INSTITUTO DE CIENCIAS ECONÓMICO ADMINISTRATIVAS

DOCTORADO EN CIENCIAS ECONÓMICO ADMINISTRATIVAS

LABORATORIO Rstudio

Labs_44A

GRADO: 3ER. SEMESTRE

MATERIA: COMPLEJIDAD ECONÓMICA

DOCENTE: Dra. Carla Carolina Pérez Hernández

ALUMNA: Mtra. Jéssica Paola Aguilar Servín

10 DE MARZO DEL 2023

title: "LABS44_A"

author: "JESSICA PAOLA AGUILAR SERVIN"

date: "2023-03-09"

output: html_document

LABORATORIO

ADICIONALES library(dplyr) library(seurat) library(patchwork) library(ggplot2) library(complexheatmap) library(seuratdata) library(hdWGCNA) library(WGCNA)

install.packages(gplots) library (gplot)

CARGAR LIBRERIA NECESARIA

```
library(stats)
```

PAQUETES DE GPLOTS. Attaching package: 'gplots'.lowess ANEXAMOS DATOS

```
h1 <- c(10,20,10,20,10,20,10,20)
h2 <- c(20,10,20,10,20,10,20,10)

l1 <- c(1,3,1,3,1,3,1,3)
l2 <- c(3,1,3,1,3,1,3,1)

mat <- rbind(h1,h2,l1,l2)
```
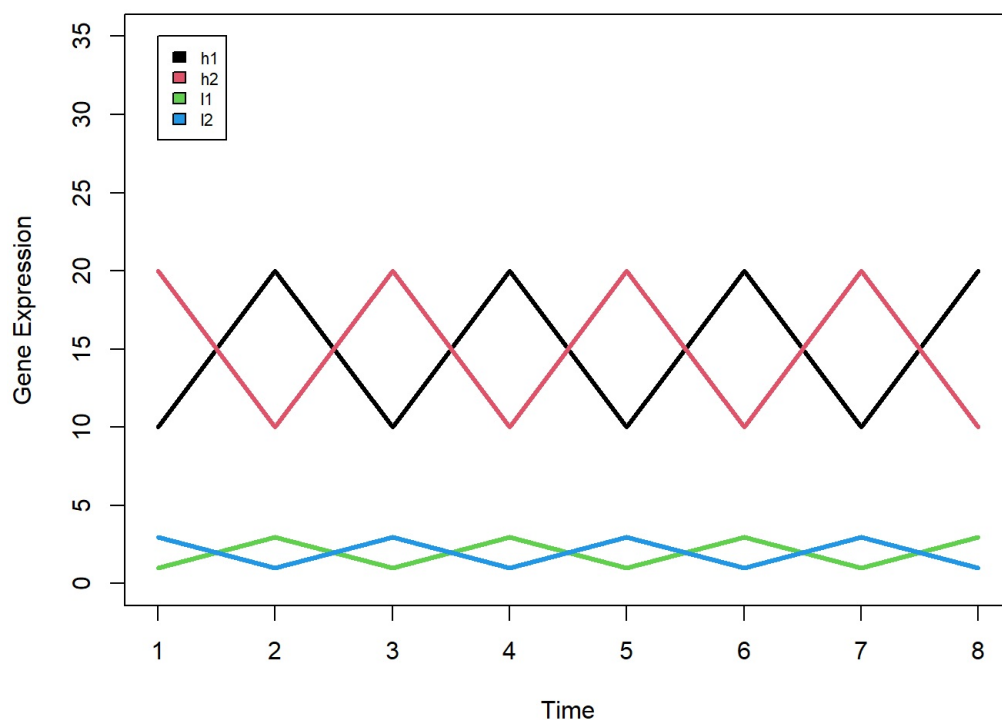
CREAR GRÁFICO

```
par(mfrow =c(1,1), mar=c(4,4,1,1))
plot(1:8,rep(0,8), ylim=c(0,35), pch="", xlab="Time", ylab="Gene Expression")

for (i in 1:nrow(mat)) {lines(1:8,mat[i,], lwd=3, col=i)}
legend(1,35,rownames(mat), 1:4, cex=0.7)
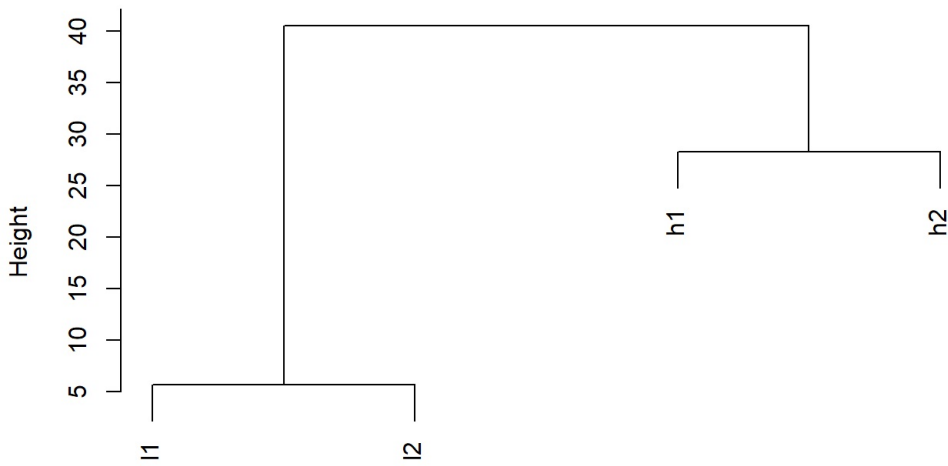```



CALCULAR DISTANCIA

```
dist(mat)
```

```
##          h1        h2        l1
## h2 28.284271
## l1 38.470768 40.496913
## l2 40.496913 38.470768  5.656854
```

SACAR PLOT-use the default for linkage method: complete

```
plot(hclust(dist(mat)))
```

Cluster Dendrogram

dist(mat)
hclust (*, "complete")

CALCULAR HEATMAP DE RENGLONES heatmap (mat, Colv=NA, col= greenred(10), scale = "row") heatmap (mat, Colv=NA, col=greenred(10), scale = "none")

```
mat.scaled<- t(scale(t(mat), center=TRUE, scale = TRUE))
mat.scaled
```

```
##         [,1]       [,2]       [,3]       [,4]       [,5]       [,6]       [,7]
## h1 -0.9354143  0.9354143 -0.9354143  0.9354143 -0.9354143  0.9354143 -0.9354143
## h2  0.9354143 -0.9354143  0.9354143 -0.9354143  0.9354143 -0.9354143  0.9354143
## l1 -0.9354143  0.9354143 -0.9354143  0.9354143 -0.9354143  0.9354143 -0.9354143
## l2  0.9354143 -0.9354143  0.9354143 -0.9354143  0.9354143 -0.9354143  0.9354143
##         [,8]
## h1  0.9354143
## h2 -0.9354143
## l1  0.9354143
## l2 -0.9354143
## attr(,"scaled:center")
## h1 h2 l1 l2
## 15 15  2  2
## attr(,"scaled:scale")
##        h1       h2       l1       l2
## 5.345225 5.345225 1.069045 1.069045
```

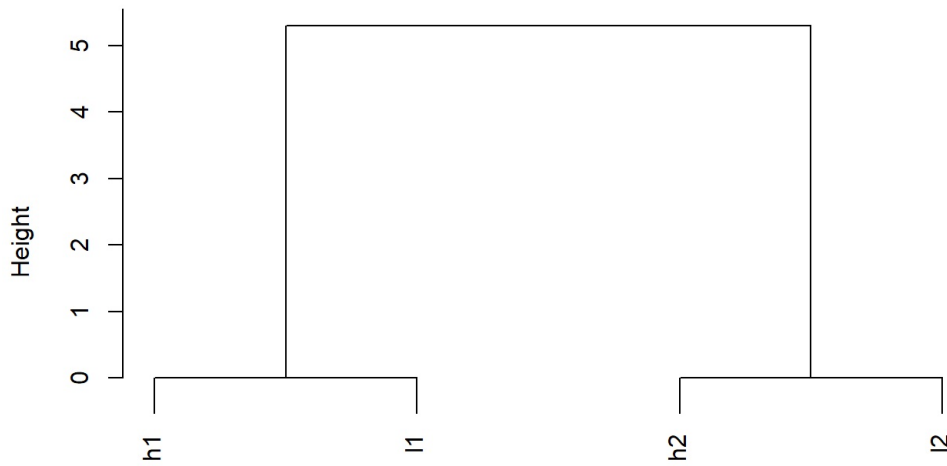DISTANCIA ENTRE GENES

```
dist(mat.scaled)
```

```
##          h1       h2       l1
## h2 5.291503
## l1 0.000000 5.291503
## l2 5.291503 0.000000 5.291503
```

NUEVO GRAFICO

```
plot(hclust(dist(mat.scaled)))
```

Cluster Dendrogram

dist(mat.scaled)
hclust (*, "complete")

heatmap(mat.scaled, Colv = NA,

scale = "none")

CORRELACION ENTRE GENES

```
cor(t(mat))
```

```
##     h1 h2 l1 l2
## h1  1 -1  1 -1
## h2 -1  1 -1  1
## l1  1 -1  1 -1
## l2 -1  1 -1  1
```
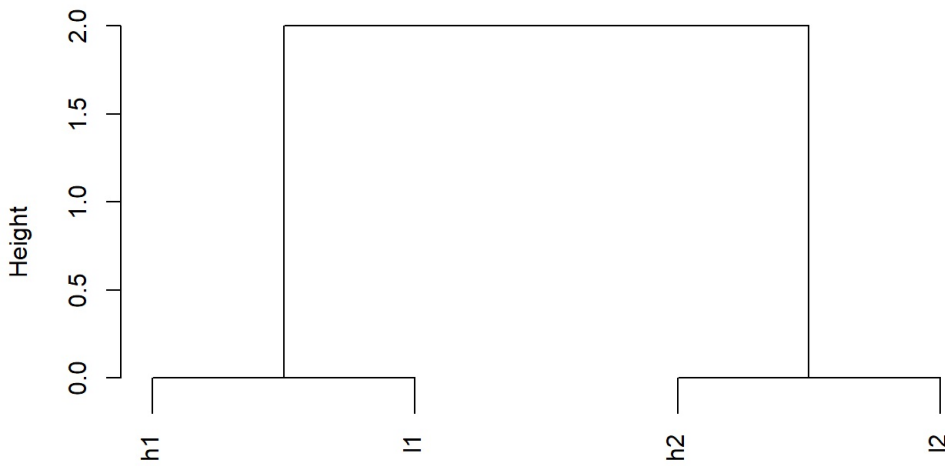
DISTANCIA EN LAS CORRELACIONES

```
1- cor(t(mat))
```

```
##     h1 h2 l1 l2
## h1  0  2  0  2
## h2  2  0  2  0
## l1  0  2  0  2
## l2  2  0  2  0
```

GRAFICAS

```
hc <- hclust(as.dist(1-cor(t(mat))))
plot(hc)
```
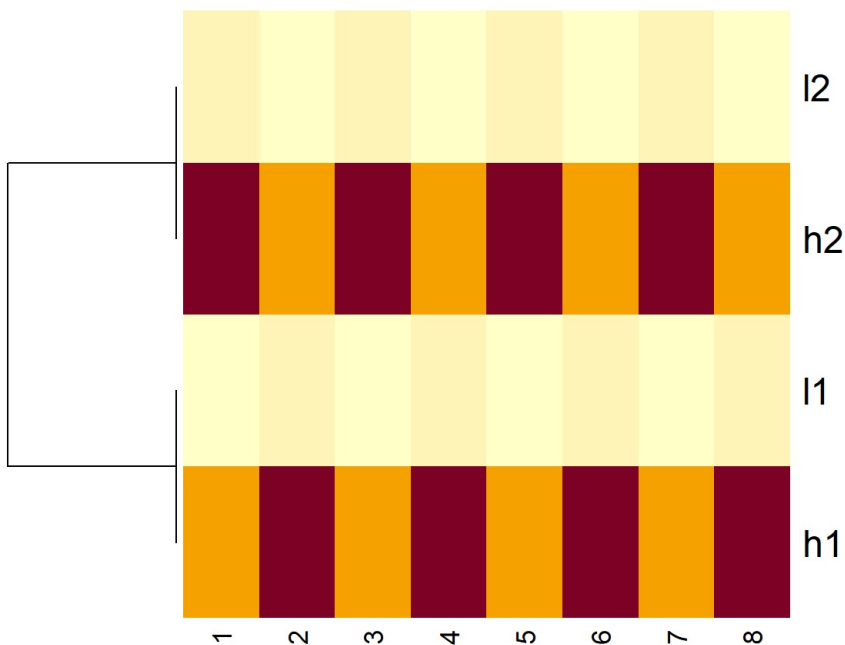
Cluster Dendrogram

as.dist(1 - cor(t(mat)))
hclust (*, "complete")

PRIMERA ADECUACION HEATMAPS

```
heatmap(mat, Colv = NA, Rowv=as.dendrogram(hc), scale = "none")
```


SEGUNDA oPCION DE HEATMAPS

```
heatmap(mat, trace = "none", Colv= NA, dendrogram = "row", scale = "none")
```

```
## Warning in plot.window(...): "trace" is not a graphical parameter
```
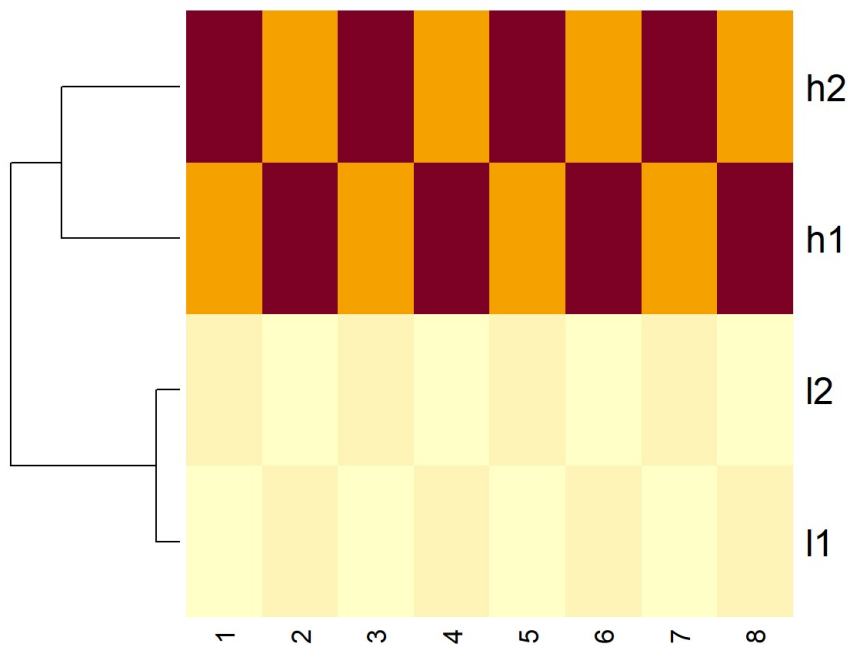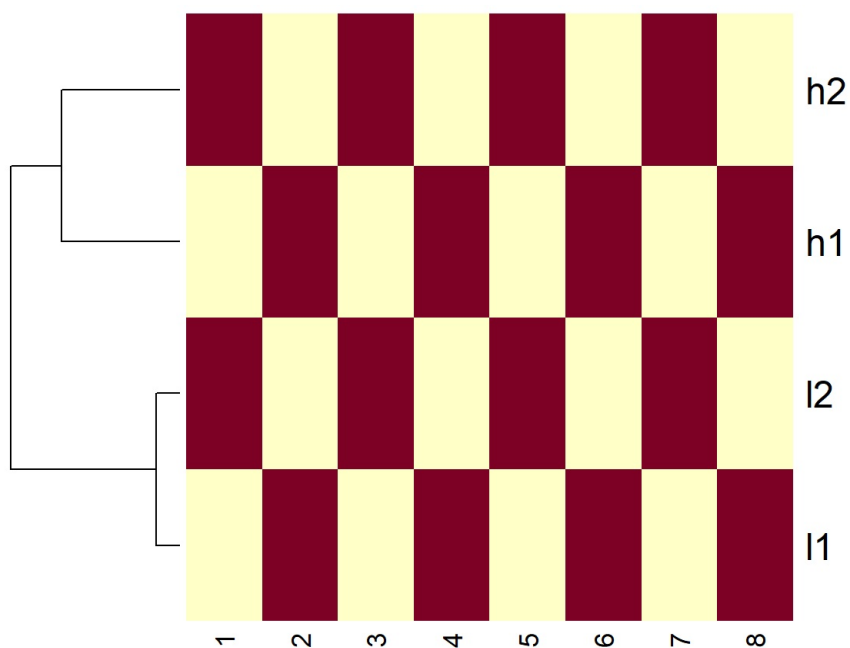
```
## Warning in plot.window(...): "dendrogram" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "trace" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "dendrogram" is not a graphical parameter
```

```
## Warning in title(...): "trace" is not a graphical parameter
```

```
## Warning in title(...): "dendrogram" is not a graphical parameter
```

```
heatmap(mat, trace = "none", Colv= NA, dendrogram = "row", scale = "row")
```

```
## Warning in plot.window(...): "trace" is not a graphical parameter
```
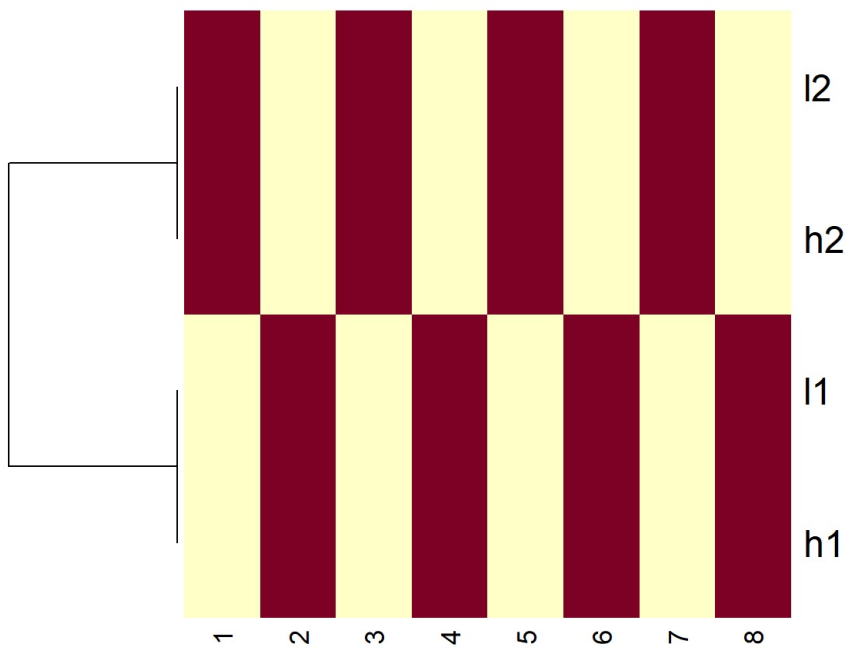
```
## Warning in plot.window(...): "dendrogram" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "trace" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "dendrogram" is not a graphical parameter
```

```
## Warning in title(...): "trace" is not a graphical parameter
```

```
## Warning in title(...): "dendrogram" is not a graphical parameter
```


CUARTA OPCION HEATMAPS USANDO DISTANCIA ECLUDIANA

```
heatmap (t(scale(t(mat), center=TRUE, scale=TRUE)), trace = "none", Colv= NA, dendrogram = "row")
```

USO 1-COR (x) DE CORRELACION EN HEAT

```
heatmap (mat, trace = "none",
  Colv= NA, dendrogram = "row",
  scale = "none",
  hclust=function(x) hclust(x, method="complete"), distfun=function(x) as.dist(1-cor(t(x))))
```

OTRA ESCALA REPRESENTADA POR LOS COLORES

```
heatmap(mat, trace = "none",
        Colv= NA, dendrogram = "row",
        scale = "row",
        hclust=function(x) hclust(x, method='complete'), distfun=function(x) as.dist(1-cor(t(x))))
```

```
## Warning in plot.window(...): "trace" is not a graphical parameter
```
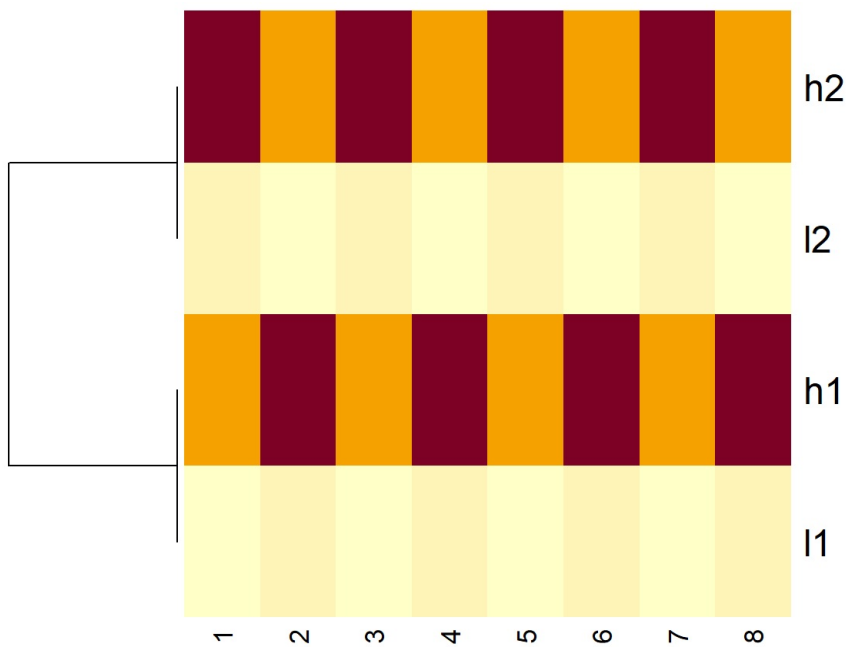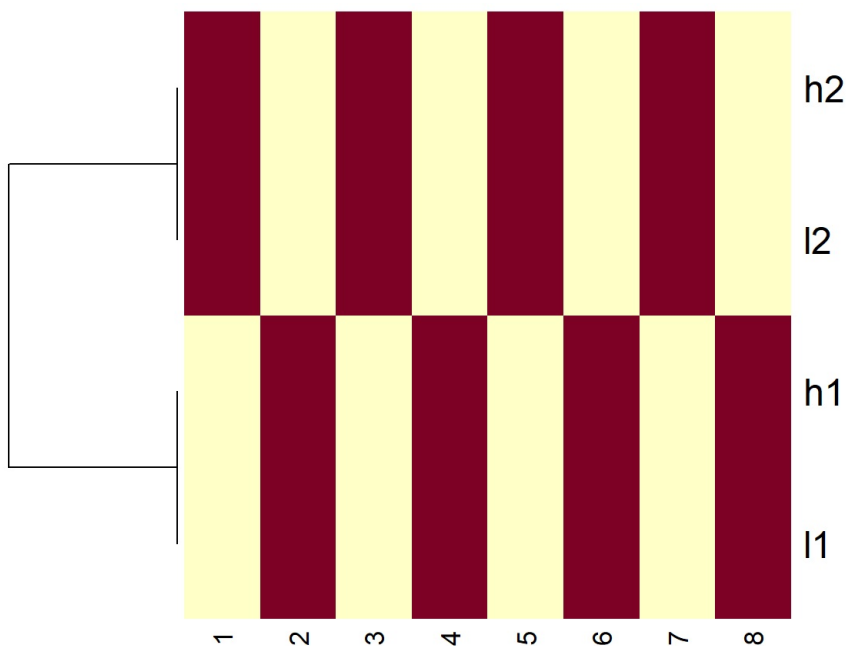
```
## Warning in plot.window(...): "dendrogram" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "trace" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "dendrogram" is not a graphical parameter
```

```
## Warning in title(...): "trace" is not a graphical parameter
```

```
## Warning in title(...): "dendrogram" is not a graphical parameter
```


ULTIMA COLORACION DE

CLUSTERS

```
heatmap(t(scale(t(mat), center=TRUE, scale=TRUE)), trace = "none",
Colv= NA, dendrogram = "row",
hclust=function(x) hclust(x, method='complete'), distfun=function(x) as.dist(1-cor(t(x))))
```

```
## Warning in plot.window(...): "trace" is not a graphical parameter
```

```
## Warning in plot.window(...): "dendrogram" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "trace" is not a graphical parameter
```

```
## Warning in plot.xy(xy, type, ...): "dendrogram" is not a graphical parameter
```

```
## Warning in title(...): "trace" is not a graphical parameter
```

```
## Warning in title(...): "dendrogram" is not a graphical parameter
```