Problem Statement: Iris Flower Classification

Import Necessary Library

In [4]:

library(ggplot2)

Load the Dataset

In [5]:

```
df <- iris
```

In [6]:

head(df)

A data.frame: 6 × 5

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	Species
	<db ></db >	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<fct></fct>
1	5.1	3.5	1.4	0.2	setosa
2	4.9	3.0	1.4	0.2	setosa
3	4.7	3.2	1.3	0.2	setosa
4	4.6	3.1	1.5	0.2	setosa
5	5.0	3.6	1.4	0.2	setosa
6	5.4	3.9	1.7	0.4	setosa

Summary of the dataset

In [14]:

summa	ary(df)			
Se	pal.Length	Sepal.Width	Petal.Length	Petal.Width
Min	. :4.300	Min. :2.000	Min. :1.000	Min. :0.100
1st	Qu.:5.100	1st Qu.:2.800	1st Qu.:1.600	1st Qu.:0.300
Med	ian :5.800	Median :3.000	Median :4.350	Median :1.300
Mea	n :5.843	Mean :3.057	Mean :3.758	Mean :1.199

3rd Qu.:5.100 3rd Qu.:1.800

Max. :2.500

Max. :6.900

Max. :7.900 Species setosa :50

versicolor:50
virginica :50

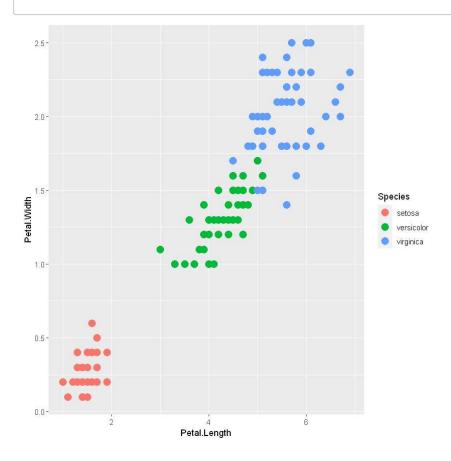
Max. :4.400

3rd Qu.:6.400 3rd Qu.:3.300

Data Visualization

In [7]:

ggplot(df, aes(Petal.Length, Petal.Width)) + geom_point(aes(col=Species), size=4)



Eliminating the target variable

In [8]:

Xtrain <- df[, -5]
head(Xtrain)</pre>

A data frame: 6 × 4

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
	<db ></db	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>
1	5.1	3.5	1.4	0.2
2	4.9	3.0	1.4	0.2
3	4.7	3.2	1.3	0.2
4	4.6	3.1	1.5	0.2
5	5.0	3.6	1.4	0.2
6	5.4	3.9	1.7	0.4

Scale the dataset

In [9]:

```
scal <- scale(Xtrain)</pre>
```

In [10]:

head(scal)

A matrix: 6 × 4 of type dbl

Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
-0.8976739	1.01560199	-1.335752	-1.311052
-1.1392005	-0.13153881	-1.335752	-1.311052
-1.3807271	0.32731751	-1.392399	-1.311052
-1.5014904	0.09788935	- 1.279104	-1.311052
-1.0184372	1.24503015	-1.335752	-1.311052
-0.5353840	1.93331463	-1.165809	-1.048667

In [11]:

```
levels(df$Species)
```

'setosa' 'versicolor' 'virginica'

In [12]:

```
ytrain <- iris[,5]</pre>
```

In [13]:

ytrain

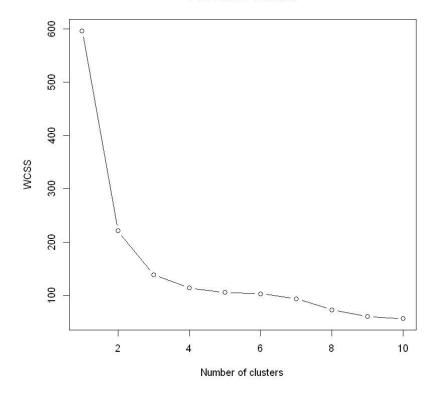
setosa versicolor virginica virginica

► Levels:

Using the elbow method to find the optimal number of clusters

In [47]:

The Elbow Method



In []:

For k=3, apply the K-means clustering algorithm.

In [15]:

```
irisCluster <- kmeans(df[,1:4], center=3, nstart=20)
irisCluster</pre>
```

K-means clustering with 3 clusters of sizes 62, 38, 50

Cluster means:

```
Sepal.Length Sepal.Width Petal.Length Petal.Width
1
      5.901613
                  2.748387
                                4.393548
                                            1.433871
2
      6.850000
                  3.073684
                                5.742105
                                            2.071053
3
      5.006000
                  3.428000
                                1.462000
                                            0.246000
```

Clustering vector:

Within cluster sum of squares by cluster:

[1] 39.82097 23.87947 15.15100 (between_SS / total_SS = 88.4 %)

Available components:

```
In [16]:
```

```
km <- kmeans(scal[,1:4], center=3, nstart=20)
km</pre>
```

K-means clustering with 3 clusters of sizes 50, 47, 53

```
Cluster means:
```

Clustering vector:

Within cluster sum of squares by cluster:

```
[1] 47.35062 47.45019 44.08754 (between_SS / total_SS = 76.7 %)
```

Available components:

In [17]:

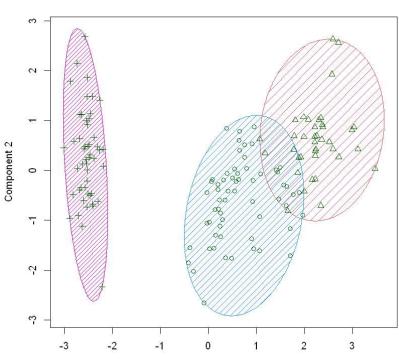
```
table(irisCluster$cluster, df$Species)
```

```
setosa versicolor virginica
1 0 48 14
2 0 2 36
3 50 0 0
```

In [18]:

library(cluster)
clusplot(iris, irisCluster\$cluster, color=T, shade=T, labels=0, lines=0)

CLUSPLOT(iris)

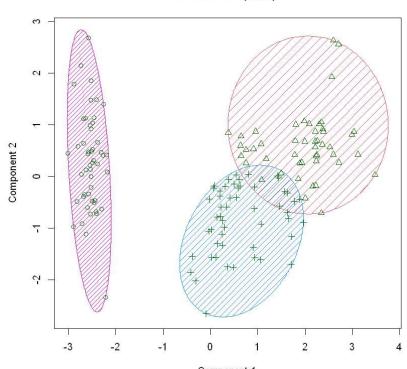


 $\label{eq:Component 1} Component \ 1$ These two components explain 95.02 % of the point variability.

In [19]:

library(cluster)
clusplot(iris, km\$cluster, color=T, shade=T, labels=0, lines=0)

CLUSPLOT(iris)



 $\label{eq:Component 1} Component \ 1$ These two components explain 95.02 % of the point variability.

In []:

In [20]:

km\$betweenss/km\$totss

0.766965839400417

In [21]:

irisCluster\$betweenss/irisCluster\$totss

0.884275251344648

In [26]:

aggregate(Xtrain, by=list(cluster=irisCluster\$cluster), mean)

A data frame: 3 × 5

cluster	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
<int></int>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>
1	5.901613	2.748387	4.393548	1.433871
2	6.850000	3.073684	5.742105	2.071053
3	5.006000	3.428000	1.462000	0.246000

If you want to add the point classifications to the original data

In [27]:

dd <- cbind(Xtrain, cluster = irisCluster\$cluster)
head(dd)</pre>

A data frame: 6 × 5

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width	cluster
	<db ></db	<dbl></dbl>	<dbl></dbl>	<dbl></dbl>	<int></int>
1	5.1	3.5	1.4	0.2	3
2	4.9	3.0	1.4	0.2	3
3	4.7	3.2	1.3	0.2	3
4	4.6	3.1	1.5	0.2	3
5	5.0	3.6	1.4	0.2	3
6	5.4	3.9	1.7	0.4	3

In [31]:

Cluster number for each of the observations
irisCluster\$cluster

```
      3
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```

In [32]:

head(irisCluster\$cluster, 4)

3 3 3 3

In [33]:

Cluster size
irisCluster\$size

62 38 50

In [34]:

Cluster means
irisCluster\$centers

A matrix: 3 × 4 of type dbl

	Sepal.Length	Sepal.Width	Petal.Length	Petal.Width
1	5.901613	2.748387	4.393548	1.433871
2	6.850000	3.073684	5.742105	2.071053
3	5 006000	3 428000	1 462000	0.246000

```
In [50]:
```

```
km2 <- kmeans(scal[,1:4], center=4, nstart=20)
km2</pre>
```

K-means clustering with 4 clusters of sizes 25, 47, 53, 25

```
Cluster means:
```

```
Sepal.Length Sepal.Width Petal.Length Petal.Width
1 -0.71894419 1.50198969 -1.2972312 -1.2165934
2 1.13217737 0.08812645 0.9928284 1.0141287
3 -0.05005221 -0.88042696 0.3465767 0.2805873
4 -1.30343857 0.19883774 -1.3040289 -1.2848136
```

Clustering vector:

Within cluster sum of squares by cluster:
[1] 12.147537 47.450194 44.087545 9.646348
(between_SS / total_SS = 81.0 %)

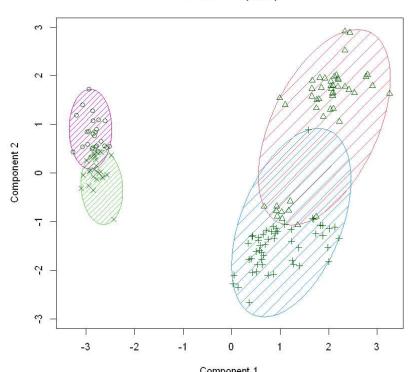
Available components:

```
[1] "cluster" "centers" "totss" "withinss" "tot.withins
s"
[6] "betweenss" "size" "iter" "ifault"
```

In [51]:

clusplot(iris, km2\$cluster, color=T, shade=T, labels=0, lines=0)

CLUSPLOT(iris)



 $\label{eq:component} \mbox{Component 1}$ These two components explain 88.99 % of the point variability.

In [52]:

km2\$tot.withinss

113.331623512778

In []: