

# Package ‘CSESA’

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**Type** Package

**Title** CRISPR-Based Salmonella Enterica Serotype Analyzer

**Version** 1.2.0

**Description** Salmonella enterica is a major cause of bacterial food-borne disease world-wide. Serotype identification is the most commonly used typing method to characterize Salmonella isolates. However, experimental serotyping needs great cost on manpower and resources. Recently, we found that the newly incorporated spacer in the clustered regularly interspaced short palindromic repeat (CRISPR) could serve as an effective marker for typing of Salmonella. It was further revealed by Li et. al (2014) <doi:10.1128/JCM.00696-14> that recognized types based on the combination of two newly incorporated spacer in both CRISPR loci showed high accordance with serotypes. Here, we developed an R package 'CSESA' to predict the serotype based on this finding. Considering it's time saving and of high accuracy, we recommend to predict the serotypes of unknown Salmonella isolates using 'CSESA' before doing the traditional serotyping.

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1

**Suggests** testthat

**Imports** Biostrings

**NeedsCompilation** no

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CSESA

*CSESA (CRISPR-based Salmonella enterica Serotype Analyzer).*


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## Description

The main function in CSESA package.

## Usage

```
CSESA(in.file1 = NULL, in.file2 = NULL, out.file = NULL,
      method = c("PCR", "WGS"))
```

## Arguments

<code>in.file1</code>	The first input file, the default value is NULL.
<code>in.file2</code>	The second input file (optional), the default value is NULL.
<code>out.file</code>	Into which results will be saved if this value is set. Otherwise results will be displayed on the screen.
<code>method</code>	The method to handle the input file(s), which can be set as "PCR" or "WGS". Choose "PCR" if the CRISPR sequence(s) from PCR amplification is entered, and choose "WGS" when entering the whole genome assembly of a Salmonella isolate.

## Note

If you use the "WGS" method, please make sure you have installed the BLAST software and included it within the working path.

## Examples

```
CSESA(system.file("extdata", "sequence_CRIPSR1.fasta", package = "CSESA"),
      system.file("extdata", "sequence_CRIPSR2.fasta", package = "CSESA"), method = "PCR")
CSESA(system.file("extdata", "sequence_CRIPSR1.fasta", package = "CSESA"), method = "PCR")
CSESA(system.file("extdata", "Salmonella_whole_genome_assembly.fasta",
      package = "CSESA"), method = "WGS")
```

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FindSerotype	<i>Find the serotype based on the analysis of the new spacers.</i>
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**Description**

Find the serotype based on the analysis of the new spacers.

**Usage**

```
FindSerotype(csesa1 = NA, csesa2 = NA)
```

**Arguments**

csesa1	The new spacer of the first sequence.
csesa2	The new spacer of the second sequence.

**Value**

The data frame which represents the serotype.

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GetAllNewSpacers	<i>Get the new spacers from the molecular sequence and its reverse complement.</i>
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**Description**

Get the new spacers from the molecular sequence and its reverse complement.

**Usage**

```
GetAllNewSpacers(molecular.seq = NULL)
```

**Arguments**

molecular.seq	The molecular sequence.
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**Value**

The vector of the new spacers, which is extracted from the molecular sequence and its reverse complement.

**Note**

If there doesn't exist any new spacer, the function would return NA.

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GetNewSpacer	<i>Get the new spacer from the molecular sequence.</i>
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**Description**

Get the new spacer from the molecular sequence.

**Usage**

```
GetNewSpacer(molecular.seq = NULL)
```

**Arguments**

`molecular.seq` The molecular sequence.

**Value**

The new spacer sequence as a string.

**Examples**

```
GetNewSpacer("AGAGGCGGACCGAAAAACCGTTTTTCAGCCAACGTAT")
```

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GetNewSpacerCode	<i>Get the new spacer from the molecular sequence and map it to the code.</i>
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**Description**

Get the new spacer from the molecular sequence and map it to the code.

**Usage**

```
GetNewSpacerCode(molecular.seq = NULL)
```

**Arguments**

`molecular.seq` The molecular sequence.

**Value**

The new spacer code as a string.

---

`GetReverseComplement`    *Return the reverse complement of the sequence.*

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**Description**

Return the reverse complement of the sequence.

**Usage**

`GetReverseComplement(x)`

**Arguments**

x                    The input sequence.

**Value**

The reverse complement sequence as a string.

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`GetStr`                    *Get the information string from the CSESA s3 object.*

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**Description**

Get the information string from the CSESA s3 object.

**Usage**

`GetStr(csesa)`

**Arguments**

csesa                The S3 object CSESA.

**Value**

The string record the newly spacers and serotype information.

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PCR                                    *Get the CSESA object through the two sequence.*

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**Description**

Get the CSESA object through the two sequence.

**Usage**

PCR(seq1, seq2, out.file)

**Arguments**

seq1	The first DNA sequence.
seq2	The second DNA sequence.
out.file	Into which results will be saved if this value is set. Otherwise results will be displayed on the screen.

---

ReadInFile                            *Read the three types of input file.*

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**Description**

Read the three types of input file.

**Usage**

ReadInFile(file.name)

**Arguments**

file.name	The input file name.
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**Value**

The molecular sequence as a string.

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WGS

*Find the serotype based on the analysis of the new spacers.*

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**Description**

Find the serotype based on the analysis of the new spacers.

**Usage**

WGS(file)

**Arguments**

file            The input fasta file.

**Value**

The two DNA molecular sequence.

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