The GSEA usage by examples

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1 Introduction

The GSEA package is generated for CCBR.

A quick way to load the vignette examples is:

```
vignette("GSEA")
```

2 do GSEA

2.1 db

The `db`

2.2 gene

```
options(stringsAsFactors = FALSE);
library(GSEA);
library(multtest);

data("TCGA.BC.cnv.2k.60", package = "OmicCircos");
gene <- as.character(TCGA.BC.cnv.2k.60[,3]);
out  <- doGSEA(db="GO", gene=gene);
write.table(out, "GO_GSEA_out.xls", quote=F, sep="\t", row.names=F);
```