



ViSEAGO: Easier data mining of biological functions organized into clusters using Gene Ontology and semantic similarity

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Visualization, **S**emantic similarity and **E**nrichment **A**nalysis of **G**ene **O**ntology.

R package publicly available on <https://forgemia.inra.fr/umr-boa/viseago>.

Objective:

Data mining of biological functions and establish links between genes

ViSEAGO:

- Allows complex experimental design (multiple comparisons, large datasets)
- Extends classical functional GO analysis to focus on functional coherence
- Provides both a synthetic and detailed view using interactive functionalities respecting the GO graph structure.

State of the art

Comparison of different tools focused on biological interpretation from GO annotation

Tool	Enrichment test	GO terms SS	Sets of GO terms SS	Visualization (focus)	Multiple lists	Graph interactivity
David https://david.ncifcrf.gov/	Fisher Exact (EASE)	No	No	genes	Yes	No
ClusterProfiler Bioconductor	Hypergeometric	IC-based, Graph-based	Yes	genes	Yes	No
gProfiler https://biit.cs.ut.ee/gprofiler/	Hypergeometric	No	No	genes	Yes	No
REVIGO http://revigo.irb.hr/	No	IC-based	No	GO terms	No	Yes
ViSEAGO https://forgemia.inr.fr/umr-boa/viseago	Fisher Exact, Hypergeometric	IC-based, Graph-based	Yes	GO terms	Yes	Yes

Pipeline

GO Annotation of list(s) of features

Annotation database (Ensembl, NCBI, Uniport...)



Enrichment Analysis

TopGO (Fisher-exact test)

	∈ GO term	∉ GO term
∈ list of interest	X	X
∉ list of interest	X	X



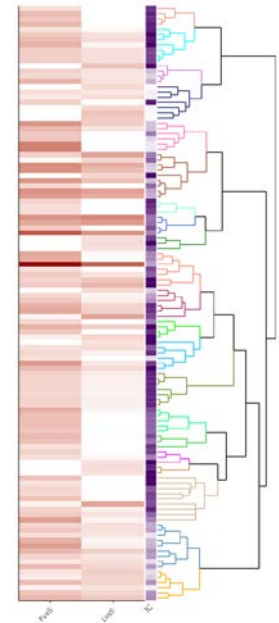
Semantic Similarity & Visualization

Semantic similarity: GOSemSim

Clustering: hclust, dynamicTreeCut

Interactivity: plotly

Wang GO terms distance clustering heatmap plot

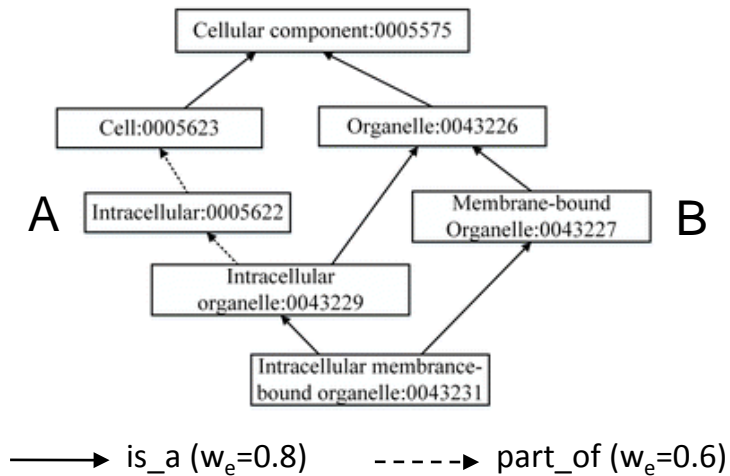


Biological Interpretation

Method: Wang's semantic similarity

Semantic similarity between 2 GO terms

$$S_{GO}(A, B) = ?$$



A	GO terms	A=0005622	0005623	0005575
	Svalue	1	0.6	0.48
B	GO terms	B=0043227	0043226	0005575
	Svalue	1	0.8	0.64

S-value of ancestor GO term (t) related to term A
 contribution of term t to the semantic of term A

$$S_A(A) = 1$$

$$S_A(t) = \max \{w_e \times S_A(t') \mid t' \in \text{children of } (t)\} \text{ if } t \neq A$$

Semantic Value of GO term A, and B

$$SV(A) = \sum_{t \in T_A} S_A(t) \quad SV(A) = 1 + 0.6 + 0.48 = 2.08$$

$$SV(B) = 1 + 0.8 + 0.64 = 2.44$$

Semantic similarity between GO terms A and B

$$S_{GO}(A, B) = \frac{\sum_{t \in T_A \cap T_B} (S_A(t) + S_B(t))}{SV(A) + SV(B)}$$

$$\sum_{t \in T_A \cap T_B} (S_A(t) + S_B(t)) = S_A(0005575) + S_B(0005575) = 0.48 + 0.64$$

$$S_{GO}(A, B) = \frac{1.12}{2.44 + 2.08} = 0.25$$

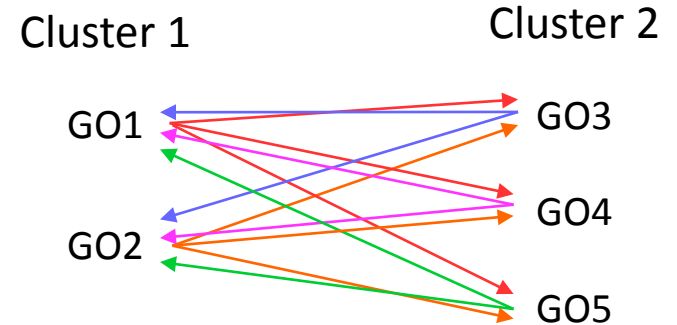
Method: BMA semantic similarity

Semantic similarity between 2 sets of GO terms

Best Match Average (BMA)

$$sim_{BMA}(g_1, g_2) = \frac{\sum_{i=1}^m \max_{1 \leq j \leq n} sim(go_{1i}, go_{2j}) + \sum_{j=1}^n \max_{1 \leq i \leq m} sim(go_{1i}, go_{2j})}{m+n}$$

→ average of all maximum similarities over all pairs of GO terms between two GO term sets



Wang's similarity between two GO terms

		Cluster 1		Cluster 2		
Cluster 1	GO1	x	x	0.3	0.3	0.4
	GO2	x	x	0.2	0.4	0.5
Cluster 2	GO3	0.3	0.2	x	x	x
	GO4	0.3	0.4	x	x	x
	GO5	0.4	0.5	x	x	x

$$sim_{BMA}(\text{cluster1}, \text{cluster2}) = \frac{(0.4+0.5) + (0.3+0.4+0.5)}{2+3} = 0.75$$

Example: Hypomethylation in bull sperm targets specific genomic functions

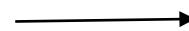
hypomethylated CpGs genomic regions (HR) and their associated functions from MeDIP datasets in bull sperm in comparison to bovine somatic cells (fibroblasts and liver cells)

→ Re-used and re-analyzed Methylated DNA immunoprecipitation (MeDIP) dataset (GSE102960, Perrier J-P, *et al.*, BMC Genomics, 2018).

Gene Sets:

bull sperm in comparison to somatic cells: fibroblast (FvsS) and Liver (LvsS).

Genes from HR with match in regulatory elements

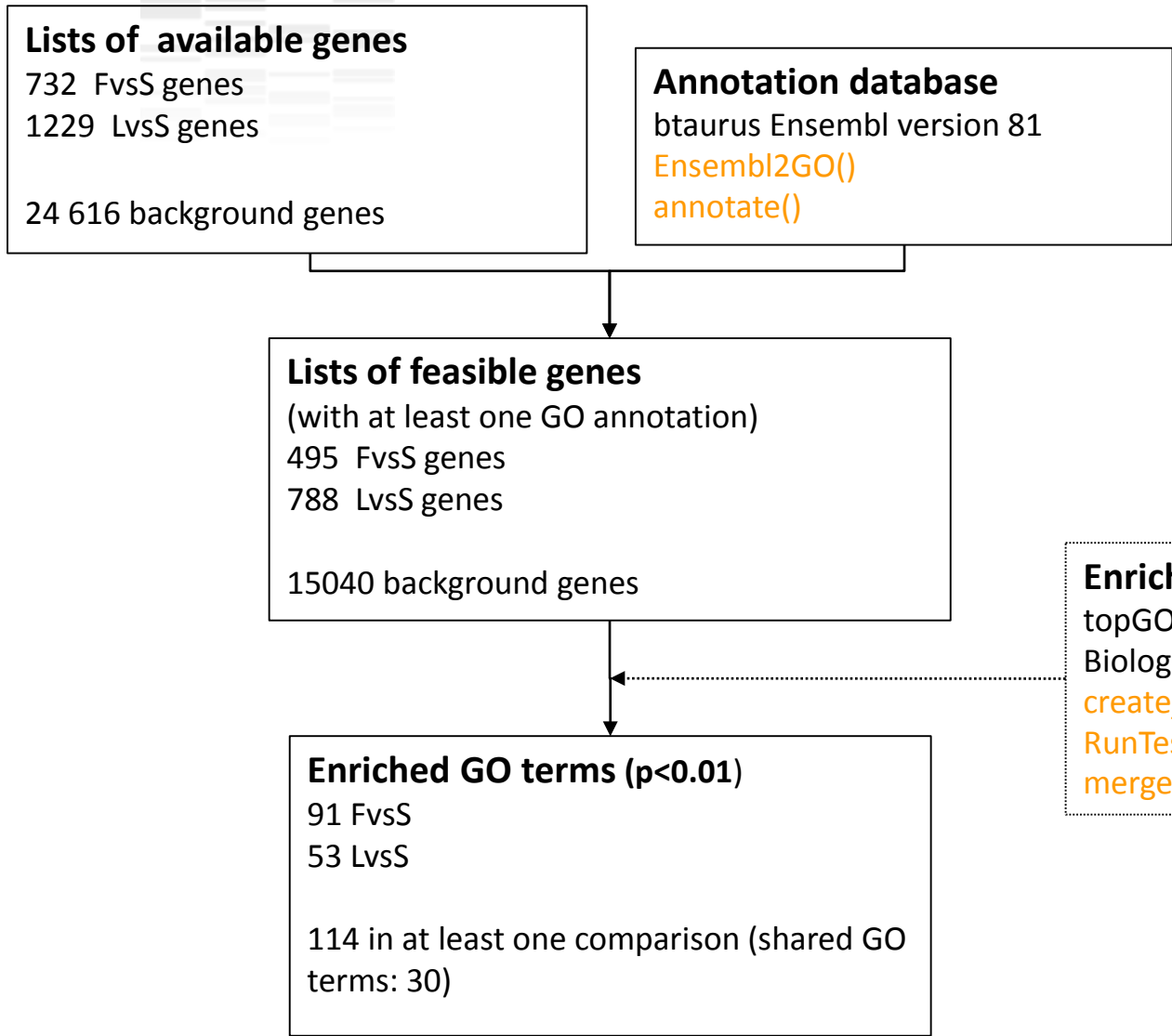


FvsS: 1632 HR, **732** genes
LvsS: 3109 HR, **1229** genes

promoter: -1kb to +0.1 kb along TSS;
downstream: +1kb along TES

background: 24 616 genes

GO annotation and enrichment analysis

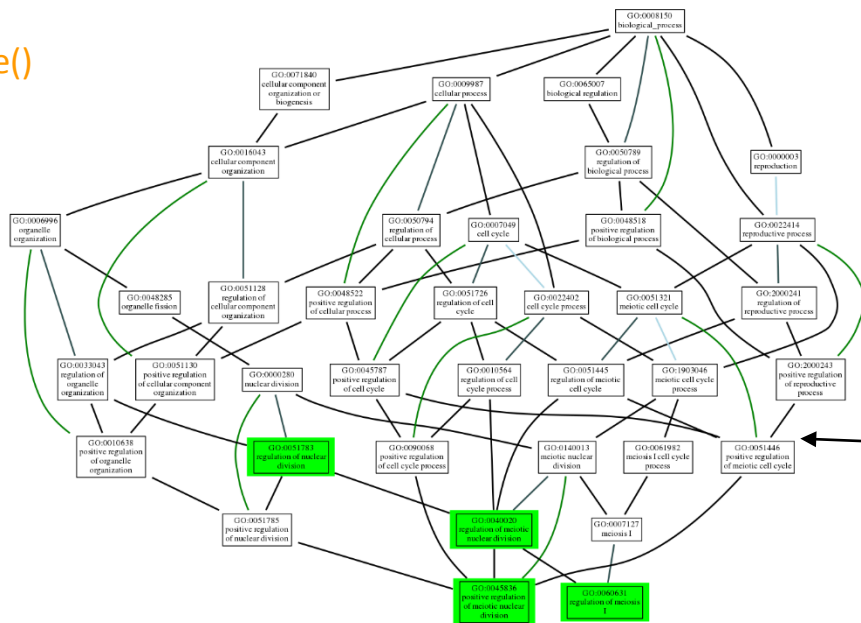


Organized enriched GO terms

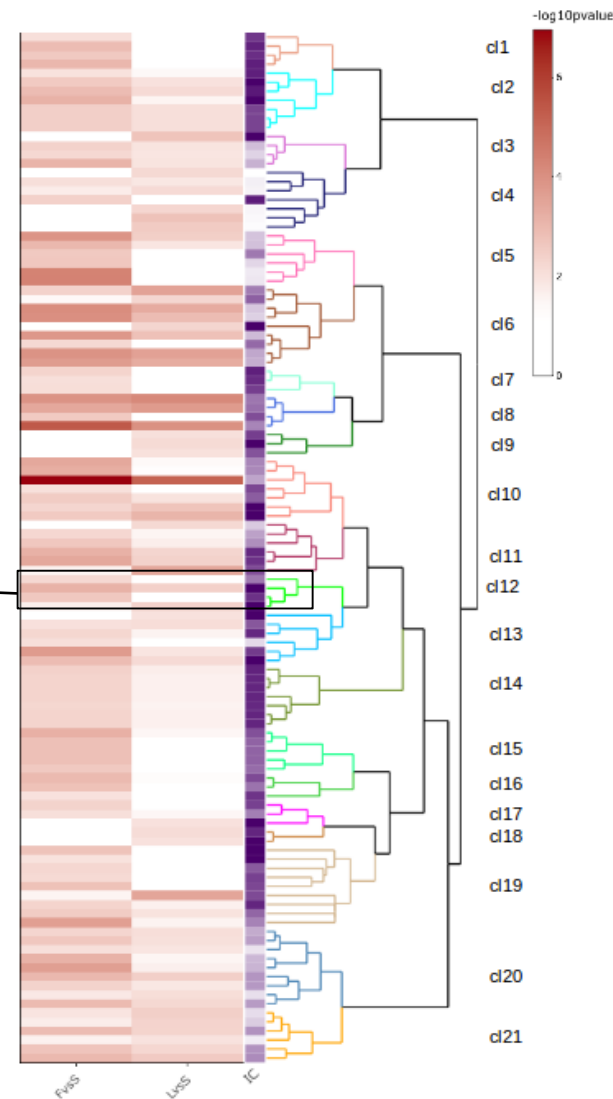
hierarchical clustering on GO terms

Wang's method, *ward.D2* aggregation criterion, dynamically cut

```
build_GO_SS()
compute_SS_distance()
GOterms_heatmap()
show_heatmap()
```



Clustering heatmap plot



Cluster 12 → 4 GO terms

13 genes involved in regulation of nuclear division (meiosis)

MAP9, PIWIL2, ENSBTAG00000005708, LCMT1, PRDM9, ENSBTAG00000024874, ENSBTAG00000035129, ENSBTAG00000035319, DAZL, CALR, UBE2C, MSX1, UBE2B

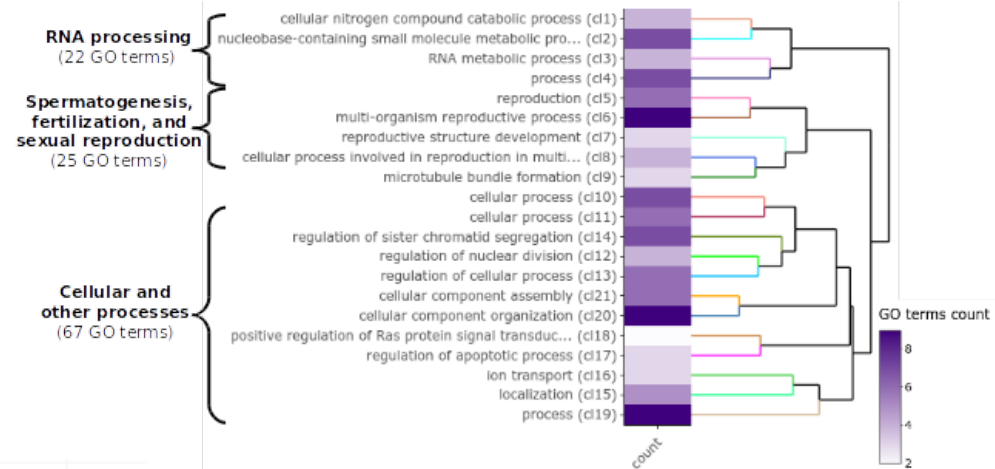
Organized sets of enriched GO terms

Heatmap and MDSplot on sets of GO terms

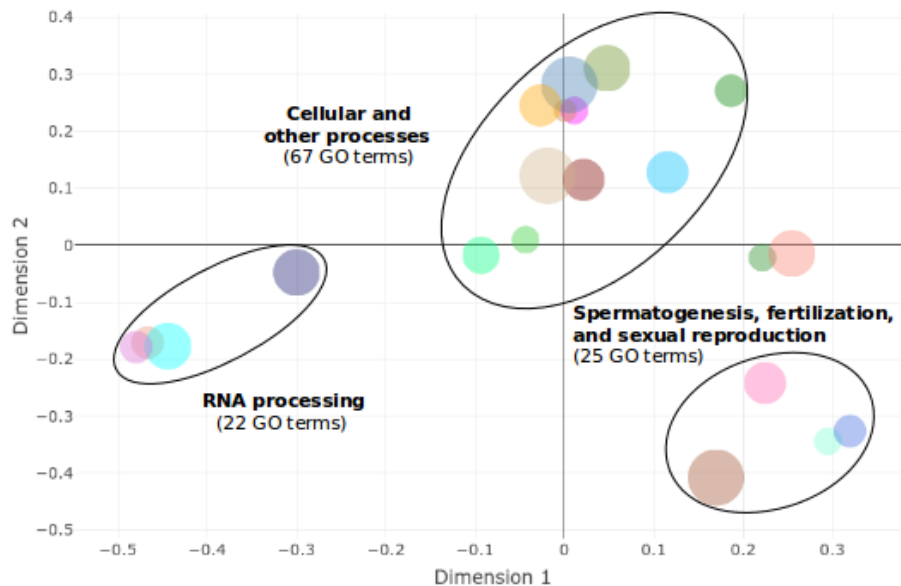
BMA method, *ward.D2* aggregation criterion

```
compute_SS_distance()  
GOclusters_heatmap()  
show_heatmap()  
MDSplot()
```

heatmap plot of functional sets of GO terms



MDS plot of functional sets of GO terms



Conclusion

ViSEAGO: data mining of biological functions using GO terms

→ Semantic similarity and visualization

ViSEAGO's functionalities:

- (1) emphasize functional coherence
- (2) reliability of the functional interpretation
- (3) facilitate biological interpretation

interactive visualization both synthetic and detailed

ViSEAGO helps users to perform a reproducible functional analysis and to prioritize genes to investigate.



Thank you for your attention

Thanks to UMR BOA

Thanks to Perrier J-P, *et al.* (BMC Genomics, 2018) for GSE102960 MeDIP dataset

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