

# Package ‘lineagespot’

September 24, 2025

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

**Version** 1.13.0

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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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**Author** Nikolaos Pechlivanis [aut, cre] (ORCID:  
<https://orcid.org/0000-0003-2502-612X>),  
 Maria Tsagiopoulou [aut],  
 Maria Christina Maniou [aut],  
 Anastasis Togkousidis [aut],  
 Evangelia Mouchtaropoulou [aut],  
 Taxiarchis Chassalevris [aut],  
 Serafeim Chaintoutis [aut],  
 Chrysostomos Dovas [aut],  
 Maria Petala [aut],  
 Margaritis Kostoglou [aut],  
 Thodoris Karapantsios [aut],  
 Stamatia Laidou [aut],  
 Elisavet Vlachonikola [aut],  
 Aspasia Orfanou [aut],  
 Styliani-Christina Fragkouli [aut],  
 Sofoklis Keisaris [aut],  
 Anastasia Chatzidimitriou [aut],  
 Agis Papadopoulos [aut],  
 Nikolaos Papaioannou [aut],  
 Anagnostis Argiriou [aut],  
 Fotis E. Psomopoulos [aut]

**Maintainer** Nikolaos Pechlivanis <inab.bioinformatics@lists.certh.gr>

## 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 |

|              |           |
|--------------|-----------|
| <b>Index</b> | <b>10</b> |
|--------------|-----------|

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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<br>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 | <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. |
|------|--------------------|

**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_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)

```

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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"
  )
)

```

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

---

### 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 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](#)