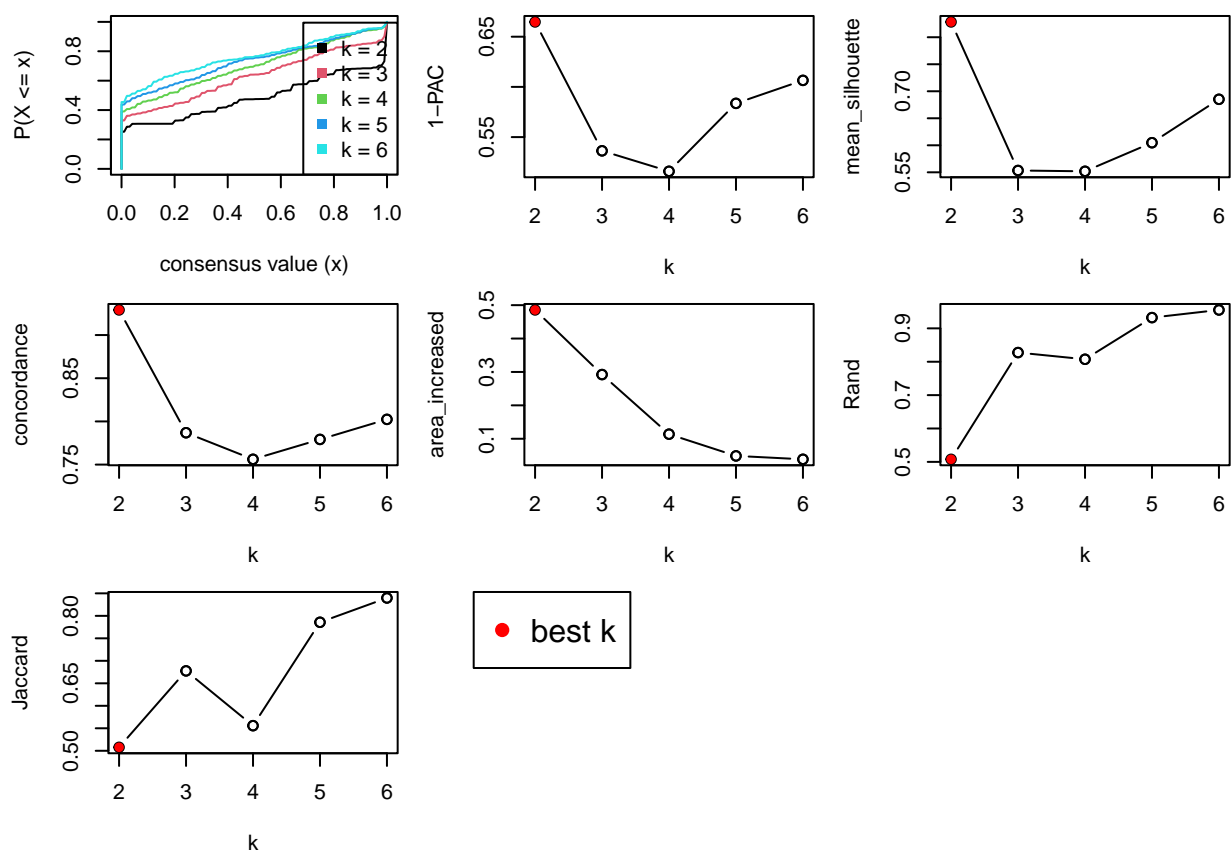


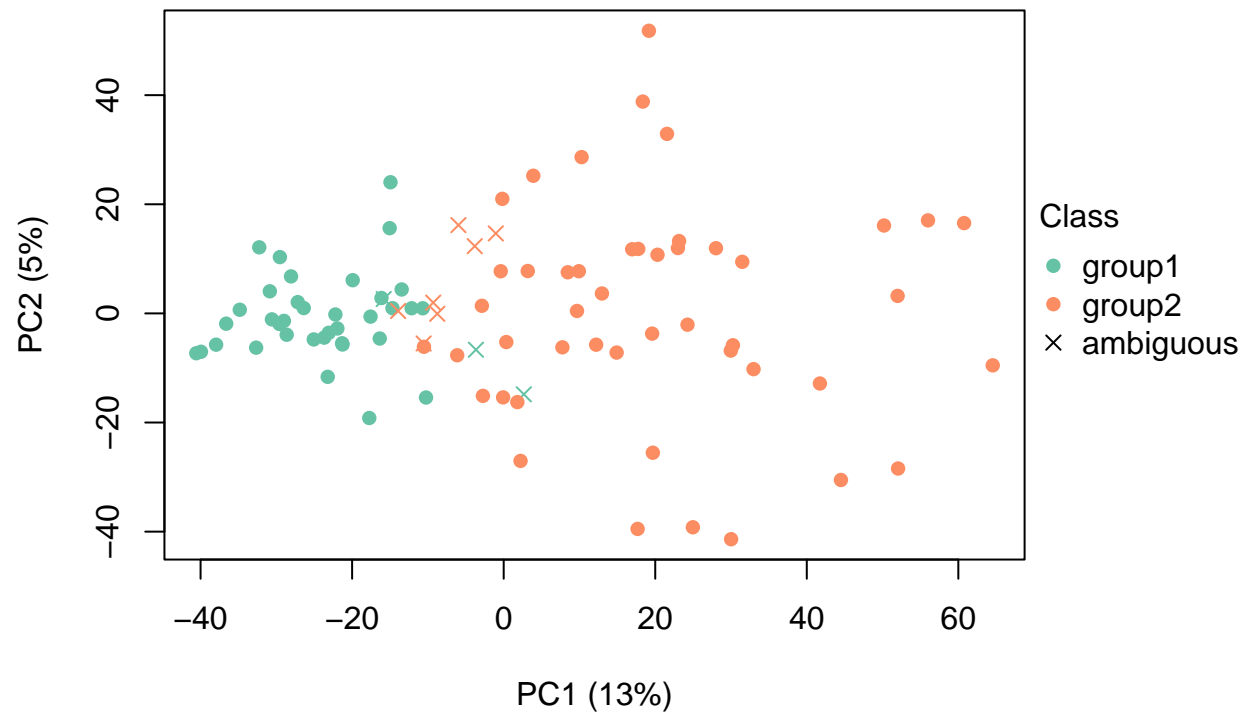
Dimension Reduction

```
library(cola)
res_list <- readRDS("Cola_res_list.rds")
res <- res_list["SD:hclust"]
select_partition_number(res)
```



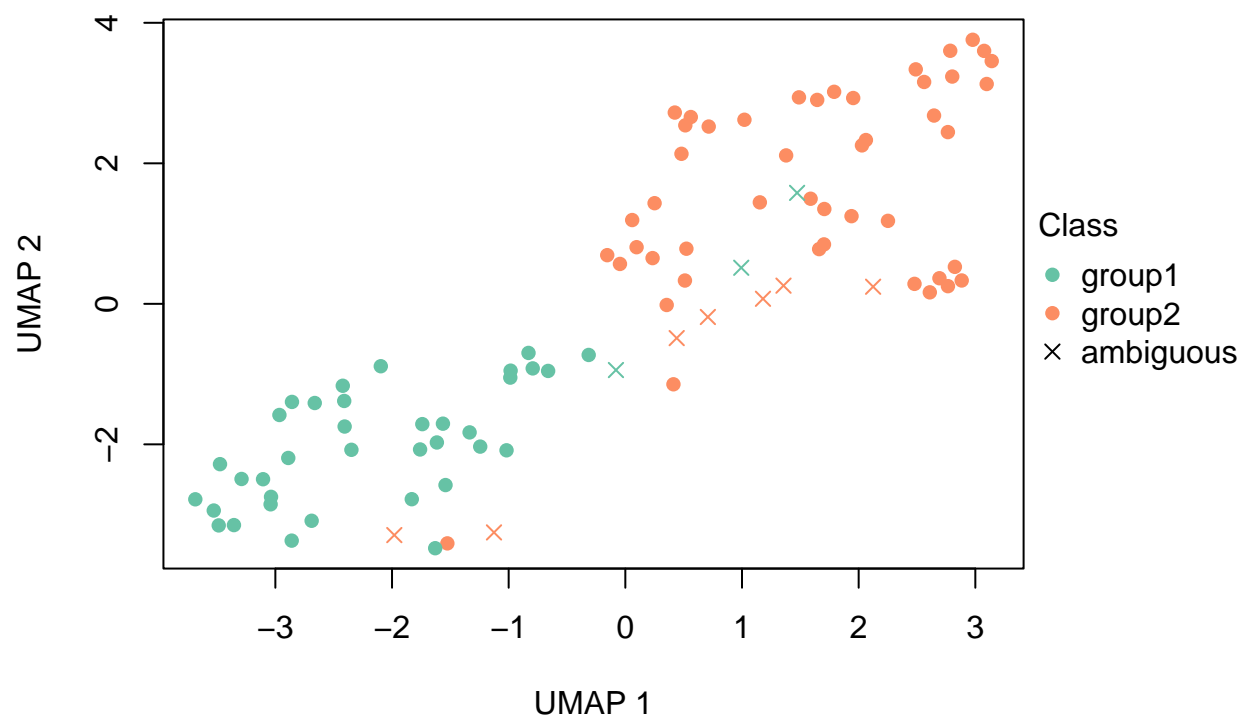
```
# PCA
dimension_reduction(res, k = 2, method = "PCA")
```

PCA on 17730 rows with highest SD scores, rows are scaled
83/93 confident samples (silhouette > 0.5)



```
# UMAP  
dimension_reduction(res, k = 2, method = "UMAP")
```

**UMAP on 17730 rows with highest SD scores, rows are scaled
83/93 confident samples (silhouette > 0.5), with 10 PCs**



```
# t-SNE  
dimension_reduction(res, k = 2, method = "t-SNE")
```

t-SNE on 17730 rows with highest SD scores, rows are scaled
83/93 confident samples (silhouette > 0.5), with 10 PCs

