

Package ‘pgen2gds’

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Type Package

Title Format Conversion from PLINK2 PGEN to GDS

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Depends methods, gdsfmt (>= 1.24.0)

Imports SeqArray (>= 1.49.6), pgenlibr

LinkingTo gdsfmt

Suggests parallel, digest, crayon, GenomicRanges, testthat (>= 3.0.0),
knitr, rmarkdown, BiocStyle, BiocGenerics

Description Provides functions to convert files from the PLINK2 pgen format
to SeqArray GDS.

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VignetteBuilder knitr

BugReports <https://github.com/zhengxwen/pgen2gds/issues>

URL <https://github.com/zhengxwen/pgen2gds>

biocViews Infrastructure, DataImport, Genetics

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seqPGEN2GDS

*Reformat PLINK2 PGEN files***Description**

Reformats PLINK2 pgen files to GDS format.

Usage

```
seqPGEN2GDS(pgen.fn, pvar.fn=NULL, psam.fn=NULL, out.gdsfn,
  compress.geno="LZMA_RA", compress.annot="LZMA_RA", variant.sel=NULL,
  sample.sel=NULL, start=1L, count=NA_integer_,
  ignore.chr.prefix=c("chr", "0"), reference=NULL, optimize=TRUE,
  digest=TRUE, parallel=FALSE, balancing=TRUE, verbose=TRUE)
```

Arguments

pgen.fn	a file name for the pgen file
pvar.fn	a file name for the pvar file, or NULL to use the default
psam.fn	a file name for the psam file, or NULL to use the default
out.gdsfn	the file name of output GDS file
compress.geno	the compression method for "genotype"; optional values are defined in the function <code>add.gdsn</code>
compress.annot	the compression method for the GDS variables, except "genotype"; optional values are defined in the function <code>add.gdsn</code>
variant.sel	NULL for no variant selection, a logical vector or a numeric vector to specify the variant selection
sample.sel	NULL for no sample selection, a logical vector or a numeric vector to specify the sample selection
start	the starting variant if importing part of the pgen file
count	the maximum count of variant if importing part of the pgen file, <code>NA_integer_</code> or any non-positive value indicates importing to the end
ignore.chr.prefix	a vector of character, indicating the prefix of chromosome which should be ignored, e.g., "chr"; it is not case-sensitive
reference	genome reference, like "GRCh37", "GRCh38"; it is not specified if <code>reference=NULL</code>
optimize	if TRUE, optimize the access efficiency by calling cleanup.gds
digest	a logical value (TRUE/FALSE) or a character (e.g., "md5"); add hash codes to the GDS file if TRUE or a digest algorithm is specified
parallel	FALSE (serial processing), TRUE (parallel processing), a numeric value indicating the number of cores, or a cluster object for parallel processing; <code>parallel</code> is passed to the argument <code>cl</code> in seqParallel , see seqParallel for more details
balancing	whether to perform workload balancing or not, only applicable when multiple cores are used; if NA, use TRUE as a default until <code>getOption("seqarray.balancing")</code> is set and not TRUE
verbose	if TRUE, show information

Value

Return the file name of SeqArray GDS file with an absolute path.

Author(s)

Xiuwen Zheng

References

<https://www.cog-genomics.org/plink/2.0/>

See Also

[seqReadPVAR](#)

Examples

```
pgen_fn <- system.file("extdata", "plink2_gen.pgen", package="pgen2gds")

seqPGEN2GDS(pgen_fn, out.gdsfn="test.gds")

# delete the temporary file
unlink("test.gds", force=TRUE)
```

seqReadPVAR

Read PLINK2 pvar file

Description

Read PLINK2 pvar file for variants

Usage

```
seqReadPVAR(pvar, sel=NULL)
```

Arguments

pvar	a file name of a pvar file (from NewPvar), or a pvar object, which can be queried for variant IDs and allele codes
sel	NULL, a logical vector or a numeric vector for specifying the variants; NULL for including all variants

Value

Return a data frame with the columns chrom, pos, allele and rsid.

Author(s)

Xiuwen Zheng

References

<https://www.cog-genomics.org/plink/2.0/>

See Also[seqPGEN2GDS](#)**Examples**

```
pvar_fn <- system.file("extdata", "plink2_gen.pvar", package="pgen2gds")  
  
head(seqReadPVAR(pvar_fn))
```

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