Description of output file headers after GO/Pathway Enrichment analysis using ImShot

ID: ID of GO process (BP, MF, CC) or Pathway

Description: Description of GO process/Pathway

GeneRatio: It is the ratio between the number of genes in your input list associated with the given GO term or Pathway (e.g., 5) and the total number of input genes.

BgRatio: It is the ratio between the number of genes in your background list associated with the given GO term or Pathway (e.g., 115) and the total number of background genes.

pvalue: To determine whether any GO/Pathway term annotate a gene list at a frequency greater than that would be expected by chance, p-values are computed using hypergeometric distribution model.

p.adjust: Adjusted pvalue using one the following correction methods: Holm's, Hochberg's, Hommel's, Bonferroni's, Benjamini and Hochberg, Benjamini and Yekutieli, FDR.

qvalue: Alternative approach to calculate FDR/control for multiple testing. The q-value of a test measures the proportion of false positives incurred (called the false discovery rate) when that particular test is called significant.

geneID: Genes from your input list that are found to be enriched in the given GO term/Pathway.

Count: Number of genes from your input list that are found to be enriched in the given GO term/Pathway.