Package ‘IBDLabels’

February 19, 2015

Type Package

Title Convert Between Different IBD-State Labelling Schemes

Version 1.1

Date 2014-12-15

Author Fiona Grimson

Maintainer Fiona Grimson `<fgrimson@uw.edu>`

Description
Convert ``label'', ``lexicographic'', ``jacquard'' and ``vec'', full state description vector. All conversions are done to and from ``label'', as used in IBD_Haplo. More information regarding IBD_Haplo can be found at http://www.stat.washington.edu/thompson/Genepi/pangaea.shtml.

License GPL-3

LazyLoad yes

LazyData yes

Repository CRAN

Repository/R-Forge/Project morgan-rtools

Repository/R-Forge/Revision 36

Repository/R-Forge/DateTimeStamp 2015-02-14 01:16:14

Date/Publication 2015-02-17 01:07:25

NeedsCompilation no

R topics documented:

`allJaq` *Jacquard ordering*

Description

Jacquard ordering for 4-gamete IBD states. Can be phased (15 states) or unphased (9 states).

Usage

```
allJaq()

jaq2label(jaq, phased = TRUE )

label2jaq(label, phased = TRUE )
```

Arguments

`jaq`	Jacquard state, either phased or unphased
`label`	IBD label
`phased`	Are the jacquard states the phased (15 states) or unphased (9 states) versions?

Details

Note that the jacquard ordering only applies to the 4-gametes case.

Value

allJaq() produces a matrix of labels (column 1), phased-jacquard (column 2) and unphased-jacquard(column 3).

label2jaq or jaq2label produces an integer converted the required index.

If label is invalid an NA is returned.

Author(s)

Fiona Grimson

Examples

```
## list all jacquard states
allJaq()

## Convert label to jacquard
label2jaq( 3, phased = TRUE )
label2jaq( 3, phased = FALSE )
```

```
## Convert jacquard to label
jaq2label( 9, phased = TRUE )
jaq2label( 9, phased = FALSE )
```

`allStates` *Conversion Table for all labelling schemes*

Description

Conversion table for all numbering schemes: label, vector, lexicographic, and if there are 4 gametes jacquard15 and jacquard9.

Usage

```
allStates(ngam)
```

Arguments

`ngam`	Number of gametes

Value

A data.frame is returned with the following variables:

$label : vector of all labels from 0 to maxlabel $vec : matrix of all state vectors (one per row) corresponding to labels. $lex : vector of lexicographic states for each label

if there are 4 gametes there is also

$jaq9 : vector of un-phased jacquard states $jaq15 : vector of phased jacquard states

Invalid labels produce NA in the other columns.

Author(s)

Fiona Grimson

Examples

```
## create lookup matrix

allStates( ngam = 4 )

allStates( ngam = 5 )
```

`IBDLabel` *Convert between different IBD-state labelling schemes*

Description

Convert "label", "lexicographic", "jacquard" and "vec", full state description vector.

All conversions are done to and from "label", as used in IBD_Haplo. More information regarding IBD_Haplo can be found at www.stat.washington.edu/thompson/Genepi/pangaea.shtml

See the tutorial by typing vignettes("IBDlabels_tutorial")

Details

Package:	IBDLabel
Type:	Package
Version:	1.1
Date:	2014-12-01
License:	GPL-3

Author(s)

Fiona Grimson <fgrimson@uw.edu>

Examples

```
## For more examples see

vignette( "IBDlabels_tutorial" )

######### All States ######################

## create lookup matrix
allStates( ngam = 4 )
allStates( ngam = 5 )

######### Jacquard Ordering ###############

## list all jacquard states
allJaq()

## Convert label to jacquard
label2jaq( 3, phased = TRUE )
label2jaq( 3, phased = FALSE )
```

```
## Convert jacquard to label
jaq2label( 9, phased = TRUE )
jaq2label( 9, phased = FALSE )

######## Lexicographic Ordering ###########

## Vector of all lexicograghic states with labels ( names of elements )
allLex( ngam = 4 )

## Convert lex to label
lex2label( lex = c( 1, 2, 15), ngam = 4 )

## Convert label to lex
## Some labels go to the same lex state
label2lex( label = c( 2, 3 ), ngam = 4 )

######## Vector Notation ##################

## Vectors for all labels
allVec( ngam = 4 )

## Convert vector to label, with renumbering
vec2label( c(1,1,1,3))
vec2label( c(1,1,1,2))

## Convert label to vector
label2vec( 1, ngam = 4 )
label2vec( 2, ngam = 4 )
label2vec( 2, ngam = 6 )

## renumbering
fgl2vec( c( 1,1,1,3) )
fgl2vec( c(5,1,5,6) )
```

`Lexicographic` *Lexicographic ordering*

Description

Lexicographic ordering of states is the same as the label order, but with invalid labels removed. For example, (1,1,1,3) will produce NA.

Usage

```
allLex(ngam)

lex2label(lex, ngam)
```

```
label2lex(label, ngam)
```

Arguments

`ngam`	Number of gametes
`lex`	Lexicographic state. Can be a vector of lexicographic states to be converted
`label`	Label. Can be a vector of labels to be converted

Details

Note that conversions are made by listing all the labels and their corrsespondign lexicographic state, so this function may not be practical for large numbers of gametes.

When converting lex to label, there may be several possible labels, in which case the minimum is taken.

Value

In allLex a vector of lexicographic states is produced for each label. The labels are the names of the vector elements.

In lex2label and label2lex the requested integer or vector of integers is produced.

Author(s)

Fiona Grimson

Examples

```
## Vector of all lexicograghic states with labels ( names of elements )
allLex( ngam = 4 )

## Convert lex to label
lex2label( lex = c( 1, 2, 15), ngam = 4 )

## Convert label to lex
label2lex( label = c( 2, 3 ), ngam = 4 )
```

`maxlabel` *Maximum Label for given number gametes*

Description

Get the maximum label for given number of gametes, the label corresponding to the vector 1:ngam.

Usage

```
maxlabel(ngam)
```

Arguments

`ngam`	Number of gametes

Value

Returns maximum label. Note that minimum label is always zero.

Author(s)

Fiona Grimson

Examples

```
maxlabel( ngam = 4 )
maxlabel( ngam = 10 )
```

`State Vectors` *IBD state vectors*

Description

These vectors are complete descriptions of the IBD state. There is one vector element per gamete. The first gamete is always numbered one, with subsequent gametes being given the same number if they are IBD with a previous gamete, or a new number if they are not.

For example in (1,2,2,3), the second and third gametes are IBD.

Note that label starts at ZERO. When converting label to vector, if the label is invalid the returned vector has NA elements.

Usage

```
allVec(ngam)

vec2label(vec)

label2vec(label, ngam)

fgl2vec(vec)
```

Arguments

`ngam`	Number of gametes if a label is supplied, otherwise number of gametes will be determined by the length of the vector.
`vec`	IBD state description vector. Must be a single vector.
`label`	IBD label. Must be an integer.

Value

For allVec, a matrix of the vectors for each label is produced, with a vector on each row and a row for each label. The labels are the row names.

For vec2label and label2vec an integer label or vector is prouduced respectively. If the input label is invalid the returned vector contains NA elements.

fgl2vec returns a vector of the same length as the input, renumbered. The vec2label function calls fgl2vec, so any vector supplied will be renumbered. If (1,1,1,3) is given, it will be renumbered (1,1,1,2) and given the label 1, not 2.

Author(s)

Fiona Grimson

Examples

```
## Vectors for all labels
allVec( ngam = 4 )

## Convert vector to label, with renumbering or without
vec2label( c(1,1,1,3))
vec2label( c(1,1,1,2))

## Convert label to vector
label2vec( 1, ngam = 4 )
label2vec( 2, ngam = 4 )
label2vec( 2, ngam = 6 )

## renumbering
fgl2vec( c(1,1,1,3) )
fgl2vec( c(5,1,5,6) )
```

Index