

Differential expression analysis with SAM			
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Differential expression analysis with SAM

Response Type

Quantitative response: is a real-valued response, such as blood pressure.

Two class (unpaired): two set of measurements (i.e.: control-treated), in which the experiments units are different in the two groups (different individuals in the two groups).

Multiclass: more than two set of measurements, each one with different experiments units. It's a generalization of two class unpaired to more than two groups.

Two class (paired): same experimental unit used in both sets of measurements. Survival data: consists of a time until an event (i.e.: death).

One class: used to test whether the mean gene expression differs from zero. Each measurement might be a red/green intensity ratio.

Time course: each experimental unit is measured at more than one time point.

Pattern discovery: ...

SAM analysis with siggenes

Start R and load siggenes package:

```
library(siggenes)
datatable = read.table('data.csv', sep = '\\t')
data = datatable[,2:7]
cl = c(rep(1,6))
genenames = datatable[,1]
sam.out <- sam(data = data, cl = cl, gene.names=genenames)
```

To obtain a delta plot:

```
plot(sam.out, 0.3)
```

To obtain a summary table:

```
summary(sam.out)
```

to write an excel file with a list of significant genes:

```
sam2excel(sam.out, delta=0.3, 'significant.csv')
```

Sam analysis with samr

Two class unpaired analysis example:

```
y <- c(1,1,2,2)
x <- as.matrix(data[,3:6])
```

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```

genenames <- as.character(data[,1])
geneids <- as.character(data[,2])
data <- list(x=x,y=y,geneids=geneids,genenames=genenames,logged2=TRUE)
samr.obj <- samr(data,resp.type="Two class unpaired",nperms=100)
delta.table <- samr.compute.delta.table(samr.obj)
samresult = list(data=data,samr.obj=samr.obj,delta.table=delta.table)

```

Delta plot generation:

```

plot(samresult$delta.table[,1],samresult$delta.table[,
5],lab=c(20,20,7),main="deltaplot",xlab="delta",ylab="fdr")

```

Sam plot generation:

```

samr.plot(samresult$samr.obj,delta)

```

Siggenes table computation:

```

siggenes.table<-samr.compute.siggenes.table(samresult$samr.obj,delta, samresult
$data, samresult$delta.table)

```

Version history

Version	Tracking of changes	Name	Date
0.1	Initial version	Alberto	March 31, 2007
0.2	Added section on analysis with samr	Alberto	November 3, 2007