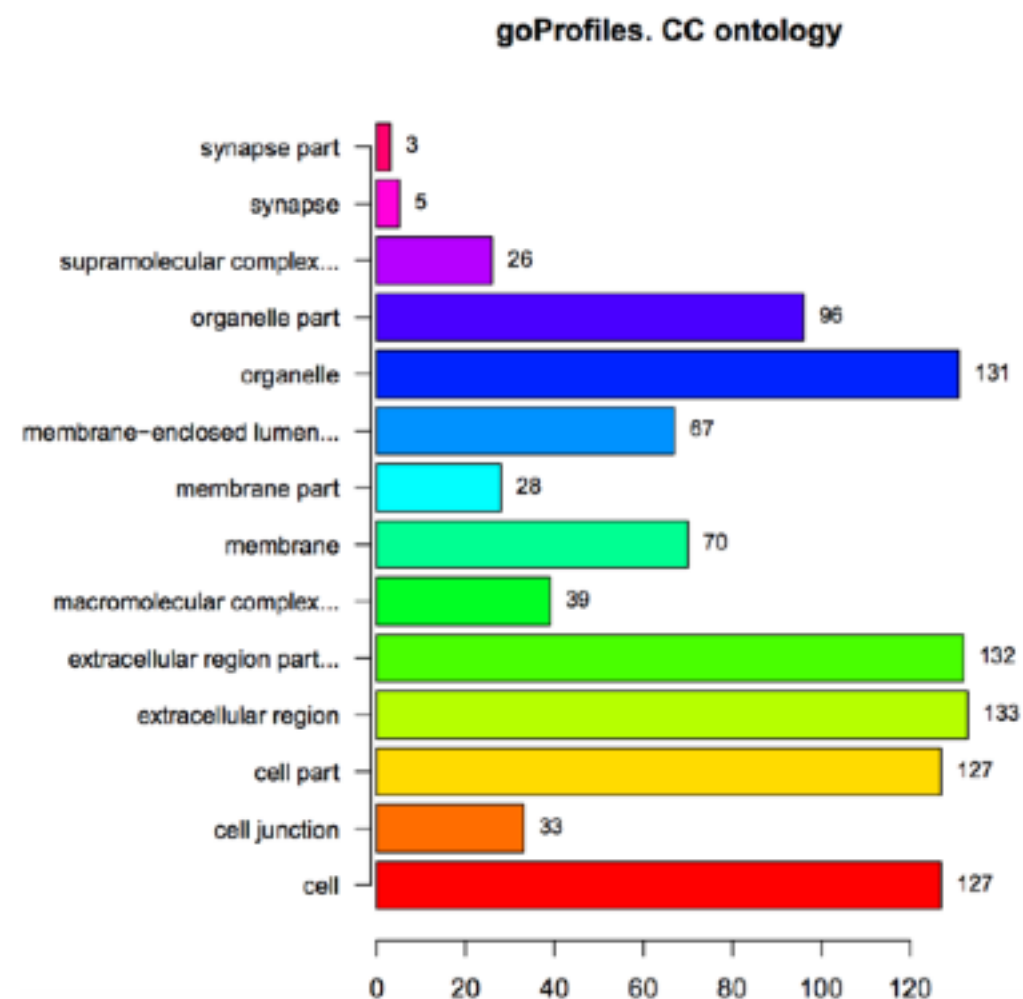


goProfiles

- Results: plot and textual output for each GO categories chosen



1	2	3
CC.Description	CC.GOID	CC.Frequency
cell	GO:0005623	127
cell junction	GO:0030054	33
cell part	GO:0044464	127
extracellular region	GO:0005576	133
extracellular region part	GO:0044421	132
macromolecular complex	GO:0032991	39
membrane	GO:0016020	70
membrane part	GO:0044425	28
membrane-enclosed lumen	GO:0031974	67
organelle	GO:0043226	131
organelle part	GO:0044422	96
supramolecular complex	GO:0099080	26
synapse	GO:0045202	5
synapse part	GO:0044456	3
MF.Description	MF.GOID	MF.Frequency
antioxidant activity	GO:0016209	8
binding	GO:0005488	127
catalytic activity	GO:0003824	60
molecular function regulator	GO:0098772	27
molecular transducer activity	GO:0060089	9
nucleic acid binding transcription factor activity	GO:0001071	1
signal transducer activity	GO:0004871	4
structural molecule activity	GO:0005198	27
transcription factor activity, protein binding	GO:0000988	1
transporter activity	GO:0005215	7

This tool uses R/Bioconductor package goProfiles - Sanchez A, Ocana J and Salicru M (2016). goProfiles: goProfiles: an R package for the statistical analysis of functional profiles. R package version 1.38.0.

topGO enrichment analysis

- Purpose: performing enrichment analysis using R package topGO
- Input: a list of Ensembl Gene IDs

topGO enrichment analysis performs enrichment analysis using R package topGO (Galaxy Version 0.1.0) Options

Select your type of input file

Input file containing your identifiers

The identifiers must be Ensembl gene IDs (e.g : ENSG00000139618). If it is not the case, please use the ID Mapping tool.

Choose an input file

15: GO Profile text output

This file must imperatively have 1 column filled with IDs consistent with the database that will be used. Please use the MappingIDs component if this is not the case.

Please specify the column where you would like to apply the comparison (e.g : Enter c1)

c1

Does your file have a header?

Yes

Select a specie

Human

Ontology category

Biological Process

Choose the topGO option for your analysis

Elim

Enter the p-value threshold level under the form 1e-level wanted (e.g : 1e-3)

1e-3

Choose a correction for multiple testing

Benjamini and Hochberg

History

Rechercher des données

23/01/18
11 shown, 10 deleted, 3 hidden
816.51 KB

15: GO Profile text output

14: GO Profile diagram outputs
a list of datasets

13: Venn diagram text output

12: Venn diagram

11: Mucilli.txt

10: Bredberg.txt

9: Expression levels by tissue (from HPA) on data 4

4: ID Converter on data 2

3: Filter lines by keywords or numerical value on Lacombe et al 2017 OK.txt - Remove