Package: plinkFile (via r-universe)

August 21, 2024

Title 'PLINK' (and 'GCTA') File Helpers

Version 0.2.1

Description reads/write binary genotype file compatable with 'PLINK' <https://www.cog-genomics.org/plink/1.9/input#bed> into/from a R matrix; traverse genotype data one windows of variants at a time, like apply() or a for loop; reads/writes genotype relatedness/kinship matrices created by 'PLINK' <https://www.cog-genomics.org/plink/1.9/distance#make_rel> or 'GCTA' <https://cnsgenomics.com/software/gcta/#MakingaGRM> into/from a R square matrix. It is best used for bringing data produced by 'PLINK' and 'GCTA' into R workflow.

Depends R (>= 3.1)

License GPL (>= 2)

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

Repository https://xiaoran831213.r-universe.dev

RemoteUrl https://github.com/xiaoran831213/plinkfile

RemoteRef HEAD

RemoteSha e1296522a3e3cd98ab1d565e9baab6b7647da2f5