# Using MLP

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# 2 Example Use

## 2.1 Preliminaries

```
> require(MLP)
> require(limma)
> pathExampleData <- system.file("exampleFiles", "expressionSetGcrma.rda",
+ package = "MLP")
> load(pathExampleData)
```

## 2.2 Prepare P Values

```
> group <- as.numeric(factor(pData(expressionSetGcrma)$subGroup1,
+ levels = c("WT", "KO"))) - 1
> design <- model.matrix(~group)
> fit <- lmFit(exprs(expressionSetGcrma), design)
> fit2 <- eBayes(fit)
> results <- limma:::topTable(fit2, coef = "group", adjust.method = "fdr",
+ number = Inf)
> pvalues <- results[, "P.Value"]
> names(pvalues) <- results$ID
> names(pvalues) <- sub("_at", "", names(pvalues))</pre>
```

## 2.3 Prepare Gene Sets

```
> geneSets <- getGeneSets(species = "Mouse", pathwaySource = "GOCC",
+ eset = expressionSetGcrma)</pre>
```

### 2.4 Run MLP

```
> mlpOut <- MLP(geneSet = geneSets, geneStatistic = pvalues, minGenes = 5,
+ maxGenes = 100, rowPermutations = TRUE, nPermutations = 50,
+ smoothPValues = TRUE, criticalValues = c(0.5, 0.9, 0.95,
+ 0.99, 0.999, 0.9999, 0.9999), df = 9)</pre>
```

#### 2.5 Visualize MLP Results

Three different types of plots are made available. The type of the plot is indicated with the type argument which can be one of

```
plot(., type = "quantileCurves")
   plot(., type = "barplot")
   plot(., type = "GOgraph")
> pdf("mlpQuantileCurves.pdf", width = 10, height = 10)
> plot(mlpOut, type = "quantileCurves")
> dev.off()
null device
> pdf("mlpBarplot.pdf", width = 10, height = 10)
> op <- par(mar = c(30, 10, 6, 2))
> plot(mlpOut, type = "barplot")
> par(op)
> dev.off()
null device
> pdf("mlpGOgraph.pdf", width = 20, height = 6)
> op <- par(mar = c(2, 1, 0, 2))
> plot(mlpOut, type = "GOgraph", nRow = 30, mainTitle = "GO graph")
> par(op)
> dev.off()
null device
```

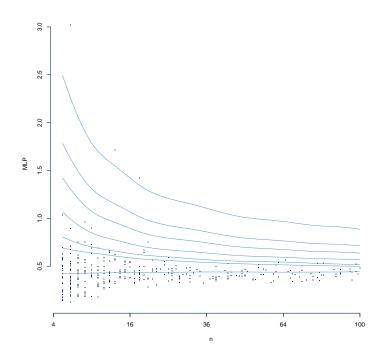


Figure 1: Example of the quantile curves for the MLP run  $\,$ 

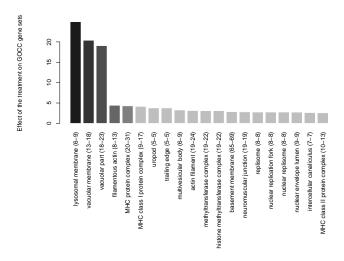


Figure 2: Example of a barplot for MLP results

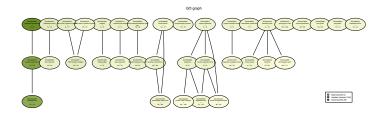


Figure 3: Example of a GOgraph for MLP results