**GOsummaries: an R package for showing Gene Ontology enrichment results in the context of experimental data**

Raivo Kolde\(^1,2,\ast\), Jaak Vilo\(^1,2\)

1. Institute of Computer Science, University of Tartu, Liivi 2- 314, 50409 Tartu, Estonia
2. Quretec, Ülikooli 6a, 51003 Tartu, Estonia
\ast Contact author: rkolde@gmail.com

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Gene Ontology (GO) enrichment analysis is a common step in analysis pipelines for large genomic datasets. With the help of various visualisation tools, the interpretation of the enrichment results is rather straightforward, when the number of queries is small. However, as the number of queries grows the tools become less effective and it gets harder to gain a good overview of results. We introduce a novel R package **GOsummaries** that visualises the GO enrichment results as concise word clouds. These word clouds can be combined together into one plot in case of multiple queries. By adding also the graphs of corresponding raw experimental data, **GOsummaries** can create informative summary plots for various analyses such as differential expression or clustering. This approach is particularly effective for Principal Component Analysis (PCA). It is possible to annotate the components using GO enrichment analysis and display this information next to the projections to the components. The **GOsummaries** package is available at GitHub (https://github.com/raivokolde/GOsummaries)