

BioinformaticsLibrary Manual

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plot_PANTHER_enrich

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Description

Generate dotplot from standard PANTHER overenrichment output test file.

Usage

```
plot_PANTHER_enrich(  
    file,  
    title='PANTHER GO Enrichment',  
    total_query_genes=None,  
    sort_by='Name',  
    output_name=None,  
    plot_width=8,  
    plot_height=10)
```

Arguments

file	Standard output .txt file from PANTHER overenrichment test.
title	Name of the figure title to be added to the top of the figure. Default is 'PANTHER GO enrichment'.
total_query_genes	Number of genes used in the GO enrichment query. This input number can be different than the number identified by PANTHER. Accepts integer values. If left blank, it will extract the number provided by the output file.
sort_by	Categories that can be used to sort the row order of the dot plot. Acceptable arguments are: 'Name', 'Pvalue', 'Counts', 'Ratio'.
output_name	Specifies the name of the output file image. The file extension will dictate the file format of the saved image. Acceptable file extensions are '.pdf', '.png', '.svg', '.eps'. If an acceptable file extension is not provided in the file name, a pdf will be generated with a default name and an error message.
plot_width	Species the width of the final image. Accepts integer values. Default is 8.
plot_height	Species the height of the final image. Accepts integer values. Default is 10.

Examples

```
plot_PANTHER_enrich(file='GOenrichment_dgcr_selected.txt',  
                    title='Example Dot Plot',  
                    total_query_genes=218,  
                    sort_by='Ratio',  
                    output_name='DGCR_Selected_Enrichment_Dotplot.png',  
                    plot_width=4,  
                    plot_height=5)
```