

# Package ‘lineagespot’

December 14, 2024

**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.

**License** MIT + file LICENSE

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

**URL** <https://github.com/BiodataAnalysisGroup/lineagespot>

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

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**VignetteBuilder** knitr

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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/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"))
```

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is\_gff3

*is\_gff3*

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**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)
```

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|-------------|--------------------|
| 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_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)

```

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| 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

*list\_input*

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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"
  )
)
```

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|          |                 |
|----------|-----------------|
| 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)
```

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| 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 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> |
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**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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