# Package 'pedtools'

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**Type** Package

**Title** Creating and Working with Pedigrees and Marker Data

**Version** 1.0.1

**Description** A comprehensive collection of tools for creating, manipulating and visualising pedigrees and genetic marker data. Pedigrees can be read from text files or created on the fly with built-in functions. A range of utilities enable modifications like adding or removing individuals, breaking loops, and merging pedigrees. Pedigree plots are produced by wrapping the plotting functionality of the 'kinship2' package. A Shiny app for creating pedigrees, based on 'pedtools', is available at <https://magnusdv.shinyapps.io/quickped>. 'pedtools' is the hub of the 'ped suite', a collection of packages for pedigree analysis. 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://github.com/magnusdv/pedtools, https://magnusdv.github.io/pedsuite/

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**VignetteBuilder** knitr

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# R topics documented:

`as.data.frame.ped` *Convert ped to data.frame*

## Description

Convert a ped object to a data.frame. The first columns are id, fid, mid and sex, followed by genotype columns for all (or a selection of) markers.

## Usage

```
## S3 method for class 'ped'
as.data.frame(x, ..., markers, sep = "/", missing = "-")
```

## Arguments

| | |
|---|---|
| `x` | Object of class ped. |
| `...` | Further parameters |
| `markers` | Vector of marker names or indices. By default, all markers are included. |
| `sep` | A single string to be used as allele separator in marker genotypes. |
| `missing` | A single string to be used for missing alleles. |

## Details

Note that the output of `as.data.frame.ped()` is quite different from that of `as.matrix.ped()`. This reflects the fact that these functions have different purposes.

Conversion to a data frame is primarily intended for pretty printing. It uses correct labels for pedigree members and marker alleles, and pastes alleles to form nice-looking genotypes.

The matrix method, on the other hand, is a handy tool for manipulating the pedigree structure. It produces a numeric matrix, using the internal index labelling both for individuals and alleles, making it very fast. In addition, all necessary meta information (loop breakers, allele frequencies a.s.o) is kept as attributes, which makes it possible to recreate the original ped object.

## Value

A `data.frame` with `pedsize(x)` rows and `4 + nMarkers(x)` columns.

## See Also

`as.matrix.ped()`

as.matrix.ped *Convert* ped *to matrix*

## Description

Converts a ped object to a numeric matrix using internal labels, with additional info necessary to recreate the original ped attached as attributes.

## Usage

```
## S3 method for class 'ped'
as.matrix(x, include.attrs = TRUE, ...)

restorePed(x, attrs = NULL, validate = TRUE)
```

## Arguments

| | |
|---|---|
| x | a ped object. In restorePed: A numerical matrix. |
| include.attrs | a logical indicating if marker annotations and other info should be attached as attributes. See Value. |
| ... | not used. |
| attrs | a list containing labels and other ped info compatible with x, in the format produced by as.matrix. If NULL, the attributes of x itself are used. |
| validate | a logical, forwarded to ped(). If FALSE, no checks for pedigree errors are performed. |

## Details

restorePed is the reverse of as.matrix.ped.

## Value

For as.matrix: A numerical matrix with pedsize(x) rows. If include.attrs = TRUE the following attributes are added to the matrix, allowing x to be exactly reproduced by restorePed:

- FAMID the family identifier (a string)
- LABELS the ID labels (a character vector)
- UNBROKEN_LOOPS a logical indicating whether x has unbroken loops
- LOOP_BREAKERS a numerical matrix, or NULL
- markerattr a list of length nMarkers(x), containing the attributes of each marker

For restorePed: A ped object.

## Author(s)

Magnus Dehli Vigeland

## See Also

ped()

## Examples

```
x = relabel(nuclearPed(1), letters[1:3])

# To examplify the ped -> matrix -> ped trick, we show how to
# reverse the internal ordering of the pedigree.
m = as.matrix(x, include.attrs = TRUE)
m[] = m[3:1, ]

# Must reverse the labels also:
attrs = attributes(m)
attrs$LABELS = rev(attrs$LABELS)

# Restore ped:
y = restorePed(m, attrs = attrs)

# Of course a simpler way is use reorderPed():
z = reorderPed(x, 3:1)
stopifnot(identical(y, z))
```

---

# as.ped *Conversions to ped objects*

---

## Description

Conversions to ped objects

## Usage

```
as.ped(x, ...)

## S3 method for class 'data.frame'
as.ped(
  x,
  famid_col = NA,
  id_col = NA,
  fid_col = NA,
  mid_col = NA,
  sex_col = NA,
  marker_col = NA,
  locusAttributes = NULL,
  missing = 0,
  sep = NULL,
```

```
  validate = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| x | Any object. |
| ... | Not used. |
| famid_col | Index of family ID column. If NA, the program looks for a column named "famid" (ignoring case). |
| id_col | Index of individual ID column. If NA, the program looks for a column named "id" (ignoring case). |
| fid_col | Index of father ID column. If NA, the program looks for a column named "fid" (ignoring case). |
| mid_col | Index of mother ID column. If NA, the program looks for a column named "mid" (ignoring case). |
| sex_col | Index of column with gender codes (0 = unknown; 1 = male; 2 = female). If NA, the program looks for a column named "sex" (ignoring case). If this is not found, genders of parents are deduced from the data, leaving the remaining as unknown. |
| marker_col | Index vector indicating columns with marker alleles. If NA, all columns to the right of all pedigree columns are used. If `sep` (see below) is non-NULL, each column is interpreted as a genotype column and split into separate alleles with `strsplit(...,split = sep,fixed = TRUE)`. |
| locusAttributes | Passed on to `setMarkers()` (see explanation there). |
| missing | Passed on to `setMarkers()` (see explanation there). |
| sep | Passed on to `setMarkers()` (see explanation there). |
| validate | A logical indicating if the pedigree structure should be validated. |

## Value

A ped object or a list of such.

## Examples

```
df = data.frame(famid = c("S1", "S2"),
                id = c("A", "B"),
                fid = 0,
                mid = 0,
                sex = 1)

# gives a list of two singletons
as.ped(df)

# Trio
df1 = data.frame(id = 1:3, fid = c(0,0,1), mid = c(0,0,2), sex = c(1,2,1))
```

```
as.ped(df1)

# Disconnected example: Trio (1-3) + singleton (4)
df2 = data.frame(id = 1:4, fid = c(2,0,0,0), mid = c(3,0,0,0),
                 M = c("1/2", "1/1", "2/2", "3/4"))
as.ped(df2)

# Two singletons
df3 = data.frame(id = 1:2, fid = 0, mid = 0, sex = 1)
as.ped(df3)
```

---

`connectedComponents` *Connected pedigree components*

---

## Description

Compute the connected parts of a pedigree. This is an important step when converting pedigree data from other formats (where disconnected pedigrees may be allowed) to `pedtools` (which requires pedigrees to be connected).

## Usage

```
connectedComponents(id, fid = NULL, mid = NULL, fidx = NULL, midx = NULL)
```

## Arguments

| | |
|---|---|
| `id` | A vector of ID labels (character or numeric). |
| `fid` | The ID labels of the fathers (or "0" if missing). |
| `mid` | The ID labels of the mothers (or "0" if missing). |
| `fidx, midx` | (For internal use mostly.) Integer vectors with paternal (resp. maternal) indices. These may be given instead of `id`, `fid`, `mid`. |

## Value

A list, where each element is a subset of `id` constituting a connected pedigree.

## Examples

```
# A trio (1-3) and a singleton (4)
x = data.frame(id = 1:4, fid = c(2,0,0,0), mid = c(3,0,0,0))
connectedComponents(x$id, x$fid, x$mid)
```

## famid *Family identifier*

### Description

Functions for getting or setting the family ID of a ped object.

### Usage

```
famid(x, ...)

## S3 method for class 'ped'
famid(x, ...)

famid(x, ...) <- value

## S3 replacement method for class 'ped'
famid(x, ...) <- value
```

### Arguments

| | |
|---|---|
| x | A ped object |
| ... | (Not used) |
| value | The new family ID, which must be (coercible to) a character string. |

### Examples

```
x = nuclearPed(1)
famid(x) # empty string

famid(x) = "trio"
famid(x)
```

## founderInbreeding *Inbreeding coefficients of founders*

### Description

Functions to get or set inbreeding coefficients for the pedigree founders.

### Usage

```
founderInbreeding(x, ids, named = FALSE, chromType = "autosomal")

founderInbreeding(x, ids, chromType = "autosomal") <- value
```

### Arguments

| | |
|---|---|
| x | A ped object. |
| ids | Any subset of `founders(x)`. If `ids` is missing in `founderInbreeding()`, it is set to `founders(x)`. |
| named | A logical: If TRUE, the output vector is named with the ID labels. |
| chromType | Either "autosomal" (default) or "x". |
| value | A numeric of the same length as `ids`, entries in the interval [0, 1]. If the vector is named, then the names are interpreted as ID labels of the founders whose inbreeding coefficients should be set. In this case, the `ids` argument should not be used. (See examples.) |

### Value

For `founderInbreeding`, a numeric vector of the same length as `ids`, containing the founder inbreeding coefficients.

For founderInbreeding<- the updated ped object is returned.

### Examples

```
x = nuclearPed(father = "fa", mother = "mo", child = 1)
founderInbreeding(x, "fa") = 1
founderInbreeding(x, named = TRUE)

# Setting all founders at once (replacement value is recycled)
founderInbreeding(x, ids = founders(x)) = 0.5
founderInbreeding(x, named = TRUE)

# Alternative syntax, using a named vector
founderInbreeding(x) = c(fa = 0.1, mo = 0.2)
founderInbreeding(x, named = TRUE)
```

---

## `freqDatabase` *Allele frequency database*

---

### Description

Functions for reading, setting and extracting allele frequency databases, in either "list" format or "allelic ladder" format.

### Usage

```
getFreqDatabase(x, markers = NULL, format = c("list", "ladder"))

setFreqDatabase(x, database, format = c("list", "ladder"), ...)
```

```
readFreqDatabase(filename, format = c("list", "ladder"), ...)

writeFreqDatabase(x, filename, markers = NULL, format = c("list", "ladder"))

setFrequencyDatabase(...)

getFrequencyDatabase(...)

readFrequencyDatabase(...)

writeFrequencyDatabase(...)
```

## Arguments

| | |
|---|---|
| x | A ped object, or a list of such. |
| markers | A character vector (with marker names) or a numeric vector (with marker indices). |
| format | Either "list" or "ladder". |
| database | Either a list or matrix/data frame with allele frequencies, or a file path (to be passed on to `readFreqDatabase()`). |
| ... | Optional arguments passed on to `read.table()`. |
| filename | The path to a text file containing allele frequencies either in "list" or "allelic ladder" format. |

## Details

A frequency database in "list" format is a list of numeric vectors; each vector named with the allele labels, and the list itself named with the marker names.

Text files containing frequencies in "list" format should look as follows, where "marker1" and "marker2" are marker names, and "a1","a2",... are allele labels (which may be characters or numeric, but will always be converted to characters):

```
marker1
a1 0.2
a2 0.5
a3 0.3

marker2
a1 0.9
a2 0.1
```

A database in "allelic ladder" format is rectangular, i.e., a numeric matrix (or data frame), with allele labels as row names and markers as column names. NA entries correspond to unobserved alleles.

## Value

- `getFreqDatabase`: either a list (if `format = "list"`) or a data frame (if `format = "ladder"`)
- `readFreqDatabase`: a list (also if `format = "ladder"`) of named numeric vectors
- `setFreqDatabase`: a modified version of `x`

## See Also

setLocusAttributes(), setMarkers(), setAlleles()

## Examples

```
loc1 = list(name = "m1", afreq = c(a = .1, b = .9))
loc2 = list(name = "m2", afreq = c("1" = .2, "10.2" = .3, "3" = .5))
x = setMarkers(singleton(1), locus = list(loc1, loc2))
db = getFreqDatabase(x)
db

y = setFreqDatabase(x, database = db)
stopifnot(identical(x, y))

# The database can also be read directly from file
tmp = tempfile()
write("m1\na 0.1\nb 0.9\n\nm2\n1 0.2\n3 0.5\n10.2 0.3", tmp)

z = setFreqDatabase(x, database = tmp)
stopifnot(all.equal(x, z))
```

---

# getAlleles *Allele matrix manipulation*

---

## Description

Functions for getting and setting the genotypes of multiple individuals/markers simultaneously

## Usage

```
getAlleles(x, ids = NULL, markers = NULL)

setAlleles(x, ids = NULL, markers = NULL, alleles)
```

## Arguments

| | |
|---|---|
| x | A ped object or a list of such |
| ids | A vector of ID labels. If NULL (default) all individuals are included. |
| markers | A vector of indices or names of markers attaches to x. If NULL (default) all markers are included. |
| alleles | A character of the same format and dimensions as the output of getAlleles(x,ids,markers), or an object which can be converted by as.matrix() into such a matrix. See Details. |

## Details

If the `alleles` argument of `setAlleles()` is not a matrix, it is recycled (if necessary), and converted into a matrix of the correct dimensions. For example, setting `alleles = 0` gives a simple way of removing the genotypes of some or all individuals (while keeping the markers attached).

## Value

`getAlleles()` returns a character matrix with `length(ids)` rows and `2 * length(markers)` columns. The ID labels of `x` are used as rownames, while the columns are named <m1>.1, <m1>.2, ... where <m1> is the name of the first marker, a.s.o.

`setAlleles()` returns a `ped` object identical to `x`, except for the modified alleles. In particular, all locus attributes are unchanged.

## See Also

`transferMarkers()`

## Examples

```
# Setup: Pedigree with two markers
x = nuclearPed(1)
m1 = marker(x, `2` = "1/2", alleles = 1:2, name = "m1")
m2 = marker(x, `3` = "2/2", alleles = 1:2, name = "m2")
x = setMarkers(x, list(m1, m2))


# Extract allele matrix:

mat1 = getAlleles(x)
mat2 = getAlleles(x, ids = 2:3, markers = "m2")
stopifnot(identical(mat1[2:3, 3:4], mat2))

# Remove all genotypes
y = setAlleles(x, alleles = 0)
y

# Setting a single genotype
z = setAlleles(y, ids = "1", marker = "m2", alleles = 1:2)

# Alternative: In-place modification with `genotype()`
genotype(y, id = "1", marker = "m2") = 1:2
stopifnot(identical(y,z))


### Manipulation of pedlist objects
s = transferMarkers(x, singleton("s"))
peds = list(x, s)

getAlleles(peds)

setAlleles(peds, ids = "s", marker = "m1", alleles = 1:2)
```

`getComponent` *Pedigree component*

## Description

Given a list of ped objects (called pedigree components), and a vector of ID labels, find the index of the component holding each individual.

## Usage

```
getComponent(x, ids, checkUnique = FALSE, errorIfUnknown = FALSE)
```

## Arguments

| | |
|---|---|
| `x` | A list of ped objects |
| `ids` | A vector of ID labels (coercible to character) |
| `checkUnique` | If TRUE an error is raised if any element of `ids` occurs more than once in `x`. Default: FALSE. |
| `errorIfUnknown` | If TRUE, the function stops with an error if not all elements of `ids` are recognised as names of members in `x`. Default: FALSE. |

## Value

An integer vector of the same length as `ids`, with NA entries where the corresponding label was not found in any of the components.

## See Also

`internalID()`

## Examples

```
x = list(nuclearPed(1), singleton(id = "A"))
getComponent(x, c(3, "A"))
```

getGenotypes *Genotype matrix*

## Description

Extract the genotypes of multiple individuals/markers in form of a matrix.

## Usage

```
getGenotypes(x, ids = NULL, markers = NULL, sep = "/", missing = "-")
```

## Arguments

| | |
|---|---|
| x | A ped object or a list of such |
| ids | A vector of ID labels. If NULL (default) all individuals are included. |
| markers | A vector of indices or names of markers attaches to x. If NULL (default) all markers are included. |
| sep | A single string to be used as allele separator in marker genotypes. |
| missing | A single string to be used for missing alleles. |

## Value

getGenotypes() returns a character matrix with length(ids) rows and length(markers) columns.

## See Also

getAlleles()

## Examples

```
x = nuclearPed(1)
m1 = marker(x, `2` = 1:2, alleles = 1:2, name = "m1")
m2 = marker(x, `3` = 2, alleles = 1:2, name = "m2")
x = setMarkers(x, list(m1, m2))

getGenotypes(x)


### A list of pedigrees

s = transferMarkers(x, singleton("s"))
peds = list(x, s)

getGenotypes(peds)
```

getMap *Tabulate marker positions*

## Description

Return a map of the markers attached to a pedigree.

## Usage

```
getMap(x, markers = NULL, na.action = 0, verbose = TRUE)

setMap(x, map, matchNames = NA, ...)
```

## Arguments

| | |
|---|---|
| x | An object of class ped or a list of such. |
| markers | A vector of names or indices referring to markers attached to x. By default, all markers are included. |
| na.action | Either 0 (default), 1 or 2. (See Details.) |
| verbose | A logical. |
| map | Either a data frame or the path to a map file. |
| matchNames | A logical; if TRUE, pre-existing marker names of x will be used to assign chromosome labels and positions from map. |
| ... | Further arguments passed to read.table(). |

## Details

The na.action argument controls how missing values are dealt with:

- na.action = 0: Return map unmodified
- na.action = 1: Replace missing values with dummy values.
- na.action = 2: Remove markers with missing data.

In setMap(), the map argument should be a data frame (or file) with the following columns in order: 1) chromosome, 2) marker name, 3) position in megabases. Column names are ignored, as are any columns after the first three.

## Value

getMap() returns a data frame with columns CHROM, MARKER and MB.

setMap() returns x with modified marker attributes.

## Examples

```
x = singleton(1)
m1 = marker(x, chrom = 1, posMb = 10, name = "m1")
m2 = marker(x, chrom = 1, posMb = 11)
m3 = marker(x, chrom = 1)
x = setMarkers(x, list(m1, m2, m3))

# Compare effect of `na.action`
getMap(x, na.action = 0)
getMap(x, na.action = 1)
getMap(x, na.action = 2)

# Getting and setting map are inverses
y = setMap(x, getMap(x))
identical(x,y)
```

---

# getSex *Get or set the sex of pedigree members*

---

## Description

Functions for retrieving or changing the sex of specified pedigree members.

## Usage

```
getSex(x, ids, named = FALSE)

setSex(x, ids = NULL, sex)

swapSex(x, ids, verbose = TRUE)
```

## Arguments

| | |
|---|---|
| x | A ped object or a list of such. |
| ids | A character vector (or coercible to one) containing ID labels. |
| named | A logical: return a named vector or not. |
| sex | A numeric vector with entries 1 (= male), 2 (= female) or 0 (= unknown). If ids is NULL, sex must be named with ID labels. If sex is unnamed and shorter than ids it is recycled to length(ids). |
| verbose | A logical: Verbose output or not. |

## Value

- `getSex(x,ids)` returns an integer vector of the same length as `ids`, with entries 0 (unknown), 1 (male) or 2 (female).
- `setSex(x,ids,sex)` returns a ped object identical to `x`, but where the sex of `ids` is set according to the entries of `sex`
- `swapSex(x,ids)` returns a ped object identical to `x`, but where the sex of `ids` (and their spouses) are swapped (1 <-> 2).

## See Also

`ped()`

## Examples

```
x = nuclearPed(father = "fa", mother = "mo", children = "ch")

stopifnot(all.equal(
  getSex(x, named = TRUE),
  c(fa = 1, mo = 2, ch = 1)
))

# Make child female
setSex(x, ids = "ch", sex = 2)

# Same, using a named vector
setSex(x, sex = c(ch = 2))

# Swapping sex is sometimes easier,
# since spouses are dealt with automatically
swapSex(x, ids = "fa")

# setting/getting sex in a pedlist
y = list(singleton(1, sex = 2), singleton(2), singleton(3))
sx = getSex(y, named = TRUE)
y2 = setSex(y, sex = sx)

stopifnot(identical(y, y2))
```

---

`inbreedingLoops` *Pedigree loops*

---

## Description

Functions for identifying, breaking and restoring loops in pedigrees.

## Usage

```
inbreedingLoops(x)

breakLoops(
  x,
  loopBreakers = NULL,
  verbose = TRUE,
  errorIfFail = TRUE,
  loop_breakers = NULL
)

tieLoops(x, verbose = TRUE)

findLoopBreakers(x)

findLoopBreakers2(x, errorIfFail = TRUE)
```

## Arguments

| | |
|---|---|
| x | a ped() object. |
| loopBreakers | either NULL (resulting in automatic selection of loop breakers) or a numeric containing IDs of individuals to be used as loop breakers. |
| verbose | a logical: Verbose output or not? |
| errorIfFail | a logical: If TRUE an error is raised if the loop breaking is unsuccessful. If FALSE, the pedigree is returned unchanged. |
| loop_breakers | Deprecated; renamed to loopBreakers. |

## Details

Pedigree loops are usually handled (by pedtools and related packages) under the hood - using the functions described here - without need for explicit action from end users. When a ped object x is created, an internal routine detects if the pedigree contains loops, in which case x$UNBROKEN_LOOPS is set to TRUE.

In cases with complex inbreeding, it can be instructive to plot the pedigree after breaking the loops. Duplicated individuals are plotted with appropriate labels (see examples).

The function findLoopBreakers identifies a set of individuals breaking all inbreeding loops, but not marriage loops. These require more machinery for efficient detection, and pedtools does this is a separate function, findLoopBreakers2, utilizing methods from the igraph package. Since this is rarely needed for most users, igraph is not imported when loading pedtools, only when findLoopBreakers2 is called.

In practice, breakLoops first calls findLoopBreakers and breaks at the returned individuals. If the resulting ped object still has loops, findLoopBreakers2 is called to break any marriage loops.

## Value

For breakLoops, a ped object in which the indicated loop breakers are duplicated. The returned object will also have a non-null loopBreakers entry, namely a matrix with the IDs of the original

loop breakers in the first column and the duplicates in the second. If loop breaking fails, then depending on `errorIfFail` either an error is raised, or the input pedigree is returned, still containing unbroken loops.

For `tieLoops`, a `ped` object in which any duplicated individuals (as given in the `x$LOOP_BREAKERS` entry) are merged. For any ped object `x`, the call `tieLoops(breakLoops(x))` should return `x`.

For `inbreedingLoops`, a list containing all inbreeding loops (not marriage loops) found in the pedigree. Each loop is represented as a list with elements `top`, `bottom`, `pathA` (individuals forming a path from top to bottom) and `pathB` (creating a different path from top to bottom, with no individuals in common with `pathA`). Note that the number of loops reported here counts all closed paths in the pedigree and will in general be larger than the genus of the underlying graph.

For `findLoopBreakers` and `findLoopBreakers2`, a numeric vector of individual ID's.

## Author(s)

Magnus Dehli Vigeland

## Examples

```
x = cousinPed(1, child = TRUE)
plot(breakLoops(x))

# Pedigree with marriage loop: Double first cousins
if(requireNamespace("igraph", quietly = TRUE)) {
  y = doubleCousins(1, 1, child = TRUE)
  findLoopBreakers(y) # --> 9
  findLoopBreakers2(y) # --> 7 and 9
  y2 = breakLoops(y)
  plot(y2)

  # Or loop breakers chosen by user
  y3 = breakLoops(y, 6:7)
  plot(y3)
}
```

---

# is.marker *Test if something is a marker*

---

## Description

Functions for testing if something is a `marker` object, or a list of such objects.

## Usage

```
is.marker(x)

is.markerList(x)
```

### Arguments

| | |
|---|---|
| x | Any object |

### Value

A logical

---

`is.ped` *Is an object a* `ped` *object?*

---

### Description

Functions for checking whether an object is a `ped()` object, a `singleton()` or a list of such.

### Usage

```
is.ped(x)

is.singleton(x)

is.pedList(x)
```

### Arguments

| | |
|---|---|
| x | Any R object. |

### Details

Note that the `singleton` class inherits from `ped`, so if `x` is a singleton, `is.ped(x)` returns TRUE.

### Value

For `is.ped()`: TRUE if `x` is a `ped` or `singleton` object, otherwise FALSE.

For `is.singleton()`: TRUE if `x` is a `singleton` object, otherwise FALSE.

For `is.pedList()`: TRUE if `x` is a list of `ped` and/or `singleton` objects, otherwise FALSE.

### Author(s)

Magnus Dehli Vigeland

### See Also

`ped()`

## Examples

```
x1 = nuclearPed(1)
x2 = singleton(1)
stopifnot(is.ped(x1), !is.singleton(x1),
          is.ped(x2), is.singleton(x2),
          is.pedList(list(x1,x2)))
```

---

`locusAttributes` *Get or set locus attributes*

---

## Description

Retrieve or modify the attributes of attached markers

## Usage

```
getLocusAttributes(
  x,
  markers = NULL,
  attribs = c("alleles", "afreq", "name", "chrom", "posMb", "mutmod")
)

setLocusAttributes(
  x,
  markers = NULL,
  locusAttributes,
  matchNames = NA,
  erase = FALSE
)
```

## Arguments

| | |
|---|---|
| `x` | A ped object, or a list of such. |
| `markers` | A character vector (with marker names) or a numeric vector (with marker indices). If NULL (default), the behaviour depends on `matchNames`, see Details. |
| `attribs` | A subset of the character vector `c("alleles","afreq","name" ,"chrom" ,"posMb","mutmod","rate'` |
| `locusAttributes` | A list of lists, with attributes for each marker. |
| `matchNames` | A logical, only relevant if `markers = NULL`. If TRUE, then the markers to be modified are identified by the 'name' component of each `locusAttributes` entry. If FALSE, all markers attached to `x` are selected in order. |
| `erase` | A logical. If TRUE, all previous attributes of the selected markers are erased. If FALSE, attributes not affected by the submitted `locusAttributes` remain untouched. |

## Details

The default setting `markers = NULL` select markers automatically, depending on the `matchNames` argument. If `matchNames = FALSE`, all markers are chosen If `matchNames = TRUE`, markers will be matched against the `name` entries in `locusAttributes` (and an error issued if these are missing).

Note that the default value `NA` of `matchNames` is changed to TRUE if all entries of `locusAttributes` have a `name` component which matches the name a an attached marker.

Possible attributes given in `locusAttributes` are as follows (default values in parenthesis):

- `alleles` : a character vector with allele labels
- `afreq` : a numeric vector with allele frequencies (`rep.int(1/L,L)`, where `L = length(alleles)`)
- `name` : marker name (NA)
- `chrom` : chromosome number (NA)
- `posMb` : physical location in megabases (NA)
- `mutmod` : mutation model, or model name (NULL)
- `rate` : mutation model parameter (NULL)

## Value

- `getLocusAttributes` : a list of lists
- `setLocusAttributes` : a modified version of `x`.

## Examples

```
x = singleton(1)
x = addMarkers(x, marker(x, name = "m1", alleles = 1:2))
x = addMarkers(x, marker(x, name = "m2", alleles = letters[1:2], chrom = "X"))

# Change frequencies at both loci
y = setLocusAttributes(x, markers = 1:2, loc = list(afreq = c(.1, .9)))
getMarkers(y, 1)

# Set the same mutation model at both loci
z = setLocusAttributes(x, markers = 1:2, loc = list(mutmod = "proportional", rate = .1))
mutmod(z, 1)

# By default, the markers to be modified are identified by name
locs = list(list(name = "m1", alleles = 1:10),
            list(name = "m2", alleles = letters[1:10]))
w = setLocusAttributes(x, loc = locs)
getMarkers(w, 1:2)

# If `erase = TRUE` attributes not explicitly given are erased
w2 = setLocusAttributes(x, loc = locs, erase = TRUE)
chrom(w2, 2) # not "X" anymore

# The getter and setter are inverses
newx = setLocusAttributes(x, loc = getLocusAttributes(x))
stopifnot(identical(x, newx))
```

marker *Marker objects*

## Description

Creating a marker object associated with a pedigree.

## Usage

```
marker(
  x,
  ...,
  geno = NULL,
  allelematrix = NULL,
  alleles = NULL,
  afreq = NULL,
  chrom = NA,
  posMb = NA,
  name = NA,
  NAstrings = c(0, "", NA, "-"),
  mutmod = NULL,
  rate = NULL,
  validate = TRUE
)
```

## Arguments

| | |
|---|---|
| x | a ped object |
| ... | one or more expressions of the form id = genotype, where id is the ID label of a member of x, and genotype is a numeric or character vector of length 1 or 2 (see Examples). |
| geno | a character vector of length pedsize(x), with genotypes written in the format "a/b". |
| allelematrix | a matrix with 2 columns and pedsize(x) rows. If this is non-NULL, then ... must be empty. |
| alleles | a character (or coercible to character) containing allele names. If not given, and afreq is named, names(afreq) is used. The default action is to take the sorted vector of distinct alleles occurring in allelematrix, geno or .... |
| afreq | a numeric of the same length as alleles, indicating the population frequency of each allele. A warning is issued if the frequencies don't sum to 1 after rounding to 3 decimals. If the vector is named, and alleles is not NULL, an error is raised if setequal(names(afreq),alleles) is not TRUE. If afreq is not specified, all alleles are given equal frequencies. |
| chrom | a single integer: the chromosome number. Default: NA. |

| | |
|---|---|
| posMb | a nonnegative real number: the physical position of the marker, in megabases. Default: NA. |
| name | a character string: the name of the marker. Default: NA. |
| NAstrings | A character vector containing strings to be treated as missing alleles. Default: c("","0",NA,"-"). |
| mutmod, rate | mutation model parameters. These are passed directly to pedmut::mutationModel(); see there for details. Note: mutmod corresponds to the model parameter. Default: NULL (no mutation model). |
| validate | if TRUE, the validity of the created marker object is checked. |

## Value

An object of class marker. This is an integer matrix with 2 columns and one row per individual, and the following attributes:

- alleles (a character vector with allele labels)
- afreq (allele frequencies; default rep.int(1/length(alleles),length(alleles)))
- chrom (chromosome number; default = NA)
- posMb (physical location in megabases; default = NA)
- name (marker identifier; default = NA)
- mutmod (a list of two (male and female) mutation matrices; default = NULL)

## See Also

marker_attach

## Examples

```
x = nuclearPed(father = "fa", mother = "mo", children = "child")

# An empty SNP with alleles "A" and "B"
marker(x, alleles = c("A", "B"))

# Alleles/frequencies can be given jointly or separately
stopifnot(identical(
  marker(x, afreq = c(A = 0.01, B = 0.99)),
  marker(x, alleles = c("A", "B"), afreq = c(0.01, 0.99)),
  ))

# Genotypes can be assigned individually ...
marker(x, fa = "1/1", mo = "1/2")

# ... or using the `geno` vector (all members in order)
marker(x, geno = c("1/1", "1/2", NA))

# For homozygous genotypes, a single allele suffices
marker(x, fa = 1)
```

```
# Attaching a marker to the pedigree
m = marker(x) # By default a SNP with alleles 1,2
x = setMarkers(x, m)

# A marker with a "proportional" mutation model,
# with different rates for males and females
mutrates = list(female = 0.1, male = 0.2)
marker(x, alleles = 1:2, mutmod = "prop", rate = mutrates)
```

---

`marker_attach` *Attach markers to pedigrees*

---

## Description

In many applications it is useful to *attach* markers to their associated ped object. In particular for bigger projects with many markers, this makes it easier to manipulate the dataset as a unit. The function `setMarkers()` replaces all existing markers with the supplied ones, while `addMarkers()` appends the supplied markers to any existing ones.

## Usage

```
setMarkers(
  x,
  m = NULL,
  alleleMatrix = NULL,
  locusAttributes = NULL,
  missing = 0,
  sep = NULL,
  checkCons = TRUE
)

addMarkers(
  x,
  m = NULL,
  alleleMatrix = NULL,
  locusAttributes = NULL,
  missing = 0,
  sep = NULL,
  checkCons = TRUE
)
```

## Arguments

| | |
|---|---|
| `x` | A ped object |
| `m` | Either a single `marker` object or a list of `marker` objects |

`alleleMatrix` A matrix with `pedsize(x)` rows, containing the observed alleles for one or several markers. The matrix must have either 1 or 2 columns per marker. If the former, then a `sep` string must be a given, and will be used to split all entries.

`locusAttributes` A list of lists, with attributes for each marker. See Details for possible attributes.

`missing` A single character (or coercible to one) indicating the symbol for missing alleles.

`sep` If this is a single string, each entry of `alleleMatrix` is interpreted as a genotype, and will be split by calling `strsplit(...,split = sep,fixed = TRUE)`. If `alleleMatrix` contains entries with "/", this will be taken as separator by default. (To override this behaviour, put `sep = FALSE`.)

`checkCons` A logical. If TRUE (default), each marker is checked for consistency with `x`.

## Details

The most general format of `locusAttributes` a list of lists, one for each marker, where possible entries in the inner lists are as follows (default values in parenthesis):

- `alleles` : a character vector with allele labels
- `afreq` : a numeric vector with allele frequencies (`rep.int(1/L,L)`, where `L = length(alleles)`)
- `chrom` : chromosome number (NA)
- `posMb` : physical location in megabases (NA)
- `name` : marker name (NA)
- `mutmod` : mutation model, or model name (NULL)
- `rate` : mutation model parameter (NULL)

If `locusAttributes` is just a single list of attributes (not a list of lists), then it is repeated to match the number of markers. In particular, the shortcut `locusAttributes = "snp-12"` sets all markers to be SNPs with alleles 1 and 2.‘

Two alternative format of `locusAttributes` are allowed: If a data.frame or matrix is given, an attempt is made to interpret it as a frequency database in allelic ladder format. Such an interpretation is also attempted if `locusAttributes` is a list of named frequency vectors (where the names are the allele labels).

## Value

A ped object.

## Examples

```
x = singleton(1)
m1 = marker(x, '1' = 1:2)
m2 = marker(x, '1' = 'a')

x = setMarkers(x, m1)
x = addMarkers(x, m2)
x
```

```
# Reversing the order of the markers
x = setMarkers(x, list(m2, m1))
x
```

---

`marker_getset` *Get/set marker attributes*

---

## Description

These functions can be used to manipulate a single attribute of one or several markers. Each getter/setter can be used in two ways: Either directly on a `marker` object, or on a `ped` object which has markers attached to it.

## Usage

```
genotype(x, ...)

## S3 method for class 'marker'
genotype(x, id, ...)

## S3 method for class 'ped'
genotype(x, markers = NULL, id, ...)

genotype(x, ...) <- value

## S3 replacement method for class 'marker'
genotype(x, id, ...) <- value

## S3 replacement method for class 'ped'
genotype(x, marker, id, ...) <- value

mutmod(x, ...)

## S3 method for class 'marker'
mutmod(x, ...)

## S3 method for class 'ped'
mutmod(x, marker, ...)

## S3 method for class 'list'
mutmod(x, marker, ...)

mutmod(x, ...) <- value

## S3 replacement method for class 'marker'
mutmod(x, ...) <- value
```

```
## S3 replacement method for class 'ped'
mutmod(x, marker = NULL, ...) <- value

## S3 replacement method for class 'list'
mutmod(x, marker = NULL, ...) <- value

alleles(x, ...)

## S3 method for class 'marker'
alleles(x, ...)

## S3 method for class 'ped'
alleles(x, marker, ...)

## S3 method for class 'list'
alleles(x, marker, ...)

afreq(x, ...)

## S3 method for class 'marker'
afreq(x, ...)

## S3 method for class 'ped'
afreq(x, marker, ...)

## S3 method for class 'list'
afreq(x, marker, ...)

afreq(x, ...) <- value

## S3 replacement method for class 'marker'
afreq(x, ...) <- value

## S3 replacement method for class 'ped'
afreq(x, marker, ...) <- value

## S3 replacement method for class 'list'
afreq(x, marker, ...) <- value

name(x, ...)

## S3 method for class 'marker'
name(x, ...)

## S3 method for class 'ped'
name(x, markers = NULL, ...)
```

```
## S3 method for class 'list'
name(x, markers = NULL, ...)

name(x, ...) <- value

## S3 replacement method for class 'marker'
name(x, ...) <- value

## S3 replacement method for class 'ped'
name(x, markers = NULL, ...) <- value

## S3 replacement method for class 'list'
name(x, markers = NULL, ...) <- value

chrom(x, ...)

## S3 method for class 'marker'
chrom(x, ...)

## S3 method for class 'ped'
chrom(x, markers = NULL, ...)

## S3 method for class 'list'
chrom(x, markers = NULL, ...)

chrom(x, ...) <- value

## S3 replacement method for class 'marker'
chrom(x, ...) <- value

## S3 replacement method for class 'ped'
chrom(x, markers = NULL, ...) <- value

## S3 replacement method for class 'list'
chrom(x, markers = NULL, ...) <- value

posMb(x, ...)

## S3 method for class 'marker'
posMb(x, ...)

## S3 method for class 'ped'
posMb(x, markers = NULL, ...)

posMb(x, ...) <- value

## S3 replacement method for class 'marker'
posMb(x, ...) <- value
```

```
## S3 replacement method for class 'ped'
posMb(x, markers = NULL, ...) <- value
```

### Arguments

| | |
|---|---|
| x | Either a marker object, a ped object or a list of ped objects. |
| ... | Further arguments, not used in most of these functions. |
| id | The ID label of a single pedigree member. |
| value | Replacement value(s). |
| marker, markers | The index or name of a marker (or a vector indicating several markers) attached to ped. Used if x is a ped object. |

### Value

The getters return the value of the query. The setters perform in-place modification of the input.

### Examples

```
x = nuclearPed(1)
x = setMarkers(x, locusAttributes = list(name = "M", alleles = 1:2))

# Set genotype
genotype(x, marker = "M", id = 1) = 1:2
genotype(x, marker = "M", id = 3) = 1

# Genotypes are returned as a vector of length 2
genotype(x, marker = "M", id = 1)

# Change allele freqs
afreq(x, "M") = c(`1` = 0.1, `2` = 0.9)

# Check the new frequencies
afreq(x, "M")
```

---

## marker_prop *Marker properties*

---

### Description

These functions are used to retrieve various properties of marker objects. Each function accepts as input either a single marker object, a ped object, or a list of ped objects.

## Usage

```
emptyMarker(x, ...)

## Default S3 method:
emptyMarker(x, ...)

## S3 method for class 'marker'
emptyMarker(x, ...)

## S3 method for class 'ped'
emptyMarker(x, markers = seq_len(nMarkers(x)), ...)

## S3 method for class 'list'
emptyMarker(x, markers = seq_len(nMarkers(x)), ...)

nTyped(x, ...)

## Default S3 method:
nTyped(x, ...)

## S3 method for class 'marker'
nTyped(x, ...)

## S3 method for class 'ped'
nTyped(x, markers = seq_len(nMarkers(x)), ...)

## S3 method for class 'list'
nTyped(x, markers = seq_len(nMarkers(x)), ...)

nAlleles(x, ...)

## Default S3 method:
nAlleles(x, ...)

## S3 method for class 'marker'
nAlleles(x, ...)

## S3 method for class 'ped'
nAlleles(x, markers = seq_len(nMarkers(x)), ...)

## S3 method for class 'list'
nAlleles(x, markers = seq_len(nMarkers(x)), ...)

isXmarker(x, ...)

## Default S3 method:
isXmarker(x, ...)
```

```
## S3 method for class 'marker'
isXmarker(x, ...)

## S3 method for class 'ped'
isXmarker(x, markers = seq_len(nMarkers(x)), ...)

## S3 method for class 'list'
isXmarker(x, markers = seq_len(nMarkers(x)), ...)

allowsMutations(x, ...)

## Default S3 method:
allowsMutations(x, ...)

## S3 method for class 'marker'
allowsMutations(x, ...)

## S3 method for class 'ped'
allowsMutations(x, markers = seq_len(nMarkers(x)), ...)

## S3 method for class 'list'
allowsMutations(x, markers = seq_len(nMarkers(x)), ...)
```

## Arguments

| | |
|---|---|
| x | A single marker object or a ped object (or a list of such) |
| ... | Not used. |
| markers | A vector of names or indices of markers attached to x, in the case that x is a ped object or a list of such. By default all attached markers are selected. |

## Details

emptyMarker() returns TRUE for markers with no genotypes. If the input is a list of pedigrees, all must be empty for the result to be TRUE.

nTyped() returns the number of typed individuals for each marker. Note that if the input is a list of pedigrees, the function returns the sum over all components.

nAlleles() returns the number of alleles of each marker.

isXmarker() returns TRUE for markers whose chrom attribute is either "X" or 23.

allowsMutations returns TRUE for markers whose mutmod attribute is non-NULL and differs from the identity matrix.

## Value

If x is a single marker object, the output is a vector of length 1.

If x is a ped object, or a list of such, the output is a vector of the same length as markers (which includes all attached markers by default), reporting the property of each marker.

## Examples

```
cmp1 = nuclearPed(1)
cmp2 = singleton(10)
loc = list(alleles = 1:2)
x = setMarkers(list(cmp1, cmp2), locus = rep(list(loc), 3))

#-------- nAlleles() ------------
# All markers have 2 alleles
stopifnot(identical(nAlleles(x), c(2L,2L,2L)))

#-------- emptyMarkers() ------------
# Add genotype for indiv 1 at marker 1
genotype(x[[1]], 1, 1) = 1:2

# Check that markers 2 and 3 are empty
stopifnot(identical(emptyMarker(x), c(FALSE,TRUE,TRUE)),
          identical(emptyMarker(x[[1]]), c(FALSE,TRUE,TRUE)),
          identical(emptyMarker(x[[2]]), c(TRUE,TRUE,TRUE)),
          identical(emptyMarker(x, markers = c(3,1)), c(TRUE,FALSE)))

#-------- nTyped() ------------
stopifnot(identical(nTyped(x), c(1L,0L,0L)))

# Add genotypes for third marker
genotype(x[[1]], marker = 3, id = 1:3) = 1
genotype(x[[2]], marker = 3, id = 10) = 2

# nTyped() returns total over all components
stopifnot(identical(nTyped(x), c(1L,0L,4L)))

#-------- allowsMutations() ------------
# Marker 2 allows mutations
mutmod(x, 2) = list("prop", rate = 0.1)

stopifnot(identical(allowsMutations(x), c(FALSE,TRUE,FALSE)),
          identical(allowsMutations(x, markers = 2:3), c(TRUE,FALSE)))

#-------- isXmarker() ------------
# Make marker 3 X-linked
chrom(x[[1]], 3) = "X"
chrom(x[[2]], 3) = "X"

stopifnot(identical(isXmarker(x), c(FALSE,FALSE,TRUE)))
```

---

`marker_select` *Select or remove attached markers*

---

## Description

Functions for manipulating markers attached to ped objects.

## Usage

```
selectMarkers(x, markers = NULL, chroms = NULL, fromPos = NULL, toPos = NULL)

getMarkers(x, markers = NULL, chroms = NULL, fromPos = NULL, toPos = NULL)

removeMarkers(x, markers = NULL, chroms = NULL, fromPos = NULL, toPos = NULL)

whichMarkers(x, markers = NULL, chroms = NULL, fromPos = NULL, toPos = NULL)
```

## Arguments

| | |
|---|---|
| x | A ped object, or a list of such |
| markers | Either a character vector (with marker names), a numeric vector (with marker indices), a logical (of length nMarkers(x)), or NULL. |
| chroms | A vector of chromosome names, or NULL |
| fromPos | A single number or NULL |
| toPos | A single number or NULL |

## Details

If markers consists of negative integers, it will be converted to its complement within 1:nMarkers(x).

## Value

The return values of these functions are:

- selectMarkers(): an object identical to x, but where only the indicated markers are kept
- removeMarkers(): an object identical to x, but where the indicated markers are removed
- getMarkers(): a list of marker objects. Note: If x is a list of pedigrees, the marker objects attached to the first component will be returned.
- whichMarkers(): an integer vector with indices of the indicated markers. If x is a list of pedigrees an error is raised unless whichMarkers() gives the same result for all components.

## See Also

setMarkers()

mendelianCheck *Check for Mendelian errors*

## Description

Check marker data for Mendelian inconsistencies

## Usage

```
mendelianCheck(x, remove = FALSE, verbose = !remove)
```

## Arguments

| | |
|---|---|
| x | a ped() object |
| remove | a logical. If FALSE, the function returns the indices of markers found to incorrect. If TRUE, a new ped object is returned, where the incorrect markers have been deleted. |
| verbose | a logical. If TRUE, details of the markers failing the tests are shown. |

## Value

A numeric containing the indices of the markers that did not pass all tests, or (if remove = TRUE) a new ped object where the failing markers are removed.

## Author(s)

Magnus Dehli Vigeland

## Examples

```
x = nuclearPed(3)

# Add a SNP with Mendelian error
m = marker(x, '1' = 1, '2' = 1, '3' = 1:2)
x = setMarkers(x, m)

mendelianCheck(x)
```

`mergePed` *Merge two pedigrees*

## Description

This function merges two ped objects, joining them at the individuals with equal ID labels. This is especially useful for building 'top-heavy' pedigrees. Only ped objects without marker data are supported.

## Usage

```
mergePed(x, y, ...)
```

## Arguments

| | |
|---|---|
| `x, y` | `ped()` objects |
| `...` | further arguments passed along to `ped()`, e.g. `famid`, `validate` and `reorder`. |

## Value

A ped object.

## Author(s)

Magnus Dehli Vigeland

## Examples

```
# Creating a trio where each parent have first cousin parents.
# (Alternatively, this could be built using many calls to addParents().)

# Paternal family
x = cousinPed(1, child = TRUE)
x = addSon(x, 9)

# Maternal family
y = cousinPed(1, child = TRUE)
y = relabel(y, c(101:108, 10))
y = swapSex(y, 10)

# Joining x and y at the common individuals (in this case: `10`)
z = mergePed(x, y)

# Plot all three pedigrees
opar = par(mfrow = c(1, 3))
plot(x); plot(y); plot(z, col = list(red = labels(y)))

# Reset graphical parameters
```

```
par(opar)
```

---

`newMarker` *Internal marker constructor*

---

## Description

This is the internal constructor of `marker` objects. It does not do any input validation and should only be used in programming scenarios, and only if you know what you are doing. Most users are recommended to use the regular constructor `marker()`.

## Usage

```
newMarker(
  alleleMatrixInt,
  alleles,
  afreq,
  name = NA_character_,
  chrom = NA_character_,
  posMb = NA_real_,
  mutmod = NULL,
  pedmembers,
  sex
)
```

## Arguments

| | |
|---|---|
| `alleleMatrixInt` | An integer matrix. |
| `alleles` | A character vector. |
| `afreq` | A numeric vector. |
| `name` | A character of length 1. |
| `chrom` | A character of length 1. |
| `posMb` | A numeric of length 1. |
| `mutmod` | A mutation model. |
| `pedmembers` | A character vector. |
| `sex` | An integer vector. |

## Details

See `marker()` for more details about the marker attributes.

## Value

A `marker` object.

## Examples

```
newMarker(matrix(c(1L, 0L, 1L, 1L, 0L, 2L), ncol = 2),
          alleles = c("A", "B"), afreq = c(0.1, 0.9), name = "M",
          pedmembers = c("1", "2", "3"), sex = c(1L, 2L, 1L))
```

---

# newPed *Internal ped constructor*

---

## Description

This is the internal constructor of ped objects. It does not do any validation of input other than simple type checking. In particular it should only be used in programming scenarios where it is known that the input is a valid, connected pedigree. End users are recommended to use the regular constructor `ped()`.

## Usage

```
newPed(ID, FIDX, MIDX, SEX, FAMID)
```

## Arguments

| | |
|---|---|
| `ID` | A character vector. |
| `FIDX` | An integer vector. |
| `MIDX` | An integer vector. |
| `SEX` | An integer vector. |
| `FAMID` | A string. |

## Details

See `ped()` for details about the input parameters.

## Value

A ped object.

## Examples

```
newPed("a", 0L, 0L, 1L, "")
```

## nMarkers *The number of markers attached to a pedigree*

### Description

The number of markers attached to a pedigree

### Usage

```
nMarkers(x)

hasMarkers(x)
```

### Arguments

| | |
|---|---|
| x | A ped object or a list of such (see Value). |

### Value

The function nMarkers returns the number of marker objects attached to x. If x is a list of pedigrees, an error is raised unless all of them have the same number of markers.

The function hasMarkers returns TRUE if nMarkers(x) > 0.

## ped *Pedigree construction*

### Description

This is the basic constructor of ped objects. Utility functions for creating many common pedigree structures are described in ped_basic.

### Usage

```
ped(
  id,
  fid,
  mid,
  sex,
  famid = "",
  reorder = TRUE,
  validate = TRUE,
  isConnected = FALSE,
  verbose = FALSE
)

singleton(id = 1, sex = 1, famid = "")
```

## Arguments

| | |
|---|---|
| id | a vector (numeric or character) of individual ID labels. |
| fid | a vector of the same length as id, containing the labels of the fathers. In other words fid[i] is the father of id[i], or 0 if id[i] is a founder. |
| mid | a vector of the same length as id, containing the labels of the mothers. In other words mid[i] is the mother of id[i], or 0 if id[i] is a founder. |
| sex | a numeric of the same length as id, describing the genders of the individuals (in the same order as id.) Each entry must be either 1 (=male), 2 (=female) or 0 (=unknown). |
| famid | a character string. Default: An empty string. |
| reorder | a logical. If TRUE, the pedigree is reordered so that all parents precede their children. |
| validate | a logical. If TRUE, validatePed() is run before returning the pedigree. |
| isConnected | a logical, by default FALSE. If it is known that the input is connected, setting this to TRUE speeds up the processing. |
| verbose | a logical. |

## Details

A singleton is a special ped object whose pedigree contains 1 individual. The class attribute of a singleton is c('singleton','ped').

Selfing, i.e. the presence of pedigree members whose father and mother are the same individual, is allowed in ped objects. Any such "self-fertilizing" parent must have undecided sex (sex = 0).

If the pedigree is disconnected, it is split into its connected components and returned as a list of ped objects.

## Value

A ped object, which is essentially a list with the following entries:

- ID : A character vector of ID labels. Unless the pedigree is reordered during creation, this equals as.character(id)
- FIDX : An integer vector with paternal indices: For each $j = 1, 2, ...$, the entry FIDX[j] is 0 if ID[j] has no father within the pedigree; otherwise ID[FIDX[j]] is the father of ID[j].
- MIDX : An integer vector with maternal indices: For each $j = 1, 2, ...$, the entry MIDX[j] is 0 if ID[j] has no mother within the pedigree; otherwise ID[MIDX[j]] is the mother of ID[j].
- SEX : An integer vector with gender codes. Unless the pedigree is reordered, this equals as.integer(sex).
- FAMID : The family ID.
- UNBROKEN_LOOPS : A logical: TRUE if the pedigree is inbred.
- LOOP_BREAKERS : A matrix with loop breaker ID's in the first column and their duplicates in the second column. All entries refer to the internal IDs. This is usually set by breakLoops().
- FOUNDER_INBREEDING : A list of two potential entries, "autosomal" and "x"; both numeric vectors with the same length as founders(x). FOUNDER_INBREEDING is always NULL when a new ped is created. See founderInbreeding().
- MARKERS : A list of marker objects, or NULL.

### Author(s)

Magnus Dehli Vigeland

### See Also

ped_basic, ped_modify, ped_subgroups, `relabel()`

### Examples

```
# Trio
x = ped(id = 1:3, fid = c(0,0,1), mid = c(0,0,2), sex = c(1,2,1))

# Female singleton
y = singleton('NN', sex = 2)

# Selfing
z = ped(id = 1:2, fid = 0:1, mid = 0:1, sex = 0:1)
stopifnot(hasSelfing(z))

# Disconnected pedigree: Trio + singleton
w = ped(id = 1:4, fid = c(2,0,0,0), mid = c(3,0,0,0), sex = c(1,1,2,1))
stopifnot(is.pedList(w), length(w) == 2)
```

---

## pedtools *pedtools: Tools for working with pedigrees in R*

---

### Description

A comprehensive collection of tools for creating, manipulating and visualising pedigrees and genetic marker data. Pedigrees can be read from text files or created on the fly with built-in functions. A range of utilities enable modifications like adding or removing individuals, breaking loops, and merging pedigrees. Pedigree plots are produced by wrapping the plotting functionality of the `kinship2` package. A Shiny app for creating pedigrees, based on `pedtools`, is available at https://magnusdv.shinyapps.io/quickped. `pedtools` is the hub of the ped suite, a collection of packages for pedigree analysis. A detailed presentation of the ped suite is given in the book Pedigree Analysis in R (Vigeland, 2021, ISBN:9780128244302).

---

## ped_basic *Create simple pedigrees*

---

### Description

Utility functions for creating some common pedigree structures.

## Usage

```
nuclearPed(nch = 1, sex = 1, father = "1", mother = "2", children = NULL)

halfSibPed(
  nch1 = 1,
  nch2 = 1,
  sex1 = 1,
  sex2 = 1,
  type = c("paternal", "maternal")
)

linearPed(n, sex = 1)

cousinPed(degree, removal = 0, side = c("right", "left"), child = FALSE)

halfCousinPed(degree, removal = 0, side = c("right", "left"), child = FALSE)

ancestralPed(g)

selfingPed(s, sex = 1)
```

## Arguments

| | |
|---|---|
| nch | The number of children, by default 1. If children is not NULL, nch is set to length(children) |
| sex | A vector with integer gender codes (0=unknown, 1=male, 2=female). In nuclearPed(), it contains the genders of the children and is recycled (if necessary) to length nch. In linearPed() it also contains the genders of the children (1 in each generation) and should have length at most n (recycled if shorter than this). In selfingPed() it should be a single number, indicating the gender of the last individual (the others must necessarily have gender code 0.) |
| father | The label of the father. Default: "1". |
| mother | The label of the mother. Default: "2". |
| children | A character with labels of the children. Default: "3", "4", ... |
| nch1, nch2 | The number of children in each sibship. |
| sex1, sex2 | Vectors of gender codes for the children in each sibship. Recycled (if necessary) to lengths nch1 and nch2 respectively. |
| type | Either "paternal" or "maternal". |
| n | The number of generations, not including the initial founders. |
| degree | A non-negative integer: 0=siblings, 1=first cousins; 2=second cousins, a.s.o. |
| removal | A non-negative integer. See Details and Examples. |
| side | Either "right" or "left"; the side on which removals should be added. |
| child | A logical: Should an inbred child be added to the two cousins? |

g — A nonnegative integer indicating the number of ancestral generations to include. The resulting pedigree has `2^(g+1)-1` members. The case `g = 0` results in a singleton.

s — A nonnegative integer indicating the number of consecutive selfings. The case `s = 0` results in a singleton.

## Details

`halfSibPed(nch1,nch2)` produces a pedigree containing two sibships (of sizes `nch1` and `nch2`) with the same father, but different mothers. If maternal half sibs are wanted instead, add `type = "maternal"`.

`cousinPed(degree = n,removal = k)` creates a pedigree with two n'th cousins, k times removed. By default, removals are added on the right side, but this can be changed by adding `side = left`. (Similarly for `halfCousinPed`.)

`ancestralPed(g)` returns the family tree of a single individual, including all ancestors g generations back.

`selfingPed(s)` returns a line of s consecutive selfings.

## Value

A ped object.

## See Also

`ped()`, `singleton()`, ped_complex, ped_subgroups

## Examples

```
# A nuclear family with 2 boys and 3 girls
nuclearPed(5, sex = c(1, 1, 2, 2, 2))

# A straight line of females
linearPed(3, sex = 2)

# Paternal half brothers
halfSibPed()

# Maternal half sisters
halfSibPed(sex1 = 2, sex2 = 2, type = "maternal")

# Larger half sibships: boy and girl on one side; 3 girls on the other
halfSibPed(nch1 = 2, sex = 1:2, nch2 = 3, sex2 = 2)

# Grand aunt:
cousinPed(degree = 0, removal = 2)

# Second cousins once removed.
cousinPed(degree = 2, removal = 1)
```

```
# Same, but with the 'removal' on the left side.
cousinPed(2, 1, side = "left")

# A child of half first cousins.
halfCousinPed(degree = 1, child = TRUE)

# The 'family tree' of a person
ancestralPed(g = 2)
```

---

ped_complex *Complex pedigree structures*

---

## Description

Functions for creating a selection of pedigrees that are awkward to construct from scratch, or by using the simple structures described in ped_basic.

## Usage

```
doubleCousins(
  degree1,
  degree2,
  removal1 = 0,
  removal2 = 0,
  half1 = FALSE,
  half2 = FALSE,
  child = FALSE
)

doubleFirstCousins()

quadHalfFirstCousins()

fullSibMating(n)

halfSibStack(n)
```

## Arguments

| | |
|---|---|
| degree1, degree2, removal1, removal2 | Nonnegative integers. |
| half1, half2 | Logicals, indicating if the fathers (resp. mothers) should be full or half cousins. |
| child | A logical: Should a child be added to the double cousins? |
| n | A positive integer indicating the number of crossings. |

## Details

The function doubleCousins returns a pedigree linking two individuals who are simultaneous paternal and maternal cousins. More precisely, they are:

- paternal (full or half) cousins of type (degree1, removal1)
- maternal (full or half) cousins of type (degree2, removal2).

For convenience, a wrapper doubleFirstCousins is provided for the most common case, double first cousins.

quadHalfFirstCousins produces a pedigree with quadruple half first cousins.

fullSibMating crosses full sibs consecutively n times.

halfSibStack produces a breeding scheme where the two individuals in the final generation are simultaneous half k'th cousins, for each k = 0,...,n-1.

## Value

A ped object.

## See Also

ped_basic

## Examples

```
# Consecutive brother-sister matings.
x = fullSibMating(2)
# plot(x)

# Simultaneous half siblings and half first cousins
x = halfSibStack(2)
# plot(x)

# Double first cousins
x = doubleFirstCousins()
# plot(x)

# Quadruple half first cousins
x = quadHalfFirstCousins()
# plot(x) # Weird plotting behaviour for this pedigree.
```

ped_internal *Internal ordering of pedigree members*

## Description

These functions give access to - and enable modifications of - the order in which the members of a pedigree are stored. (This is the order in which the members are listed when a ped object is printed to the screen.)

## Usage

```
reorderPed(x, neworder = NULL)

parentsBeforeChildren(x)

hasParentsBeforeChildren(x)

foundersFirst(x)

internalID(x, ids, errorIfUnknown = TRUE)
```

## Arguments

| | |
|---|---|
| x | A ped object. Most of these functions also accepts ped lists. |
| neworder | A permutation of labels(x) or of vector 1:pedsize(x). By default, the sorting order of the ID labels is used. |
| ids | A character vector (or coercible to one) of original ID labels. |
| errorIfUnknown | A logical. If TRUE (default), the function stops with an error if not all elements of ids are recognised as names of members in x. |

## Details

The internal ordering is usually of little importance for end users, with one important exception: Certain pedigree-traversing algorithms require parents to precede their children. A special function, parentsBeforeChildren() is provided for this purpose. This is a wrapper of the more general reorderPed() which allows any permutation of the members.

It should be noted that ped() by default calls parentsBeforeChildren() whenever a pedigree is created, unless explicitly avoided with reorder = FALSE.

hasParentsBeforeChildren() can be used as a quick test to decide if it is necessary to call parentsBeforeChildren().

The foundersFirst() function reorders the pedigree so that all the founders come first.

The utility internalID() converts ID labels to indices in the internal ordering. If x is a list of pedigrees, the output is a data frame containing both the component number and internal ID (within the component).

## See Also

ped()

## Examples

```
x = ped(id = 3:1, fid = c(1,0,0), mid = c(2,0,0), sex = c(1,2,1), reorder = FALSE)
x

# The 'ids' argument is converted to character, hence these are equivalent:
internalID(x, ids = 3)
internalID(x, ids = "3")

hasParentsBeforeChildren(x)

# Fix the ordering
y = parentsBeforeChildren(x)
internalID(y, ids = 3)

# A different ordering
reorderPed(x, c(2,1,3))
```

---

# ped_modify *Add/remove pedigree members*

---

## Description

Functions for adding or removing individuals in a 'ped' object.

## Usage

```
addChildren(
  x,
  father = NULL,
  mother = NULL,
  nch = NULL,
  sex = 1,
  ids = NULL,
  verbose = TRUE
)

addSon(x, parent, id = NULL, verbose = TRUE)

addDaughter(x, parent, id = NULL, verbose = TRUE)

addParents(x, id, father = NULL, mother = NULL, verbose = TRUE)

removeIndividuals(x, ids, verbose = TRUE)
```

```
branch(x, id)

## S3 method for class 'ped'
subset(x, subset, ...)
```

## Arguments

| | |
|---|---|
| x | A ped object. |
| father, mother | Single ID labels. At least one of these must belong to an existing pedigree member. The other label may either: 1) belong to an existing member, 2) not belong to any existing member, or 3) be missing (i.e. not included in the function call). In cases 2 and 3 a new founder is added to the pedigree. In case 2 its label is the one given, while in case 3 a suitable label is created by the program (see Details). |
| nch | A positive integer indicating the number of children to be created. Default: 1. |
| sex | Gender codes of the created children (recycled if needed). |
| ids | A character vector (or coercible to such) with ID labels. In addChildren the (optional) ids argument is used to specify labels for the created children. If given, its length must equal nch. If not given, labels are assigned automatically as explained in Details. |
| verbose | A logical: Verbose output or not. |
| parent | The ID label (coercible to character) of a single pedigree member, which will be the father or mother (depending on its gender) of the new child. |
| id | The ID label of some existing pedigree member. |
| subset | A character vector (or coercible to such) with ID labels forming a connected sub-pedigree. |
| ... | Not used. |

## Details

In addChildren() and addParents(), labels of added individuals are created automatically if they are not specified by the user. In the automatic case, the labelling depends on whether the existing labels are integer-like or not (i.e. if labels(x) equals as.character(as.integer(labels(x)))). If so, the new labels are integers subsequent to the largest of the existing labels. If not, the new labels are "NN_1", "NN_2", ... If any such label already exists, the numbers are adjusted accordingly.

addSon() and addDaughter() are wrappers for a common use of addChildren(), namely adding a single child to a pedigree member. Note that its argument parent is gender-neutral, unlike in addChildren() where you have to know the parental genders. Also note that the other parent is always created as a new individual. Thus, applying addDaughter() twice with the same parent will create half sisters.

In removeIndividuals() all descendants of ids are also removed. Any individuals (spouses) left unconnected to the remaining pedigree are also removed.

The branch() function extracts the sub-pedigree formed by id and all his/her spouses and descendants.

Finally, `subset()` can be used to extract any connected sub-pedigree. (Note that in the current implementation, the function does not actually check that the indicated subset forms a connected pedigree; failing to comply with this may lead to obscure errors.)

## Value

The modified ped object.

## Author(s)

Magnus Dehli Vigeland

## See Also

`ped()`, `relabel()`, `swapSex()`

## Examples

```
x = nuclearPed(1)

# To see the effect of each command below, use plot(x) in between.
x = addSon(x, 3)
x = addParents(x, id = 4, father = 6, mother = 7)
x = removeIndividuals(x, 4)
```

---

# ped_subgroups *Pedigree subgroups*

---

## Description

A collection of utility functions for identifying pedigree members with certain properties.

## Usage

```
founders(x, internal = FALSE)

nonfounders(x, internal = FALSE)

leaves(x, internal = FALSE)

males(x, internal = FALSE)

females(x, internal = FALSE)

typedMembers(x, internal = FALSE)
```

```
untypedMembers(x, internal = FALSE)

father(x, id, internal = FALSE)

mother(x, id, internal = FALSE)

children(x, id, internal = FALSE)

offspring(x, id, internal = FALSE)

spouses(x, id, internal = FALSE)

unrelated(x, id, internal = FALSE)

parents(x, id, internal = FALSE)

grandparents(x, id, degree = 2, internal = FALSE)

siblings(x, id, half = NA, internal = FALSE)

nephews_nieces(x, id, removal = 1, half = NA, internal = FALSE)

ancestors(x, id, inclusive = FALSE, internal = FALSE)

commonAncestors(x, ids, inclusive = FALSE, internal = FALSE)

descendants(x, id, inclusive = FALSE, internal = FALSE)

commonDescendants(x, ids, inclusive = FALSE, internal = FALSE)
```

## Arguments

| | |
|---|---|
| x | A ped() object or a list of such. |
| internal | A logical indicating whether id (or ids) refers to the internal order. |
| id, ids | A character (or coercible to such) with one or several ID labels. |
| degree, removal | Non-negative integers. |
| half | a logical or NA. If TRUE (resp. FALSE), only half (resp. full) siblings/cousins/nephews/nieces are returned. If NA, both categories are included. |
| inclusive | A logical indicating whether an individual should be counted among his or her own ancestors/descendants |

## Value

The functions ancestors(x,id) and descendants(x,id) return a vector containing the IDs of all ancestors (resp. descendants) of the individual id within the pedigree x. If inclusive = TRUE, id is included in the output.

For `commonAncestors(x,ids)` and `commonDescendants(x,ids)`, a vector containing the IDs of common ancestors to all of `ids`.

The functions `founders`, `nonfounders`, `males`, `females`, `leaves` each return a vector containing the IDs of all pedigree members with the wanted property. (Recall that a founder is a member without parents in the pedigree, and that a leaf is a member without children in the pedigree.)

The functions `father`, `mother`, `cousins`, `grandparents`, `nephews_nieces`, `children`, `parents`, `siblings`, `spouses`, `unrelated`, each returns a vector containing the IDs of all pedigree members having the specified relationship with `id`.

## Author(s)

Magnus Dehli Vigeland

## Examples

```
x = ped(id = 2:9,
         fid = c(0,0,2,0,4,4,0,2),
         mid = c(0,0,3,0,5,5,0,8),
         sex = c(1,2,1,2,1,2,2,2))

spouses(x, id = 2) # 3, 8
children(x, 2)     # 4, 9
descendants(x, 2)  # 4, 6, 7, 9
siblings(x, 4)     # 9 (full or half)
unrelated(x, 4)    # 5, 8
father(x, 4)       # 2
mother(x, 4)       # 3

siblings(x, 4, half = FALSE) # none
siblings(x, 4, half = TRUE)  # 9

leaves(x)          # 6, 7, 9
founders(x)        # 2, 3, 5, 8
```

---

# ped_utils *Pedigree utilities*

---

## Description

Various utility functions for ped objects.

## Usage

```
pedsize(x)

generations(x, maxComp = TRUE)
```

```
hasUnbrokenLoops(x)

hasInbredFounders(x, chromType = "autosomal")

hasSelfing(x)

hasCommonAncestor(x)

subnucs(x)

peelingOrder(x)
```

## Arguments

| | |
|---|---|
| x | A ped object, or (in some functions - see Details) a list of such. |
| maxComp | A logical, by default TRUE. See Value. |
| chromType | Either "autosomal" (default) or "x". |

## Value

- `pedsize(x)` returns the number of pedigree members in each component of `x`.
- `generations(x)` returns the number of generations in `x`, defined as the number of individuals in the longest line of parent-child links. (Note that this definition is valid also if `x` has loops.) If `x` has multiple components, the output depends on the parameter `maxComp`. If this is FALSE, the output is a vector containing the result for each component. If TRUE (default), only the highest number is returned.
- `hasUnbrokenLoops(x)` returns TRUE if `x` has loops, otherwise FALSE. (No computation is done here; the function simply returns the value of `x$UNBROKEN_LOOPS`).
- `hasInbredFounders(x)` returns TRUE is founder inbreeding is specified for `x` and at least one founder has positive inbreeding coefficient. See `founderInbreeding()` for details.
- `hasSelfing(x)` returns TRUE if the pedigree contains selfing events. This is recognised by father and mother begin equal for some child. (Note that for this to be allowed, the gender code of the parent must be 0.)
- `hasCommonAncestor(x)` computes a logical matrix `A` whose entry `A[i,j]` is TRUE if pedigree members i and j have a common ancestor in `x`, and FALSE otherwise. By convention, `A[i,i]` is TRUE for all i.
- `subnucs(x)` returns a list of all nuclear sub-pedigrees of `x`, wrapped as `nucleus` objects. Each nucleus is a list with entries `father`, `mother` and `children`.
- `peelingOrder(x)` calls `subnucs(x)` and extends each entry with a `link` individual, indicating a member linking the nucleus to the remaining pedigree. One application of this function is the fact that if *fails* to find a complete peeling order if and only if the pedigree has loops. (In fact it is called each time a new ped object is created by `ped()` in order to detect loops.) The main purpose of the function, however, is to prepare for probability calculations in other packages, as e.g. in `pedprobr::likelihood`.

## Examples

```
x = fullSibMating(1)
stopifnot(pedsize(x) == 6)
stopifnot(hasUnbrokenLoops(x))
stopifnot(generations(x) == 3)

# All members have common ancestors except the grandparents
CA = hasCommonAncestor(x)
stopifnot(!CA[1,2], !CA[2,1], sum(CA) == length(CA) - 2)

# Effect of breaking the loop
y = breakLoops(x)
stopifnot(!hasUnbrokenLoops(y))
stopifnot(pedsize(y) == 7)

# A pedigree with selfing (note the necessary `sex = 0`)
z1 = singleton(1, sex = 0)
z2 = addChildren(z1, father = 1, mother = 1, nch = 1)
stopifnot(!hasSelfing(z1), hasSelfing(z2))

# Nucleus sub-pedigrees
stopifnot(length(subnucs(z1)) == 0)
peelingOrder(cousinPed(1))
```

---

# plot.ped *Plot pedigrees with genotypes*

---

## Description

This is the main function for pedigree plotting, with many options for controlling the appearance of pedigree symbols and accompanying labels. Most of the work is done by the plotting functionality in the kinship2 package.

## Usage

```
## S3 method for class 'ped'
plot(
  x,
  marker = NULL,
  sep = "/",
  missing = "-",
  showEmpty = FALSE,
  labs = labels(x),
  title = NULL,
  col = 1,
  aff = NULL,
  carrier = NULL,
```

```
  hatched = NULL,
  shaded = NULL,
  deceased = NULL,
  starred = NULL,
  twins = NULL,
  textInside = NULL,
  textAbove = NULL,
  hints = NULL,
  fouInb = "autosomal",
  margins = c(0.6, 1, 4.1, 1),
  keep.par = FALSE,
  ...
)

## S3 method for class 'singleton'
plot(
  x,
  marker = NULL,
  sep = "/",
  missing = "-",
  showEmpty = FALSE,
  labs = labels(x),
  title = NULL,
  col = 1,
  aff = NULL,
  carrier = NULL,
  hatched = NULL,
  shaded = NULL,
  deceased = NULL,
  starred = NULL,
  textInside = NULL,
  textAbove = NULL,
  fouInb = "autosomal",
  margins = c(8, 0, 0, 0),
  yadj = 0,
  ...
)

as_kinship2_pedigree(
  x,
  deceased = NULL,
  aff = NULL,
  twins = NULL,
  hints = NULL
)

## S3 method for class 'pedList'
plot(x, ...)
```

## Arguments

| | |
|---|---|
| x | A ped() object. |
| marker | Either a vector of names or indices referring to markers attached to x, a marker object, or a list of such. The genotypes for the chosen markers are written below each individual in the pedigree, in the format determined by sep and missing. See also showEmpty. If NULL (the default), no genotypes are plotted. |
| sep | A character of length 1 separating alleles for diploid markers. |
| missing | The symbol (integer or character) for missing alleles. |
| showEmpty | A logical, indicating if empty genotypes should be included. |
| labs | A vector or function controlling the individual labels included in the plot. Alternative forms:<br>• If labs is a vector with nonempty intersection with labels(x), these individuals will be labelled. If the vector is named, then the (non-empty) names are used instead of the ID label. (See Examples.)<br>• If labs is NULL, or has nonempty intersection with labels(x), then no labels are drawn.<br>• If labs is the word "num", then all individuals are numerically labelled following the internal ordering.<br>• If labs is a function, it will be replaced with labs(x) and handled as above. (See Examples.) |
| title | The plot title. If NULL (default) or '', no title is added to the plot. |
| col | A vector of colours for the pedigree members, recycled if necessary. Alternatively, col can be a list assigning colours to specific members. For example if col = list(red = "a",blue = c("b","c")) then individual "a" will be red, "b" and "c" blue, and everyone else black. By default everyone is black. |
| aff | A vector of labels identifying members whose plot symbols should be filled. (This is typically used in medical pedigrees to indicate affected members.) |
| carrier | A vector of labels identifying members whose plot symbols should be marked with a dot. (This is typically used in medical pedigrees to indicate unaffected carriers of the disease allele.) |
| hatched | A vector of labels identifying members whose plot symbols should be hatched. |
| shaded | (Deprecated) synonym of hatched |
| deceased | A vector of labels indicating deceased pedigree members. |
| starred | A vector of labels indicating pedigree members that should be marked with a star in the pedigree plot. |
| twins | A data frame with columns id1, id2 and code, passed on to the relation parameter of kinship2::plot.pedigree(). |
| textInside, textAbove | Character vectors of text to be printed inside or above pedigree symbols. |
| hints | A list with alignment hints passed on to kinship2::align.pedigree(). Rarely necessary, but see Examples. |

| | |
|---|---|
| fouInb | Either "autosomal" (default), "x" or NULL. If "autosomal" or "x", inbreeding coefficients are added to the plot above the inbred founders. If NULL, or if no founders are inbred, nothing is added. |
| margins | A numeric of length 4 indicating the plot margins. For singletons only the first element (the 'bottom' margin) is used. |
| keep.par | A logical (default = FALSE). If TRUE, the graphical parameters are not reset after plotting, which may be useful for adding additional annotation. |
| ... | Arguments passed on to plot.pedigree in the kinship2 package. In particular symbolsize and cex can be useful. |
| yadj | A tiny adjustment sometimes needed to fix the appearance of singletons. |

## Details

plot.ped is in essence an elaborate wrapper for kinship2::plot.pedigree().

## Author(s)

Magnus Dehli Vigeland

## See Also

kinship2::plot.pedigree()

## Examples

```
x = nuclearPed(father = "fa", mother = "mo", child = "boy")
m = marker(x, fa = "1/1", boy = "1/2", name = "SNP")

plot(x, marker = m)

# Markers attached to `x` may be called by name
x = setMarkers(x, m)
plot(x, marker = "SNP")

# Other options
plot(x, marker = "SNP", hatched = typedMembers(x),
     starred = "fa", deceased = "mo")

# Filled symbols
plot(x, aff = males(x))

# Label only some members
plot(x, labs = c("fa", "boy"))

# Label only some members; rename the father
plot(x, labs = c(FATHER = "fa", "boy"))

# Label males only
plot(x, labs = males)
```

```
# Colours
plot(x, col = list(red = "fa", green = "boy"), hatched = "boy")

# Founder inbreeding is shown by default
founderInbreeding(x, "mo") = 0.1
plot(x)

# ... but can be suppressed
plot(x, fouInb = NULL)

# Twins
x = nuclearPed(children = c("tw1", "tw2", "tw3"))
plot(x, twins = data.frame(id1 = "tw1", id2 = "tw2", code = 1)) # MZ
plot(x, twins = data.frame(id1 = "tw1", id2 = "tw2", code = 1)) # DZ

# Triplets
plot(x, twins = data.frame(id1 = c("tw1", "tw2"),
                           id2 = c("tw2", "tw3"),
                           code = 2))

#-----------------------------
# In some cases, the plotting machinery of `kinship2` needs a hint
# (see ?kinship2::align.pedigree)

# Example with 3/4-siblings
y = nuclearPed(2)
y = addChildren(y, 3, mother = 5, nch = 1)
y = addChildren(y, 4, mother = 5, nch = 1)

plot(y) # bad

hints = list(order = 1:7, spouse = rbind(c(3,5,0), c(5,4,0)))
plot(y, hints = hints) # good
```

---

`plotPedList` *Plot a collection of pedigrees.*

---

## Description

This function creates a row of pedigree plots, each created by `plot.ped()`. Any parameter accepted by `plot.ped()` can be applied, either to all plots simultaneously, or to individual plots. Some effort is made to guess a reasonable window size and margins, but in general the user must be prepared to do manual resizing of the plot window. See various examples in the Examples section below.

## Usage

```
plotPedList(
  plots,
```

```
  widths = NULL,
  groups = NULL,
  titles = NULL,
  frames = TRUE,
  fmar = NULL,
  frametitles = NULL,
  source = NULL,
  dev.height = NULL,
  dev.width = NULL,
  newdev = !is.null(dev.height) || !is.null(dev.width),
  verbose = FALSE,
  ...
)
```

## Arguments

| | |
|---|---|
| plots | A list of lists. Each element of plots is a list, where the first element is a pedigree, and the remaining elements are passed on to plot.ped. These elements must be correctly named. See examples below. |
| widths | A numeric vector of relative widths of the subplots. Recycled to length(plots) if necessary, before passed on to layout(). Note that the vector does not need to sum to 1. |
| groups | A list of vectors, each consisting of consecutive integers, indicating subplots to be grouped. By default the grouping follows the list structure of plots. |
| titles | A character vector of titles for each group. Overrides titles given in individuals subplots. |
| frames | A logical indicating if groups should be framed. |
| fmar | A single number in the interval $[0, 0.5)$ controlling the position of the frames. |
| frametitles | Deprecated; use titles instead. |
| source | NULL (default), or the name or index of an element of plots. If given, marker data is temporarily transferred from this to all the other pedigrees. This may save some typing when plotting the same genotypes on several pedigrees. |
| dev.height, dev.width | The dimensions of the new plot window. If these are NA suitable values are guessed from the pedigree sizes. |
| newdev | A logical, indicating if a new plot window should be opened. |
| verbose | A logical. |
| ... | Further arguments passed on to each call to plot.ped(). |

## Details

Note that for tweaking dev.height and dev.width the function dev.size() is useful to determine the size of the active device.

## Author(s)

Magnus Dehli Vigeland

## See Also

plot.ped()

## Examples

```
##################
# Basic examples #
##################

# Simples use: Just give a list of ped objects.
peds = list(nuclearPed(3), cousinPed(2), singleton(12), halfSibPed())
plotPedList(peds, newdev = TRUE)

# Modify the relative widths (which are not guessed)
w = c(2, 3, 1, 2)
plotPedList(peds, widths = w)

# In most cases the guessed dimensions are ok but not perfect.
# Resize plot window manually and re-plot with `newdev = FALSE` (default)
# plotPedList(peds, widths = w)

## Remove frames
plotPedList(peds, widths = w, frames = FALSE)

# Non-default grouping
plotPedList(peds, widths = w, groups = list(1, 2:3), titles = 1:2)

# Parameters added in the main call are used in each sub-plot
plotPedList(peds, widths = w, margins = c(2, 4, 2, 4), labs = leaves,
            hatched = leaves, symbolsize = 1.3, col = list(red = 1))

dev.off()

################################
# Example of automatic grouping #
################################
H1 = nuclearPed()
H2 = list(singleton(1), singleton(3))  # grouped!

plotPedList(list(H1, H2), dev.height = 2, dev.width = 4,
            titles = c(expression(H[1]), expression(H[2])))

dev.off()

#############################################################
# Complex example with individual parameters for each plot #
#############################################################

# For more control of individual plots, each plot and all
# its parameters can be specified in its own list.

x1 = nuclearPed(nch = 3)
```

```
m1 = marker(x1, `3` = 1:2)
marg1 = c(7, 4, 7, 4)
plot1 = list(x1, marker = m1, margins = marg1, title = "Plot 1",
             deceased = 1:2, cex = 1.3)

x2 = cousinPed(2)
m2 = marker(x2, alleles = "A")
genotype(m2, leaves(x2)) = "A"
marg2 = c(3, 4, 2, 4)
plot2 = list(x2, marker = m2, margins = marg2, title = "Plot 2",
             symbolsize = 1.2, labs = NULL)

x3 = singleton("Mr. X")
marg3 = c(10, 0, 0, 0)
plot3 = list(x3, margins = marg3, title = "Plot 3",
             symbolsize = 1, cex = 2)

x4 = halfSibPed()
hatched = 4:5
col = list(red = founders(x4), blue = leaves(x4))
marg4 = marg1
plot4 = list(x4, margins = marg4, title = "Plot 4", cex = 1.3,
             hatched = hatched, col = col)

plotPedList(list(plot1, plot2, plot3, plot4), widths = c(2,3,1,2),
            groups = list(1, 2:3, 4), newdev = TRUE)

dev.off()

################################
# Example with large pedigrees #
################################

# Important to set device dimensions here

plotPedList(list(halfCousinPed(4), cousinPed(7)),
            titles = c("Large", "Very large"),
            dev.height = 8, dev.width = 5)

dev.off()
```

---

`print.nucleus` *S3 methods*

---

## Description

S3 methods

### Usage

```
## S3 method for class 'nucleus'
print(x, ...)
```

### Arguments

| | |
|---|---|
| x | An object |
| ... | Not used |

---

`print.ped` *Printing pedigrees*

---

### Description

Print a ped object using original labels.

### Usage

```
## S3 method for class 'ped'
print(x, ..., markers, verbose = TRUE)
```

### Arguments

| | |
|---|---|
| x | object of class ped. |
| ... | (optional) arguments passed on to `print.data.frame()`. |
| markers | (optional) vector of marker indices. If missing, and x has less than 10 markers, they are all displayed. If x has 10 or more markers, the first 5 are displayed. |
| verbose | If TRUE, a message is printed if only the first 5 markers are printed. (See above). |

### Details

This first calls `as.data.frame.ped()` and then prints the resulting data.frame. The data.frame is returned invisibly.

randomPed *Random pedigree*

## Description

Generate a random pedigree by applying random mating starting from a finite population. The resulting pedigree will have f + g members, where f is the number of founders and g is the number of matings.

## Usage

```
randomPed(g, founders = rpois(1, 3) + 1, selfing = FALSE, seed = NULL)
```

## Arguments

| | |
|---|---|
| g | A positive integer: The number of matings. |
| founders | A positive integer: The size of the initial population. |
| selfing | A logical indicating if selfing is allowed. |
| seed | A numerical seed for random number generation. (Optional.) |

## Details

The sampling scheme for choosing parents in each mating depends on the selfing parameter. If selfing = FALSE, a father is randomly sampled from the existing males, and a mother from the existing females. If selfing = TRUE then one parent P1 is sampled first (among all members), and then a second parent from the set consisting of P1 and all members of the opposite sex. The gender of the child is randomly chosen with equal probabilities.

## Value

A ped object.

## Examples

```
randomPed(3, 3)
randomPed(3, 3, selfing = TRUE)
```

readPed *Read a pedigree from file*

## Description

Read a pedigree from file

## Usage

```
readPed(
  pedfile,
  header = NA,
  famid_col = NA,
  id_col = NA,
  fid_col = NA,
  mid_col = NA,
  sex_col = NA,
  marker_col = NA,
  locusAttributes = NULL,
  missing = 0,
  sep = NULL,
  validate = TRUE,
  ...
)
```

## Arguments

| | |
|---|---|
| pedfile | A file name |
| header | A logical. If NA, the program will interpret the first line as a header line if the first entry contains "id" AND the word "sex" is an entry. |
| famid_col | Index of family ID column. If NA, the program looks for a column named "famid" (ignoring case). |
| id_col | Index of individual ID column. If NA, the program looks for a column named "id" (ignoring case). |
| fid_col | Index of father ID column. If NA, the program looks for a column named "fid" (ignoring case). |
| mid_col | Index of mother ID column. If NA, the program looks for a column named "mid" (ignoring case). |
| sex_col | Index of column with gender codes (0 = unknown; 1 = male; 2 = female). If NA, the program looks for a column named "sex" (ignoring case). If this is not found, genders of parents are deduced from the data, leaving the remaining as unknown. |
| marker_col | Index vector indicating columns with marker alleles. If NA, all columns to the right of all pedigree columns are used. If sep (see below) is non-NULL, each column is interpreted as a genotype column and split into separate alleles with strsplit(...,split = sep,fixed = TRUE). |

| | |
|---|---|
| locusAttributes | Passed on to setMarkers() (see explanation there). |
| missing | Passed on to setMarkers() (see explanation there). |
| sep | Passed on to setMarkers() (see explanation there). |
| validate | A logical indicating if the pedigree structure should be validated. |
| ... | Further parameters passed on to read.table(), e.g. sep, comment.char and quote. |

## Value

A ped object or a list of such.

## Examples

```
tf = tempfile()

### Write and read a trio
trio = data.frame(id = 1:3, fid = c(0,0,1), mid = c(0,0,2), sex = c(1,2,1))
write.table(trio, file = tf, row.names = FALSE)
readPed(tf)

# With marker data in one column
trio.marker = cbind(trio, M = c("1/1", "2/2", "1/2"))
write.table(trio.marker, file = tf, row.names = FALSE)
readPed(tf)

# With marker data in two allele columns
trio.marker2 = cbind(trio, M.1 = c(1,2,1), M.2 = c(1,2,2))
write.table(trio.marker2, file = tf, row.names = FALSE)
readPed(tf)

### Two singletons in the same file
singles = data.frame(id = c("S1", "S2"),
                     fid = c(0,0), mid = c(0,0), sex = c(2,1),
                     M = c("9/14.2", "9/9"))
write.table(singles, file = tf, row.names = FALSE)
readPed(tf)

### Two trios in the same file
trio2 = cbind(famid = rep(c("trio1", "trio2"), each = 3), rbind(trio, trio))

# Without column names
write.table(trio2, file = tf, row.names = FALSE)
readPed(tf)

# With column names
write.table(trio2, file = tf, col.names = FALSE, row.names = FALSE)
readPed(tf, famid = 1, id = 2, fid = 3, mid = 4, sex = 5)

# Cleanup
```

```
unlink(tf)
```

---

`relabel` *Get or modify pedigree labels*

---

## Description

Functions for getting or changing the ID labels of pedigree members.

## Usage

```
relabel(x, new, old = labels(x), reorder = FALSE)

## S3 method for class 'ped'
labels(object, ...)

## S3 method for class 'list'
labels(object, ...)
```

## Arguments

| | |
|---|---|
| `x` | A ped object or a list of such. |
| `new, old` | Character vectors (or coercible to character) of the same length. ID labels in `old` are replaced by those in `new`. |
| `reorder` | A logical. If TRUE, `reorderPed()` is called on `x` after relabelling. Default: FALSE. |
| `object` | A ped object |
| `...` | Not used |

## Value

- `labels()` returns a character vector containing the ID labels of all pedigree members. If the input is a list of ped objects, the output is a list of character vectors.
- `relabel()` returns ped object similar to the input except for the labels.

## Author(s)

Magnus Dehli Vigeland

## See Also

`ped()`

## Examples

```
x = nuclearPed()
x
labels(x)

relabel(x, new = "girl", old = 3)
```

---

`sortGenotypes` *Sort the alleles in each genotype*

---

## Description

Ensure that all genotypes are sorted internally. For example, if a marker attached to x has alleles 1 and 2, then running this function will replace all genotypes "2/1" by "1/2".

## Usage

```
sortGenotypes(x)
```

## Arguments

| | |
|---|---|
| x | A ped object or a list of such |

## Value

An object identical to x except that the all genotypes are sorted.

## Examples

```
x = singleton(1)

# Various markers with misordered genotypes
m1 = marker(x, `1` = 2:1)
m2 = marker(x, `1` = c('b','a'))
m3 = marker(x, `1` = c("100.3", "99.1"))
x = setMarkers(x, list(m1, m2, m3))
x

# Sort all genotypes
y = sortGenotypes(x)
y

# Also works when input is a list of peds
sortGenotypes(list(x, x))
```

`transferMarkers` *Transfer marker data*

## Description

Transfer marker data between pedigrees. Any markers attached to the target are overwritten.

## Usage

```
transferMarkers(
  from,
  to,
  ids = NULL,
  idsFrom = ids,
  idsTo = ids,
  erase = TRUE,
  matchNames = TRUE,
  checkSex = FALSE
)
```

## Arguments

| | |
|---|---|
| `from` | A ped or `singleton` object, or a list of such objects. |
| `to` | A ped or `singleton` object, or a list of such objects. |
| `ids` | A vector of ID labels. This should be used only if the individuals have the same name in both pedigrees; otherwise use `idsFrom` and `idsTo` instead. |
| `idsFrom, idsTo` | Vectors of equal length, denoting source individuals (in the `from` pedigree) and target individuals (in the `to` pedigree), respectively. |
| `erase` | A logical. If `TRUE` (default), all markers attached to `to` are erased prior to transfer, and new marker objects are created with the same attributes as in `from`. If `FALSE` no new marker objects are attached to `to`. Only the genotypes of the `ids` individuals are modified, while genotypes for other pedigree members - and marker attributes - remain untouched. |
| `matchNames` | A logical, only relevant if `erase = FALSE`. If `matchNames = TRUE` (default) marker names are used to ensure genotypes are transferred into the right markers, The output contains only markers present in `from`, in the same order. (An error is raised if the markers are not named.) |
| `checkSex` | A logical. If TRUE, it is checked that `fromIds` and `toIds` have the same sex. Default: FALSE. |

## Details

By default, genotypes are transferred between all individuals present in both pedigrees.

## Value

A ped object (or a list of such) similar to `to`, but where all individuals also present in `from` have marker genotypes copied over. Any previous marker data is erased.

## Examples

```
x = nuclearPed(fa = "father", mo = "mother", children = "boy")
m = marker(x, father = 1:2, mother = 1, boy = 1:2)
x = setMarkers(x, m)

y = list(singleton("father"), nuclearPed(mo = "mother", children = "boy"))

# By default all common individuals are transferred
transferMarkers(x, y)

# Transfer data for the boy only
transferMarkers(x, y, ids = "boy")

# Transfer without erasing marker attributes or others genotypes
# Note that `erase = FALSE` requires markers to be named
z = nuclearPed(children = "boy")
z = setMarkers(z, marker(z, '1' = c(2,2), alleles = 1:2, afreq = c(.1, .9)))
name(x, 1) = name(z, 1) = 'M1'
z2 = transferMarkers(x, z, ids = "boy", erase = FALSE)
z2
# Frequencies are not transferred
afreq(z2, 1)
```

---

`validatePed` *Pedigree errors*

---

## Description

Validate the internal structure of a ped object.

## Usage

```
validatePed(x)
```

## Arguments

| | |
|---|---|
| `x` | object of class ped. |

## Value

If no errors are detected, the function returns NULL invisibly. Otherwise, messages describing the errors are printed to the screen and an error is raised.

`writePed` *Write a pedigree to file*

## Description

Write a pedigree to file

## Usage

```
writePed(
  x,
  prefix,
  what = "ped",
  famid = is.pedList(x),
  header = TRUE,
  merlin = FALSE,
  verbose = TRUE
)
```

## Arguments

| | |
|---|---|
| `x` | A ped object |
| `prefix` | A character string giving the prefix of the files. For instance, if `prefix = "myped"` and `what = c("ped","map")`, the output files are "myped.ped" and "myped.map" in the current directory. Paths to other folder may be included, e.g. `prefix = "path-to-my-dir/myped"`. |
| `what` | A subset of the character vector `c("ped","map","dat","freq")`, indicating which files should be created. By default only the "ped" file is created. This option is ignored if `merlin = TRUE`. |
| `famid` | A logical indicating if family ID should be included as the first column in the ped file. The family ID is taken from `famid(x)`. If `x` is a pedlist, the family IDs are taken from `names(x)`, or if this is NULL, the component-wise `famid()` values. Missing values are replaced by natural numbers. This option is ignored if `merlin = TRUE`. |
| `header` | A logical indicating if column names should be included in the ped file. This option is ignored if `merlin = TRUE`. |
| `merlin` | A logical. If TRUE, "ped", "map", "dat" and "freq" files are written in a format readable by the MERLIN software. In particular MERLIN requires non-numerical allele labels in the frequency file. |
| `verbose` | A logical. |

## Value

A character vector with the file names.

## Examples

```
x = nuclearPed(1)
x = setMarkers(x, marker(x, "3" = "a/b", name = "m1"))

# Write to file
fn = writePed(x, prefix = tempfile("test"))

# Read
y = readPed(fn)

stopifnot(identical(x, y))
```

# Index