

# Package ‘Pedixplorer’

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**Title** Pedigree Functions

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**Description** Routines to handle family data with a Pedigree object. The initial purpose was to create correlation structures that describe family relationships such as kinship and identity-by-descent, which can be used to model family data in mixed effects models, such as in the coxme function. Also includes a tool for Pedigree drawing which is focused on producing compact layouts without intervention. Recent additions include utilities to trim the Pedigree object with various criteria, and kinship for the X chromosome.

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'alignped2.R' 'alignped1.R' 'auto\_hint.R' 'align.R'  
'best\_hint.R' 'bit\_size.R' 'data.R' 'descendants.R'

'family\_check.R' 'find\_unavailable.R' 'find\_avail\_affected.R'  
 'find\_avail\_noninform.R' 'fix\_parents.R' 'generate\_aff\_inds.R'  
 'generate\_colors.R' 'ibd\_matrix.R' 'is\_informative.R'  
 'make\_famid.R' 'min\_dist\_inf.R' 'norm\_data.R' 'num\_child.R'  
 'ped\_to\_legdf.R' 'ped\_to\_plotdf.R' 'plot\_fct.R' 'plot\_fromdf.R'  
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**Author** Louis Le Nézet [aut, cre] (<<https://orcid.org/0009-0000-0202-2703>>),  
 Jason Sinnwell [aut],  
 Terry Therneau [aut],  
 Daniel Schaid [ctb],  
 Elizabeth Atkinson [ctb],  
 Louis Le Nezet [ctb]

**Maintainer** Louis Le Nézet <louislenezet@gmail.com>

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Pedixplorerer-package	<i>The Pedixplorerer package for pedigree data</i>
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**Description**

The Pedixplorerer package for pedigree data an updated package of the kinship2 package. The kinship2 package was originally written by Terry Therneau and Jason Sinnwell. The Pedixplorerer package is a fork of the kinship2 package with additional functionality and bug fixes.

**Details**

The package download, NEWS, and README are available on CRAN: [urlhttps://cran.r-project.org/package=kinship2](https://cran.r-project.org/package=kinship2) for the previous version of the package.

**Functions**

- Below are listed some of the most widely used functions available in arsenal:
- `Pedigree()`: Contstructor of the Pedigree class, given identifiers, sex, affection status(es), and special relationships
  - `kinship()`: Calculates the kinship matrix, the probability having an allele sampled from two individuals be the same via IBD.
  - `plot()` : Method to transform a Pedigree object into a graphical plot. Allows extra information to be included in the id under the plot symbol. This method use the `plot_fromdf()` function to transform the Pedigree object into a data frame of graphical elements, the same is done for the legend with the `ped_to_legdf()` function. When done, the data frames are plotted with the `plot_fromdf()` function.
  - `shrink()`: Shrink a Pedigree to a specific bit size, removing non-informative members first.
  - `bit_size()`: Approximate the output from SAS’s PROC FREQ procedure when using the /list option of the TABLE statement.

**Data**

- `sampleped()`: Pedigree example data sets with two pedigrees
- `minnbreast()`: Larger cohort of pedigrees from MN breast cancer study

**Author(s)**

**Maintainer:** Louis Le Nézet <louislenezet@gmail.com> ([ORCID](#))

Authors:

- Jason Sinnwell <sinnwell.jason@mayo.edu>
- Terry Therneau

Other contributors:

- Daniel Schaid [contributor]
- Elizabeth Atkinson [contributor]
- Louis Le Nezet [contributor]

**See Also**

Useful links:

- <https://github.com/LouisLeNezet/Pedexplorer>
- Report bugs at <https://github.com/LouisLeNezet/Pedexplorer/issues>

**Examples**

```
library(Pedexplorer)
```

---

align

*Align a Pedigree object*

---

**Description**

Given a Pedigree, this function creates helper matrices that describe the layout of a plot of the Pedigree.

**Usage**

```
## S4 method for signature 'Pedigree'
align(
  obj,
  packed = TRUE,
  width = 10,
  align = TRUE,
  hints = NULL,
  missid = "NA_character_"
)
```

## Arguments

<code>obj</code>	A Pedigree object
<code>packed</code>	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
<code>width</code>	For a packed output, the minimum width of the plot, in inches.
<code>align</code>	For a packed Pedigree, align children under parents TRUE, to the extent possible given the page width, or align to the left margin FALSE. This argument can be a two element vector, giving the alignment parameters, or a logical value. If TRUE, the default is <code>c(1.5, 2)</code> , or if numeric the routine <code>alignedped4()</code> will be called.
<code>hints</code>	A Hints object or a named list containing <code>horder</code> and <code>spouse</code> . If NULL then the Hints stored in <b>obj</b> will be used.
<code>missid</code>	A character vector with the missing values identifiers. All the <code>id</code> , <code>dadid</code> and <code>momid</code> corresponding to those values will be set to <code>NA_character_</code> .

## Details

This is an internal routine, used almost exclusively by `ped_to_plotdf()`.

The subservient functions `auto_hint()`, `alignedped1()`, `alignedped2()`, `alignedped3()`, and `alignedped4()` contain the bulk of the computation.

If the **hints** are missing the `auto_hint()` routine is called to supply an initial guess.

If multiple families are present in the **obj** Pedigree, this routine is called once for each family, and the results are combined in the list returned.

For more information you can read the associated vignette: `vignette("pedigree_alignment")`.

## Value

A list with components

- `n`: A vector giving the number of subjects on each horizontal level of the plot
- `nid`: A matrix with one row for each level, giving the numeric id of each subject plotted. (A value of 17 means the 17th subject in the Pedigree).
- `pos`: A matrix giving the horizontal position of each plot point
- `fam`: A matrix giving the family id of each plot point. A value of 3 would mean that the two subjects in positions 3 and 4, in the row above, are this subject's parents.
- `spouse`: A matrix with values
  - 0 = not a spouse
  - 1 = subject plotted to the immediate right is a spouse
  - 2 = subject plotted to the immediate right is an inbred spouse
- `twins`: Optional matrix which will only be present if the Pedigree contains twins :
  - 0 = not a twin
  - 1 = sibling to the right is a monozygotic twin
  - 2 = sibling to the right is a dizygotic twin
  - 3 = sibling to the right is a twin of unknown zygosity

See Also

[alignped1\(\)](#), [alignped2\(\)](#), [alignped3\(\)](#), [alignped4\(\)](#), [auto\\_hint\(\)](#)

Examples

```
data(sampleped)
ped <- Pedigree(sampleped)
align(ped)
```

---

alignped1	<i>Alignment first routine</i>
-----------	--------------------------------

---

Description

First alignment routine which create the subtree founded on a single subject as though it were the only tree.

Usage

```
alignped1(idx, dadx, momx, level, horder, packed, spouselist)
```

Arguments

idx	Indexes of the subjects
dadx	Indexes of the fathers
momx	Indexes of the mothers
level	Vector of the level of each subject
horder	A named numeric vector with one element per subject in the Pedigree. It determines the relative horizontal order of subjects within a sibship, as well as the relative order of processing for the founder couples. (For this latter, the female founders are ordered as though they were sisters). The names of the vector should be the individual identifiers.
packed	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
spouselist	Matrix of spouses with 4 columns: <ul style="list-style-type: none"><li>• 1: husband index</li><li>• 2: wife index</li><li>• 3: husband anchor</li><li>• 4: wife anchor</li></ul>

## Details

In this routine the **nid** array consists of the final **nid** array + 1/2 of the final spouse array. Note that the **spouselist** matrix will only contain spouse pairs that are not yet processed. The logic for anchoring is slightly tricky.

### 1. Anchoring::

First, if col 4 of the spouselist matrix is 0, we anchor at the first opportunity. Also note that if `spouselist[, 3] == spouselist[, 4]` it is the husband who is the anchor (just write out the possibilities).

### 2. Return values initialization::

Create the set of 3 return structures, which will be matrices with 1 + nspouse columns. If there are children then other routines will widen the result.

### 3. Create lspouse and rspouse::

This two complimentary lists denote the spouses plotted on the left and on the right. For someone with lots of spouses we try to split them evenly. If the number of spouses is odd, then men should have more on the right than on the left, women more on the right. Any hints in the spouselist matrix override. We put the undecided marriages closest to **idx**, then add predetermined ones to the left and right. The majority of marriages will be undetermined singletons, for which **nleft** will be 1 for female (put my husband to the left) and 0 for male. In one bug found by plotting canine data, **lspouse** could initially be empty but `length(rspouse) > 1`. This caused `nleft > length(idx)`. A fix was to not let **idx** to be indexed beyond its length, fix by JPS 5/2013.

### 4. List the children::

For each spouse get the list of children. If there are any we call `alignedped2()` to generate their tree and then mark the connection to their parent. If multiple marriages have children we need to join the trees.

### 5. Splice the tree::

To finish up we need to splice together the tree made up from all the kids, which only has data from `lev + 1` down, with the data here. There are 3 cases:

1. No children were found.
2. The tree below is wider than the tree here, in which case we add the data from this level onto theirs.
3. The tree below is narrower, for instance an only child.

## Value

A list containing the elements to plot the Pedigree. It contains a set of matrices along with the spouselist matrix. The latter has marriages removed as they are processed.

- **n** : A vector giving the number of subjects on each horizontal level of the plot
- **nid** : A matrix with one row for each level, giving the numeric id of each subject plotted. (A value of 17 means the 17th subject in the Pedigree).
- **pos** : A matrix giving the horizontal position of each plot point
- **fam** : A matrix giving the family id of each plot point. A value of 3 would mean that the two subjects in positions 3 and 4, in the row above, are this subject's parents.
- **spouselist** : Spouse matrix with anchors informations



**See Also**[align\(\)](#)**Examples**

```
data(sampleped)
ped <- Pedigree(sampleped)
align(ped)
```

alignped2

*Alignment second routine***Description**

Second of the four co-routines which takes a collection of siblings, grows the tree for each, and appends them side by side into a single tree.

**Usage**

```
alignped2(idx, dadx, momx, level, horder, packed, spouselist)
```

**Arguments**

idx	Indexes of the subjects
dadx	Indexes of the fathers
momx	Indexes of the mothers
level	Vector of the level of each subject
horder	A named numeric vector with one element per subject in the Pedigree. It determines the relative horizontal order of subjects within a sibship, as well as the relative order of processing for the founder couples. (For this latter, the female founders are ordered as though they were sisters). The names of the vector should be the individual identifiers.
packed	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
spouselist	Matrix of spouses with 4 columns: <ul style="list-style-type: none"> <li>• 1: husband index</li> <li>• 2: wife index</li> <li>• 3: husband anchor</li> <li>• 4: wife anchor</li> </ul>

### Details

The input arguments are the same as those to `alignped1()` with the exception that **idx** will be a vector. This routine does nothing to the `spouselist` matrix, but needs to pass it down the tree and back since one of the routines called by `alignped2()` might change the matrix.

The code below has one non-obvious special case. Suppose that two sibs marry. When the first sib is processed by `alignped1` then both partners (and any children) will be added to the `rval` structure below. When the second sib is processed they will come back as a 1 element tree (the marriage will no longer be on the **spouselist**), which should be added onto `rval`. The rule thus is to not add any 1 element tree whose value (which must be `idx[i]`) is already in the `rval` structure for this level.

### Value

A list containing the elements to plot the Pedigree. It contains a set of matrices along with the `spouselist` matrix. The latter has marriages removed as they are processed.

- `n` : A vector giving the number of subjects on each horizontal level of the plot
- `nid` : A matrix with one row for each level, giving the numeric id of each subject plotted. (A value of 17 means the 17th subject in the Pedigree).
- `pos` : A matrix giving the horizontal position of each plot point
- `fam` : A matrix giving the family id of each plot point. A value of 3 would mean that the two subjects in positions 3 and 4, in the row above, are this subject's parents.
- `spouselist` : Spouse matrix with anchors informations

### See Also

[align\(\)](#)

### Examples

```
data(sampleped)
ped <- Pedigree(sampleped)
align(ped)
```

---

alignped3

*Alignment third routine*

---

### Description

Third of the four co-routines to merges two pedigree trees which are side by side into a single object.

### Usage

```
alignped3(alt1, alt2, packed, space = 1)
```

**Arguments**

alt1	Alignment of the first tree
alt2	Alignment of the second tree
packed	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
space	Space between two subjects

**Details**

The primary special case is when the rightmost person in the left tree is the same as the leftmost person in the right tree; we need not plot two copies of the same person side by side. (When initializing the output structures do not worry about this, there is no harm if they are a column bigger than finally needed.) Beyond that the work is simple book keeping.

**1. Slide::**

For the unpacked case, which is the traditional way to draw a Pedigree when we can assume the paper is infinitely wide, all parents are centered over their children. In this case we think of the two trees to be merged as solid blocks. On input they both have a left margin of 0. Compute how far over we have to slide the right tree.

**2. Merge::**

Now merge the two trees. Start at the top level and work down.

**Value**

A list containing the elements to plot the Pedigree. It contains a set of matrices along with the spouseslist matrix. The latter has marriages removed as they are processed.

- `n` : A vector giving the number of subjects on each horizontal level of the plot
- `nid` : A matrix with one row for each level, giving the numeric id of each subject plotted. (A value of 17 means the 17th subject in the Pedigree).
- `pos` : A matrix giving the horizontal position of each plot point
- `fam` : A matrix giving the family id of each plot point. A value of 3 would mean that the two subjects in positions 3 and 4, in the row above, are this subject's parents.
- `spouseslist` : Spouse matrix with anchors informations

**See Also**

[align\(\)](#)

**Examples**

```
data(sampleped)
ped <- Pedigree(sampleped)
align(ped)
```

alignped4

*Alignment fourth routine***Description**

Last routines which attempts to line up children under parents and put spouses and siblings "close" to each other, to the extent possible within the constraints of page width.

**Usage**

```
alignped4(rval, spouse, level, width, align)
```

**Arguments**

rval	A list with components n, nid, pos, and fam.
spouse	A boolean matrix with one row per level representing if the subject is a spouse or not.
level	Vector of the level of each subject
width	For a packed output, the minimum width of the plot, in inches.
align	For a packed Pedigree, align children under parents TRUE, to the extent possible given the page width, or align to the left margin FALSE. This argument can be a two element vector, giving the alignment parameters, or a logical value. If TRUE, the default is c(1.5, 2), or if numeric the routine alignped4() will be called.

**Details**

The alignped4() routine is the final step of alignment. The current code does necessary setup and then calls the quadprog::solve.QP() function.

There are two important parameters for the function:

1. The maximum width specified. The smallest possible width is the maximum number of subjects on a line, if the user suggestion is too low it is increased to that 1 + that amount (to give just a little wiggle room).
2. The align vector of 2 alignment parameters a and b. For each set of siblings x with parents at p\_1 and p\_2 the alignment penalty is :

$$(1/k^a) \sum i = 1k(x_i - (p_1 + p_2))^2$$

where k is the number of siblings in the set.

Using the fact that when a = 1 :

$$\sum (x_i - c)^2 = \sum (x_i - \mu)^2 + k(c - \mu)^2$$

then moving a sibship with  $k$  sibs one unit to the left or right of optimal will incur the same cost as moving one with only 1 or two sibs out of place.

If  $a = 0$  then large sibships are harder to move than small ones, with the default value  $a = 1.5$  they are slightly easier to move than small ones. The rationale for the default is as long as the parents are somewhere between the first and last siblings the result looks fairly good, so we are more flexible with the spacing of a large family. By tethering all the sibs to a single spot they tend to be kept close to each other.

The alignment penalty for spouses is  $b(x_1 - x_2)^2$ , which tends to keep them together. The size of  $b$  controls the relative importance of sib-parent and spouse-spouse closeness.

1. We start by adding in these penalties. The total number of parameters in the alignment problem (what we hand to quadprog) is the set of  $\text{sum}(n)$  positions. A work array `myid` keeps track of the parameter number for each position so that it is easy to find. There is one extra penalty added at the end. Because the penalty amount would be the same if all the final positions were shifted by a constant, the penalty matrix will not be positive definite; `solve.QP()` does not like this. We add a tiny amount of leftward pull to the widest line.
2. If there are  $k$  subjects on a line there will be  $k+1$  constraints for that line. The first point must be  $\geq 0$ , each subsequent one must be at least 1 unit to the right, and the final point must be  $\leq$  the max width.

### Value

The updated position matrix

### See Also

[align\(\)](#)

### Examples

```
data(sampleped)
ped <- Pedigree(sampleped)
align(ped)
```

---

ancestors

*Ancestors indexes of a subject*

---

### Description

Given the index of one or multiple individual(s), this function iterate through the mom and dad indexes to list out all the ancestors of the said individual(s). This function is use in the [align\(\)](#) function to identify which spouse pairs has a common ancestor and therefore if they need to be connected with a double line (i.e. inbred).

### Usage

```
ancestors(idx, momx, dadx)
```

**Arguments**

idx	Indexes of the subjects
momx	Indexes of the mothers
dadx	Indexes of the fathers

**Value**

A vector of ancestor indexes

**See Also**

[align\(\)](#)

**Examples**

```
ancestors(c(1), c(3, 4, 5, 6), c(7, 8, 9, 10))
ancestors(c(1, 2), c(3, 4, 5, 6), c(7, 8, 9, 10))
```

---

anchor_to_factor	<i>Anchor variable to ordered factor</i>
------------------	--

---

**Description**

Anchor variable to ordered factor

**Usage**

```
anchor_to_factor(anchor)
```

**Arguments**

anchor	A character, factor or numeric vector corresponding to the anchor of the individuals. The following values are recognized: <ul style="list-style-type: none"> <li>• <code>character()</code> or <code>factor()</code> : "0", "1", "2", "left", "right", "either"</li> <li>• <code>numeric()</code> : 1 = "left", 2 = "right", 0 = "either"</li> </ul>
--------	---

**Value**

An ordered factor vector containing the transformed variable "either" < "left" < "right"

**Examples**

```
anchor_to_factor(c(1, 2, 0, "left", "right", "either"))
```

---

auto\_hint

*Initial hint for a Pedigree alignment*


---

## Description

Compute an initial guess for the alignment of a Pedigree

## Usage

```
## S4 method for signature 'Pedigree'
auto_hint(obj, hints = NULL, packed = TRUE, align = FALSE, reset = FALSE)
```

## Arguments

obj	A Pedigree object
hints	A Hints object or a named list containing horder and spouse. If NULL then the Hints stored in <b>obj</b> will be used.
packed	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
align	For a packed Pedigree, align children under parents TRUE, to the extent possible given the page width, or align to to the left margin FALSE. This argument can be a two element vector, giving the alignment parameters, or a logical value. If TRUE, the default is c(1.5, 2), or if numeric the routine alignedped4() will be called.
reset	If TRUE, then even if the Ped object has Hints, reset them to the initial values.

## Details

A Pedigree structure can contain a [Hints](#) object which helps to reorder the Pedigree (e.g. left-to-right order of children within family) so as to plot with minimal distortion. This routine is used to create an initial version of the hints. They can then be modified if desired.

This routine would not normally be called by a user. It moves children within families, so that marriages are on the "edge" of a set children, closest to the spouse. For pedigrees that have only a single connection between two families this simple-minded approach works surprisingly well. For more complex structures hand-tuning of the hints may be required.

When auto\_hint() is called with a a vector of numbers as the **hints** argument, the values for the founder females are used to order the founder families left to right across the plot. The values within a sibship are used as the preliminary order of siblings within a family; this may be changed to move one of them to the edge so as to match up with a spouse. The actual values in the vector are not important, only their order.

## Value

The initial [Hints](#) object.

**See Also**

[align\(\)](#), [best\\_hint\(\)](#), [Hints](#)

**Examples**

```
data(sampleped)
ped <- Pedigree(sampleped[sampleped$famid == 1, ])
auto_hint(ped)
```

---

best\_hint

*Best hint for a Pedigree alignment*

---

**Description**

When computer time is cheap, use this routine to get a *best* Pedigree alignment. This routine will try all possible founder orders, and return the one with the least **stress**.

**Usage**

```
## S4 method for signature 'Pedigree'
best_hint(obj, wt = c(1000, 10, 1), tolerance = 0)
```

**Arguments**

obj	A Pedigree object
wt	A vector of three weights for the three error measures. Default is c(1000, 10, 1). <ol style="list-style-type: none"> <li>1. The number of duplicate individuals in the plot</li> <li>2. The sum of the absolute values of the differences in the positions of duplicate individuals</li> <li>3. The sum of the absolute values of the differences between the center of the children and the parents.</li> </ol>
tolerance	The maximum stress level to accept. Default is 0

**Details**

The [auto\\_hint\(\)](#) routine will rearrange sibling order, but not founder order. This calls [auto\\_hint\(\)](#) with every possible founder order, and finds that plot with the least "stress". The stress is computed as a weighted sum of three error measures:

- nbArcs The number of duplicate individuals in the plot
- lgArcs The sum of the absolute values of the differences in the positions of duplicate individuals
- lgParentsChilds The sum of the absolute values of the differences between the center of the children and the parents



$$stress = wt[1] * nbArcs + wt[2] * lgArcs + wt[3] * lgParentsChilds$$

If during the search, a plot is found with a stress level less than **tolerance**, the search is terminated.

### Value

The best Hints object out of all the permutations

### See Also

[auto\\_hint\(\)](#), [align\(\)](#)

### Examples

```
data(sampleped)
ped <- Pedigree(sampleped[sampleped$famid == 1,])
best_hint(ped)
```

---

bit\_size

*Bit size of a Pedigree*


---

### Description

Utility function used in the `shrink()` function to calculate the bit size of a Pedigree.

### Usage

```
## S4 method for signature 'character_OR_integer'
bit_size(obj, momid, missid = NA_character_)
```

```
## S4 method for signature 'Pedigree'
bit_size(obj)
```

```
## S4 method for signature 'Ped'
bit_size(obj)
```

### Arguments

obj	A Ped or Pedigree object or a vector of fathers identifiers
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.

**Details**

The bit size of a Pedigree is defined as :

$$2 \times NbNonFounders - NbFounders$$

Where NbNonFounders is the number of non founders in the Pedigree (i.e. individuals with identified parents) and NbFounders is the number of founders in the Pedigree (i.e. individuals without identified parents).

**Value**

A list with the following components:

- bit\_size The bit size of the Pedigree
- nFounder The number of founders in the Pedigree
- nNonFounder The number of non founders in the Pedigree

**See Also**

[shrink\(\)](#)

**Examples**

```
data(sampleped)
ped <- Pedigree(sampleped)
bit_size(ped)
```

---

check\_columns

*Check columns presence in a dataframe*

---

**Description**

Check for presence / absence of columns names depending on their need

**Usage**

```
check_columns(
  df,
  cols_needed = NULL,
  cols_used = NULL,
  cols_to_use = NULL,
  others_cols = FALSE,
  cols_used_init = FALSE,
  cols_to_use_init = FALSE,
  cols_used_del = FALSE,
  verbose = FALSE
)
```

**Arguments**

df	The dataframe to use
cols_needed	A vector of columns needed
cols_used	A vector of columns that are used by the script and that will be overwritten.
cols_to_use	A vector of optional columns that are authorized.
others_cols	Boolean defining if non defined columns should be allowed.
cols_used_init	Boolean defining if the columns that will be used should be initialised to NA.
cols_to_use_init	Boolean defining if the optional columns should be initialised to NA.
cols_used_del	Boolean defining if the columns that will be used should be deleted.
verbose	Should message be prompted to the user

**Details**

3 types of columns are here checked:

- cols\_needed : those columns need to be present if any is missing an error will be prompted and the script will stop
- cols\_used : those columns will be used in the script and will be overwritten to NA.
- cols\_to\_use : those columns are optional and will be recognise if present. The last two types of columns can be initialised to NA if needed.

**Value**

Dataframe with only the column allowed and all the column correctly initialised.

**Examples**

```
data.frame
df <- data.frame(ColN1 = c(1, 2), ColN2 = 4,
  ColU1 = 'B', ColU2 = '1',
  ColTU1 = 'A', ColTU2 = 3,
  ColNR1 = 4, ColNR2 = 5)
tryCatch(
  check_columns(df,
    c('ColN1', 'ColN2'), c('ColU1', 'ColU2'),
    c('ColTU1', 'ColTU2')
  ), error = function(e) print(e))
```

---

check_num_na	<i>Is numeric or NA</i>
--------------	-------------------------

---

**Description**

Check if a variable given is numeric or NA

**Usage**

```
check_num_na(var, na_as_num = TRUE)
```

**Arguments**

var	Vector of value to test
na_as_num	Boolean defining if the NA string should be considered as numerical values

**Details**

Check if the values in **var** are numeric or if they are NA in the case that na\_as\_num is set to TRUE.

**Value**

A vector of boolean of the same size as **var**

---

check_slot_fd	<i>Check if the fields are present in an object slot</i>
---------------	--

---

**Description**

Check if the fields are present in an object slot

**Usage**

```
check_slot_fd(obj, slot = NULL, fields = character())
```

**Arguments**

obj	An object.
slot	A slot of object.
fields	A character vector with the fields to check.

**Value**

A character vector with the errors if any.

---

check_values	<i>Check values in a slot</i>
--------------	-------------------------------

---

**Description**

Check if the all the values in a slot are in a vector of values.

**Usage**

```
check_values(val, ref, name = NULL, present = TRUE)
```

**Arguments**

val	A vector of values to check.
ref	A vector of reference values.
name	A character vector with the name of the values to check.
present	A logical value indicating if the values should be present or not

**Value**

A character vector with the errors if any.

---

circfun	<i>Circular element</i>
---------	-------------------------

---

**Description**

Create a list of x and y coordinates for a circle with a given number of slices.

**Usage**

```
circfun(nslice, n = 50)
```

**Arguments**

nslice	Number of slices in the circle
n	Total number of points in the circle

**Value**

A list of x and y coordinates per slice.

**Examples**

```
circfun(1)
circfun(1, 10)
circfun(4, 50)
```

---

descendants	<i>Descendants of individuals</i>
-------------	-----------------------------------

---

### Description

Find all the descendants of a particular list of individuals given a Pedigree object.

### Usage

```
## S4 method for signature 'character_OR_integer,character_OR_integer'
descendants(idlist, obj, dadid, momid)
```

```
## S4 method for signature 'character_OR_integer,Pedigree'
descendants(idlist, obj)
```

```
## S4 method for signature 'character_OR_integer,Ped'
descendants(idlist, obj)
```

### Arguments

idlist	List of individuals identifiers to be considered
obj	A Ped or Pedigree object or a vector of the individuals identifiers.
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.

### Value

Vector of all descendants of the individuals in idlist. The list is not ordered.

### Examples

```
data("sampleped")
ped <- Pedigree(sampleped)
descendants(c("1_101", "2_208"), ped)
```

---

draw_arc	<i>Draw arcs</i>
----------	------------------

---

### Description

Draw arcs

### Usage

```
draw_arc(x0, y0, x1, y1, p, ggplot_gen = FALSE, lwd = 1, col = "black")
```

**Arguments**

x0	x coordinate of the first point
y0	y coordinate of the first point
x1	x coordinate of the second point
y1	y coordinate of the second point
p	ggplot object
ggplot_gen	If TRUE add the segments to the ggplot object
lwd	Line width
col	Line color

**Value**

Plot the arcs to the current device or add it to a ggplot object

---

draw_polygon	<i>Draw a polygon</i>
--------------	-----------------------

---

**Description**

Draw a polygon

**Usage**

```
draw_polygon(
  x,
  y,
  p,
  ggplot_gen = FALSE,
  fill = "grey",
  border = NULL,
  density = NULL,
  angle = 45
)
```

**Arguments**

x	x coordinates
y	y coordinates
p	ggplot object
ggplot_gen	If TRUE add the segments to the ggplot object
fill	Fill color
border	Border color
density	Density of shading
angle	Angle of shading

**Value**

Plot the polygon to the current device or add it to a ggplot object

---

draw_segment	<i>Draw segments</i>
--------------	----------------------

---

**Description**

Draw segments

**Usage**

```
draw_segment(  
  x0,  
  y0,  
  x1,  
  y1,  
  p,  
  ggplot_gen,  
  col = par("fg"),  
  lwd = par("lwd"),  
  lty = par("lty")  
)
```

**Arguments**

x0	x coordinate of the first point
y0	y coordinate of the first point
x1	x coordinate of the second point
y1	y coordinate of the second point
p	ggplot object
ggplot_gen	If TRUE add the segments to the ggplot object
col	Line color
lwd	Line width
lty	Line type

**Value**

Plot the segments to the current device or add it to a ggplot object



---

draw_text	<i>Draw texts</i>
-----------	-------------------

---

## Description

Draw texts

## Usage

```
draw_text(  
  x,  
  y,  
  label,  
  p,  
  ggplot_gen = FALSE,  
  cex = 1,  
  col = NULL,  
  adjx = 0,  
  adjy = 0  
)
```

## Arguments

x	x coordinates
y	y coordinates
label	Text to be displayed
p	ggplot object
ggplot_gen	If TRUE add the segments to the ggplot object
cex	Character expansion of the text
col	Text color
adjx	x adjustment
adjy	y adjustment

## Value

Plot the text to the current device or add it to a ggplot object

---

duporder	<i>Find the duplicate pairs of a subject</i>
----------	--

---

**Description**

Find the duplicate pairs of a subject

**Usage**

```
duporder(idlist, plist, lev, obj)
```

**Arguments**

idlist	List of individuals identifiers to be considered
plist	The alignment structure representing the Pedigree layout. See <a href="#">align()</a> for details.
lev	The generation level of the subject
obj	A Pedigree object

**Details**

This routine is used by `auto_hint()`. It finds the duplicate pairs of a subject and returns them in the order they should be plotted.

**Value**

A matrix of duplicate pairs

**See Also**

[auto\\_hint\(\)](#)

---

exclude_stray_marryin	<i>Exclude stray marry-ins</i>
-----------------------	--------------------------------

---

**Description**

Exclude any founders who are not parents.

**Usage**

```
exclude_stray_marryin(id, dadid, momid)
```

**Arguments**

id	A character vector with the identifiers of each individuals
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.

**Value**

Returns a data frame of subject identifiers and their parents. The data frame is trimmed of any founders who are not parents.

**See Also**

[shrink\(\)](#)

---

exclude\_unavail\_founders

*Exclude unavailable founders*

---

**Description**

Exclude any unavailable founders.

**Usage**

```
exclude_unavail_founders(id, dadid, momid, avail, missid = NA_character_)
```

**Arguments**

id	A character vector with the identifiers of each individuals
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
avail	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.

**Value**

Returns a list with the following components:

- n\_trimmed Number of trimmed individuals
- id\_trimmed Vector of IDs of trimmed individuals
- id Vector of subject identifiers
- dadid Vector of father identifiers
- momid Vector of mother identifiers

**See Also**[shrink\(\)](#)

family\_check

*Check family***Description**

Error check for a family classification

**Usage**

```
## S4 method for signature 'character_OR_integer'
family_check(obj, dadid, momid, famid, newfam)
```

```
## S4 method for signature 'Pedigree'
family_check(obj)
```

```
## S4 method for signature 'Ped'
family_check(obj)
```

**Arguments**

obj	A character vector with the id of the individuals or a <code>data.frame</code> with all the informations in corresponding columns.
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
famid	A character vector with the family identifiers of the individuals. If provide, will be aggregated to the individuals identifiers separated by an underscore.
newfam	The result of a call to <code>make_famid()</code> . If this has already been computed by the user, adding it as an argument shortens the running time somewhat.

**Details**

Given a family id vector, also compute the familial grouping from first principles using the parenting data, and compare the results.

The [make\\_famid\(\)](#) function is used to create a de novo family id from the parentage data, and this is compared to the family id given in the data.

If there are any joins, then an attribute 'join' is attached. It will be a matrix with family as row labels, new-family-id as the columns, and the number of subjects as entries.

**Value**

a data frame with one row for each unique family id in the famid argument or the one detected in the Pedigree object. Components of the output are:

- famid : The family id, as entered into the data set
- n : Number of subjects in the family
- unrelated : Number of them that appear to be unrelated to anyone else in the entire Pedigree. This is usually marry-ins with no children (in the Pedigree), and if so are not a problem.
- split : Number of unique 'new' family ids.
  - 0 = no one in this 'family' is related to anyone else (not good)
  - 1 = everything is fine
  - 2 and + = the family appears to be a set of disjoint trees. Are you missing some of the people?
- join : Number of other families that had a unique family, but are actually joined to this one. 0 is the hope.

**See Also**

[make\\_famid\(\)](#)

**Examples**

```
# use 2 samplepeds
data(sampleped)
pedAll <- Pedigree(sampleped)

## check them giving separate ped ids
fcheck.sep <- family_check(pedAll)
fcheck.sep

## check assigning them same ped id
fcheck.combined <- with(sampleped, family_check(id, dadid, momid,
rep(1, nrow(sampleped))))
fcheck.combined
```

---

findsibs

*Find the siblings of a subject*


---

**Description**

Find the siblings of a subject

**Usage**

```
findsibs(idpos, plist, lev)
```

**Arguments**

idpos	The position of the subject
plist	The alignment structure representing the Pedigree layout. See <a href="#">align()</a> for details.
lev	The generation level of the subject

**Details**

This routine is used by `auto_hint()`. It finds the siblings of a subject.

**Value**

The positions of the siblings

**See Also**

[auto\\_hint\(\)](#)

---

findspouse	<i>Find the spouse of a subject</i>
------------	-------------------------------------

---

**Description**

Find the spouse of a subject

**Usage**

```
findspouse(idpos, plist, lev, obj)
```

**Arguments**

idpos	The position of the subject
plist	The alignment structure representing the Pedigree layout. See <a href="#">align()</a> for details.
lev	The generation level of the subject
obj	A Pedigree object

**Details**

This routine is used by `auto_hint()`. It finds the spouse of a subject.

**Value**

The position of the spouse

**See Also**

[auto\\_hint\(\)](#)

---

find\_avail\_affected      *Find single affected and available individual from a Pedigree*

---

### Description

Finds one subject from among available non-parents with indicated affection status.

### Usage

```
## S4 method for signature 'Ped'
find_avail_affected(obj, avail = NULL, affected = NULL, affstatus = NA)

## S4 method for signature 'Pedigree'
find_avail_affected(obj, avail = NULL, affected = NULL, affstatus = NA)
```

### Arguments

obj	A Ped or Pedigree object.
avail	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
affected	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).
affstatus	Affection status to search for.

### Details

When used within [shrink\(\)](#), this function is called with the first affected indicator, if the affected item in the Pedigree is a matrix of multiple affected indicators.

If **avail** or **affected** is null, then the function will use the corresponding Ped accessor.

### Value

A list is returned with the following components

- ped The new Ped object
- newAvail Vector of availability status of trimmed individuals
- idTrimmed Vector of IDs of trimmed individuals
- isTrimmed logical value indicating whether Ped object has been trimmed
- bit\_size Bit size of the trimmed Ped

### See Also

[shrink\(\)](#)

### Examples

```
data(sampleped)
ped <- Pedigree(sampleped)
find_avail_affected(ped, affstatus = 1)
```

---

find\_avail\_noninform    *Find uninformative but available subject*

---

### Description

Finds subjects from among available non-parents with all affection equal to 0.

### Usage

```
## S4 method for signature 'Ped'
find_avail_noninform(obj, avail = NULL, affected = NULL)

## S4 method for signature 'Pedigree'
find_avail_noninform(obj, avail = NULL, affected = NULL)
```

### Arguments

obj	A Ped or Pedigree object.
avail	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
affected	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).

### Details

Identify subjects to remove from a Pedigree who are available but non-informative (unaffected). This is the second step to remove subjects in [shrink\(\)](#) if the Pedigree does not meet the desired bit size.

If **avail** or **affected** is null, then the function will use the corresponding Ped accessor.

### Value

Vector of subject ids who can be removed by having lowest informativeness.

### See Also

[shrink\(\)](#)

### Examples

```
data(sampleped)
ped <- Pedigree(sampleped)
find_avail_noninform(ped)
```



---

find_unavailable	<i>Find unavailable subjects in a Pedigree</i>
------------------	--

---

## Description

Find the identifiers of subjects in a Pedigree iteratively, as anyone who is not available and does not have an available descendant by successively removing unavailable terminal nodes.

## Usage

```
## S4 method for signature 'Ped'
find_unavailable(obj, avail = NULL)

## S4 method for signature 'Pedigree'
find_unavailable(obj, avail = NULL)
```

## Arguments

obj	A Ped or Pedigree object.
avail	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).

## Details

If **avail** is null, then the function will use the corresponding Ped accessor.

Originally written as `pedTrim` by Steve Iturria, modified by Dan Schaid 2007, and now split into the two separate functions: `find_unavailable()`, and `trim()` to do the tasks separately. `find_unavailable()` calls `exclude_stray_marryin()` to find stray available marry-ins who are isolated after trimming their unavailable offspring, and `exclude_unavail_founders()`. If the subject ids are character, make sure none of the characters in the ids is a colon (":"), which is a special character used to concatenate and split subjects within the utility. The `trim()` functions is now replaced by the `subset()` function.

## Value

Returns a vector of subject ids for who can be removed.

## Side Effects

Relation matrix from subsetting is trimmed of any special relations that include the subjects to trim.

## See Also

[shrink\(\)](#)

## Examples

```
data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == "1",])
find_unavailable(ped1)
```

---

fix\_parents

*Fix parents relationship and gender*


---

## Description

Fix the sex of parents, add parents that are missing from the data. Can be used with a dataframe or a vector of the different individuals informations.

## Usage

```
## S4 method for signature 'character'
fix_parents(obj, dadid, momid, sex, famid = NULL, missid = NA_character_)

## S4 method for signature 'data.frame'
fix_parents(obj, delete = FALSE, filter = NULL, missid = NA_character_)
```

## Arguments

obj	A data.frame or a vector of the individuals identifiers. If a dataframe is given it must contain the columns id, dadid, momid, sex and famid (optional).
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
sex	A character, factor or numeric vector corresponding to the gender of the individuals. This will be transformed to an ordered factor with the following levels: male < female < unknown < 'terminated'. The following values are recognized: <ul style="list-style-type: none"> <li>• character() or factor() : "f", "m", "woman", "man", "male", "female", "unknown", "terminated"</li> <li>• numeric() : 1 = "male", 2 = "female", 3 = "unknown", 4 = "terminated"</li> </ul>
famid	A character vector with the family identifiers of the individuals. If provide, will be aggregated to the individuals identifiers separated by an underscore.
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.
delete	Boolean defining if missing parents needs to be: <ul style="list-style-type: none"> <li>• TRUE : added as a new row</li> <li>• FALSE : be deleted</li> </ul>
filter	Filtering column containing 0 or 1 for the rows to kept before proceeding.

## Details

First look to add parents whose ids are given in momid/dadid. Second, fix sex of parents. Last look to add second parent for children for whom only one parent id is given. If a **famid** vector is given the family id will be added to the ids of all individuals (id, dadid, momid) separated by an underscore before proceeding.

### Special case for dataframe:

Check for presence of both parents id in the **id** field. If not both presence behaviour depend of **delete** parameter

- If TRUE then use fix\_parents function and merge back the other fields in the dataframe then set availability to O for non available parents.
- If FALSE then delete the id of missing parents

## Value

A data.frame with id, dadid, momid, sex as columns with the relationships fixed.

## Author(s)

Jason Sinnwell

## Examples

```
test1char <- data.frame(
  id = paste('fam', 101:111, sep = ''),
  sex = c('male', 'female')[c(1, 2, 1, 2, 1, 1, 2, 2, 1, 2, 1)],
  father = c(
    0, 0, 'fam101', 'fam101', 'fam101', 0, 0,
    'fam106', 'fam106', 'fam106', 'fam109'
  ),
  mother = c(
    0, 0, 'fam102', 'fam102', 'fam102', 0, 0,
    'fam107', 'fam107', 'fam107', 'fam112'
  )
)
test1newmom <- with(test1char, fix_parents(id, father, mother,
  sex,
  missid = NA_character_
))
Pedigree(test1newmom)
```

## Description

Perform transformation upon a vector given as the one containing the affection status to obtain an affected binary state.

**Usage**

```
generate_aff_inds(
  values,
  mods_aff = NULL,
  threshold = NULL,
  sup_thres_aff = NULL
)
```

**Arguments**

values	Vector containing the values of the column to process.
mods_aff	Vector of modality to consider as affected in the case where the values is a factor.
threshold	Numeric value separating the affected and healthy subject in the case where the values is numeric.
sup_thres_aff	Boolean defining if the affected individual are above the threshold or not. If TRUE, the individuals will be considered affected if the value of values is stricly above the threshold. If FALSE, the individuals will be considered affected if the value is stricly under the threshold.

**Details**

This function helps to configure a binary state from a character or numeric variable.

**If the variable is a character or a factor::**

In this case the affected state will depend on the modality provided as an affected status. All individuals with a value corresponding to one of the element in the vector **mods\_aff** will be considered as affected.

**If the variable is numeric::**

In this case the affected state will be TRUE if the value of the individual is above the **threshold** if **sup\_thres\_aff** is TRUE and FALSE otherwise.

**Value**

A dataframe with the affected column processed accordingly. The different columns are:

- mods: The different modalities of the column
- labels: The labels of the different modalities
- affected: The column processed to have only TRUE/FALSE values

**Author(s)**

Louis Le Nézet

**Examples**

```
generate_aff_inds(c(1, 2, 3, 4, 5), threshold = 3, sup_thres_aff = TRUE)
generate_aff_inds(c("A", "B", "C", "A", "V", "B"), mods_aff = c("A", "B"))
```

---

generate_border	<i>Process the border colors based on availability</i>
-----------------	--

---

### Description

Perform transformation upon a vector given as the one containing the availability status to compute the border color. The vector given will be transformed using the `vect_to_binary()` function.

### Usage

```
generate_border(values, colors_avail = c("green", "black"))
```

### Arguments

values	The vector containing the values to process as available.
colors_avail	Set of 2 colors to use for the box's border of an individual. The first color will be used for available individual (avail == 1) and the second for the unavailable individual (avail == 0).

### Value

A list of three elements

- `mods` : The processed values column as a numeric factor
- `avail` : A logical vector indicating if the individual is available
- `sc_bord` : A dataframe containing the description of each modality of the scale

### Examples

```
generate_border(c(1, 0, 1, 0, NA, 1, 0, 1, 0, NA))
```

---

generate_colors	<i>Process the filling and border colors based on affection and availability</i>
-----------------	--

---

### Description

Perform transformation upon a dataframe given to compute the colors for the filling and the border of the individuals based on the affection and availability status.

**Usage**

```
## S4 method for signature 'character'
generate_colors(
  obj,
  avail,
  mods_aff = NULL,
  keep_full_scale = FALSE,
  colors_aff = c("yellow2", "red"),
  colors_unaff = c("white", "steelblue4"),
  colors_avail = c("green", "black")
)

## S4 method for signature 'numeric'
generate_colors(
  obj,
  avail,
  threshold = 0.5,
  sup_thres_aff = TRUE,
  keep_full_scale = FALSE,
  breaks = 3,
  colors_aff = c("yellow2", "red"),
  colors_unaff = c("white", "steelblue4"),
  colors_avail = c("green", "black")
)

## S4 method for signature 'Pedigree'
generate_colors(
  obj,
  col_aff = "affected",
  add_to_scale = TRUE,
  col_avail = "avail",
  mods_aff = NULL,
  threshold = 0.5,
  sup_thres_aff = TRUE,
  keep_full_scale = FALSE,
  breaks = 3,
  colors_aff = c("yellow2", "red"),
  colors_unaff = c("white", "steelblue4"),
  colors_avail = c("green", "black"),
  reset = TRUE
)
```

**Arguments**

<code>obj</code>	A Pedigree object or a vector containing the affection status for each individuals. The affection status can be numeric or a character.
<code>avail</code>	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).

mods_aff	Vector of modality to consider as affected in the case where the values is a factor.
keep_full_scale	Boolean defining if the affection values need to be set as a scale. If values is numeric the filling scale will be calculated based on the values and the number of breaks given. If values isn't numeric then each levels will get it's own color
colors_aff	Set of increasing colors to use for the filling of the affected individuals.
colors_unaff	Set of increasing colors to use for the filling of the unaffected individuals.
colors_avail	Set of 2 colors to use for the box's border of an individual. The first color will be used for available individual (avail == 1) and the second for the unavailable individual (avail == 0).
threshold	Numeric value separating the affected and healthy subject in the case where the values is numeric.
sup_thres_aff	Boolean defining if the affected individual are above the threshold or not. If TRUE, the individuals will be considered affected if the value of values is stricly above the threshold. If FALSE, the individuals will be considered affected if the value is stricly under the threshold.
breaks	Number of breaks to use when using full scale with numeric values. The same number of breaks will be done for values from affected individuals and unaffected individuals.
col_aff	A character vector with the name of the column to be used for the affection status.
add_to_scale	Boolean defining if the scales need to be added to the existing scales or if they need to replace the existing scales.
col_avail	A character vector with the name of the column to be used for the availability status.
reset	If TRUE the scale of the specified column will be reset if already present.

## Details

The colors will be set using the `generate_fill()` and the `generate_border()` functions respectively for the filling and the border.

## Value

### When used with a vector:

A list of two elements

- The list containing the filling colors processed and their description
- The list containing the border colors processed and their description

### When used with a Pedigree object:

The Pedigree object with the affected and avail columns processed accordingly as well as the scales slot updated.

**Examples**

```

generate_colors(
  c("A", "B", "A", "B", NA, "A", "B", "A", "B", NA),
  c(1, 0, 1, 0, NA, 1, 0, 1, 0, NA),
  mods_aff = "A",
)

generate_colors(
  c(10, 0, 5, 7, NA, 6, 2, 1, 3, NA),
  c(1, 0, 1, 0, NA, 1, 0, 1, 0, NA),
  threshold = 3, keep_full_scale = TRUE
)
data("sampleped")
ped <- Pedigree(sampleped)
ped <- generate_colors(ped, "affected", add_to_scale=FALSE)
scales(ped)

```

generate\_fill

*Process the filling colors based on affection***Description**

Perform transformation upon a column given as the one containing affection status to compute the filling color.

**Usage**

```

generate_fill(
  values,
  affected,
  labels,
  keep_full_scale = FALSE,
  breaks = 3,
  colors_aff = c("yellow2", "red"),
  colors_unaff = c("white", "steelblue4")
)

```

**Arguments**

values	The vector containing the values to process as affection.
affected	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).
labels	The vector containing the labels to use for the affection.
keep_full_scale	Boolean defining if the affection values need to be set as a scale. If values is numeric the filling scale will be calculated based on the values and the number of breaks given. If values isn't numeric then each levels will get it's own color



breaks	Number of breaks to use when using full scale with numeric values. The same number of breaks will be done for values from affected individuals and unaffected individuals.
colors_aff	Set of increasing colors to use for the filling of the affected individuals.
colors_unaff	Set of increasing colors to use for the filling of the unaffected individuals.

### Details

The colors will be set using the `grDevices::colorRampPalette()` function with the colors given as parameters.

The colors will be set as follow:

- If **keep\_full\_scale** is FALSE: Then the affected individuals will get the first color of the **colors\_aff** vector and the unaffected individuals will get the first color of the **colors\_unaff** vector.
- If **keep\_full\_scale** is TRUE:
  - If **values** isn't numeric: Each levels of the affected **values** vector will get it's own color from the **colors\_aff** vector using the `grDevices::colorRampPalette()` and the same will be done for the unaffected individuals using the **colors\_unaff**.
  - If **values** is numeric: The mean of the affected individuals will be compared to the mean of the unaffected individuals and the colors will be set up such as the color gradient follow the direction of the affection.

### Value

A list of three elements

- **mods** : The processed values column as a numeric factor
- **affected** : A logical vector indicating if the individual is affected
- **sc\_fill** : A dataframe containing the description of each modality of the scale

### Examples

```
aff <- generate_aff_inds(seq_len(5), threshold = 3, sup_thres_aff = TRUE)
generate_fill(seq_len(5), aff$affected, aff$labels)
generate_fill(seq_len(5), aff$affected, aff$labels, keep_full_scale = TRUE)
```

---

get_twin_rel	<i>Get twin relationships</i>
--------------	-------------------------------

---

### Description

Get twin relationships

### Usage

```
get_twin_rel(obj)
```

Arguments

obj                    A Pedigree object

Details

This routine function determine the twin relationships in a Pedigree. It determine the order of the twins in the Pedigree. It is used by `auto_hint()`.

Value

A list containing components

- 1. `twinset` the set of twins
- 2. `twinrel` the twins relationships
- 3. `twinord` the order of the twins

See Also

[auto\\_hint\(\)](#)

---

Hints-class	<i>Hints object</i>
-------------	---------------------

---

Description

The hints are used to specify the order of the individuals in the pedigree and to specify the order of the spouses.

Constructor ::

You either need to provide **horder** or **spouse** in the dedicated parameters (together or separately), or inside a list.

Usage

```
Hints(horder, spouse)

## S4 method for signature 'list,missing_OR_NULL'
Hints(horder, spouse)

## S4 method for signature 'numeric,data.frame'
Hints(horder, spouse)

## S4 method for signature 'numeric,missing_OR_NULL'
Hints(horder, spouse)
```

**Arguments**

horder	A named numeric vector with one element per subject in the Pedigree. It determines the relative horizontal order of subjects within a sibship, as well as the relative order of processing for the founder couples. (For this latter, the female founders are ordered as though they were sisters). The names of the vector should be the individual identifiers.
spouse	A data.frame with one row per hinted marriage, usually only a few marriages in a pedigree will need an added hint, for instance reverse the plot order of a husband/wife pair. Each row contains the id of the left spouse (i.e. idl), the id of the right hand spouse (i.e. idr), and the anchor (i.e : anchor : 1 = left, 2 = right, 0 = either). Children will preferentially appear under the parents of the anchored spouse.

**Value**

A Hints object.

**Slots**

horder	A numeric named vector with one element per subject in the Pedigree. It determines the relative horizontal order of subjects within a sibship, as well as the relative order of processing for the founder couples. (For this latter, the female founders are ordered as though they were sisters).
spouse	A data.frame with one row per hinted marriage, usually only a few marriages in a Pedigree will need an added hint, for instance reverse the plot order of a husband/wife pair. Each row contains the identifiers of the left spouse, the right hand spouse, and the anchor (i.e : 1 = left, 2 = right, 0 = either).

**Accessors**

- `horder(x)` : Get the horder vector
- `horder(x) <- value` : Set the horder vector
- `spouse(x)` : Get the spouse data.frame
- `spouse(x) <- value` : Set the spouse data.frame

**Generics**

- `as.list(x)`: Convert a Hints object to a list
- `subset(x, i, keep = TRUE)`: Subset a Hints object based on the individuals identifiers given.
  - `i` : A vector of individuals identifiers to keep.
  - `keep` : A logical value indicating if the individuals should be kept or deleted.

**See Also**

[Pedigree\(\)](#)

**Examples**

```
Hints(  
  list(  
    horder = c("1" = 1, "2" = 2, "3" = 3),  
    spouse = data.frame(  
      idl = c("1", "2"),  
      idr = c("2", "3"),  
      anchor = c(1, 2)  
    )  
  )  
)  
  
Hints(  
  horder = c("1" = 1, "2" = 2, "3" = 3),  
  spouse = data.frame(  
    idl = c("1", "2"),  
    idr = c("2", "3"),  
    anchor = c(1, 2)  
  )  
)  
  
Hints(  
  horder = c("1" = 1, "2" = 2, "3" = 3)  
)
```

---

<i>ibd_matrix</i>	<i>IBD matrix</i>
-------------------	-------------------

---

**Description**

Transform identity by descent (IBD) matrix data from the form produced by external programs such as SOLAR into the compact form used by the *coxme* and *lmekin* routines.

**Usage**

```
ibd_matrix(id1, id2, ibd, idmap, diagonal)
```

**Arguments**

- id1*                    A character vector with the id of the first individuals of each pairs
- id2*                    A character vector with the id of the second individuals of each pairs
- ibd*                    the IBD value for that pair
- idmap*                  an optional 2 column matrix or data frame whose first element is the internal value (as found in *id1* and *id2*, and whose second element will be used for the *dimnames* of the result
- diagonal*              optional value for the diagonal element. If present, any missing diagonal elements in the input data will be set to this value.

## Details

The IBD matrix for a set of  $n$  subjects will be an  $n$  by  $n$  symmetric matrix whose  $i,j$  element contains, for some given genetic location, a 0/1 indicator of whether 0, 1/2 or 2/2 of the alleles for  $i$  and  $j$  are identical by descent. Fractional values occur if the IBD fraction must be imputed. The diagonal will be 1. Since a large fraction of the values will be zero, programs such as Solar return a data set containing only the non-zero elements. As well, Solar will have renumbered the subjects as `seq_len(n)` in such a way that families are grouped together in the matrix; a separate index file contains the mapping between this new id and the original one. The final matrix should be labeled with the original identifiers.

## Value

a sparse matrix of class `dsCMatrix`. This is the same form used for kinship matrices.

## See Also

[kinship\(\)](#)

---

<code>is_disconnected</code>	<i>Are individuals disconnected</i>
------------------------------	-------------------------------------

---

## Description

Check which individuals are disconnected.

## Usage

```
is_disconnected(id, dadid, momid)
```

## Arguments

<code>dadid</code>	A vector containing for each subject, the identifiers of the biologicals fathers.
<code>momid</code>	A vector containing for each subject, the identifiers of the biologicals mothers.

## Details

An individual is considered disconnected if the kinship with all the other individuals is 0.

## Value

A vector of boolean of the same size as **id** with TRUE if the individual is disconnected and FALSE otherwise

**Examples**

```
is_disconnected(
  c("1", "2", "3", "4", "5"),
  c("3", "3", NA, NA, NA),
  c("4", "4", NA, NA, NA)
)
```

---

is_founder	<i>Are individuals founders</i>
------------	---------------------------------

---

**Description**

Check which individuals are founders.

**Usage**

```
is_founder(momid, dadid, missid = NA_character_)
```

**Arguments**

momid	A vector containing for each subject, the identifiers of the biologicals mothers.
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.

**Value**

A vector of boolean of the same size as **dadid** and **momid** with TRUE if the individual has no parents (i.e is a founder) and FALSE otherwise.

**Examples**

```
is_founder(c("3", "3", NA, NA), c("4", "4", NA, NA))
```

---

is_informative	<i>Find informative individuals</i>
----------------	-------------------------------------

---

**Description**

Select the ids of the informative individuals.

**Usage**

```
## S4 method for signature 'character_OR_integer'
is_informative(obj, avail, affected, informative = "AvAf")

## S4 method for signature 'Pedigree'
is_informative(obj, col_aff = NULL, informative = "AvAf", reset = FALSE)
```

**Arguments**

obj	A character vector with the id of the individuals or a data.frame with all the informations in corresponding columns.
avail	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
affected	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).
informative	Informative individuals selection can take 5 values: <ul style="list-style-type: none"> <li>• 'AvAf' (available and affected),</li> <li>• 'AvOrAf' (available or affected),</li> <li>• 'Av' (available only),</li> <li>• 'Af' (affected only),</li> <li>• 'All' (all individuals)</li> <li>• A numeric/character vector of individuals id</li> <li>• A boolean</li> </ul>
col_aff	A character vector with the name of the column to be used for the affection status.
reset	If TRUE, the isinf slot is reset

**Details**

Depending on the **informative** parameter, the function will extract the ids of the informative individuals. In the case of a numeric vector, the function will return the same vector. In the case of a boolean, the function will return the ids of the individuals if TRUE, NA otherwise. In the case of a string, the function will return the ids of the corresponding informative individuals based on the avail and affected columns.

**Value****When obj is a vector:**

A vector of individuals informative identifiers.

**When obj is a Pedigree:**

The Pedigree object with its isinf slot updated.

## Examples

```
is_informative(c("A", "B", "C", "D", "E"), informative = c("A", "B"))
is_informative(c("A", "B", "C", "D", "E"), informative = c(1, 2))
is_informative(c("A", "B", "C", "D", "E"), informative = c("A", "B"))
is_informative(c("A", "B", "C", "D", "E"), avail = c(1, 0, 0, 1, 1),
  affected = c(0, 1, 0, 1, 1), informative = "AvAf")
is_informative(c("A", "B", "C", "D", "E"), avail = c(1, 0, 0, 1, 1),
  affected = c(0, 1, 0, 1, 1), informative = "AvOrAf")
is_informative(c("A", "B", "C", "D", "E"),
  informative = c(TRUE, FALSE, TRUE, FALSE, TRUE))

data("sampleped")
ped <- Pedigree(sampleped)
ped <- is_informative(ped, col_aff = "affection_mods")
isinf(ped(ped))
```

---

is_parent	<i>Are individuals parents</i>
-----------	--------------------------------

---

## Description

Check which individuals are parents.

## Usage

```
## S4 method for signature 'character_OR_integer'
is_parent(obj, dadid, momid, missid = NA_character_)

## S4 method for signature 'Ped'
is_parent(obj, missid = NA_character_)
```

## Arguments

obj	A vector of each subjects identifiers or a Ped object
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.

## Value

A vector of boolean of the same size as **obj** with TRUE if the individual is a parent and FALSE otherwise



**Examples**

```
is_parent(c("1", "2", "3", "4"), c("3", "3", NA, NA), c("4", "4", NA, NA))

data(sampleped)
ped <- Pedigree(sampleped)
is_parent(ped(ped))
```

---

is_valid_hints	<i>Check if a Hints object is valid</i>
----------------	---

---

**Description**

Check if horder and spouse slots are valid:

- horder is named numeric vector
- spouse is a data.frame
  - Has the three idr, idl, anchor columns
  - idr and idl are different and doesn't contains NA
  - idr and idl couple are unique
  - anchor column only have right, left, either values
- all ids in spouse needs to be in the names of the horder vector

**Usage**

```
is_valid_hints(object)
```

**Arguments**

object            A Hints object.

**Value**

A character vector with the errors or TRUE if no errors.

---

is_valid_ped	<i>Check if a Ped object is valid</i>
--------------	---------------------------------------

---

**Description**

Multiple checks are done here

**Usage**

```
is_valid_ped(object)
```

**Arguments**

object            A Ped object.

**Details**

- 1. Check that the ped ids slots have the right values
- 2. Check that the sex, steril, status, avail and affected slots have the right values
- 3. Check that dad are male and mom are female
- 4. Check that individuals have both parents or none

**Value**

A character vector with the errors or TRUE if no errors.

---

is_valid_pedigree	<i>Check if a Pedigree object is valid</i>
-------------------	--

---

**Description**

Multiple checks are done here

**Usage**

```
is_valid_pedigree(object)
```

**Arguments**

object            A Ped object.

**Details**

1. Check that the all Rel id are in the Ped object
2. Check that twins have same parents
3. Check that MZ twins have same sex
4. Check that all columns used in scales are in the Ped object
5. Check that all fill & border modalities are in the Ped object column
6. Check that all id used in Hints object are in the Ped object
7. Check that all spouse in Hints object are male / female

**Value**

A character vector with the errors or TRUE if no errors.

---

is_valid_rel	<i>Check if a Rel object is valid</i>
--------------	---------------------------------------

---

**Description**

Multiple checks are done here

**Usage**

```
is_valid_rel(object)
```

**Arguments**

object	A Ped object.
--------	---------------

**Details**

1. Check that the "id1", "id2", "code", "famid" slots exist
2. Check that the "code" slots have the right values (i.e. "MZ twin", "DZ twin", "UZ twin", "Spouse")
3. Check that all "id1" are different to "id2"
4. Check that all "id1" are smaller than "id2"
5. Check that no duplicate relation are present

**Value**

A character vector with the errors or TRUE if no errors.

---

is_valid_scales	<i>Check if a Scales object is valid</i>
-----------------	--

---

### Description

Check if the fill and border slots are valid:

- fill slot is a data.frame with "order", "column\_values", "column\_mods", "mods", "labels", "affected", "fill", "density", "angle" columns.
  - "affected" is logical.
  - "density", "angle", "order", "mods" are numeric.
  - "column\_values", "column\_mods", "labels", "fill" are character.
- border slot is a data.frame with "column\_values", "column\_mods", "mods", "labels", "border" columns.
  - "column\_values", "column\_mods", "labels", "border" are character.
  - "mods" is numeric.

### Usage

```
is_valid_scales(object)
```

### Arguments

object            A Scales object.

### Value

A character vector with the errors or TRUE if no errors.

---

kindepth	<i>Individual's depth in a pedigree</i>
----------	---

---

### Description

Computes the depth of each subject in the Pedigree.

### Usage

```
kindepth(obj, ...)
```

```
## S4 method for signature 'character_OR_integer'
kindepth(obj, dadid, momid, align_parents = FALSE)
```

```
## S4 method for signature 'Pedigree'
kindepth(obj, align_parents = FALSE)
```

```
## S4 method for signature 'Ped'
kindepth(obj, align_parents = FALSE)
```

### Arguments

<code>obj</code>	A character vector with the id of the individuals or a <code>data.frame</code> with all the informations in corresponding columns.
<code>...</code>	Additional arguments
<code>dadid</code>	A vector containing for each subject, the identifiers of the biologicals fathers.
<code>momid</code>	A vector containing for each subject, the identifiers of the biologicals mothers.
<code>align_parents</code>	If <code>align_parents = TRUE</code> , go one step further and try to make both parents of each child have the same depth. (This is not always possible). It helps the drawing program by lining up pedigrees that 'join in the middle' via a marriage.

### Details

Mark each person as to their depth in a Pedigree; 0 for a founder, otherwise :

$$depth = 1 + \max(fatherDepth, motherDepth)$$

In the case of an inbred Pedigree a perfect alignment may not exist.

### Value

An integer vector containing the depth for each subject

### Author(s)

Terry Therneau, updated by Louis Le Nézet

### See Also

[align\(\)](#)

### Examples

```
kindepth(
  c("A", "B", "C", "D", "E"),
  c("C", "D", "0", "0", "0"),
  c("E", "E", "0", "0", "0")
)
data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == "1",])
kindepth(ped1)
```

kinship

*Kinship matrix***Description**

Compute the kinship matrix for a set of related autosomal subjects. The function is generic, and can accept a Pedigree, a Ped or a vector as the first argument.

**Usage**

```
## S4 method for signature 'Ped'
kinship(obj, chrtype = "autosome")

## S4 method for signature 'character'
kinship(obj, dadid, momid, sex, chrtype = "autosome")

## S4 method for signature 'Pedigree'
kinship(obj, chrtype = "autosome")
```

**Arguments**

obj	A Pedigree or Ped object or a vector of subject identifiers.
chrtype	chromosome type. The currently supported types are 'autosome' and 'X' or 'x'.
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
sex	A character, factor or numeric vector corresponding to the gender of the individuals. This will be transformed to an ordered factor with the following levels: male < female < unknown < 'terminated'. The following values are recognized: <ul style="list-style-type: none"> <li>• character() or factor() : "f", "m", "woman", "man", "male", "female", "unknown", "terminated"</li> <li>• numeric() : 1 = "male", 2 = "female", 3 = "unknown", 4 = "terminated"</li> </ul>

**Details**

The function will usually be called with a Pedigree. The call with a Ped or a vector is provided for backwards compatibility with an earlier release of the library that was less capable. Note that when using with a Ped or a vector, any information on twins is not available to the function.

When called with a Pedigree, the routine will create a block-diagonal-symmetric sparse matrix object of class `dsCMatrix`. Since the `[i, j]` value of the result is 0 for any two unrelated individuals `i` and `j` and a `Matrix` utilizes sparse representation, the resulting object is often orders of magnitude smaller than an ordinary matrix.

Two genes `G1` and `G2` are identical by descent (IBD) if they are both physical copies of the same ancestral gene; two genes are identical by state if they represent the same allele. So the brown eye gene that I inherited from my mother is IBD with hers; the same gene in an unrelated individual is not.

The kinship coefficient between two subjects is the probability that a randomly selected allele from a locus will be IBD between them. It is obviously 0 between unrelated individuals. For an autosomal site and no inbreeding it will be 0.5 for an individual with themselves, .25 between mother and child, .125 between an uncle and neice, etc.

The computation is based on a recursive algorithm described in Lange, which assumes that the founder alleles are all independent.

## Value

### When obj is a vector:

A matrix of kinship coefficients.

### When obj is a Pedigree:

A matrix of kinship coefficients ordered by families present in the Pedigree object.

## References

K Lange, Mathematical and Statistical Methods for Genetic Analysis, Springer-Verlag, New York, 1997.

## See Also

`make_famid()`, `kindepth()`

## Examples

```
kinship(c("A", "B", "C", "D", "E"), c("C", "D", "0", "0", "0"),
        c("E", "E", "0", "0", "0"), sex = c(1, 2, 1, 2, 1))
kinship(c("A", "B", "C", "D", "E"), c("C", "D", "0", "0", "0"),
        c("E", "E", "0", "0", "0"), sex = c(1, 2, 1, 2, 1),
        chrtype = "x"
)

data(sampleped)
ped <- Pedigree(sampleped)
kinship(ped)
```

---

make\_famid

*Compute family id*

---

## Description

Construct a family identifier from pedigree information

**Usage**

```
## S4 method for signature 'character'
make_famid(obj, dadid, momid)

## S4 method for signature 'Pedigree'
make_famid(obj)
```

**Arguments**

obj	A character vector with the id of the individuals or a <code>data.frame</code> with all the informations in corresponding columns.
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.

**Details**

Create a vector of length `n`, giving the family 'tree' number of each subject. If the Pedigree is totally connected, then everyone will end up in tree 1, otherwise the tree numbers represent the disconnected subfamilies. Singleton subjects give a zero for family number.

**Value****When used with a character vector:**

An integer vector giving family groupings

**When used with a Pedigree object:**

An updated Pedigree object with the family id added and with all ids updated

**See Also**

[kinship\(\)](#)

**Examples**

```
make_famid(
  c("A", "B", "C", "D", "E", "F"),
  c("C", "D", "0", "0", "0", "0"),
  c("E", "E", "0", "0", "0", "0")
)

data(sampleped)
ped1 <- Pedigree(sampleped[, -1])
make_famid(ped1)
```



---

`minnbreast`*Minnesota Breast Cancer Study*

---

## Description

Data from the Minnesota Breast Cancer Family Study. This contains extended pedigrees from 426 families, each identified by a single proband in 1945-1952, with follow up for incident breast cancer.

## Usage

```
data(minnbreast)
```

## Format

A data frame with 28081 observations, one line per subject, on the following 14 variables.

- `id` : Subject identifier
- `proband` : If 1, this subject is one of the original 426 probands
- `fatherid` : Identifier of the father, if the father is part of the data set; zero otherwise
- `motherid` : Identifier of the mother, if the mother is part of the data set; zero otherwise
- `famid` : Family identifier
- `endage` : Age at last follow-up or incident cancer
- `cancer` : 1 = breast cancer (females) or prostate cancer (males), 0 = censored
- `yob` : Year of birth
- `education` : Amount of education: 1-8 years, 9-12 years, high school graduate, vocational education beyond high school, some college but did not graduate, college graduate, post-graduate education, refused to answer on the questionnaire
- `marstat` : Marital status: married, living with someone in a marriage-like relationship, separated or divorced, widowed, never married, refused to answer the questionnaire
- `everpreg` : Ever pregnant at the time of baseline survey
- `parity` : Number of births
- `nbreast` : Number of breast biopsies
- `sex` : M or F
- `bcpc` : Part of one of the families in the breast / prostate cancer substudy: 0 = no, 1 = yes. Note that subjects who were recruited to the overall study after the date of the BP substudy are coded as zero.

## Details

The original study was conducted by Dr. Elving Anderson at the Dight Institute for Human Genetics at the University of Minnesota. From 1944 to 1952, 544 sequential breast cancer cases seen at the University Hospital were enrolled, and information gathered on parents, siblings, offspring, aunts / uncles, and grandparents with the goal of understanding possible familial aspects of breast cancer. In 1991 the study was resurrected by Dr Tom Sellers.

Of the original 544 he excluded 58 prevalent cases, along with another 19 who had less than 2 living relatives at the time of Dr Anderson's survey. Of the remaining 462 families 10 had no living members, 23 could not be located and 8 refused, leaving 426 families on whom updated pedigrees were obtained.

This gave a study with 13351 males and 12699 females (5183 marry-ins). Primary questions were the relationship of early life exposures, breast density, and pharmacogenomics on incident breast cancer risk. For a subset of the families data was gathered on prostate cancer risk for male subjects via questionnaires sent to men over 40. Other than this, data items other than parentage are limited to the female subjects. In 2003 a second phase of the study was instituted. The pedigrees were further extended to the numbers found in this data set, and further data gathered by questionnaire.

## References

Epidemiologic and genetic follow-up study of 544 Minnesota breast cancer families: design and methods. Sellers TA, Anderson VE, Potter JD, Bartow SA, Chen PL, Everson L, King RA, Kuni CC, Kushi LH, McGovern PG, et al. Genetic Epidemiology, 1995; 12(4):417-29.

Evaluation of familial clustering of breast and prostate cancer in the Minnesota Breast Cancer Family Study. Grabrick DM, Cerhan JR, Vierkant RA, Therneau TM, Cheville JC, Tindall DJ, Sellers TA. Cancer Detect Prev. 2003; 27(1):30-6.

Risk of breast cancer with oral contraceptive use in women with a family history of breast cancer. Grabrick DM, Hartmann LC, Cerhan JR, Vierkant RA, Therneau TM, Vachon CM, Olson JE, Couch FJ, Anderson KE, Pankratz VS, Sellers TA. JAMA. 2000; 284(14):1791-8.

## Examples

```
data(minnbreast)
breastped <- Pedigree(minnbreast,
  cols_ren_ped = list(
    "indId" = "id", "fatherId" = "fatherid",
    "motherId" = "motherid", "gender" = "sex", "family" = "famid"
  ), missid = "0", col_aff = "cancer"
)
summary(breastped)
scales(breastped)
#plot family 8, proband is solid, slash for cancers
#plot(breastped[famid(breastped) == "8"])
```

---

min_dist_inf	<i>Minimum distance to the informative individuals</i>
--------------	--

---

## Description

Compute the minimum distance between the informative individuals and all the others. This distance is a transformation of the maximum kinship degree between the informative individuals and all the others. This transformation is done by taking the log2 of the inverse of the maximum kinship degree.

$$\text{minDist} = \log_2(1 / \max(\text{kinship}))$$

Therefore, the minimum distance is 0 when the maximum kinship is 1 and is infinite when the maximum kinship is 0. For siblings, the kinship value is 0.5 and the minimum distance is 1. Each time the kinship degree is divided by 2, the minimum distance is increased by 1.

## Usage

```
## S4 method for signature 'character'
min_dist_inf(obj, dadid, momid, sex, id_inf)

## S4 method for signature 'Pedigree'
min_dist_inf(obj, col_aff = NULL, informative = "AvAf", reset = FALSE, ...)

## S4 method for signature 'Ped'
min_dist_inf(obj, informative = "AvAf", reset = FALSE)
```

## Arguments

obj	A character vector with the id of the individuals or a data.frame with all the informations in corresponding columns.
...	Additional arguments
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
sex	A character, factor or numeric vector corresponding to the gender of the individuals. This will be transformed to an ordered factor with the following levels: male < female < unknown < 'terminated'. The following values are recognized: <ul style="list-style-type: none"> <li>• character() or factor() : "f", "m", "woman", "man", "male", "female", "unknown", "terminated"</li> <li>• numeric() : 1 = "male", 2 = "female", 3 = "unknown", 4 = "terminated"</li> </ul>
id_inf	An identifiers vector of informative individuals.
col_aff	A character vector with the name of the column to be used for the affection status.
informative	Informative individuals selection can take 5 values: <ul style="list-style-type: none"> <li>• 'AvAf' (available and affected),</li> </ul>

- 'AvOrAf' (available or affected),
  - 'Av' (available only),
  - 'Af' (affected only),
  - 'All' (all individuals)
  - A numeric/character vector of individuals id
  - A boolean
- reset                      If TRUE, the kin and if isinf columns is reset

**Value**

**When obj is a vector:**  
A vector of the minimum distance between the informative individuals and all the others corresponding to the order of the individuals in the obj vector.

**When obj is a Pedigree:**  
The Pedigree object with a new slot named 'kin' containing the minimum distance between each individuals and the informative individuals. The isinf slot is also updated with the informative individuals.

**See Also**

[kinship\(\)](#)

**Examples**

```
min_dist_inf(  
  c("A", "B", "C", "D", "E"),  
  c("C", "D", "0", "0", "0"),  
  c("E", "E", "0", "0", "0"),  
  sex = c(1, 2, 1, 2, 1),  
  id_inf = c("D", "E")  
)  
  
data(sampleped)  
ped <- Pedigree(sampleped)  
kin(ped(min_dist_inf(ped, col_aff = "affection_mods")))
```

---

na_to_length	<i>NA to specific length</i>
--------------	------------------------------

---

**Description**

Check if all value in a vector is NA. If so set all of them to a new value matching the length of the template. If not check that the size of the vector is equal to the template.

**Usage**

```
na_to_length(x, temp, value)
```

**Arguments**

x	The vector to check.
temp	A template vector to use to determine the length.
value	The value to use to fill the vector.

**Value**

A vector with the same length as temp.

**Examples**

```
na_to_length(NA, rep(0, 4), "NewValue")
na_to_length(c(1, 2, 3, NA), rep(0, 4), "NewValue")
```

---

norm_ped	<i>Normalise a Ped object dataframe</i>
----------	---

---

**Description**

Normalise dataframe for a Ped object

**Usage**

```
norm_ped(
  ped_df,
  na_strings = c("NA", ""),
  missid = NA_character_,
  try_num = FALSE
)
```

**Arguments**

ped_df	A data.frame with the individuals informations. The minimum columns required are: <ul style="list-style-type: none"> <li>- <code>`indID`</code> individual identifiers -&gt; <code>`id`</code></li> <li>- <code>`fatherId`</code> biological fathers identifiers -&gt; <code>`dadid`</code></li> <li>- <code>`motherId`</code> biological mothers identifiers -&gt; <code>`momdid`</code></li> <li>- <code>`gender`</code> sex of the individual -&gt; <code>`sex`</code></li> <li>- <code>`family`</code> family identifiers -&gt; <code>`famid`</code></li> </ul>
--------	---

The family column, if provided, will be merged to the *ids* field separated by an underscore using the `upd_famid_id()` function.

The following columns are also recognize and will be transformed with the `vect_to_binary()` function:

```
- `sterilisation` status -> `steril`
- `available` status -> `avail`
- `vitalStatus`, is the individual dead -> `status`
- `affection` status -> `affected`
```

The values recognized for those columns are 1 or 0, TRUE or FALSE.

na_strings	Vector of strings to be considered as NA values.
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.
try_num	Boolean defining if the function should try to convert all the columns to numeric.

## Details

Normalise a dataframe and check for columns correspondance to be able to use it as an input to create a Ped object. Multiple test are done and errors are checked. Sex is calculated based on the gender column.

The steril column need to be a boolean either TRUE, FALSE or 'NA'. Will be considered available any individual with no 'NA' values in the available column. Duplicated indId will nullify the relationship of the individual. All individuals with errors will be remove from the dataframe and will be transfered to the error dataframe.

A number of checks are done to ensure the dataframe is correct:

### On identifiers::

- All ids (id, dadid, momid, famid) are not empty (`!= ""`)
- All id are unique (no duplicated)
- All dadid and momid are unique in the id column (no duplicated)
- id is not the same as dadid or momid
- Either have both parents or none

### On sex:

- All sex code are either male, female, terminated or unknown.
- No parents are steril
- All fathers are male
- All mothers are female

## Value

A dataframe with different variable correctly standardized and with the errors identified in the error column

## See Also

[Ped\(\)](#), [Ped](#), [Pedigree\(\)](#)

Examples

```
df <- data.frame(
  indId = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),
  fatherId = c("A", 0, 1, 3, 0, 4, 1, 0, 6, 6),
  motherId = c(0, 0, 2, 2, 0, 5, 2, 0, 8, 8),
  gender = c(1, 2, "m", "man", "f", "male", "m", "m", "f", "f"),
  available = c("A", "1", 0, NA, 1, 0, 1, 0, 1, 0),
  famid = c(1, 1, 1, 1, 1, 1, 1, 2, 2, 2),
  sterilisation = c("TRUE", "FALSE", TRUE, FALSE, 1, 0, 1, 0, 1, "TRUE"),
  vitalStatus = c("TRUE", "FALSE", TRUE, FALSE, 1, 0, 1, 0, 1, 0),
  affection = c("TRUE", "FALSE", TRUE, FALSE, 1, 0, 1, 0, 1, 0)
)
tryCatch(
  norm_ped(df),
  error = function(e) print(e)
)
```

---

norm_rel	<i>Normalise a Rel object dataframe</i>
----------	---

---

Description

Normalise a dataframe and check for columns correspondance to be able to use it as an input to create a Ped object.

Usage

```
norm_rel(rel_df, na_strings = c("NA", ""), missid = NA_character_)
```

Arguments

rel_df	<p>A data.frame with the special relationships between individuals. See <a href="#">Rel()</a> for more informations. The minimum columns required are id1, id2 and code. The famid column can also be used to specify the family of the individuals. If a matrix is given, the columns needs to be ordered as id1, id2, code and famid. The code values are:</p> <ul style="list-style-type: none"><li>• 1 = Monozygotic twin</li><li>• 2 = Dizygotic twin</li><li>• 3 = twin of unknown zygotity</li><li>• 4 = Spouse</li></ul> <p>The value relation code recognized by the function are the one defined by the <a href="#">rel_code_to_factor()</a> function.</p>
na_strings	<p>Vector of strings to be considered as NA values.</p>
missid	<p>A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.</p>

Details

The famid column, if provided, will be merged to the *ids* field separated by an underscore using the `upd_famid_id()` function. The code column will be transformed with the `rel_code_to_factor()`. Multiple test are done and errors are checked.

A number of checks are done to ensure the dataframe is correct:

On identifiers::

- All ids (id1, id2) are not empty (`!= ""`)
- id1 and id2 are not the same

On code:

- All code are recognised as either "MZ twin", "DZ twin", "UZ twin" or "Spouse"

Value

A dataframe with the errors identified

Examples

```
df <- data.frame(
  id1 = c(1, 2, 3, 4, 5, 6, 7, 8, 9, 10),
  id2 = c(2, 3, 4, 5, 6, 7, 8, 9, 10, 1),
  code = c("MZ twin", "DZ twin", "UZ twin", "Spouse", 1, 2,
    3, 4, "MzTwin", "sp oUse"),
  famid = c(1, 1, 1, 1, 1, 1, 1, 2, 2, 2)
)
norm_rel(df)
```

---

num_child	<i>Number of childs</i>
-----------	-------------------------

---

Description

Compute the number of childs per individual

Usage

```
## S4 method for signature 'character_OR_integer'
num_child(obj, dadid, momid, rel_df = NULL, missid = NA_character_)

## S4 method for signature 'Pedigree'
num_child(obj, reset = FALSE)
```



**Arguments**

obj	A character vector with the id of the individuals or a <code>data.frame</code> with all the informations in corresponding columns.
dadid	A vector containing for each subject, the identifiers of the biologicals fathers.
momid	A vector containing for each subject, the identifiers of the biologicals mothers.
rel_df	A <code>data.frame</code> with the special relationships between individuals. See <a href="#">Rel()</a> for more informations. The minimum columns required are <code>id1</code> , <code>id2</code> and <code>code</code> . The <code>famid</code> column can also be used to specify the family of the individuals. If a matrix is given, the columns needs to be ordered as <code>id1</code> , <code>id2</code> , <code>code</code> and <code>famid</code> . The code values are: <ul style="list-style-type: none"> <li>• 1 = Monozygotic twin</li> <li>• 2 = Dizygotic twin</li> <li>• 3 = twin of unknown zygotity</li> <li>• 4 = Spouse</li> </ul> The value relation code recognized by the function are the one defined by the <a href="#">rel_code_to_factor()</a> function.
missid	A character vector with the missing values identifiers. All the <code>id</code> , <code>dadid</code> and <code>momid</code> corresponding to those values will be set to <code>NA_character_</code> .
reset	If <code>TRUE</code> , the <code>num_child_tot</code> , <code>num_child_ind</code> and the <code>num_child_dir</code> columns are reset.

**Details**

Compute the number of direct child but also the number of indirect child given by the ones related with the linked spouses. If a relation ship dataframe is given, then even if no children is present between 2 spouses, the indirect childs will still be added.

**Value****When obj is a vector:**

A dataframe with the columns `num_child_dir`, `num_child_ind` and `num_child_tot` giving respectively the direct, indirect and total number of child.

**When obj is a Pedigree object:**

An updated Pedigree object with the columns `num_child_dir`, `num_child_ind` and `num_child_tot` added to the Pedigree ped slot.

**Examples**

```
num_child(
  obj = c("1", "2", "3", "4", "5", "6", "7", "8", "9", "10"),
  dadid = c("3", "3", "6", "8", "0", "0", "0", "0", "0", "0"),
  momid = c("4", "5", "7", "9", "0", "0", "0", "0", "0", "0"),
  rel_df = data.frame(
    id1 = "10",
    id2 = "3",
```

```
        code = "Spouse"
      )
    )

data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == "1",])
ped1 <- num_child(ped1, reset = TRUE)
summary(ped(ped1))
```

---

paste0max	<i>Print0 to max</i>
-----------	----------------------

---

**Description**

Print0 the elements inside a vector until a maximum is reached.

**Usage**

```
paste0max(x, max = 5, sep = "", ...)
```

**Arguments**

x	A vector.
max	The maximum number of elements to print.
...	Additional arguments passed to print0

**Value**

The character vector aggregated until the maximum is reached.

---

Ped-class	<i>Ped object</i>
-----------	-------------------

---

**Description**

S4 class to represent the identity informations of the individuals in a pedigree.

**Constructor ::**

You either need to provide a vector of the same size for each slot or a data.frame with the corresponding columns.

The metadata will correspond to the columns that do not correspond to the Ped slots.

**Usage**

```
## S4 method for signature 'data.frame'
Ped(obj, cols_used_init = FALSE, cols_used_del = FALSE)

## S4 method for signature 'character_OR_integer'
Ped(
  obj,
  sex,
  dadid,
  momid,
  famid = NA,
  steril = NA,
  status = NA,
  avail = NA,
  affected = NA,
  missid = NA_character_
)
```

**Arguments**

<code>obj</code>	A character vector with the id of the individuals or a <code>data.frame</code> with all the informations in corresponding columns.
<code>cols_used_init</code>	Boolean defining if the columns that will be used should be initialised to NA.
<code>cols_used_del</code>	Boolean defining if the columns that will be used should be deleted.
<code>sex</code>	A character, factor or numeric vector corresponding to the gender of the individuals. This will be transformed to an ordered factor with the following levels: <code>male &lt; female &lt; unknown &lt; 'terminated'</code> The following values are recognized: <ul style="list-style-type: none"> <li>• <code>character()</code> or <code>factor()</code> : "f", "m", "woman", "man", "male", "female", "unknown", "terminated"</li> <li>• <code>numeric()</code> : 1 = "male", 2 = "female", 3 = "unknown", 4 = "terminated"</li> </ul>
<code>dadid</code>	A vector containing for each subject, the identifiers of the biologicals fathers.
<code>momid</code>	A vector containing for each subject, the identifiers of the biologicals mothers.
<code>famid</code>	A character vector with the family identifiers of the individuals. If provide, will be aggregated to the individuals identifiers separated by an underscore.
<code>steril</code>	A logical vector with the sterilisation status of the individuals (i.e. FALSE = not sterilised, TRUE = sterilised, NA = unknown).
<code>status</code>	A logical vector with the affection status of the individuals (i.e. FALSE = alive, TRUE = dead, NA = unknown).
<code>avail</code>	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
<code>affected</code>	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).
<code>missid</code>	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to <code>NA_character_</code> .

## Details

The minimal needed informations are `id`, `dadid`, `momid` and `sex`. The other slots are used to store recognized informations. Additional columns can be added to the Ped object and will be stored in the `elementMetadata` slot of the Ped object.

## Value

A Ped object.

## Slots

`id` A character vector with the id of the individuals.  
`dadid` A character vector with the id of the father of the individuals.  
`momid` A character vector with the id of the mother of the individuals.  
`sex` An ordered factor vector for the sex of the individuals (i.e. `male < female < unknown < terminated`).  
`famid` A character vector with the family identifiers of the individuals (optional).  
`steril` A logical vector with the sterilisation status of the individuals (i.e. `FALSE` = not sterilised, `TRUE` = sterilised, `NA` = unknown).  
`status` A logical vector with the affection status of the individuals (i.e. `FALSE` = alive, `TRUE` = dead, `NA` = unknown).  
`avail` A logical vector with the availability status of the individuals (i.e. `FALSE` = not available, `TRUE` = available, `NA` = unknown).  
`affected` A logical vector with the affection status of the individuals (i.e. `FALSE` = not affected, `TRUE` = affected, `NA` = unknown).  
`useful` A logical vector with the usefulness status of the individuals (i.e. `FALSE` = not useful, `TRUE` = useful).  
`isinf` A logical vector indicating if the individual is informative or not (i.e. `FALSE` = not informative, `TRUE` = informative).  
`kin` A numeric vector with minimal kinship value between the individuals and the useful individuals.  
`num_child_tot` A numeric vector with the total number of children of the individuals.  
`num_child_dir` A numeric vector with the number of children of the individuals.  
`num_child_ind` A numeric vector with the number of children of the individuals.  
`elementMetadata` A `DataFrame` with the additional metadata columns of the Ped object.  
`metadata` Meta informations about the pedigree.

## Accessors

For all the following accessors, the `x` parameters is a Ped object. Each getters return a vector of the same length as `x` with the values of the corresponding slot. For each getter, you have a setter with the same name, to be use as `slot(x) <- value`. The value parameter is a vector of the same length as `x`, except for the `mcols()` accessors where value is a list or a `data.frame` with each elements with the same length as `x`.

- `id(x)` : Individuals identifiers
- `dadid(x)` : Individuals' father identifiers
- `momid(x)` : Individuals' mother identifiers
- `famid(x)` : Individuals' family identifiers
- `sex(x)` : Individuals' gender
- `affected(x)` : Individuals' affection status
- `avail(x)` : Individuals' availability status
- `status(x)` : Individuals' death status
- `isinf(x)` : Individuals' informativeness status
- `kin(x)` : Individuals' kinship distance to the informative individuals
- `useful(x)` : Individuals' usefullness status
- `mcols(x)` : Individuals' metadata

### Generics

- `summary(x)`: Compute the summary of a Ped object
- `show(x)`: Convert the Ped object to a `data.frame` and print it with its summary.
- `as.list(x)`: Convert a Ped object to a list with the metadata columns at the end.
- `as.data.frame(x)`: Convert a Ped object to a `data.frame` with the metadata columns at the end.
- `subset(x, i, del_parents = FALSE, keep = TRUE)`: Subset a Ped object based on the individuals identifiers given.
  - `i` : A vector of individuals identifiers to keep.
  - `del_parents` : A logical value indicating if the parents of the individuals should be deleted.
  - `keep` : A logical value indicating if the individuals should be kept or deleted.

### See Also

[Pedigree\(\)](#)

**Examples**

```
data(sampleped)
Ped(sampleped)

Ped(
  obj = c("1", "2", "3", "4", "5", "6"),
  dadid = c("4", "4", "6", "0", "0", "0"),
  momid = c("5", "5", "5", "0", "0", "0"),
  sex = c(1, 2, 3, 1, 2, 1),
  missid = "0"
)
```

Pedigree-class

*Pedigree object***Description**

A pedigree is a ensemble of individuals linked to each other into a family tree. A Pedigree object store the informations of the individuals and the special relationships between them. It also permit to store the informations needed to plot the pedigree (i.e. scales and hints).

**Constructor ::**

Main constructor of the package. This constructor help to create a Pedigree object from different data.frame or a set of vectors.

If any errors are found in the data, the function will return the data.frame with the errors of the Ped object and the Rel object.

**Usage**

```
Pedigree(obj, ...)
```

```
## S4 method for signature 'character_OR_integer'
```

```
Pedigree(
  obj,
  dadid,
  momid,
  sex,
  famid = NA,
  avail = NULL,
  affected = NULL,
  status = NULL,
  steril = NULL,
  rel_df = NULL,
  missid = NA_character_,
  col_aff = "affection",
  normalize = TRUE,
  ...
)
```

```

)

## S4 method for signature 'data.frame'
Pedigree(
  obj = data.frame(indId = character(), fatherId = character(), motherId = character(),
    gender = numeric(), family = character(), available = numeric(), vitalStatus =
    numeric(), affection = numeric(), sterilisation = numeric()),
  rel_df = data.frame(id1 = character(), id2 = character(), code = numeric(), famid =
    character()),
  cols_ren_ped = list(indId = "id", fatherId = "dadid", motherId = "momid", family =
    "famid", gender = "sex", sterilisation = "steril", affection = "affected", available
    = "avail", vitalStatus = "status"),
  cols_ren_rel = list(id1 = "indId1", id2 = "indId2", famid = "family"),
  hints = list(horder = NULL, spouse = NULL),
  normalize = TRUE,
  missid = NA_character_,
  col_aff = "affection",
  ...
)

```

## Arguments

<code>obj</code>	A vector of the individuals identifiers or a data.frame with the individuals informations. See <a href="#">Ped()</a> for more informations.
<code>...</code>	Arguments passed on to <a href="#">generate_colors</a>
<code>dadid</code>	A vector containing for each subject, the identifiers of the biologicals fathers.
<code>momid</code>	A vector containing for each subject, the identifiers of the biologicals mothers.
<code>sex</code>	A character, factor or numeric vector corresponding to the gender of the individuals. This will be transformed to an ordered factor with the following levels: male < female < unknown < 'terminated'. The following values are recognized: <ul style="list-style-type: none"> <li>• <code>character()</code> or <code>factor()</code> : "f", "m", "woman", "man", "male", "female", "unknown", "terminated"</li> <li>• <code>numeric()</code> : 1 = "male", 2 = "female", 3 = "unknown", 4 = "terminated"</li> </ul>
<code>famid</code>	A character vector with the family identifiers of the individuals. If provide, will be aggregated to the individuals identifiers separated by an underscore.
<code>avail</code>	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
<code>affected</code>	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown). Can also be a data.frame with the same length as <code>obj</code> . If it is a matrix, it will be converted to a data.frame and the columns will be named after the <code>col_aff</code> argument.
<code>status</code>	A logical vector with the affection status of the individuals (i.e. FALSE = alive, TRUE = dead, NA = unknown).
<code>steril</code>	A logical vector with the sterilisation status of the individuals (i.e. FALSE = not sterilised, TRUE = sterilised, NA = unknown).

<code>rel_df</code>	<p>A data.frame with the special relationships between individuals. See <code>Rel()</code> for more informations. The minimum columns required are <code>id1</code>, <code>id2</code> and <code>code</code>. The <code>famid</code> column can also be used to specify the family of the individuals. If a matrix is given, the columns needs to be ordered as <code>id1</code>, <code>id2</code>, <code>code</code> and <code>famid</code>. The code values are:</p> <ul style="list-style-type: none"> <li>• 1 = Monozygotic twin</li> <li>• 2 = Dizygotic twin</li> <li>• 3 = twin of unknown zygoty</li> <li>• 4 = Spouse</li> </ul> <p>The value relation code recognized by the function are the one defined by the <code>rel_code_to_factor()</code> function.</p>
<code>missid</code>	A character vector with the missing values identifiers. All the <code>id</code> , <code>dadid</code> and <code>momid</code> corresponding to those values will be set to <code>NA_character_</code> .
<code>col_aff</code>	A character vector with the name of the column to be used for the affection status.
<code>normalize</code>	A logical to know if the data should be normalised.
<code>cols_ren_ped</code>	A named list with the columns to rename for the pedigree dataframe. This is useful if you want to use a dataframe with different column names. The names of the list should be the new column names and the values should be the old column names. The default values are to be used with <code>normalize = TRUE</code> .
<code>cols_ren_rel</code>	A named list with the columns to rename for the relationship matrix. This is useful if you want to use a dataframe with different column names. The names of the list should be the new column names and the values should be the old column names.
<code>hints</code>	A Hints object or a named list containing <code>horder</code> and <code>spouse</code> .

## Details

If the normalization is set to `TRUE`, then the data will be standardized using the function `norm_ped()` and `norm_rel()`.

If a data.frame is given, the columns names needed will depend if the normalization is selected or not. If the normalization is selected, the columns names needed are as follow and if not the columns names needed are in parenthesis:

- `indID`: the individual identifier (`id`)
- `fatherId`: the identifier of the biological father (`dadid`)
- `motherId`: the identifier of the biological mother (`momid`)
- `gender`: the sex of the individual (`sex`)
- `family`: the family identifier of the individual (`famid`)
- `sterilisation`: the sterilisation status of the individual (`steril`)
- `available`: the availability status of the individual (`avail`)
- `vitalStatus`: the death status of the individual (`status`)
- `affection`: the affection status of the individual (`affected`)



- ...: other columns that will be stored in the elementMetadata slot

The minimum columns required are :

- indID / id
- fatherId / dadid
- motherId / momid
- gender / sex

The family / famid column can also be used to specify the family of the individuals and will be merge to the indId / id field separated by an underscore. The columns sterilisation, available, vitalStatus, affection will be transformed with the [vect\\_to\\_binary\(\)](#) function when the normalisation is selected. If you do not use the normalisation, the columns will be checked to be 0 or 1.

If affected is a data.frame, **col\_aff** will be overwritten by the column names of the data.frame.

## Value

A Pedigree object.

## Slots

**ped** A Ped object for the identity informations. See [Ped\(\)](#) for more informations.

**rel** A Rel object for the special relationships. See [Rel\(\)](#) for more informations.

**scales** A Scales object for the filling and bordering colors used in the plot. See [Scales\(\)](#) for more informations.

**hints** A Hints object for the ordering of the individuals in the plot. See [Hints\(\)](#) for more informations.

## Accessors

For all the following accessors, the x parameters is a Pedigree object. Each getters return a vector of the same length as x with the values of the corresponding slot.

- **famid(x)** : Get the family identifiers of a Pedigree object. This function is a wrapper around **famid(ped(x))**.
- **ped(x, slot)** : Get the value of a specific slot of the Ped object
- **ped(x)** : Get the Ped object
- **ped(x, slot) <- value** : Set the value of a specific slot of the Ped object Wrapper of **slot(ped(x)) <- value**
- **ped(x) <- value** : Set the Ped object
- **mcols(x)** : Get the metadata of a Pedigree object. This function is a wrapper around **mcols(ped(x))**.
- **mcols(x) <- value** : Set the metadata of a Pedigree object. This function is a wrapper around **mcols(ped(x)) <- value**.

- `rel(x, slot)` : Get the value of a specific slot of the Rel object
- `rel(x)` : Get the Rel object
- `rel(x, slot) <- value` : Set the value of a specific slot of the Rel object Wrapper of `slot(rel(x)) <- value`
- `rel(x) <- value` : Set the Rel object
- `scales(x)` : Get the Scales object
- `scales(x) <- value` : Set the Scales object
- `fill(x)` : Get the fill data.frame from the Scales object. Wrapper of `fill(scales(x))`
- `fill(x) <- value` : Set the fill data.frame from the Scales object. Wrapper of `fill(scales(x)) <- value`
- `border(x)` : Get the border data.frame from the Scales object. Wrapper of `border(scales(x))`
- `border(x) <- value` : Set the border data.frame from the Scales object. Wrapper of `border(scales(x)) <- value`
- `hints(x)` : Get the Hints object
- `hints(x) <- value` : Set the Hints object
- `horder(x)` : Get the horder vector from the Hints object. Wrapper of `horder(hints(x))`
- `horder(x) <- value` : Set the horder vector from the Hints object. Wrapper of `horder(hints(x)) <- value`
- `spouse(x)` : Get the spouse data.frame from the Hints object. Wrapper of `spouse(hints(x))`.
- `spouse(x) <- value` : Set the spouse data.frame from the Hints object. Wrapper of `spouse(hints(x)) <- value`.

## Generics

- `length(x)`: Get the length of a Pedigree object. Wrapper of `length(ped(x))`.
- `show(x)`: Print the information of the Ped and Rel object inside the Pedigree object.
- `summary(x)`: Compute the summary of the Ped and Rel object inside the Pedigree object.
- `as.list(x)`: Convert a Pedigree object to a list
- `subset(x, i, keep = TRUE)`: Subset a Pedigree object based on the individuals identifiers given.
  - `i` : A vector of individuals identifiers to keep.
  - `del_parents` : A logical value indicating if the parents of the individuals should be deleted.
  - `keep` : A logical value indicating if the individuals should be kept or deleted.
- `x[i, del_parents, keep]`: Subset a Pedigree object based on the individuals identifiers given.

**See Also**

[Pedigree\(\)](#), [Ped\(\)](#), [Rel\(\)](#), [Scales\(\)](#), [Hints\(\)](#)

[Ped\(\)](#), [Rel\(\)](#), [Scales\(\)](#)

**Examples**

```
Pedigree(
  obj = c("1", "2", "3", "4", "5", "6"),
  dadid = c("4", "4", "6", "0", "0", "0"),
  momid = c("5", "5", "5", "0", "0", "0"),
  sex = c(1, 2, 3, 1, 2, 1),
  avail = c(0, 1, 0, 1, 0, 1),
  affected = matrix(c(
    0, 1, 0, 1, 0, 1,
    1, 1, 1, 1, 1, 1
  ), ncol = 2),
  col_aff = c("aff1", "aff2"),
  missid = "0",
  rel_df = matrix(c(
    "1", "2", 2
  ), ncol = 3, byrow = TRUE),
)

data(sampleped)
Pedigree(sampleped)
```

---

ped\_to\_legdf

---

Create plotting legend data frame from a Pedigree

---

**Description**

Convert a Pedigree to a legend data frame for it to be plotted afterwards with [plot\\_fromdf\(\)](#).

**Usage**

```
## S4 method for signature 'Pedigree'
ped_to_legdf(obj, boxh = 1, boxw = 1, cex = 1, adjx = 0, adjy = 0)
```

**Arguments**

obj	A Pedigree object
boxh	Height of the polygons elements
boxw	Width of the polygons elements
cex	Character expansion of the text
adjx	default=0. Controls the horizontal text adjustment of the labels in the legend.
adjy	default=0. Controls the vertical text adjustment of the labels in the legend.

## Details

The data frame contains the following columns:

- `x0, y0, x1, y1`: coordinates of the elements
- `type`: type of the elements
- `fill`: fill color of the elements
- `border`: border color of the elements
- `angle`: angle of the shading of the elements
- `density`: density of the shading of the elements
- `cex`: size of the elements
- `label`: label of the elements
- `tips`: tips of the elements (used for the tooltips)
- `adjx`: horizontal text adjustment of the labels
- `adjy`: vertical text adjustment of the labels

All those columns are used by `plot_fromdf()` to plot the graph.

## Value

A list containing the legend data frame and the user coordinates.

## Examples

```
data("sampleped")
ped <- Pedigree(sampleped)
leg_df <- ped_to_legdf(ped)
summary(leg_df$df)
plot_fromdf(leg_df$df, usr = c(-1,15,0,7))
```

---

ped\_to\_plotdf

*Create plotting data frame from a Pedigree*

---

## Description

Convert a Pedigree to a data frame with all the elements and their characteristic for them to be plotted afterwards with `plot_fromdf()`.

**Usage**

```
## S4 method for signature 'Pedigree'
ped_to_plotdf(
  obj,
  packed = TRUE,
  width = 6,
  align = c(1.5, 2),
  subreg = NULL,
  cex = 1,
  symbolsize = cex,
  pconnect = 0.5,
  branch = 0.6,
  aff_mark = TRUE,
  label = NULL,
  ...
)
```

**Arguments**

<code>obj</code>	A Pedigree object
<code>...</code>	Other arguments passed to <a href="#">par()</a>
<code>packed</code>	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
<code>width</code>	For a packed output, the minimum width of the plot, in inches.
<code>align</code>	For a packed Pedigree, align children under parents TRUE, to the extent possible given the page width, or align to the left margin FALSE. This argument can be a two element vector, giving the alignment parameters, or a logical value. If TRUE, the default is <code>c(1.5, 2)</code> , or if numeric the routine <code>alignedped4()</code> will be called.
<code>subreg</code>	A 4-element vector for (min x, max x, min depth, max depth), used to edit away portions of the plot coordinates returned by <a href="#">align()</a> . This is useful for zooming in on a particular region of the Pedigree.
<code>cex</code>	Character expansion of the text
<code>symbolsize</code>	Size of the symbols
<code>pconnect</code>	When connecting parent to children the program will try to make the connecting line as close to vertical as possible, subject to it lying inside the endpoints of the line that connects the children by at least <code>pconnect</code> people. Setting this option to a large number will force the line to connect at the midpoint of the children.
<code>branch</code>	defines how much angle is used to connect various levels of nuclear families.
<code>aff_mark</code>	If TRUE, add a <code>aff_mark</code> to each box corresponding to the value of the affection column for each filling scale.
<code>label</code>	If not NULL, add a label to each box corresponding to the value of the column given.

## Details

The data frame contains the following columns:

- `x0`, `y0`, `x1`, `y1`: coordinates of the elements
- `type`: type of the elements
- `fill`: fill color of the elements
- `border`: border color of the elements
- `angle`: angle of the shading of the elements
- `density`: density of the shading of the elements
- `cex`: size of the elements
- `label`: label of the elements
- `tips`: tips of the elements (used for the tooltips)
- `adjx`: horizontal text adjustment of the labels
- `adjy`: vertical text adjustment of the labels

All those columns are used by `plot_fromdf()` to plot the graph.

## Value

A list containing the data frame and the user coordinates.

## See Also

`plot_fromdf()` `ped_to_legdf()`

## Examples

```
data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == 1,])
plot_df <- ped_to_plotdf(ped1)
summary(plot_df$df)
plot_fromdf(plot_df$df, usr = plot_df$par_usr$usr,
            boxh = plot_df$par_usr$boxh, boxw = plot_df$par_usr$boxw
)
```

---

permute

*Generate all possible permutation*

---

## Description

Given a vector of length **n**, generate all possible permutations of the numbers 1 to **n**. This is a recursive routine, and is not very efficient.

**Usage**

```
permute(x)
```

**Arguments**

**x**                      A vector of length **n**

**Value**

A matrix with **n** cols and **n!** rows

---

```
plot, Pedigree, missing-method
```

*Plot Pedigrees*

---

**Description**

This function is used to plot a Pedigree object.

It is a wrapper for [plot\\_fromdf\(\)](#) and [ped\\_to\\_plotdf\(\)](#) as well as [ped\\_to\\_legdf\(\)](#) if legend = TRUE.

**Usage**

```
## S4 method for signature 'Pedigree,missing'
plot(
  x,
  aff_mark = TRUE,
  label = NULL,
  ggplot_gen = FALSE,
  cex = 1,
  symbolsize = 1,
  branch = 0.6,
  packed = TRUE,
  align = c(1.5, 2),
  width = 6,
  title = NULL,
  subreg = NULL,
  pconnect = 0.5,
  fam_to_plot = 1,
  legend = FALSE,
  leg_cex = 0.8,
  leg_symbolsize = 0.5,
  leg_loc = NULL,
  leg_adjx = 0,
  leg_adjy = 0,
  ...
)
```

**Arguments**

<code>x</code>	A Pedigree object.
<code>aff_mark</code>	If TRUE, add a <code>aff_mark</code> to each box corresponding to the value of the affection column for each filling scale.
<code>label</code>	If not NULL, add a label to each box corresponding to the value of the column given.
<code>ggplot_gen</code>	If TRUE add the segments to the ggplot object
<code>cex</code>	Character expansion of the text
<code>symbolsize</code>	Size of the symbols
<code>branch</code>	defines how much angle is used to connect various levels of nuclear families.
<code>packed</code>	Should the Pedigree be compressed. (i.e. allow diagonal lines connecting parents to children in order to have a smaller overall width for the plot.)
<code>align</code>	For a packed Pedigree, align children under parents TRUE, to the extent possible given the page width, or align to the left margin FALSE. This argument can be a two element vector, giving the alignment parameters, or a logical value. If TRUE, the default is <code>c(1.5, 2)</code> , or if numeric the routine <code>alignped4()</code> will be called.
<code>width</code>	For a packed output, the minimum width of the plot, in inches.
<code>title</code>	The title of the plot.
<code>subreg</code>	A 4-element vector for (min x, max x, min depth, max depth), used to edit away portions of the plot coordinates returned by <code>align()</code> . This is useful for zooming in on a particular region of the Pedigree.
<code>pconnect</code>	When connecting parent to children the program will try to make the connecting line as close to vertical as possible, subject to it lying inside the endpoints of the line that connects the children by at least <code>pconnect</code> people. Setting this option to a large number will force the line to connect at the midpoint of the children.
<code>fam_to_plot</code>	default=1. If the Pedigree contains multiple families, this parameter can be used to select which family to plot. It can be a numeric value or a character value. If numeric, it is the index of the family to plot returned by <code>unique(x\$ped\$famid)</code> . If character, it is the family id to plot.
<code>legend</code>	default=FALSE. If TRUE, a legend will be added to the plot.
<code>leg_cex</code>	default=0.8. Controls the size of the legend text.
<code>leg_symbolsizes</code>	default=0.5. Controls the size of the legend symbols.
<code>leg_loc</code>	default=NULL. If NULL, the legend will be placed in the upper right corner of the plot. Otherwise, a 4-element vector of the form (x0, x1, y0, y1) can be used to specify the location of the legend.
<code>leg_adjx</code>	default=0. Controls the horizontal labels adjustment of the legend.
<code>leg_adjy</code>	default=0. Controls the vertical labels adjustment of the legend.
<code>...</code>	Extra options that feed into the plot function.



## Details

Two important parameters control the looks of the result. One is the user specified maximum width. The smallest possible width is the maximum number of subjects on a line, if the user's suggestion is too low it is increased to 1 + that amount (to give just a little wiggle room).

To make a Pedigree where all children are centered under parents simply make the width large enough, however, the symbols may get very small.

The second is `align`, a vector of 2 alignment parameters `a` and `b`. For each set of siblings at a set of locations `x` and with parents at `p=c(p1, p2)` the alignment penalty is

$$(1/k^a) \sum_i (x_i - (p1 + p2)/2)^2$$

$$\sum (x - \bar{p})^2 / (k^a)$$

Where `k` is the number of siblings in the set.

When `a = 1` moving a sibship with `k` sibs one unit to the left or right of optimal will incur the same cost as moving one with only 1 or two sibs out of place.

If `a = 0` then large sibships are harder to move than small ones, with the default value `a = 1.5` they are slightly easier to move than small ones. The rationale for the default is as long as the parents are somewhere between the first and last siblings the result looks fairly good, so we are more flexible with the spacing of a large family. By tethering all the sibs to a single spot they are kept close to each other. The alignment penalty for spouses is  $b(x_1 - x_2)^2$ , which tends to keep them together. The size of `b` controls the relative importance of sib-parent and spouse-spouse closeness.

## Value

an invisible list containing

- `df` : the data.frame used to plot the Pedigree
- `par_usr` : the user coordinates used to plot the Pedigree
- `ggplot` : the ggplot object if `ggplot_gen = TRUE`

## Side Effects

Creates plot on current plotting device.

## See Also

[Pedigree\(\)](#)

## Examples

```
data(sampleped)
pedAll <- Pedigree(sampleped)
#plot(pedAll)
```

---

plot_fromdf	<i>Create a plot from a data.frame</i>
-------------	--

---

### Description

This function is used to create a plot from a data.frame.

If ggplot\_gen = TRUE, the plot will be generated with ggplot2 and will be returned invisibly.

### Usage

```
plot_fromdf(
  df,
  usr = NULL,
  title = NULL,
  ggplot_gen = FALSE,
  boxw = 1,
  boxh = 1,
  add_to_existing = FALSE
)
```

### Arguments

df	<p>A data.frame with the following columns:</p> <ul style="list-style-type: none"> <li>• type: The type of element to plot. Can be text, segments, arc or other polygons. For polygons, the name of the polygon must be in the form poly_*_* where poly is one of the type given by <a href="#">polygons()</a>, the first * is the number of slice in the polygon and the second * is the position of the division of the polygon.</li> <li>• x0: The x coordinate of the center of the element.</li> <li>• y0: The y coordinate of the center of the element.</li> <li>• x1: The x coordinate of the end of the element. Only used for segments and arc.</li> <li>• y1: The y coordinate of the end of the element. Only used for segments and arc.</li> <li>• fill: The fill color of the element.</li> <li>• border: The border color of the element.</li> <li>• density: The density of the element.</li> <li>• angle: The angle of the element.</li> <li>• label: The label of the element. Only used for text.</li> <li>• cex: The size of the element.</li> <li>• adjx: The x adjustment of the element. Only used for text.</li> <li>• adjy: The y adjustment of the element. Only used for text.</li> </ul>
usr	The user coordinates of the plot.
title	The title of the plot.

ggplot\_gen        If TRUE add the segments to the ggplot object  
boxw              Width of the polygons elements  
boxh              Height of the polygons elements  
add\_to\_existing    If TRUE, the plot will be added to the current plot.

**Value**

an invisible ggplot object and a plot on the current plotting device

**Examples**

```
data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == 1,])
lst <- ped_to_plotdf(ped1)
#plot_fromdf(lst$df, lst$par_usr$usr,
#   boxw = lst$par_usr$boxw, boxh = lst$par_usr$boxh
#)
```

---

polyfun	<i>Polygonal element</i>
---------	--------------------------

---

**Description**

Create a list of x and y coordinates for a polygon with a given number of slices and a list of coordinates for the polygon.

**Usage**

```
polyfun(nslice, coord)
```

**Arguments**

nslice            Number of slices in the polygon  
coord            Element form which to generate the polygon containing x and y coordinates and theta

**Value**

a list of x and y coordinates

**Examples**

```
polyfun(2, list(
  x = c(-0.5, -0.5, 0.5, 0.5),
  y = c(-0.5, 0.5, 0.5, -0.5),
  theta = -c(3, 5, 7, 9) * pi / 4
))
```

---

polygons	<i>List of polygonal elements</i>
----------	-----------------------------------

---

**Description**

Create a list of polygonal elements with x, y coordinates and theta for the square, circle, diamond and triangle. The number of slices in each element can be specified.

**Usage**

```
polygons(nslice = 1)
```

**Arguments**

nslice	Number of slices in each element If nslice > 1, the elements are created with <code>polyfun()</code> .
--------	--

**Value**

a list of polygonal elements with x, y coordinates and theta by slice.

**Examples**

```
polygons()
polygons(4)
```

---

Rel-class	<i>Rel object</i>
-----------	-------------------

---

**Description**

S4 class to represent the special relationships in a Pedigree.

**Constructor ::**

You either need to provide a vector of the same size for each slot or a `data.frame` with the corresponding columns.

**Usage**

```
## S4 method for signature 'data.frame'
Rel(obj)

## S4 method for signature 'character_OR_integer'
Rel(obj, id2, code, famid = NA_character_)
```

**Arguments**

obj	A character vector with the id of the first individuals of each pairs or a data . frame with all the informations in corresponding columns.
id2	A character vector with the id of the second individuals of each pairs
code	A character, factor or numeric vector corresponding to the relation code of the individuals: <ul style="list-style-type: none"> <li>• MZ twin = Monozygotic twin</li> <li>• DZ twin = Dizygotic twin</li> <li>• UZ twin = twin of unknown zygosity</li> <li>• Spouse = Spouse The following values are recognized: <ul style="list-style-type: none"> <li>• character() or factor() : "MZ twin", "DZ twin", "UZ twin", "Spouse" with or without space between the words. The case is not important.</li> <li>• numeric() : 1 = "MZ twin", 2 = "DZ twin", 3 = "UZ twin", 4 = "Spouse"</li> </ul> </li> </ul>
famid	A character vector with the family identifiers of the individuals. If provide, will be aggregated to the individuals identifiers separated by an underscore.

**Details**

A Rel object is a list of special relationships between individuals in the pedigree. It is used to create a Pedigree object. The minimal needed informations are id1, id2 and code.

If a famid is provided, the individuals id will be aggregated to the famid character to ensure the uniqueness of the id.

**Value**

A Rel object.

**Slots**

id1	A character vector with the id of the first individual.
id2	A character vector with the id of the second individual.
code	An ordered factor vector with the code of the special relationship. (i.e. MZ twin < DZ twin < UZ twin < Spouse).
famid	A character vector with the famid of the individuals.

**Accessors**

For all the following accessors, the x parameters is a Rel object. Each getters return a vector of the same length as x with the values of the corresponding slot.

- code(x) : Relationships' code
- id1(x) : Relationships' first individuals' identifier
- id2(x) : Relationships' second individuals' identifier

- famid(x) : Relationships' individuals' family identifier
- famid(x) <- value : Set the relationships' individuals' family identifier
  - value : A character or integer vector of the same length as x with the family identifiers

### Generics

- summary(x): Compute the summary of a Rel object
- show(x): Convert the Rel object to a data.frame and print it with its summary.
- as.list(x): Convert a Rel object to a list
- as.data.frame(x): Convert a Rel object to a data.frame
- subset(x, i, keep = TRUE): Subset a Rel object based on the individuals identifiers given.
  - i : A vector of individuals identifiers to keep.
  - keep : A logical value indicating if the individuals should be kept or deleted.

### See Also

[Pedigree\(\)](#)

### Examples

```
rel_df <- data.frame(
  id1 = c("1", "2", "3"),
  id2 = c("2", "3", "4"),
  code = c(1, 2, 3)
)
Rel(rel_df)

Rel(
  obj = c("1", "2", "3"),
  id2 = c("2", "3", "4"),
  code = c(1, 2, 3)
)
```

---

rel_code_to_factor	<i>Relationship code variable to ordered factor</i>
--------------------	---

---

### Description

Relationship code variable to ordered factor

### Usage

```
rel_code_to_factor(code)
```

**Arguments**

- code                      A character, factor or numeric vector corresponding to the relation code of the individuals:
- MZ twin = Monozygotic twin
  - DZ twin = Dizygotic twin
  - UZ twin = twin of unknown zygosity
  - Spouse = Spouse The following values are recognized:
  - character() or factor() : "MZ twin", "DZ twin", "UZ twin", "Spouse" with or without space between the words. The case is not important.
  - numeric() : 1 = "MZ twin", 2 = "DZ twin", 3 = "UZ twin", 4 = "Spouse"

**Value**

an ordered factor vector containing the transformed variable "MZ twin" < "DZ twin" < "UZ twin" < "Spouse"

**Examples**

```
rel_code_to_factor(c(1, 2, 3, 4, "MZ twin", "DZ twin", "UZ twin", "Spouse"))
```

---

sampleped

*Sampleped data*


---

**Description**

Small sample pedigree data set for testing purposes.

**Usage**

```
data("sampleped")
```

**Format**

A data frame with 55 observations, one line per subject, on the following 7 variables.

- famid : Family identifier
- id : Subject identifier
- dadid : Identifier of the father, if the father is part of the data set; zero otherwise
- momid : Identifier of the mother, if the mother is part of the data set; zero otherwise
- sex : 1 for male or 2 for female
- affected : 1 or 0
- avail : 1 or 0

## Details

This is a small fictive pedigree data set, with 55 individuals in 2 families. The aim was to create a data set with a variety of pedigree structures.

## Examples

```
data("sampleped")
ped <- Pedigree(sampleped)
summary(ped)
#plot(ped)
```

---

Scales-class

*Scales object*


---

## Description

A Scales object is a list of two data.frame. The first one is used to represent the affection status of the individuals and therefore the filling of the individuals in the pedigree plot. The second one is used to represent the availability status of the individuals and therefore the border color of the individuals in the pedigree plot.

### Constructor ::

You need to provide both **fill** and **border** in the dedicated parameters. However this is usually done using the [generate\\_colors\(\)](#) function with a Pedigree object.

## Usage

```
Scales(fill, border)
```

```
## S4 method for signature 'data.frame,data.frame'
Scales(fill, border)
```

## Arguments

- |      |  |
|------|--|
| fill | <p>A data.frame with the informations for the affection status. The columns needed are:</p> <ul style="list-style-type: none"> <li>• 'order': the order of the affection to be used</li> <li>• 'column_values': name of the column containing the raw values in the Ped object</li> <li>• 'column_mods': name of the column containing the mods of the transformed values in the Ped object</li> <li>• 'mods': all the different mods</li> <li>• 'labels': the corresponding labels of each mods</li> <li>• 'affected': a logical value indicating if the mod correspond to an affected individuals</li> <li>• 'fill': the color to use for this mods</li> </ul> |
|------|--|



- 'density': the density of the shading
  - 'angle': the angle of the shading
- border A data.frame with the informations for the availability status. The columns needed are:
- 'column\_values': name of the column containing the raw values in the Ped object
  - 'column\_mods': name of the column containing the mods of the transformed values in the Ped object
  - 'mods': all the different mods
  - 'labels': the corresponding labels of each mods
  - 'border': the color to use for this mods

### Value

A Scales object.

### Slots

- fill A data.frame with the informations for the affection status. The columns needed are:
- 'order': the order of the affection to be used
  - 'column\_values': name of the column containing the raw values in the Ped object
  - 'column\_mods': name of the column containing the mods of the transformed values in the Ped object
  - 'mods': all the different mods
  - 'labels': the corresponding labels of each mods
  - 'affected': a logical value indicating if the mod correspond to an affected individuals
  - 'fill': the color to use for this mods
  - 'density': the density of the shading
  - 'angle': the angle of the shading
- border A data.frame with the informations for the availability status. The columns needed are:
- 'column\_values': name of the column containing the raw values in the Ped object
  - 'column\_mods': name of the column containing the mods of the transformed values in the Ped object
  - 'mods': all the different mods
  - 'labels': the corresponding labels of each mods
  - 'border': the color to use for this mods

### Accessors

- fill(x) : Get the fill data.frame
- fill(x) <- value : Set the fill data.frame
- border(x) : Get the border data.frame
- border(x) <- value : Set the border data.frame

Generics

- `as.list(x)`: Convert a Scales object to a list

See Also

[Pedigree\(\)](#)  
[generate\\_colors\(\)](#)

Examples

```
Scales(  
  fill = data.frame(  
    order = 1,  
    column_values = "affected",  
    column_mods = "affected_mods",  
    mods = c(0, 1),  
    labels = c("unaffected", "affected"),  
    affected = c(FALSE, TRUE),  
    fill = c("white", "red"),  
    density = c(NA, 20),  
    angle = c(NA, 45)  
  ),  
  border = data.frame(  
    column_values = "avail",  
    column_mods = "avail_mods",  
    mods = c(0, 1),  
    labels = c("not available", "available"),  
    border = c("black", "blue")  
  )  
)
```

---

set_plot_area	<i>Set plotting area</i>
---------------	--------------------------

---

Description

Set plotting area

Usage

```
set_plot_area(cex, id, maxlev, xrange, symbolsize, ...)
```

Arguments

cex	Character expansion of the text
id	A character vector with the identifiers of each individuals
maxlev	Maximum level

xrange	Range of x values
symbolsize	Size of the symbols
...	Other arguments passed to <code>par()</code>

**Value**

List of user coordinates, old par, box width, box height, label height and leg height

---

sex_to_factor	<i>Gender variable to ordered factor</i>
---------------	--

---

**Description**

Gender variable to ordered factor

**Usage**

`sex_to_factor(sex)`

**Arguments**

- |     |   |
|-----|---|
| sex | <p>A character, factor or numeric vector corresponding to the gender of the individuals. This will be transformed to an ordered factor with the following levels: male &lt; female &lt; unknown &lt; 'terminated' The following values are recognized:</p> <ul style="list-style-type: none"><li>• <code>character()</code> or <code>factor()</code> : "f", "m", "woman", "man", "male", "female", "unknown", "terminated"</li><li>• <code>numeric()</code> : 1 = "male", 2 = "female", 3 = "unknown", 4 = "terminated"</li></ul> |
|-----|---|

**Value**

an ordered factor vector containing the transformed variable "male" < "female" < "unknown" < "terminated"

**Examples**

`sex_to_factor(c(1, 2, 3, 4, "f", "m", "man", "female"))`

---

shift	<i>Shift set of siblings to the left or right</i>
-------	---

---

## Description

Shift set of siblings to the left or right

## Usage

```
shift(id, sibs, goleft, hint, twinrel, twinset)
```

## Arguments

id	The id of the subject to be shifted
sibs	The ids of the siblings
goleft	If TRUE, shift to the left, otherwise to the right
hint	The current hint vector
twinrel	The twin relationship matrix
twinset	The twinset vector

## Details

This routine is used by `auto_hint()`. It shifts a set of siblings to the left or right, so that the marriage is on the edge of the set of siblings, closest to the spouse. It also shifts the subject himself, so that he is on the edge of the set of siblings, closest to the spouse. It also shifts the monozygotic twins, if any, so that they are together within the set of twins.

## Value

The updated hint vector

## See Also

[auto\\_hint\(\)](#)

---

shrink	<i>Shrink Pedigree object</i>
--------	-------------------------------

---

## Description

Shrink Pedigree object to specified bit size with priority placed on trimming uninformative subjects. The algorithm is useful for getting a Pedigree condensed to a minimally informative size for algorithms or testing that are limited by size of the Pedigree.

If **avail** or **affected** are NULL, they are extracted with their corresponding accessors from the Ped object.

## Usage

```
## S4 method for signature 'Pedigree'
shrink(obj, avail = NULL, affected = NULL, max_bits = 16)

## S4 method for signature 'Ped'
shrink(obj, avail = NULL, affected = NULL, max_bits = 16)
```

## Arguments

<code>obj</code>	A Pedigree or Ped object.
<code>avail</code>	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
<code>affected</code>	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).
<code>max_bits</code>	Optional, the bit size for which to shrink the Pedigree

## Details

Iteratively remove subjects from the Pedigree. The random removal of members was previously controlled by a seed argument, but we remove this, forcing users to control randomness outside the function. First remove uninformative subjects, i.e., unavailable (not genotyped) with no available descendants. Next, available terminal subjects with unknown phenotype if both parents available. Last, iteratively shrinks Pedigrees by preferentially removing individuals (chosen at random if there are multiple of the same status):

1. Subjects with unknown affected status
2. Subjects with unaffected affected status
3. Affected subjects.

**Value**

A list containing the following elements:

- pedObj: Pedigree object after trimming
- id\_trim: Vector of ids trimmed from Pedigree
- id\_lst: List of ids trimmed by category
- bit\_size: Vector of bit sizes after each trimming step
- avail: Vector of availability status after trimming
- pedSizeOriginal: Number of subjects in original Pedigree
- pedSizeIntermed: Number of subjects after initial trimming
- pedSizeFinal: Number of subjects after final trimming

**Author(s)**

Original by Dan Schaid, updated by Jason Sinnwell and Louis Le Nézet

**See Also**

[Pedigree\(\)](#), [bit\\_size\(\)](#)

**Examples**

```
data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == '1',])
shrink(ped1, max_bits = 12)
```

---

subregion	<i>Subset a region of a Pedigree</i>
-----------	--------------------------------------

---

**Description**

Subset a region of a Pedigree

**Usage**

```
subregion(plist, subreg)
```

**Arguments**

plist	The alignment structure representing the Pedigree layout. See <a href="#">align()</a> for details.
subreg	A 4-element vector for (min x, max x, min depth, max depth), used to edit away portions of the plot coordinates returned by <a href="#">align()</a> . This is useful for zooming in on a particular region of the Pedigree.

**Value**

A Pedigree structure with the specified region

---

unrelated	<i>Find Unrelated subjects</i>
-----------	--------------------------------

---

**Description**

Determine set of maximum number of unrelated available subjects from a Pedigree.

**Usage**

```
## S4 method for signature 'Ped'
unrelated(obj, avail = NULL)

## S4 method for signature 'Pedigree'
unrelated(obj, avail = NULL)
```

**Arguments**

obj	A Pedigree or Ped object.
avail	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).

**Details**

Determine set of maximum number of unrelated available subjects from a Pedigree, given vectors id, father, and mother for a Pedigree structure, and status vector of TRUE / FALSE for whether each subject is available (e.g. has DNA).

This is a greedy algorithm that uses the kinship matrix, sequentially removing rows/cols that are non-zero for subjects that have the most number of zero kinship coefficients (greedy by choosing a row of kinship matrix that has the most number of zeros, and then remove any cols and their corresponding rows that are non-zero. To account for ties of the count of zeros for rows, a random choice is made. Hence, running this function multiple times can return different sets of unrelated subjects.

If **avail** is NULL, it is extracted with its corresponding accessor from the Ped object.

**Value**

A vector of the ids of subjects that are unrelated.

**Author(s)**

Dan Schaid and Shannon McDonnell updated by Jason Sinnwell

## Examples

```
data(sampleped)
fam1 <- sampleped[sampleped$famid == 1, ]
ped1 <- Pedigree(fam1)
unrelated(ped1)
## some possible vectors
## [1] '110' '113' '133' '109'
## [1] '113' '118' '141' '109'
## [1] '113' '118' '140' '109'
## [1] '110' '113' '116' '109'
## [1] '113' '133' '141' '109'
```

---

upd\_famid\_id

*Update family prefix in individuals id*

---

## Description

Update the family prefix in the individuals identifiers. Individuals identifiers are constructed as follow **famid\_id**. Therefore to update their family prefix the ids are split by the first underscore and the first part is overwritten by **famid**.

## Usage

```
## S4 method for signature 'character,ANY'
upd_famid_id(obj, famid, missid = NA_character_)

## S4 method for signature 'Ped,character_OR_integer'
upd_famid_id(obj, famid)

## S4 method for signature 'Ped,missing'
upd_famid_id(obj)

## S4 method for signature 'Rel,character_OR_integer'
upd_famid_id(obj, famid)

## S4 method for signature 'Rel,missing'
upd_famid_id(obj)

## S4 method for signature 'Pedigree,character_OR_integer'
upd_famid_id(obj, famid)

## S4 method for signature 'Pedigree,missing'
upd_famid_id(obj)
```



**Arguments**

obj	Ped or Pedigree object or a character vector of individual ids
famid	A character vector with the family identifiers of the individuals. If provide, will be aggregated to the individuals identifiers separated by an underscore.
missid	A character vector with the missing values identifiers. All the id, dadid and momid corresponding to those values will be set to NA_character_.

**Details**

If famid is *missing*, then the famid() function will be called on the object.

**Value**

A character vector of individual ids with family prefix updated

**Examples**

```

upd_famid_id(c("1", "2", "B_3"), c("A", "B", "A"))
upd_famid_id(c("1", "B_2", "C_3", "4"), c("A", NA, "A", NA))

data(sampleped)
ped1 <- Pedigree(sampleped[, -1])
id(ped(ped1))
new_fam <- make_famid(id(ped(ped1)), dadid(ped(ped1)), momid(ped(ped1)))
id(ped(upd_famid_id(ped1, new_fam)))

data(sampleped)
ped1 <- Pedigree(sampleped[, -1])
make_famid(ped1)

```

---

useful\_inds

*Usefulness of individuals*


---

**Description**

Compute the usefulness of individuals

**Usage**

```

## S4 method for signature 'character'
useful_inds(
  obj,
  dadid,
  momid,
  avail,
  affected,
  num_child_tot,

```

```

    informative = "AvAf",
    keep_infos = FALSE
)

## S4 method for signature 'Pedigree'
useful_inds(obj, informative = "AvAf", keep_infos = FALSE, reset = FALSE)

## S4 method for signature 'Ped'
useful_inds(obj, informative = "AvAf", keep_infos = FALSE, reset = FALSE)

```

## Arguments

<code>obj</code>	A character vector with the id of the individuals or a <code>data.frame</code> with all the informations in corresponding columns.
<code>dadid</code>	A vector containing for each subject, the identifiers of the biologicals fathers.
<code>momid</code>	A vector containing for each subject, the identifiers of the biologicals mothers.
<code>avail</code>	A logical vector with the availability status of the individuals (i.e. FALSE = not available, TRUE = available, NA = unknown).
<code>affected</code>	A logical vector with the affection status of the individuals (i.e. FALSE = unaffected, TRUE = affected, NA = unknown).
<code>num_child_tot</code>	A numeric vector of the number of children of each individuals
<code>informative</code>	Informative individuals selection can take 5 values: <ul style="list-style-type: none"> <li>• 'AvAf' (available and affected),</li> <li>• 'AvOrAf' (available or affected),</li> <li>• 'Av' (available only),</li> <li>• 'Af' (affected only),</li> <li>• 'All' (all individuals)</li> <li>• A numeric/character vector of individuals id</li> <li>• A boolean</li> </ul>
<code>keep_infos</code>	Boolean to indicate if individuals with unknown status but available or reverse should be kept
<code>reset</code>	Boolean to indicate if the useful column should be reset

## Details

Check for the informativeness of the individuals based on the informative parameter given, the number of children and the usefulness of their parents. A useful slot is added to the Ped object with the usefulness of the individual. This boolean is hereditary.

## Value

### When `obj` is a vector:

A vector of useful individuals identifiers

### When `obj` is a Pedigree or Ped object:

The Pedigree or Ped object with the slot 'useful' containing TRUE for useful individuals and FALSE otherwise.

**Examples**

```
data(sampleped)
ped1 <- Pedigree(sampleped[sampleped$famid == "1",])
ped(useful_inds(ped1, informative = "AvAf"))
```

---

vect_to_binary	<i>Vector variable to binary vector</i>
----------------	---

---

**Description**

Transform a vector to a binary vector. All values that are not 0, 1, TRUE, FALSE, or NA are transformed to NA.

**Usage**

```
vect_to_binary(vect, logical = FALSE)
```

**Arguments**

<b>vect</b>	A character, factor, logical or numeric vector corresponding to a binary variable (i.e. 0 or 1). The following values are recognized: <ul style="list-style-type: none"> <li>• character() or factor() : "TRUE", "FALSE", "0", "1", "NA" will be respectively transformed to 1, 0, 0, 1, NA. Spaces and case are ignored. All other values will be transformed to NA.</li> <li>• numeric() : 0 and 1 are kept, all other values are transformed to NA.</li> <li>• logical() : TRUE and FALSE are transformed to 1 and 0.</li> </ul>
<b>logical</b>	Boolean defining if the output should be a logical vector instead of a numeric vector (i.e. 0 and 1 becomes FALSE and TRUE).

**Value**

numeric binary vector of the same size as **vect** with 0 and 1

**Examples**

```
vect_to_binary(
  c(0, 1, 2, 3.6, "TRUE", "FALSE", "0", "1", "NA", "B", TRUE, FALSE, NA)
)
```

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