

Package ‘PlinkMatrix’

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Title DelayedArray interface for plink bed files

Version 1.0.0

Description This package provides a DelayedArray interface for plink bed files.

There is support for interfacing to plink genotype data via RangedSummarizedExperiment.

Example data from the GEUVADIS project (internationalgenome.org) are used for demonstration.

Depends R (>= 4.1.0), methods, Rcpp, DelayedArray,
SummarizedExperiment

Suggests knitr, BiocStyle, testthat, rmarkdown, irlba, GenomeInfoDb

Imports BiocFileCache, GenomicRanges, IRanges

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VignetteBuilder knitr

biocViews Infrastructure, Genetics

Encoding UTF-8

URL <https://github.com/vjcitn/PlinkMatrix>

BugReports <https://github.com/vjcitn/PlinkMatrix/issues>

RoxygenNote 7.3.3

LinkingTo Rcpp

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decode_bed_genotypes	<i>Helper function to decode BED format</i>
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Description

Helper function to decode BED format

Usage

decode_bed_genotypes(raw_bytes, n_samples)

Arguments

raw_bytes	byte stream from file
n_samples	number of samples

Value

numeric vector

Examples

PlinkMatrix:::decode_bed_genotypes(raw(4), 4L)

dim,PlinkSeed-method *Method: dim for delayed plink*

Description

Method: dim for delayed plink

Usage

```
## S4 method for signature 'PlinkSeed'  
dim(x)
```

Arguments

x PlinkSeed instance

Value

2-vector

Examples

```
methods(class="PlinkSeed")
```

dimnames,PlinkSeed-method
 Method: dimnames for delayed plink

Description

Method: dimnames for delayed plink

Usage

```
## S4 method for signature 'PlinkSeed'  
dimnames(x)
```

Arguments

x PlinkSeed instance

Value

list of dimnames

example_GRanges	<i>sample GRanges coordinated with example_PlinkMatrix</i>
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Description

sample GRanges coordinated with example_PlinkMatrix

Usage

```
data("example_GRanges", package="PlinkMatrix")
```

Format

GRanges

Examples

```
data("example_GRanges", package="PlinkMatrix")
head(example_GRanges)
```

example_PlinkMatrix	<i>produce PlinkMatrix from example data</i>
---------------------	--

Description

produce PlinkMatrix from example data

Usage

```
example_PlinkMatrix(folder = tempdir(), as_RSE = FALSE)
```

Arguments

folder	a path where unzipped example data will be managed
as_RSE	logical(1) if TRUE (default is FALSE) a RangedSummarizedExperiment is returned

Value

a SummarizedExperiment or RangedSummarizedExperiment with rowRanges calculated from SNP ids

Examples

```
example_PlinkMatrix()
```

extract_array,PlinkSeed-method
<i>Method: extract_array, internal</i>

Description

Method: extract_array, internal

Usage

```
## S4 method for signature 'PlinkSeed'  
extract_array(x, index)
```

Arguments

x	seed instance
index	list of suitable values for extracting elements

Value

method definition

Examples

```
methods(class="PlinkSeed")
```

g445samples	<i>sample characteristics of 445 GEUVADIS samples</i>
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Description

sample characteristics of 445 GEUVADIS samples

Usage

```
data("g445samples", package="PlinkMatrix")
```

Format

data.frame

Note

Example data are those provided with tensorqtl, see <https://github.com/broadinstitute/tensorqtl/tree/0c4db65a0cdc47f3b824ae530b89d270ef5e0096/example/data>.

Examples

```
data("g445samples", package="PlinkMatrix")
g445samples[seq_len(4), seq_len(4)]
```

getSampleData	<i>Get sample metadata</i>
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Description

Get sample metadata

Usage

```
getSampleData(x)
```

Arguments

x DelayedArray instance

Value

data.frame

Examples

```
tst <- example_PlinkMatrix()
head(getSampleData(tst))
```

getVariantData	<i>Get variant metadata</i>
----------------	-----------------------------

Description

Get variant metadata

Usage

```
getVariantData(x)
```

Arguments

x DelayedArray instance

Value

data.frame

Examples

```
tst <- example_PlinkMatrix()
dim(getVariantData(tst))
```

```
get_plink_example_path
```

operate with BiocFileCache to retrieve zip file of plink example data

Description

operate with BiocFileCache to retrieve zip file of plink example data

Usage

```
get_plink_example_path(ca = BiocFileCache::BiocFileCache())
```

Arguments

ca BiocFileCache instance

Value

character string with path to example in cache

Examples

```
get_plink_example_path()
```

```
plid2gr
```

produce GRanges from variant notation for plink example from geuvadis

Description

produce GRanges from variant notation for plink example from geuvadis

Usage

```
plid2gr(x, sepused = "_")
```

Arguments

x character vector of variant names
sepused single character, defaults to "_"

Value

GRanges instance

Examples

```
plid2gr("chr18_80259028_AG_A_b38")
```

PlinkMatrix	<i>Constructor for DelayedArray</i>
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Description

Constructor for DelayedArray

Usage

```
PlinkMatrix(filepath)
```

Arguments

filepath path to plink bed, bim, fam resources without suffixes

Value

An instance of PlinkMatrix

Examples

```
PlinkMatrix
```

PlinkMatrix-pkg	<i>Delayed interface to Plink genotype files</i>
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Description

This package includes C++ code to interface to Plink files. Large-scale genotype calls can be managed in a RangedSummarized Experiment instance.

Value

side effects

PlinkSeed	<i>Constructor function for seed for plink bed format</i>
-----------	---

Description

Constructor function for seed for plink bed format

Usage

```
PlinkSeed(filepath)
```

Arguments

filepath	character string without suffixes
----------	-----------------------------------

Value

PlinkSeed instance

Examples

```
PlinkSeed
```

PlinkSeed-class	<i>Define the PlinkSeed class</i>
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Description

Define the PlinkSeed class

Value

class definition

Examples

```
getClass("PlinkSeed")
```

read_bed_subset	<i>read subset for use in delayed matrix approach</i>
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Description

read subset for use in delayed matrix approach

Usage

```
read_bed_subset(prefix, snp_indices, sample_indices, n_total_samples = NULL)
```

Arguments

prefix	character path to bed resources and file prefix
snp_indices	integer vector of snp indices
sample_indices	integer vector of sample indices
n_total_samples	optional

Value

matrix

Examples

```
read_bed_subset
```

selectSome	<i>abbreviated display</i>
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Description

abbreviated display

Usage

```
selectSome(obj, maxToShow = 5)
```

Value

abbreviated display

show,PlinkSeed-method *present seed concisely*

Description

present seed concisely

Usage

```
## S4 method for signature 'PlinkSeed'  
show(object)
```

Arguments

object instance of PlinkSeed

Value

side effect of cat

Examples

```
ex <- example_PlinkMatrix()  
ex
```

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