Package 'rrbgen'

June 6, 2018

Type Package

Title Robbie's lightweight limited functionality R bgen read/write library

Version 0.0.0

Date 2019-06-07

Author Robert William Davies

Maintainer Robert William Davies <robertwilliamdavies@gmail.com>

Description A lightweight R bgen library with limited functionality

Imports Rcpp

LinkingTo Rcpp

License GPL | file LICENSE

SystemRequirements C++11

NeedsCompilation yes

Suggests testthat

RoxygenNote 6.0.1

R topics documented:

---

rrbgen_load   *Load entire bgen file*

Usage

```
rrbgen_load(bgen_file, gp_names_col = "snpid")
```

Arguments

bgen_file   Path to bgen file to load

gp_names_col   Which column to use to label the variants in the first dimension of the genotype
probabilities. Note that bgen has two variant ID columns, a variant identifier
(here labelled snpid) and rsid (here labelled rsid)

Value

gp, sample_names and var_info

Author(s)

Robert Davies

---

rrbgen_load_samples   *Load samples names only from a bgen file*

Usage

```
rrbgen_load_samples(bgen_file)
```

Arguments

bgen_file   Path to bgen file to load

Value

sample_names

Author(s)

Robert Davies

---

rrbgen_load_variant_info

Load variant information only from a bgen file

Usage

```
rrbgen_load_variant_info(bgen_file)
```

Arguments

bgen_file   Path to bgen file to load

Value

var_info

Author(s)

Robert Davies

---

rrbgen_write   *Write variant information to a bgen file*

Usage

```
rrbgen_write(bgen_file, sample_names = NULL, var_info = NULL, gp = NULL,
    list_of_gp_raw_t = NULL, free = NULL, Layout = 2,
    CompressedSNPBlocks = 1, B_bit_prob = 8)
```

Arguments

bgen_file	Path to bgen file to be written to
sample_names	character vector of sample names
var_info	var_info (6 first columns of gen file, or chr, snpid, rsid, position (1-based), ref, alt)
gp	genotype probabilities as 3-dimensional array, where dim1 = variants, dim2 = samples, dim3 = hom ref, het, hom alt
list_of_gp_raw_t	
	list of raw data. bespoke format. to understand, investigate the tests
free	free text for header. Should probably remain NULL. Not read if written in rrbgen_read
Layout	Only supported 2 (see bgen spec)
CompressedSNPBlocks	
	Only supported 1. Whether to (1) or not to (0) compress genotype probabilities
B_bit_prob	How many bits to use to encode genotype probabilities (only supported 8, 16, 24, 32)

Author(s)

Robert Davies

Index