

Package ‘lineagespot’

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

Version 1.11.0

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

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| <code>get_lineage_report</code> | <i>get_lineage_report</i> |
|---------------------------------|---------------------------|

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/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 | <i>lineagespot</i> |
|-------------|--------------------|

Description

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

Usage

```
lineagespot(
  vcf_files = 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_files</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> |
|------------------|-------------------------|

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 | <i>list_vcf</i> |
|----------|-----------------|

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> |
|-----------|------------------|

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 containing 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"
  )
)
```

| | |
|----------------|-----------------------|
| uniqu_variants | <i>uniqu_variants</i> |
|----------------|-----------------------|

Description

Lineage report for variants overlapping

Usage

```
uniqu_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 be 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)
```

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