API Documentation

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1 Script script-GTEvaluator

GTEvaluator workfow. First, run GTEvaluator_matrixMaker then run GTEvaluator_statistic.

Requires:

- python 2.7[1] (tested with 2.7.6)
- Biopython[2]
- scipy[3]
- EMBOSS[4]
- 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 workfow. First, run GTEvaluator_matrixMaker then run GTEvaluator_statistic.

Requires:

- python 2.7[5] (tested with 2.7.6)
- Biopython[6]
- scipy[7]
- EMBOSS[8]
- 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, 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)

---

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 ambigous 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 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

dictionnary 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

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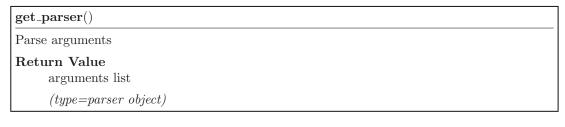
(type=dictionnary)

---

main()

3.2 Variables

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

4   Script script-GTEvaluator_statistic

4.1   Functions

get_parser()
Parse arguments
Return Value
arguments list
(type=parser object)

main()

4.2   Variables

Name	Description
__doc__	**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(*self, Ci_min, Ci_max*)
Compute the sensitivity confidence interval

computeCi_Sp(*self, Ci_min, Ci_max*)
Compute the specificity confidence interval

Inherited from object

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

4.3.2 Properties

Name	Description
Inherited from object	
__class__	

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