### Clustering

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```
clust <- read_csv("clust.csv")

## Rows: 32 Columns: 13

## -- Column specification -------

## Delimiter: ","

## chr (1): Team

## dbl (12): MPasstoRush, MPasses, MTD, MScore, Rushes, Passes, Wins, favorby, ...

##

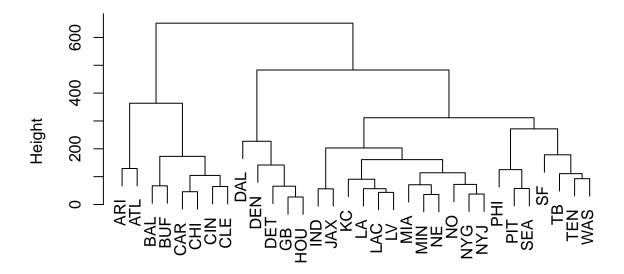
## i Use `spec()` to retrieve the full column specification for this data.

## i Specify the column types or set `show_col_types = FALSE` to quiet this message.</pre>
```

#### Hclust

```
dist.map <- dist(clust)
## Warning in dist(clust): NAs introduced by coercion
hclustavg <- hclust(dist.map,method= "complete")
labels(hclustavg) <- clust$Team
p1<-plot(hclustavg)</pre>
```

# **Cluster Dendrogram**

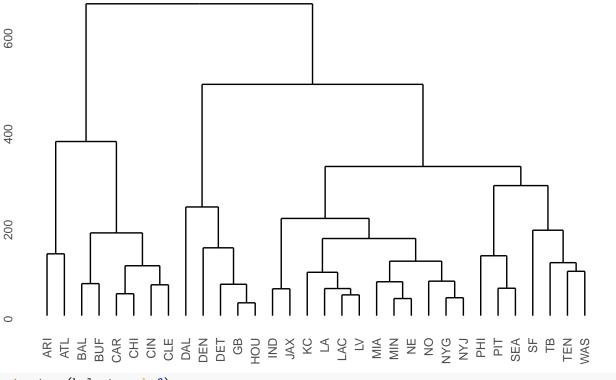


dist.map hclust (\*, "complete")

p1 ## NULL

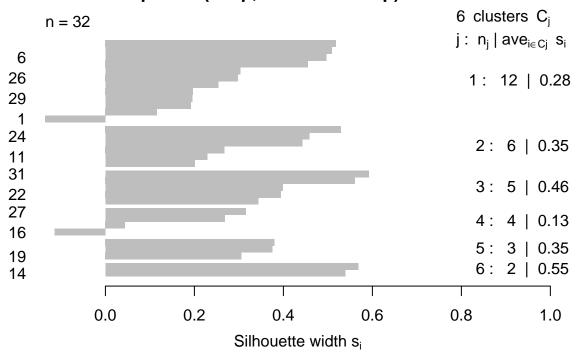
ggdendrogram(hclustavg, rotate = FALSE, size = 2) + labs(title = "complete Linkage")

# complete Linkage



p<-cutree(hclustavg,k=6)
s<-silhouette(p,dist.map)
plot(s)</pre>

#### Silhouette plot of (x = p, dist = dist.map)



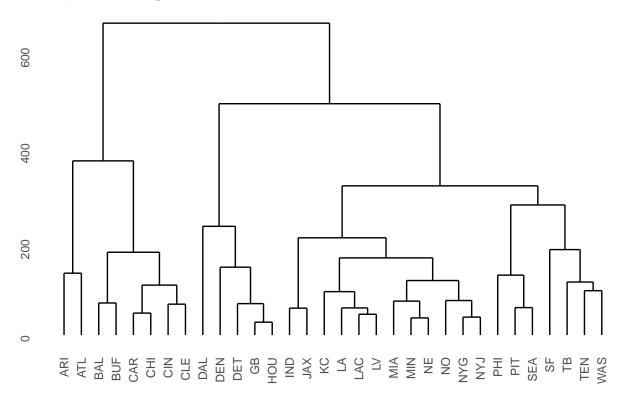
Average silhouette width: 0.33

so 2 is the

best number of clusters for complete Linkage using the silhouette diagram  $\,$ 

ggdendrogram(hclustavg, rotate = FALSE, size = 2) + labs(title = "complete Linkage")

#### complete Linkage



```
dend<-as.dendrogram(hclustavg)%>%
color_branches(k=6)

plot(dend)

##heat map

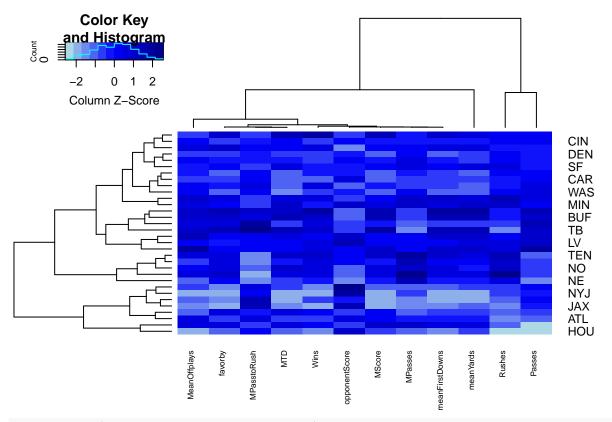
mycol <- colorRampPalette(c("lightblue", "blue", "darkblue"))(12)

C<-clust[,2:13]

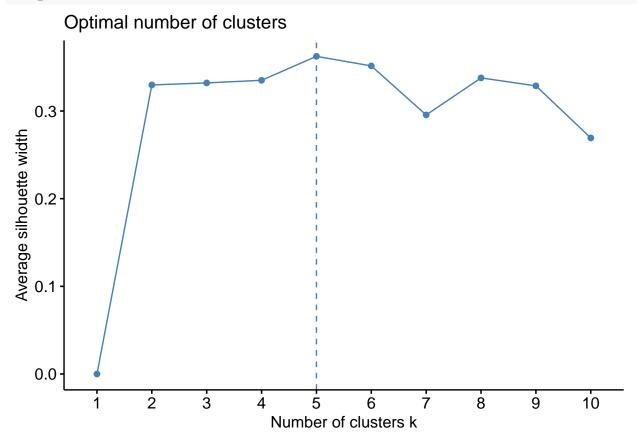
c<-data.matrix(C)

rownames(c) <- clust$Team

heatmap.2(c, col=mycol, trace="none", scale="column", cexCol =0.65 ,margins=c(7,5))
```

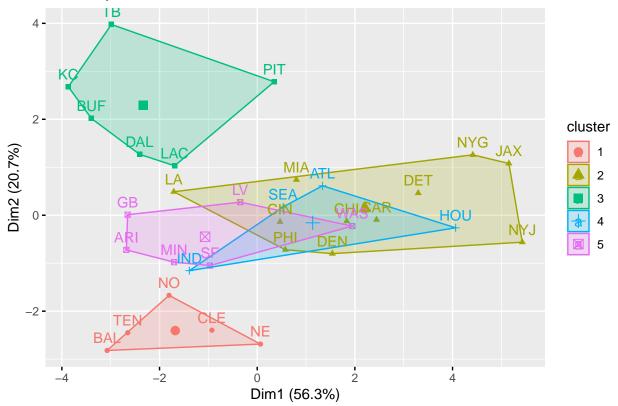


fviz\_nbclust(c, kmeans, method='silhouette')



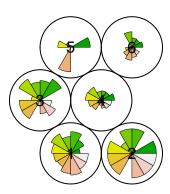
```
k<-kmeans(c, centers = 5)
fviz_cluster(k, data = c)</pre>
```

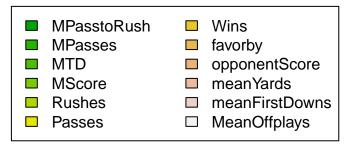
#### Cluster plot



```
SOM<-som(c,grid=somgrid(2,3,topo="hexagonal"),rlen=1000)
fitted<-SOM$unit.classif
wts<-SOM$codes
plot(SOM,type="codes")
coords<-SOM$grid$pts
text(coords,labels=seq(1,6))</pre>
```

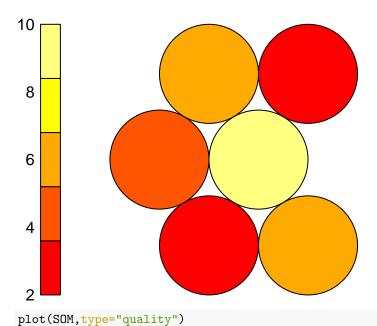
# **Codes plot**



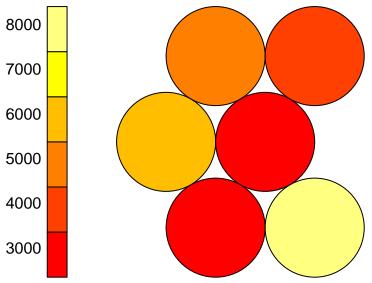


plot(SOM, type="counts")

# **Counts plot**

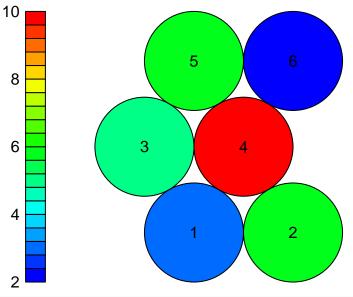


### **Quality plot**



```
coolBlue.hotRed<-colorRampPalette(c("blue","cyan","green","yellow","red"))
plot(SOM,type="counts",palette.name=coolBlue.hotRed,ncolors=20)
coords<-SOM$grid$pts
text(coords,labels=seq(1,6))</pre>
```

### **Counts plot**



```
par(bg = rgb(0,0.5,0.5), font = 1, pch = 16, pch = 16, cex = 0.5)
plot(SOM, type="mapping", labels = rownames(c), cex.lab = 0.65,
```

```
main = "NFL Team mapping", cex.main = 5.4)
text(coords,labels=seq(1,6), col = "blue")
```

