

Code ▼

```
m1 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID01.csv')
m2 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID02.csv')
m3 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID03.csv')
m4 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID11.csv')
m5 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID12.csv')
m6 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID13.csv')
m7 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID21.csv')
m8 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID22.csv')
m9 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID23.csv')
m10 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID29.csv')
m11 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID30.csv')
m12 = read.csv('~\\Desktop\\NCSA\\CGManalyzer-datasets\\ID31.csv')
```

```
training_frame = rbind.data.frame(
  m1$glucoseValue,
  m2$glucoseValue,
  m3$glucoseValue,
  m4$glucoseValue,
  m5$glucoseValue,
  m6$glucoseValue,
  m7$glucoseValue,
  m8$glucoseValue,
  m9$glucoseValue,
  m10$glucoseValue,
  m11$glucoseValue,
  m12$glucoseValue
)
```

training_frame

[illegible]

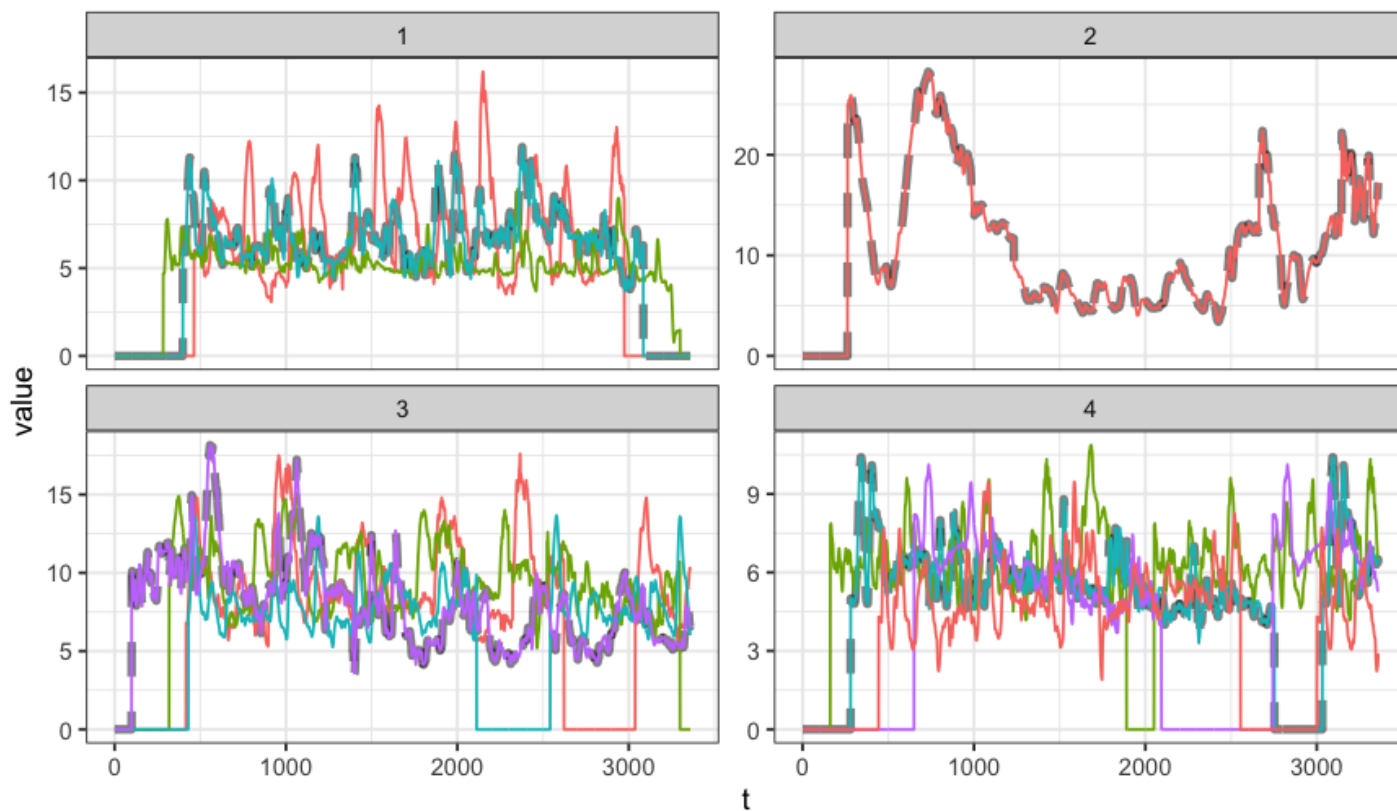
Calculating distance matrix...
Performing hierarchical clustering...
Extracting centroids...

Elapsed time is 105.74 seconds.

Hide

```
plot(clust.hier, type="sc")
```

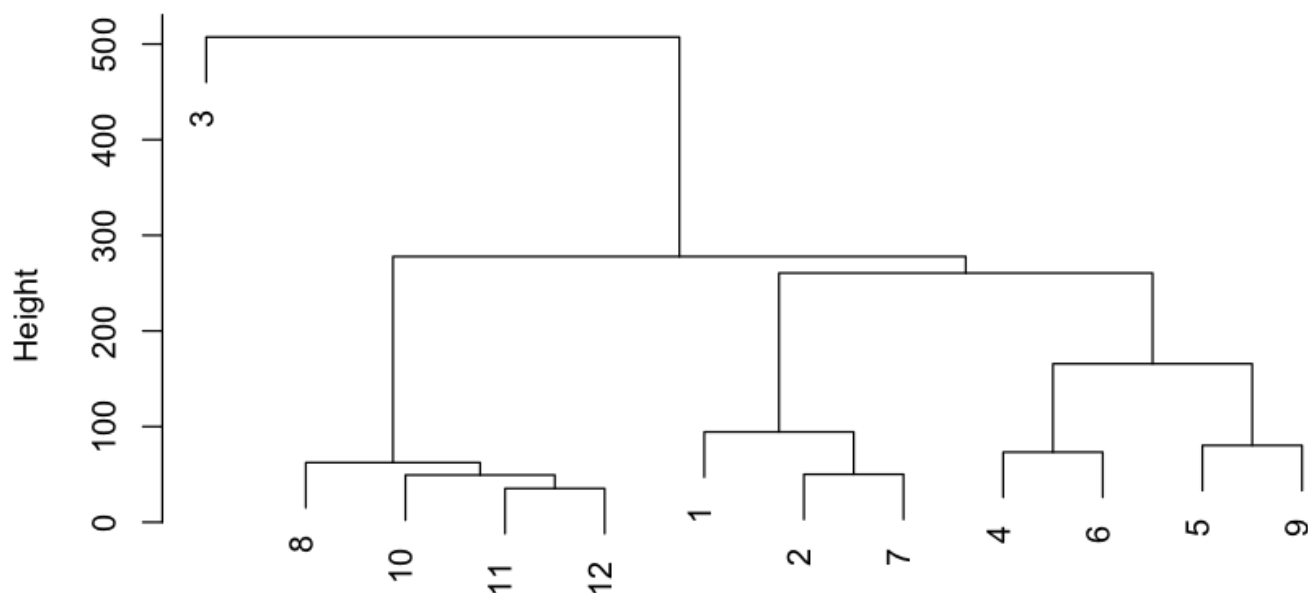
Clusters' members



Hide

```
plot(clust.hier)
```

Cluster Dendrogram



```
stats::as.dist(distmat)
stats::hclust (*, "ward.D")
```

Hide

```
t(cbind(training_frame[,0], cluster = clust.hier@cluster))
```

```
      1 2 3 4 5 6 7 8 9 10 11 12
cluster 1 1 2 3 3 3 1 4 3 4 4 4
```

Hide

```
l_hier <- clust.hier@cluster
```

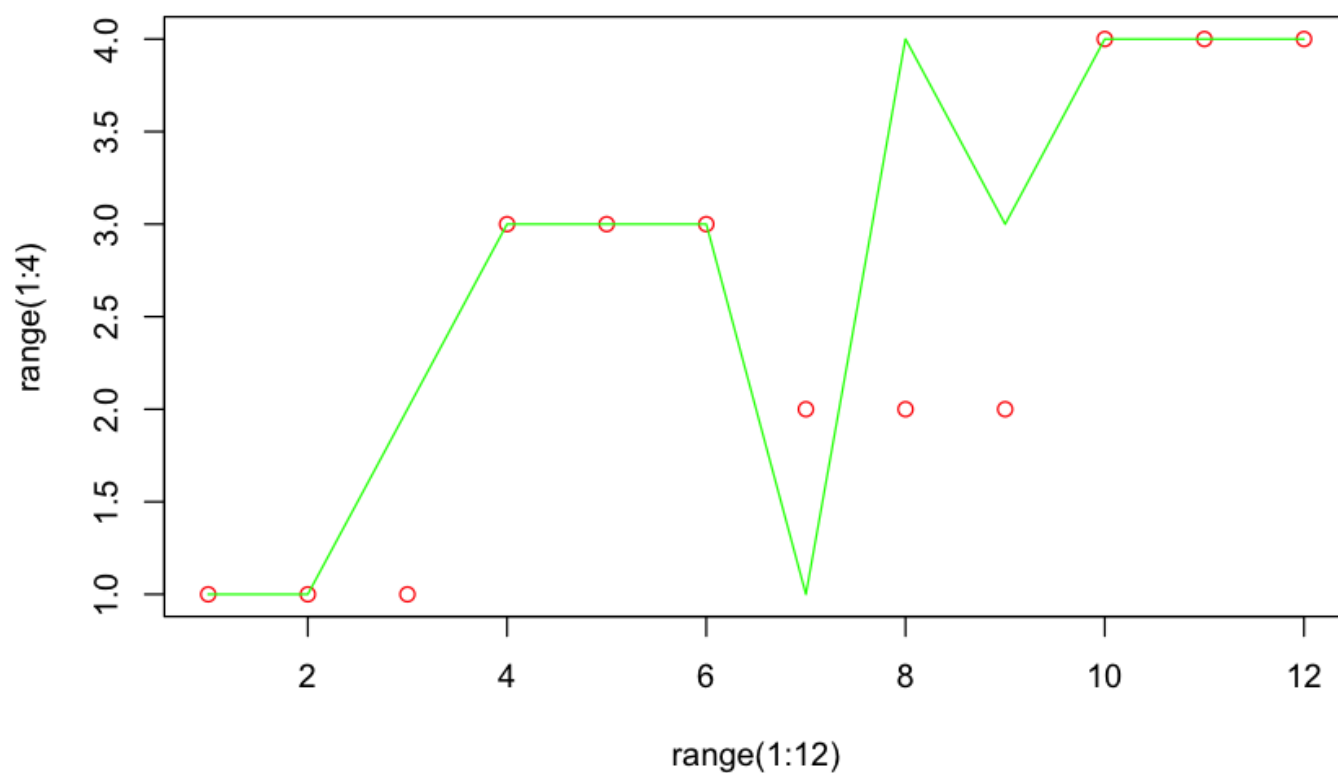
```
m_hier <- c(1,1,1,3,3,3,2,2,2,4,4,4)
```

Hide

```
plot(range(1:12),range(1:4), type='n')
points(m_hier, col='red')
```

Hide

```
lines(l_hier, col='green')
```

[Hide](#)

```
predict(clust.hier,newdata=unlist(m3$glucoseValue))
```

```
[1] 2
```

[Hide](#)

```
predict(clust.hier,newdata=unlist(m6$glucoseValue))
```

```
[1] 3
```

[Hide](#)

```
predict(clust.hier,newdata=unlist(m9$glucoseValue))
```

```
[1] 3
```

[Hide](#)

```
predict(clust.hier,newdata=unlist(m12$glucoseValue))
```

```
[1] 4
```

[Hide](#)

```
clust.par <- tsclust(training_frame, type = "partitional", k = 4L, distance = "dtw2", trace=TRUE)
```

Precomputing distance matrix...

Iteration 1: Changes / Distsum = 12 / 611.5245

Iteration 2: Changes / Distsum = 1 / 545.6121

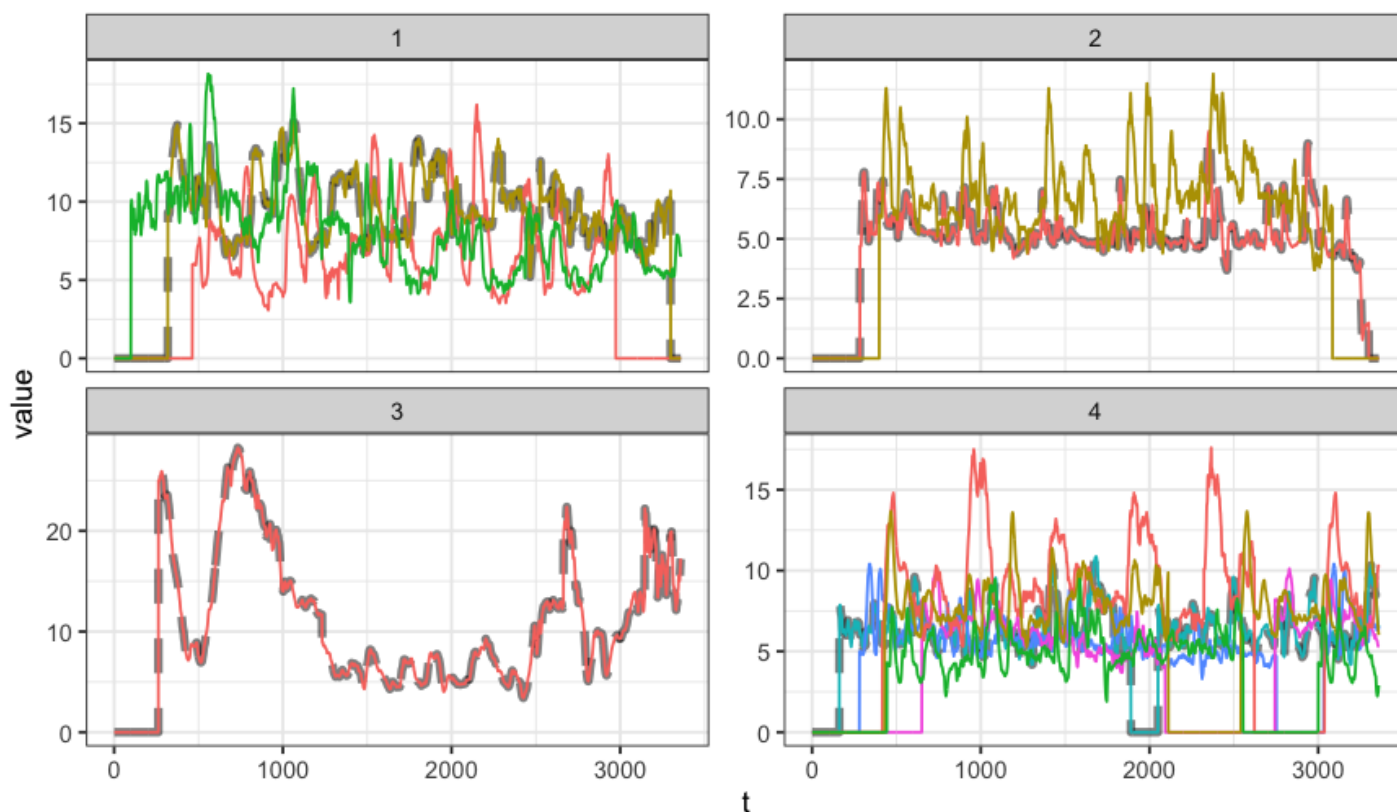
Iteration 3: Changes / Distsum = 0 / 545.6121

Elapsed time is 62.168 seconds.

[Hide](#)

```
plot(clust.par, type="sc")
```

Clusters' members


[Hide](#)

```
t(cbind(training_frame[,0], cluster = clust.par@cluster))
```

```
      [,1] [,2] [,3] [,4] [,5] [,6] [,7] [,8] [,9] [,10] [,11] [,12]
cluster  1    2    3    4    1    4    2    4    1    4    4    4
```

[Hide](#)

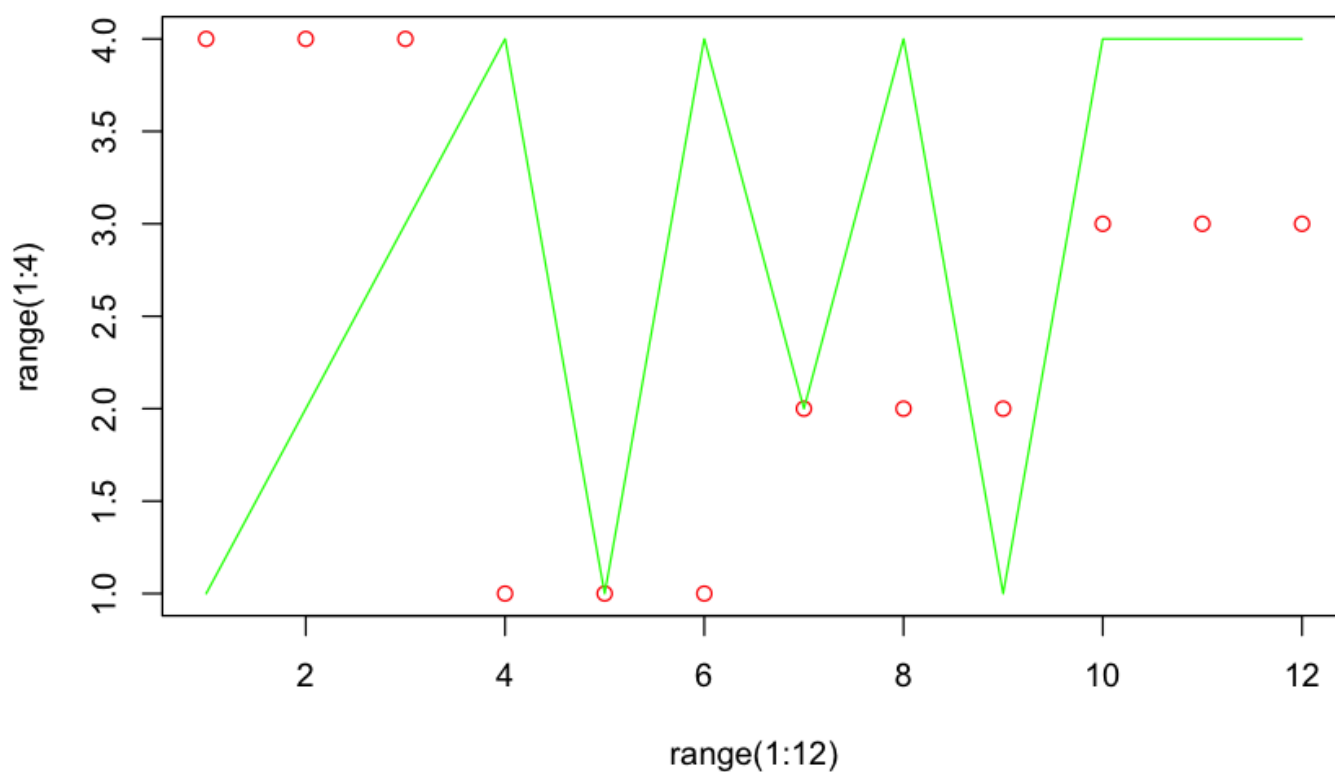
```
l_par <- clust.par@cluster  
  
m_par <- c(4,4,4,1,1,1,2,2,2,3,3,3)
```

Hide

```
plot(range(1:12),range(1:4), type='n')  
points(m_par, col='red')
```

Hide

```
lines(l_par, col='green')
```



Hide

```
predict(clust.par,newdata=unlist(m3$glucoseValue))
```

```
[1] 3
```

Hide

```
predict(clust.par,newdata=unlist(m6$glucoseValue))
```

```
[1] 1
```

Hide

```
predict(clust.par,newdata=unlist(m9$glucoseValue))
```

```
[1] 1
```

Hide

```
predict(clust.par,newdata=unlist(m12$glucoseValue))
```

```
[1] 2
```

Hide

```
#predicted_labels  
#test_labels  
index_hier=arandi(l_hier,m_hier)  
unadjusted_hier=arandi(l_hier,m_hier,adjust=FALSE)  
index_hier
```

```
[1] 0.3966245
```

Hide

```
unadjusted_hier
```

```
[1] 0.8030303
```

Hide

```
index_par=arandi(l_par,m_par)  
unadjusted_par=arandi(l_par,m_par,adjust=FALSE)  
index_par
```

```
[1] 0.04528302
```

Hide

```
unadjusted_par
```

```
[1] 0.6515152
```

Hide

```
colors = c('red','blue')  
types = c('Hierarchical Clustering','Partitional Clustering')
```

Hide


```
plot(NULL,NULL, type='n',ylim=c(0,1), xlim=c(0,2), xlab='Index', ylab='Rand Index', main  
='Random Index of Hierarchical and Partitional Clustering')
```

```
legend("topright",legend = types, col = colors, title = 'Clustering Types', pch=1)
```

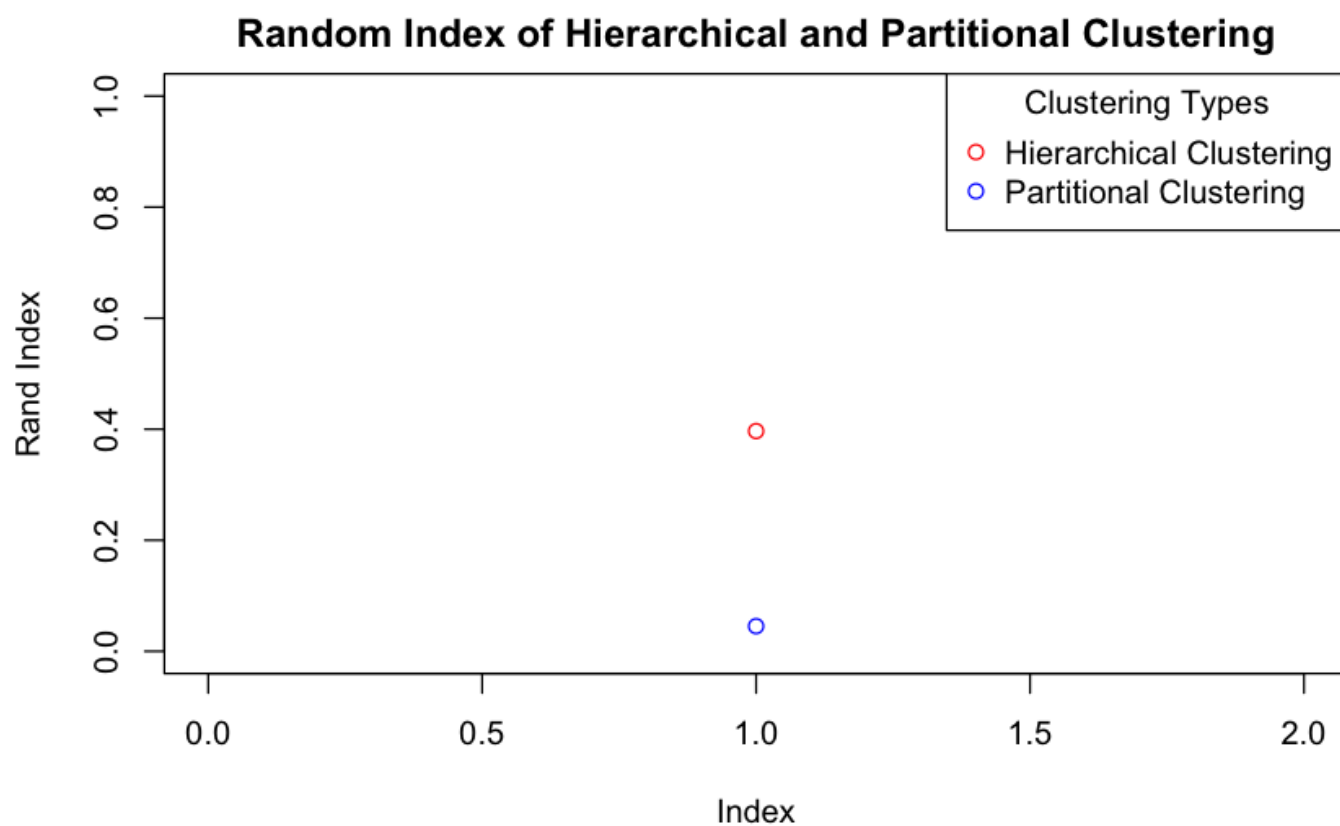
[Hide](#)

```
par(new=TRUE)
```

```
points(index_hier, col='red')
```

[Hide](#)

```
points(index_par, col='blue')
```

[Hide](#)

```
NA
```

```
NA
```

[Hide](#)

```
plot(NULL,NULL, type='n',ylim=c(0,1), xlim=c(0,2), xlab='Index', ylab='Rand Index', main  
='Adjusted Index of Hierarchical and Partitional Clustering')
```

```
legend("topright",legend = types, col = colors, title = 'Clustering Types', pch=1)
```

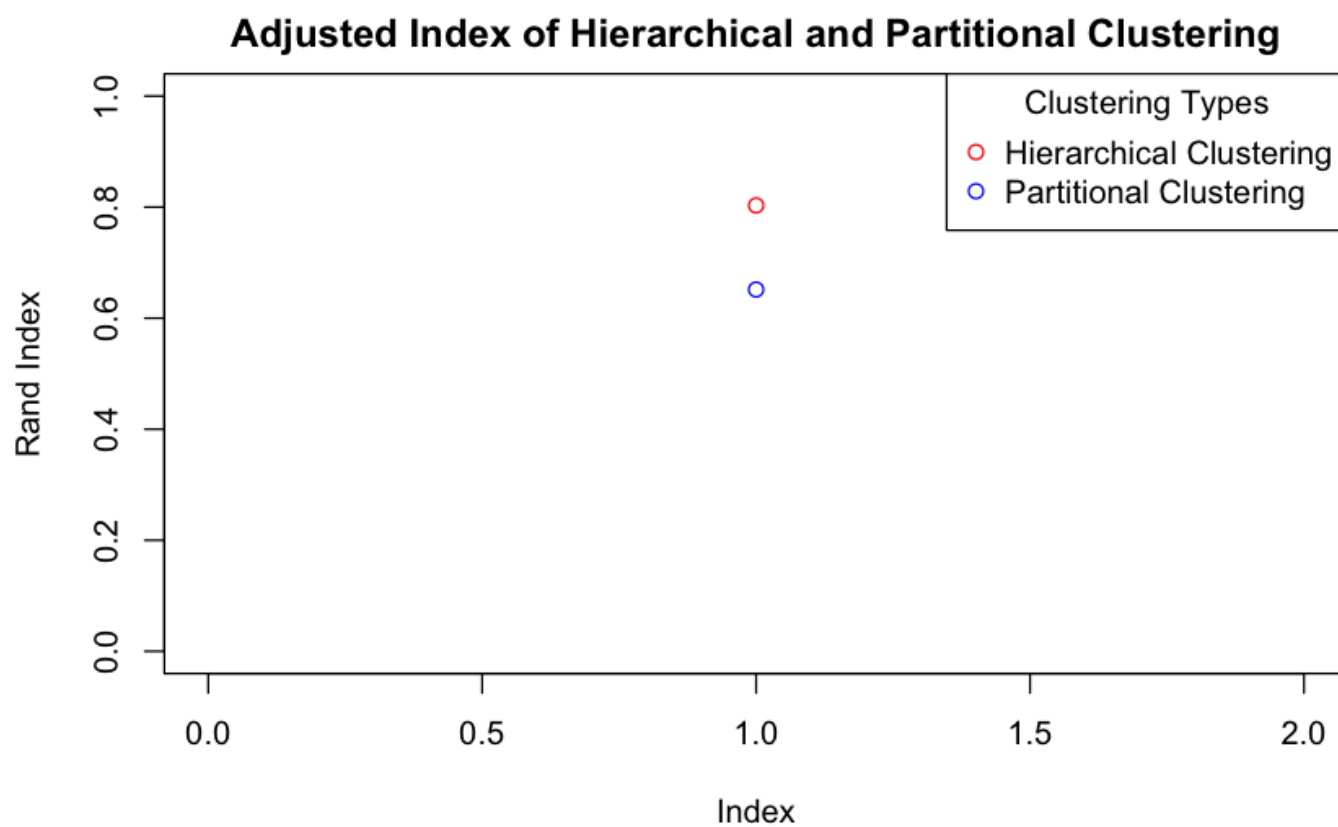
Hide

```
par(new=TRUE)
```

```
points(unadjusted_hier, col='red')
```

Hide

```
points(unadjusted_par,col='blue')
```



Hide

```
NA
```

```
NA
```