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### --- BIOINFORMATICS TRAINING SCHOOL (EuGESMA) --- ###  
### --- 23-24 Marzo 2010 - Barcelona - Spain --- ###
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# 2nd SESSION:  
# Microarray data analysis:  
analysis of exon arrays and miRNA arrays; mapping of different RNAs to the genome  
landscape.  
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# See WEB SITE: GATEplorer  
# http://bioinfow.dep.usal.es/xgate/
```

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### ANALYSIS OF EXON MICROARRAYS FROM Affymetrix (HUMAN_EXON_1.0) TO FIND GENES ###  
# Example of how to install a CDF package (in LINUX command line):  
cd ../exon-arrays_protocol/Data_PackagesANNOT  
R CMD INSTALL genemapperhumanexon1.0cdf_2.0.tar.gz
```

```
# Load libraries  
library(affy)  
library(siggenes)
```

```
# Set directory  
setwd("../exon-arrays_protocol")
```

```
# Load annotation package taken from GATEplorer  
load('Data_PackagesANNOT/genes-human-annotation.R')
```

```
# Read and normalization of samples  
setwd('Data_CELs')  
rma <- justRMA(cdfname="genemapperhumanexon1.0cdf")  
exprs <- exprs(rma)
```

```
# Differential expression using SAM algorithm  
diffExp <-  
sam(exprs,c(0,0,0,1,1,1),method=d.stat,var.equal=FALSE,na.method="median",rand=123)
```

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diffExp  
plot(diffExp)  
plot(diffExp,2.4)  
sigGenes <- summary(diffExp,2.4)@mat.sig
```

```
# Annotation  
annotGenes <- genes.human.Annotation[rownames(sigGenes),]  
annotGenes <- cbind(sigGenes[c("d.value","stdev","rawp","q.value","R.fold")],annotGenes)
```

```
# Export to file  
setwd("../exon-arrays_protocol")  
write.table(annotGenes,quote=FALSE,sep='\t',row.names=FALSE,file='gene_list.tsv')
```

```
### ANALYSIS OF EXON MICROARRAYS FROM Affymetrix (HUMAN_EXON_1.0) TO FIND ncRNAs ###  
  
# ncRNA  
setwd('../exon-arrays_protocol/Data_CELs')  
rma.ncRNA <- justRMA(cdfname="ncrnamapperhumanexon1.0cdf")  
exprs.ncRNA <- exprs(rma.ncRNA)  
  
# differential expression using SAM algorithm  
diffExp.ncRNA <-  
sam(exprs.ncRNA,c(0,0,0,1,1,1),method=d.stat,var.equal=FALSE,na.method="median",rand=123  
)  
  
diffExp.ncRNA  
plot(diffExp.ncRNA)  
plot(diffExp.ncRNA,12)  
sigGenes.ncRNA <- summary(diffExp.ncRNA,12)@mat.sig  
  
sigGenes.ncRNA <- cbind(rownames(sigGenes.ncRNA),sigGenes.ncRNA)  
  
# export to file  
setwd("../exon-arrays_protocol")  
write.table(sigGenes.ncRNA,quote=FALSE,sep='\t',row.names=FALSE,file='ncRNA_list.tsv')
```