Package: PlinkMatrix (via r-universe)

November 25, 2026

Title DelayedArray interface for plink bed files

Version 1.2.0

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, learnr, shiny, later

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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Contents

dim,PlinkSeed-method . . . 2
dimnames,PlinkSeed-method . . . 3
example_GRanges . . . 3
example_PlinkMatrix . . . 4
g445samples . . . 4
get_plink_example_path . . . 5
getSampleData . . . 5
getVariantData . . . 6
plid2gr . . . 6
PlinkMatrix . . . 7
PlinkMatrix-pkg . . . 7
PlinkMatrix_tutorials . . . 8
read_bed_subset . . . 9
show,PlinkSeed-method . . . 9

Index **11**

`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()
```

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)]
```

`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()
```

`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))
```

`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

`PlinkMatrix_tutorials` *browse and launch the learnr tutorials bundled with PlinkMatrix*

Description

browse and launch the learnr tutorials bundled with PlinkMatrix

Usage

```
PlinkMatrix_tutorials(name)
```

Arguments

`name`	character(1) name of a tutorial to launch directly (the tutorial's directory name under `inst/tutorials`, as reported by `learnr::available_tutorials(package = "PlinkMatrix")`). If missing, a menu is presented in interactive sessions; in non-interactive sessions the available tutorial names are printed and an error is raised.

Details

Lists the `learnr` tutorials shipped with this package – covering matrix foundations, the Singular Value Decomposition, Principal Components Analysis, and ancestry discrimination using the package's example genotype data. With `name` supplied, that tutorial is launched directly. With `name` missing in an interactive session, a menu is shown with a checkbox beside each tutorial already marked done; the menu keeps returning after each tutorial finishes (offering to mark it done) until you choose 0 to quit. Progress is kept in a small file in your own R user data directory (see `R_user_dir`), so it survives restarting R; it is self-reported and is not sent anywhere. Each tutorial has its own "Exit tutorial" button that cleanly stops the tutorial's web server and returns control to the R console, so there is no need to interrupt with Ctrl-C. Requires the `learnr` package.

Value

invisible(NULL) if `name` is supplied; otherwise, invisibly, a named logical vector recording which tutorials are marked done. As a side effect, launches one or more `learnr` tutorials, typically in the default web browser, via `learnr::run_tutorial`.

Examples

```
if (interactive()) PlinkMatrix_tutorials()
```

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
```

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
```

Index

∗ **datasets**
example_GRanges, 3
g445samples, 4

dim,PlinkSeed-method, 2
dimnames,PlinkSeed-method, 3

example_GRanges, 3
example_PlinkMatrix, 4

g445samples, 4
get_plink_example_path, 5
getSampleData, 5
getVariantData, 6

plid2gr, 6
PlinkMatrix, 7
PlinkMatrix-pkg, 7
PlinkMatrix_tutorials, 8

R_user_dir, *8*
read_bed_subset, 9

show,PlinkSeed-method, 9