

Package ‘parati’

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Type Package

Title Parental Allele Transmission Inference for Trio Genotype Data

Version 0.99.8

Description Infers maternal and paternal transmitted and non-transmitted alleles from phased trio genotype data. The package supports SNP-level analyses of genetic nurture and transgenerational effects. It interoperates with Bioconductor VCF infrastructure through support for VariantAnnotation::VCF objects and returns R objects for downstream analysis.

URL <https://github.com/newche/parati>

BugReports <https://github.com/newche/parati/issues>

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Encoding UTF-8

RoxygenNote 7.3.3

Imports data.table, methods, openxlsx, R.utils, vcfR,
VariantAnnotation, SummarizedExperiment, BiocGenerics,
GenomeInfoDb

Suggests BiocStyle, knitr, optparse, rmarkdown, testthat (>= 3.0.0),
waldo

VignetteBuilder knitr

biocViews Genetics, SNP, Sequencing, VariantAnnotation, Software

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|-----------------|---|
| haplotype_infer | <i>Infer parental transmitted and non-transmitted alleles</i> |
|-----------------|---|

Description

Given trio genotype data for a single family, infer maternal and paternal transmitted and non-transmitted alleles.

Usage

```
haplotype_infer(vcf_dt, hap_length = 5e+05)
```

Arguments

| | |
|------------|---|
| vcf_dt | A 'data.table' containing fixed VCF columns and genotype columns named 'M', 'P', and 'B'. |
| hap_length | Integer, haplotype window length. |

Details

This function preserves the original PARATI inference semantics: - deterministic Mendelian inference for non-triple-heterozygote patterns - local haplotype matching for triple-heterozygote sites - low-similarity / ambiguous sites are left as missing (".l.")

Value

A named list containing:

vcf_trans A 'data.table' with transmitted alleles.

vcf_nontrans A 'data.table' with non-transmitted alleles.

sim_perc_summary A 'data.table' summarizing inference statistics.

| | |
|------------|--------------------------------------|
| parati_run | <i>Run PARATI inference workflow</i> |
|------------|--------------------------------------|

Description

Main function to infer parental transmitted and non-transmitted alleles from phased trio genotype data. The function accepts either a VCF file path or a 'VCF' object from 'VariantAnnotation', and returns R objects without writing files by default.

Usage

```
parati_run(vcf, fam, chr = NULL, hap_length = 5e+05)
```

Arguments

| | |
|------------|--|
| vcf | Either a character path to a phased VCF/VCF.GZ file, or a 'VariantAnnotation::VCF' object. |
| fam | Either a character path to a family index table ('.xlsx') or a 'data.frame' / 'data.table' with columns 'FamilyIndex', 'IndividualID', and 'Role'. |
| chr | Optional chromosome identifier to subset variants. |
| hap_length | Integer, haplotype window length. |

Value

A named list containing:

vcf_trans A 'data.table' with transmitted alleles.

vcf_nontrans A 'data.table' with non-transmitted alleles.

sim_perc_summary A 'data.table' summarizing inference statistics.

Examples

```
vcf_file <- system.file("extdata", "Toy_TrioGenotype.vcf.gz", package = "parati")
fam_file <- system.file("extdata", "Toy_FamilyIndexTable.xlsx", package = "parati")
res <- parati_run(vcf = vcf_file, fam = fam_file, chr = 1)
names(res)
```

| | |
|-----------------|-------------------------------|
| read_vcf_by_chr | <i>Read VCF by chromosome</i> |
|-----------------|-------------------------------|

Description

Reads a VCF file and subsets variants to a given chromosome.

Usage

```
read_vcf_by_chr(vcf_file, chr)
```

Arguments

| | |
|----------|--|
| vcf_file | Character scalar, path to a VCF/VCF.GZ file. |
| chr | Character or integer chromosome identifier. |

Value

A 'data.table' containing VCF rows for the selected chromosome.

Examples

```
vcf_file <- system.file("extdata", "Toy_TrioGenotype.vcf.gz", package = "parati")
vcf_chr <- read_vcf_by_chr(vcf_file, chr = 1)
dim(vcf_chr)
```

| | |
|----------------|--|
| vcf_dt_to_vcfR | <i>Convert data.table to vcfR object</i> |
|----------------|--|

Description

Converts a 'data.table' representing VCF rows into a 'vcfR' object.

Usage

```
vcf_dt_to_vcfR(df, meta = character())
```

Arguments

| | |
|------|-------------------------------------|
| df | A 'data.table' containing VCF rows. |
| meta | Character vector of VCF meta lines. |

Value

A 'vcfR' object.

Examples

```
vcf_file <- system.file("extdata", "Toy_TrioGenotype.vcf.gz", package = "parati")
vcf_dt <- read_vcf_by_chr(vcf_file, chr = 1)
vcf_obj <- vcf_dt_to_vcfR(vcf_dt)
class(vcf_obj)
stopifnot(inherits(vcf_obj, "vcfR"))
```

| | |
|--------------|-------------------------------------|
| write_vcf_dt | <i>Write VCF data.table to file</i> |
|--------------|-------------------------------------|

Description

Writes a 'data.table' representing VCF rows to a VCF file.

Usage

```
write_vcf_dt(df, file)
```

Arguments

| | |
|------|-------------------------------------|
| df | A 'data.table' containing VCF rows. |
| file | Character scalar, output file path. |

Value

'NULL', invisibly. The VCF file is written to 'file'.

Examples

```
vcf_file <- system.file("extdata", "Toy_TrioGenotype.vcf.gz", package = "parati")
vcf_dt <- read_vcf_by_chr(vcf_file, chr = 1)
outfile <- tempfile(fileext = ".vcf")
write_vcf_dt(vcf_dt, outfile)
file.exists(outfile)
```

| | |
|---------------|----------------------------------|
| write_vcf_obj | <i>Write vcfR object to file</i> |
|---------------|----------------------------------|

Description

Writes a 'vcfR' object to a VCF file.

Usage

```
write_vcf_obj(vcf_obj, file)
```

Arguments

| | |
|---------|-------------------------------------|
| vcf_obj | A 'vcfR' object. |
| file | Character scalar, output file path. |

Value

'NULL', invisibly. The VCF file is written to 'file'.

Examples

```
vcf_file <- system.file("extdata", "Toy_TrioGenotype.vcf.gz", package = "parati")
vcf_dt <- read_vcf_by_chr(vcf_file, chr = 1)
vcf_obj <- vcf_dt_to_vcfR(vcf_dt)
stopifnot(inherits(vcf_obj, "vcfR"))
outfile <- tempfile(fileext = ".vcf")
write_vcf_obj(vcf_obj, outfile)
stopifnot(file.exists(outfile))
```

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