

Column1	Column2	Column3	Column4	Column5
Function	Library	databaseUsed	Input (demonstrated examples)	Sample Configuration
<b>Enrich functions</b>				
enricher	clusterProfiler	msigdb/wiki-download/others	vectorOfGenes	enricher(gene, TERM2GENE = wpid2gene, TERM2NAME = wpid2name)
enrichKEGG	clusterProfiler	organism='hsa'	vectorOfGenes	enrichKEGG(gene=gene,organism='hsa',pvalueCutoff=0.05)
enrichMKEGG	clusterProfiler	organism='hsa'	vectorOfGenes	enrichMKEGG(gene = gene,organism = 'hsa')
enrichGO	clusterProfiler	OrgDb=org.Hs.eg.db	vectorOfGenes	enrichGO(gene=gene,universe=names(geneList),OrgDb=org.Hs.eg.db,ont="CC",pAdjustMethod="BH",pvalueCutoff=0.01,qvalueCutoff=0.05,readable=TRUE)
enrichPathway	ReactomePA	automatic	vectorOfGenes	
enrichMeSH	ReactomePA	MeSHDb="Mesh.Hsa.eg.db"	vectorOfGenes	enrichMeSH(de, MeSHDb = ***"MeSH.Hsa.eg.db"**, database='gendoo', category = 'C')
enrichDO	DOSE	ont="DO"	vectorOfGenes	enrichDO(gene=gene,ont="DO",pvalueCutoff=0.05,pAdjustMethod="BH",universe=names(geneList),minGSSize=5,maxGSSize=500,qvalueCutoff=0.05,readable=FALSE)
enrichNCG	DOSE	automatic	vectorOfGenes	
enrichDGN	DOSE	automatic	vectorOfGenes	enrichDGN(gene)
enrichDGNv	DOSE	automatic	vectorOfGenes	enrichDGNv(snp)
groupGO	clusterProfiler	OrgDb=org.Hs.eg.db	vectorOfGenes	groupGO(gene= gene,OrgDb= org.Hs.eg.db,ont="CC",level= 3,universe= names(geneList),readable = TRUE)
<b>GSEA functions</b>				
GSEA	clusterProfiler	msigdb/wiki-download/others	NamedVectorOfFoldchange	GSEA(geneList, TERM2GENE = wpid2gene, TERM2NAME = wpid2name, verbose=FALSE)
gseKEGG	clusterProfiler	organism='hsa'	NamedVectorOfFoldchange	gseKEGG(geneList=geneList,organism='mcc',nPerm=1000,minGSSize=120,pvalueCutoff=0.05,verbose=FALSE)
gseMKEGG	clusterProfiler	organism='hsa'	NamedVectorOfFoldchange	
gseGO	clusterProfiler	OrgDb=org.Hs.eg.db	NamedVectorOfFoldchange	gseGO(geneList=geneList,OrgDb=org.Hs.eg.db,ont="CC",nPerm=1000,minGSSize=100,maxGSSize=500,pvalueCutoff=0.05,verbose=FALSE)
gsePathway	ReactomePA	?	NamedVectorOfFoldchange	
gseMeSH	ReactomePA	MeSHDb="Mesh.Hsa.eg.db"	NamedVectorOfFoldchange	gseMeSH(geneList, MeSHDb = "MeSH.Hsa.eg.db", database = 'gene2pubmed', category = "G")
gseDO	DOSE	ont="DO"	NamedVectorOfFoldchange	gseDO(geneList,nPerm=100,minGSSize=120,pvalueCutoff=0.2,pAdjustMethod="BH",verbose=FALSE)

<b>gseNCG</b>	<b>DOSE</b>	automatic	<b>NamedVectorOfFoldchange</b>	<b>gseNCG(geneList,nPerm=100,minGSSize=120,pvalueCutoff=0.2,pAdjustMethod="BH",verbose=FALSE)</b>
<b>gseDGN</b>	<b>DOSE</b>	automatic	<b>NamedVectorOfFoldchange</b>	<b>gseDGN(geneList,nPerm=100,minGSSize=120,pvalueCutoff=0.2,pAdjustMethod="BH",verbose=FALSE)</b>
<b>Database &amp; ID conversion</b>				
<b>get .gmt files</b>	<b>msigdb</b>	no	<b>species &amp; category</b>	<b>msigdb(species = "Homo sapiens", category = "C2") %&gt;% dplyr::select(gs_name, gene_symbol) or read.gmt("./wikipathways-20200510-gmt- Homo_sapiens.gmt")</b>
<b>bitr</b>	<b>clusterProfiler</b>	no	<b>avector of gene ids</b>	<b>bitr(wpid2gene\$gene,fromType="ENTREZID",toType=c("ENSEMBL","SYMBOL"),OrgDb=org.Hs.eg.db)</b>
<b>Visulization</b>				
<b>barplot</b>	<b>graphics</b>	no	<b>enrichResult</b>	<b>barplot(enricherRes, showCategory=20)</b>
<b>dotplot</b>	<b>enrichplot</b>	no	<b>enrichRseult, gseaResult &amp; compareClusterResult</b>	<b>dotplot(edo2, showCategory=30) + ggtitle("dotplot for GSEA") &amp;&amp; plot_grid(p1, p2, ncol=2)</b>
<b>cnetplot</b>	<b>enrichplot</b>	no	<b>enrichResult</b>	<b>options(repr.plot.width=16, repr.plot.height=24) &amp;&amp; cnetplot(edox, foldChange=geneList, showCategory = 10,colorEdge=TRUE,circular=TRUE, node_label="all")</b>
<b>upsetplot</b>	<b>enrichplot</b>	no	<b>enrichRseult and gseaResult</b>	<b>upsetplot(kk2)</b>
<b>ridgeplot</b>	<b>enrichplot</b>	no	<b>gseaResult</b>	<b>ridgeplot(edo2)</b>
<b>gseaplot</b>	<b>enrichplot</b>	no	<b>gseaResult</b>	<b>gseaplot2(edo2, geneSetID = 2, title = edo2\$Description[2]) # geneSetID are the row number in the edo2 object</b>
<b>multiple category</b>				
<b>compareCluster</b>	<b>clusterProfiler</b>	automatic	<b>list of gene sets/ genes with different factor labels</b>	<b>formula_res &lt;- compareCluster(Entrez~group+othergroup, data=mydf, fun="enrichKEGG"); ck &lt;- compareCluster(geneCluster = gcSample, fun = "enrichKEGG")</b>
<b>emapplot</b>	<b>enrichplot</b>	no	<b>compareClusterResult</b>	<b>options(repr.plot.width=8, repr.plot.height=6) &amp;&amp; emapplot(xx,pie="count", pie_scale=2, layout="kk",legend_n=4)ridgeplot(edo2) # show the fold change of core genes in the GSEA analysis.</b>