Package: lineagespot (via r-universe)

June 30, 2024

Title Detection of SARS-CoV-2 lineages in wastewater samples using next-generation sequencing

Version 1.9.0

Date 2021-03-24

Description Lineagespot is a framework written in R, and aims to identify SARS-CoV-2 related mutations based on a single (or a list) of variant(s) file(s) (i.e., variant calling format). The method can facilitate the detection of SARS-CoV-2 lineages in wastewater samples using next generation sequencing, and attempts to infer the potential distribution of the SARS-CoV-2 lineages.

License MIT + file LICENSE

Encoding UTF-8

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.2

biocViews VariantDetection, VariantAnnotation, Sequencing

Imports VariantAnnotation, MatrixGenerics, SummarizedExperiment, data.table, stringr, httr, utils

Suggests BiocStyle, RefManageR, rmarkdown, knitr, testthat (>= 3.0.0)

URL https://github.com/BiodataAnalysisGroup/lineagespot

BugReports https://github.com/BiodataAnalysisGroup/lineagespot/issues

BiocType Software

VignetteBuilder knitr

Config/testthat/edition 3

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

RemoteUrl https://github.com/bioc/lineagespot

RemoteRef HEAD

RemoteSha ae4993ee5b07bc61748d2e4b20eeb3c4fa453b9f

Contents

`get_lineage_report` *get_lineage_report*

Description

Retrieve information about lineages' variants vie outbreak.info's API

Usage

```
get_lineage_report(
  lineages,
 base.url = "https://api.outbreak.info/genomics/lineage-mutations?pangolin_lineage="
)
```

Arguments

`lineages`	a character vector containing the names of the lineages of interest
`base.url`	The base API URL used to search for lineage reports Default value is "https://api.outbreak.info/genomics/lineage-mutations?pangolin_lineage="

Value

A list of data table elements of lineage reports

Examples

```
get_lineage_report(lineages = c("B.1.1.7", "B.1.617.2"))
```

is_gff3 *is_gff3*

Description

Identify whether a file is in GFF3 format.

Usage

```
is_gff3(file)
```

Arguments

file	Path to GFF3 file.

Value

result; TRUE if the input file is in GFF3 format, FALSE if not.

Examples

```
gff3_path <- system.file("extdata", "NC_045512.2_annot.gff3",
  package = "lineagespot"
)
is_gff3(gff3_path)
```

lineagespot *lineagespot*

Description

Identify SARS-CoV-2 related mutations based on a single (or a list) of variant(s) file(s)

Usage

```
lineagespot(
  vcf_fls = NULL,
  vcf_folder = NULL,
  gff3_path = NULL,
  ref_folder = NULL,
  voc = c("B.1.617.2", "B.1.1.7", "B.1.351", "P.1"),
  AF_threshold = 0.8
)
```

Arguments

vcf_fls	A character vector of paths to VCF files
vcf_folder	A path to a folder containing all VCF files that will be integrated into a single table
gff3_path	Path to GFF3 file containing SARS-CoV-2 gene coordinates.
ref_folder	A path to a folder containing lineage reports
voc	A character vector containing the names of the lineages of interest
AF_threshold	A parameter indicating the AF threshold for identifying variants per sample

Value

A list of three elements;

- Variants' table; A data table containing all variants that are included in the input VCF files
- Lineage hits; A data table containing identified hits between the input variants and outbreak.info's lineage reports
- Lineage report; A data table with computed metrics about the prevalence of the lineage of interest per sample.

Examples

```
results <- lineagespot(
    vcf_folder = system.file("extdata", "vcf-files",
        package = "lineagespot"
    ),
    gff3_path = system.file("extdata",
        "NC_045512.2_annot.gff3",
        package = "lineagespot"
    ),
    ref_folder = system.file("extdata", "ref",
        package = "lineagespot"
    )
)

head(results$lineage.report)
```

---

lineagespot_hits *lineagespot_hits*

Description

Find overlapping variants with SARS-CoV-2 reference lineages coming from outbreak.info reports

Usage

```
lineagespot_hits(
  vcf_table = NULL,
  ref_folder = NULL,
  voc = c("B.1.617.2", "B.1.1.7", "B.1.351", "P.1")
)
```

Arguments

vcf_table	A tab-delimited table containing all variants for all samples. This input is generated by the merge_vcf function.
ref_folder	A path to lineages' reports
voc	A character vector containing the names of the lineages of interest

Value

A data table containing all identified SARS-CoV-2 variants based on the provided reference files

Examples

```
variants_table <- merge_vcf(
    vcf_folder = system.file("extdata",
        "vcf-files",
        package = "lineagespot"
    ),
    gff3_path = system.file("extdata",
        "NC_045512.2_annot.gff3",
        package = "lineagespot"
    )
)

# retrieve lineage reports using outbreak.info's API

# use user-specified references
lineage_hits_table <- lineagespot_hits(
    vcf_table = variants_table,
    ref_folder = system.file("extdata", "ref",
        package = "lineagespot"
    )
)
```

---

list_input *list_input*

Description

Check the validity of input parameters from lineagespot function.

Usage

```
list_input(vcf_fls = NULL, vcf_folder = NULL, gff3_path = NULL)
```

Arguments

vcf_fls	A character vector of paths to VCF files.
vcf_folder	A path to a folder containing all VCF files that will be integrated into a single table.
gff3_path	Path to GFF3 file containing SARS-CoV-2 gene coordinates.

Value

Return a character vector of paths to VCF files.

Examples

```
vcflist <- list_input(
  vcf_folder = system.file("extdata", "vcf-files",
    package = "lineagespot"
  ),
  gff3_path = system.file("extdata",
    "NC_045512.2_annot.gff3",
    package = "lineagespot"
  )
)
```

---

list_vcf *list_vcf*

Description

Identify VCF files from a group of files.

Usage

```
list_vcf(vcf_fls = NULL, vcf_folder = NULL, gff3_path = NULL)
```

Arguments

vcf_fls	A character vector of paths to VCF files
vcf_folder	A path to a folder containing all VCF files that will be integrated into a single table
gff3_path	Path to GFF3 file containing SARS-CoV-2 gene coordinates.

Value

- VCF list; A list where only VCF files are stored.

Examples

```
list_vcf_info <- list_vcf(
  vcf_folder = system.file("extdata", "vcf-files",
    package = "lineagespot"
  ),
  gff3_path = system.file("extdata",
    "NC_045512.2_annot.gff3",
    package = "lineagespot"
  )
)
print(list_vcf_info)
```

`merge_vcf` *merge_vcf*

Description

Merge Variant Calling Format (VCF) files into a single tab-delimited table

Usage

```
merge_vcf(vcf_fls = NULL, vcf_folder = NULL, gff3_path = NULL)
```

Arguments

`vcf_fls`	A list of paths to VCF files
`vcf_folder`	A path to a folder containing all VCF file that will be integrated into a single table
`gff3_path`	Path to GFF3 file

Value

A data table contaiing all variants from each sample of the input VCF files

Examples

```
merge_vcf(
    vcf_folder = system.file("extdata",
        "vcf-files",
        package = "lineagespot"
    ),
    gff3_path = system.file("extdata",
        "NC_045512.2_annot.gff3",
        package = "lineagespot"
    )
)
```

uniq_variants *uniq_variants*

Description

Lineage report for variants overlapping

Usage

```
uniq_variants(hits_table = NULL, AF_threshold = 0.8)
```

Arguments

hits_table	A tab-delimited table containing the identified overlaps/hits between the input files and the lineages' reports. This input is generated by the lineagespot_hits function.
AF_threshold	A parameter indicating the AF threshold that is going to applied in order to identify the presence or not of a variant. This is used to compute the number of variants in a sample and eventually the proportion of a lineage.

Value

A data table with metrics assessing the abundance of every lineage in each samples

Examples

```
variants_table <- merge_vcf(
    vcf_folder = system.file("extdata", "vcf-files",
        package = "lineagespot"
    ),
    gff3_path = system.file("extdata",
        "NC_045512.2_annot.gff3",
        package = "lineagespot"
    )
)

lineage_hits_table <- lineagespot_hits(
    vcf_table = variants_table,
    ref_folder = system.file("extdata", "ref",
        package = "lineagespot")
)

report <- uniq_variants(hits_table = lineage_hits_table)
head(report)
```

Index