

Single GO term

HBG

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NetBAS calculation based on a single GO term

```
#Read the network
network <- read.csv("../Data/human.pin.csv", colClasses = c("character", "character"))
names(network) = c("geneA", "geneB")
geneA <- network$geneA
geneB <- network$geneB
go.category <- c("GO:0005049") #a single GO term

go.file <- read.csv("../Data/human.all.go.csv", header=T, stringsAsFactors=F)
go.orf <- go.file$gene
go.id <- go.file$goid
genes.list <- go.orf[which(go.id %in% go.category)]

panc.file <- read.csv("../rnf43.csv",header=TRUE,stringsAsFactors=F)
panc.gene <- panc.file$gene
panc.z <- panc.file$zPanc_vs_other

gene.list <- panc.gene[which(panc.z > 2)]
background.list <- panc.gene[which(panc.z <=2)]
glA <- geneB[which(geneA %in% gene.list)]
glB <- geneA[which(geneB %in% gene.list)]
gl.all <- c(glA, glB)

bgA <- geneB[which(geneA %in% background.list)]
bgB <- geneA[which(geneB %in% background.list)]
bg.all <- c(bgA, bgB)

gl.count <- length(which(gl.all %in% genes.list))
#bg.count <- length(which(bg.all %in% genes.list))

gl.perm.count <- c()

for (p in 1:100) {
permutation.file <- paste("../ms02star/human/", "ms02.", p, ".csv", sep="")
permutation <- read.csv(permutation.file, header=T, stringsAsFactors = F)
geneA <- permutation$id1
geneB <- permutation$id2

gl.perm.A <- geneB[which(geneA %in% gene.list)]
gl.perm.B <- geneA[which(geneB %in% gene.list)]
gl.perm.all <- c(gl.perm.A, gl.perm.B)
gl.count.2 <- length(which(gl.perm.all %in% genes.list))
gl.perm.count <- rbind(gl.perm.count, gl.count.2)
}
```

```
z <- (gl.count - mean(gl.perm.count))/sd(gl.perm.count)
z
```

```
## [1] 0.3627597
```