

Annotation with DAVID

BST 226

Statistical Methods for

Bioinformatics

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DAVID Bioinformatics Resources

- Provides tools for functional annotation including enrichment and gene classification
- Easy to use
- Free
- Nature Protocols paper describing the methods is available and on the website
- <http://david.abcc.ncifcrf.gov/>

```
require(affy)
require(LMGene)
rrdata <- ReadAffy()
eset <- rma(rrdata)
group <- as.factor(c(0,0,1,1,2,2,3,3,4,4,5,5))
vlist <- list(group=group)
eset.lmg <- neweS(exprs(eset),vlist)
pv1 <- genediff(eset.lmg)
gene.background <- featureNames(eset)
sig.genes <- gene.background[pv1$Gene.Specific < .05]
write(sig.genes, "sig.genes.txt")
write(gene.background, "gene.background.txt")
```

Using DAVID

- Upload list of significant probes
- Identify type of identifier
- Identify species
- Upload list of background probes, which is all the probes on the array
- Use tools