

# 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](http://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

**License** MIT + file LICENSE

**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*

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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      *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)]
```

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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>
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---

**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")
```

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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

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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

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

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show,PlinkSeed-method	<i>present seed concisely</i>
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---

**Description**

present seed concisely

**Usage**

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

**Arguments**

object	instance of PlinkSeed
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**Value**

side effect of cat

**Examples**

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

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