

Package: BEDMatrix (via r-universe)

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Title Extract Genotypes from a PLINK .bed File

Description A matrix-like data structure that allows for efficient, convenient, and scalable subsetting of binary genotype/phenotype files generated by PLINK (<<https://www.cog-genomics.org/plink2>>), the whole genome association analysis toolset, without loading the entire file into memory.

URL <https://github.com/QuantGen/BEDMatrix>

BugReports <https://github.com/QuantGen/BEDMatrix/issues>

Depends R (>= 3.4.0)

Imports methods, crochet (>= 2.3.0)

Suggests data.table, LinkedMatrix, tinytest

Repository <https://quantgen.r-universe.dev>

RemoteUrl <https://github.com/quantgen/bedmatrix>

RemoteRef HEAD

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BEDMatrix-package *A Package to Extract Genotypes from a PLINK .bed File*

Description

The BEDMatrix package provides a matrix-like wrapper around `.bed` files, one of the genotype/phenotype file formats of **PLINK**, the whole genome association analysis toolset. BEDMatrix objects are created by simply providing the path to a `.bed` file and once created, they behave similarly to regular matrices with the advantage that genotypes are retrieved on demand without loading the entire file into memory. This allows handling of very large files with limited use of memory.

.bed Files

`.bed` files (sometimes referred to as binary `.ped` files) are binary representations of genotype calls at biallelic variants. This very compact file format (2 bits per genotype call) is used and generated by **PLINK**. `.bed` files should not be confused with the **UCSC Genome Browser's BED format**, which is totally different.

A `.bed` file can be created from a `.ped` file with **PLINK** using `plink --file myfile --make-bed`.

See Also

[BEDMatrix-class](#) to learn more about the BEDMatrix class.

BEDMatrix *Create a BEDMatrix Object from a PLINK .bed File*

Description

This function constructs a new BEDMatrix object by mapping the specified **PLINK** `.bed` file into memory.

Usage

```
BEDMatrix(path, n = NULL, p = NULL, simple_names = FALSE)
```

Arguments

<code>path</code>	Path to the <code>.bed</code> file (with or without extension).
<code>n</code>	The number of samples. If <code>NULL</code> (the default), this number will be determined from the accompanying <code>.fam</code> file (of the same name as the <code>.bed</code> file). If a positive integer, the <code>.fam</code> file is not read and <code>rownames</code> will be set to <code>NULL</code> and have to be provided manually.

p	The number of variants. If NULL (the default) the number of variants will be determined from the accompanying <code>.bim</code> file (of the same name as the <code>.bed</code> file). If a positive integer, the <code>.bim</code> file is not read and <code>colnames</code> will be set to NULL and have to be provided manually.
simple_names	Whether to simplify the format of the dimension names. If FALSE (the default), row names are concatenations of family IDs, <code>_</code> , and within-family IDs, while column names are concatenations of variant names, <code>_</code> , and allele codes for the first allele of the <code>.bim</code> file (A1). If TRUE, row names are within-family IDs only and column names are variant names only.

Details

`.bed` files must be accompanied by `.fam` and `.bim` files: `.fam` files contain sample information, and `.bim` files contain variant information. If the name of the `.bed` file is `plink.bed` then the names of the `.fam` and `.bim` files have to be `plink.fam` and `plink.bim`, respectively. The `.fam` and `.bim` files are used to extract the number and names of samples and variants.

For very large `.bed` files, reading the `.fam` and `.bim` files can take a long time. If `n` and `p` are provided, these files are not read and `dimnames` have to be provided manually.

Currently, only the variant-major mode of `.bed` files is supported. **PLINK2** "dropped" support for the sample-major mode by automatically converting files in this format to the variant-major mode. Therefore, it is recommended to run files in sample-major mode through **PLINK2** first.

Value

A `BEDMatrix` object.

See Also

[BEDMatrix-package](#) to learn more about the `BEDMatrix` package, [BEDMatrix-class](#) to learn more about the `BEDMatrix` class.

Examples

```
# Get the path to the example .bed file
path <- system.file("extdata", "example.bed",
                   package = "BEDMatrix")

# Create a BEDMatrix object the example .bed file
m1 <- BEDMatrix(path)

# Create a BEDMatrix object the example .bed file without loading
# the .fam and .bim files
m2 <- BEDMatrix(path, n = 50, p = 1000)
```

Description

BEDMatrix is a class that maps a **PLINK .bed** file into memory and behaves similarly to a regular matrix by implementing key methods such as `[]`, `dim`, and `dimnames`. Subsets are extracted directly and on-demand from the .bed file without loading the entire file into memory.

Details

The subsets extracted from a BEDMatrix object are coded as the allelic dosages of the first allele in the .bim file (A1), similarly to .raw files generated with the `--recode A` argument in **PLINK**.

Internally, this class is an S4 class with the following slots that should not be relied upon in actual code: `xptr`, `dims`, `dnames`, and `path`. The .bed file is mapped into memory using `mmap` on Unix and `MapViewOfFile` on Windows.

Slots

`xptr`: An external pointer to the underlying C code.

`dims`: An integer vector specifying the number of samples and variants as determined by the accompanying .fam and .bim files or by the `n` and `p` parameters of the BEDMatrix constructor function.

`dnames`: A list describing the row names and column names of the object as determined by the accompanying .fam and .bim files, or NULL if the `n` and `p` parameters of the BEDMatrix constructor function were provided.

`path`: A character string containing the path to the .bed file.

Methods

`[]`: Extract parts of an object

`dim`: Retrieve the dimension of an object

`dimnames`: Retrieve the dimnames of an object

`dimnames<-`: Set the dimnames of an object

`as.matrix`: Turn the object into a matrix

`is.matrix`: Test if the object is a matrix

`length`: Get the length of an object

`str`: Display the internal structure of an object

`show`: Display the object

See Also

[BEDMatrix](#) to create a BEDMatrix object from a .bed file, [BEDMatrix-package](#) to learn more about the BEDMatrix package, [LinkedMatrix](#) to link several BEDMatrix objects together.

Examples

```
# Get the path to the example .bed file
path <- system.file("extdata", "example.bed",
                    package = "BEDMatrix")

# Create a BEDMatrix object the example .bed file
m <- BEDMatrix(path)

# Get the dimensions of the BEDMatrix object
dim(m)

# Get the row names of the BEDMatrix object
rownames(m)

# Get the column names of the BEDMatrix object
colnames(m)

# Extract genotypes for the specified sample(s)
m[1, ]
m[1:3, ]
m["per0_per0", ]
m[c("per0_per0", "per1_per1", "per2_per2"), ]

# Extract genotypes for a particular variant
m[, 1]
m[, c("snp0_A", "snp1_C", "snp2_G")]

# Extract genotypes for the specified samples and variants
m[
  c("per0_per0", "per1_per1", "per2_per2"),
  c("snp0_A", "snp1_C", "snp2_G")
]
```

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