HW3a

Part 1 – Phylogenetic Trees

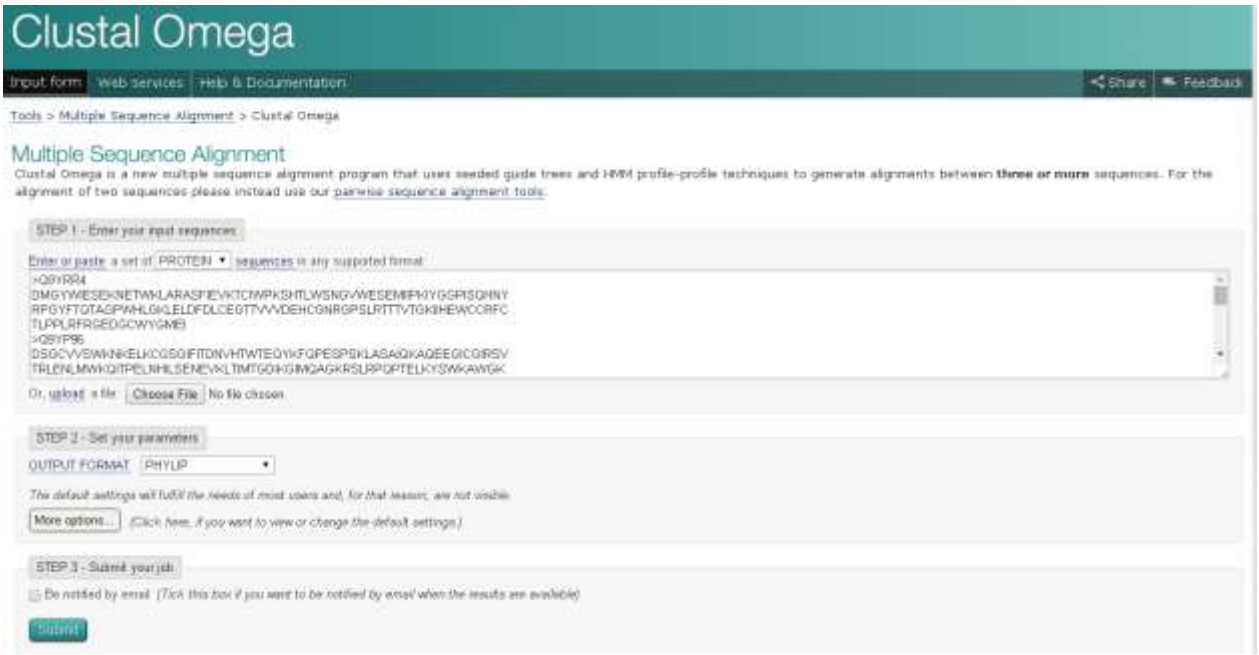
One can use the power of phylogenetic trees and alignment algorithms to visually assess distances between protein sequences while appreciating hierarchical structure.

In this HW we will calculate distances between different strains of Dengue virus strains. Specifically between *Dengue virus 1 NS1 protein (Uniprot Q9YRR4), Dengue virus 2 NS1 protein (UniProt Q9YP96), Dengue virus 3 NS1 protein (UniProt B0LSS3), and Dengue virus 4 NS1 protein (UniProt Q6TFL5).* The main question is which of those strains are the mostly related? This information could be used to better understand dangers of unknown viral strains most similar to the known strain.

1) Retrieve sequences programmatically and save into one *.fasta file

```
library("seqinr");          # Load the SeqinR package
# Make a vector containing the names of the sequences
seqnames <- c("Q9YRR4", "Q9YP96", "B0LSS3", "Q6TFL5");
seqs <- retrieveseqs(seqnames,"swissprot");
```

2) Align sequences via the online tool Clustal Omega, choose PHYLIP output. E.g. save file DengueViruses.phylip



3) Calculate distances between sequences

```
NS1aln  <- read.alignment(file = "Dengueviruses.phylip", format =
"phylip")
```

```
NS1dist <- dist.alignment(NS1aln)
```

4) Build hierarchical tree. Which of the viruses is closest to Q6TFL5?

```
plot(hclust(NS1dist))
```

Appendix of auxiliary functions

```
retrieveseqs <- function(seqnames,acnucdb)
  {
     myseqs <- list()   # Make a list to store the sequences
     require("seqinr")  # This function requires the SeqinR R package
     choosebank(acnucdb)
     for (i in 1:length(seqnames))
     {
        seqname <- seqnames[i]
        print(paste("Retrieving sequence",seqname,"..."))
        queryname <- "query2"
        query <- paste("AC=",seqname,sep="")
        query2 <-query(`queryname`,`query`)
        seq <- getSequence(query2$req[[1]])
        myseqs[[i]] <- seq
     }
     closebank()
     return(myseqs)
  }
```

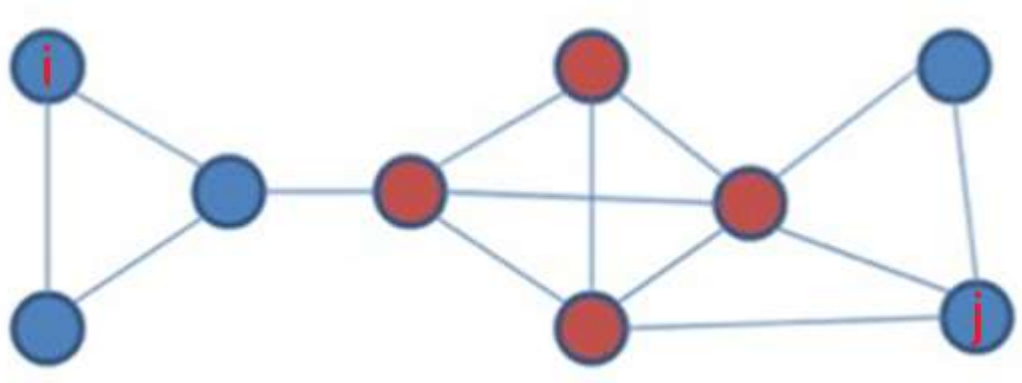
Part 2 – Decision Trees

5) Describe how decision trees could be used to predict gene expression and build gene regulatory networks
6) What are strength and weaknesses of RF? Comment on bias of the Gini Index of a split measure
7) Given a tree root node, calculate its GINI Index.

Table 1: Sample values

	Sample 1	Sample 2	Sample 3
class 1	3	6	2
class 2	1	5	9

8) What are the two main components of any network?
9) Find the shortest path between the node i and j shown in a graph. Use color (red, black) to trace the shortest path



10) Define scale-free network and its properties. Give an examples both biological and non-biological networks