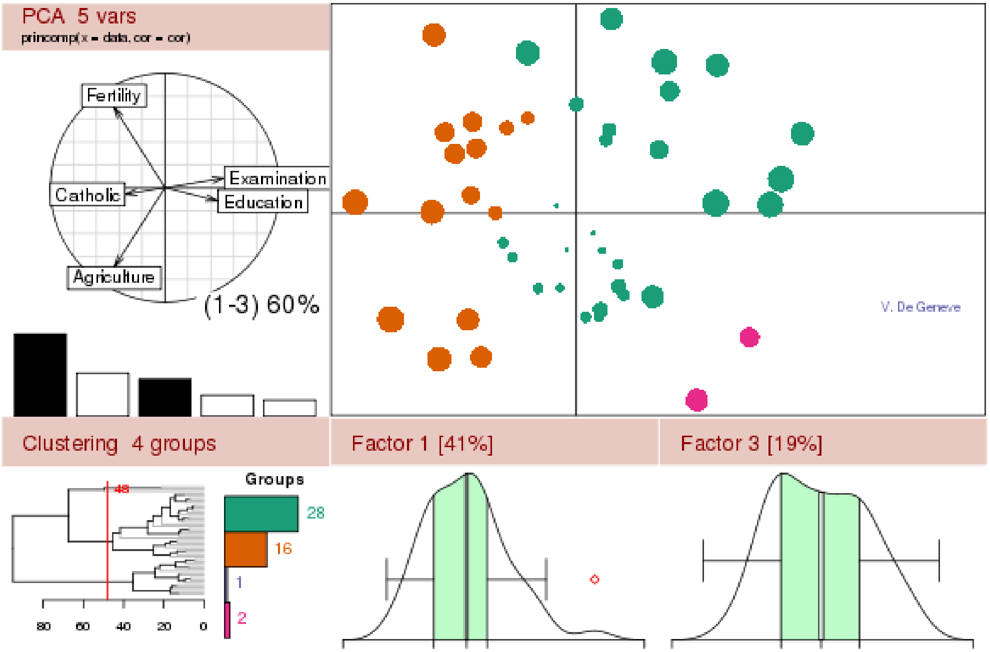
Zpracování microarray dat pomocí programů R a Bioconductor

www.r-project.org



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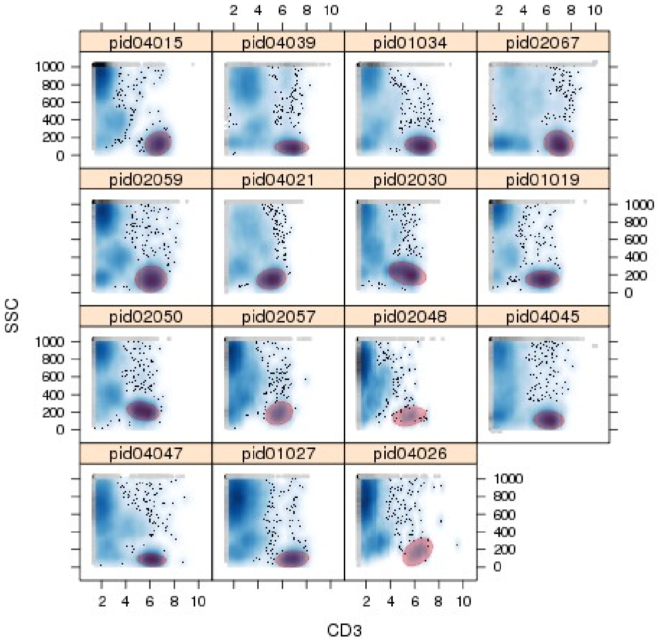
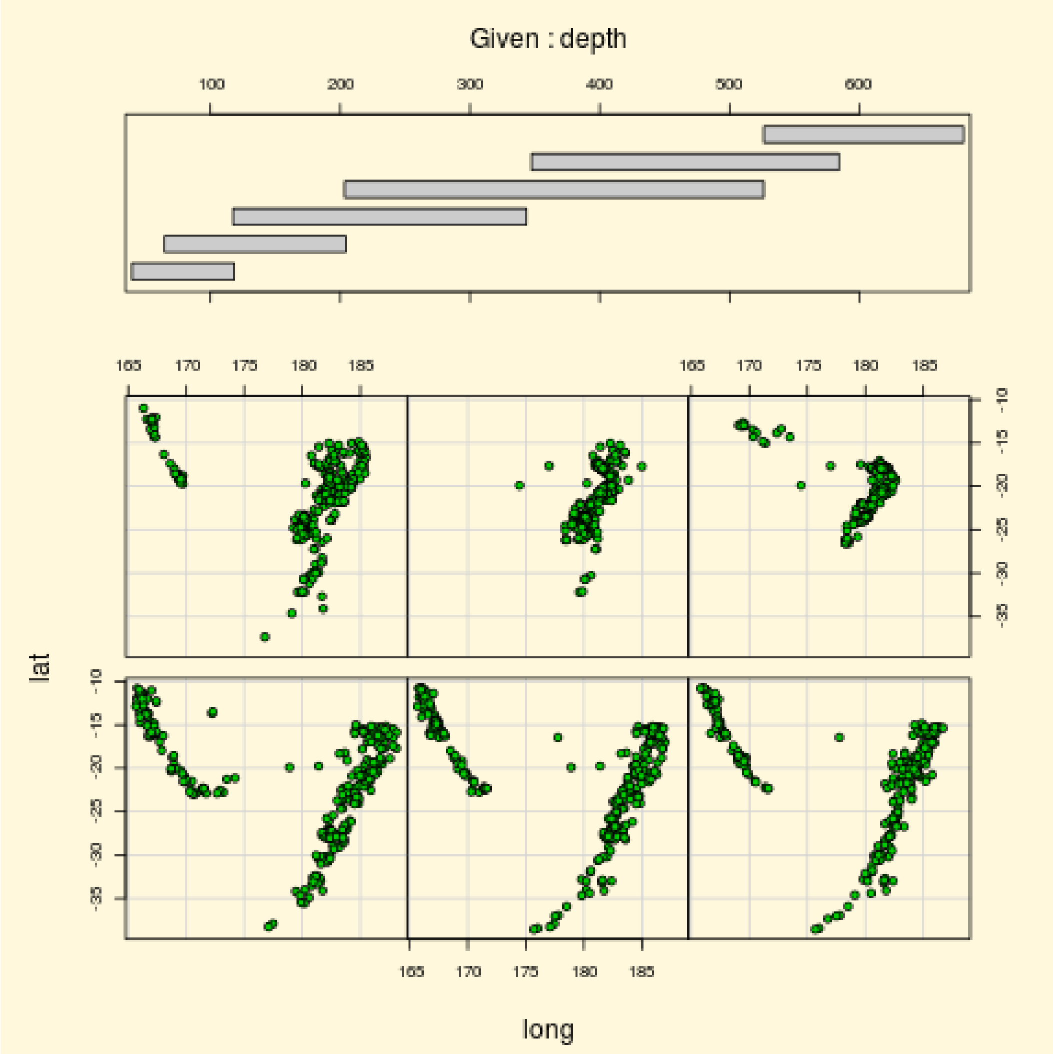
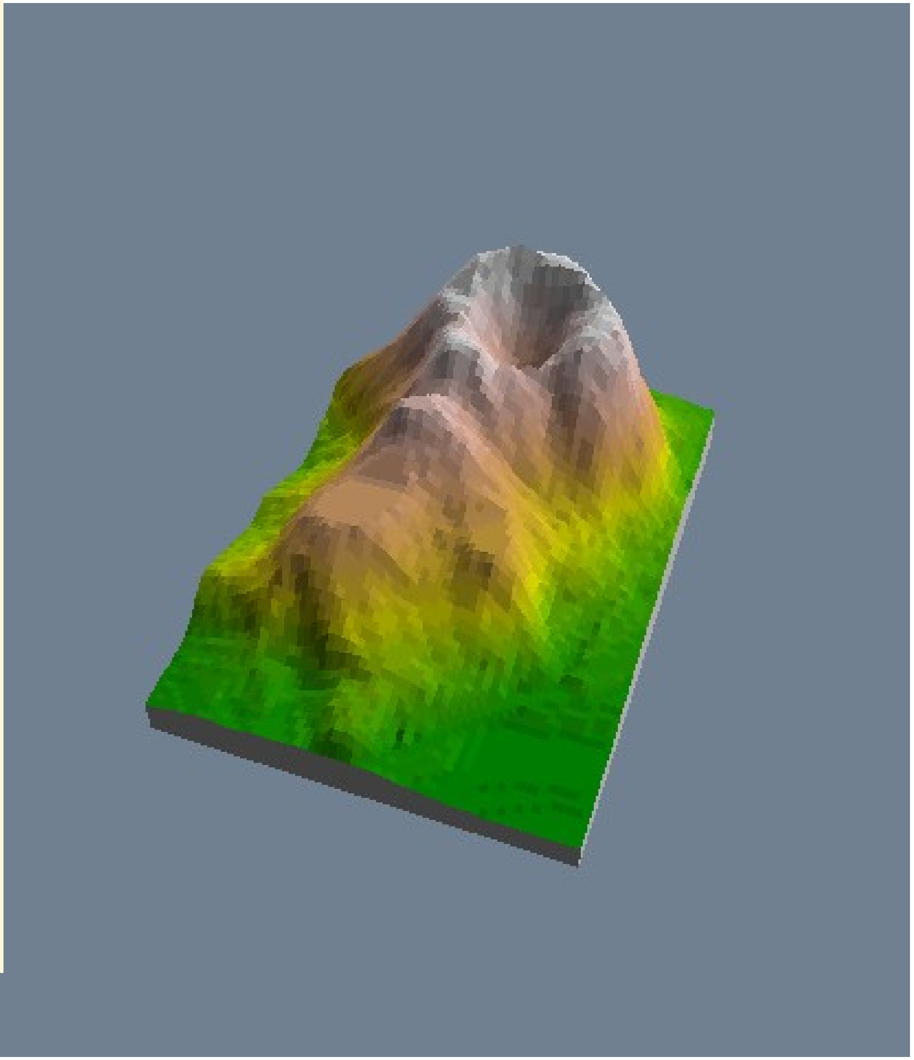


```
> 1 + 1
[1] 2
> x <- 1
> x
[1] 1
> x <- c(1, 2, 5)
> x
[1] 1 2 5
> x <- 1:10
> x
 [1]  1  2  3  4  5  6  7  8  9 10
> x <- 1:10*2
> x
 [1]  2  4  6  8 10 12 14 16 18 20
>
```

```
> demo(graphics)
...
> demo(persp)
...
```





Public on Oct 31, 2010
Title 0.6% Methamphetamine feeding experiments
Organism Drosophila melanogaster
Experiment type Expression profiling by array
Summary Methamphetamine can trigger dopamine releasing in human brain, now used as abuse drug. Some studies have shown that specific genes and proteins responded to, methamphetamine, but little is known about the overall “omic” response of organisms to this illicit substance. Here we demonstrate that Drosophila melanogaster has the potential to give us significant insights into evolutionarily conserved responses to methamphetamine. We performed metabolome, proteome, and transciptome profiling with Drosophila treated with methamphetamine. The proteomic profiling revealed responses associated with known physiological problems that occur with methamphetamine usage in mammals. The metabolomic result showed that the metabolite trehalose was decreased significantly after methamphetamine exposure, suggesting an oxidative stress response to this drug. Many of the differential transcribed genes, including detoxification enzymes, had the potential transcription factor-binding motif YY1 associated with their upstream regulatory regions. YY1 is known to be responsive to amphetamines in mammals.

GSM406533.CEL GSM406534.CEL GSM406535.CEL
GSM406536.CEL GSM406537.CEL GSM406538.CEL

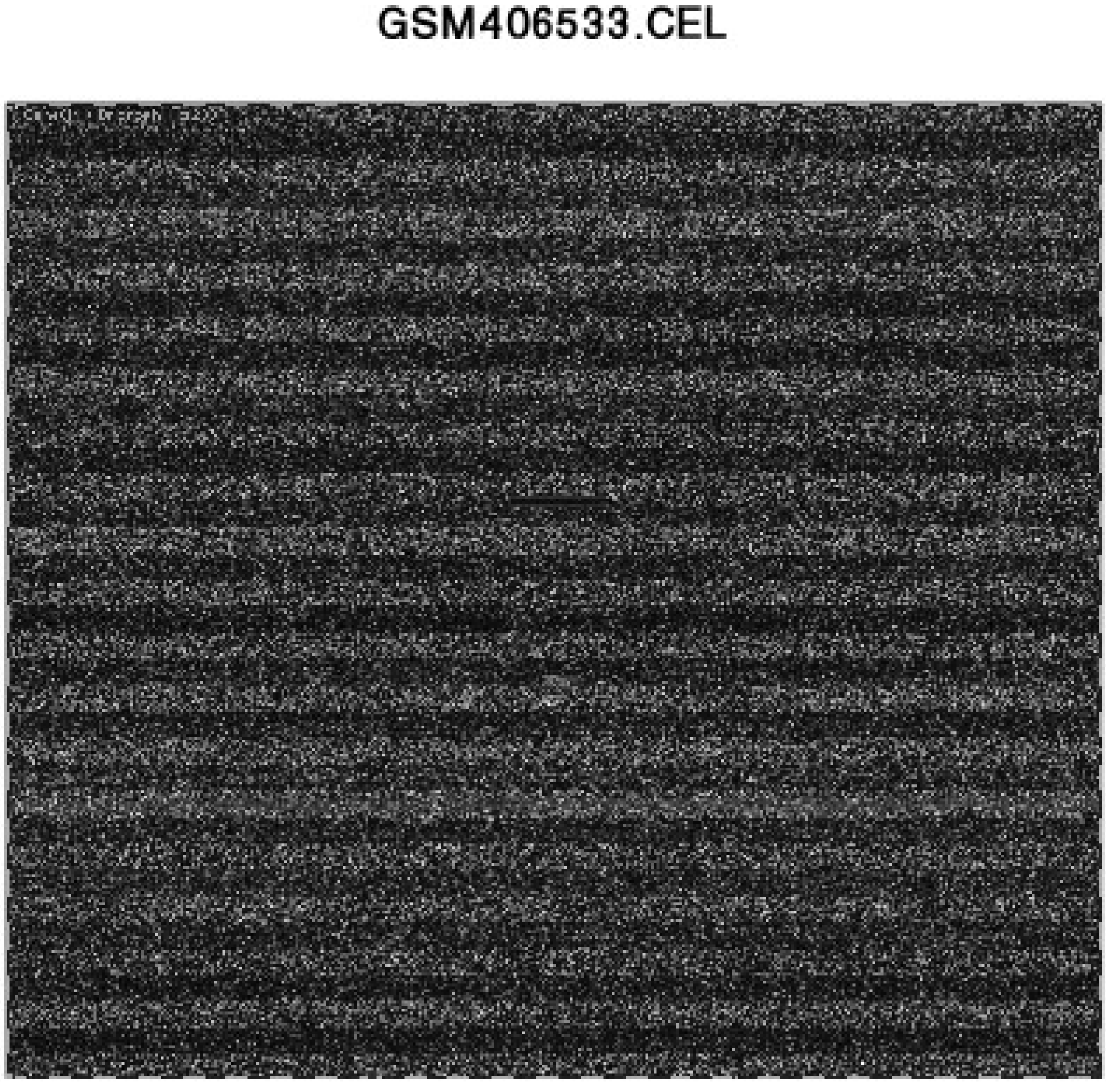
experiment.txt

```
file          methamphetamine
GSM406533.CEL control
GSM406534.CEL control
GSM406535.CEL control
GSM406536.CEL smazka
GSM406537.CEL smazka
GSM406538.CEL smazka
```

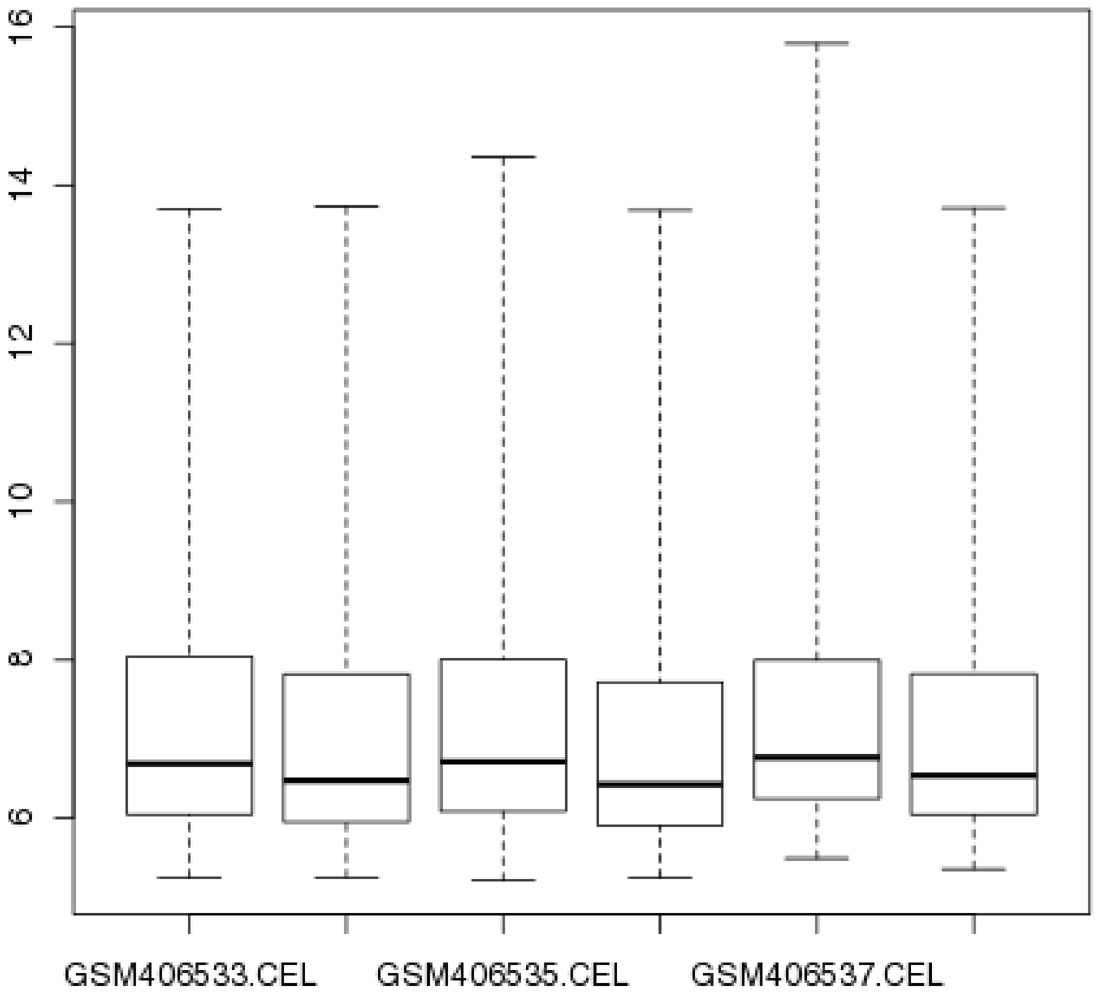
```
> source("http://bioconductor.org/biocLite.R")
> biocLite()
...
> library(affy)
Loading required package: Biobase
Welcome to Bioconductor
Vignettes contain introductory material. To view, type
'openVignette()'. To cite Bioconductor, see
'citation("Biobase")' and for packages 'citation(pkgname)'.
> library(limma)
>
```

```
> targets <- readTargets("experiment.txt", sep="")
> targets
file methamphetamine
1 GSM406533.CEL control
2 GSM406534.CEL control
3 GSM406535.CEL control
4 GSM406536.CEL smazka
5 GSM406537.CEL smazka
6 GSM406538.CEL smazka
> samples <- ReadAffy(filenames=targets$filename)
> samples
AffyBatch object
size of arrays=732x732 features (18 kb)
cdf=Drosophila_2 (18952 affyids)
number of samples=6
number of genes=18952
annotation=drosophila2
notes=
>
```

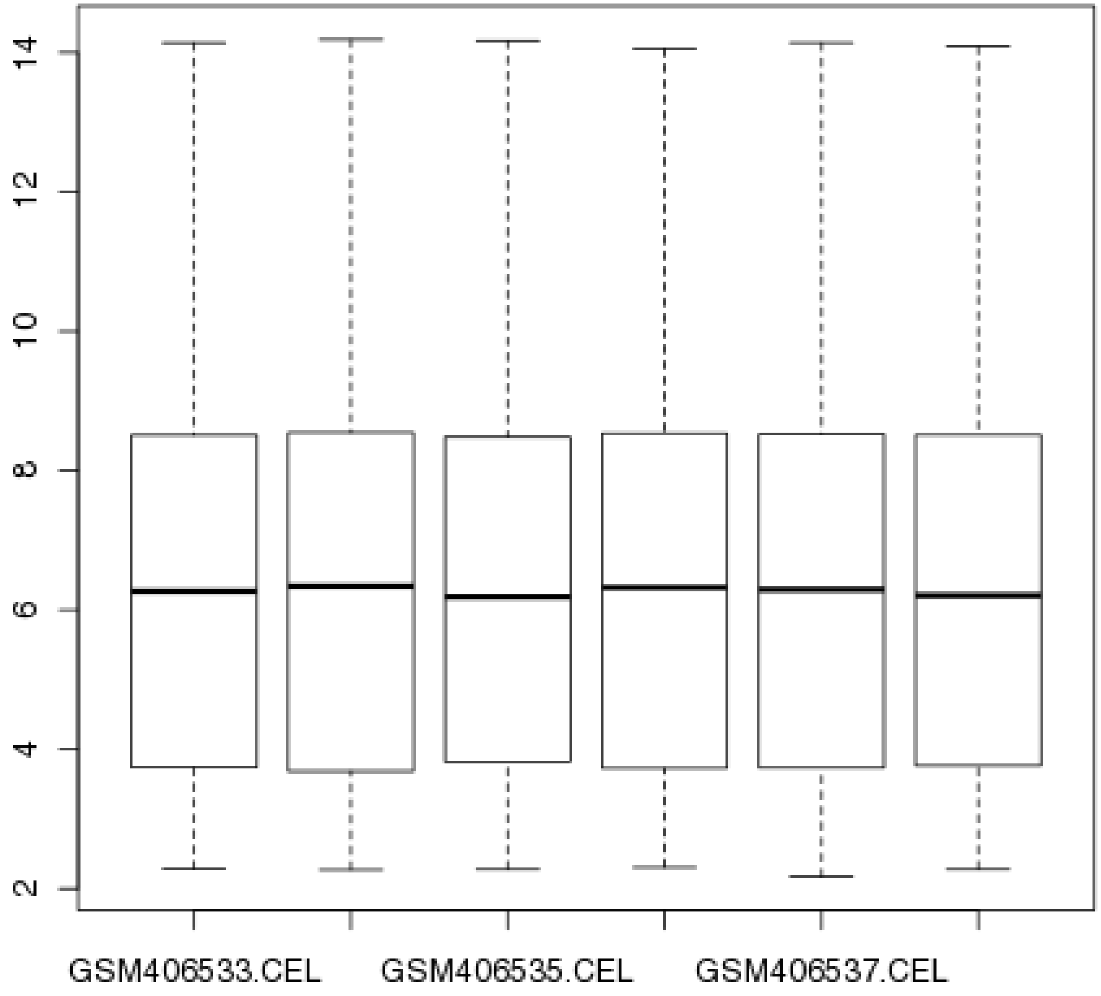
```
> image(samples[,1])
```



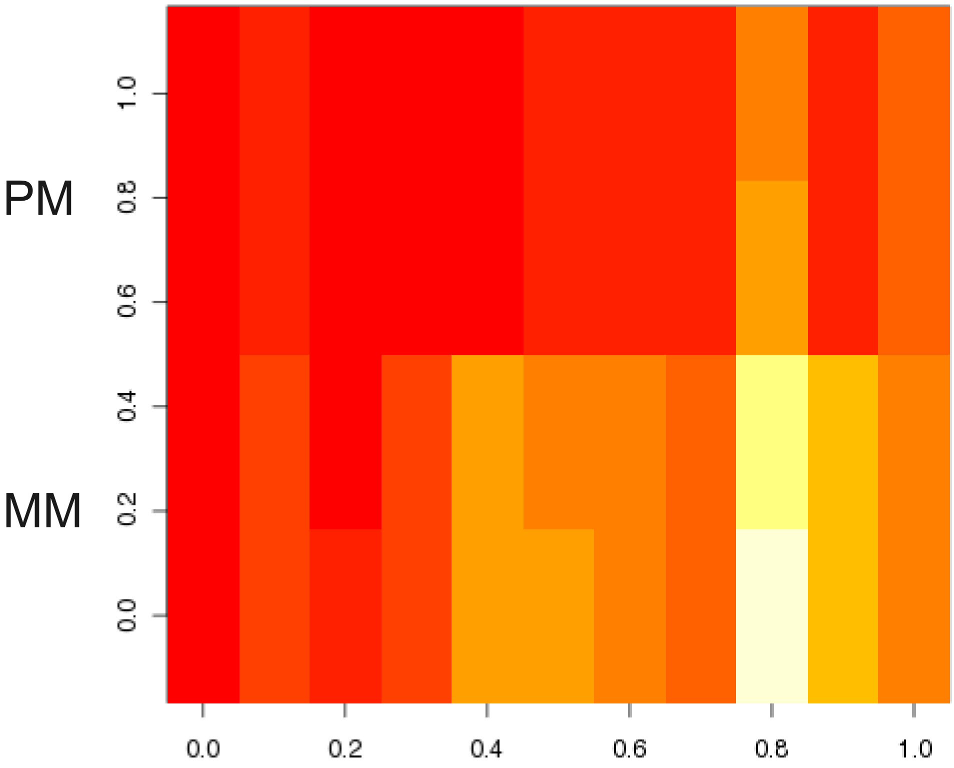
```
> boxplot(samples)
```



```
> samples.rma <- rma(samples)
> boxplot(exprs(samples.rma))
```



```
> geneNames(samples)[1000]
[1] "1368451_at"
> probeset1000<-probeset(samples,
+ geneNames(samples)[1000])[[1]]
> myprobeset1000<-as.matrix(
+ cbind(pm(probeset1000), mm(probeset1000)))
> image(myprobeset1000)
```



```
> samples.fit1 <- lmFit(samples.rma, design)
> cont.matrix <- makeContrasts(
+ methamfetamine="smazka-control",levels=design)
> cont.matrix
Contrasts
Levels     methamfetamine
control    -1
smazka     1
> samples.fit2 <- contrasts.fit(samples.fit1, cont.matrix)
> samples.fit3 <- eBayes(samples.fit2)
> topTable(samples.fit3,coef=1)
      ID            logFC     AveExpr   t         P.Value      adj.P.Val
10423 1633401_s_at  3.961135  8.700558  35.96214 1.834874e-10 3.477454e-06
15446 1638424_at   -3.211559  8.532248 -31.93537 4.920771e-10 4.662923e-06
56    1622946_at    2.974180  9.711813  29.92491 8.439401e-10 5.331451e-06
17777 1640755_at    3.676179  9.802488  28.56372 1.241342e-09 5.881479e-06
7361  1630258_at    3.962029  9.512164  25.37734 3.303628e-09 1.252207e-05
11165 1634143_at    3.390006 10.289132  24.62514 4.235979e-09 1.286656e-05
8773  1631670_at   -3.605631  7.223845 -24.15459 4.967542e-09 1.286656e-05
6112  1629009_at    2.197367 11.268665  23.89484 5.431219e-09 1.286656e-05
18503 1641481_at    2.539188 10.801977  22.66981 8.382841e-09 1.765240e-05
2002  1624892_s_at -2.584324 10.176756 -22.11663 1.027481e-08 1.836464e-05
      B
10423 12.63752
15446 12.14307
56    11.84536
17777 11.62051
7361  11.00602
11165 10.84004
8773  10.73160
6112  10.67015
18503 10.36423
2002  10.21681
```

```
> selected<-topTable(samples.fit3, coef=1,
+ number=100000, lfc=1, p.value=0.01)
> expressions<-exprs(samples.rma[selected[,"ID"],])
> heatmap(expressions, scale="none")
> pca<-prcomp(t(expressions))
> biplot(pca, xlim=c(-0.6,0.6))
```