How To Use topOnto

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1 Overview

This vignette demonstrates how to easily use the **topOnto** package.

To start with **topOnto** package, type following code below:

```
> library(topOnto)
> help(topOnto)
```

2 Load ontology

```
> topOnto::initWHAT()
> topOnto::initONT('HDO')
```

3 Load Annotation and gene list

```
> a<-system.file("extdata/annotation","human_g2d_omim.txt", package ="topOnto")
> g<-system.file("extdata/genelist","testList", package ="topOnto")
> geneID2GO <- readMappings(file = a)
> geneNames=names(geneID2GO)
> myInterestingGenes=(read.csv(header = FALSE, file = g))$V1
> geneList <- factor(as.integer(geneNames %in% myInterestingGenes))
> names(geneList) <- geneNames
```

4 GSEA

```
> GOdata <- new("topGOdata", ontology = "HDO", allGenes = geneList,annot = annFUN.gen
> resultFis <- runTest(GOdata, algorithm = "classic", statistic = "fisher")
> resultElimFis<- runTest(GOdata, algorithm = "elim", statistic = "fisher")
> allRes <- GenTable(GOdata,  elim = resultElimFis,elim = resultElimFis,topNodes = 30
```