AnalisisGAGE

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2/6/2021

Cargar la base de datos

```
data(kegg.sets.hs)
data(sigmet.idx.hs)
kegg.sets.hs <- kegg.sets.hs[sigmet.idx.hs]
kegg.sets.hs <- kegg.sets.hs[1:131]
```

Hacer los grupos

```
earlyOnset <- which(colnames(countData)%in%samplesToStudy$LessThan70Years)
lateOnset <- which(colnames(countData)%in%samplesToStudy$GreaterThan70Years)
```

Analisis con GAGE teniendo en cuenta las perturbaciones en solo una dirección

```
earlyOnset_v_LateOnsetSAMEDIR <- gage(exprs = countData,
                                      gsets = kegg.sets.hs,
                                      ref = earlyOnset,
                                      samp = lateOnset,
                                      compare = "unpaired",
                                      same.dir = TRUE)
```

```
earlyOnset_v_LateOnset.SigSAMEDIR <- sigGeneSet(earlyOnset_v_LateOnsetSAMEDIR)
```

```
## [1] "No heatmap produced for up- or down-regulated gene sets, only 1 or none signficant."
## [1] "there are 0 signficantly up-regulated gene sets"
## [1] "there are 0 signficantly down-regulated gene sets"
```

Analisis con GAGE teniendo en cuenta las perturbaciones en ambas direcciones

```
earlyOnset_v_LateOnsetBOTHDIR <- gage(exprs = countData,
                                      gsets = kegg.sets.hs,
                                      ref = earlyOnset,
                                      samp = lateOnset,
                                      compare = "unpaired",
                                      same.dir = FALSE)
```

```
earlyOnset_v_LateOnset.SigBOTHDIR <- sigGeneSet(earlyOnset_v_LateOnsetBOTHDIR,
                                                outname = "earlyOnset_v_lateOnset")
```

```
## [1] "there are 30 signficantly two-direction perturbed gene sets"
```