

# API Documentation

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# 1 Script script-GTSelector

GTSelector workflow. First, run GTSelector\_matrixMaker then run GTSelector\_statistic.

## Requires:

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

## 1.1 Functions

<b>get_parser()</b>
Parse arguments
<b>Return Value</b>
arguments list
<i>(type=parser object)</i>

  

<b>main()</b>
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## 1.2 Variables

Name	Description
__doc__	<b>Value:</b> ...
__package__	<b>Value:</b> None

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

<sup>2</sup><http://biopython.org/wiki/Download>

<sup>3</sup><http://www.scipy.org/scipylib/download.html>

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

## 2 Script script-GTSelector\_matrixMaker

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

### Requires:

- python 2.7<sup>5</sup> (tested with 2.7.6)
- Biopython<sup>6</sup>
- EMBOSS<sup>7</sup>

### 2.1 Functions

#### **get\_parser()**

Parse arguments

#### **Return Value**

arguments list

(*type=parser object*)

#### **exec\_commands(cmds, 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 ambiguous nucleotides for the regex matching

#### **Parameters**

**seq:** nucleic sequence

(*type=string*)

#### **Return Value**

transformed sequence

(*type=string*)

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

<sup>6</sup><http://biopython.org/wiki/Download>

<sup>7</sup><http://emboss.sourceforge.net/download/>

**primerReader**(*file*, *trim*, *maxDistance*)

Reads the primer file and stocks informations in a dictionary

**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**

dictionary with the primer name for key and a list composed by the primers sequences and the regex pattern as value  
*(type=dictionnary)*

**genomeReader**(*file*)

Reads the genomes list file

**Parameters**

**file:** file name  
*(type=string)*

**Return Value**

dictionary with genome file for key and the serovar name as value  
*(type=dictionnary)*

**main**()

## 2.2 Variables

Name	Description
<code>__doc__</code>	<b>Value:</b> ...
<code>__package__</code>	<b>Value:</b> None

### 3 Script *script-GTSelector\_statistic*

Compute specificity and sensitivity for each target and variant from matrix.

**Requires:**

- python 2.7<sup>8</sup> (tested with 2.7.6)
- scipy<sup>9</sup>

#### 3.1 Functions

##### **get\_parser()**

Parse arguments

**Return Value**

arguments list

(*type=parser object*)

##### **main()**

#### 3.2 Variables

Name	Description
<code>__doc__</code>	<b>Value:</b> ...
<code>__package__</code>	<b>Value:</b> None

#### 3.3 Class *primerStat*

object — **script-GTSelector\_statistic.primerStat**

Create *primerStat* object to stock statistic about this primer combinaison

<sup>8</sup><https://www.python.org/downloads/>

<sup>9</sup><http://www.scipy.org/scipylib/download.html>

### 3.3.1 Methods

<b>__init__</b> ( <i>self</i> , <i>primer</i> )
Initialize the node class
<b>Parameters</b>
<b>primer:</b> combinaison name ( <i>type=string</i> )
<b>primer:</b> combinaison name ( <i>type=string</i> )
<b>sensitivity:</b> combinaison sensitivity ( <i>type=float</i> )
<b>specificity:</b> combinaison specificity ( <i>type=float</i> )
<b>distance:</b> combinaison distance ( <i>type=float</i> )
<b>Ci_Se:</b> sensitivity confidence ( <i>type=float</i> )
<b>Ci_Sp:</b> specificity confidence ( <i>type=float</i> )
<b>TP:</b> number of true positif ( <i>type=integer</i> )
<b>FP:</b> number of false positif ( <i>type=integer</i> )
<b>FN:</b> number of false negatif ( <i>type=integer</i> )
<b>TN:</b> number of false negatif ( <i>type=integer</i> )
Overrides: object.__init__

  

<b>computeSensitivity</b> ( <i>self</i> )
Compute the sensitivity

  

<b>computeSpecificity</b> ( <i>self</i> )
Compute the specificity

  

<b>computeDistance</b> ( <i>self</i> )
Compute the distance

<b>computeCi_Se</b> (self, Ci_min, Ci_max)
--

Compute the sensitivity confidence interval
---

<b>computeCi_Sp</b> (self, Ci_min, Ci_max)
--

Compute the specificity confidence interval
---

### ***Inherited from object***

\_\_delattr\_\_(), \_\_format\_\_(), \_\_getattr\_\_(), \_\_hash\_\_(), \_\_new\_\_(),  
 \_\_reduce\_\_(), \_\_reduce\_ex\_\_(), \_\_repr\_\_(), \_\_setattr\_\_(), \_\_sizeof\_\_(),  
 \_\_str\_\_(), \_\_subclasshook\_\_()

### **3.3.2 Properties**

Name	Description
<i>Inherited from object</i>	
__class__	

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