Exercises

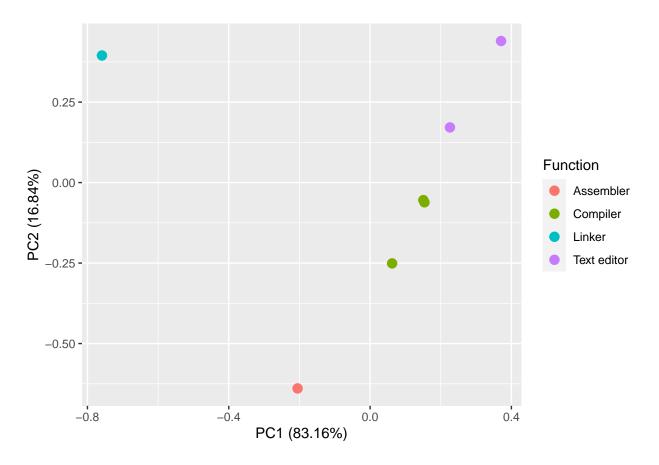
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6.1 The CPU time and disk I/O's of seven programs are shown in Table 6.7. Determine the equation for principal factors.

Load the dataset

```
dataset <- read.csv("table-6.7.csv")</pre>
print(dataset)
##
     Program.Name
                      Function CPU.Time I.O.s
## 1
                                      14 2735
               TKB
                        Linker
## 2
                     Assembler
                                      13
                                          253
              MAC
## 3
            COBOL
                      Compiler
                                       8
                                             27
## 4
            BASIC
                      Compiler
                                       6
                                             27
## 5
           Pascal
                      Compiler
                                       6
                                            12
## 6
               EDT Text editor
                                             91
               SOS Text editor
## 7
                                             33
Run principal-component analysis algorithm
pca_result <- prcomp(dataset[3:4], scale = TRUE)</pre>
print(pca_result)
## Standard deviations (1, .., p=2):
## [1] 1.2896552 0.5803357
## Rotation (n x k) = (2 \times 2):
                    PC1
## CPU.Time -0.7071068 -0.7071068
## I.O.s
            -0.7071068 0.7071068
Plot the values of principal factors
library(ggfortify)
autoplot(pca_result, data = dataset, colour = 'Function', size = 3)
```



6.2 Using a spanning-tree algorithm for cluster analysis, prepare a dendrogram for the data shown in Table 6.7. Interpret the result of your analysis.

Make program name the row name, remove "Function" collumn

```
library(tibble)
dataset <- column_to_rownames(dataset, var = "Program.Name")[,-1]
print(dataset)</pre>
```

##		${\tt CPU.Time}$	I.O.s
##	TKB	14	2735
##	MAC	13	253
##	COBOL	8	27
##	BASIC	6	27
##	Pascal	6	12
##	EDT	4	91
##	SOS	1	33

Compute the intercluster distance matrix and do the agglomerative hierarchical clustering

```
dist <- dist(scale(dataset), method = "euclidean")
clust <- hclust(dist, method = "ward.D2")</pre>
```

Plot the dendrogram

```
dend <- as.dendrogram(clust)
plot(dend)</pre>
```

