Package ‘PlinkMatrix’

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Title DelayedArray interface for plink bed files

Version 1.1.0

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` *Helper function to decode BED format*

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` *sample GRanges coordinated with example_PlinkMatrix*

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` *produce PlinkMatrix from example data*

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`
Method: extract_array, internal

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` *sample characteristics of 445 GEUVADIS samples*

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` *Get sample metadata*

Description

Get sample metadata

Usage

```
getSampleData(x)
```

Arguments

`x`	DelayedArray instance

Value

data.frame

Examples

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

`getVariantData` *Get variant metadata*

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` *Constructor for DelayedArray*

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` *Delayed interface to Plink genotype files*

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` *Constructor function for seed for plink bed format*

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` *Define the PlinkSeed class*

Description

Define the PlinkSeed class

Value

class definition

Examples

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

`read_bed_subset` *read subset for use in delayed matrix approach*

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` *abbreviated display*

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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