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## Abstract

The main objective of *ViSEAGO* workflow is to carry out a data mining of biological functions and establish links between genes involved in the study. We developed *ViSEAGO* in R to facilitate functional Gene Ontology (GO) analysis of complex experimental design with multiple comparisons of interest. It allows to study large-scale datasets together and visualize GO profiles to capture biological knowledge. The acronym stands for three major concepts of the analysis: *Vi*sualization, *S*emantic similarity and *E*nrichment *A*nalysis of *G*ene *O*ntology. It provides access to the last current GO annotations, which are retrieved from one of NCBI EntrezGene, Ensembl or Uniprot databases for available species. *ViSEAGO* extends classical functional GO analysis to focus on functional coherence by aggregating closely related biological themes while studying multiple datasets at once. It provides both a synthetic and detailed view using interactive functionalities respecting the GO graph structure and ensuring functional coherence supplied by semantic similarity. *ViSEAGO* has been successfully applied on several datasets from different species with a variety of biological questions. Results can be easily shared between bioinformaticians and biologists, enhancing reporting capabilities while maintaining reproducibility.

*ViSEAGO* is publicly available on https://forgemia.inra.fr/umr-boa/viseago.