# API Documentation

## API Documentation

# July 17, 2017

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#### Script script-GTEvaluator 1

 $GTE valuator\_matrix Maker\ then\ run\ GTE valuator\_statistic.$ 

## Requires:

- python  $2.7^1$  (tested with 2.7.6)
- $Biopython^2$
- $scipy^3$
- $\bullet$  EMBOSS<sup>4</sup>
- GTEvaluator\_matrixMaker
- GTEvaluator\_statistic

#### 1.1 **Functions**

$\mathbf{get\_parser}()$	
Parse arguments	
Return Value	
arguments list	
$(type=parser\ object)$	

main()

#### 1.2Variables

Name	Description
doc	Value:
package	Value: None

<sup>&</sup>lt;sup>1</sup>https://www.python.org/downloads/

<sup>&</sup>lt;sup>2</sup>http://biopython.org/wiki/Download <sup>3</sup>http://www.scipy.org/scipylib/download.html

<sup>&</sup>lt;sup>4</sup>http://emboss.sourceforge.net/download/

#### ${\bf Script\ script\text{-}GTEvaluator}\_$ 2

 $GTE valuator\_matrix Maker\ then\ run\ GTE valuator\_statistic.$ 

## ${\bf Requires:}$

- python  $2.7^5$  (tested with 2.7.6)
- Biopython $^6$
- $scipy^7$
- $EMBOSS^8$
- GTEvaluator\_matrixMaker
- GTEvaluator\_statistic

#### 2.1**Functions**

$\mathbf{get\_parser}()$	
Parse arguments	
Return Value	
arguments list	
$(type=parser\ object)$	

main()

## 2.2 Variables

Name	Description
doc	Value:
package	Value: None

<sup>&</sup>lt;sup>5</sup>https://www.python.org/downloads/

<sup>6</sup> http://biopython.org/wiki/Download 7 http://www.scipy.org/scipylib/download.html

 $<sup>^8 \</sup>rm http://emboss.sourceforge.net/download/$ 

## 3 Script script-GTEvaluator\_matrixMaker

For each genomes, matchs targets against sequences. Make a matrix with 1 if the target is present, 0 otherwise.

#### Requires:

- python  $2.7^9$  (tested with 2.7.6)
- Biopython  $^{10}$
- $EMBOSS^{11}$

## 3.1 Functions

#### get\_parser()

Parse arguments

#### Return Value

arguments list

(type=parser object)

### $\mathbf{exec\_commands}(\mathit{cmds}, \mathit{nbThreads})$

Exec commands in parallel in multiple process (as much as we have CPU)

### transformDegeneratedSeq(seq, trim)

#### **Parameters**

seq: nucleic sequence

(type=string)

trim: number of 5' nucleotides to trim

(type=integer)

#### Return Value

transformed sequence

(type=string)

#### replaceDegenerated(seq)

Transform sequence degenerated with ambigous nucleotides for the regex matching

#### Parameters

seq: nucleic sequence

(type=string)

#### Return Value

transformed sequence

(type=string)

<sup>&</sup>lt;sup>9</sup>https://www.python.org/downloads/

 $<sup>^{10} \</sup>rm http://biopython.org/wiki/Download$ 

 $<sup>^{11} \</sup>rm http://emboss.source forge.net/download/$ 

## primerReader(file, trim, maxDistance)

Reads the primer file and stocks informations in a dictionnary

#### Parameters

file: file name

(type=string)

trim: number of 5' nucleotides to trim

(type=integer)

maxDistance: maximum distance between the 2 primers

(type=integer)

### Return Value

diction nary with the primer name for key and a list composed by the primers sequences and the regex pattern as value

(type=dictionnary)

### $\mathbf{genomeReader}(file)$

Reads the genomes list file

### Parameters

file: file name

(type=string)

#### Return Value

dictionnary with genome file for key and the serovar name as value

(type=dictionnary)

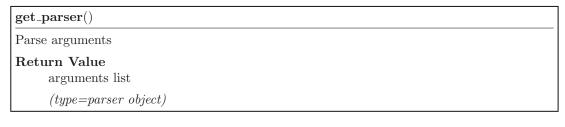
| main()

### 3.2 Variables

Name	Description
doc	Value:
package	Value: None

# 4 Script script-GTEvaluator\_statistic

## 4.1 Functions



main()

## 4.2 Variables

Name	Description
doc	Value:

## 4.3 Class primerStat

 $\begin{array}{c} \text{object} & \\ \\ & \text{script-GTEvaluator\_statistic.primerStat} \end{array}$ 

Create primerStat object to stock statistic about this primer combinaison

#### 4.3.1 Methods

 $\_$ **init** $\_$ (self, primer)

Initialize the node class

Parameters

primer: primer combinaison name

(type=string)

primer: primer combinaison name

(type=string)

sensitivity: combinaison sensitivity

(type=float)

specificity: combinaison specificity

(type=float)

distance: combinaison distance

(type=float)

Ci\_Se: sensitivity confidence

(type=float)

Ci\_Sp: specificity confidence

(type=float)

TP: number of true positif

(type=integer)

FP: number of false positif

(type=integer)

FN: number of false negatif

(type=integer)

TN: number of false negatif

(type=integer)

Overrides: object.\_\_init\_\_

 ${f compute Sensitivity}(self)$ 

Compute the sensitivity

 ${\bf compute Specificity}(\mathit{self})$ 

Compute the specificity

computeDistance(self)

Compute the distance

$computeCi\_Se(self, Ci\_min, Ci\_max)$	
Compute the sensitivity confidence interval	

```
Compute Ci_Sp(self, Ci_min, Ci_max)

Compute the specificity confidence interval
```

## Inherited from object

```
\label{lem:condition} $$ $\_delattr_{-}(), \_format_{-}(), \_getattribute_{-}(), \_hash_{-}(), \_new_{-}(), \_reduce_{-}(), \_reduce_{-}(), \_reduce_{-}(), \_reduce_{-}(), \_sizeof_{-}(), \_str_{-}(), \_subclasshook_{-}() $
```

## 4.3.2 Properties

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class	

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