

API Documentation

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Contents

Contents	1
1 Script script-GTEvaluator	2
1.1 Functions	2
1.2 Variables	2
2 Script script-GTEvaluator_	3
2.1 Functions	3
2.2 Variables	3
3 Script script-GTEvaluator_matrixMaker	4
3.1 Functions	4
3.2 Variables	5
4 Script script-GTEvaluator_statistic	6
4.1 Functions	6
4.2 Variables	6
4.3 Class primerStat	6
4.3.1 Methods	7
4.3.2 Properties	8

1 Script script-GTEvaluator

GTEvaluator workflow. First, run GTEvaluator_matrixMaker then run GTEvaluator_statistic.

Requires:

- python 2.7¹ (tested with 2.7.6)
- Biopython²
- scipy³
- EMBOSS⁴
- GTEvaluator_matrixMaker
- GTEvaluator_statistic

1.1 Functions

get_parser()

Parse arguments

Return Value

arguments list

(*type=parser object*)

main()

1.2 Variables

Name	Description
__doc__	Value: ...
__package__	Value: None

¹<https://www.python.org/downloads/>

²<http://biopython.org/wiki/Download>

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

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

2 Script script-GTEvaluator_

GTEvaluator workflow. First, run GTEvaluator_matrixMaker then run GTEvaluator_statistic.

Requires:

- python 2.7⁵ (tested with 2.7.6)
- Biopython⁶
- scipy⁷
- EMBOSS⁸
- GTEvaluator_matrixMaker
- GTEvaluator_statistic

2.1 Functions

get_parser()

Parse arguments

Return Value

arguments list

(*type=parser object*)

main()

2.2 Variables

Name	Description
__doc__	Value: ...
__package__	Value: None

⁵<https://www.python.org/downloads/>

⁶<http://biopython.org/wiki/Download>

⁷<http://www.scipy.org/scipylib/download.html>

⁸<http://emboss.sourceforge.net/download/>

3 Script script-GTEvaluator_matrixMaker

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

Requires:

- python 2.7⁹ (tested with 2.7.6)
- Biopython¹⁰
- EMBOSS¹¹

3.1 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*)

⁹<https://www.python.org/downloads/>

¹⁰<http://biopython.org/wiki/Download>

¹¹<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=dictionary)

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=dictionary)

main()

3.2 Variables

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

4 Script *script-GTEvaluator_statistic*

4.1 Functions

get_parser()

Parse arguments

Return Value

arguments list


(*type=parser object*)

main()

4.2 Variables

Name	Description
<code>__doc__</code>	Value: ...

4.3 Class *primerStat*

object  **script-GTEvaluator_statistic.primerStat**

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__`

`computeSensitivity(self)`

Compute the sensitivity

`computeSpecificity(self)`

Compute the specificity

`computeDistance(self)`

Compute the distance

computeCi_Se (<i>self</i> , <i>Ci_min</i> , <i>Ci_max</i>)

Compute the sensitivity confidence interval

computeCi_Sp (<i>self</i> , <i>Ci_min</i> , <i>Ci_max</i>)

Compute the specificity confidence interval

Inherited from object

`__delattr__()`, `__format__()`, `__getattr__()`, `__hash__()`, `__new__()`, `__reduce__()`, `__reduce_ex__()`,
`__repr__()`, `__setattr__()`, `__sizeof__()`, `__str__()`, `__subclasshook__()`

4.3.2 Properties

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

Index

script-GTEvaluator (*script*), 2
 script-GTEvaluator.get_parser (*function*),
 2
 script-GTEvaluator.main (*function*), 2
script-GTEvaluator_ (*script*), 3
 script-GTEvaluator_.get_parser (*function*),
 3
 script-GTEvaluator_.main (*function*), 3
script-GTEvaluator_matrixMaker (*script*), 4–
 5
 script-GTEvaluator_matrixMaker.exec_commands
 (*function*), 4
 script-GTEvaluator_matrixMaker.genomeReader
 (*function*), 5
 script-GTEvaluator_matrixMaker.get_parser
 (*function*), 4
 script-GTEvaluator_matrixMaker.main (*func-*
 tion), 5
 script-GTEvaluator_matrixMaker.primerReader
 (*function*), 4
 script-GTEvaluator_matrixMaker.replaceDegenerated
 (*function*), 4
 script-GTEvaluator_matrixMaker.transformDegeneratedSeq
 (*function*), 4
script-GTEvaluator_statistic (*script*), 6–8
 script-GTEvaluator_statistic.get_parser (*func-*
 tion), 6
 script-GTEvaluator_statistic.main (*func-*
 tion), 6
 script-GTEvaluator_statistic.primerStat (*class*),
 6–8
 script-GTEvaluator_statistic.primerStat.computeCi_Se
 (*method*), 7
 script-GTEvaluator_statistic.primerStat.computeCi_Sp
 (*method*), 8
 script-GTEvaluator_statistic.primerStat.computeDistance
 (*method*), 7
 script-GTEvaluator_statistic.primerStat.computeSensitivity
 (*method*), 7
 script-GTEvaluator_statistic.primerStat.computeSpecificity
 (*method*), 7