

Input

Gene_ID / ontology annotation / associated variable(s)	Annotation (GO format)
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Test

Hypergeometric Associated var.: binary	Wilcoxon rank Associated var: Floating point	Binomial Associated vars: Two integers	2 x 2 contingency Associated vars: four integers
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Options

Minimum number of genes per category	Top categories (default: biological process, molecular function, cellular component)
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Calculations

1) Sum up gene associated variables per category 2) Perform the chosen test on all selected categories 3) Generate 10,000 sets with permuted gene associated variables 4) Perform the chosen test on all random sets 5) Calculate overall significance by comparing p-value distribution of the data set against the random sets 6) Calculate FDR and FWER per category based on the random sets
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Output

Global p-value, summary statistics Categories with raw p-values
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Refinement

1) Choose raw p-value cut-off 2) Refinement algorithm recursively removes genes contained in significant child categories 3) Generates output table with p-values before and after refinement for each category
