



## GSAn: An alternative to gene set enrichment analysis

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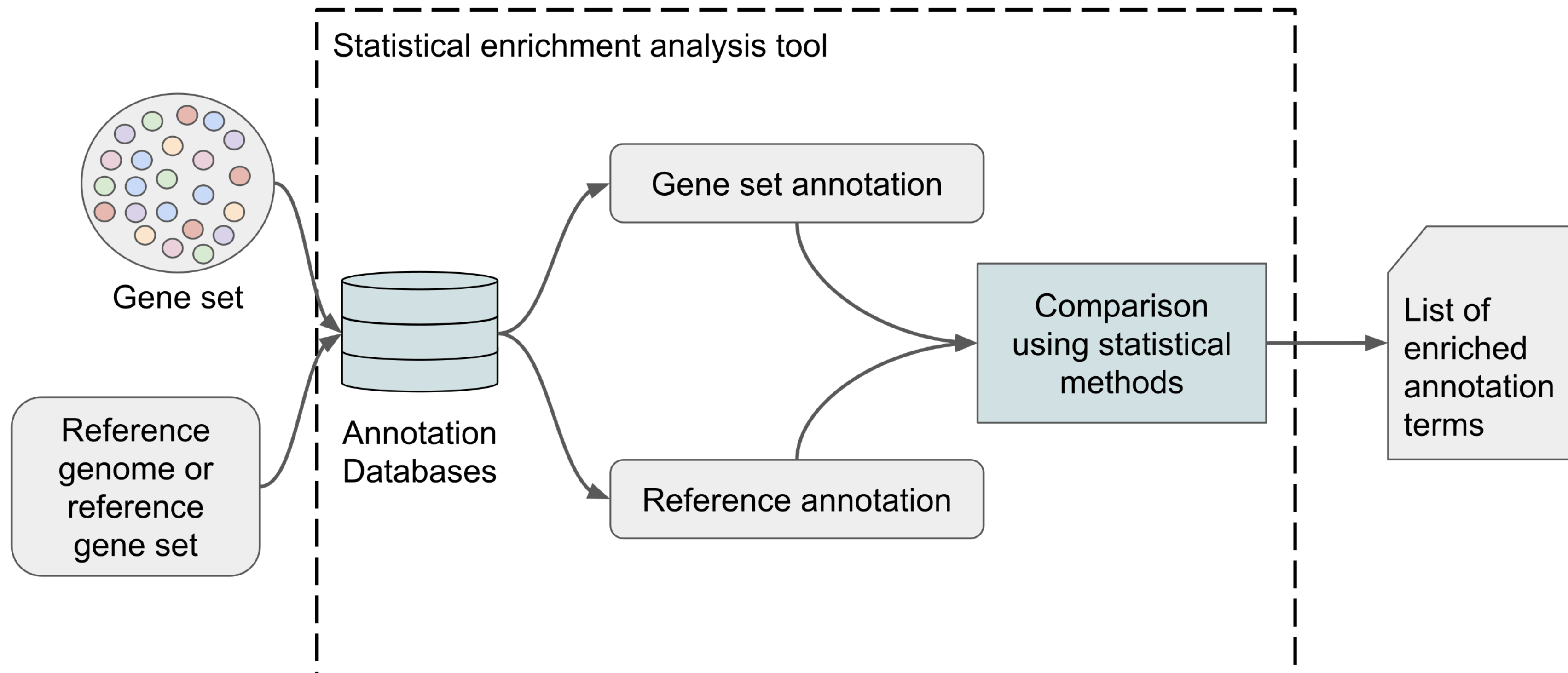
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## 1 - Introduction

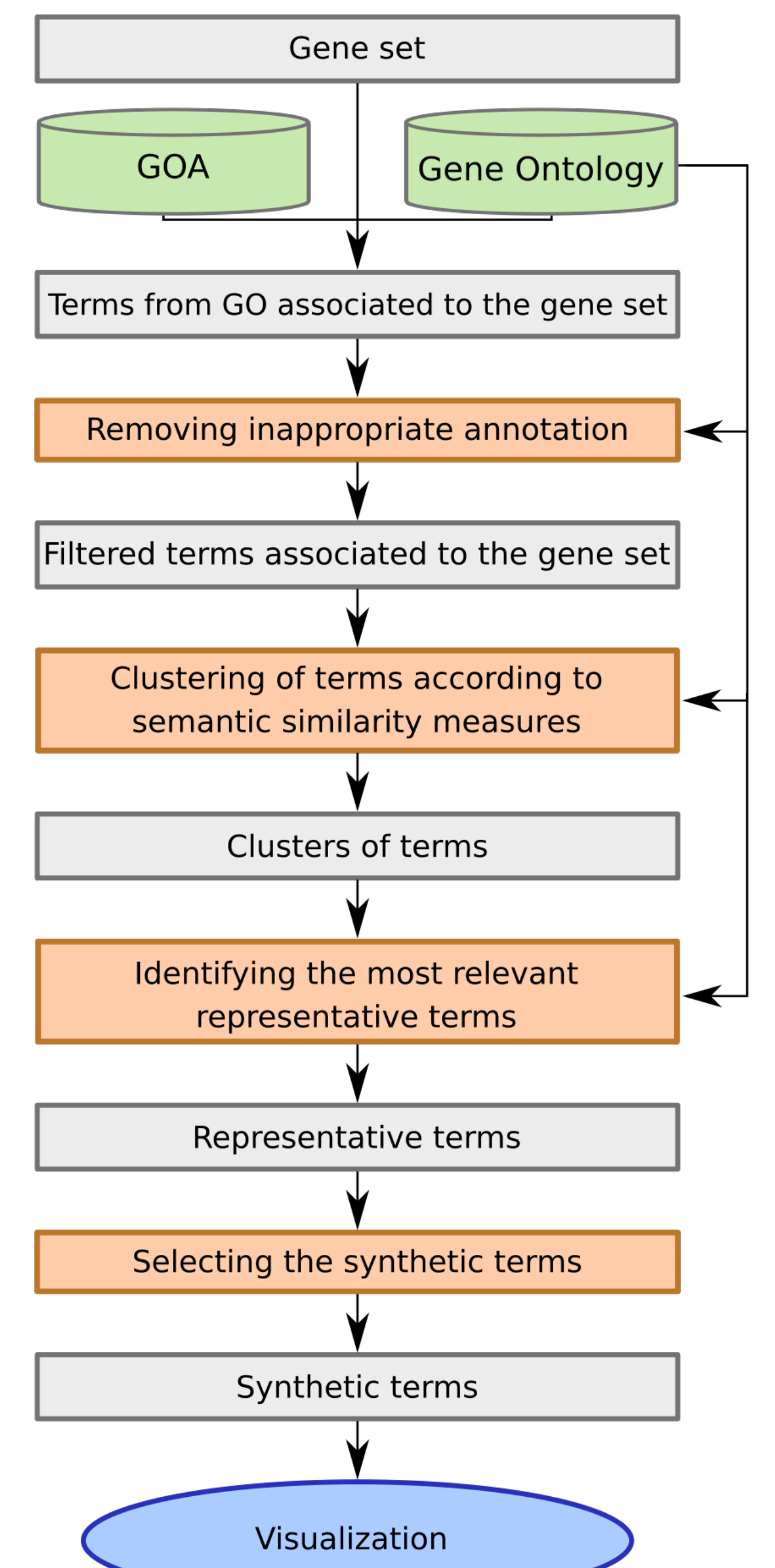
- The revolution in new sequencing technologies has strongly supported the production of omics data to improve our understanding of the relations between genotype and phenotype.
- Analyzing gene sets to identify their biological function and to synthesize the key annotation information aims to help biologists in their interpretation.

## 2 - Statistical enrichment limitations



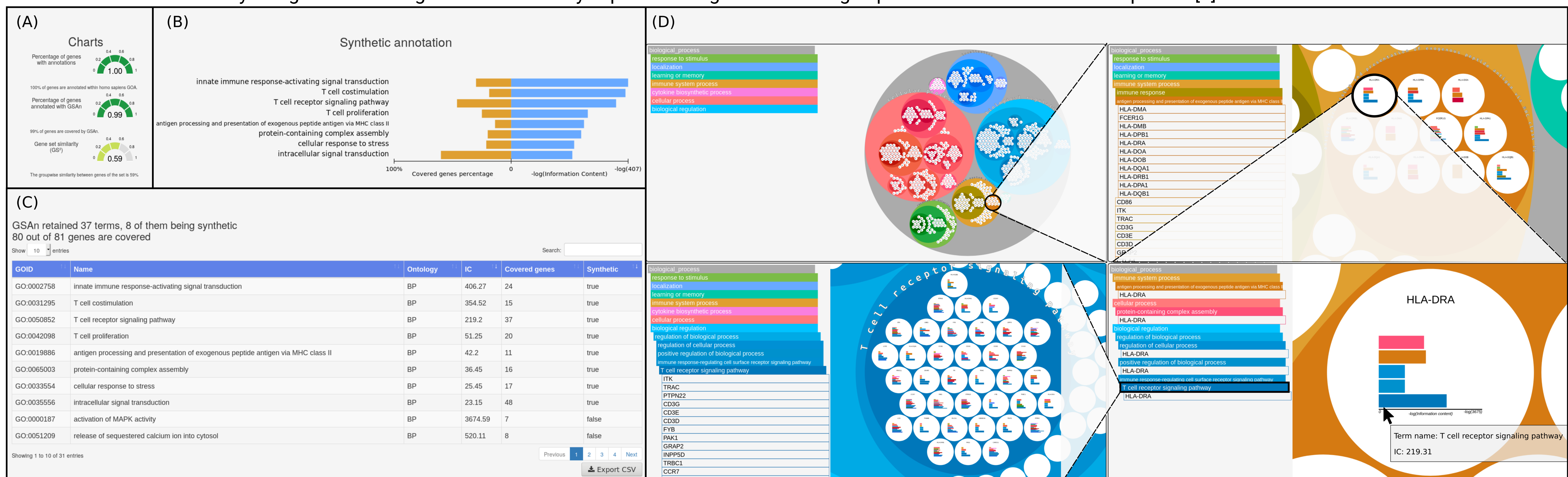
- These statistical methods tend to focus on the most studied genes and provide gene set annotation results that cover a limited number of annotated genes [1, 2, 3].
- Visualization facilities often suffer from a lack of capacity to perform multi-scale analyses which may help users while interpreting their results.

## 3 - Method



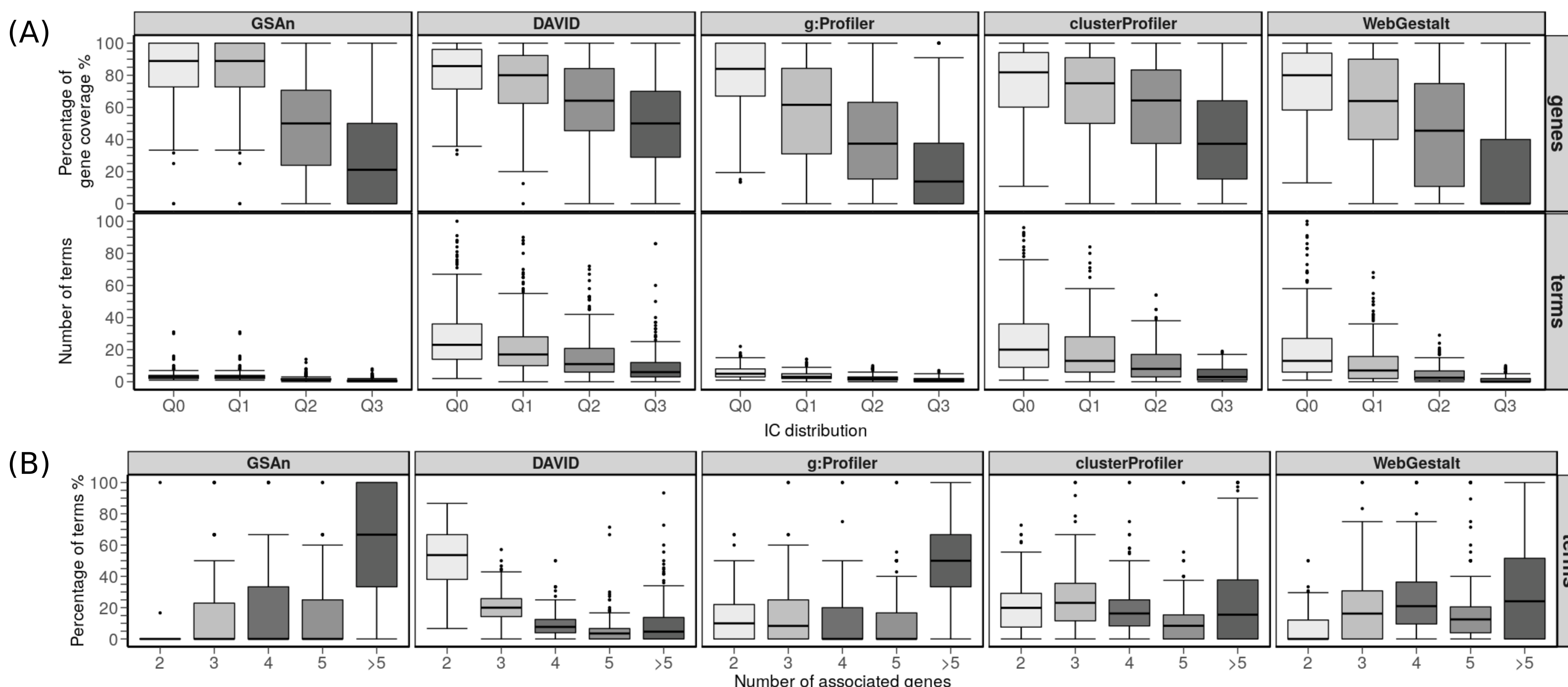
## 4 - GSAN results using an immunological gene set

- We used GSAN to analyze a gene set of 81 genes annotated by experts as “regulation of antigen presentation and immune response” [4].



## 5 - Comparison with other gene set annotation tools

Four enrichment analysis were compared in order to observe their impact in the annotation of gene set by using 346 gene sets provided by [4]. (A) We used four thresholds (from Q0 to Q3) corresponding to the quartiles of the Information Content (IC) distribution (0.0, 18.4, 44.4 and 155.3, respectively) to filter out the results of each tool. Each threshold filters out the terms with an IC below their value. (B) To further investigate this comparison, we analyzed the percentage of terms according to the number of genes that are annotated by these terms (2, 3, 4, 5, and more than 5 genes).



## Availability

GSAN web service is available at <https://gsan.labri.fr>

## References

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- [6] Ayllón-Benítez A. et al. Deciphering gene sets annotations with ontology based visualization. 21st international conference Information Visualization 2017

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