

gse20986

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Packages

```
pacman::p_load("Biobase", "GEOquery")
```

Downloading CEL files

```
gcel = getGEOSuppFiles("GSE20986")
```

The directory **GSE20986** has been created.

```
setwd("GSE20986/")
system("tar xvf GSE20986_RAW.tar")
gse20986raw = affy::ReadAffy()
setwd("../")
system("rm -fr GSE20986")
```

Phenotype

```
tissue = factor(c(1,2,2,1,2,1,3,3,3,4,4,4),levels = 1:4,
  labels=c("iris","retina","choroides","huvec"))
pd = data.frame(tissue)
rownames(pd) = colnames(gse20986raw)
pData(gse20986raw) = pd
```

The normalization is performed using the method GC-RMA.

```
pacman::p_load("gcrma","hgu133plus2probe")
gse20986 = gcrma(gse20986raw)
```

Annotation

```
pacman::p_load(hgu133plus2.db)
a = AnnotationDbi::select(hgu133plus2.db,keys=featureNames(gse20986),
  columns=c("ENTREZID","ENSEMBL","GO"),keytype="PROBEID")
b = BiocGenerics::match(featureNames(gse20986),a[, "PROBEID"])
fData(gse20986) = a[b,]
```

Saving data

```
save(gse20986,file="gse20986.rda")
```