# getListGIF module

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## 1 Introduction

`getListGIF` is a utility function to interact with ListGIF web server (`http://listgif.nubic.northwestern.edu`). ListGIF provides a comprehensive analysis solution to identify the overrepresented biomedical concepts from a list of query genes. It combines Tag cloud, Wordle-like graph to present the analysis results to the end-user [1][2]. ListGIF assumes the co-occurring functional annotation terms of many genes from a list can reveal some common features of the genes [2]. The hypergeometric test is performed to identify the enriched Gene Reference Into Function (GeneRIF) and Gene Ontology (GO) terms. To reduce the bias that unbalanced GeneRIF distribution among genes might introduce to the result, both gene level and GeneRIF level analysis are provided. Result is rendered as a "word cloud"-like graph for easy viewing.

## 2 Description

The followings are requirement for input query gene list and arguments of `getListGIF`:

*glist*: This should be a character vector consisting of gene symbols in query

*output*: Optional. User can specify the name and location of the output word cloud png file; otherwise the file name from ListGIF web server is used and the output file is saved in current working directory.

*background*: This argument specifies the background of the output word cloud png file. Only `white` and `black` are supported. Default is `white`.

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*type*: This argument specifies which ListGIF analysis can be performed on the query gene list. User can specify either `genelevel`, `riflevel` or `goterm` enrichment analysis.

- *genelevel*: Gene level enrichment analysis.
- *riflevel*: GeneRIF level enrichment analysis. Warning: this option may take long depending on the length of the query gene list.
- *goterm*: GO term enrichment analysis.

# 3 Example

The following is an example to generate the ListGIF word cloud graph for gene list: MRPS35, NBL1, PSMD14, PGK1, SMC4, SLC16A1 and CAV1.

```
> #glist <- c("MRPS35","NBL1","PSMD14","PGK1","SMC4","SLC16A1","CAV1")
```

To get the graph at gene level (Figure 1):

```
> #getListGIF(glist=glist, output="tmp.png", background="white", type="genelevel")
```

To get the graph at GeneRIF level (note this may take a considerable amount of time on ListGIF web server):

```
> #getListGIF(glist=glist, output="tmp.png", background="white", type="riflevel")
```

To get the graph for enriched GO terms:

```
> #getListGIF(glist=glist, output="tmp.png", background="white", type="goterm")
```

# 4 References

1.Wen, J., Wang X., Kibbe, W., Lin S., Lu, H., "Visual Annotation of the Gene Database", Conf Proc IEEE Eng Med Biol Soc. 2009;2009:4175-7
2.Wen, J., "Visual Annotation of Gene List with Functional Enrichment", MS Thesis, University of Illinois at Chicago (2012) http://hdl.handle.net/10027/9072
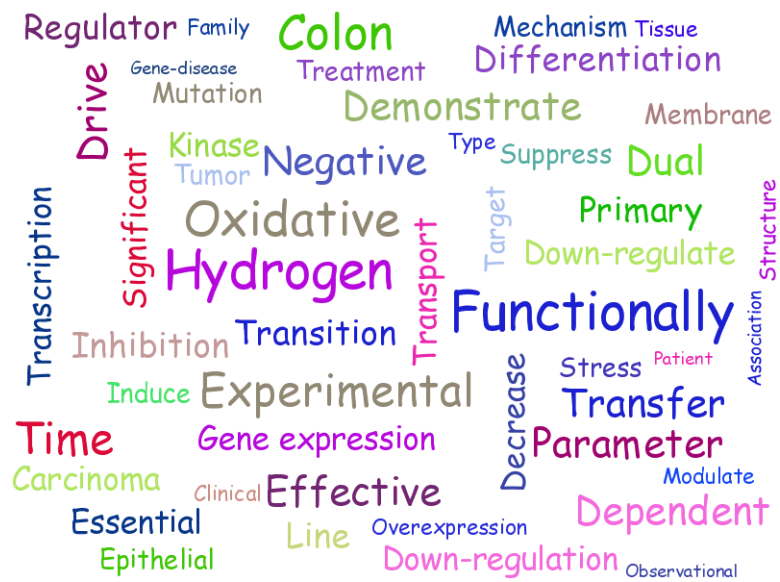
Figure 1: An example of ListGIF word-cloud graph. The query genes are MRPS35, NBL1, PSMD14, PGK1, SMC4, SLC16A1 and CAV1.