

Introduction to PCA

UNSUPERVISED LEARNING IN R



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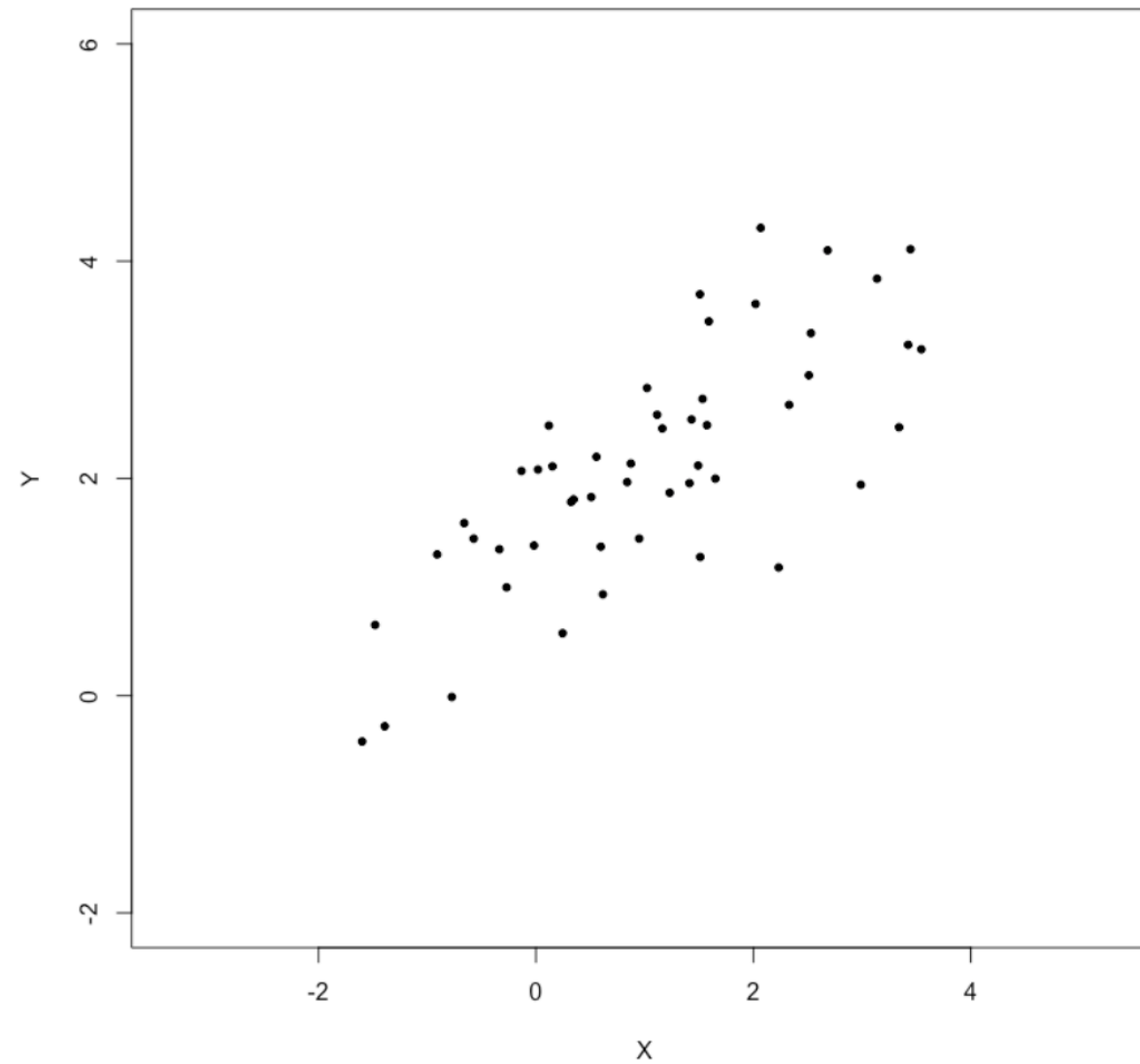
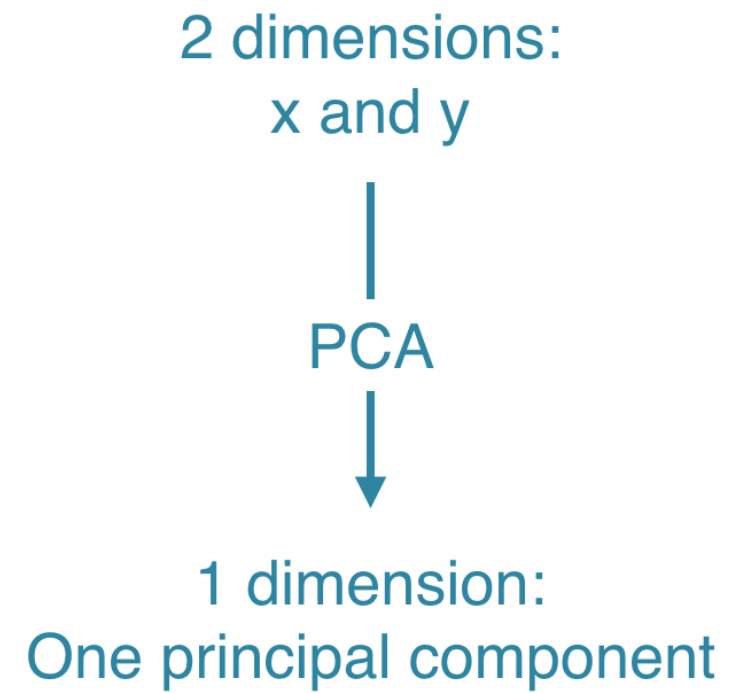
Two methods of clustering

- Two methods of clustering - finding groups of homogeneous items
- Next up, dimensionality reduction
 - Find structure in features
 - Aid in visualization

Dimensionality reduction

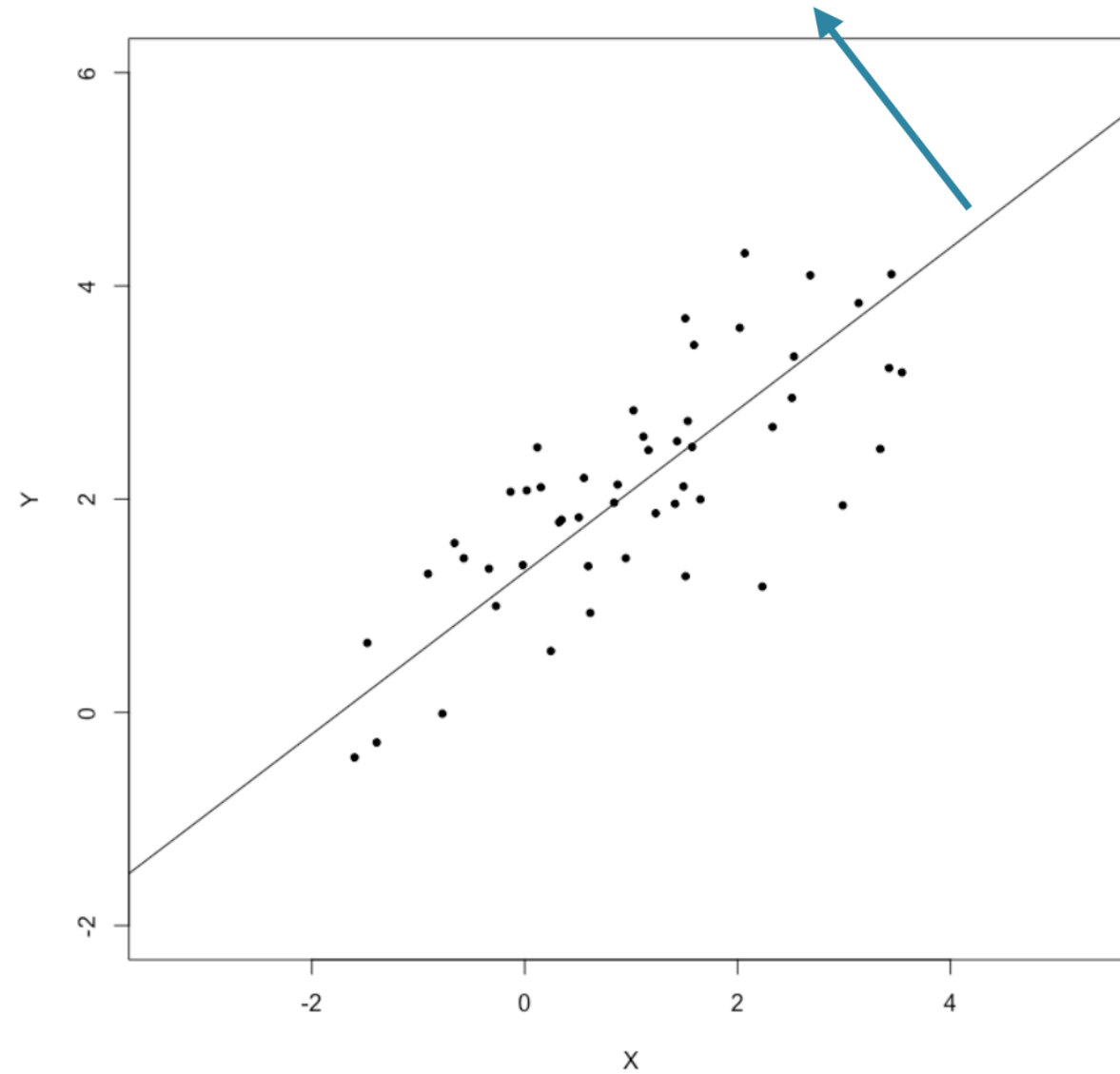
- A popular method is principal component analysis (PCA)
- Three goals when finding lower dimensional representation of features:
 - Find linear combination of variables to create principal components
 - Maintain most variance in the data
 - Principal components are uncorrelated (i.e., orthogonal to each other)

PCA intuition



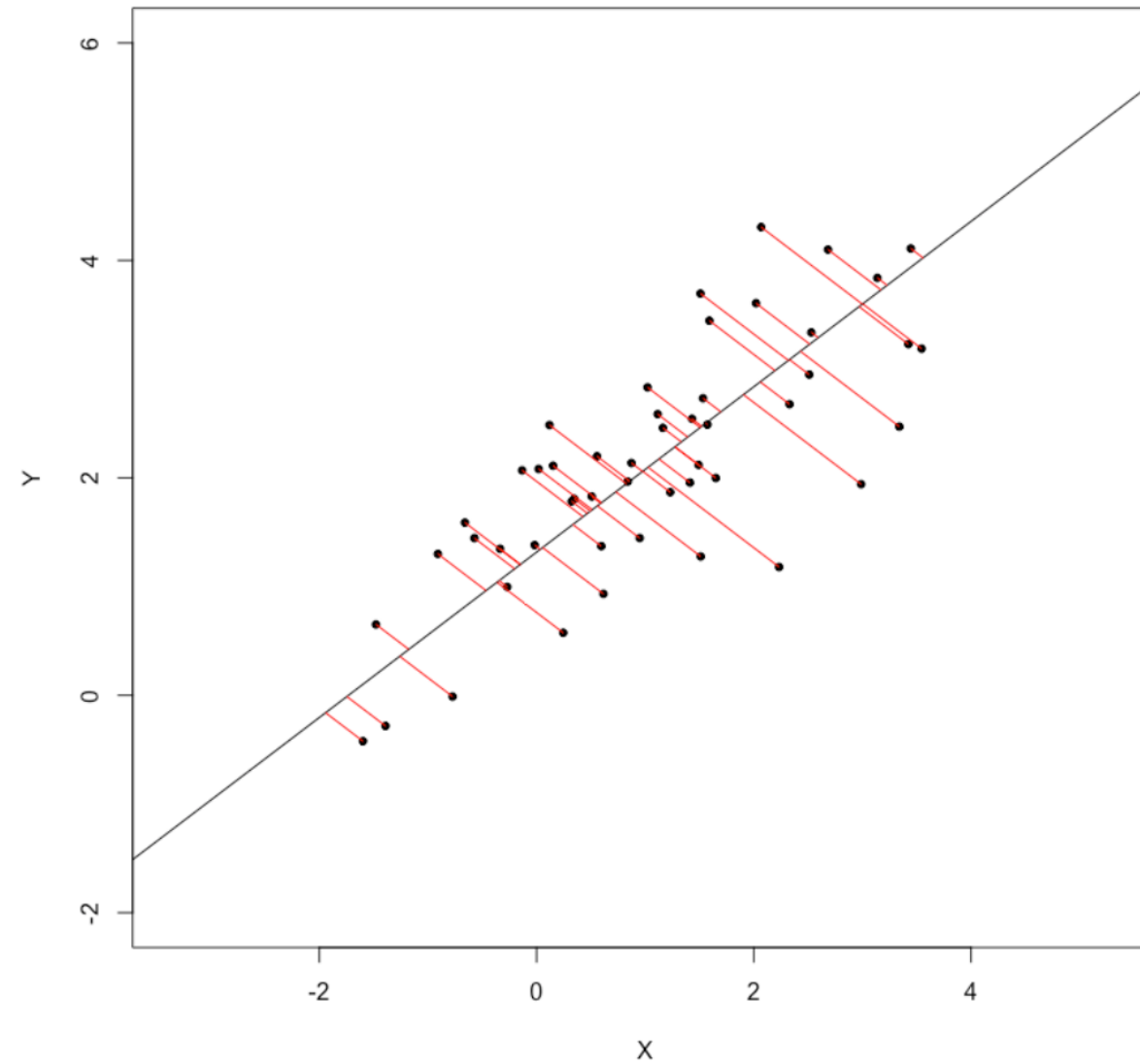
PCA intuition

Regression line represents the principal component

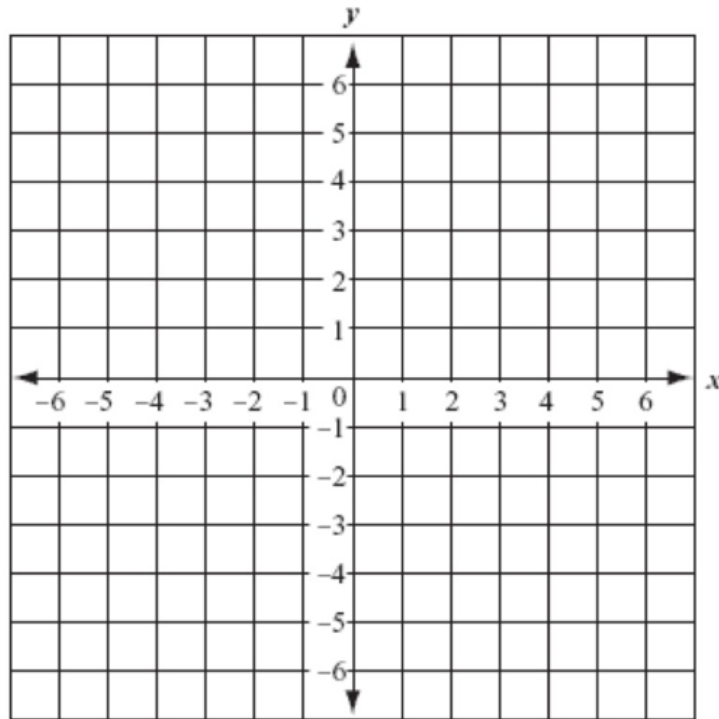


PCA intuition

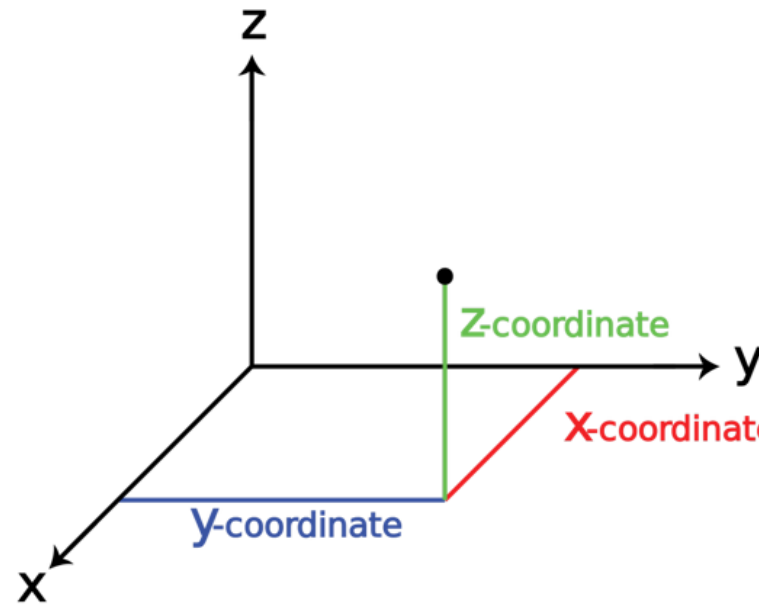
Projected values on principal component is called component scores or factor scores



Visualization of high dimensional data



Two-dimensional

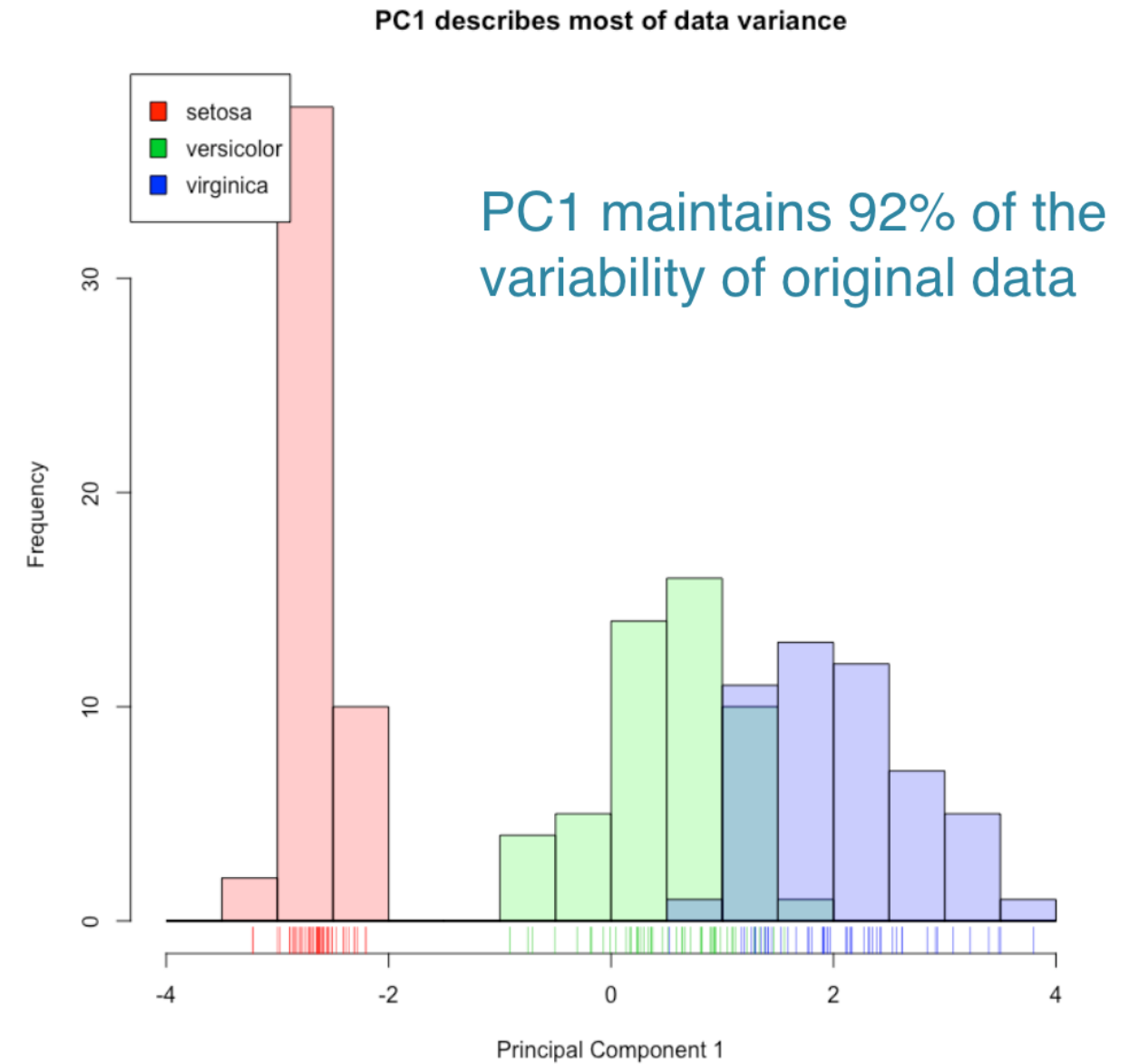
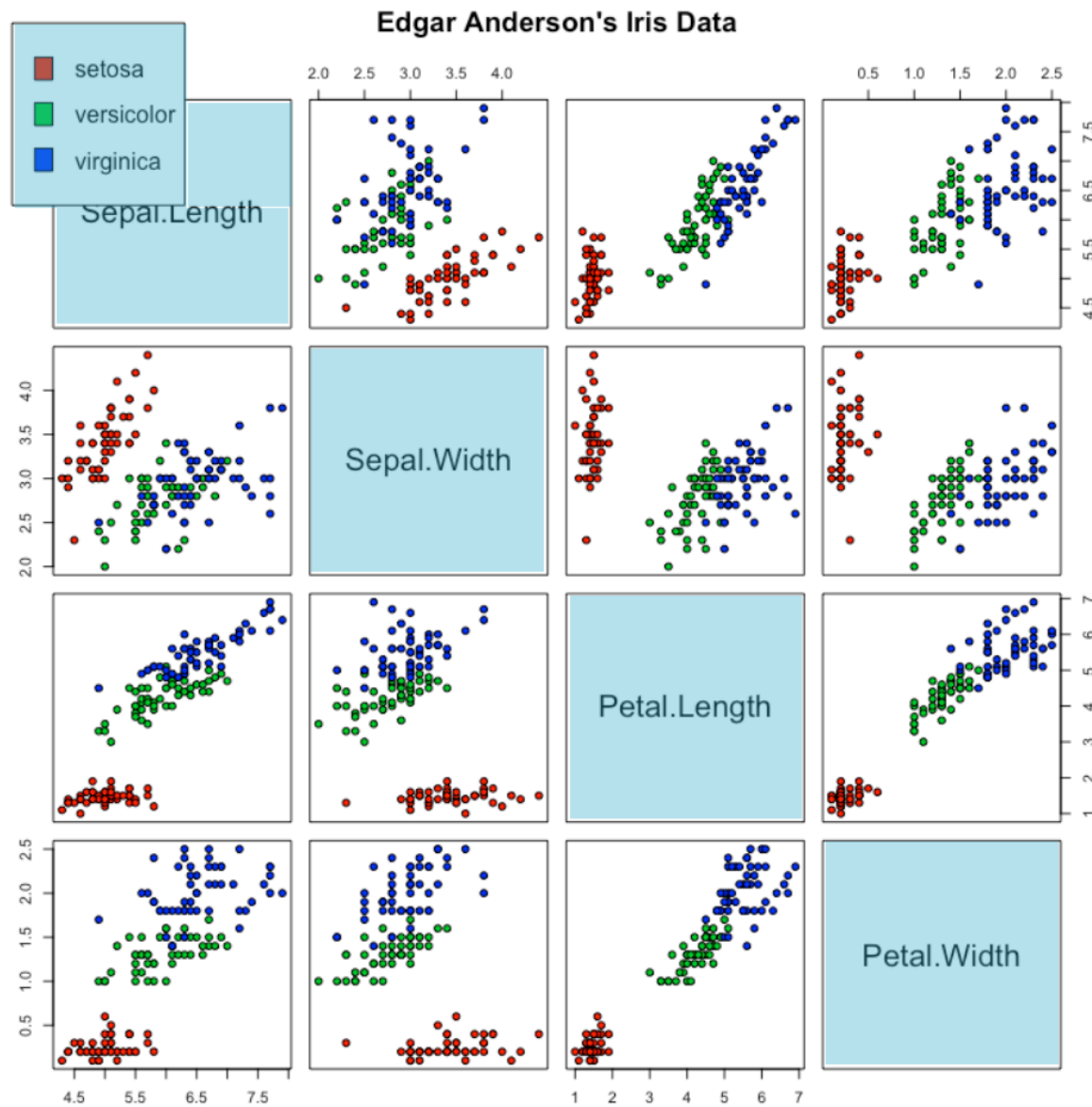


Three-dimensional



Four-dimensional

Visualization



PCA in R

```
pr.iris <- prcomp(x = iris[-5],  
                  scale = FALSE,  
                  center = TRUE)  
  
summary(pr.iris)
```

Importance of components:

	PC1	PC2	PC3	PC4
Standard deviation	2.0563	0.49262	0.2797	0.15439
Proportion of Variance	0.9246	0.05307	0.0171	0.00521
Cumulative Proportion	0.9246	0.97769	0.9948	1.00000

Let's practice!
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Visualizing and interpreting PCA results

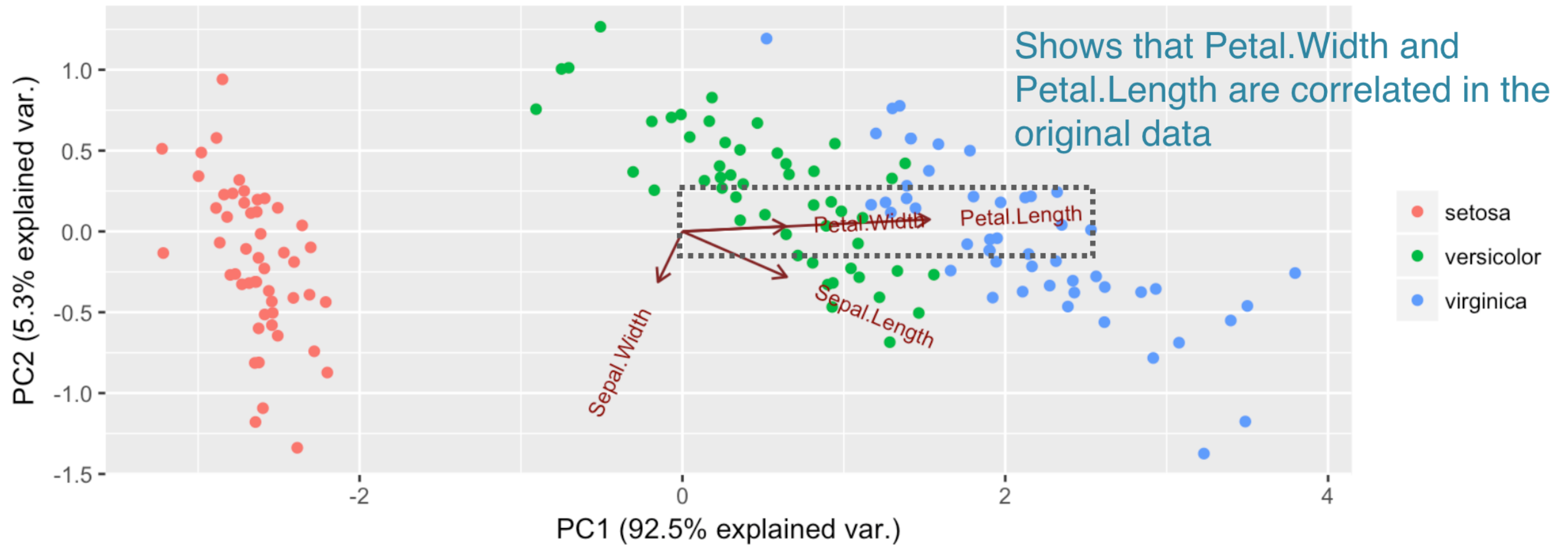
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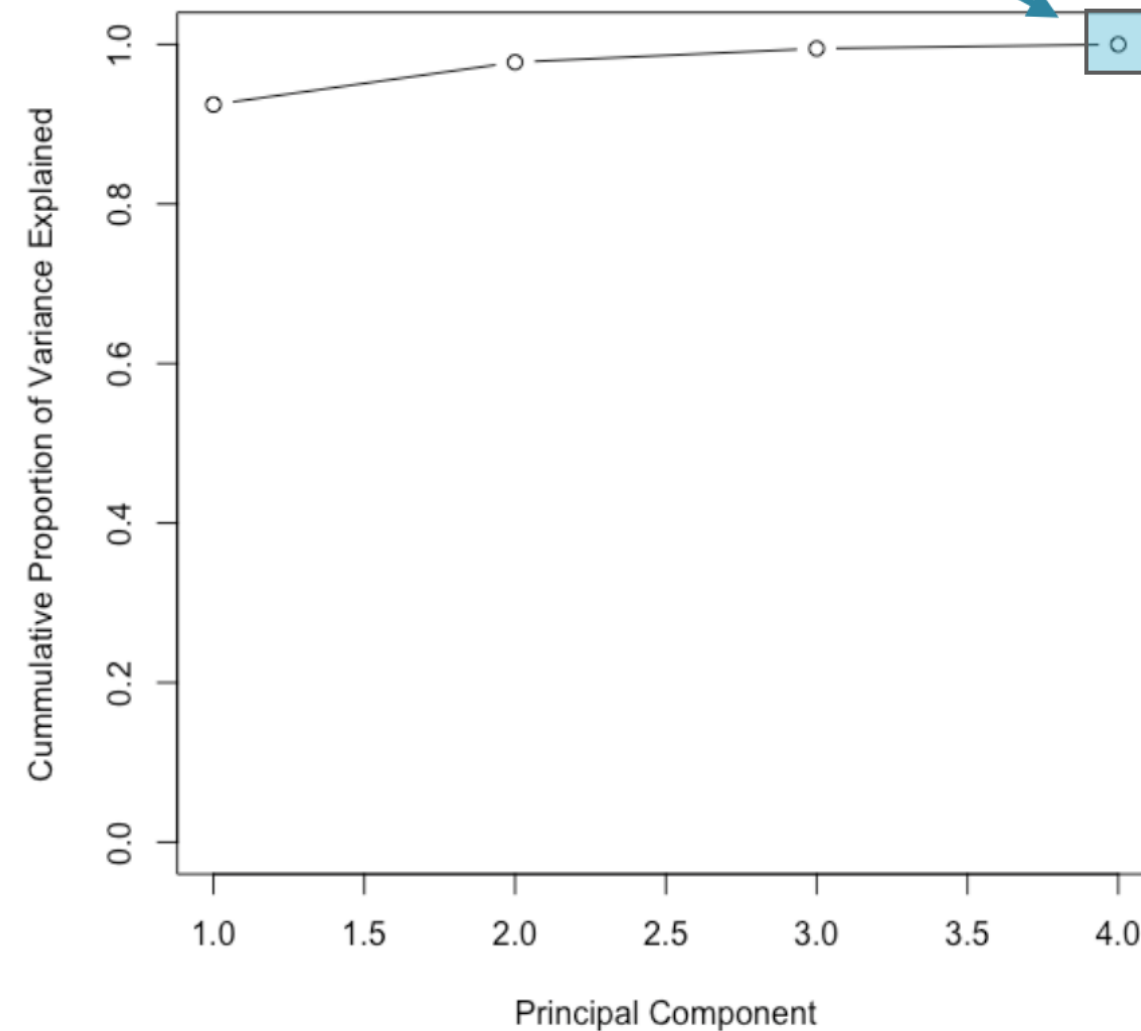
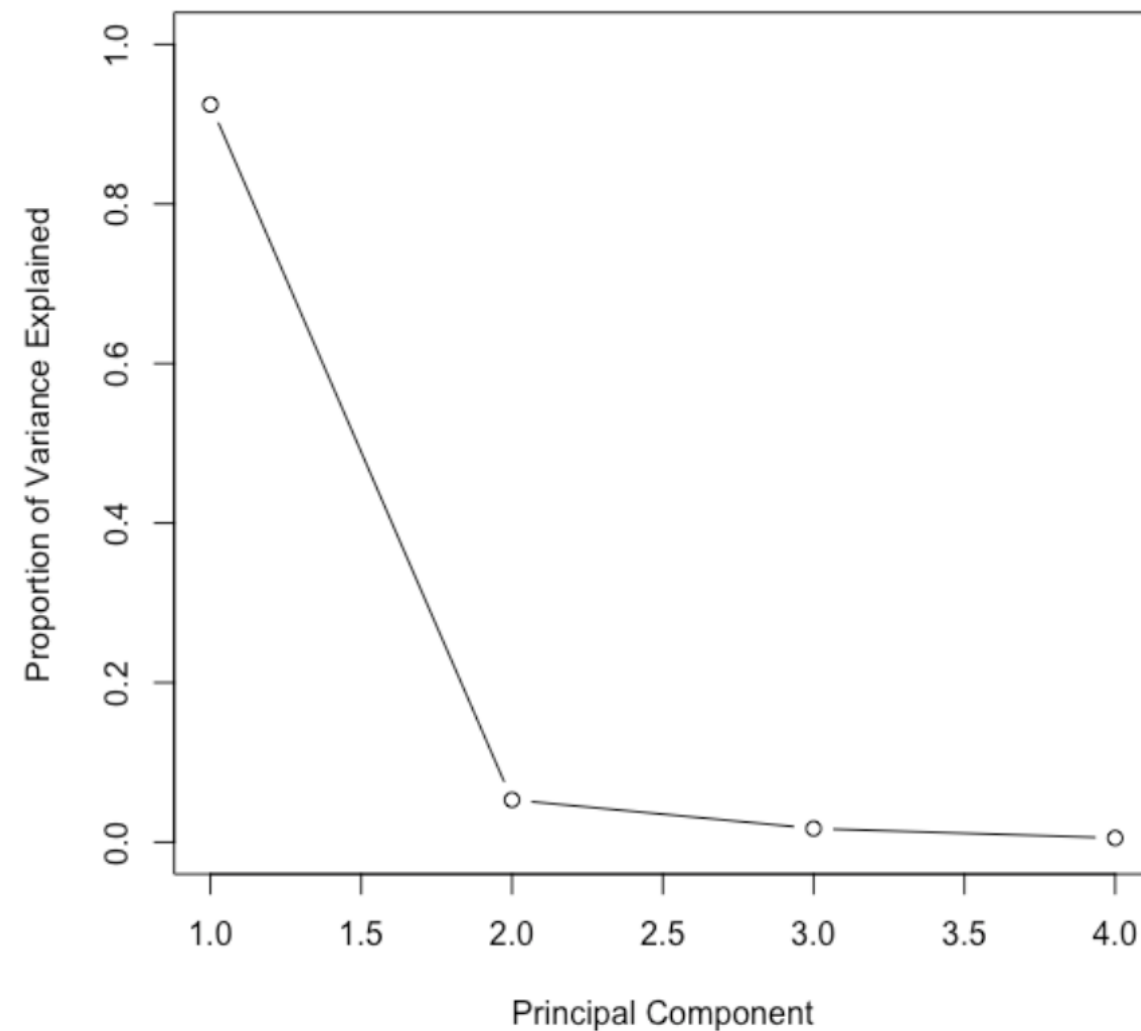
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Biplot



Scree plot

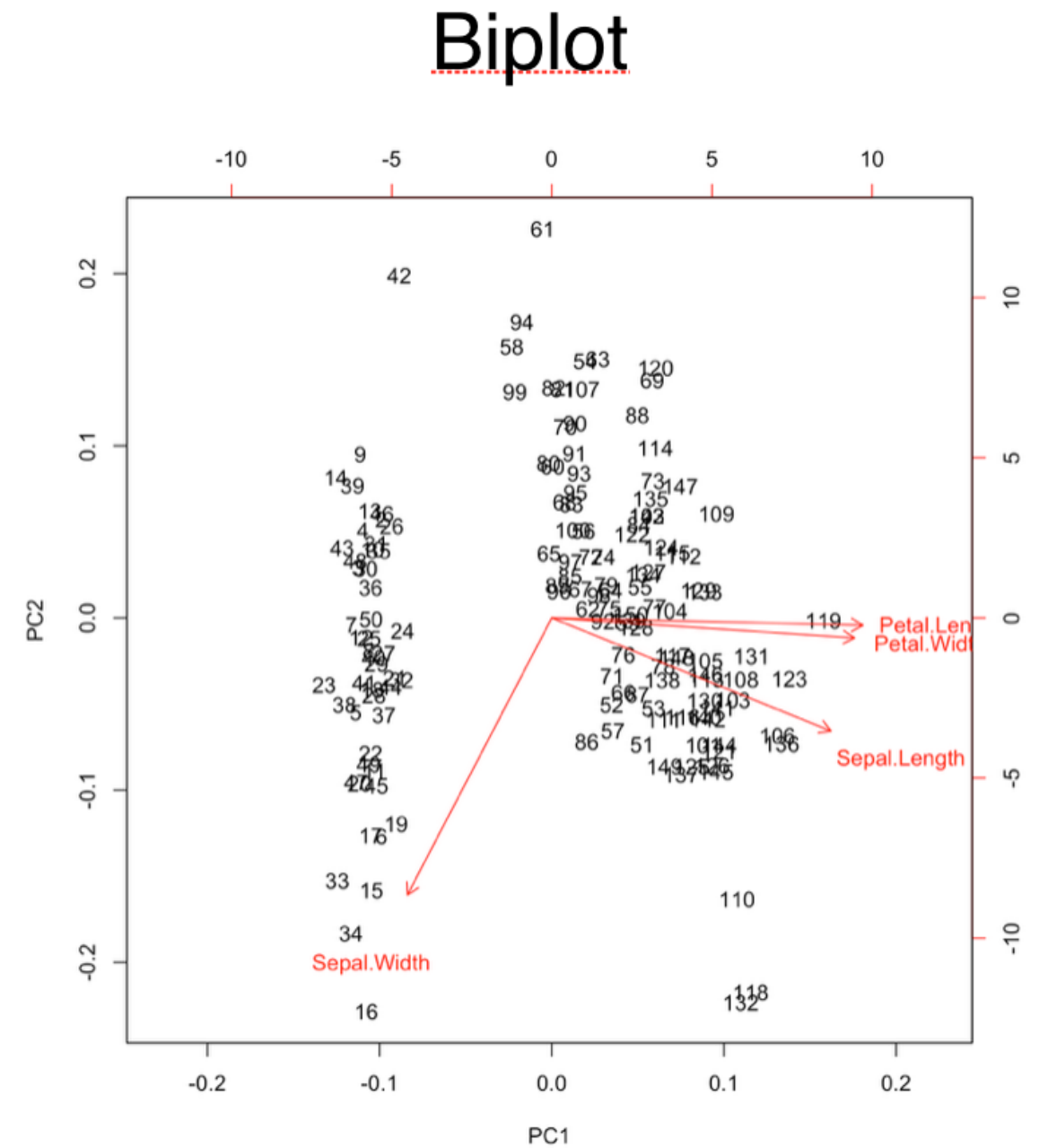
When number of PCs and number of original features are the same, the cumulative proportion of variance explained is 1



Biplots in R

```
# Creating a biplot
pr.iris <- prcomp(x = iris[-5],
                  scale = FALSE,
                  center = TRUE)

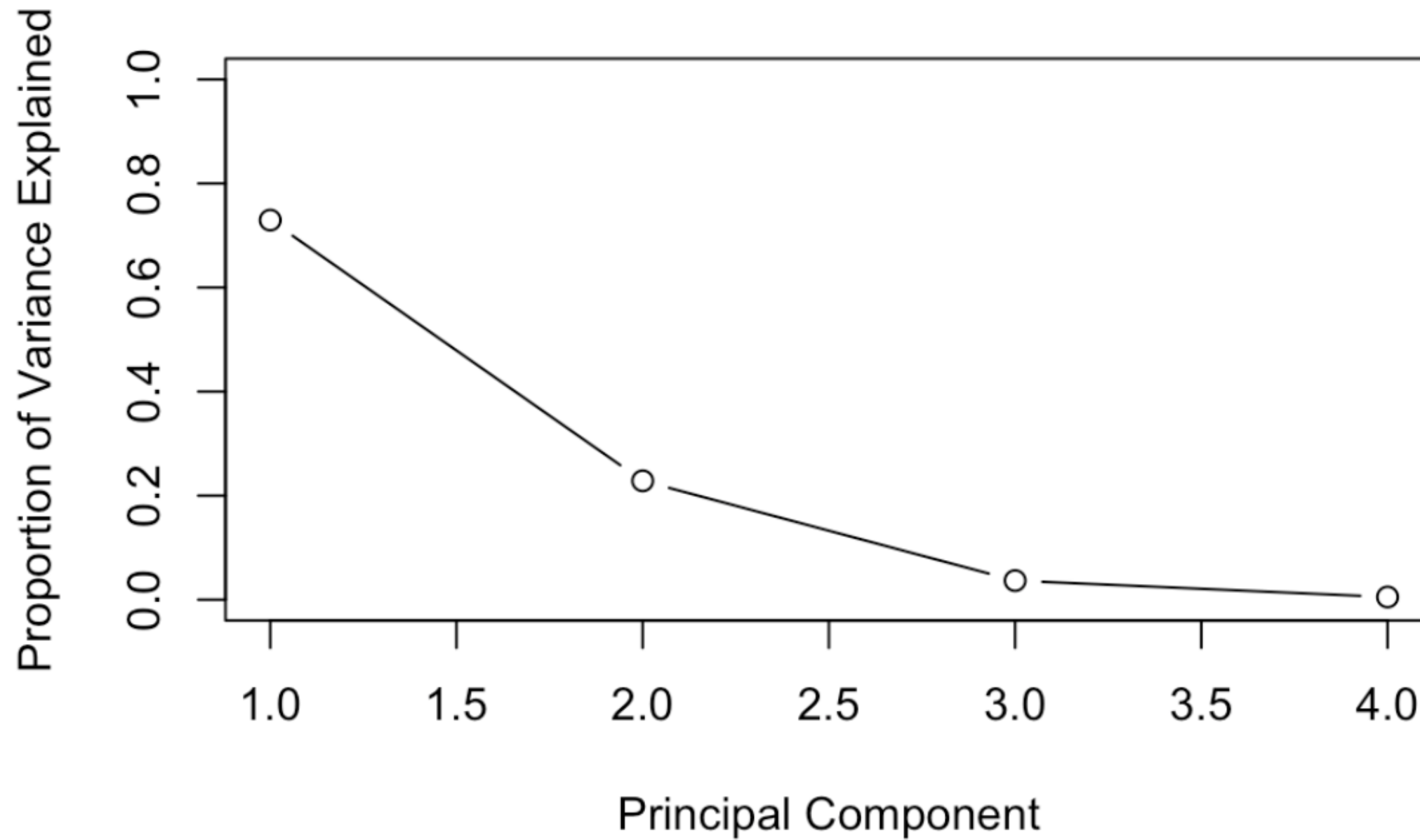
biplot(pr.iris)
```



Scree plots in R

```
# Getting proportion of variance for a scree plot
pr.var <- pr.iris$sdev^2
pve <- pr.var / sum(pr.var)
# Plot variance explained for each principal component
plot(pve, xlab = "Principal Component",
      ylab = "Proportion of Variance Explained",
      ylim = c(0, 1), type = "b")
```

Scree plot



Let's practice!
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Practical issues with PCA

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Practical issues with PCA

- Scaling the data
- Missing values:
 - Drop observations with missing values
 - Impute / estimate missing values
- Categorical data:
 - Do not use categorical data features
 - Encode categorical features as numbers

mtcars dataset

```
data(mtcars)
head(mtcars)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0
Valiant	18.1	6	225	105	2.76	3.460	20.22	1

Scaling

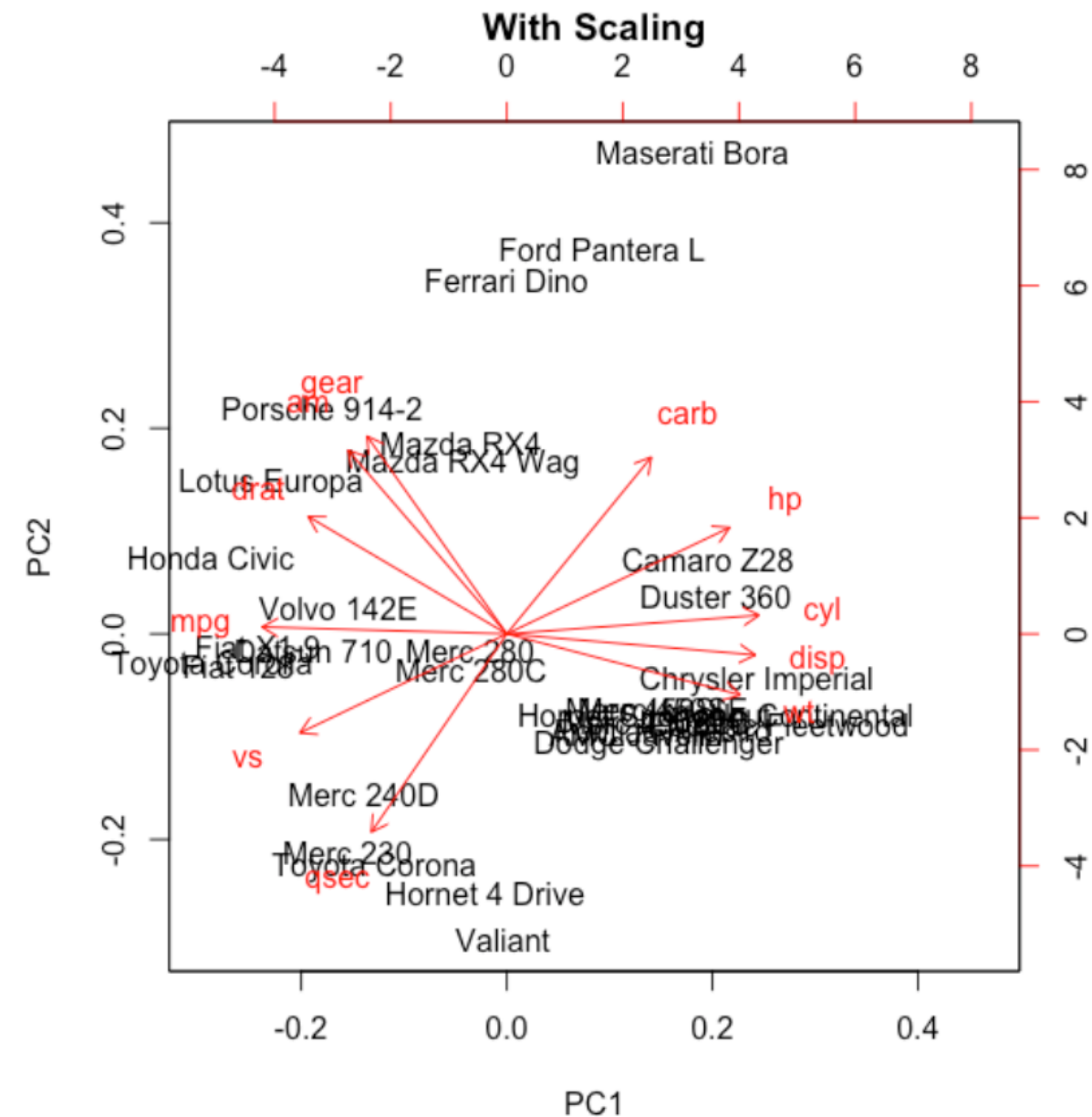
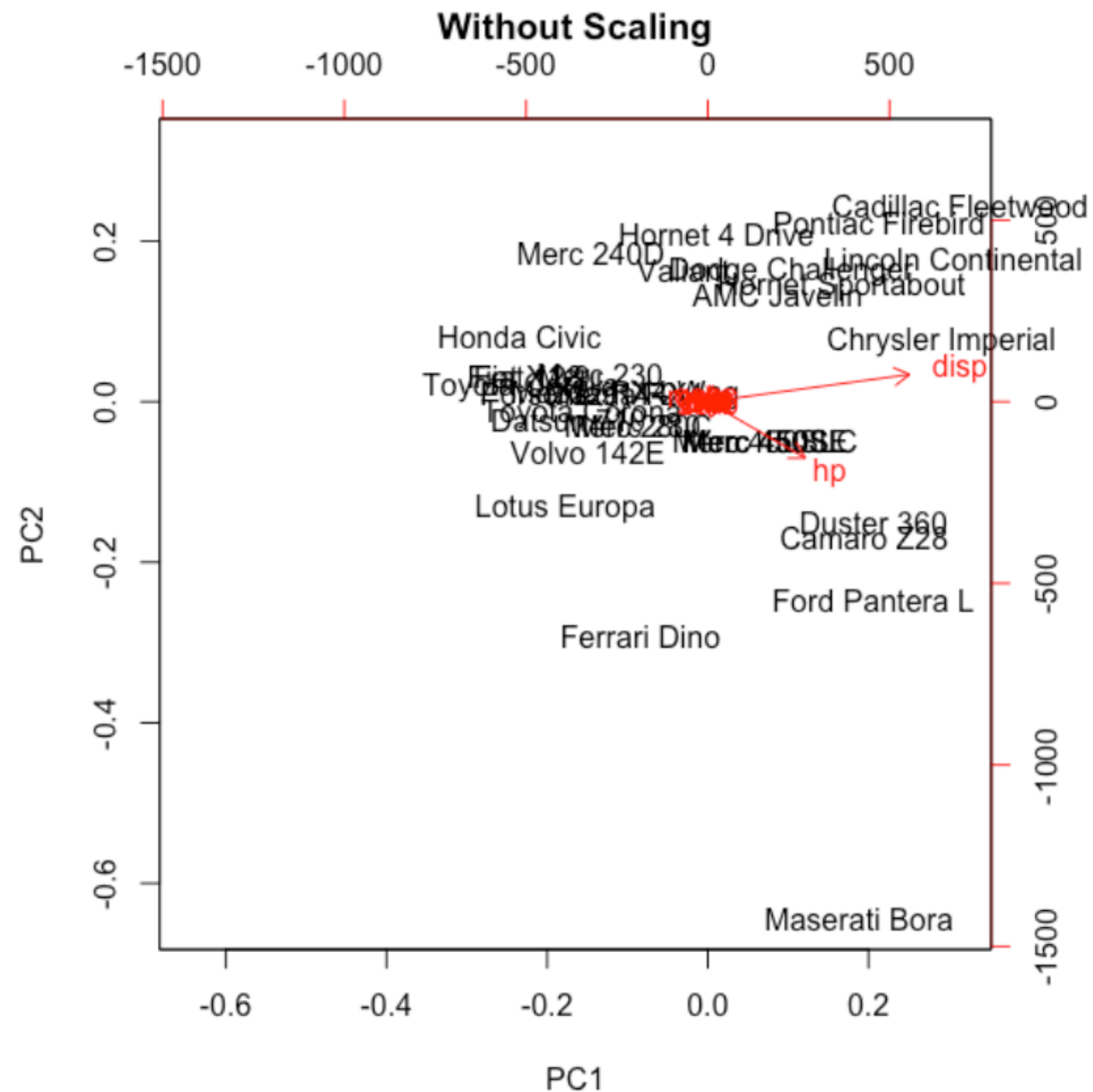
```
# Means and standard deviations vary a lot  
round(colMeans(mtcars), 2)
```

mpg	cyl	disp	hp	drat	wt	qsec	vs
20.09	6.19	230.72	146.69	3.60	3.22	17.85	0.44

```
round(apply(mtcars, 2, sd), 2)
```

mpg	cyl	disp	hp	drat	wt	qsec	vs
6.03	1.79	123.94	68.56	0.53	0.98	1.79	0.50

Importance of scaling data



Scaling and PCA in R

```
prcomp(x, center = TRUE, scale = FALSE)
```

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Additional uses of PCA and wrap-up

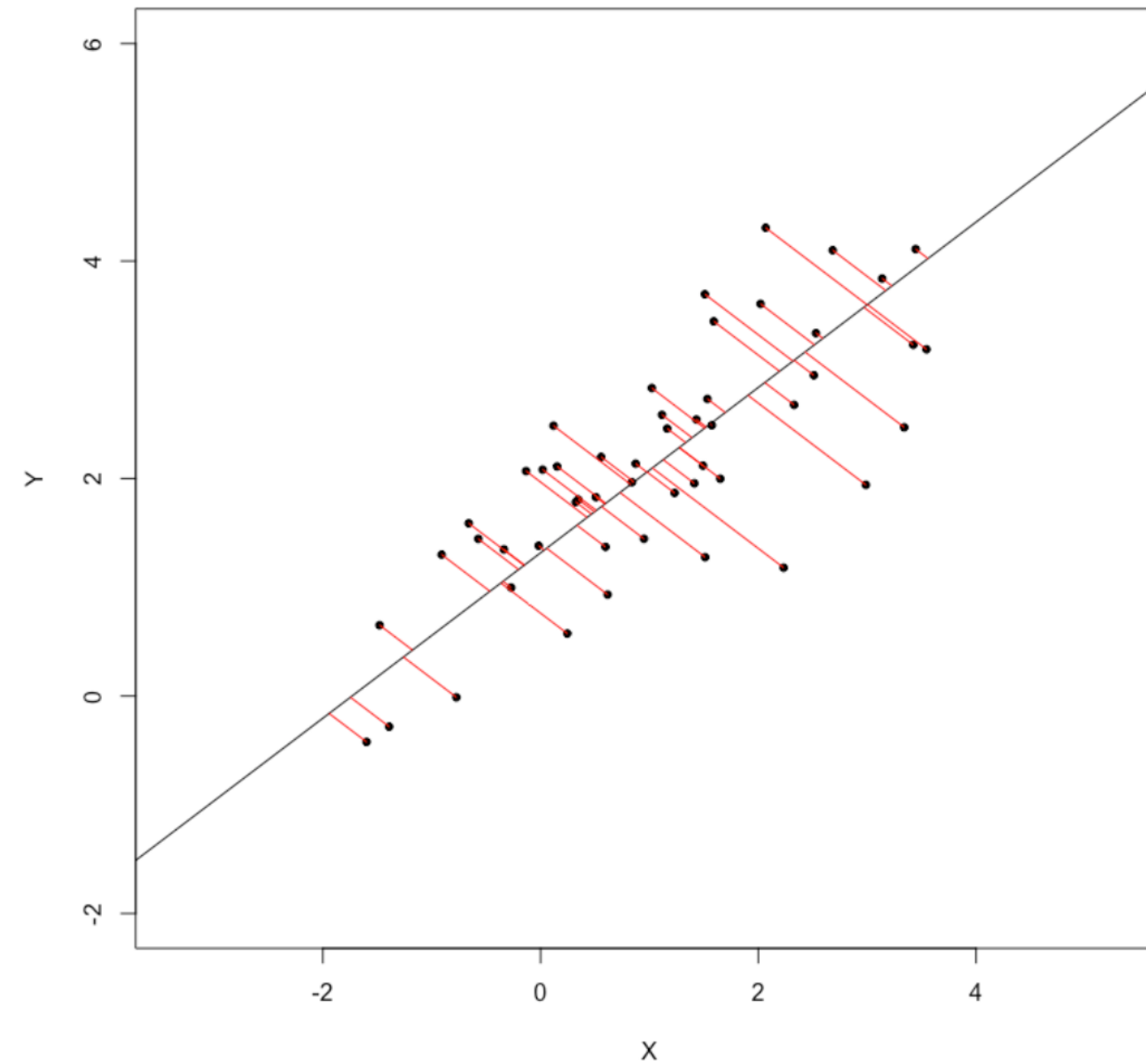
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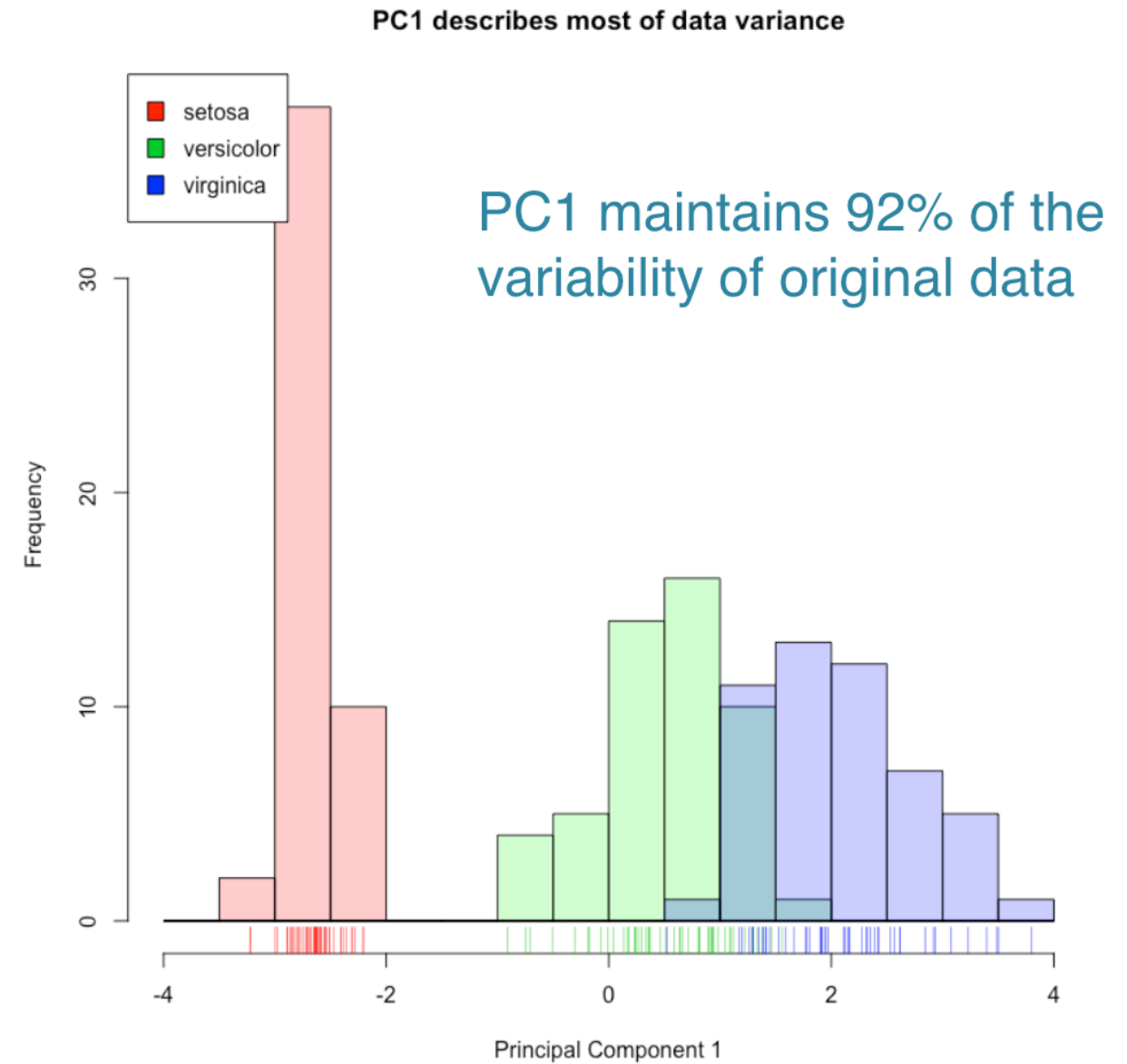
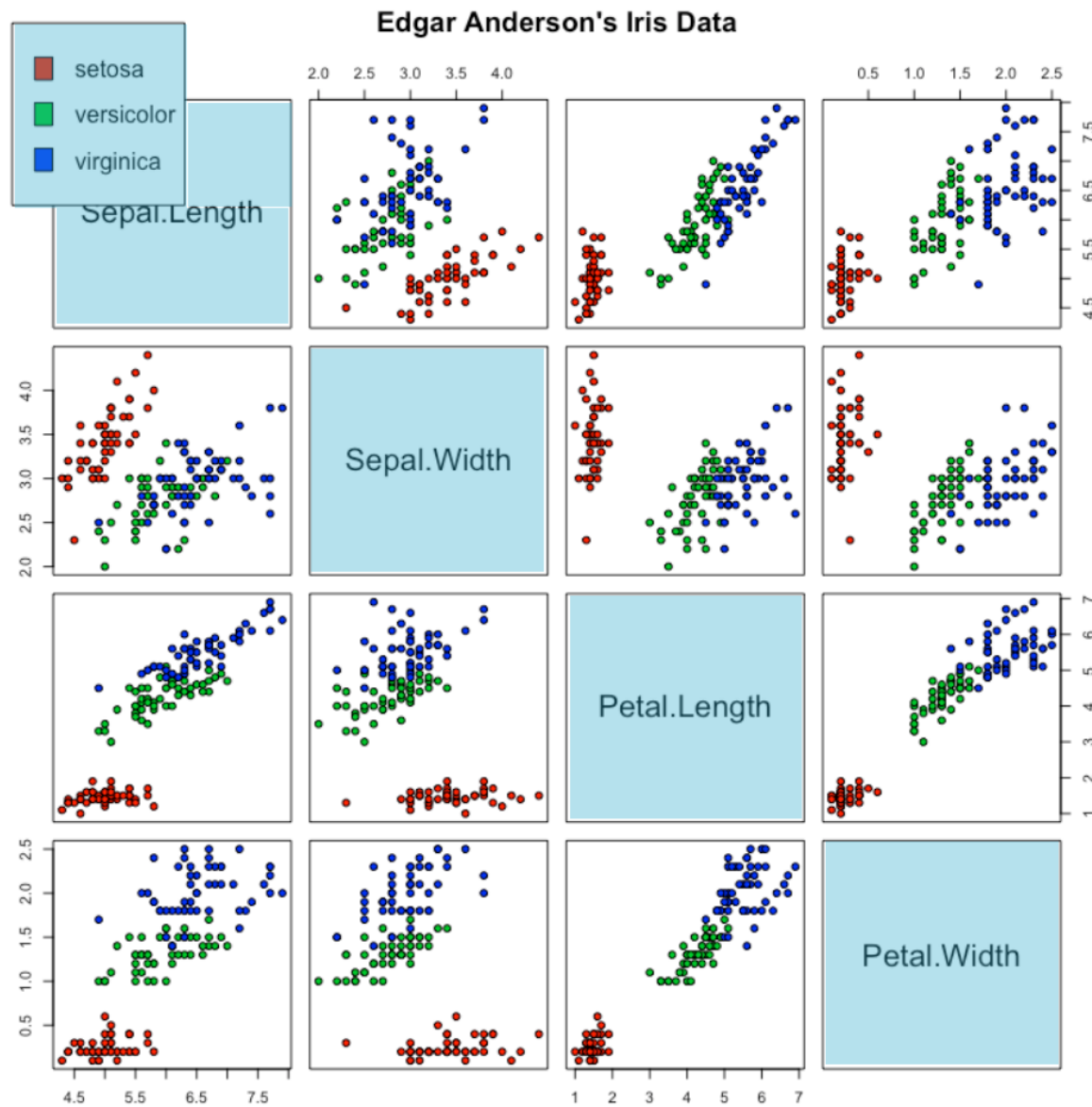
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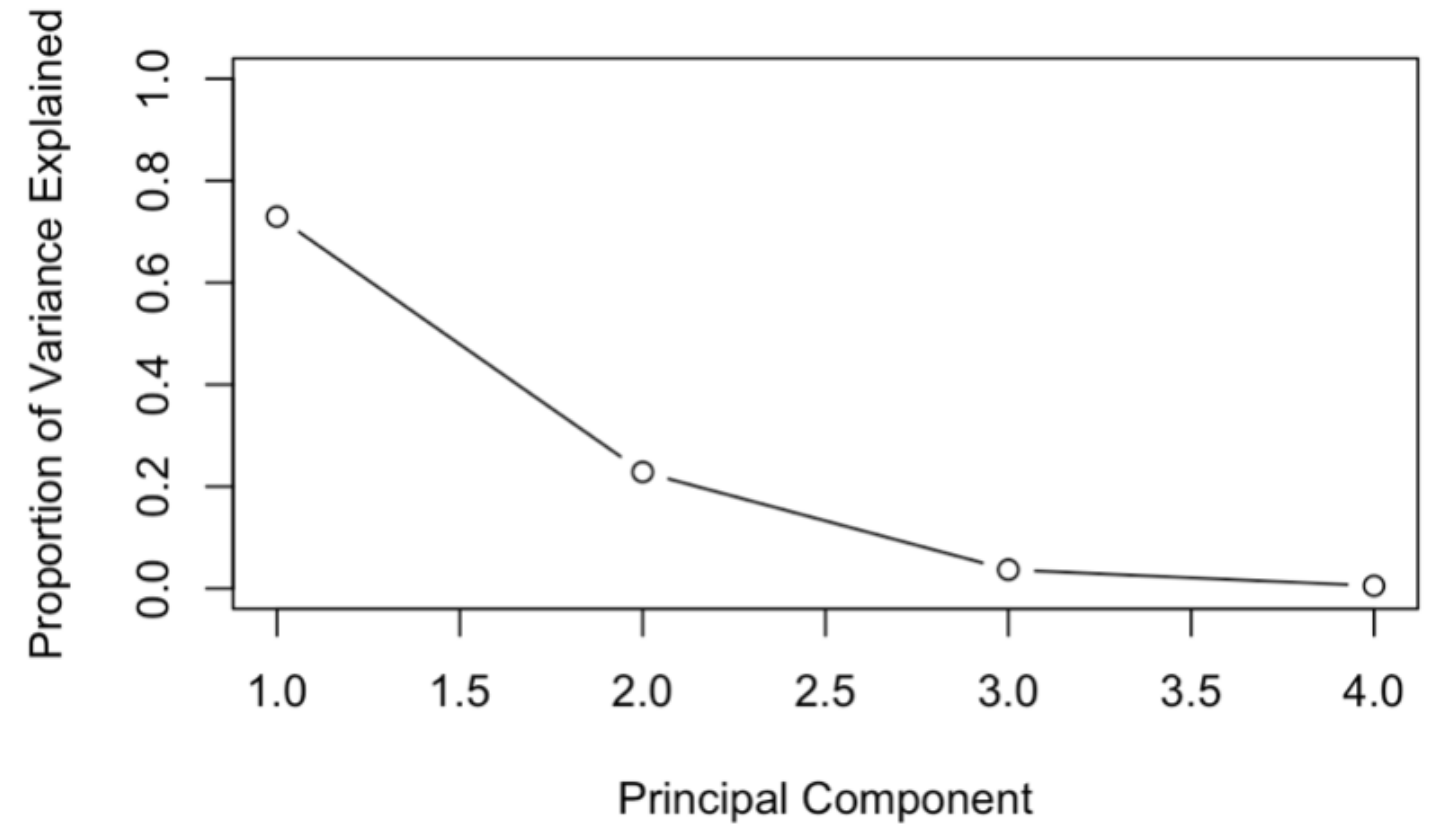
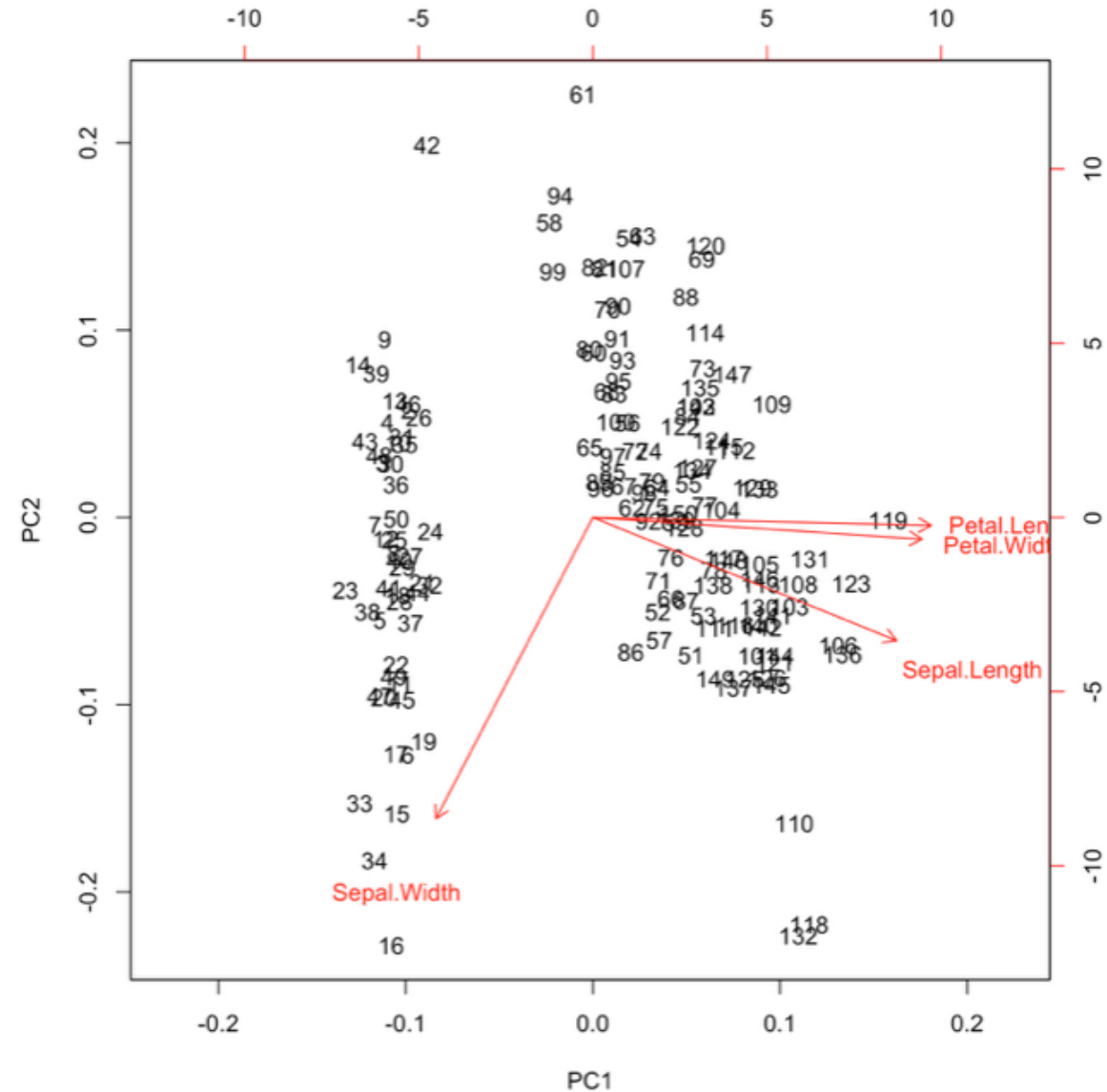
Dimensionality reduction



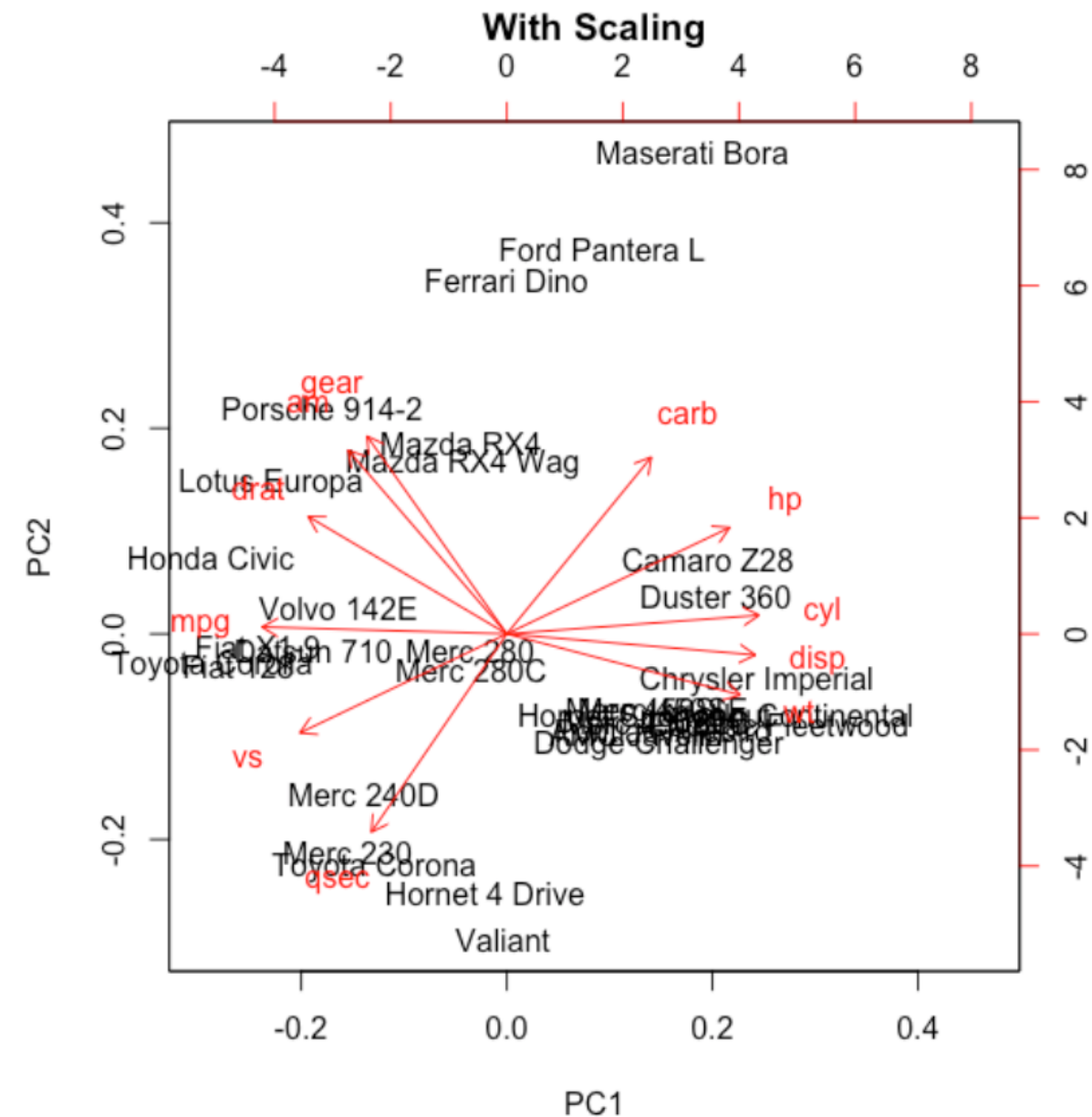
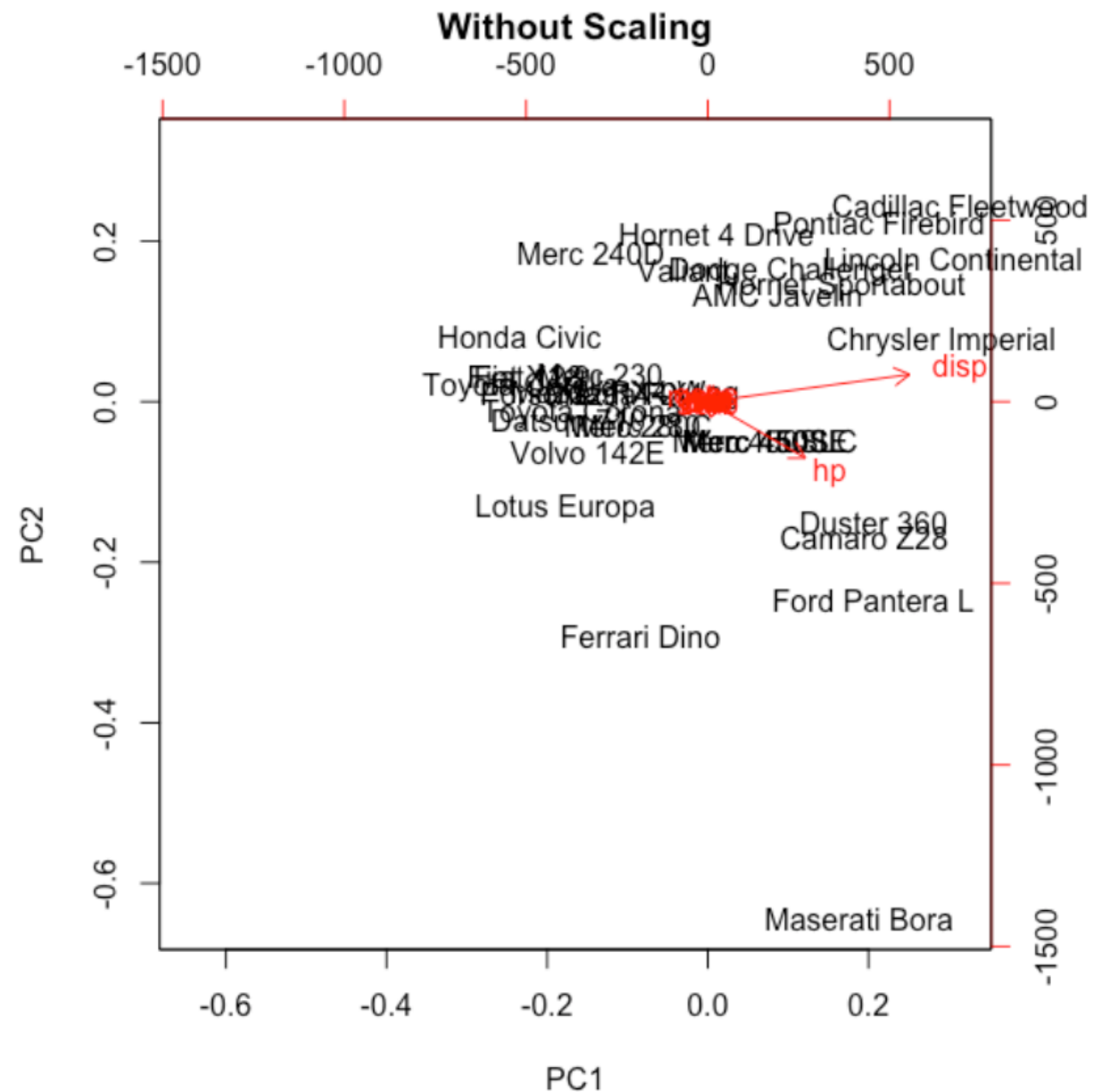
Data visualization



Interpreting PCA results



Importance of data scaling



Up next

```
# URL to cancer dataset hosted on DataCamp servers
url <- "https://assets.datacamp.com/production/course_1903/datasets/WisconsinCancer.csv"
```

```
# Download the data: wisc.df
wisc.df <- read.csv(url)
wisc.data[1:6, 1:5]
```

	radius_mean	texture_mean	perimeter_mean	area_mean	smoothness_mean
842302	17.99	10.38	122.80	1001.0	0.11840
842517	20.57	17.77	132.90	1326.0	0.08474
84300903	19.69	21.25	130.00	1203.0	0.10960
84348301	11.42	20.38	77.58	386.1	0.14250
84358402	20.29	14.34	135.10	1297.0	0.10030
843786	12.45	15.70	82.57	477.1	0.12780

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