

Course: Bioinformatics

Instructor: Zaynab Mousavian



Homework 2

Deadline: 17 Khordad

Problem 1:

How do you calculate the trimming parameter δ in ADDITIVEPHYLOGENY?

Problem 2:

Answer to the following questions using the GSE19143 dataset from the GEO database in R:

- A) Which genes are differentially expressed between PRED-sensitive and PRED-resistant infant ALL samples?
- B) Which genes are differentially expressed between PRED-sensitive and PRED-resistant non-infant ALL samples?
- C) Which genes are differentially expressed between infant and non-infant PRED-sensitive ALL samples?
- D) Which genes are differentially expressed between infant and non-infant PRED-resistant ALL samples?

Problem 3:

Perform a GO functional enrichment analysis on each of the outputs obtained in problem 2 using DAVID database. For each list of differential expressed genes (i.e. the output of sections A to D in problem 2), which GO terms are highly enriched?