Package: hirisplexr (via r-universe)

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Type Package

Title From PLINK to HIrisPlex

Version 0.1.0

Author Andrea Giardina [aut, cre]

Maintainer Andrea Giardina <r@andreagiardina.com>

Description Read PLINK 1.9 binary datasets (BED/BIM/FAM) and generate the CSV files required by the Erasmus MC HIrisPlex / HIrisPlex-S webtool. It maps PLINK alleles to the webtool's required 'rsID_Allele' columns (0/1/2/NA). No external tools (e.g., PLINK CLI) are required.

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URL https://github.com/agiardina/hirisplexr

BugReports https://github.com/agiardina/hirisplexr/issues

Depends R (>= 3.6)

Imports BEDMatrix, data.table, utils

Suggests testthat (>= 3.0.0), knitr, rmarkdown

Config/testthat/edition 3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

VignetteBuilder knitr

Repository https://adhikari-statgen-lab.r-universe.dev

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`write_hirisplex_csv` *Write HIrisPlex / HIrisPlex-S CSV from a PLINK BED/BIM/FAM prefix*

Description

Given a PLINK 1.9 binary dataset (prefix.bed/.bim/.fam), this function produces a CSV ready to upload to the HIrisPlex(-S) webtool.

Usage

```
write_hirisplex_csv(
  prefix,
  panel = c("hirisplexs", "hirisplex", "irisplex"),
  out = NULL,
  sample_id = c("IID", "FID_IID"),
  allow_strand_flip = TRUE
)
```

Arguments

`prefix`	Character. Path prefix to PLINK files, without extension.
`panel`	Character. One of "hirisplexs" (default), "hirisplex", "irisplex".
`out`	Character. Output CSV path. Defaults to `<panel>.csv` in the working directory.
`sample_id`	Character. How to form 'SampleID': "IID" or "FID_IID". Default is "IID".
`allow_strand_flip`	Logical. If TRUE, attempt to match the required allele by allowing strand complements.

Details

Columns are 'SampleID' followed by one column per required SNP in the form `rsID_Allele` (e.g., `rs12203592_T`). Each cell contains 0/1/2 (count of the input allele) or NA when the SNP is missing. The column set and order are defined by the selected panel (IrisPlex, HIrisPlex, HIrisPlex-S).

Allele counting is based on the PLINK .bim alleles. Genotype dosage is read on demand from the .bed using `BEDMatrix::BEDMatrix()`, which encodes the dosage of the first allele in the .bim file (A1). If the webtool's required input allele equals A1, we use the dosage directly; if it equals A2, we use (2 - dosage). If `allow_strand_flip = TRUE`, we also reconcile complements (A<->T, C<->G) to account for strand orientation differences.

Value

(Invisibly) the output file path.

Examples

```
## Not run:
write_hirisplex_csv("/path/to/prefix", panel = "hirisplexs")

## End(Not run)
```

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