

# **gse6647**

Maribel Alcoriza Balaguer and Guillermo Ayala

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## **Packages**

```
pacman::p_load(Biobase,affy,ygs98.db)

gcel = GEOquery::getGEOSuppFiles("GSE6647")
system("tar xvf GSE6647/GSE6647_RAW.tar")
gse6647raw = affy::ReadAffy()
system("rm GSM*.gz")
gse6647 = affy::rma(gse6647raw)
type = factor(rep(1:2,4),levels=1:2,labels=c("wt","edc3D"))
x = data.frame(type)
rownames(x) = rownames(pData(gse6647))
datosexperimento = new('MIAME',name = "Singer RH et al.",title = "Expression
                        analysis of edc3 cell", abstract = "El objetivo de este experimento
que participa en la eliminación del grupo CAP del mRNA. Para ello se realizan microarrays

pData(gse6647) = x
experimentData(gse6647) = datosexperimento
annotation(gse6647) = "ygs98.db"
```

Removing genes without ORF.

```
a = AnnotationDbi::select(ygs98.db,keys=featureNames(gse6647),
                          columns=c("ORF","ENTREZID","ENSEMBL"),keytype="PROBEID")
```

```
b = match(featureNames(gse6647),a[,"PROBEID"])
fData(gse6647) = a[b,]
dim(gse6647)
gse6647 = gse6647[which(!is.na(fData(gse6647)[,"ORF"])),]
dim(gse6647)
sel = match(unique(fData(gse6647)[,"ORF"]),fData(gse6647)[,"ORF"])
gse6647 = gse6647[sel,]
featureNames(gse6647) = fData(gse6647)[,"ORF"]
```

Guardamos el ExpressionSet.

```
save(gse6647,file="gse6647.rda")
```