Math 189 HW5

Group Members:

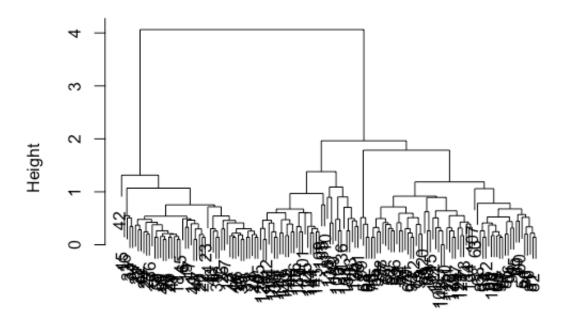
```
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Problem 1

```
install.packages("factoextra")
library(factoextra)
data(iris)
data<-iris[c(1,2,3,4)]
data<-na.omit(data)</pre>
d<-dist(data,method="euclidean")</pre>
hc<- hclust(d,method="average")</pre>
plot(hc,main=" Dendrogram: Average Linkage ")
sub grp<-cutree(hc,k=3)</pre>
fviz_cluster(list(data = data, cluster = sub_grp))
species \leftarrow c(rep(1,50), rep(2,50), rep(3,50))
count <- 0
for (i in 1:150){
  if (sub_grp[i] == species[i]){
    count <- count + 1</pre>
  }
rate <- count/150
print(paste("Correct clustering rate =",rate))
```

[&]quot;Correct clustering rate = 0.906666666666667"

Dendrogram: Average Linkage



d hclust (*, "average")

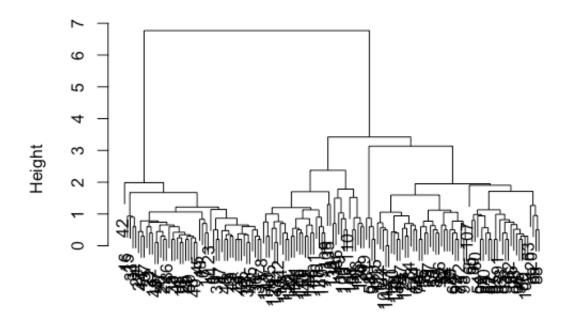
Dim1 (73%)

Problem 2A

```
d2<-dist(data,method="manhattan")
hc2<- hclust(d2,method="average")
plot(hc2,main=" Dendrogram: Average Linkage ")
sub_grp2<-cutree(hc2,k=3)
fviz_cluster(list(data = data, cluster = sub_grp2))
count <- 0
for (i in 1:150){
   if (sub_grp2[i] == species[i]){
      count <- count + 1
   }
}
rate <- count/150
print(paste("Correct clustering rate =",rate))</pre>
```

[&]quot;Correct clustering rate = 0.9"

Dendrogram: Average Linkage



d2 hclust (*, "average")

110

Problem 2B

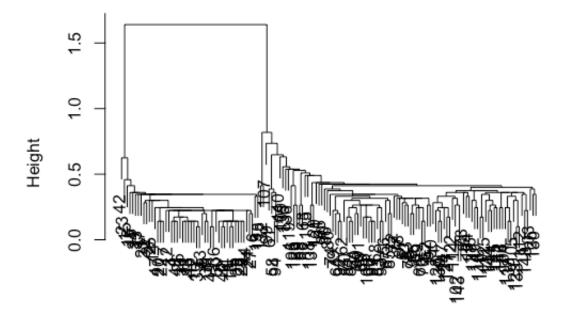
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```
d3<-dist(data,method="euclidean")
hc3<- hclust(d3,method="single")
plot(hc3,main=" Dendrogram: Single Linkage ")
sub_grp3<-cutree(hc3,k=3)
fviz_cluster(list(data = data, cluster = sub_grp3))
count <- 0
for (i in 1:150){
   if (sub_grp3[i] == species[i]){
      count <- count + 1
   }
}
rate <- count/150
print(paste("Correct clustering rate =",rate))</pre>
```

Dim1 (73%)

[&]quot;Correct clustering rate = 0.68"

Dendrogram: Single Linkage



d3 hclust (*, "single")

Cluster plot 2 42 59 88 1088

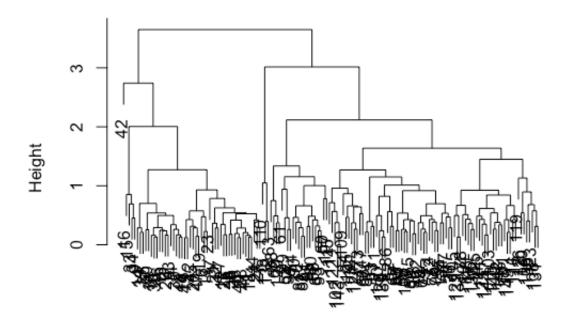
Dim1 (73%)

Problem 2C

```
data_standard <- scale(data, center = TRUE, scale = TRUE)
d4<-dist(data_standard,method="euclidean")
hc4<- hclust(d4,method="average")
plot(hc4,main=" Dendrogram: Average Linkage ")
sub_grp4<-cutree(hc4,k=3)
fviz_cluster(list(data = data_standard, cluster = sub_grp4))
count <- 0
for (i in 1:150){
   if (sub_grp4[i] == species[i]){
      count <- count + 1
   }
}
rate <- count/150
print(paste("Correct clustering rate =",rate))</pre>
```

[&]quot;Correct clustering rate = 0.686666666666667"

Dendrogram: Average Linkage



d4 hclust (*, "average")

