Clue60 v1.5 Get CluePedia Extension! Cluster Analysis Type Single Compare Load Gene Cluster List(s) Homo Sapiens 2 * # Automatic # 3 File 4 Text Field Netw /home/gabi/.cluegoplugin/v1.5/ClueGOFiles/ClueG Choose Cluster ClueGO Settings Select Ontology Evidence Type Name Date 5 Go CellularComponent 23.05.2 GO CellularComponent 23.05.2 GO CellularComponent 23.05.2 So MolecularFunction 23.05.2 Show Ontology Update Options Select Ontology Update Options Select Ontology Update Options Select Ontology Update Options Select Ontology Update Options	
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1, 12 Show Advanced Settings	
ClueGO Functional Analysis	
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Remaining Free Cytoscape Memory	
13 99%	
13 99%	

ClueGO v.1.5 new features

- 1. Get CluePedia plugin
- 2. New organisms were added
- 3. Automatic identification of ids
- 4. Import of ids from text field
- 5. Ontologies were updated
- 6. Ontologies can be created from a term of interest
- 7. All experimental evidence codes can be selected
- 8. Automatic update of Reactome and of IDs
- 9. Automatic download of data sets
- 10. New options for the reference used to calculate stats
- Refinement of the percentage based term selection
 Show only significant terms feature

13. Memory bar showing the free Cytoscape memory

	Show Ontology Update Options Update Ontology / KEGG Annotation Files
8	GO ClueGO Update
	Update
9	Show New Available Downloads Options Download New Example/Additional Files
	Example data sets ClueG0 Repository Download
	Download
	Select Statistical Test Enrichment (Right-sided hypergeometric test)
	Bonferroni step down
10	 Show Advanced Statistical Options Show Advanced Reference Set Options Reference Set Options
	 Selected Ontologies Reference Set Predefined IDs Reference Set Custom Reference Set
	Set Network Specificity
	Global Medium Detailed
	Show Advanced Settings
	GO Term Restriction (GO Tree Levels)
	3 Min Level 8 Max Level
	GO Term Restriction (#/% Genes)
	Cluster #1
	2 Min #Genes 4.11 🔹 %Genes 11
	GO Term Restriction (Significant Only)
12	Show only Terms with pVal>= 0.05

- 8. Automatic update of Reactome and Identifier's Annotation (NCBI)
- 9. Automatic download of example data sets (can be used for CluePedia as well) and of additional files (new annotation files, new identifier lists)

New files are available for download

10. New options for the reference used to calculate stats (Standard: Selected Ontologies).

a) Predefined IDs Reference Set
 ○ Selected Ontologies Reference Set ● Predefined IDs Reference Set △ Affymetrix_GeneChipHT_HG-U133plus_2_ID ○ Custom Reference Set
b) Custom Reference Set
 Selected Ontologies Reference Set Predefined IDs Reference Set

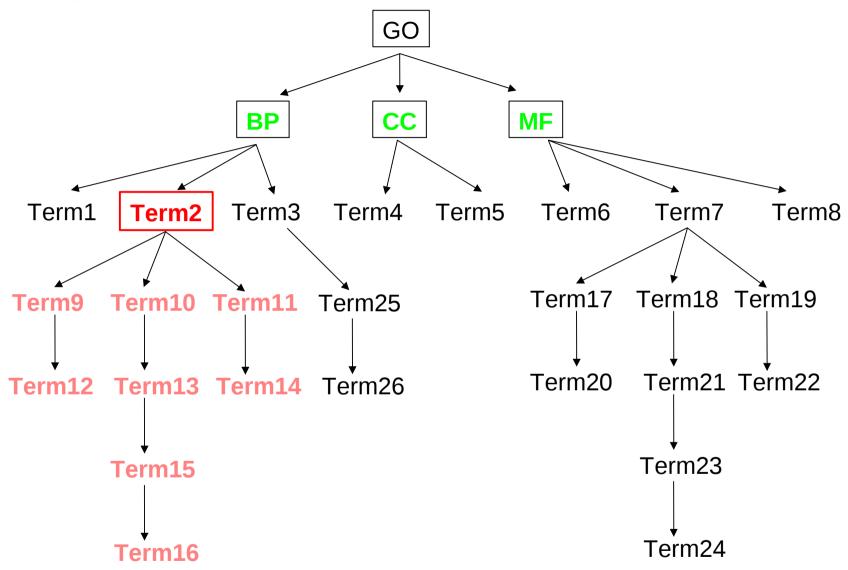
🖲 Custom Reference Set

11. Refinement of percentage based term selection

Choose ...

12. Show only significant terms on the network matching the set threshold.

6. Ontologies created from a term of interest



GO has three parts: Biological Process (BP), Cellular Component (CC) and Molecular Function (MF).

In ClueGO, the user can create a custom ontology, by specifying in the .properties file the GO id and the name of the term of interest (e.g. GO:0002376|ImmuneSystemProcess). This term will be the root of the new ontology. All the children terms will be included. The ontology is created after updating ClueGO ontologies.

10. New options for the reference used to calculate stats (Standard: Selected Ontologies).

The enrichment compares the annotated genes from the list of interest to a reference set. By default, the reference set is the ontology/ontologies used. Other available options are predefined IDs lists (e.g. Affymetrix HG-133plus) or a custom list that can be uploaded by the user. More, in the case of a list1 and list2 comparison analysis, the user can choose to calculate the significance of annotations found for list1 as compared to the second list. The reference set selection influences the enrichment result. Importantly, only functions/terms with at least one gene found in the ontology and in the reference set used will be kept in the initial selection.

