API Documentation

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1 Module EveryGO

EveryGO workfow. In order to perform GO-terms enrichment analysis for one or more nodes/comparisons of the phylogeny stored in the XML file.

Requires:

- python 2.7^1 (tested with 2.7.6)
- $lxml^2$
- \bullet GOtrimmer_xml
- GOwalker
- GoView

1.1 Functions

$get_parser()$

Arguments setting and parsing

Return Value

arguments list

 $(type=parser\ object)$

$\mathbf{getcomp}(complist)$

Get comparisons values

Parameters

complist: list of comparisons values (-comp argument)

(type=string)

Return Value

list of comparisons values (-comp argument)

(type=string)

makeuniverse(xmlname)

Make universe of GO-terms from the XML file

Parameters

xmlname: the xml filename

(type=string)

¹https://www.python.org/downloads/

 $^{^2}$ https://github.com/lxml/lxml

Variables Module EveryGO

everygo(compvalues, view, xmlname)

Make enrichment analysis for each comparison values

Parameters

compvalues: comparisons values returned by getcomp()

(type=string)

 $extsf{view}$: -view argument -> if view != 0 , graphical representation of

enrichment will be processed

(type=int)

xmlname: the xml filename

(type=string)

main()

Name	Description
doc	Value:
package	Value: None

Variables Module GOtrimmer

2 Module GOtrimmer

GOtrimmer script. In order to keep prokaryotic terms only in VCFtoGO universe output file, based on GOslim (GO-basic.obo)

Requires:

- $\bullet~$ VCFtoGO output file (GO-terms universe)
- GO-basic.obo file (GOslim)

2.1 Functions

$\mathbf{get} _\mathbf{parser}()$

Arguments setting and parsing

Return Value

arguments list

(type=parser object)

$\mathbf{add_object}(\mathit{d})$

collect prokaryotic terms in GO-basic.obo

Parameters

d: go-term related data collected from GO-basic.obo (type=object data)

main()

Name	Description
doc	Value:
package	Value: None

3 Module GoXML

GoXML workfow. In order to add GO-terms from a XML file and generate a non-enriched universe of GO-terms.

Requires:

- python 2.7^3 (tested with 2.7.6)
- PyVCF⁴
- $lxml^5$
- GOtrimmer xml

3.1 Functions

get_parser()

Arguments setting and parsing

Return Value

arguments list

(type=parser object)

readDBFile(fichier)

Read NP-EBI local storage file

Parameters

fichier: NP-EBI_databases.tsv file

(type=.tsv file)

Return Value

dictionnary of NP identifiers

(type=dictionnary)

${f readDBGOFile}(fichier)$

Read EBI-GO local storage file

Parameters

fichier: EBI-GO_databases.tsv file

(type=.tsv file)

Return Value

dictionnary of GO identifiers

(type=dictionnary)

³https://www.python.org/downloads/

⁴https://github.com/jamescasbon/PyVCF

 $^{^5 \}rm https://github.com/lxml/lxml$

Functions Module GoXML

extractNP(path)

Retrieve NP ids from XML file

Parameters

path: relative path to the XML file

(type=string)

Return Value

dictionnary of NP identifiers

(type=dictionnary)

idmapping(nplist, dicoNP, NPfile)

Make ID mapping from NP identifiers to Uniprot identifiers requesting Online(Uniprot database) of Offline(NP-EBI_databases.tsv)

Parameters

 ${\tt nplist: list used in ONLINE \ request -> values} = {\tt NP \ identifiers}$

(type=list)

dicoNP: dictionnary used in OFFLINE request -> keys = NP identifiers,

values = uniprot id retrieved

(type=dictionnary)

NPfile: Storage of uniprot identifiers to NP identifiers (NP-EBI databases.tsv)

(type=.tsv file)

UNIPROTtoGO(path, output, protlist, dicoGO, GOFile)

Make ID mapping from Uniprot identifiers to GO identifiers requesting Online(Quick-GO database) of Offline(EBI-GO_databases.tsv)

Parameters

path: relative path to the XML file

(type=string)

output: Universe of GO identifiers (univers.txt)

(type=.txt file)

protlist: list used in ONLINE request -> values = UNIPROT identifiers

(type=list)

dicog0: dictionnary used in ONLINE requests -> keys = Uniprot identifiers,

values = GO identifiers list

 $(type{=}dictionnary)$

GOFile: Storage of uniprot identifiers to GO identifiers

(EBI-GO databases.tsv)

(type=.tsv file)

main()

Variables Module GoXML

Name	Description
doc	Arguments settings
	Value:
package	Value: None

4 Module VCFtoGO

VCFtoGO workfow. In order to generate non-enriched universe of GO-terms from a VCF.

Requires:

- python 2.7^6 (tested with 2.7.6)
- \bullet PyVCF⁷
- GOtrimmer

4.1 Functions

get_parser()

Arguments setting and parsing

Return Value

arguments list

(type=parser object)

${f readDBFile}(fichier)$

Read NP-EBI local storage file

Parameters

fichier: NP-EBI_databases.tsv file

(type=.tsv file)

Return Value

dictionnary of NP identifiers

(type=dictionnary)

readDBGOFile(fichier)

Read EBI-GO local storage file

Parameters

 ${\tt fichier: EBI\text{-}GO_databases.tsv~file}$

(type=.tsv file)

Return Value

dictionnary of GO identifiers

(type=dictionnary)

 $^{\ \ \, \}underline{^{6}} https://www.python.org/downloads/$

 $^{^{7} \}rm https://github.com/jamescasbon/PyVCF$

Functions Module VCFtoGO

extractinfopos(fichier, pos)

Parse NP identifiers from VCF file

Parameters

fichier: VCF file

(type=.vcf file)

Return Value

dictionnary of NP identifiers

(type=dictionnary)

idmapping(dico, dicoNP, NPfile)

Make ID mapping from NP identifiers to Uniprot identifiers requesting Online(Uniprot database) of Offline(NP-EBI_databases.tsv)

Parameters

 $\mbox{\tt dictionnary used in ONLINE request $->$ keys = NP$ identifiers , values}$

= uniprot id retrieved

(type=dictionnary)

dicoNP: dictionnary used in OFFLINE request -> keys = NP identifiers,

values = uniprot id retrieved

(type=dictionnary)

NPfile: Storage of uniprot identifiers to NP identifiers (NP-EBI_databases.tsv)

(type=.tsv file)

UNIPROTtoGO(dico, output, pos, dicoGO, GOfile)

Make ID mapping from Uniprot identifiers to GO identifiers requesting Online(Quick-GO database) of Offline(EBI-GO_databases.tsv)

Parameters

dico: dictionnary used in OFFLINE requests -> keys = Uniprot identifiers,

values = GO identifiers list

(type=dictionnary)

output: Universe of GO identifiers (univers.txt)

(type=.txt file)

pos: positions requested if -pos argument was used

(type=int)

dicoGO: dictionnary used in ONLINE requests -> keys = Uniprot identifiers,

values = GO identifiers list

(type=dictionnary)

GOfile: Storage of uniprot identifiers to GO identifiers (EBI-GO_databases.tsv)

(type=.tsv file)

main()

Variables Module VCFtoGO

Name	Description
doc	Value:
package	Value: None

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