

Protein

MP

2015-06-18

```
> setwd("D:/Dropbox/R/2015-NUS/Session-3/(a) Hierarchical/Protein")
```

```
> Dataset <-  
+ read.table("D:/Dropbox/R/2015-NUS/Session-3/(a) Hierarchical/Protein/Protein.csv",  
+ header=TRUE, sep=",", na.strings="NA", dec=".", strip.white=TRUE)
```

```
> HClust.1 <- hclust(dist(model.matrix(~1 +  
+ Cereals+Eggs+Fish+FruitVegetable+Milk+Nuts+RedMeat+Starch+WhiteMeat,  
+ Dataset)), method="single")  
> plot(HClust.1, main="Cluster Dendrogram for Solution HClust.1", xlab=  
+ "Observation Number in Data Set Dataset",  
+ sub="Method=single; Distance=euclidian")
```

