

Protein-k

MP

2015-06-24

```
> setwd("D:/Dropbox/R/2015-NUS/Session-3/(b) k-Means/Protein")
```

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

```
> .cluster <- KMeans(model.matrix(~-1 + Fish + RedMeat, Dataset), centers =  
+ 3, iter.max = 10, num.seeds = 10)  
> .cluster$size # Cluster Sizes
```

```
[1] 6 11 8
```

```
> .cluster$centers # Cluster Centroids
```

```
new.x.Fish new.x.RedMeat  
1 3.733333 14.550000  
2 1.754545 7.918182  
3 8.175000 8.912500
```

```
> .cluster$withinss # Within Cluster Sum of Squares
```

```
[1] 42.86833 51.00364 78.92375
```

```
> .cluster$tot.withinss # Total Within Sum of Squares
```

```
[1] 172.7957
```

```
> .cluster$betweenss # Between Cluster Sum of Squares
```

```
[1] 373.9283
```

```
> Dataset$KMeans <- assignCluster(model.matrix(~-1 + Fish + RedMeat, Dataset),  
+ Dataset, .cluster$cluster)  
> remove(.cluster)
```