Package ‘ldblock’

October 12, 2016

Title data structures for linkage disequilibrium measures in populations

Version 1.2.2

Author VJ Carey <`stvjc@channing.harvard.edu`>

Description Define data structures for linkage disequilibrium measures in populations.

Suggests RUnit, BiocGenerics, knitr

Imports Matrix, snpStats

Depends R (>= 3.1), methods

Maintainer VJ Carey <`stvjc@channing.harvard.edu`>

License Artistic-2.0

LazyLoad yes

BiocViews genetics, SNP, GWAS

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

`ldblock-package` *data structures for linkage disequilibrium measures in populations*

Description

Define data structures for linkage disequilibrium measures in populations.

Details

The DESCRIPTION file:

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VignetteBuilder:	knitr

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`ldstruct-class`	`Class '"ldstruct"'`

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Maintainer: VJ Carey <stvjc@channing.harvard.edu>

Examples

```
# see vignette
```

`downloadPopByChr` *download hapmap resource with LD estimates*

Description

download hapmap resource with LD estimates

Usage

```
downloadPopByChr(chrname = "chr1",
 popname = "CEU",
 urlTemplate = "http://hapmap.ncbi.nlm.nih.gov/downloads/ld_data/2009-02_phaseIII_r2/ld_%%CHRN%%_%%P
 targfolder = Sys.getenv("LDBLOCK_TXTGZ_DIR"))
```

Arguments

`chrname`	UCSC format tag for chromosome
`popname`	hapmap three letter code for population, e.g. 'CEU'
`urlTemplate`	pattern for creating URL given chr and pop
`targfolder`	destination

Details

delivers HapMap LD data to ‘targfolder‘

Value

just run for side effect of download.file

Examples

```
## Not run:
 downloadPopByChr()

## End(Not run)
```

`expandSnpSet` *Given a set of SNP identifiers, use LD to expand the set to include linked loci*

Description

Given a set of SNP identifiers, use LD to expand the set to include linked loci

Usage

```
expandSnpSet(rsl, lb = 0.8, ldstruct, chrn = "chr17", popn = "CEU",
  txtgzfn = dir(system.file("hapmap", package = "ldblock"), full.names = TRUE))
```

Arguments

`rsl`	input list – SNPs not found in the LD structure are simply returned along with those found, and the expansion list, all combined in a vector
`lb`	lower bound on statistic used to retrieve loci in LD
`ldstruct`	instance of `ldstruct-class`
`chrn`	chromosome identifier
`popn`	population identifier (one of 'CEU', 'MEX', ...)
`txtgzfn`	path to gzipped hapmap file with LD information

Details

direct use of elementwise arithmetic comparison

Value

character vector

Note

As of 2015, it appears that locus names are more informative than addresses for determining SNP identity across resources.

Examples

```
og = Sys.getenv("LDBLOCK_TXTGZ_DIR")
on.exit( Sys.setenv("LDBLOCK_TXTGZ_DIR" = og ) )
Sys.setenv("LDBLOCK_TXTGZ_DIR"=system.file("hapmap", package="ldblock"))
ld17 = hmld(chr="chr17", pop="CEU")
ee = expandSnpSet( ld17@allrs[1:10], ldstruct = ld17 )
```

`hmld` *import hapmap LD data and create a structure for its management*

Description

import hapmap LD data and create a structure for its management

Usage

```
hmld(hmgztxt, poptag, chrom, genome = "hg19", stat = "Dprime")
```

Arguments

`hmgztxt`	name of gzipped text file as distributed at `hapmap.ncbi.nlm.nih.gov/downloads/ld_data/2009-02_phaseIII_r2/`. It will be processed by `read.delim`.
`poptag`	heuristic tag identifying population
`chrom`	heuristic tag for chromosome name
`genome`	genome tag
`stat`	statistic to use, "Dprime", "R2", and "LOD" are options

Details

generates a sparse matrix representation of pairwise LD statistics and binds metadata on variant name and position

Value

instance of ldstruct class

Examples

```
getClass("ldstruct")
# see vignette
```

`ldstruct-class` *Class* `"ldstruct"`

Description

Manage information about LD statistics as reported by HapMap.

Objects from the Class

Objects can be created by calls of the form `new("ldstruct", ...)`.

Slots

- `ldmat`**:** Object of class `"dsCMatrix"` sparse representation of statistics
- `chrom`**:** Object of class `"character"` chromosome tag in UCSC format
- `genome`**:** Object of class `"character"` genome tag
- `allpos`**:** Object of class `"numeric"` coordinates
- `poptag`**:** Object of class `"character"` hapmap founder population tag, 'CEU', 'MEX' etc.
- `statInUse`**:** Object of class `"character"` code for statistic retrieved, one of 'Dprime', 'LOD', 'R2'
- `allrs`**:** Object of class `"character"` all SNP identifiers, sometimes in affy format

Methods

ldmat `signature(x = "ldstruct")`: extract sparse matrix

Examples

```
showClass("ldstruct")
```

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