Clustering of differentially expressed genes

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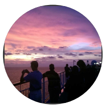
MP2Lab



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Protocol status: Working
We use this protocol and it's working

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ABSTRACT

This differentially expressed genes clustering pipeline utilizes coseq v3.17 package (Rau & Maugis-Rabusseau, 2018) in R.

Clustering of differentially expressed genes (DEG) using Co...

1 Load the package (coseq).

Command

```
library(coseq)
library(matrixStats)
```

2 Run Coseq on transformed and normalized counts.
Example:
Performing clustering on bud data with expected clusters, K=5-16.
Clustering process is repeated for 10x.

Command

```
coseq_bud_logclr_1 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_2 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_3 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_4 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_5 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_6 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_7 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_8 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_9 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
coseq_bud_logclr_10 = coseq(tcounts_logclr_exp_bud_ORF_scTMM[,1:15], K=5:16,
normFactor = "none", transformation = "none")
```

3 Manually inspect the results and decide on the average number of clusters
Choose one clustering result to proceed with the subsequent steps

Command

```
summary(coseq_bud_logclr_1)
summary(coseq_bud_logclr_2)
summary(coseq_bud_logclr_3)
summary(coseq_bud_logclr_4)
summary(coseq_bud_logclr_5)
summary(coseq_bud_logclr_6)
summary(coseq_bud_logclr_7)
summary(coseq_bud_logclr_8)
summary(coseq_bud_logclr_9)
summary(coseq_bud_logclr_10)
```

Assigning clusters to transcripts

4 Retrieve and tabulate the clustering information based on the chose clustering from the previous step.
Example:
coseq_bud_logclr_1 is chosen as the best clustering
results_coseq_bud_logclr: the new table/vector.

Command

```
results_coseq_bud_logclr = clusters(coseq_bud_logclr_1)
```

5 Convert the vector into a data frame.

Command

```
results_coseq_bud_logclr = data.frame(results_coseq_bud_logclr)
```

6 Create a column containing the assigned cluster number for each transcript in the read count data frame.
Example:
the new column: bud_logclr
the data frame with read counts: tcounts_logclr_exp_bud_ORF_scTMM

Command

```
tcounts_logclr_exp_bud_ORF_scTMM$bud_logclr =
results_coseq_bud_logclr_1$results_coseq_bud_logclr
```