.
- detailed: The detailed identity coefficients of Jacquard, computed by identityCoefs(..., detailed = TRUE). Columns: d1, ..., d15.

Value

A data frame with one row for each pair of individuals. The first two columns are characters named id1 and id2, while remaining columns are numeric. Columns containing X-chromosomal coefficients are suffixed with ".X".

If "f" (inbreeding) is the only coefficient, the data frame has one row per individual, and the first column is named id.

Note: If x has members with unknown sex, all X-chromosomal coefficients are NA.

Examples

```
# Uncle-nephew pedigree
x = addSon(nuclearPed(2), 4)

# Complete table
coeffTable(x)

# Only relevant coefficients
coeffTable(x, coeff = c("phi", "deg", "kappa"))

# Only the uncle-nephew pair
coeffTable(x, ids = c(3, 6), coeff = c("phi", "deg", "kappa"))

# X-chromosomal coefficients
coeffTable(x, Xchrom = TRUE)

# Both autosomal and X
coeffTable(x, Xchrom = NA)
```

`condensedIdentity` *Condensed identity coefficients*

Description

Computes the 9 condensed identity coefficients of pairwise relationships in a pedigree. Founders of the pedigree may be inbred; use `pedtools::founderInbreeding()` to set this up.

Usage

```
condensedIdentity(
  x,
  ids,
  sparse = NA,
  simplify = TRUE,
  self = FALSE,
  verbose = FALSE
)
```

Arguments

`x`	A pedigree in the form of a `pedtools::ped` object
`ids`	A character (or coercible to character) containing ID labels of two or more pedigree members.
`sparse`	A positive integer, indicating the pedigree size limit for using sparse arrays (as implemented by the slam package) instead of ordinary arrays.
`simplify`	Simplify the output (to a numeric of length 9) if `ids` has length 2. Default: TRUE.

self	A logical indicating if self-relationships (i.e., between a pedigree member and itself) should be included. FALSE by default.
verbose	A logical

Details

The implementation is a modified version of Karigl's recursive algorithm (1981).

Value

If ids has length 2 and simplify = TRUE: A vector of length 9, containing the condensed identity coefficients.

Otherwise, a data frame with 11 columns and one row for each pair of individuals. The first two columns contain the ID labels, and columns 3-11 contain the condensed identity coefficients.

References

G. Karigl (1981). *A recursive algorithm for the calculation of identity coefficients.* Annals of Human Genetics, vol. 45.

See Also

kappa(), identityCoefs(), pedtools::founderInbreeding()

Examples

```
# One generation of full sib mating.
# (One of the simplest examples with all 9 coefficients nonzero.)
x = fullSibMating(1)
j1 = condensedIdentity(x, ids = 5:6)

stopifnot(all.equal(j1, c(2, 1,4, 1, 4, 1, 7, 10, 2)/32))

# Recalculate the coefficients when the founders are 100% inbred
founderInbreeding(x, 1:2) = 1
condensedIdentity(x, ids = 5:6)
```

---

condensedIdentityX *Identity coefficients on X*

Description

Computes the X chromosomal condensed identity coefficients of a pairwise relationship.

Usage

```
condensedIdentityX(x, ids, sparse = NA, simplify = TRUE, verbose = FALSE)
```

Arguments

x	A pedigree in the form of a pedtools::ped object
ids	A character (or coercible to character) containing ID labels of two or more pedigree members.
sparse	A positive integer, indicating the pedigree size limit for using sparse arrays (as implemented by the slam package) instead of ordinary arrays.
simplify	Simplify the output (to a numeric of length 9) if ids has length 2. Default: TRUE.
verbose	A logical

Details

The implementation is inspired by Karigl's recursive algorithm (1981) for the autosomal case, modified to account for X-linked inheritance.

The X chromosomal pairwise identity states depend on the sexes of the two individuals. If both are female, the states are the same as in the autosomal case. When males are involved, the two individuals have less than 4 alleles, hence the states differ from the autosomal ones. However, to avoid drawing (and learning) new pictures we re-use the autosomal states by using the following simple rule: **Replace any hemizygous male allele with a pair of autozygous alleles**. In this way each X state corresponds to a unique autosomal state.

For simplicity the output always contains 9 coefficients, but with NA's in the positions of undefined states (depending on the sex combination). The README file on the GitHub home page of ribd has a table illustrating this.

Value

If ids has length 2 and simplify = TRUE: A vector of length 9, containing the condensed identity coefficients. If any of the individuals are male, certain states are undefined, and the corresponding coefficients are NA. (See Details.)

Otherwise, a data frame with 11 columns and one row for each pair of individuals. The first two columns contain the ID labels, and columns 3-11 contain the condensed identity coefficients.

See Also

kinship(), identityCoefs(), pedtools::founderInbreeding()

Examples

```
x = fullSibMating(1)
x_sisters = swapSex(x, 5)
x_brothers = swapSex(x, 6)

condensedIdentityX(x, ids = 5:6)
condensedIdentityX(x_sisters, ids = 5:6)
condensedIdentityX(x_brothers, ids = 5:6)
```

`constructPedigree` *Pedigree construction*

Description

Construct a pedigree yielding a prescribed set of IBD coefficients.

Usage

```
constructPedigree(kappa, describe = TRUE, verbose = FALSE)
```

Arguments

`kappa`	A probability vector of length 3; $(kappa0, kappa1, kappa2)$.
`describe`	A logical. If TRUE, a textual description of the resulting relationship is printed.
`verbose`	A logical. If TRUE, various details about the calculations are printed.

Details

The construction follows the method and formulae given in Vigeland (2020).

Value

A ped object containing a pair of double half cousins with inbred founders. (In corner cases the relationship collapses into siblings.)

References

M. D. Vigeland (2020). *Relatedness coefficients in pedigrees with inbred founders*. Journal of mathematical biology. doi:10.1007/s0028502001505x

Examples

```
# Full siblings
x = constructPedigree(kappa = c(0.25, 0.5, 0.25))
kappaIBD(x, leaves(x))

# A relationship halfway between parent-child and full sibs
kap = c(1/8, 6/8, 1/8)
showInTriangle(kap, label = " (1/8, 1/8)", pos = 4)

y = constructPedigree(kappa = kap)
plot(y)

stopifnot(all.equal(kappaIBD(y, leaves(y)), kap))

# kappa = (0,1,0) does not give a parent-child relationship,
```

```
# but half siblings whose shared parent is completely inbred.
z = constructPedigree(kappa = c(0,1,0))
plot(z)
```

ELR *Expected LR of a pairwise kinship test*

Description

Calculates the exact likelihood ratio of a pairwise kinship test, implementing formulas of Egeland & Slooten (2016).

Usage

```
ELR(x, true = x, ids = leaves(x), L1, L2 = NULL, rho = NULL)
```

Arguments

x	An hypothesised pedigree connecting two individuals.
true	The true relationship between the two individuals.
ids	A vector containing the names of the two individuals. Note: These must occur in both x and true.
L1	The number of alleles at the first locus.
L2	The number of alleles at the second locus, or NULL (default).
rho	(If L2 is not NULL.) A numeric vector of recombination fractions. Values outside the interval $[0, 0.5]$ will raise an error.

Value

A single number, the expected LR.

References

Egeland, T. and Slooten, K. (2016). *The likelihood ratio as a random variable for linked markers in kinship analysis*. Int J Legal Med.

Examples

```
############################
# Fig. 2 of Egeland & Slooten
############################

rhos = seq(0, 0.5, length = 11)

dat = cbind(
  Grand = ELR(linearPed(2), ids = c(1,5), L1 = 10, L2 = 30, rho = rhos),
```

```
  Half = ELR(halfSibPed(), ids = c(4,5), L1 = 10, L2 = 30, rho = rhos),
  Uncle = ELR(avuncularPed(), ids = c(3,6), L1 = 10, L2 = 30, rho = rhos))

matplot(rhos, dat, type = "l",  lwd = 2, ylab = "E[LR]", ylim = c(0, 8))
legend("bottomleft", legend = colnames(dat), lty = 1:3, col = 1:3, lwd = 2)
```

`external_coefs` *Relatedness coefficients by other programs*

Description

Wrappers for functions in other packages or external programs.

Usage

```
kinship2_kinship(x, ids = NULL, Xchrom = FALSE)

kinship2_inbreeding(x, Xchrom = FALSE)
```

Arguments

`x`	A pedigree, in the form of a `pedtools::ped` object.
`ids`	A integer vector of length 2.
`Xchrom`	A logical, indicating if the autosomal (default) or X-chromosomal coefficients should be computed.

Details

`kinship2_kinship()` and `kinship2_inbreeding()` both wrap `kinship2::kinship()`.

Value

For `kinship2_inbreeding()`, a numerical vector with inbreeding coefficients, named with ID labels.

For `kinship2_kinship()`, either a single numeric (if `ids` is a pair of pedigree members) or the whole kinship matrix, with the ID labels as dimnames.

See Also

`kinship2::kinship()`

Examples

```
# A random pedigree with 2 founders and 5 matings
p = randomPed(g = 5, founders = 2, seed = 123)

### Kinship matrix

# Autosomal: Check that ribd agrees with kinship2
stopifnot(identical(
  kinship(p),          # ribd
  kinship2_kinship(p)  # kinship2

))

# X chromosomal kinship
stopifnot(identical(
  kinship(p, Xchrom = TRUE),          # ribd
  kinship2_kinship(p, Xchrom = TRUE)  # kinship2
))


### Inbreeding coefficients

# Autosomal
stopifnot(identical(
  inbreeding(p),          # ribd
  kinship2_inbreeding(p)  # kinship2

))

# X chromosomal
stopifnot(identical(
  inbreeding(p, Xchrom = TRUE),          # ribd
  kinship2_inbreeding(p, Xchrom = TRUE)  # kinship2
))
```

---

gKinship *Generalised kinship coefficients*

Description

Computes single-locus generalised kinship coefficients of various kinds. These are fundamental for computing identity coefficients (see `identityCoefs()`), but are also interesting in their own right. Each generalised kinship coefficient is defined as the probability of observing a corresponding *generalised IBD pattern*, as defined and discussed in the Details section below.

Usage

```
gKinship(
  x,
  pattern,
  distinct = TRUE,
  Xchrom = FALSE,
  method = c("auto", "K", "WL", "LS", "GC"),
  verbose = FALSE,
  debug = FALSE,
  mem = NULL,
  ...
)

gip(x, pattern, distinct = TRUE)
```

Arguments

x	A ped object.
pattern	A gip object, or a list of vectors to be passed onto gip(). Each vector should contain members of x constituting an IBD block. (See Details and Examples.)
distinct	A logical indicating if different blocks are required to be non-IBD. Default: TRUE. (Irrelevant for single-block patterns.)
Xchrom	A logical, by default FALSE.
method	Either "auto", "K", "WL", "LS" or "GC".
verbose	A logical, by default FALSE.
debug	A logical, by default FALSE.
mem	For internal use.
...	Further arguments.

Details

The starting point: standard kinship coefficients:

The classical kinship coefficient phi between two pedigree members A and B, is the probability that two alleles sampled from A and B (one from each), at a random autosomal locus, are identical by descent (IBD).

In the language and notation to be introduced shortly, we would write `phi = Pr[(A,B)]` where `(A,B)` is an *IBD pattern*.

Generalised IBD patterns:

We define a *generalised IBD pattern* (GIP) to be a partition of a set of alleles drawn from members of a pedigree, such that the alleles in each subset are IBD. Each subset (also referred to as a *group* or a *block*) is written as a collection of pedigree members (A, B, ...), with the understanding that each member represents one of its alleles at the given locus. A member may occur in multiple blocks, and also more than once within a block.

Additional requirements give rise to different flavours of GIPs (and their corresponding coefficients):

- `Distinct` (resp. `non-distinct`): alleles in different blocks are non-IBD (resp. may be IBD)
- `Deterministic` (resp. `random`): the parental origin (paternal or maternal) of each allele is fixed (resp. unknown).

We may say that a GIP is *partially* (rather than *fully*) deterministic if the parental origin is fixed for some, but not all alleles involved.

Notational examples:

Our notation distinguishes the different types of patterns, as exemplified below. Blocks are separated with "/" if they are distinct, and "&" otherwise. Deterministically sampled alleles are suffixed by either ":p" (paternal) or ":m" (maternal).

- `(A, B) & (A, C)`: 4 alleles are sampled randomly; two from A, one from B and one from C. The first from A is IBD with that from B, and the second from A is IBD with that from C. All four alleles may be IBD. [Random, non-distinct]
- `(A, B) / (A, C)`: Same as the previous, but the two allele pairs must be non-IBD. [Random, distinct]
- `(A:p, C:p) / (C:m)`: The paternal alleles of A and C are IBD, and different from the maternal allele of C. [Deterministic, distinct]
- `(A, C:p) & (B, C:m)`: The paternal and maternal alleles of C are IBD with random alleles of from A and B, respectively. The two pairs are not necessarily different. [Partially deterministic, non-distinct]
- `(A:p, A, A)`: Here we have just one group, specifying that the paternal allele of A is IBD with two other alleles sampled randomly from A. (If A is non-inbred, this must have probability 1/4.) [Partially deterministic, single-block]

In the `gip()` constructor, deterministic sampling is indicated by naming elements with "p" or "m", e.g., `c(p = A)` produces `(A:p)`. See Examples for how to create the example patterns listed above.

Internal structure of `gip` objects:

(Note: This section is included only for completeness; `gip` objects should not be directly manipulated by end users.)

Internally, a GIP is stored as a list of integer vectors, each vector giving the indices of pedigree members constituting an IBD block. In addition, the object has three attributes:

- `labs`: A character vector containing the names of all pedigree members
- `deterministic`: A logical, which is TRUE if the pattern is (partially or fully) deterministic
- `distinct`: A logical.

If `deterministic = TRUE`, the last digit of each integer encodes the parental origin of the allele (0 = unknown; 1 = paternal; 2 = maternal). For example:

- 12 = the maternal origin of individual 1
- 231 = the paternal allele of individual 23
- 30 = a random allele of individual 3

A brief history of generalised kinship coefficients:

The notion of generalised kinship coefficients originated with Karigl (1981) who used a selection of random, non-distinct patterns (in our terminology) to compute identity coefficients.

Weeks & Lange (1988), building on Karigl's work, defined random, distinct patterns in full generality and gave an algorithm for computing the corresponding coefficients.

In a follow-up paper, Lange & Sinsheimer (1992) introduced partially deterministic (distinct) patterns, and used these to compute detailed identity coefficients.

In another follow-up, Weeks et al. (1995) extended the work on random, distinct patterns by Weeks & Lange (1988) to X-chromosomal loci.

Garcia-Cortes (2015) gave an alternative algorithm for the detailed identity coefficients, based on (in our terminology) fully deterministic, non-distinct patterns.

Implemented algorithms:

The following are valid options for the `methods` parameters, and what they implement.

- `auto`: Chooses method automatically, based on the pattern type.
- `K`: Karigl's algorithm for random, non-distinct patterns. Only the cases considered by Karigl are currently supported, namely single groups up to length 4, and two groups of length two. The implementation in **ribd** includes an X-chromosomal version, and allows inbred founders.
- `WL`: Weeks & Lange's algorithm for random, distinct patterns of any size. [TODO: Include the extension to X by Weeks et al. (1995).]
- `LS`: Lange & Sinsheimer's algorithm for partially deterministic, distinct patterns of any size. Does not support X, nor patterns involving inbred founders.
- `GC`: Garcia-Cortes' algorithm for fully deterministic, non-distinct patterns. The current implementation only covers the patterns needed to compute identity coefficients, namely single blocks and two blocks of length two. The original algorithm has been extended to an X-chromosomal version, and to pedigrees with inbred founders.

Value

`gKinship()` returns a single number, the probability of the given IBD pattern.

`gip()` returns an object of class `gip`. This is internally a list of integer vectors, with attributes `labs`, `deterministic` and `distinct`. (See also Details.)

References

- G. Karigl (1981). A recursive algorithm for the calculation of identity coefficients. Ann. Hum. Genet.
- D.E. Weeks & K. Lange (1988). The affected-pedigree-member method of linkage analysis. Am. J. Hum. Genet
- K. Lange & J.S. Sinsheimer (1992). Calculation of genetic identity coefficients. Ann. Hum. Genet.
- D.E. Weeks, T.I. Valappil, M. Schroeder, D.L. Brown (1995) An X-linked version of the affected-pedigree-member method of linkage analysis. Hum Hered.
- L.A. García-Cortés (2015). A novel recursive algorithm for the calculation of the detailed identity coefficients. Gen Sel Evol.

See Also

`kinship()`, `identityCoefs()`

Examples

```
### Trivial examples ###

x = nuclearPed(father = "A", mother = "B", children = "C")

# Random, distinct
patt1 = gip(x, list(c("A", "B"), c("A", "C")))
patt1

# Random, non-distinct
patt2 = gip(x, list(c("A", "B"), c("A", "C")), distinct = FALSE)
patt2

# Fully deterministic, distinct
patt3 = gip(x, list(c(p="A", p="C"), c(m="C")))
patt3

# Partially deterministic, non-distinct`
patt4 = gip(x, list(c("A", p="C"), c("B", m="C")), distinct = FALSE)
patt4

# Partially deterministic, single block
patt5 = gip(x, list(c(p="A", "A", "A")))
patt5

stopifnot(
  gKinship(x, patt1) == 0,      # (since A and B are unrelated)
  gKinship(x, patt2) == 0,      # (same as previous)
  gKinship(x, patt3) == 0.5,    # (only uncertainty is which allele A gave to C)
  gKinship(x, patt4) == 0.25,   # (distinct irrelevant)
  gKinship(x, patt5) == 0.25   # (both random must hit the paternal)
)



### Kappa coefficients via generalised kinship ###

# NB: Much less efficient than `kappaIBD()`; only for validation

kappa_from_gk = function(x, ids, method = "WL") {
  fa1 = father(x, ids[1])
  fa2 = father(x, ids[2])
  mo1 = mother(x, ids[1])
  mo2 = mother(x, ids[2])

  GK = function(...) gKinship(x, list(...), method = method)

  k0 = GK(fa1, fa2, mo1, mo2)
  k1 = GK(c(fa1, fa2), mo1, mo2) + GK(c(fa1, mo2), fa2, mo1) +
       GK(c(mo1, fa2), fa1, mo2) + GK(c(mo1, mo2), fa1, fa2)
  k2 = GK(c(fa1, fa2), c(mo1, mo2)) + GK(c(fa1, mo2), c(mo1, fa2))
```

```
  c(k0, k1, k2)
}

y1 = nuclearPed(2); ids = 3:4
stopifnot(kappa_from_gk(y1, ids) == kappaIBD(y1, ids))

y2 = quadHalfFirstCousins(); ids = 9:10
stopifnot(kappa_from_gk(y2, ids) == kappaIBD(y2, ids))


### Detailed outputs and debugging ###

x = fullSibMating(1)

# Probability of sampling IBD alleles from 1, 5 and 6
p1 = gip(x, list(c(1,5,6)))
p1
gKinship(x, p1, method = "K", verbose = TRUE, debug = TRUE)
gKinship(x, p1, method = "WL", verbose = TRUE, debug = TRUE)

# Probability that paternal of 5 is IBD with maternal of 6
p2 = gip(x, list(c(p=5, m=6)))
p2
gKinship(x, p2, method = "LS", verbose = TRUE, debug = TRUE)
gKinship(x, p2, method = "GC", verbose = TRUE, debug = TRUE)

# Probability that paternal of 5 is *not* IBD with maternal of 6
p3 = gip(x, list(c(p=5), c(m=6)), distinct = TRUE)
p3
gKinship(x, p3, method = "LS", verbose = TRUE, debug = TRUE)
```

---

ibdDraw *Colourised IBD plot*

Description

This is a pedagogical tools for illustrating the concept of identity-by-descent, by representing the alleles in a pedigree by coloured points or letters. By default, the alleles are placed below each pedigree symbols, but any positions are possible, including inside. (See examples.)

Usage

```
ibdDraw(
  x,
  alleles,
  symbol = c("point", "text"),
  pos = 1,
  cols = NULL,
```

```
  cex = NA,
  sep = NULL,
  dist = 1,
  labs = FALSE,
  checkFounders = TRUE,
  checkParents = TRUE,
  margin = c(1, 1, 1, 1),
  ...
)
```

Arguments

x	A ped object.
alleles	A list of length pedsize(x). Each element should consist of one or two integers, representing different colours. Zeroes produce "greyed-out" alleles.
symbol	Either "point" or "text".
pos	A vector recycled to the length of labels(x), indicating allele placement relative to the pedigree symbols: 0 = inside; 1 = below; 2 = left; 3 = above; 4 = right. By default, all are placed below.
cols	A colour vector corresponding to the integers occurring in alleles.
cex	An expansion factor for the allele points/letters. Default: 3 for points and 2 for text.
sep	The separation between haplotypes within a pair, given as a multiple of the width of a pedigree symbol. Default: 0.5 when pos = 0 and 1 otherwise.
dist	The distance between pedigree symbols and the alleles, given as a multiple of the height of a pedigree symbol. Default: 1. Ignored when pos = 0.
labs	A logical indicating if labels should be included.
checkFounders	A logical. If TRUE (default), a warning is issued if a founder has two equal alleles other than 0.
checkParents	A logical. If TRUE (default), a warning is issued if someone's alleles don't match those of the parents. This a superficial test and does not catch all Mendelian errors.
margin	Plot margins (bottom, left, top, right).
...	Further arguments passed on to plot.ped().

Value

The plot structure is returned invisibly.

See Also

pedtools::plot.ped(), ibdsim2::haploDraw()

Examples

```
op = par(no.readonly = TRUE)

##############################
# Example 1: A family quartet #
##############################

x = nuclearPed(2)
als = list(1:2, 3:4, c(1,3), c(2,3))

# Default options
ibdDraw(x, als)

# Nicer colors
cols = c(7, 3, 2, 4)
ibdDraw(x, als, cols = cols)

# Inside the pedigree symbols
ibdDraw(x, als, cols = cols, pos = 0, symbolsize = 2.5)

# Other placements (margins depend on device - may need adjustment)
ibdDraw(x, als, cols = cols, pos = c(2, 4, 1, 1),
        margin = c(2, 6, 2, 6))

# Letters instead of points
ibdDraw(x, als, cols = cols, symbol = "text", cex = 2)

# Further arguments (note that `col` is an argument of `ped.plot()`)
ibdDraw(x, als, cols = cols, pos = 0, symbolsize = 2,
        labs = TRUE, hatched = 3:4, col = "blue")

# Mutations are warned about (unless `checkParents = FALSE`)
ibdDraw(x, alleles = list(1:2, 3:4, 5, 6))


##############################
# Example 2: Cousin pedigree #
##############################

x = swapSex(cousinPed(1), 3)
als = list(1:2, 3:4, NULL, c(1,3), c(2,3), NULL, 3, 3)

cols = c(7, 3, 2, 4)
ibdDraw(x, als, cols = cols, dist = 0.8)
ibdDraw(x, als, cols = cols, dist = 0.8, symbol = "text")

# Alternative: 0's give greyed-out alleles
als2 = list(1:2, 3:4, c(0,0), c(1,3), c(2,3), c(0,0), c(0,3), c(3,0))

ibdDraw(x, als2, cols = cols, dist = 0.8)
ibdDraw(x, als2, cols = cols, dist = 0.8, symbol = "text")
```

```
############################
# Example 3: X inheritance #
############################

x = nuclearPed(2, sex = c(1, 2))
als = list(1, 2:3, 3, c(1, 3))
ibdDraw(x, als, cols = c(3, 7, 2))


################################
# Example 4: mtDNA inheritance  #
################################

x = linearPed(2, sex = 2)
als = list(1, 2, 2, 3, 2)
ibdDraw(x, als, cols = 2:4)


# Restore graphics parameters
par(op)
```

---

ibdTriangle *IBD triangle plot*

Description

The IBD triangle is typically used to visualize the pairwise relatedness of non-inbred individuals. Various annotations are available, including points marking the most common relationships, contour lines for the kinship coefficients, and shading of the unattainable region.

Usage

```
ibdTriangle(
  relationships = c("UN", "PO", "MZ", "S", "H,U,G", "FC"),
  pch = 16,
  cexPoint = 1.2,
  cexText = 1.2,
  kinshipLines = numeric(),
  shading = "lightgray",
  xlim = c(0, 1),
  ylim = c(0, 1),
  axes = FALSE,
  xlab = expression(kappa[0]),
  ylab = expression(kappa[2]),
  cexLab = cexText,
  mar = c(3.1, 3.1, 1, 1),
  xpd = TRUE,
```

```
  keep.par = TRUE
)
```

Arguments

relationships	A character vector indicating relationships points to be included in the plot. See Details for a list of valid entries.
pch	Symbol used for the relationship points (see par()).
cexPoint	A number controlling the symbol size for the relationship points.
cexText	A number controlling the font size for the relationship labels.
kinshipLines	A numeric vector (see Details).
shading	The shading colour for the unattainable region.
xlim, ylim, mar, xpd	Graphical parameters; see par().
axes	A logical: Draw surrounding axis box? Default: FALSE.
xlab, ylab	Axis labels.
cexLab	A number controlling the font size for the axis labels.
keep.par	A logical. If TRUE, the graphical parameters are not reset after plotting, which may be useful for adding additional annotation.

Details

For any pair of non-inbred individuals A and B, their genetic relationship can be summarized by the IBD coefficients $(\kappa_0, \kappa_1, \kappa_2)$, where κ_i = P(A and B share i alleles IBD at random autosomal locus). Since $\kappa_0 + \kappa_1 + \kappa_2 = 1$, any relationship corresponds to a point in the triangle in the (κ_0, κ_2)-plane defined by $\kappa_0 \geq 0, \kappa_2 \geq 0, \kappa_0 + \kappa_2 \leq 1$. The choice of κ_0 and κ_2 as the axis variables is done for reasons of symmetry and is not significant (other authors have used different views of the triangle).

As shown by Thompson (1976), points in the subset of the triangle defined by $4\kappa_0\kappa_2 > \kappa_1^2$ are unattainable for pairwise relationships. By default this region in shaded in a 'light grey' colour, but this can be modified with the shading argument.

The IBD coefficients are linearly related to the kinship coefficient ϕ by the formula

$$\phi = 0.25\kappa_1 + 0.5\kappa_2.$$

By indicating values for ϕ in the kinshipLines argument, the corresponding contour lines are shown as dashed lines in the triangle plot.

The following abbreviations are valid entries in the relationships argument:

- UN = unrelated
- PO = parent/offspring
- MZ = monozygotic twins
- S = full siblings
- H,U,G = half sibling/avuncular (**u**ncle)/grandparent
- FC = first cousins
- SC = second cousins
- DFC = double first cousins
- Q = quadruple first half cousins

Value

None

Author(s)

Magnus Dehli Vigeland

References

- E. A. Thompson (1975). *The estimation of pairwise relationships.* Annals of Human Genetics 39.
- E. A. Thompson (1976). *A restriction on the space of genetic relationships.* Annals of Human Genetics 40.

Examples

```
opar = par(no.readonly = TRUE) # store graphical parameters

ibdTriangle()
ibdTriangle(kinshipLines = c(0.25, 0.125), shading = NULL, cexText = 0.8)

par(opar) # reset graphical parameters
```

---

identityCoefs *Omnibus function for identity coefficients*

Description

This function calculates the pairwise identity coefficients described by Jacquard (1974). Unlike the previous `condensedIdentity()` (which will continue to exist), this function also computes the 15 *detailed* identity coefficients. The implementation supports pedigrees with inbred founders, and X-chromosomal coefficients.

Usage

```
identityCoefs(
  x,
  ids = labels(x),
  detailed = FALSE,
  Xchrom = FALSE,
  self = FALSE,
  simplify = TRUE,
  method = c("auto", "K", "WL", "LS", "GC", "idcoefs", "identity", "merlin"),
  verbose = FALSE,
  ...
)

detailed2condensed(d)
```

Arguments

x	A pedigree in the form of a pedtools::ped object.
ids	A vector of two ID labels.
detailed	A logical. If FALSE (default), the 9 condensed coefficients are computed; otherwise the 15 detailed identity coefficients.
Xchrom	A logical, by default FALSE.
self	A logical indicating if self-relationships (i.e., between a pedigree member and itself) should be included. FALSE by default.
simplify	Simplify the output (to a numeric of length 9) if ids has length 2. Default: TRUE.
method	Either "auto", "K", "WL", "LS", "GC", "idcoefs", "identity" or "merlin". By default ("auto") a suitable algorithm is chosen automatically.
verbose	A logical.
...	Further arguments.
d	Either a numeric vector of length 15, or a data frame with 17 columns.

Details

Both the condensed and detailed coefficients are given in the orders used by Jacquard (1974). The function detailed2condensed() converts from detailed coefficients (d1, ..., d15) to condensed ones (D1, ..., D9) using the following relations:

- D1 = d1
- D2 = d6
- D3 = d2 + d3
- D4 = d7
- D5 = d4 + d5
- D6 = d8
- D7 = d9 + d12
- D8 = d10 + d11 + d13 + d14
- D9 = d15

Algorithms for computing identity coefficients:

The following is a brief overview of various algorithms for computing (single-locus) condensed and/or detailed identity coefficients. This topic is closely linked to that of *generalised kinship coefficients*, which is further described in the documentation of gKinship().

For each algorithm below, it is indicated in brackets how to enforce it in identityCoefs().

- Karigl (1981) gave the first recursive algorithm for the 9 condensed identity coefficients. [method = "K"]
- Weeks & Lange (1988) suggested a broader and more natural generalisation of kinship coefficients, leading to a slightly different algorithm for condensed coefficients. [method = "WL"]

- Lange & Sinsheimer (1992) described an even further generalisation of kinship coefficients, allowing a mix of deterministic and random sampling of alleles. They used this to give (i) an alternative algorithm for the 9 condensed identity coefficients, and (ii) an algorithm for the 15 detailed coefficients. [`method = "LS"`]
- The C program `IdCoefs` (version 2.1.1) by Mark Abney (2009) uses a graph model to obtain very fast computation of condensed identity coefficients. This requires `IdCoefs` to be installed on the computer (see link under References) and available on the system search path. The function then writes the necessary files to disk and calls `IdCoefs` via `system()`. [`method = "idcoefs"`]
- The R package `identity` provides an R interface for `IdCoefs`, avoiding calls to `system()`. [`method = "identity"`]
- The MERLIN software (Abecasis et al, 2002) offers an option "–extended" for computing detailed identity coefficients. This option requires MERLIN to be installed on the system. The function then writes the necessary files to disk and calls MERLIN via `system()`. If `detailed = FALSE`, the coefficients are transformed with `detailed2condensed()` before returning. Note: MERLIN rounds all numbers to 3 decimal places. Since this rounding is done on the detailed coefficients, rounding errors may happen when converting to the condensed ones. [`method = "merlin"`]

Value

A data frame with L + 2 columns, where L is either 9 or 15 (if `detailed = TRUE`).

If `simplify = TRUE` and `length(ids) = 2`: A numeric vector of length `L`.

References

- Jacquard, A. (1974). The Genetic Structure of Populations. Springer.
- Karigl, G. (1981). A recursive algorithm for the calculation of identity coefficients. Ann. Hum. Genet.
- Weeks, D.E. & Lange, K. (1988). The affected-pedigree-member method of linkage analysis. Am. J. Hum. Genet
- Lange, K. & Sinsheimer, J.s. (1992). Calculation of genetic identity coefficients. Ann. Hum. Genet.
- Abney, M. (2009). A graphical algorithm for fast computation of identity coefficients and generalized kinship coefficients. Bioinformatics, 25, 1561-1563. https://home.uchicago.edu/~abney/abney_web/Software.html

See Also

`condensedIdentity()`, `gKinship()`

Examples

```
x = fullSibMating(1)

### Condensed coefficients
j1 = identityCoefs(x, method = "K")
j2 = identityCoefs(x, method = "WL")
```

```
j3 = identityCoefs(x, method = "LS")
j4 = identityCoefs(x, method = "GC")
j5 = condensedIdentity(x, ids = 1:6) # legacy version

stopifnot(all.equal(j1,j2), all.equal(j1,j3), all.equal(j1,j4), all.equal(j1,j5))

### Detailed coefficients
jdet1 = identityCoefs(x, detailed = TRUE, method = "LS")
jdet2 = identityCoefs(x, detailed = TRUE, method = "GC")

stopifnot(all.equal(jdet1,jdet2))

### X-chromosomal coefficients
jx1 = identityCoefs(x, Xchrom = TRUE, method = "K")
jx2 = identityCoefs(x, Xchrom = TRUE, method = "GC")
jx3 = condensedIdentityX(x, ids = 1:6)  # legacy version

stopifnot(all.equal(jx1,jx2), all.equal(jx1,jx3))

### Detailed X-chromosomal coefficients
jdx = identityCoefs(x, detailed = TRUE, Xchrom = TRUE, method = "GC")

stopifnot(all.equal(detailed2condensed(jdx), jx1))
```

`inbreeding` *Inbreeding coefficients*

Description

Compute the inbreeding coefficients of all members of a pedigree. Both autosomal and X-chromosomal coefficients are supported. This function is a simple wrapper of `kinship()`. Note that pedigree founders are allowed to be inbred; see `pedtools::founderInbreeding()` for how to set this up, and see Examples below.

Usage

```
inbreeding(x, ids = NULL, Xchrom = FALSE)

inbreedingX(x, ids = NULL)
```

Arguments

`x`	A pedigree in the form of a ped object, or a list of such.
`ids`	A vector of ID labels, or NULL (default).
`Xchrom`	A logical, indicating if the autosomal (default) or X-chromosomal inbreeding coefficients should be computed.

Details

The autosomal inbreeding coefficient of a pedigree member is defined as the probability that, at a random autosomal locus, the two alleles carried by the member are identical by descent relative to the pedigree. It follows from the definition that the inbreeding coefficient of a non-founder equals the kinship coefficient of the parents.

The implementation here uses `kinship()` to compute the kinship matrix, and computes the inbreeding coefficients from the diagonal, by the formula

$$f_a = 2 * \phi_{aa} - 1.$$

The X chromosomal inbreeding coefficient of females are defined (and computed) similarly to the autosomal case above. For males is it always defined as 1.

Value

If `ids` has length 1, the inbreeding coefficient of this individual is returned as a single unnamed number.

Otherwise, the output is a named numeric vector containing the inbreeding coefficients of the indicated pedigree members (if `ids = NULL`: all).

See Also

`kinship()`

Examples

```
# Child of half siblings: f = 1/8
x = halfCousinPed(0, child = TRUE)

# Inbreeding vector
inbreeding(x)

# Simpler output using the `ids` argument:
inbreeding(x, ids = 6)


### X-chromosomal inbreeding ###

# Males have inbreeding coefficient 1
stopifnot(inbreeding(x, ids = 6, Xchrom = TRUE) == 1)

y1 = swapSex(x, ids = 6)  # female child
stopifnot(inbreeding(y1, ids = 6, Xchrom = TRUE) == 0)

y2 = swapSex(y1, ids = 2) # female ancestor
stopifnot(inbreeding(y2, ids = 6, Xchrom = TRUE) == 0.25)


### Inbred founder ###
```

```
# Mother 100% inbred
founderInbreeding(x, ids = 2) = 1

inbreeding(x)


# Example with selfing and complete inbreeding
s = selfingPed(1)
founderInbreeding(s, 1) = 1
stopifnot(inbreeding(s, ids = 2) == 1)
```

`jicaque` *Jicaque pedigree*

Description

A data frame describing a pedigree from the Jicaque tribe, studied by Chapman and Jacquard (1971).

Usage

```
jicaque
```

Format

A data frame with 22 rows and four columns:

- `id` : individual ID
- `fid` : father's ID (or 0 if not included)
- `mid` : mother's ID (or 0 if not included)
- `sex` : Gender codes, where 1 = male and 2 = female

References

Chapman, A.M and Jacquard, A. (1971). Un isolat d'Amerique Centrale: les Indiens Jicaques de Honduras. In Genetique et Population. Paris: Presses Universitaires de France.

kappaIBD *IBD (kappa) coefficients*

Description

Computes the three IBD coefficients summarising the relationship between two non-inbred individuals. Both autosomal and X chromosomal versions are implemented. The pedigree founders (other than the individuals in question) are allowed to be inbred; see `pedtools::founderInbreeding()` for how to set this up, and see Examples below.

Usage

```
kappaIBD(x, ids = labels(x), inbredAction = 1, simplify = TRUE, Xchrom = FALSE)
```

Arguments

`x`	A pedigree in the form of a ped object (or a list of such).
`ids`	A character (or coercible to character) containing ID labels of two or more pedigree members.
`inbredAction`	An integer telling the program what to do if either of the `ids` individuals are inbred. Possible values are: 0 = do nothing; 1 = print a warning message (default); 2 = raise an error. In the first two cases the coefficients are reported as `NA`.
`simplify`	Simplify the output (to a numeric of length 3) if `ids` has length 2. Default: TRUE.
`Xchrom`	A logical, indicating if the autosomal (default) or X-chromosomal kappa coefficients should be computed.

Details

For non-inbred individuals a and b, their autosomal IBD coefficients $(\kappa 0, \kappa 1, \kappa 2)$ are defined as follows:

$$\kappa_i = P(aandbshareexactlyiallelesIBDatarandomautosomallocus)$$

The autosomal kappa coefficients are computed from the kinship coefficients. When a and b are both nonfounders, the following formulas hold:

- $\kappa 2 = \phi_M M * \phi_F F + \phi_M F * \phi_F M$
- $\kappa 1 = 4 * \phi_a b - 2 * \kappa 2$
- $\kappa 0 = 1 - \kappa 1 - \kappa 2$

Here $\phi_M M$ denotes the kinship coefficient between the mothers of a and b, and so on. If either a or b is a founder, then $\kappa 2 = 0$, while the other two formulas remain as above.

The X-chromosomal IBD coefficients are defined similarly to the autosomal case. Here $\kappa 2$ is undefined when one or both individuals are male, which greatly simplifies the calculations when males are involved. The formulas are (with $\phi_a b$ referring to the X-chromosomal kinship coefficient):

- Both male: $(\kappa 0, \kappa 1, \kappa 2) = (1 - \phi_a b, \phi_a b, NA)$
- One male, one female: $(\kappa 0, \kappa 1, \kappa 2) = (1 - 2 * \phi_a b, 2 * \phi_a b, NA)$
- Two females: Similar formulas as in the autosomal case.

Value

If `ids` has length 2 and `simplify = TRUE`: A numeric vector of length 3: $(\kappa 0, \kappa 1, \kappa 2)$.

Otherwise: A data frame with one row for each pair of individuals, and 5 columns. The first two columns contain the ID labels, and columns 3-5 contain the IBD coefficients.

Unless `inbredAction = 2`, the coefficients of pairs involving inbred individuals (X-inbred females if `Xchrom = T`) are reported as NA. Furthermore, the X-chromosomal $\kappa 2$ is NA whenever at least one of the two individuals is male.

See Also

`kinship()`, `identityCoefs()`

Examples

```
### Siblings
x = nuclearPed(2)
kappaIBD(x)

k = kappaIBD(x, 3:4)
stopifnot(identical(k, c(.25, .5, .25)))

### Quad half first cousins
x = quadHalfFirstCousins()
k = kappaIBD(x, ids = leaves(x))
stopifnot(identical(k, c(17/32, 14/32, 1/32)))

### Paternal half brothers with 100% inbred father
# Genetically indistinguishable from an (outbred) father-son relationship
x = halfSibPed()
ids = 4:5

# Set founder inbreeding
fou = commonAncestors(x, ids) # robust to label change
founderInbreeding(x, fou) = 1

k = kappaIBD(x, ids)
stopifnot(identical(k, c(0, 1, 0)))

### X-chromosomal kappa
y = nuclearPed(2, sex = 2)
kappaIBD(y, Xchrom = TRUE)
```

`kin2deg` *Degree of relationship*

Description

Converts a vector of kinship coefficients to "degrees of relationship", as used by some software for relatedness inference (e.g. KING).

Usage

```
kin2deg(kin, unrelated = Inf)
```

Arguments

`kin`	A vector of kinship coefficients, i.e., numbers in `[0, 1]`.
`unrelated`	The conversion of unrelated individuals (`kin = 0`). Mathematically this corresponds to `degree = Inf`, but in some situations `degree = NA` or something else might be preferable.

Details

The implementation uses the conversion formula

$$deg = round(-log2(kin) - 1).$$

The first degrees correspond to the following approximate kinship ranges:

- `[0.354, 1]`: 0th degree (MZ twins or duplicates)
- `[0.177, 0.354)`: 1st degree (parent-offspring, full siblings)
- `[0.0884, 0.177)`: 2nd degree (half sibs, grandparent-grandchild, avuncular)
- `[0.0442, 0.0884)` 3rd degree (half-avuncular, first cousins, great-grandparent etc)

Value

An integer vector of the same length as `kin`.

References

KING manual with thresholds for relationship degrees: https://www.kingrelatedness.com/manual.shtml

See Also

`kinship()`, `coeffTable()`

Examples

```
x = cousinPed(1)

# Kinship matrix
k = kinship(x)

# Degrees
deg = kin2deg(k)
deg

# First cousins are 3rd degree
stopifnot(deg['7', '8'] == 3)
```

---

kinship *Kinship coefficients*

Description

Compute the matrix of kinship coefficients of all members of a pedigree. Both autosomal and X-chromosomal versions are supported. The pedigree founders are allowed to be inbred; see `pedtools::founderInbreeding()` for how to set this up, and see Examples below.

Usage

```
kinship(x, ids = NULL, Xchrom = FALSE)

kinshipX(x, ids = NULL)
```

Arguments

`x`	A ped object or a list of such.
`ids`	Either NULL (default), or a vector of length 2, containing the IDs of two (possibly equal) members of `x`.
`Xchrom`	A logical, indicating if the autosomal (default) or X-chromosomal kinship coefficients should be computed.

Details

For two (possibly equal) members A, B of a pedigree, their autosomal (resp. X-chromosomal) *kinship coefficient* is defined as the probability that a random allele from A and a random allele from B, sampled at the same autosomal (resp. X-chromosomal) locus, are identical by descent relative to the pedigree.

Value

If `ids = NULL`, a symmetric matrix containing all pairwise kinship coefficients in `x`. If `ids` has length 2, the function returns a single number.

See Also

inbreeding(), kappa()

Examples

```
# Kinship coefficients in a nuclear family with two children
x = nuclearPed(2)
kinship(x)

# X chromosomal kinship coefficients in the same family
kinship(x, Xchrom = TRUE)

# Autosomal kinships if the mother is 100% inbred
founderInbreeding(x, 2) = 1
kinship(x)

# Similar for X:
founderInbreeding(x, 2, chromType = "X") = 1
kinship(x, Xchrom = TRUE)
```

---

minimalPattern *Minimal IBD pattern*

Description

Compute the minimal form of given multiperson IBD pattern.

Usage

```
minimalPattern(x)
```

Arguments

x	An integer vector of even length.

Value

An integer vector of the same length as x.

Examples

```
v = c(1,2,2,3)
stopifnot(identical(minimalPattern(v), c(1,2,1,3)))
```

`multiPersonIBD` *Multi-person IBD coefficients*

Description

Computes the probabilities (coefficients) of all possible patterns of identity by descent (IBD) sharing at a single locus, among N>1 non-inbred members of a pedigree. The reported coefficients are "condensed" in the sense that allele ordering within each individual is ignored. For N = 2, the result should agree with the traditional "kappa" coefficients, as computed by `kappaIBD()`. This function is under development, and should be regarded as experimental. For now, the only cases handled are those with: N = 2 or 3, autosomal locus.

Usage

```
multiPersonIBD(x, ids, complete = FALSE, verbose = FALSE)
```

Arguments

`x`	A ped object.
`ids`	A vector of ID labels.
`complete`	A logical. If FALSE, only IBD patterns with nonzero probability are included in the output.
`verbose`	A logical. If TRUE, some computational details are printed.

Details

Consider N members of a pedigree, i1, i2, ... iN. A pattern of IBD sharing between these individuals is a sequence of N ordered pairs of labels, (a1_1, a1_2), (a2_1, a2_2), ... (aN_1, aN_2), where ai_1 and ai_2 represent the paternal and maternal allele of individual i, respectively. Equality of labels means that the corresponding alleles are IBD, and vice versa.

We say that two IBD patterns are equivalent if one can be transformed into the other by some combination of

- renaming the labels (without changing the structure)
- swapping the paternal/maternal labels of some individuals

Each equivalence class has a "minimal" element, using integer labels, and being minimal with respect to standard sorting. For example, the minimal element equivalent to `(a,c),(d,c),(b,b)` is `(1,2),(2,3),(4,4)`.

Value

A data frame in which each row corresponds to an equivalence class of multi-person IBD patterns. The first column gives the calculated probability, followed by one column for each `ids` individual, describing the minimal element of the equivalence class. (See Details.) If `complete = FALSE` (the default) rows with probability 0 are removed.

Examples

```
### Trivial example: Trio ###
x = nuclearPed(1)
ids = 1:3
multiPersonIBD(x, ids, complete = TRUE)

### Example due to Peter Green ###
# Three (pariwise) cousins arranged in two different ways,
# with different 3-way IBD coefficients.

threeCousins1 = ped(
  id  = c('gf','gm','gf1','gf2','gf3','gm1','gm2','gm3',
          'f1','f2','f3','m1','m2','m3','c1','c2','c3'),
  fid = c(0,0,0,0,0,0,0,0,'gf1','gf2','gf3','gf','gf','gf',
          'f1','f2','f3'),
  mid = c(0,0,0,0,0,0,0,0,'gm1','gm2','gm3','gm','gm','gm',
          'm1','m2','m3'),
  sex = c(1,2,1,1,1,2,2,2,1,1,1,2,2,2,1,1,1))

threeCousins2 = ped(
  id  = c('gf1','gf2','gf3','gm1','gm2','gm3','f1','f2','f3',
          'm1','m2','m3','c1','c2','c3'),
  fid = c(0,0,0,0,0,0,'gf2','gf3','gf1','gf3','gf1','gf2',
          'f1','f2','f3'),
  mid = c(0,0,0,0,0,0,'gm2','gm3','gm1','gm3','gm1','gm2',
          'm1','m2','m3'),
  sex = c(1,1,1,2,2,2,1,1,1,2,2,2,1,1,1))

ids = c('c1','c2','c3')
multiPersonIBD(threeCousins1, ids)
multiPersonIBD(threeCousins2, ids)
```

`realisedIbdVariance` *Variance of realised relatedness coefficients*

Description

Compute the variance of realised relatedness coefficients, by doubly integrating the corresponding two-locus coefficients.

Usage

```
realisedIbdVariance(x, ids = leaves(x), coeff, L = 1)
```

Arguments

`x`	A ped object.
`ids`	A vector naming two members of `x`.

coeff	A string naming a coefficient for which the variance is to be computed. See Details for legal values.
L	A positive number; the chromosome length in Morgan.

Details

The double integral method was used by Guo to compute the variation in proportion of the genome shared IBD (Guo 1995, see also Thompson 2013). The method extends directly to other coefficients. The implementation here supports Cotterman's kappa coefficients (of noninbred individuals), and Jacquard's condensed identity coefficients.

This function is a bare-bones implementation of the double integral method, based on `stats::integrate`, and can probably be optimised in various ways.

The `coeff` parameter must be either a character naming the coefficient to compute, or a function. If a character, it must be one of the following names:

- "inb" (inbreeding coefficient)
- "kinship", "phi" (synonyms for the kinship coefficient)
- "k0", "k1", "k2" (kappa coefficients of noninbred individuals)
- "D1", "D2", ... "D9" (condensed identity coefficients)

Value

A positive number.

References

- Guo (1995) *Proportion of genome shared identical by descent by relatives: concept, computation, and applications*. Am J Hum Genet.
- Hill & Weir (2011). *Variation in actual relationship as a consequence of Mendelian sampling and linkage*. Genet Res.
- Thompson (2013). *Identity by Descent: Variation in Meiosis, Across Genomes, and in Populations*. Genetics.

Examples

```
###################################
### Box 1 of Hill & Weir (2011) ###
###################################

# Eq. 4b of Hill & Weir
phi = function(n, l) {
 1/(2*l^2) * (1/4)^n * sum(sapply(1:n, function(r)
   choose(n, r) * (2*r*l - 1 + exp(-2*r*l))/r^2))
}

# Chromosome of 1 Morgan
L = 1
```

```
### Full sibs ###

x = nuclearPed(2)
realisedIbdVariance(x, ids = 3:4, coeff = "k2", L = L)

# Hill & Weir (Box 1)
16*phi(4,L) - 16*phi(3,L) + 8*phi(2,L) - 2*phi(1,L)


### Double first cousins ###

## Not run:
dfc = doubleFirstCousins()

# Runtime ~1 min
realisedIbdVariance(dfc, coeff = "k0", L = L)
realisedIbdVariance(dfc, coeff = "k1", L = L)
realisedIbdVariance(dfc, coeff = "k2", L = L)

# Hill & Weir, Box 1
var_k2 = 64*phi(8,L) - 64*phi(7,L) + 40*phi(6,L) - 20*phi(5,L) +
 33/4*phi(4,L) - 5/2*phi(3,L) + 5/8*phi(2,L)-1/8*phi(1,L)
var_k1 = 4*var_k2
var_k0 = var_k2 + 2 * (4*phi(4,L) - 2*phi(3,L) + 3/4*phi(2,L) - 1/4*phi(1,L))

var_k0
var_k1
var_k2


## End(Not run)
```

`ribd` *ribd: Computation of pedigree-based relatedness coefficients*

Description

Recursive algorithms for computing various relatedness coefficients, including Jacquard's condensed identity coefficients. The standard algorithms are extended to allow inbred founders. Both autosomal and X-linked coefficients are computed.

`showInTriangle` *Add points to the IBD triangle*

Description

Utility function for plotting points in the IBD triangle.

Usage

```
showInTriangle(
  kappa,
  new = TRUE,
  col = 6,
  cex = 1,
  pch = 4,
  lwd = 2,
  labels = FALSE,
  colLab = col,
  cexLab = 0.8,
  pos = 1,
  adj = NULL,
  keep.par = TRUE,
  ...
)
```

Arguments

`kappa`	Coordinates of points to be plotted in the IBD triangle. Valid input types are: • A numerical vector of length 2 or 3. In the latter case `kappa[c(1, 3)]` is used. • A matrix of data frame, whose column names must include either `k0` and `k2`, `kappa0` and `kappa2`, or `ibd0` and `ibd2`. • A list (and not a data frame), in which case an attempt is made to bind the elements row-wise.
`new`	A logical indicating if a new triangle should be drawn.
`col, cex, pch, lwd`	Parameters passed onto `points()`.
`labels`	A character of same length as the number of points, or a single logical `TRUE` or `FALSE`. If `TRUE`, an attempt is made to create labels by pasting columns `ID1` and `ID2` in `kappa`, if these exist. By default, no labels are plotted.
`colLab, cexLab, pos, adj`	Parameters passed onto `text()` (if `labels` is non-NULL).
`keep.par`	A logical. If TRUE, the graphical parameters are not reset after plotting, which may be useful for adding additional annotation.
`...`	Plot arguments passed on to `ibdTriangle()`.

Value

None

Author(s)

Magnus Dehli Vigeland

Examples

```
showInTriangle(c(3/8, 1/8), label = "3/4 siblings", pos = 1)
```

`twoLocusIBD` *Two-locus IBD coefficients*

Description

Computes the 3*3 matrix of two-locus IBD coefficients of a pair of non-inbred pedigree members, for a given recombination rate.

Usage

```
twoLocusIBD(
  x,
  ids,
  rho,
  coefs = NULL,
  detailed = FALSE,
  uniMethod = 1,
  verbose = FALSE
)
```

Arguments

`x`	A pedigree in the form of a `pedtools::ped` object.
`ids`	A character (or coercible to character) containing ID labels of two pedigree members.
`rho`	A number in the interval $[0, 0.5]$; the recombination rate between the two loci.
`coefs`	A character indicating which coefficient(s) to compute. A subset of `c('k00', 'k01', 'k02', 'k10', 'k11', 'k12', 'k20', 'k21', 'k22')`. By default, all coefficients are computed.
`detailed`	A logical, indicating whether the condensed (default) or detailed coefficients should be returned.
`uniMethod`	Either 1 or 2 (for testing purposes)
`verbose`	A logical.

Details

Let A, B be two pedigree members, and L1, L2 two loci with a given recombination rate ρ. The two-locus IBD coefficients $\kappa_{i,j}(\rho)$, for $0 \leq i, j \leq 2$ are defined as the probability that A and B have `i` alleles IBD at L1 and `j` alleles IBD at L2 simultaneously. Note that IBD alleles at the two loci are not required to be *in cis* (or *in trans* for that matter).

The method of computation depends on the (single-locus) IBD coefficient κ_2. If this is zero (e.g. if A is a direct ancestor of B, or vice versa) the two-locus IBD coefficients are easily computable from the two-locus kinship coefficients, as implemented in `twoLocusKinship()`. In the general case, the computation is more involved, requiring *generalised two-locus kinship* coefficients. This is implemented in the function `twoLocusGeneralisedKinship()`, which is not exported yet.

Value

By default, a symmetric 3*3 matrix containing the two-locus IBD coefficients $\kappa_{i,j}$.

If either `coefs` is explicitly given (i.e., not NULL), or `detailed = TRUE`, the computed coefficients are returned as a named vector.

See Also

`twoLocusKinship()`, `twoLocusIdentity()`, `twoLocusPlot()`

Examples

```
# Plot title used in several examples below
main = expression(paste("Two-locus IBD:  ", kappa[`1,1`]))

######################################################################
# Example 1: A classic example of three relationships with the same
# one-locus IBD coefficients, but different two-locus coefficients.
# As a consequence, these relationships cannot be separated using
# unlinked markers, but are (theoretically) separable with linked
# markers.
######################################################################
peds = list(
    GrandParent = list(ped = linearPed(2),   ids = c(1, 5)),
    HalfSib     = list(ped = halfSibPed(),   ids = c(4, 5)),
    Uncle       = list(ped = avuncularPed(), ids = c(3, 6)))

twoLocusPlot(peds, coeff = "k11", main = main, lty = 1:3, col = 1)


############################################################
# Example 2: Inspired by Fig. 3 in Thompson (1988),
# and its erratum: https://doi.org/10.1093/imammb/6.1.1.
#
# These relationships are also analysed in ?twoLocusKinship,
# where we show that they have identical two-locus kinship
# coefficients. Here we demonstrate that they have different
# two-locus IBD coefficients.
############################################################

peds = list(
  GreatGrand = list(ped = linearPed(3),              ids = c(1, 7)),
  HalfUncle  = list(ped = avuncularPed(half = TRUE), ids = c(4, 7))
)

twoLocusPlot(peds, coeff = "k11", main = main, lty = 1:2, col = 1)
```

```
#########################################################################
# Example 3: Fig. 15 of Vigeland (2021).
# Two-locus IBD of two half sisters whose mother have inbreeding
# coefficient 1/4. We compare two different realisations of this:
#   PO: the mother is the child of parent-offspring
#  SIB: the mother is the child of full siblings
#
# The fact that these relationships have different two-locus coefficients
# exemplifies that a single-locus inbreeding coefficient cannot replace
# the genealogy in analyses of linked loci.
#########################################################################

po = addChildren(nuclearPed(1, sex = 2), 1, 3, nch = 1, sex = 2)
po = addDaughter(addDaughter(po, 4), 4)

sib = addChildren(nuclearPed(2, sex = 1:2), 3, 4, nch = 1)
sib = addDaughter(addDaughter(sib, 5), 5)

# plotPedList(list(po, sib), new = TRUE, title = c("PO", "SIB"))

# List of pedigrees and ID pairs
peds = list(PO =  list(ped = po,  ids = leaves(po)),
            SIB = list(ped = sib, ids = leaves(sib)))

twoLocusPlot(peds, coeff = "k11", main = main, lty = 1:2, col = 1)


### Check against exact formulas
rho = seq(0, 0.5, length = 11)  # recombination values

kvals = sapply(peds, function(x)
  sapply(rho, function(r) twoLocusIBD(x$ped, x$ids, r, coefs = "k11")))

k11.po = 1/8*(-4*rho^5 + 12*rho^4 - 16*rho^3 + 16*rho^2 - 9*rho + 5)
stopifnot(all.equal(kvals[, "PO"], k11.po, check.names = FALSE))

k11.s = 1/16*(8*rho^6 - 32*rho^5 + 58*rho^4 - 58*rho^3 + 43*rho^2 - 20*rho + 10)
stopifnot(all.equal(kvals[, "SIB"], k11.s, check.names = FALSE))


#################################################
# Example 4:
# The complete two-locus IBD matrix of full sibs
#################################################

x = nuclearPed(2)
k2_mat = twoLocusIBD(x, ids = 3:4, rho = 0.25)
k2_mat

### Compare with exact formulas
IBDSibs = function(rho) {
```

```
  R = rho^2 + (1-rho)^2
  nms = c("ibd0", "ibd1", "ibd2")
  m = matrix(0, nrow = 3, ncol = 3, dimnames = list(nms, nms))
  m[1,1] = m[3,3] = 0.25 *R^2
  m[2,1] = m[1,2] = 0.5 * R * (1-R)
  m[3,1] = m[1,3] = 0.25 * (1-R)^2
  m[2,2] = 0.5 * (1 - 2 * R * (1-R))
  m[3,2] = m[2,3] = 0.5 * R * (1-R)
  m
}

stopifnot(all.equal(k2_mat, IBDSibs(0.25)))


######################################################
# Example 5: Two-locus IBD of quad half first cousins
#
# We use this to exemplify two simple properties of
# the two-locus IBD matrix.
######################################################

x = quadHalfFirstCousins()
ids = leaves(x)

# First compute the one-locus IBD coefficients (= c(17, 14, 1)/32)
k1 = kappaIBD(x, ids)

### Case 1: Complete linkage (`rho = 0`).
# In this case the two-locus IBD matrix has `k1` on the diagonal,
# and 0's everywhere else.
k2_mat_0 = twoLocusIBD(x, ids = ids, rho = 0)

stopifnot(all.equal(k2_mat_0, diag(k1), check.attributes = FALSE))

#' ### Case 2: Unlinked loci (`rho = 0.5`).
# In this case the two-locus IBD matrix is the outer product of
# `k1` with itself.
k2_mat_0.5 = twoLocusIBD(x, ids = ids, rho = 0.5)
stopifnot(all.equal(k2_mat_0.5, k1 %o% k1, check.attributes = FALSE))


#########################################################
# Example 6: By Donnelly (1983) these relationships are
# genetically indistinguishable
#########################################################

x1 = halfCousinPed(1)
x2 = halfCousinPed(0, removal = 2)
stopifnot(identical(
  twoLocusIBD(x1, ids = leaves(x1), rho = 0.25),
  twoLocusIBD(x2, ids = leaves(x2), rho = 0.25)))
```

```
############################################################
# Example 7: Detailed coefficients of double first cousins.
# Compare with exact formulas by Denniston (1975).
############################################################

x = doubleFirstCousins()
ids = leaves(x)
rho = 0.25

kapDetailed = twoLocusIBD(x, ids, rho, detailed = TRUE)

# Example 1 of Denniston (1975)
denn = function(rho) {
  F = (1-rho)^2 * (rho^2 + (1-rho)^2)/4 + rho^2/8
  U = 1 + 2*F
  V = 1 - 4*F

  # Note that some of Denniston's definitions differ slightly;
  # some coefficients must be multiplied with 2
  c(k00 = U^2/4,
    k01 = U*V/8  *2,
    k02 = V^2/16,
    k10 = U*V/8  *2,
    k11.cc = F*U/2  *2,
    k11.ct = 0,
    k11.tc = 0,
    k11.tt = V^2/16  *2,
    k12.h = F*V/4  *2,
    k12.r = 0,
    k20 = V^2/16,
    k21.h = F*V/4  *2,
    k21.r = 0,
    k22.h = F^2,
    k22.r = 0)
}

stopifnot(all.equal(kapDetailed, denn(rho)))
```

`twoLocusIdentity` *Two-locus identity coefficients*

Description

Computes the 9*9 matrix of two-locus condensed identity coefficients of a pair of pedigree members, for a given recombination rate.

Usage

```
twoLocusIdentity(x, ids, rho, coefs = NULL, detailed = FALSE, verbose = FALSE)
```

Arguments

x	A pedigree in the form of a pedtools::ped object.
ids	A character (or coercible to character) containing ID labels of two pedigree members.
rho	A number in the interval $[0, 0.5]$; the recombination rate between the two loci.
coefs	A character indicating which coefficient(s) to compute. A subset of c('D00', 'D01', ..., 'D99'). By default, all coefficients are computed.
detailed	A logical, indicating whether the condensed (default) or detailed coefficients should be returned.
verbose	A logical.

Details

Let A, B be two pedigree members, and L1, L2 two loci with a given recombination rate ρ. The two-locus identity coefficient $\Delta_{i,j}(\rho)$, for $1 \leq i, j \leq 9$ is defined as the probability that the identity state of the alleles of A and B are Σ_i at L1 and Σ_j at L2 simultaneously. (The ordering of the 9 states follows Jacquard (1974).)

For details about the algorithm, see Vigeland (2022).

Value

By default, a symmetric 9*9 matrix containing the two-locus condensed identity coefficients $\Delta_{i,j}$.

If either coefs is explicitly given (i.e., not NULL), or detailed = TRUE, the computed coefficients are returned as a named vector.

References

- Jacquard (1974). The Genetic Structure of Populations. Springer.
- Vigeland (2022) *Two-locus identity coefficients in pedigrees* (In progress)

See Also

twoLocusIBD(), identityCoefs()

Examples

```
### Full sibs ###
x = nuclearPed(2)
kapp = twoLocusIBD(x, ids = 3:4, rho = 0.25)
jacq = twoLocusIdentity(x, ids = 3:4, rho = 0.25)

stopifnot(all.equal(jacq[9:7,9:7], kapp, check.attributes = FALSE))

### Parent-child ###
x = nuclearPed(1)
jacq = twoLocusIdentity(x, ids = c(1,3), rho = 0.25)
```

```
stopifnot(jacq[8,8] == 1)

### Full sib mating ###
x = fullSibMating(1)
j = condensedIdentity(x, ids = 5:6)
j2 = twoLocusIdentity(x, ids = 5:6, rho = 0.25)

stopifnot(identical(unname(rowSums(j2)), j))
```

`twoLocusInbreeding` *Two-locus inbreeding*

Description

Computes the two-locus inbreeding coefficient of a pedigree member, for a given recombination rate.

Usage

```
twoLocusInbreeding(x, id, rho, verbose = FALSE, debug = FALSE)
```

Arguments

`x`	A pedigree in the form of a `pedtools::ped` object.
`id`	The ID label of a pedigree member.
`rho`	A numeric vector of recombination rates; all entries must be in the interval $[0, 0.5]$.
`verbose`	A logical.
`debug`	A logical. If TRUE, detailed messages are printed during the recursion process.

Details

Let A be a pedigree member, and L1, L2 two autosomal loci with recombination rate ρ. The two-locus inbreeding coefficient $f_{11}(\rho)$ is defined as the probability that A is autozygous at both L1 and L2 simultaneously.

As in the one-locus case, the two-locus inbreeding coefficient of A equals the two-locus kinship coefficient of the parents.

References

Weir & Cockerham (1969). *Pedigree mating with two linked loci*. Genetics, 61:923-940.

See Also

`twoLocusKinship()`, `twoLocusIBD()`, `twoLocusIdentity()`

Examples

```
#####################################################
# Reproducing an example of Weir & Cockerham (1969)
#####################################################

# Pedigree
x = nuclearPed(2, sex = 1:2) |>
  addDaughter(3:4) |>
  addSon(c(3,5)) |>
  addDaughter(5:6) |>
  relabel(new = strsplit("GHDECBA","")[[1]])

plot(x)

# The two-locus inbreeding of A
twoLocusPlot(list(ped = x, ids = "A"), coeff = "inb")

# W&C formula (expressed by linkage parameter a = 1-2*rho)
rho = seq(0, 0.5, length = 11)
a = 1 - 2*rho
WC = (128 + 10*a + 36*a^2 + 47*a^3 + 20*a^4 + 10*a^5 + 4*a^6 + a^7)/512

points(rho, WC, col = 2)
```

---

twoLocusKinship *Two-locus kinship coefficients*

Description

Computes the two-locus kinship coefficient of a pair of pedigree members, at a given recombination rate.

Usage

```
twoLocusKinship(
  x,
  ids,
  rho,
  recombinants = NULL,
  verbose = FALSE,
  debug = FALSE
)
```

Arguments

x	A pedigree in the form of a `pedtools::ped` object.

ids	A character (or coercible to character) containing ID labels of two or more pedigree members.
rho	A numeric vector of recombination rates; all entries must be in the interval $[0, 0.5]$.
recombinants	A logical of length 2, applicable only when ids has length 2. When given, it indicates whether each of the two gametes is a recombinant or non-recombinant. This parameter is mainly used by twoLocusIBD().
verbose	A logical.
debug	A logical. If TRUE, detailed messages are printed during the recursion process.

Details

Let A, B be two pedigree members, and L1, L2 two loci with a given recombination rate rho. The two-locus kinship coefficient $\phi_{AB}(rho)$ is defined as the probability that random gametes segregating from A and B has IBD alleles at both L1 and L2 simultaneously.

The implementation is based on the recursive algorithm described by Thompson (1988).

References

E. A. Thompson (1988). *Two-locus and Three-locus Gene Identity by Descent in Pedigrees*. IMA Journal of Mathematics Applied in Medicine & Biology, vol. 5.

Examples

```
######################
# Example 1: Full sibs
######################
x = nuclearPed(2)

k_0 = twoLocusKinship(x, ids = 3:4, rho = 0)
k_0.5 = twoLocusKinship(x, ids = 3:4, rho = 0.5)

stopifnot(k_0 == 1/4, k_0.5 == 1/16)


################################################
# Example 2: Reproducing Fig. 3 in Thompson (1988)
# Note that in the article, curve (a) is wrong.
# See Erratum: https://doi.org/10.1093/imammb/6.1.1
################################################

# Pedigrees (a) - (d)
ped.a = linearPed(3)
ped.b = avuncularPed(half = TRUE)
ped.c = cousinPed(1)
ped.d = doubleCousins(1, 1, half1 = TRUE, half2 = TRUE)

peds = list(
  a = list(ped = ped.a, ids = c(1,7)),
  b = list(ped = ped.b, ids = leaves(ped.b)),
```

```
  c = list(ped = ped.c, ids = leaves(ped.c)),
  d = list(ped = ped.d, ids = leaves(ped.d))
)

twoLocusPlot(peds, coeff = "kinship", lty = 1:4)
```

`twoLocusPlot` *Two-locus coefficient plot*

Description

Plot two-locus kinship or IBD coefficients as function of the recombination rate.

Usage

```
twoLocusPlot(
  peds,
  coeff = "k11",
  rseq = seq(0, 0.5, length = 11),
  xlab = "Recombination rate",
  ylab = NA,
  col = seq_along(peds),
  lty = 1,
  lwd = 1,
  ...
)
```

Arguments

`peds`	A list of lists. See details.
`coeff`	A string identifying which coefficient to compute. See Details for legal values.
`rseq`	A numeric vector of recombination rates. By default `seq(from = 0, by = 0.5, length = 11)`.
`xlab, ylab`	Axis labels.
`col, lty, lwd`	Plotting parameters.
`...`	Further parameters passed on to `matplot()`.

Details

Each entry of `peds` must be a list with the following (named) entries:

- ped: A ped object
- ids: A pair of labels identifying two members of `ped`

The `coeff` parameter must be either a character naming the coefficient to compute, or a function. If a character, it must be one of the following names: "inb", "kinship", "phi", "phi11", "k00", "k01", "k02", "k10", "k11", "k12", "k20", "k21" or "k22".

If `coeff` is a function, it must take three arguments named `ped`, `ids` and `rho`, and produce a single number for each set of input data. See Examples.

The first three are synonymous and indicate the two-locus kinship coefficient. The remaining choices are two-locus IBD coefficients. (See `twoLocusIBD()`.)

Examples

```
##############################
# Classic example of three relationships with equal one-locus coeffs
peds = list(
    GrandParent = list(ped = linearPed(2),    ids = c(1, 5)),
    HalfSib     = list(ped = halfSibPed(),    ids = c(4, 5)),
    Uncle       = list(ped = cousinPed(0, 1), ids = c(3, 6)))

twoLocusPlot(peds, coeff = "kinship")
twoLocusPlot(peds, coeff = "k11")

##############################

peds = list(
    PO = list(ped = nuclearPed(1), ids = c(1,3)),
    S  = list(ped = nuclearPed(2), ids = c(3,4)))

twoLocusPlot(peds, coeff = "kinship")
twoLocusPlot(peds, coeff = "k11")

##############################

ped1 = addChildren(halfSibPed(sex2 = 2), 4, 5, nch = 2)
ped2 = addChildren(addDaughter(nuclearPed(1), 3), 1, 5, nch = 2)
ped3 = addChildren(addDaughter(nuclearPed(2), 4), 3, 6, nch = 2)

peds = list(
   `H-sibs` = list(ped = ped1, ids = leaves(ped1)),
   `G-sibs` = list(ped = ped2, ids = leaves(ped2)),
   `U-sibs` = list(ped = ped3, ids = leaves(ped3))
)
# plotPedList(peds)
twoLocusPlot(peds, coeff = "kinship")

##############################

### Reproducing Fig 2 of Bishop & Williamson (1990)
### This example illustrates `coeff` as a function.

# The coefficient d11(rho) is the conditional probability of IBD = 1
# in the first locus, given IBD = 1 in the second.
```

```
G = linearPed(2)
H = halfSibPed()
U = cousinPed(0, removal = 1)
FC = cousinPed(1)
FC1R = cousinPed(1, removal = 1)
SC = cousinPed(2)

peds = list(
    GrandParent = list(ped = G,    ids = c(1, 5)),
    HalfSib     = list(ped = H,    ids = leaves(H)),
    Uncle       = list(ped = U,    ids = leaves(U)),
    FirstCous   = list(ped = FC,   ids = leaves(FC)),
    FirstCous1R = list(ped = FC1R, ids = leaves(FC1R)),
    SecondCous  = list(ped = SC,   ids = leaves(SC)))


d11 = function(ped, ids, rho) {
  twoLocusIBD(ped, ids, rho, coefs = "k11")/kappaIBD(ped, ids)[2]
}

twoLocusPlot(peds, coeff = d11)
```

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