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GOsummaries basics Raivo Kolde rkolde@gmail.com

Introduction s:introduction GOsummaries is a package to visualise Gene Ontology (GO) enrichment analysis results on gene lists arising from different analyses such clustering or PCA. The significant GO categories are visualised as word clouds that can be combined with different plots summarising the underlying data.

Elements of a GOsummaries plot s:elements

Figure fig:gs shows an example of plot generated with GOsummaries package. All the GOsummaries plots have more or less the same layout, however, the elements are adjusted corresponding to the underlying analysis. The plot is built of components (Fig fig:gsA) that represent a gene list or a pair of gene lists as in Fig fig:gs. Each component is composed of two parts the word cloud(s) (Fig fig:gsE), representing the GO annotations of the gene lists, and a panel (Fig fig:gsC) that displays the underlying data experimental data. In this case the panel shows the expression values of the corresponding genes. There are also slots for the component title (Fig fig:gsB) and some additional information about the gene lists (Fig fig:gsD).

In the word clouds the sizes of the GO categories indicate the strength of enrichment, relative to the other results of the same query. To make global comparison of the strength of enrichment possible we use different shades of grey.

figure[ht] [width=140mm]GS.pdf Elements of a GO summaries figure fig:gs