

Package ‘lineagespot’

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

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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.

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

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

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Contents

get_lineage_report	2
is_gff3	3
lineagespot	4
lineagespot_hits	5
list_input	6
list_vcf	6
merge_vcf	7
uniq_variants	8

Index	10
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get_lineage_report	<i>get_lineage_report</i>
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Description

Retrieve information about lineages' variants via 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/genom 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	<i>is_gff3</i>
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Description

Identify whether a file is in GFF3 format.

Usage

```
is_gff3(file)
```

Arguments

file	Path to GFF3 file.
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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	<i>lineagespot</i>
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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

<code>vcf_fls</code>	A character vector of paths to VCF files
<code>vcf_folder</code>	A path to a folder containing all VCF files that will be integrated into a single table
<code>gff3_path</code>	Path to GFF3 file containing SARS-CoV-2 gene coordinates.
<code>ref_folder</code>	A path to a folder containing lineage reports
<code>voc</code>	A character vector containing the names of the lineages of interest
<code>AF_threshold</code>	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 out-break.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	<i>lineagespot_hits</i>
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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	<i>list_input</i>
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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	<i>list_vcf</i>
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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	<i>merge_vcf</i>
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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 containiing 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	<i>uniq_variants</i>
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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

`get_lineage_report`, [2](#)

`is_gff3`, [3](#)

`lineagespot`, [4](#)

`lineagespot_hits`, [5](#)

`list_input`, [6](#)

`list_vcf`, [6](#)

`merge_vcf`, [7](#)

`uniq_variants`, [8](#)