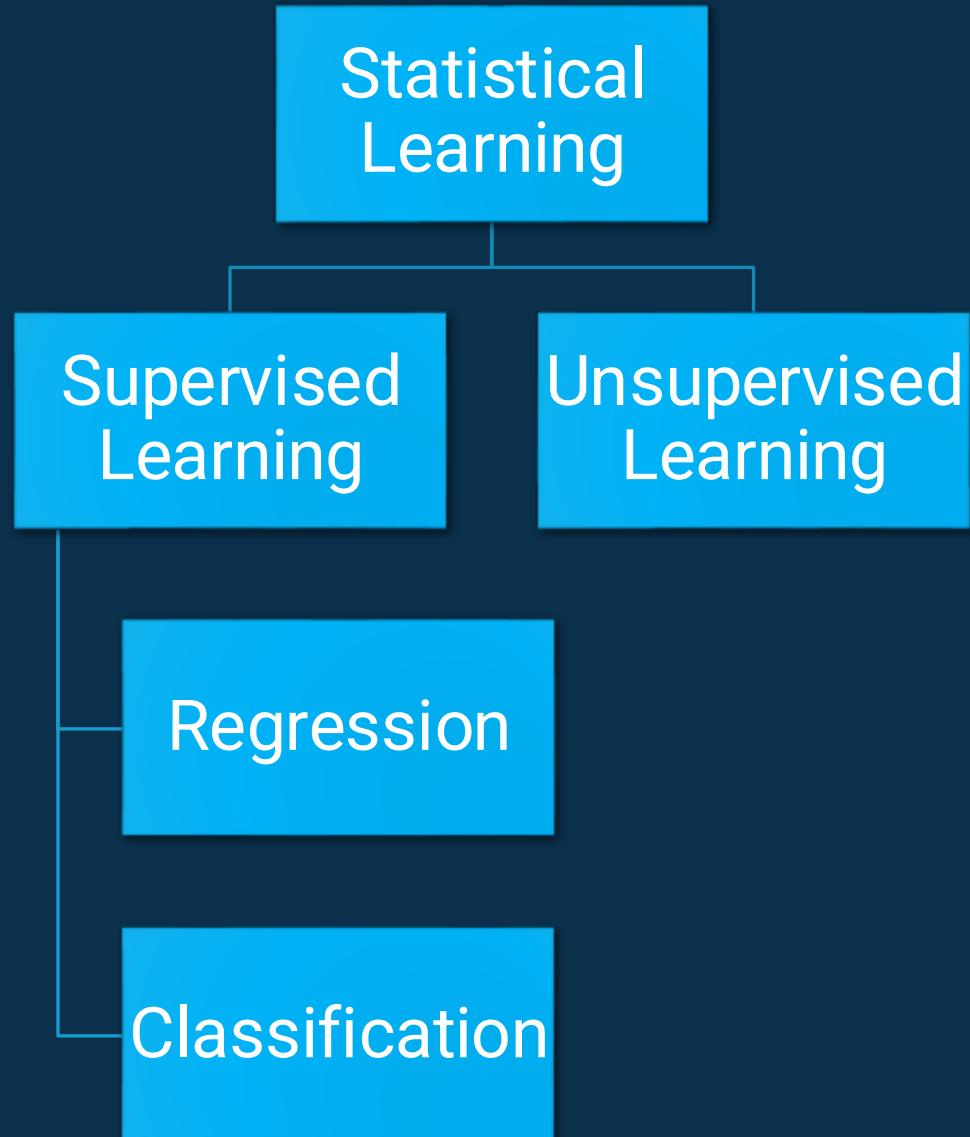


# Session 1 (DAY 1)

## Statistical and Machine Learning Models

Workshop on Quantitative Literacy and Statistics





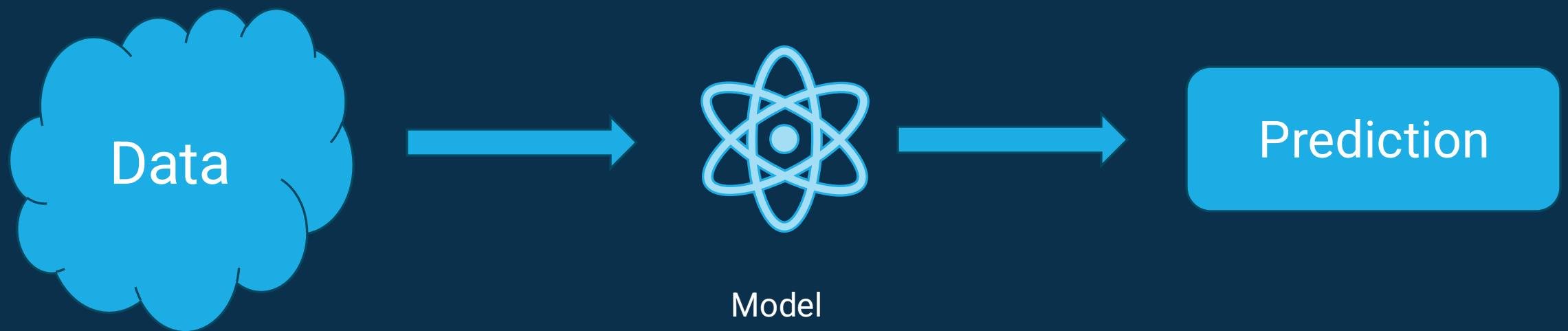
# Session 2: Part 1

## Supervised Learning

Workshop on Quantitative Literacy and Statistics

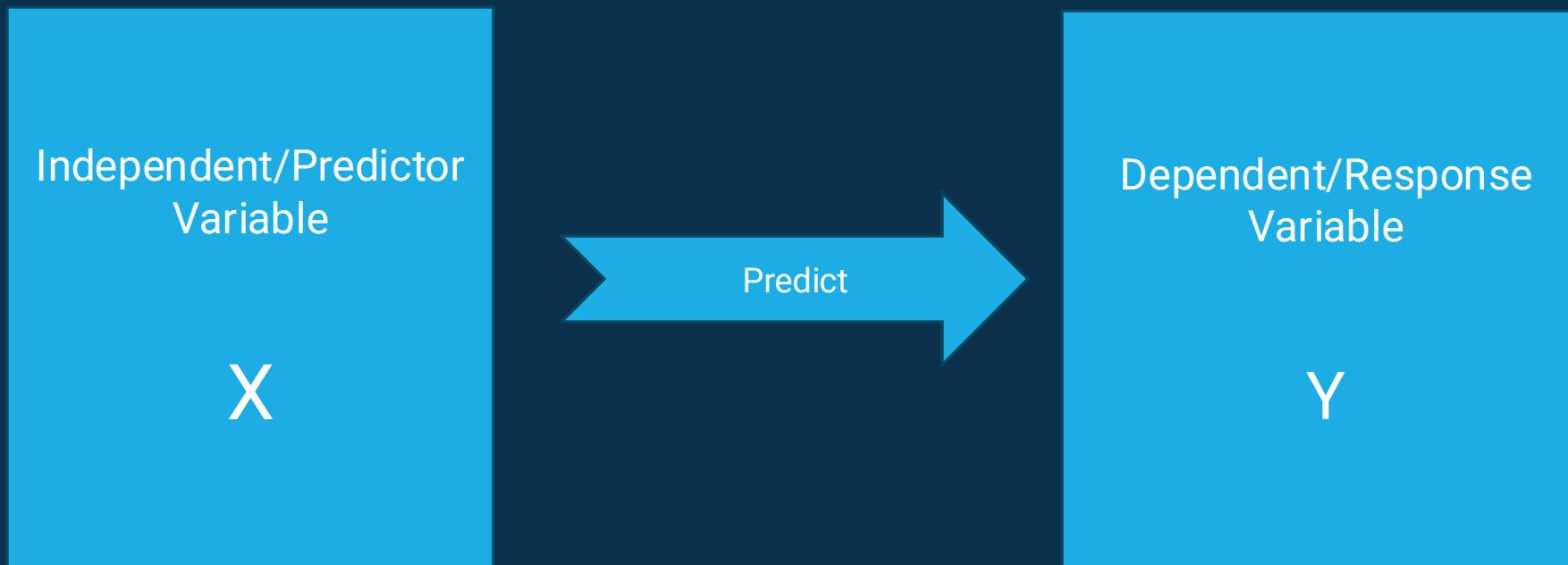


# Supervised Learning



# Supervised Learning

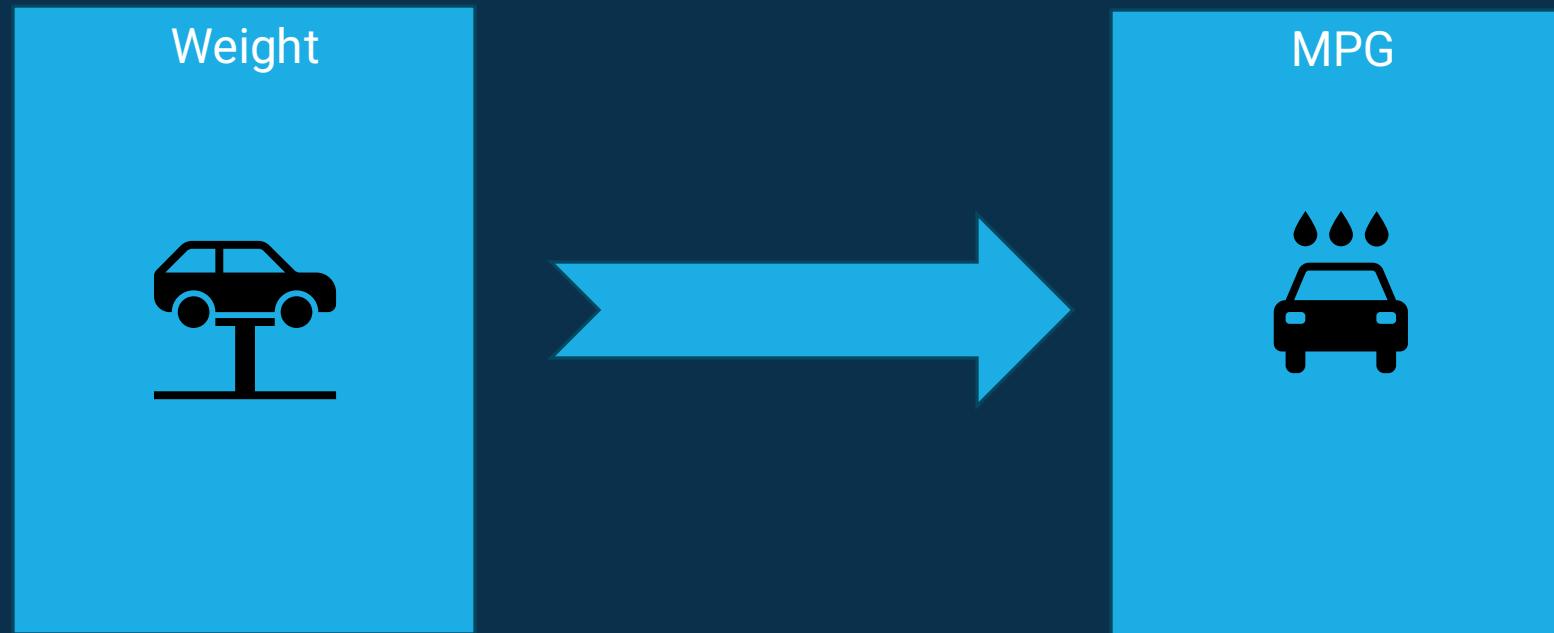
Learning techniques to find a function to **predict a response** variable (Y) from set of independent variables (X)



$$Y = f(x)$$

# Supervised Learning: Regression

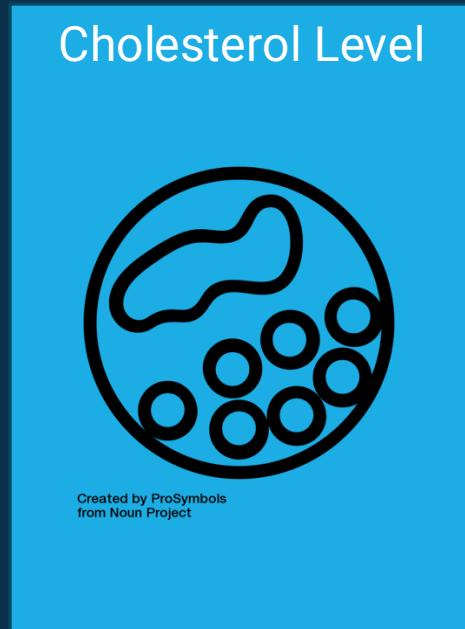
Predict **Continuous Response (Y)** from set of Independent Variables (X)



$$MPG = f(Weight)$$

# Supervised Learning: Classification

Predict a **Categorical Response Variable** from a set of Independent Variables



$$\text{Heart Disease}_{(Yes \text{ or } No)} = f(\text{Cholesterol Level})$$

# Supervised Learning

## 1. Linear Models

Regression : Linear Regression  
Classification : Logistic Regression

## 2. Bagging Methods

Regression : Random Forest Regression  
Classification : Random Forest Classification

## 3. Boosting Methods

Regression : Gradient Boost Regression  
Classification : Gradient Boost Classification

# 1. Linear Models

Regression

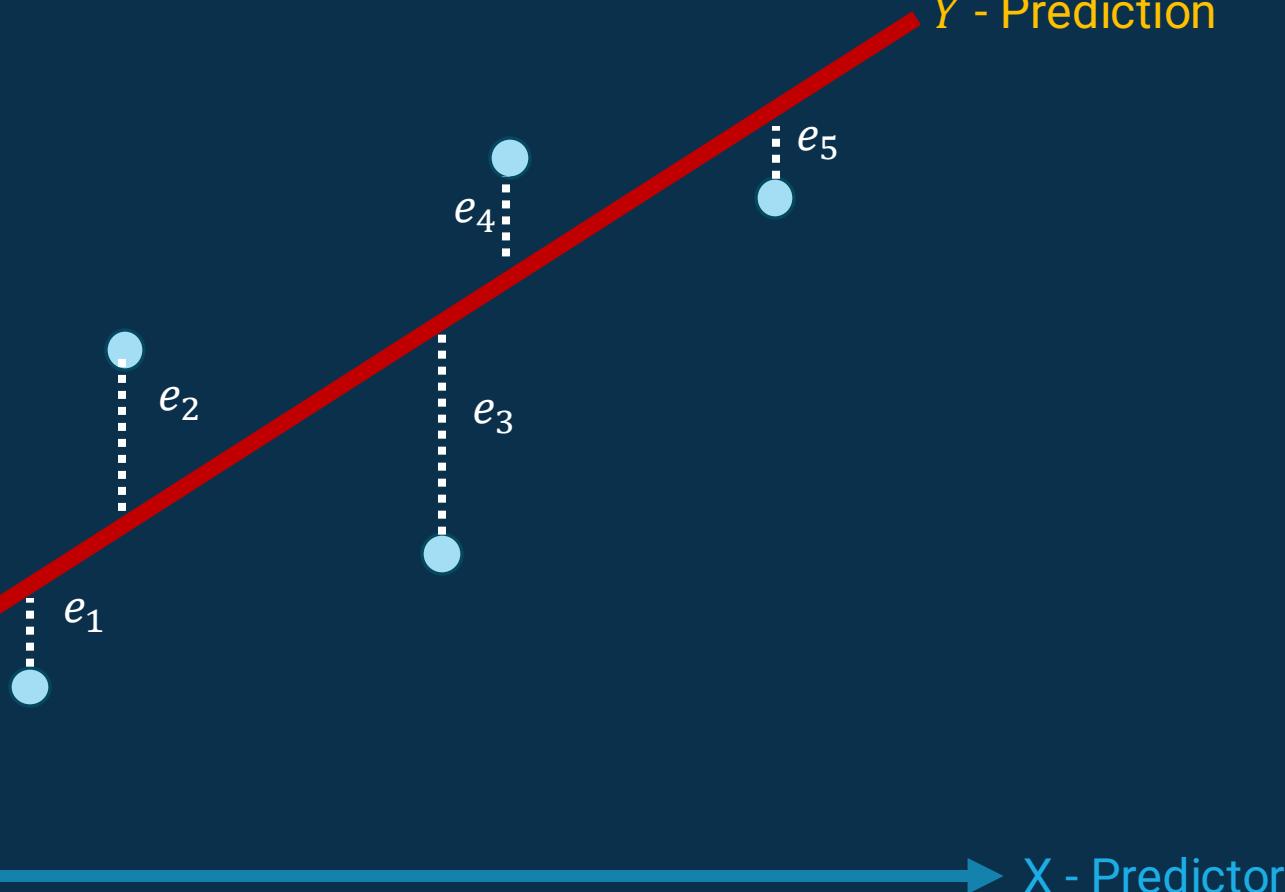
# Linear Regression

Y - Response



$$\hat{Y} = \hat{\beta}_0 + \hat{\beta}_1 X$$

$\hat{Y}$  - Prediction



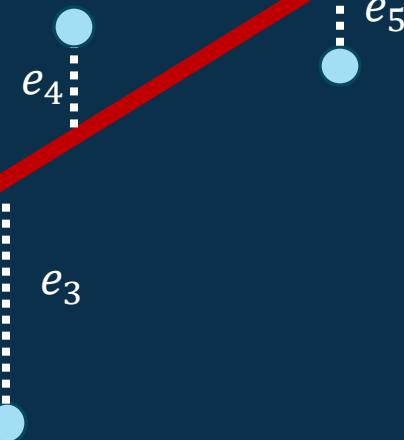
X	Y
$x_1$	$y_1$
$x_2$	$y_2$
$x_3$	$y_3$
$x_4$	$y_4$
$x_5$	$y_5$

Simple Linear Regression Model:  $Y = \beta_0 + \beta_1 X + \text{Error}$

$\beta_0$  - Response when  $X = 0$

$\beta_1$  - Increase of Response when  $X$  increase by 1-unit

Y - Response



$$\begin{aligned}\hat{Y} &= \hat{\beta}_0 + \hat{\beta}_1 X \\ \hat{Y} &- \text{Prediction}\end{aligned}$$

$$\text{Residual: } e_i = y_i - \hat{y}_i$$

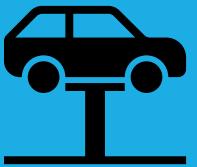
$$\text{Residual Sum of Square: RSS} = e_1^2 + e_2^2 + e_3^2 + e_4^2 + e_5^2$$

$$\text{RSS} = \sum(Y - \hat{Y})^2$$

Find  $\beta_0$  and  $\beta_1$  which minimize the RSS

X - Predictor

Weight



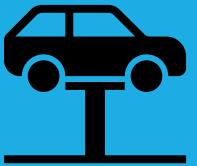
MPG



$$\widehat{MPG} = \hat{\beta}_0 + \hat{\beta}_1 \text{Weight}$$

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160.0	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160.0	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108.0	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258.0	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360.0	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225.0	105	2.76	3.460	20.22	1	0	3	1
Duster 360	14.3	8	360.0	245	3.21	3.570	15.84	0	0	3	4
Merc 240D	24.4	4	146.7	62	3.69	3.190	20.00	1	0	4	2
Merc 230	22.8	4	140.8	95	3.92	3.150	22.90	1	0	4	2
Merc 280	19.2	6	167.6	123	3.92	3.440	18.30	1	0	4	4
Merc 280C	17.8	6	167.6	123	3.92	3.440	18.90	1	0	4	4
Merc 450SE	16.4	8	275.8	180	3.07	4.070	17.40	0	0	3	3
Merc 450SL	17.3	8	275.8	180	3.07	3.730	17.60	0	0	3	3
Merc 450SLC	15.2	8	275.8	180	3.07	3.780	18.00	0	0	3	3
Cadillac Fleetwood	10.4	8	472.0	205	2.93	5.250	17.98	0	0	3	4
Lincoln Continental	10.4	8	460.0	215	2.93	5.424	17.82	0	0	3	4

Weight



MPG



$$\widehat{MPG} = \hat{\beta}_0 + \hat{\beta}_1 \text{Weight}$$

```
lm(formula = mpg ~ wt , data = mtcars)
```

$$\begin{aligned}\hat{\beta}_0 &= 37.28 \\ \hat{\beta}_1 &= -5.34\end{aligned}$$

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
--	----------	------------	---------	----------

(Intercept)	37.2851	1.8776	19.858	< 2e-16 ***
wt	-5.3445	0.5591	-9.559	1.29e-10 ***

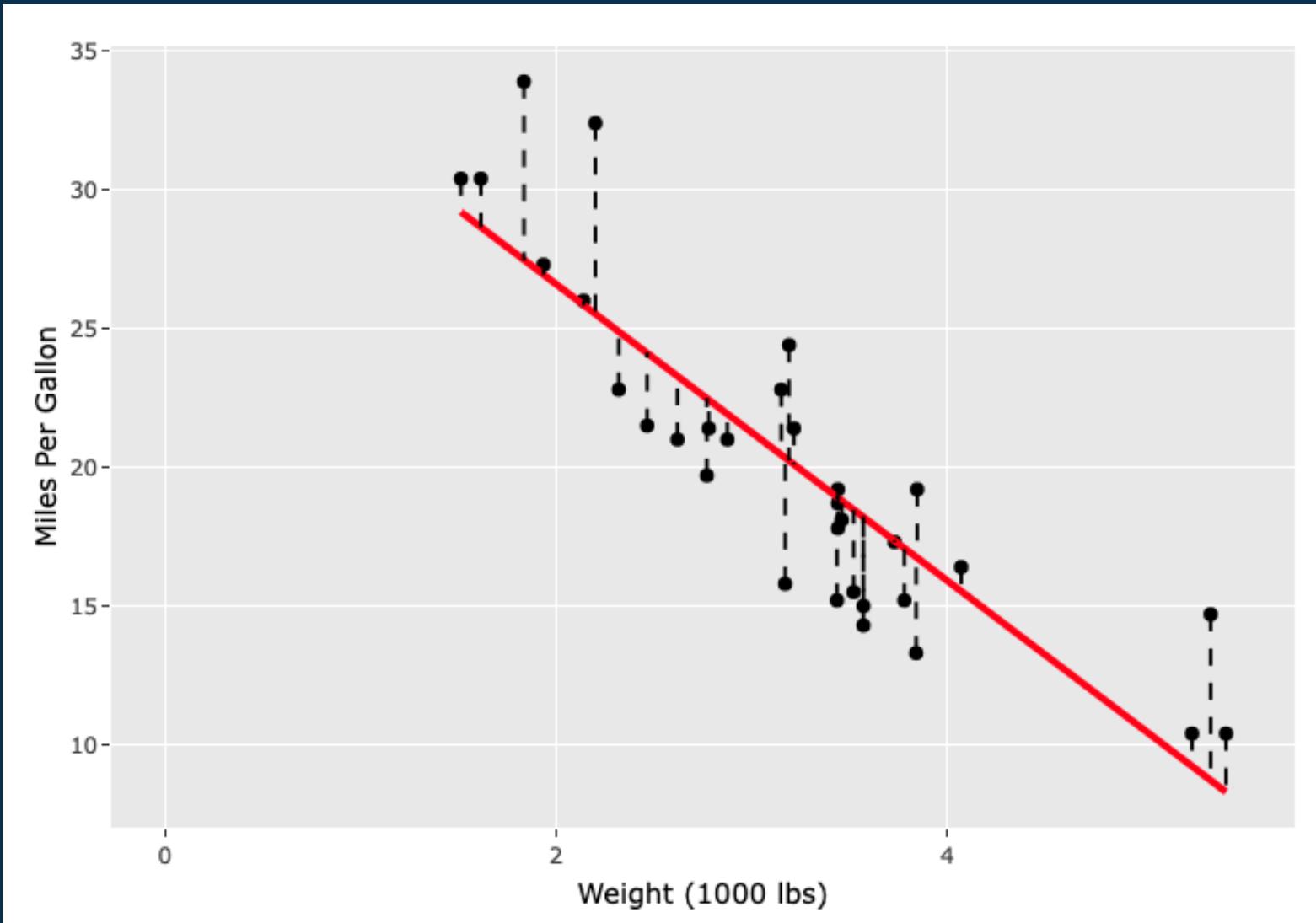
---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

$$\widehat{mpg} = 37.28 - 5.34 \text{Weight}$$

*p*-value will provide statistical significance  
 $\beta_1$  – Weight is a significant variable in estimating MPG

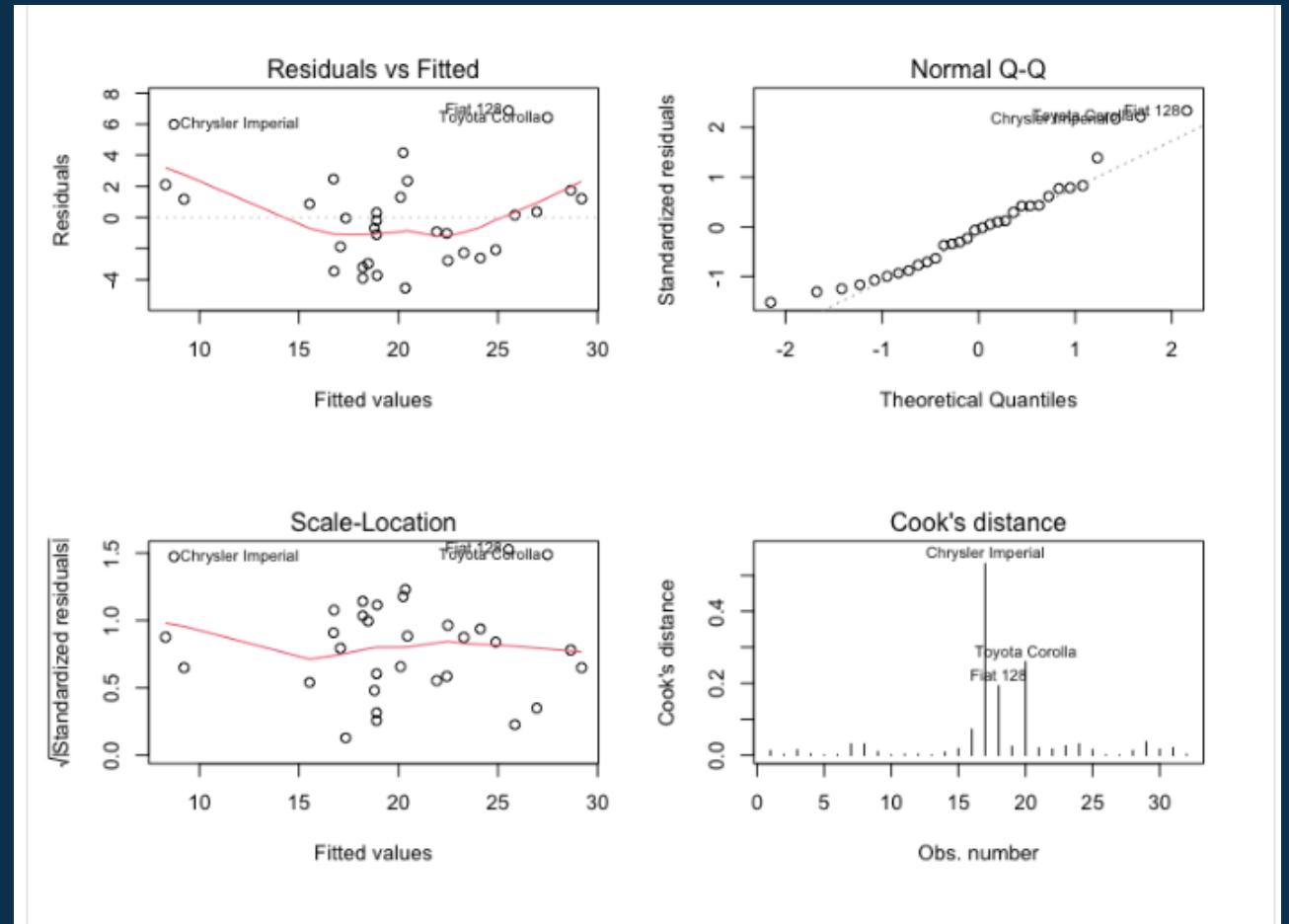
$$\widehat{mpg} = 37.28 - 5.34 \text{Weight}$$



# Linear Regression Assumptions

## Assumptions

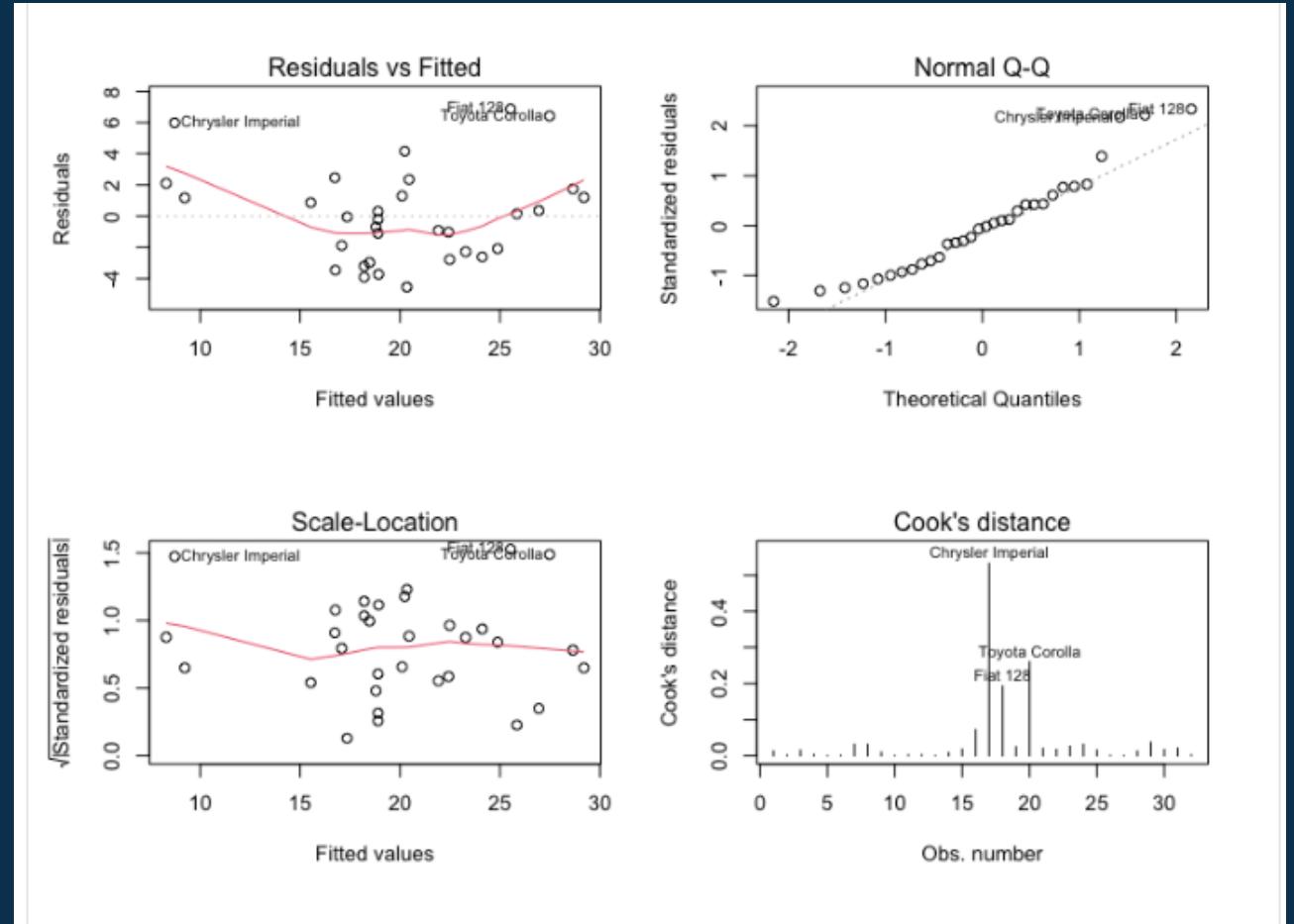
- Linearity of Data
- Independence of Errors
- Constant Variance of residuals
- Normality of Residuals
- No Multicollinearity



# Linear Regression Assumptions

## Assumptions

- Linearity of Data
  - Transform X variables
- Independence of Errors
  - Use Autoregressive Models
- Constant Variance of residuals
  - Transform dependent variable
- Normality of Residuals
  - Remove/impute outliers
  - Transform dependent variables
- No Multicollinearity
  - Remove or combine highly correlated X variables
  - Use Principal component analysis



# Linear Regression: Evaluation Model Performance

**$R^2$  - Coefficient of Determination = 0.75**

- How much variability of response is explained by the predictor variables
- $0 \leq R^2 \leq 1$
- Higher the better

**Adjusted  $R^2$  = 0.74**

- Penalize for additional predictor variables
- $R_{adj}^2 \leq 1$
- Higher the better

```
Residual standard error: 3.046 on 30 degrees of freedom
Multiple R-squared:  0.7528,    Adjusted R-squared:  0.7446
F-statistic: 91.38 on 1 and 30 DF,  p-value: 1.294e-10
```

RMSE – Root mean squared error = 3.04

- Lower the Better

# Multiple Linear Regression

$$MPG = \beta_0 + \beta_1 Weight + \beta_2 Cylinders + \beta_3 Rear_axle_Ratio + Error$$

```
multiple_linear_regression = lm(formula = mpg ~ wt + cyl + drat ,data = mtcars)
summary(multiple_linear_regression)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	39.7677	6.8729	5.786	3.26e-06 ***
wt	-3.1947	0.8293	-3.852	0.000624 ***
cyl	-1.5096	0.4464	-3.382	0.002142 **
drat	-0.0162	1.3231	-0.012	0.990317

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 2.613 on 28 degrees of freedom

Multiple R-squared: 0.8302, Adjusted R-squared: 0.812

F-statistic: 45.64 on 3 and 28 DF, p-value: 6.569e-11

$$R^2 = 0.83$$

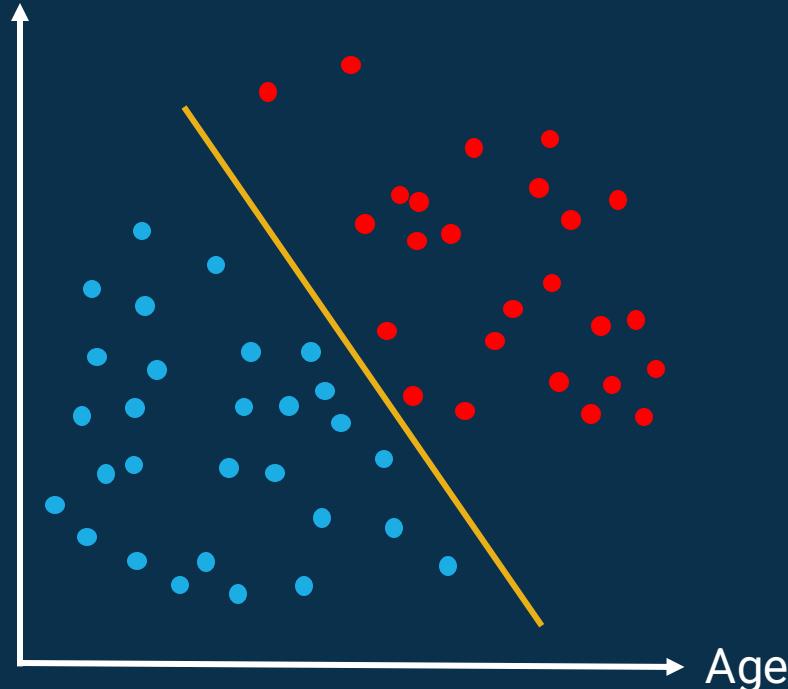
$$R_{adj}^2 = 0.81$$

$$\widehat{MPG} = 39.76 - 3.19 Weight - 1.51 Cylinders - 0.016 Rear_axle_Ratio$$

Classification

# Logistic Regression

Cholesterol



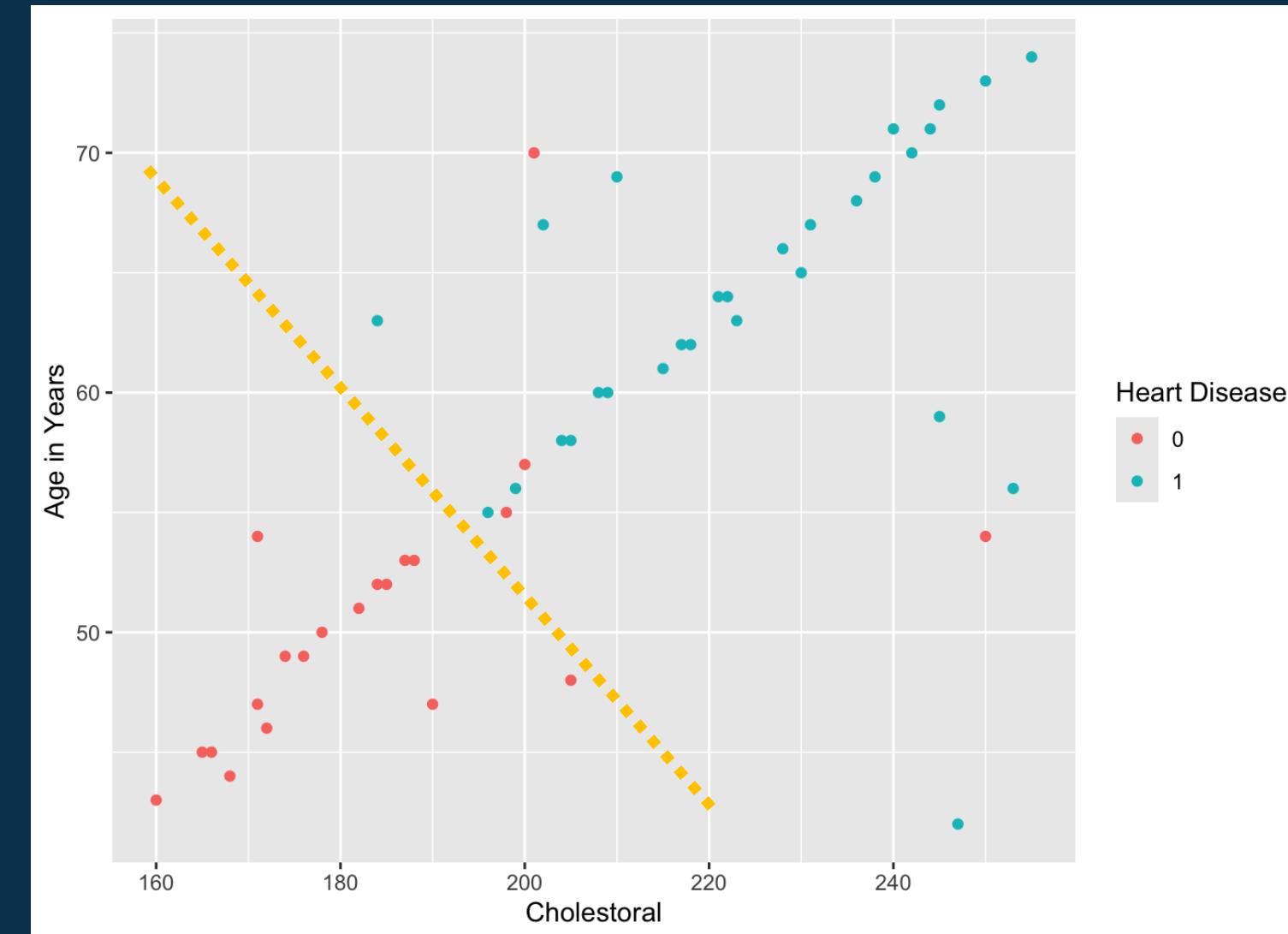
No Heart Disease

Heart Disease

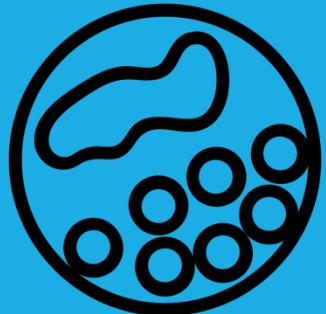
# 50 Subjects

age	cholesterol	heart_disease
56	253	1
63	184	1
59	245	1
48	205	0
62	218	1
54	171	0
71	240	1
67	202	1
44	168	0
53	188	0
58	205	1
65	230	1
49	176	0
72	245	1
61	215	1
47	190	0
55	196	1
69	238	1
52	185	0
64	222	1

And more ....

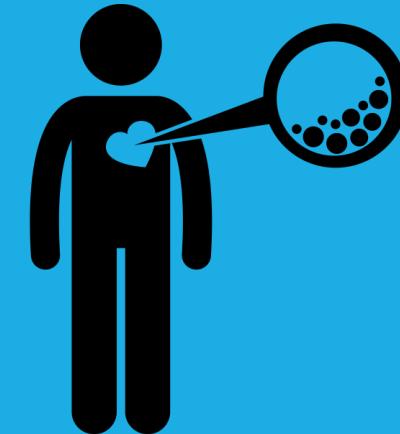


Cholesterol Level



Created by ProSymbols  
from Noun Project

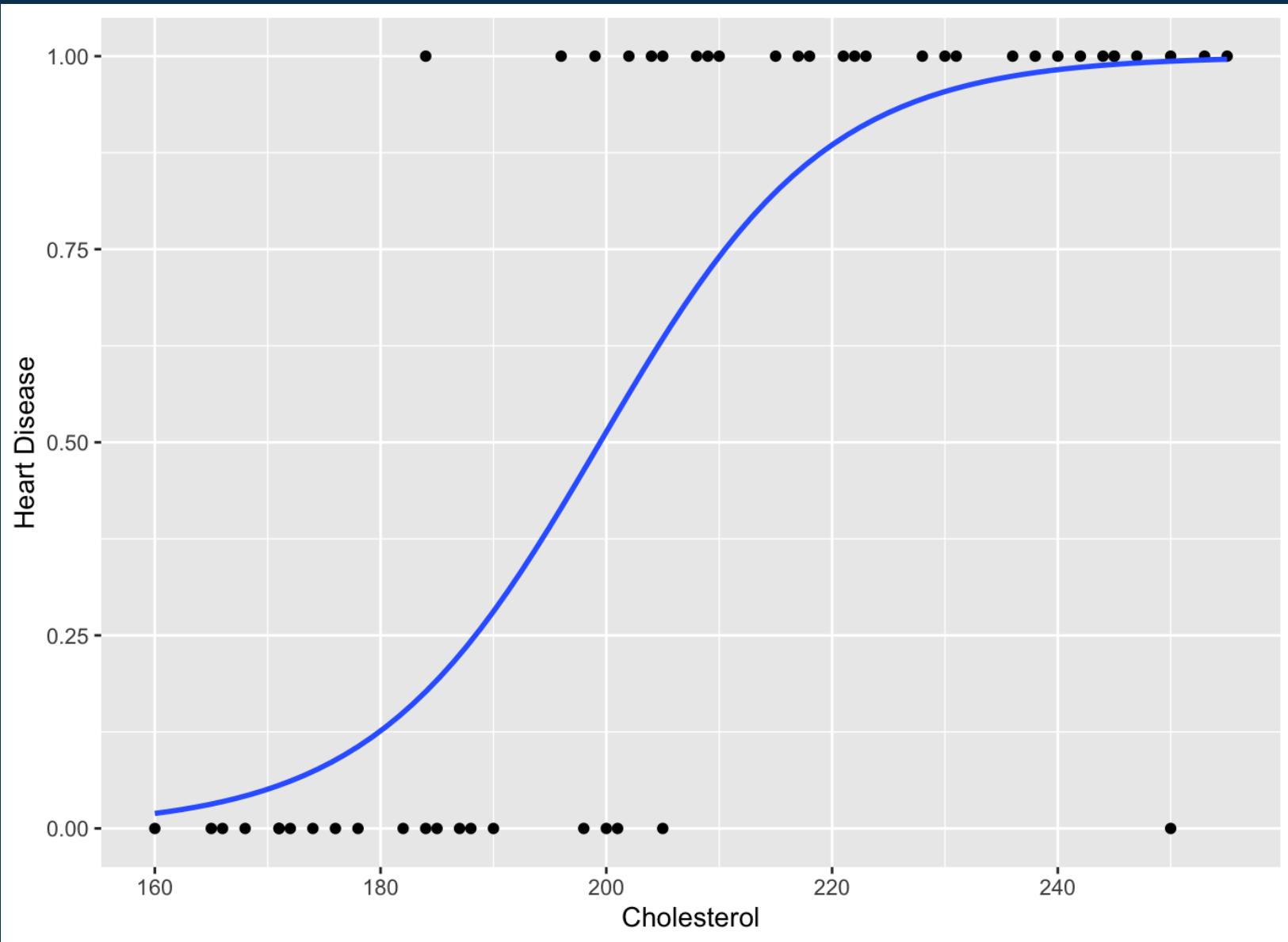
Get a Heart Disease or Not



Created by Gan Khoon Lay  
from Noun Project

$p$  – Probability of Getting a Heart Disease

$$\text{Log} \left[ \frac{p}{1 - p} \right] = \beta_0 + \beta_1 \text{Cholesterol}$$



$$p(x) = \frac{\exp(x)}{1 + \exp(x)}$$

$p$  – Probability of Getting a Heart Disease

$$\text{Logit } p = \text{Log} \left[ \frac{p}{1-p} \right] = \beta_0 + \beta_1 \text{Cholesterol}$$

Estimate  $\beta_0$  and  $\beta_1$  such that maximizing:

$$L = \sum \{y \ln p + (1-y) \ln(1-p)\}$$

$p$  – Probability of Getting a Heart Disease

$$\text{Logit } \{p\} = \beta_0 + \beta_1 \text{Cholesterol}$$

$$\text{Logit } p = \log \left[ \frac{p}{1-p} \right] = \beta_0 + \beta_1 \text{Cholesterol}$$

This is also equivalent to:

$$p = \frac{\exp(\beta_0 + \beta_1 \text{Cholesterol})}{1 + \exp(\beta_0 + \beta_1 \text{Cholesterol})}$$

```

logistic_regression = glm(formula = heart_disease ~ cholesterol,
                         data = loan_df,family = 'binomial')

summary(logistic_regression)

```

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-19.82515	5.50299	-3.603	0.000315	***
cholesterol	0.09940	0.02745	3.621	0.000293	***
<hr/>					

$$\text{logit } (\hat{p}) = -19.82 + 0.099 \text{ Cholesterol}$$

$$\hat{p} = \frac{\exp(-19.82 + 0.099 \text{ Cholesterol})}{1 + \exp(-19.82 + 0.099 \text{ Cholesterol})}$$

$\hat{p}$  - Probability of getting a heart disease given the Cholesterol Level

If  $p > 0.5 \rightarrow$  Heart Disease

We can change 0.5 to a different probability threshold.

```

logistic_regression = glm(formula = heart_disease ~ cholesterol + age ,
                         data = heart_df, family = 'binomial')

summary(logistic_regression)

```

Coefficients:					
	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-25.27279	7.08238	-3.568	0.000359	***
cholesterol	0.06902	0.02652	2.603	0.009249	**
age	0.20247	0.07907	2.561	0.010449	*

$$\text{logit } (\hat{p}) = -25.3 + 0.069 \text{ Cholesterol} + 0.2 \text{ Age}$$

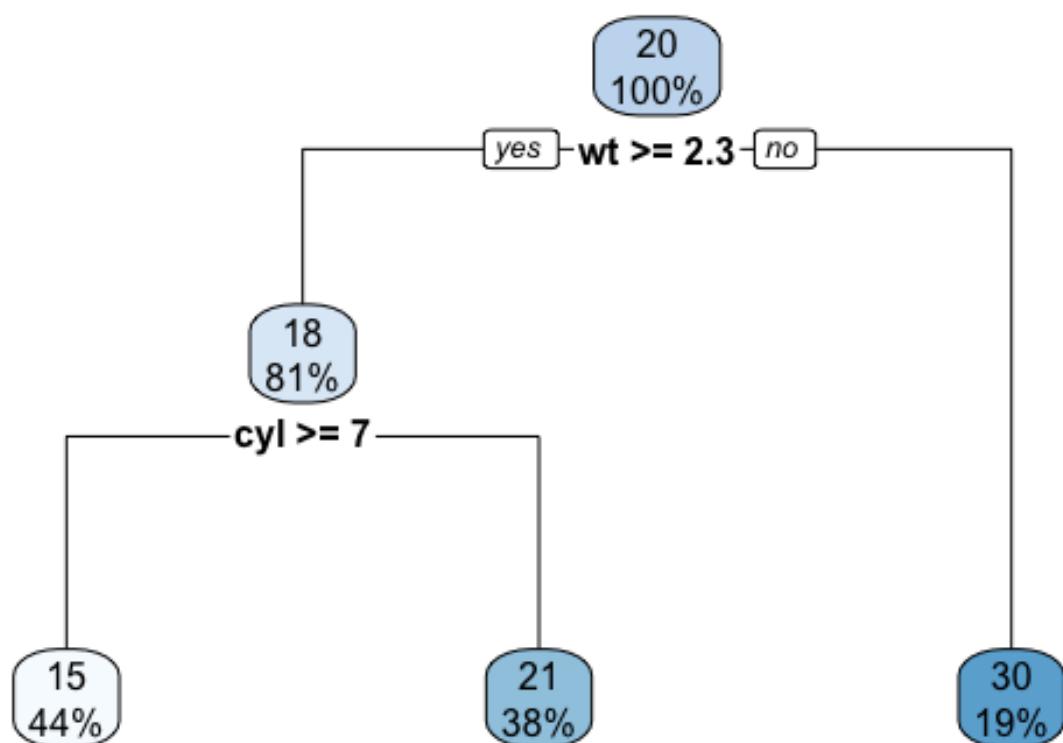
$$\hat{p} = \frac{\exp(-25.3 + 0.069 \text{ Cholesterol} + 0.2 \text{ Age})}{1 + \exp(-25.3 + 0.069 \text{ Cholesterol} + 0.2 \text{ Age})}$$

$\hat{p}$  - Probability of approving the loan when income and age is known

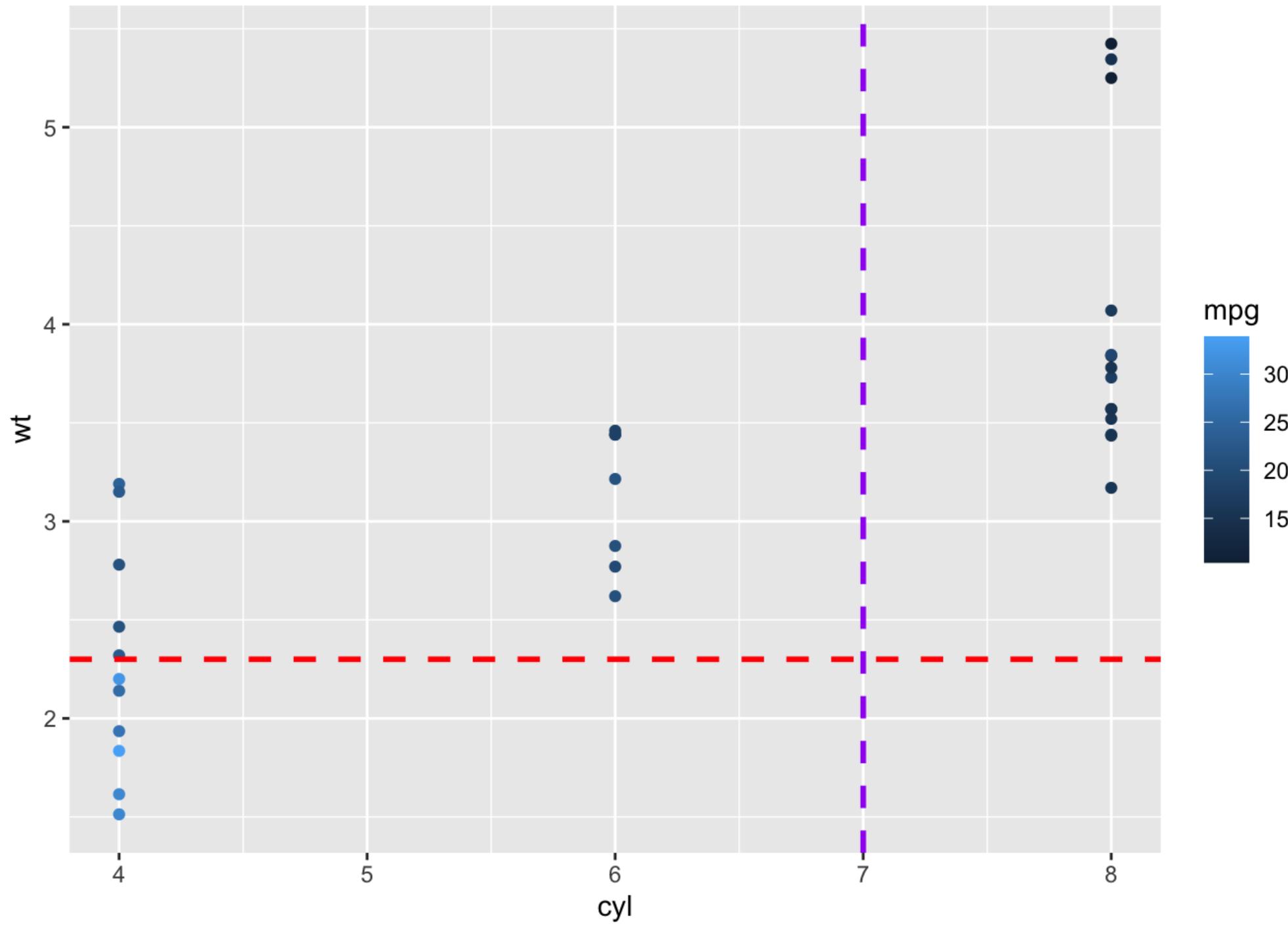
- The odds of getting a heart disease will increase by 7.1% (i.e.,  $\exp(0.069) = 1.071$ ) when the Cholesterol level increases by 1 unit.
- The odds of getting heart disease will increase by 22% (i.e.,  $\exp(0.2) = 1.22$ ) when the age increases by 1 year.

## 2. Bagging Methods

# Regression Trees (Decision Trees)



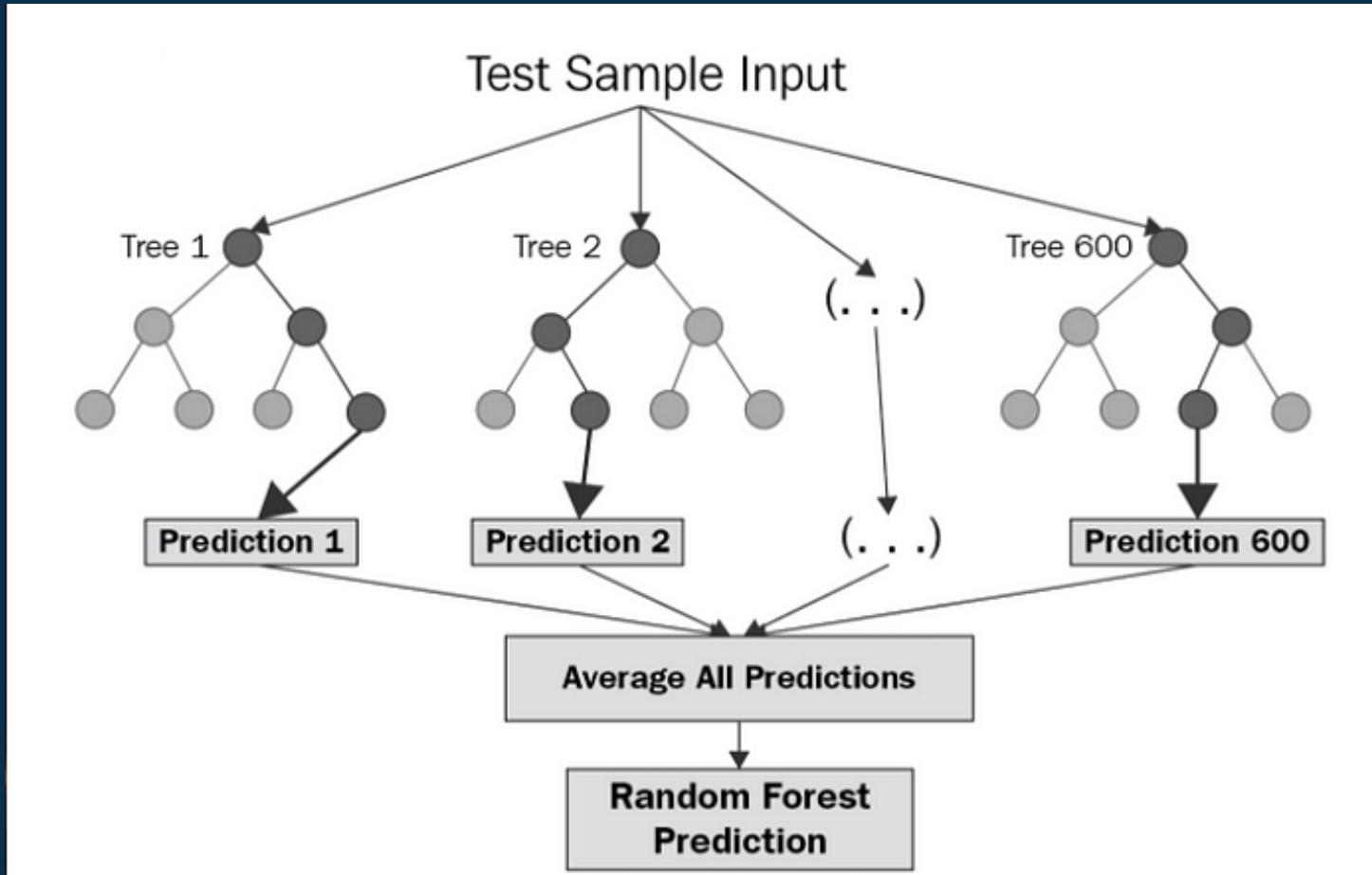
Partition the data set into decision boundaries.



Regression

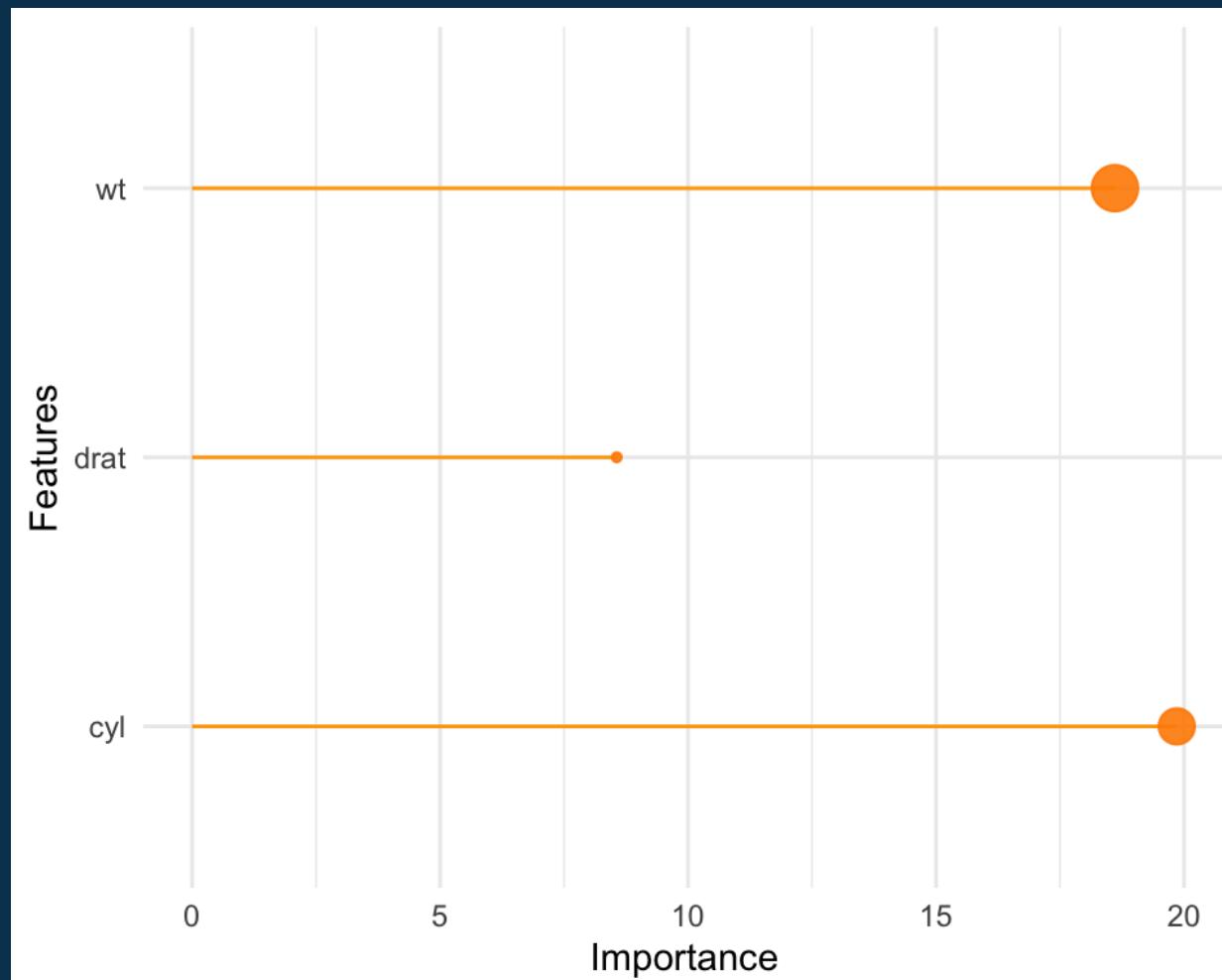
# Random Forest Regression

# Random Forest Regression use the “Bagging” Technique



Source: <https://levelup.gitconnected.com/random-forest-regression-209c0f354c84>

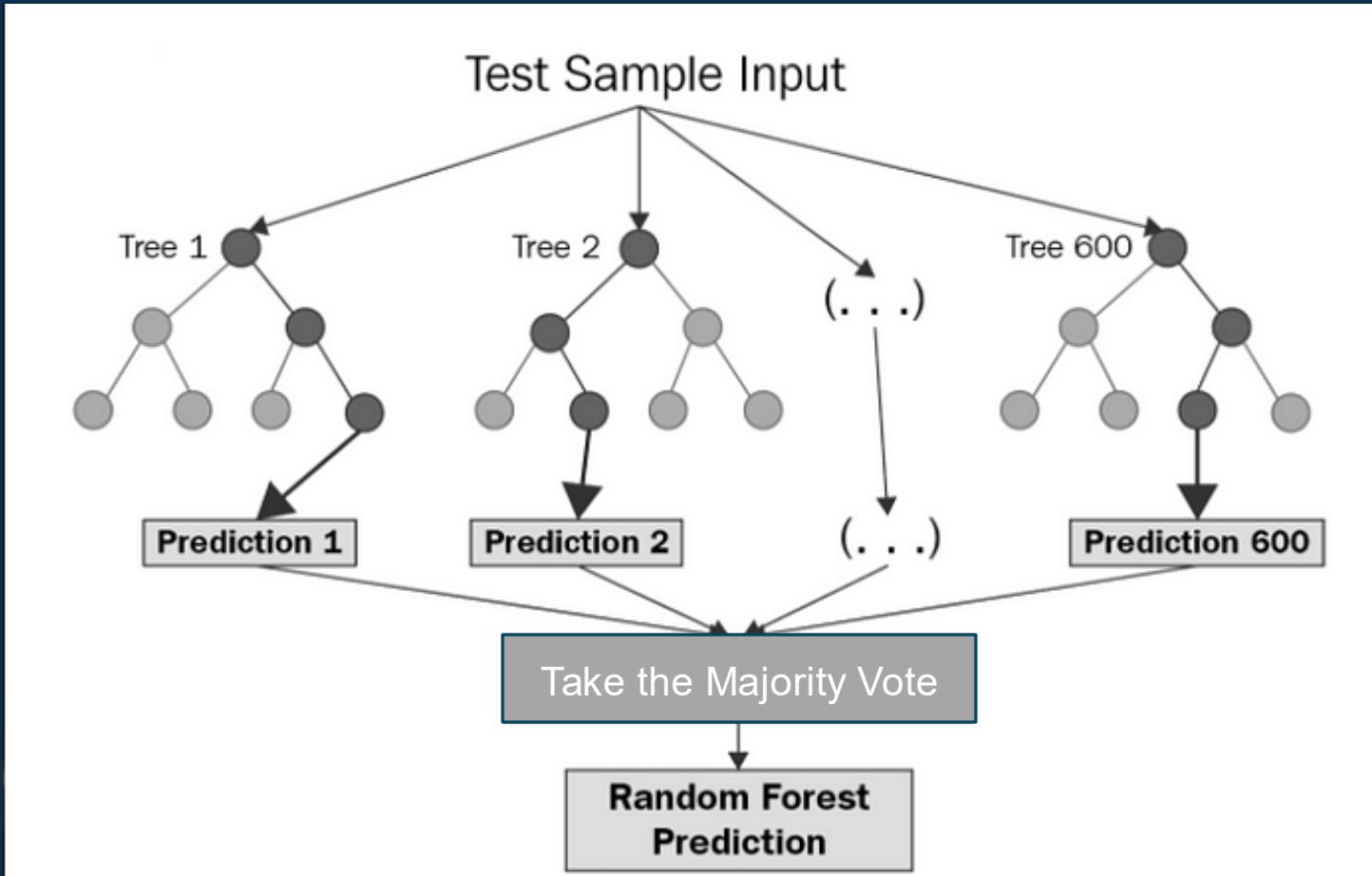
```
library(randomForest)
Random_Forest_model = randomForest(formula = mpg ~ wt + cyl + drat,
                                    data = mtcars,
                                    ntree=500, importance=TRUE)
```



Classification

# Random Forest Classification

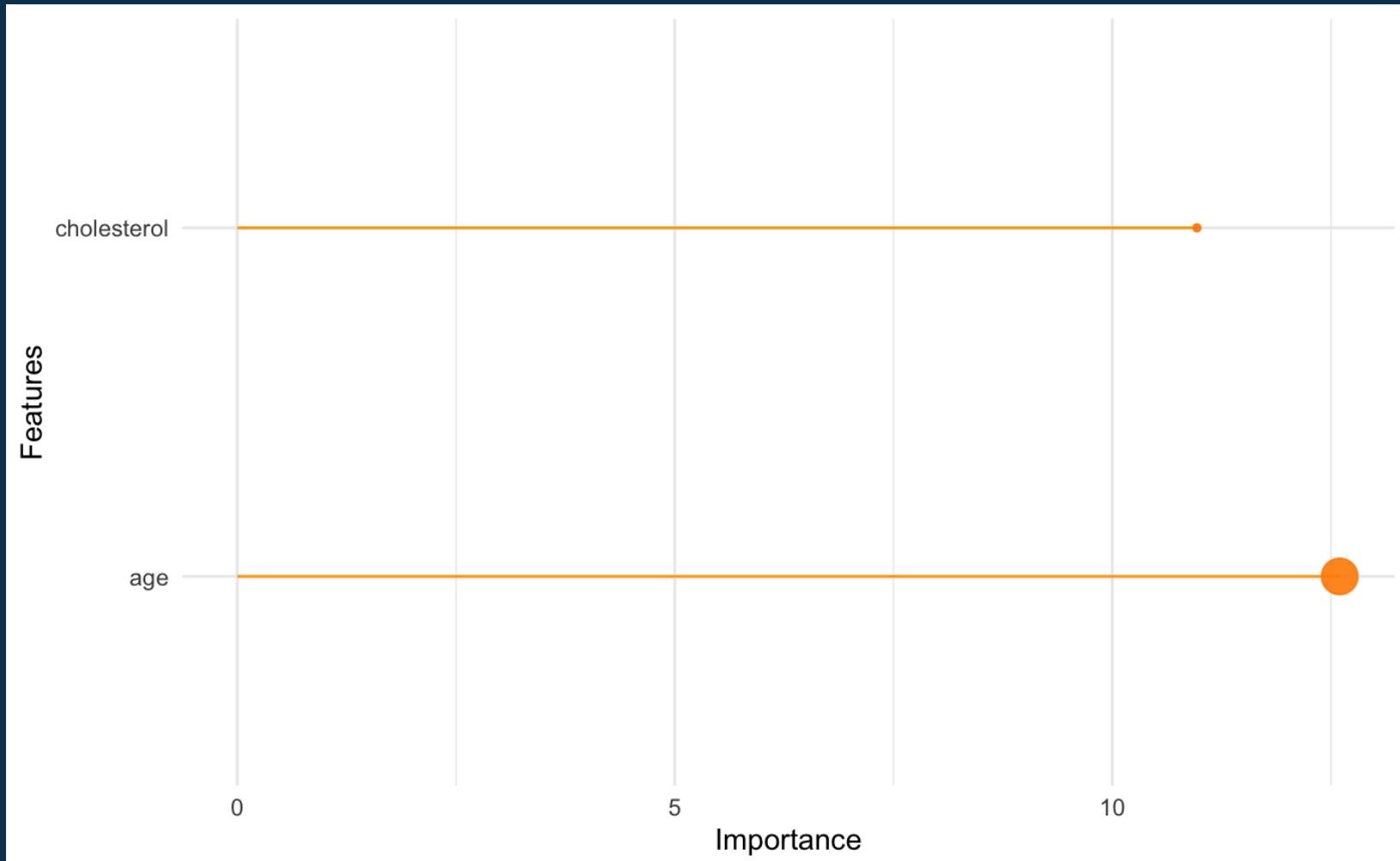
# Random Forest Classification



Source: <https://levelup.gitconnected.com/random-forest-regression-209c0f354c84>

```
library(randomForest)

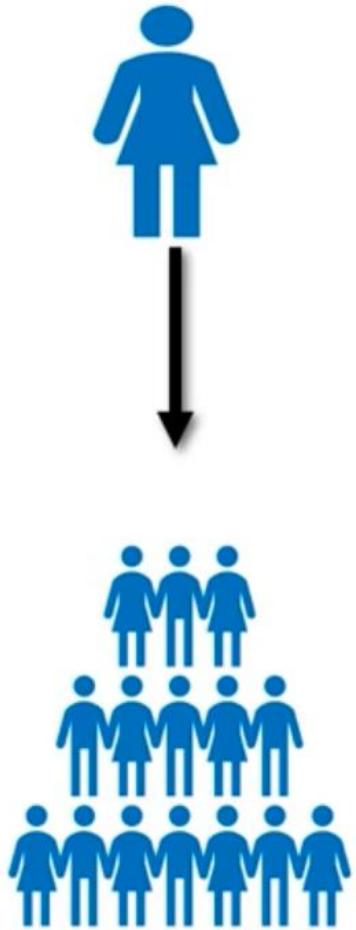
Random_Forest_Classifier = randomForest(as.factor(heart_disease) ~ cholesterol + age,
                                         data=heart_df, importance = TRUE, ntree=500)
```



# 3. Boosting Methods

Trees are built in parallel

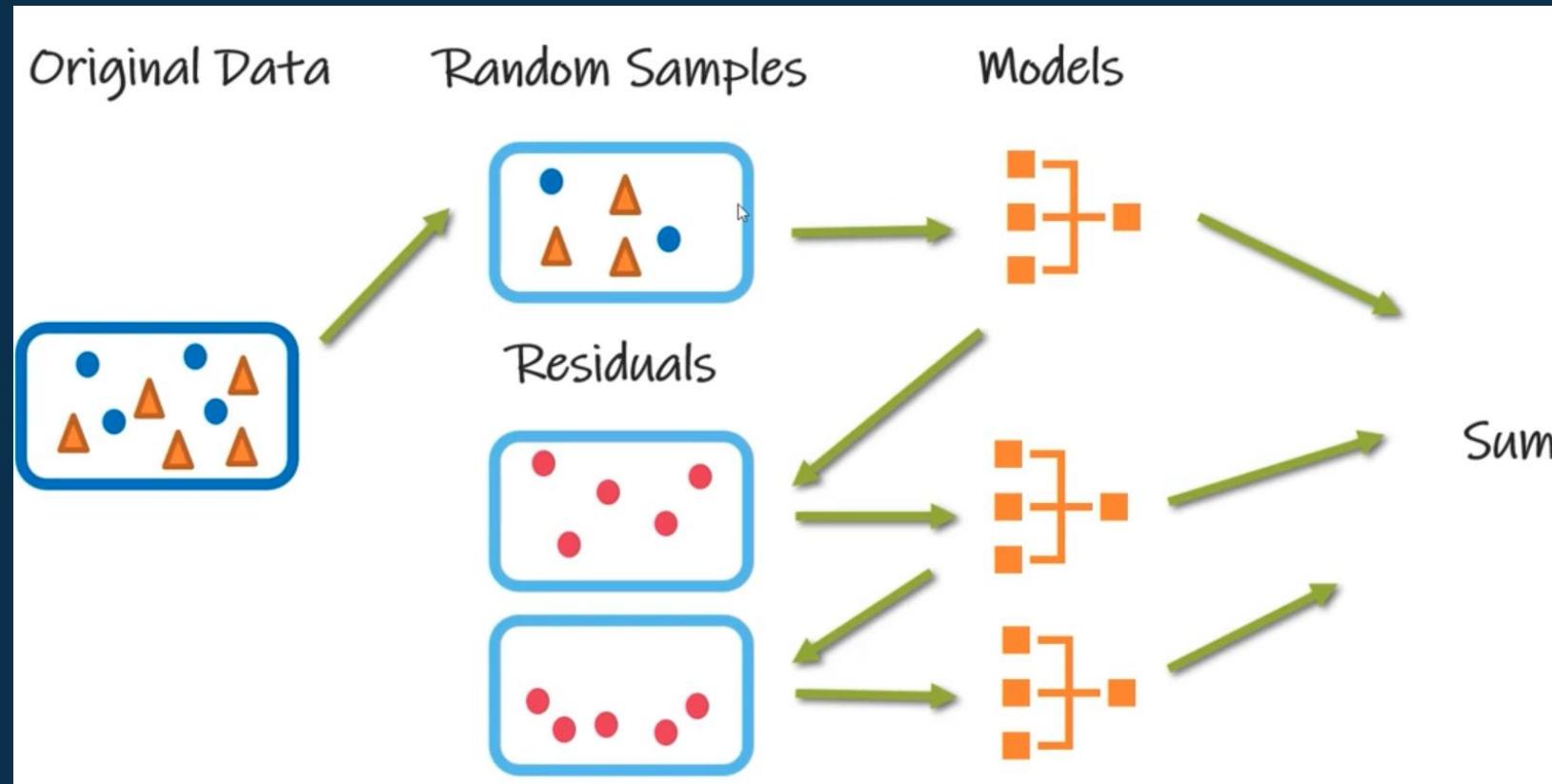
## Bagging



Trees are built in sequentially

## Boosting

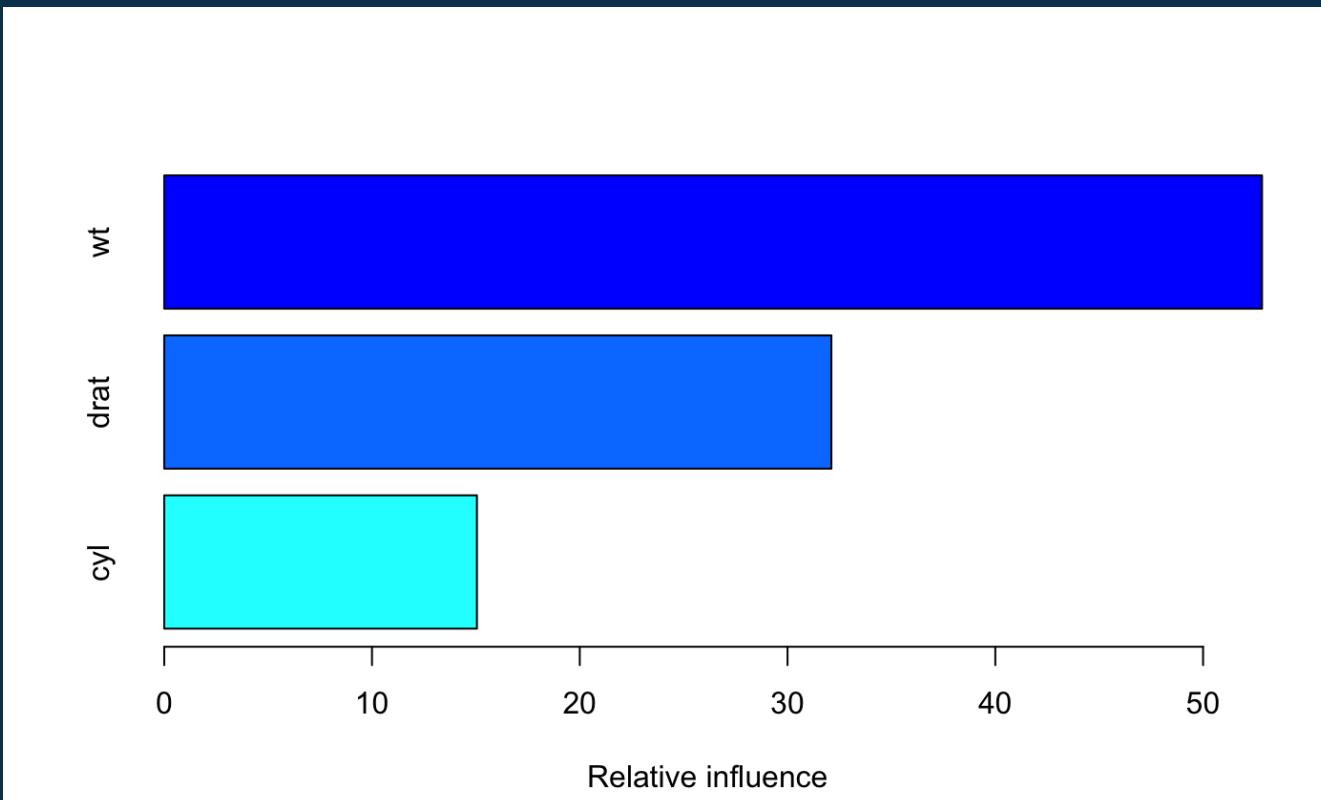




# Gradient Boost Regression

```
library(gbm)

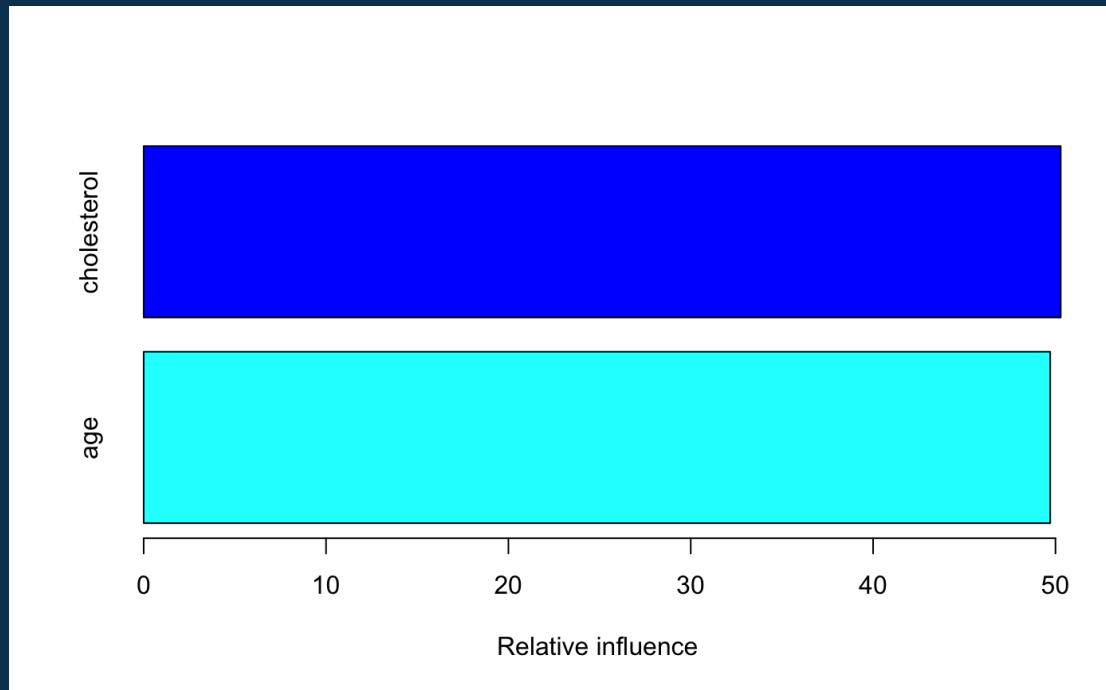
Gradient_Boost_Regression = gbm(formula = mpg ~ wt + cyl + drat,
                                 data = mtcars, n.trees = 2000,
                                 n.minobsinnode = 5
                               )
```



# Gradient Boost Classification

```
library(gbm)

Gradient_Boost_Classifier = gbm(heart_disease ~ cholesterol + age,
                                data=heart_df,
                                n.trees = 2000)
```



# Performance Metrics in Supervised Learning

# Evaluate Model Performance in Regression

Coefficient of Determination:  $0 \leq R^2 \leq 1$

$$-\infty < R_{\text{adjusted}}^2 \leq 1$$

$$\text{Mean Squared Error} = MSE = \frac{1}{N} \sum (Y_i - \hat{Y}_i)^2$$

$$\text{Root Mean Squared Error} = RMSE = \sqrt{\frac{1}{N} \sum (Y_i - \hat{Y}_i)^2}$$

$Y$  – Observed Value

$\hat{Y}$  – Predicted Value

N – Total Number of Observations

# Evaluate Model Performance in Classification

Confusion Matrix

		Actual Classes	
		0	1
Predicted Classes	0	True Negative	False Negative
	1	False Positive	True Positive

$$\text{Accuracy} = \frac{TP + TN}{N}$$

$$\text{Precision} = \frac{TP}{TP + FP}$$

$$\text{Sensitivity} = \text{True Positive Rate} = \frac{TP}{TP + FN}$$

$$\text{Specificity} = 1 - \text{False Positive Rate} = \frac{TN}{TN + FP}$$

N – Total Number of Observations

# Evaluate Model Performance in Classification

```
library(caret)

random_forest_prediction = predict(Random_Forest_Classifier)

observed_data = as.factor(heart_df$heart_disease)

confusionMatrix( random_forest_prediction, observed_data, positive = '1')
```

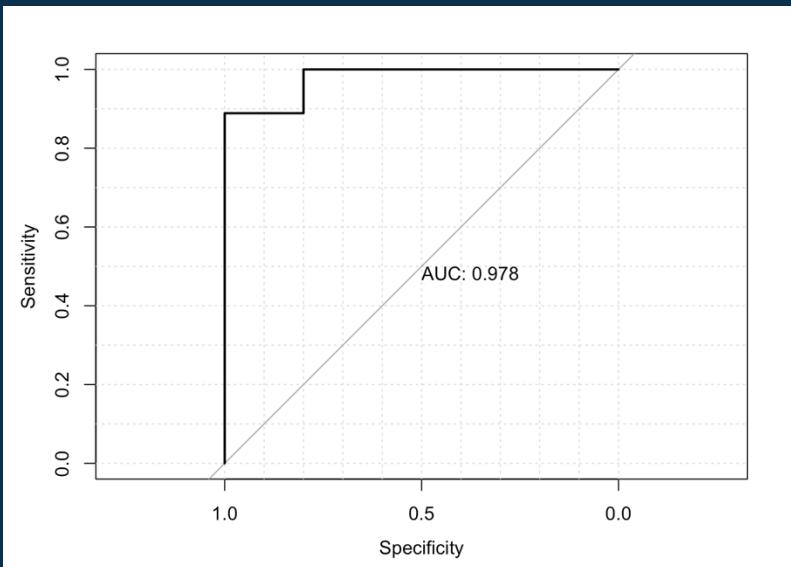
## Confusion Matrix and Statistics

		Reference
		0 1
Prediction	0	1
0	3	2
1	2	7

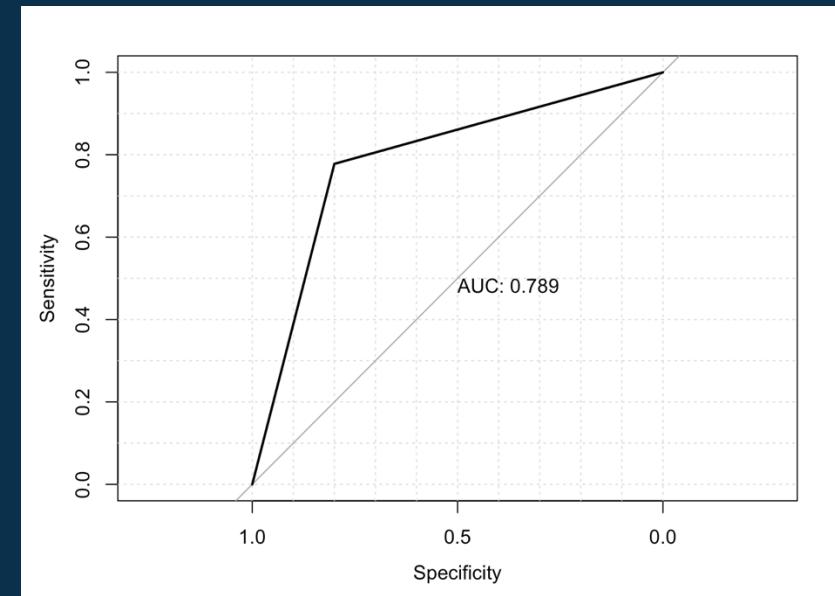
Accuracy : 0.7143  
95% CI : (0.419, 0.9161)  
No Information Rate : 0.6429  
P-Value [Acc > NIR] : 0.4007  
  
Kappa : 0.3778  
  
McNemar's Test P-Value : 1.0000  
  
Sensitivity : 0.7778  
Specificity : 0.6000  
Pos Pred Value : 0.7778  
Neg Pred Value : 0.6000  
Prevalence : 0.6429  
Detection Rate : 0.5000  
Detection Prevalence : 0.6429  
Balanced Accuracy : 0.6889

# Evaluate Model Performance in Classification

## Receiver Operating Characteristic (ROC) Curve



Logistic Regression



Random Forest Classifier

- ROC curve is a plot between the Sensitivity and Specificity of a classification model
- If the area under the curve is 0.5, we are making random guesses
- If the area under the curve is close to 1, we are making accurate predictions

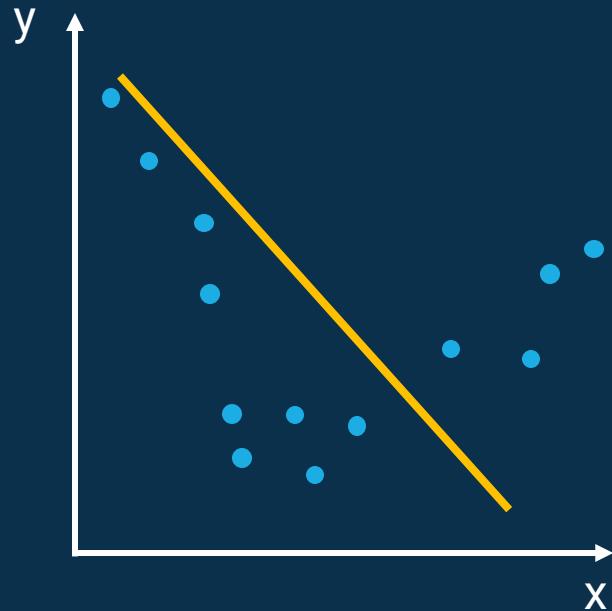
$$\text{Sensitivity} = \frac{TP}{TP + FN}$$

$$\text{Specificity} = \frac{TN}{TN + FP}$$

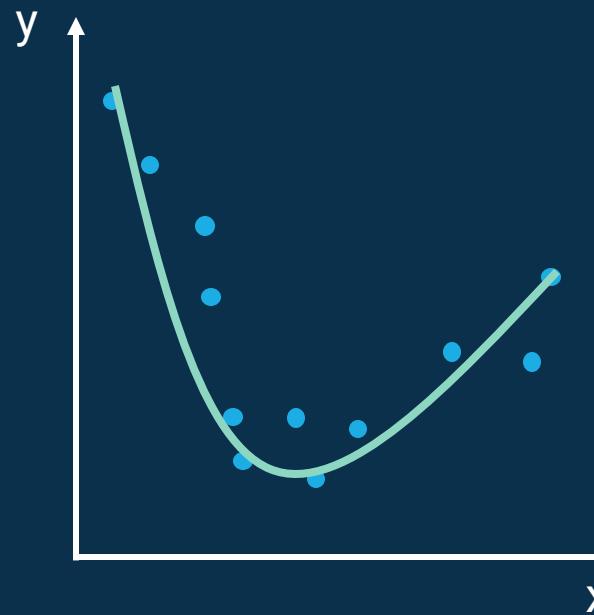
Method Type	Examples	Advantages	Disadvantages
<b>Linear Models</b>	Linear Regression Logistic Regression	- Easy to interpret - Works well for simple, linear patterns	- Struggles with nonlinear relationships - Sensitive to outliers - Requires assumptions (linearity, independence, multicollinearity)
<b>Bagging Methods</b>	Random Forest	- Handles nonlinear patterns - Robust to noise/outliers	- Less interpretable - Can be slow for large data
<b>Boosting Methods</b>	Gradient Boosting XGBoost GBM	- Handles complex nonlinearities - Good for small-to-medium datasets	- Can overfit if not tuned - Less interpretable - Slower training

# Overfitting & Cross-Validation

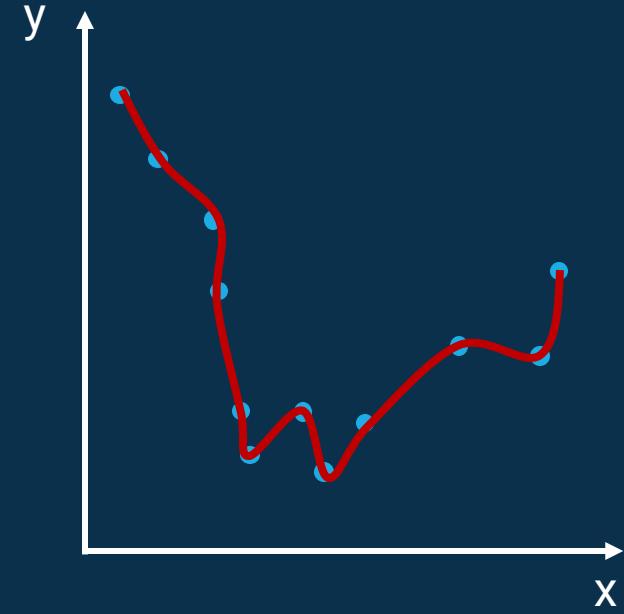
# Overfitting in Regression



Underfit  
– less complex model

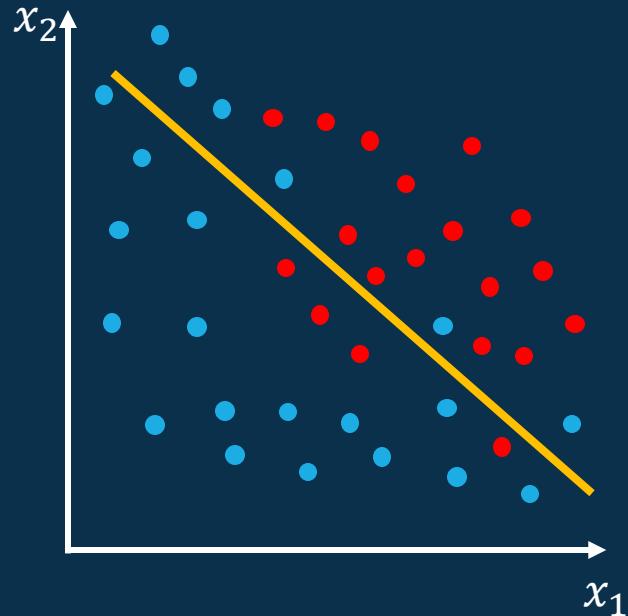


Better Fit  
- moderately complex model

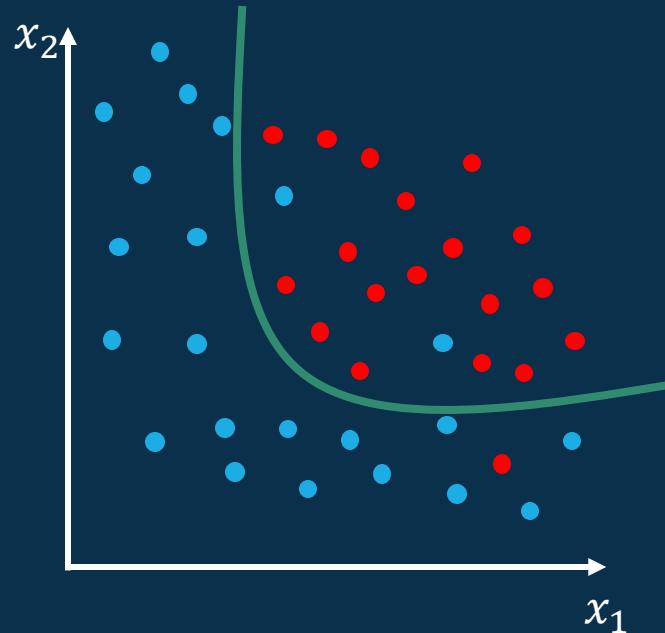


Overfit  
– high complex model

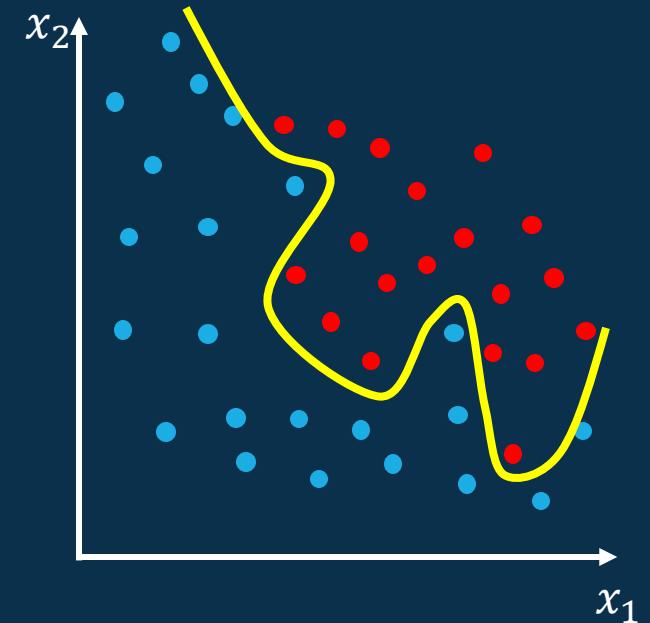
# Overfitting in Classification



Underfit  
– less complex model



Better Fit  
- moderately complex model



Overfit  
– high complex model

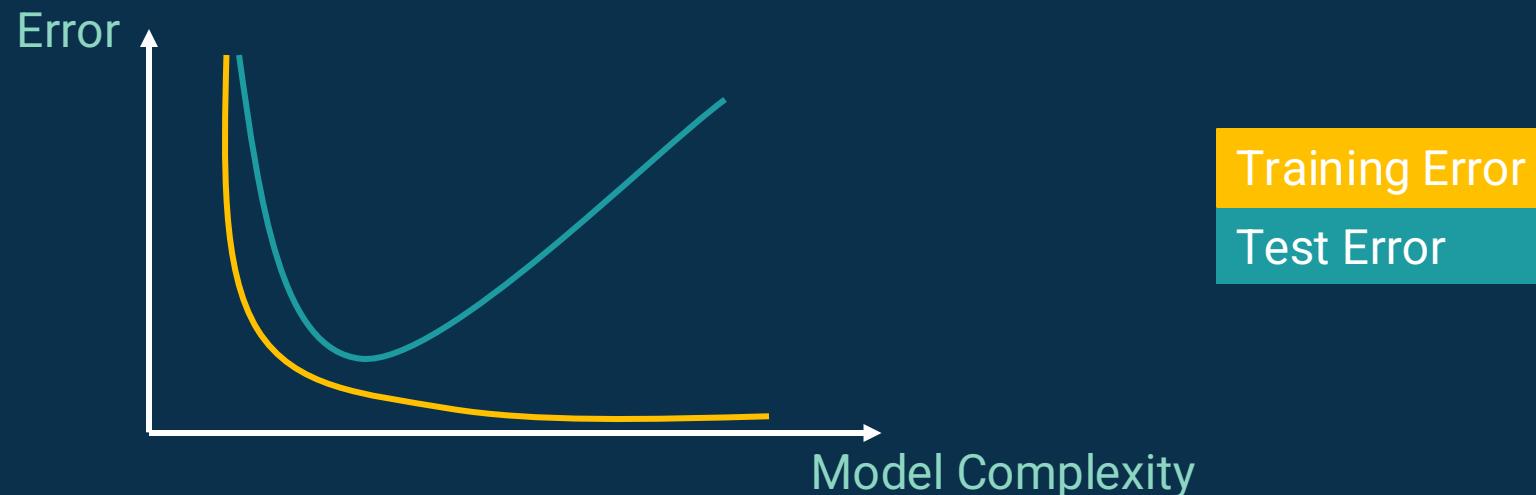
# How to Overcome Overfitting

Train/Test Data Split

Regularization

Cross Validation

# Train/Test Data Split

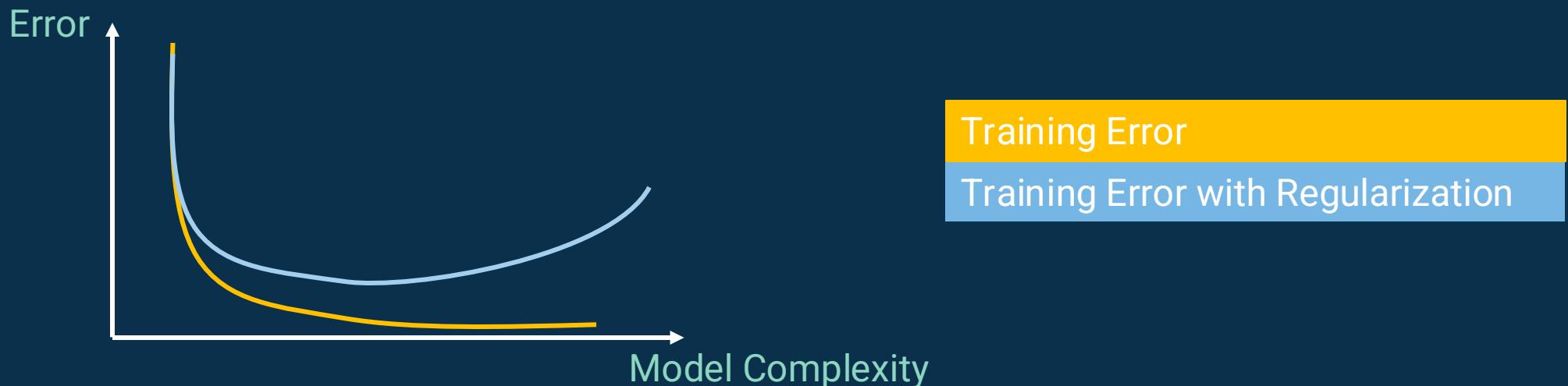


Error = Actual - Predicted

# Regularization

Total Error = Training Error + Regularization

Regularization is proportional to the model complexity and prevents overfitting  
Regularization prevents the training error from going to zero



# Cross-validation

## K-Fold Cross-Validation

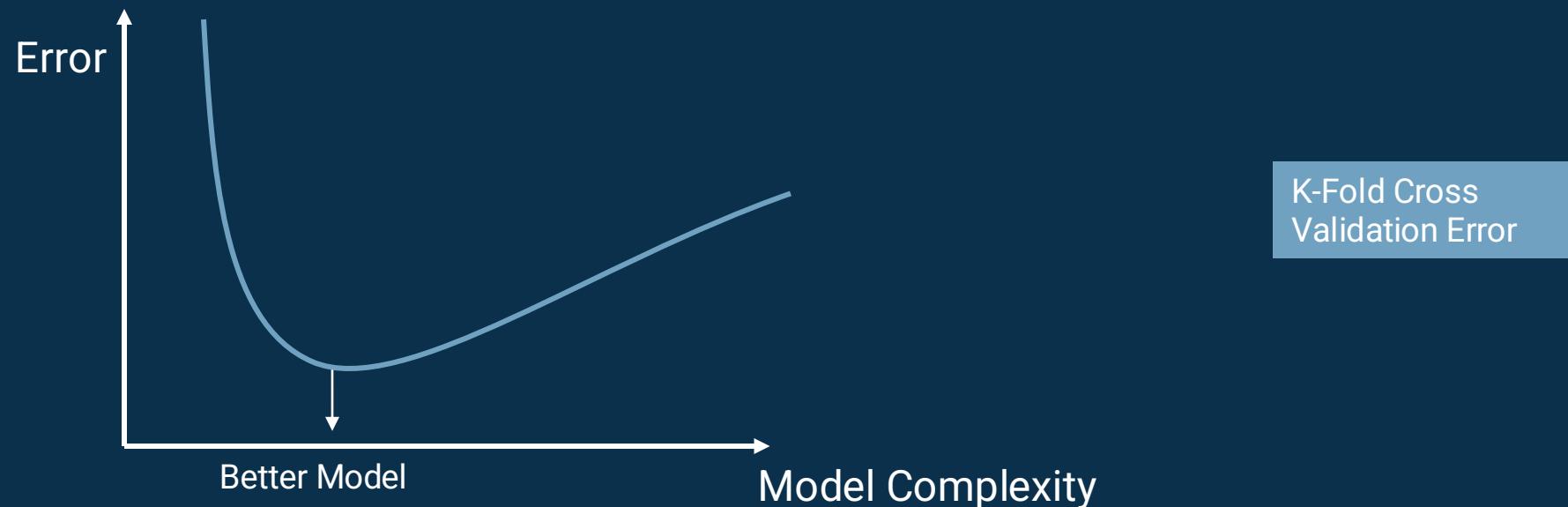


K-Fold Cross Validation Error

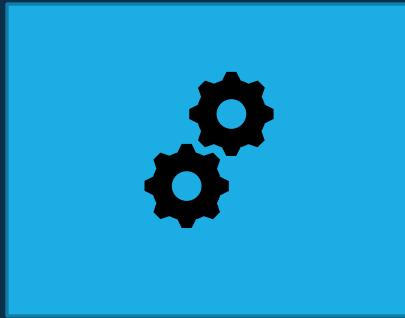
**Take average of all Validation Errors**

# Cross-validation

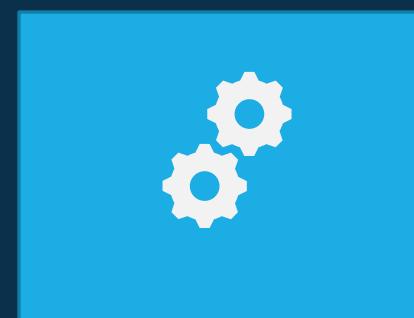
## K-Fold Cross-validation



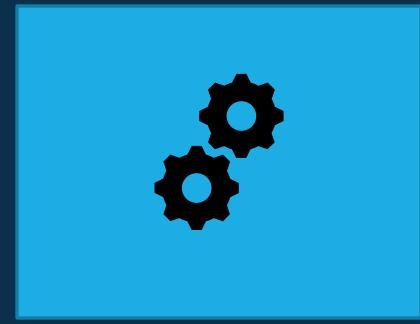
# Cross-validation: Hyperparameter Tuning



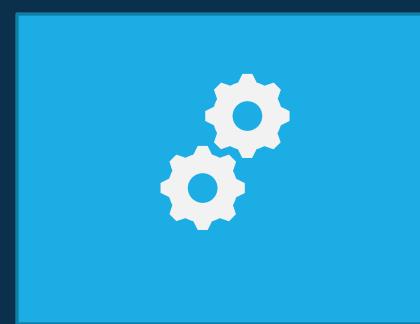
Equipment 1 Settings



Equipment 2 Settings



Model 1 Settings



Model 2 Settings

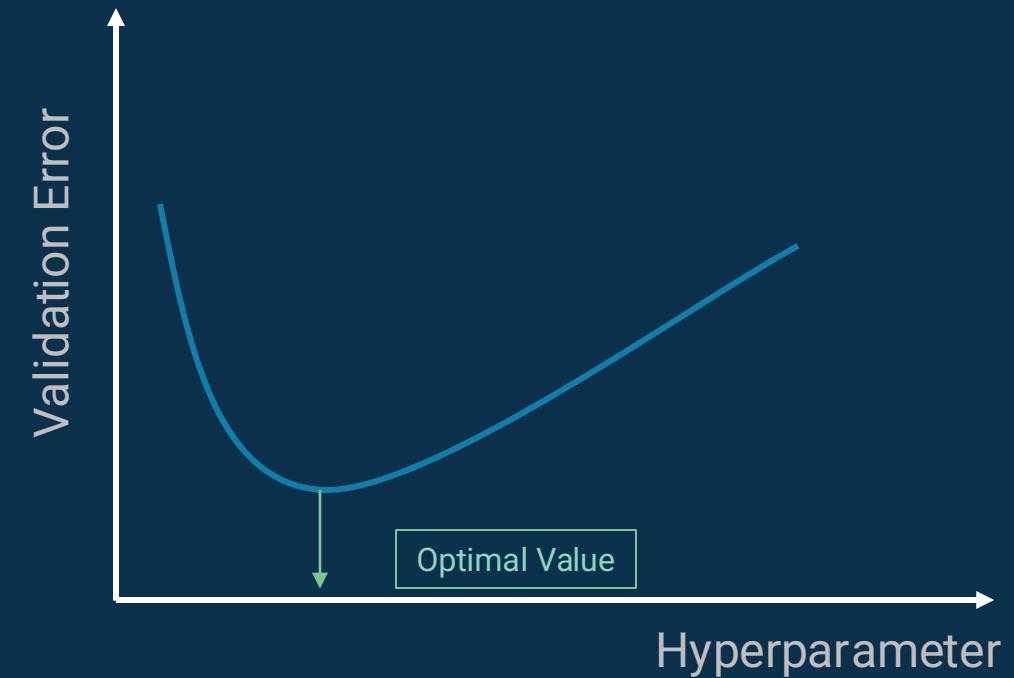
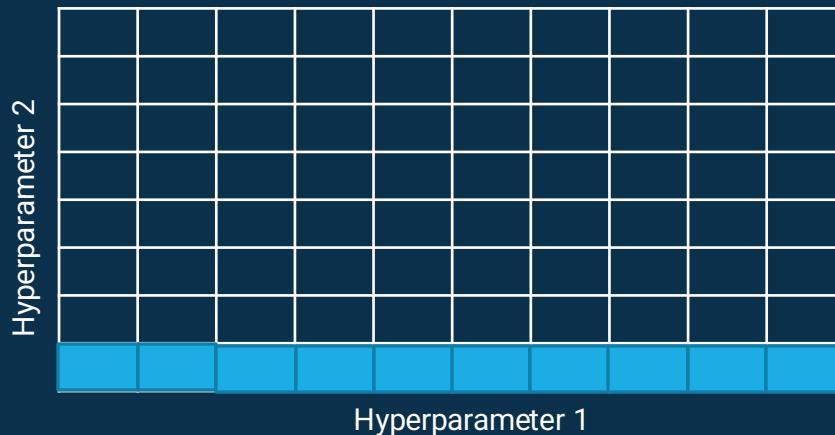
# Cross-validation: Hyperparameter Tuning

## Hyperparameters

- Model specific parameters which can not be estimated with data
- Example: ntrees and mtry in Random Forest

## Grid Search

- Require to find optimal values with a search



## Training Data

Use to Train Model

## Validation Data

- Use to control overfit
- Use to tune model parameters

## Test Data

Test model with unseen data

# Session 1: Part 2

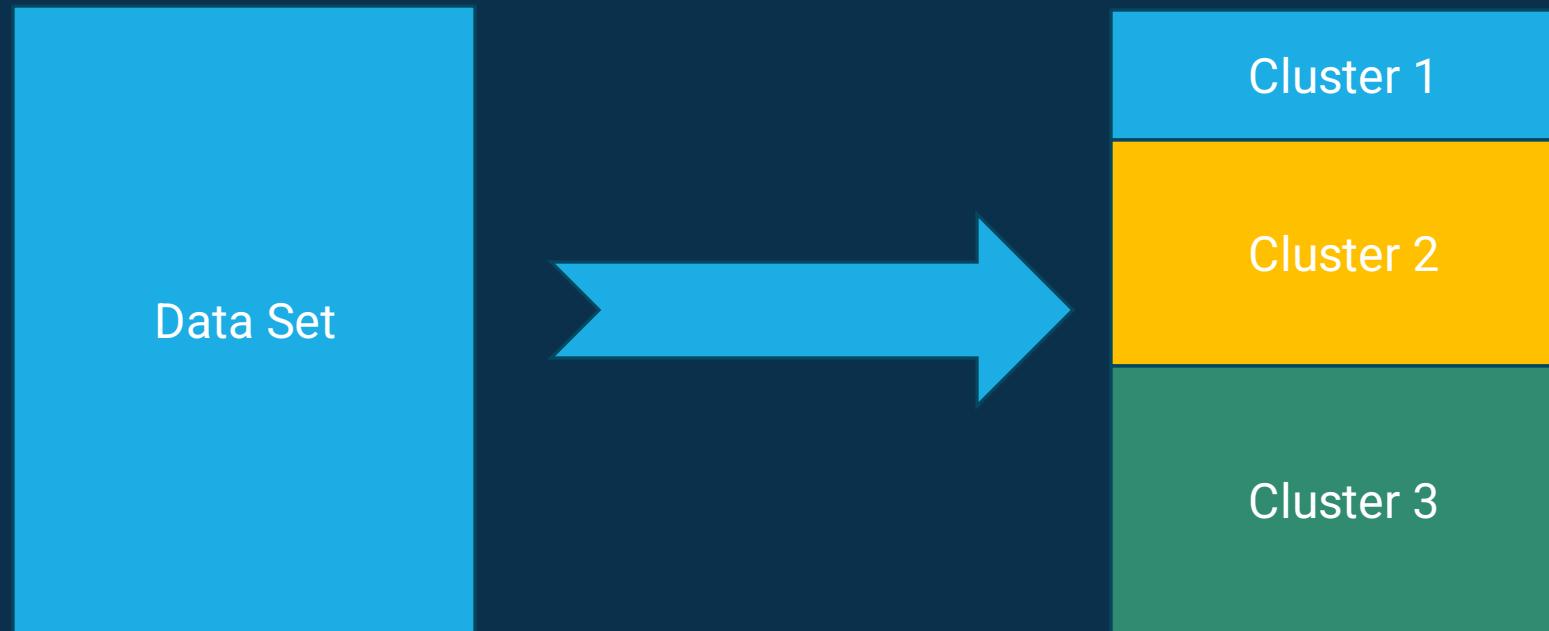
## Unsupervised Learning

Workshop on Quantitative Literacy and Statistics

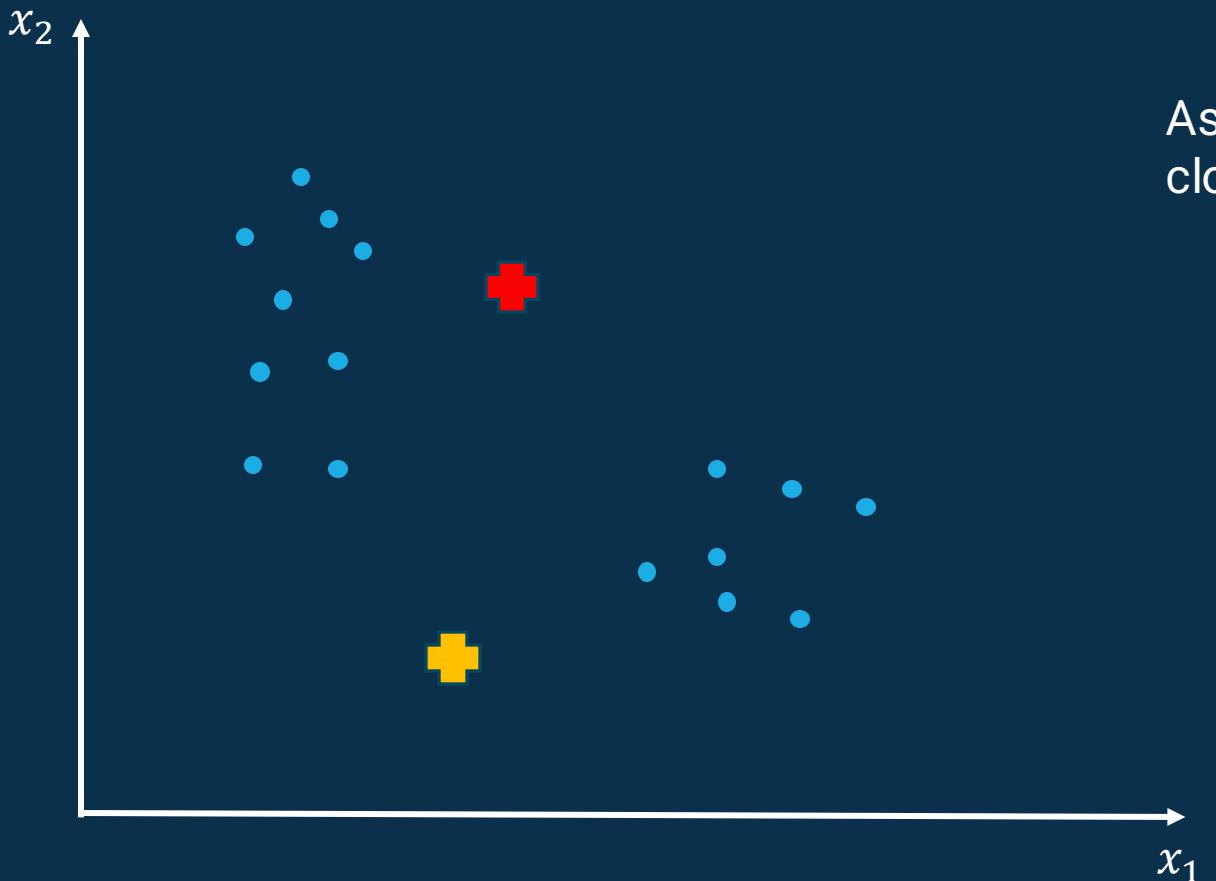


# Unsupervised Learning

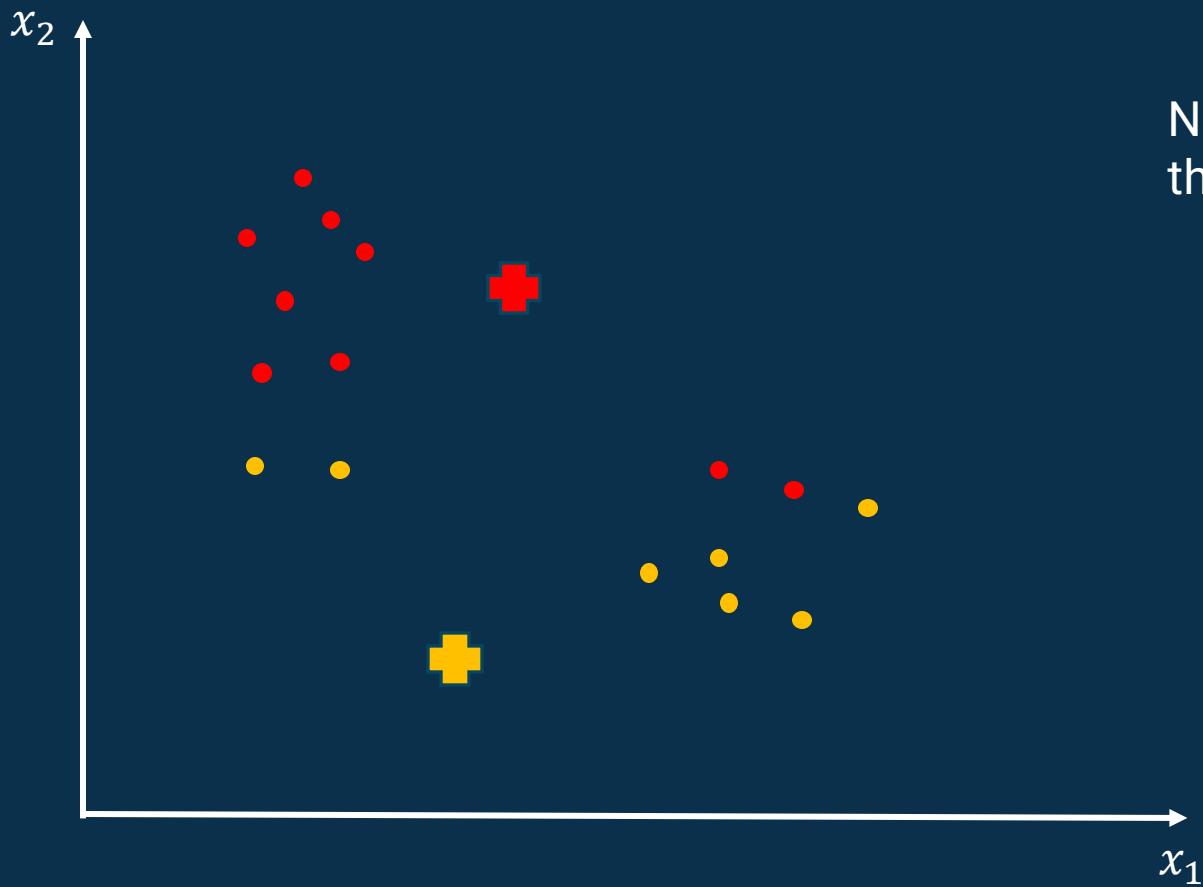
Learning techniques to find patterns and cluster unlabeled data



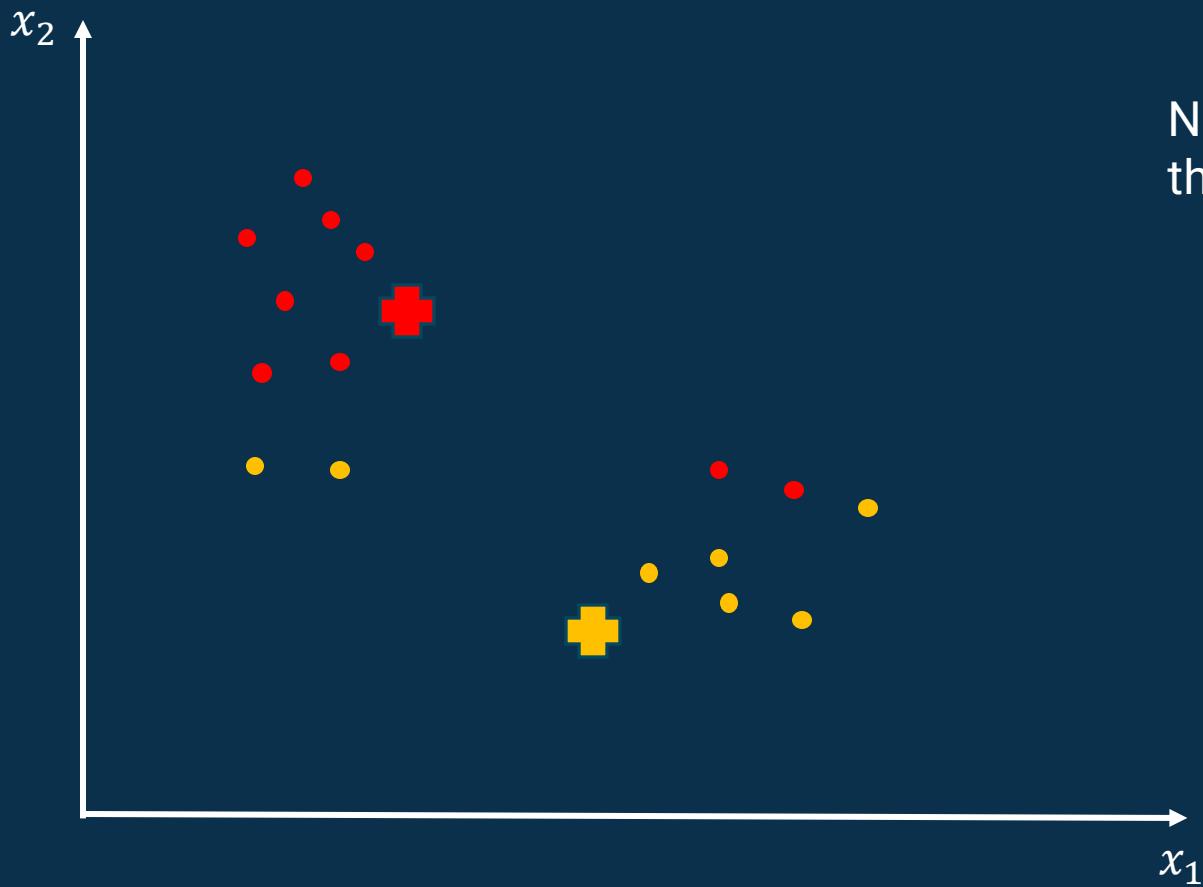
# K-Means Clustering



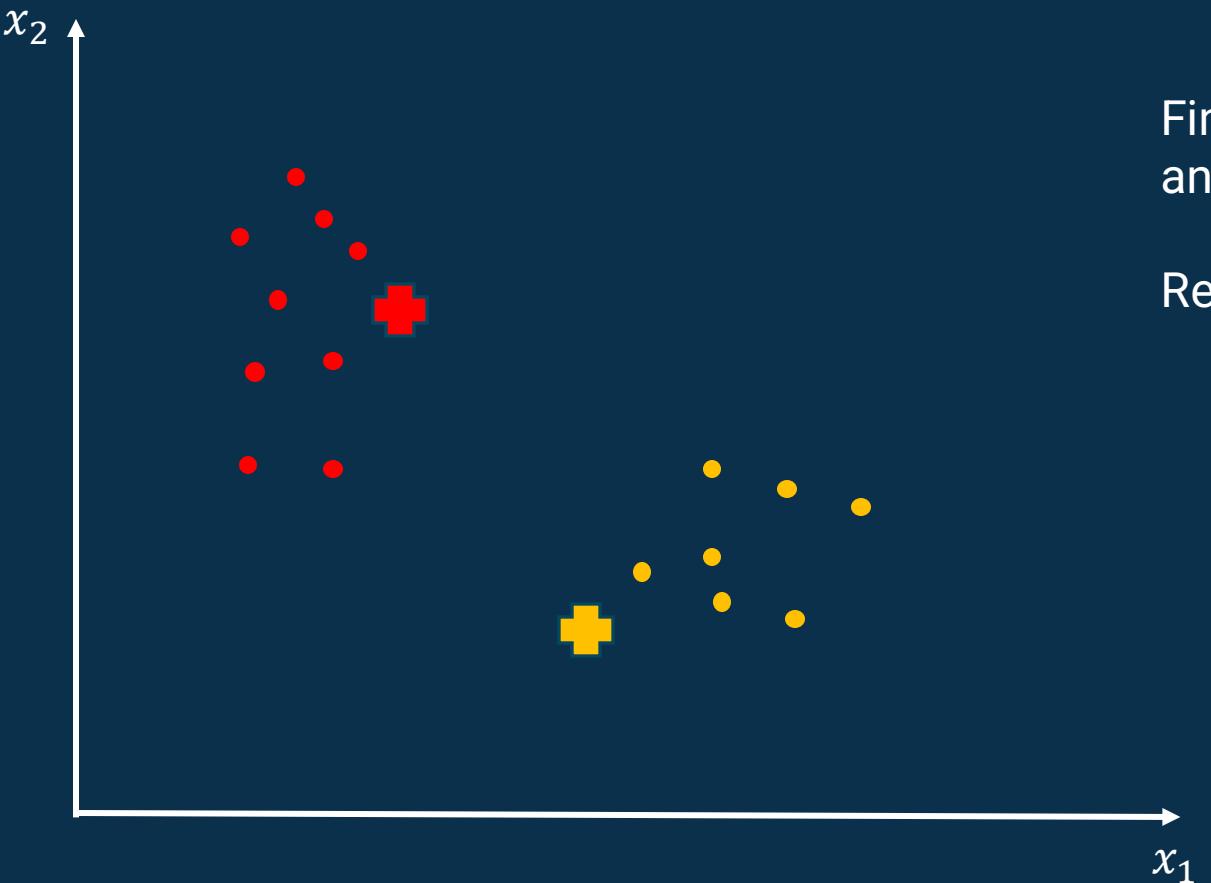
Assign data points for the  
closest centroid



Now update the center of  
the centroids

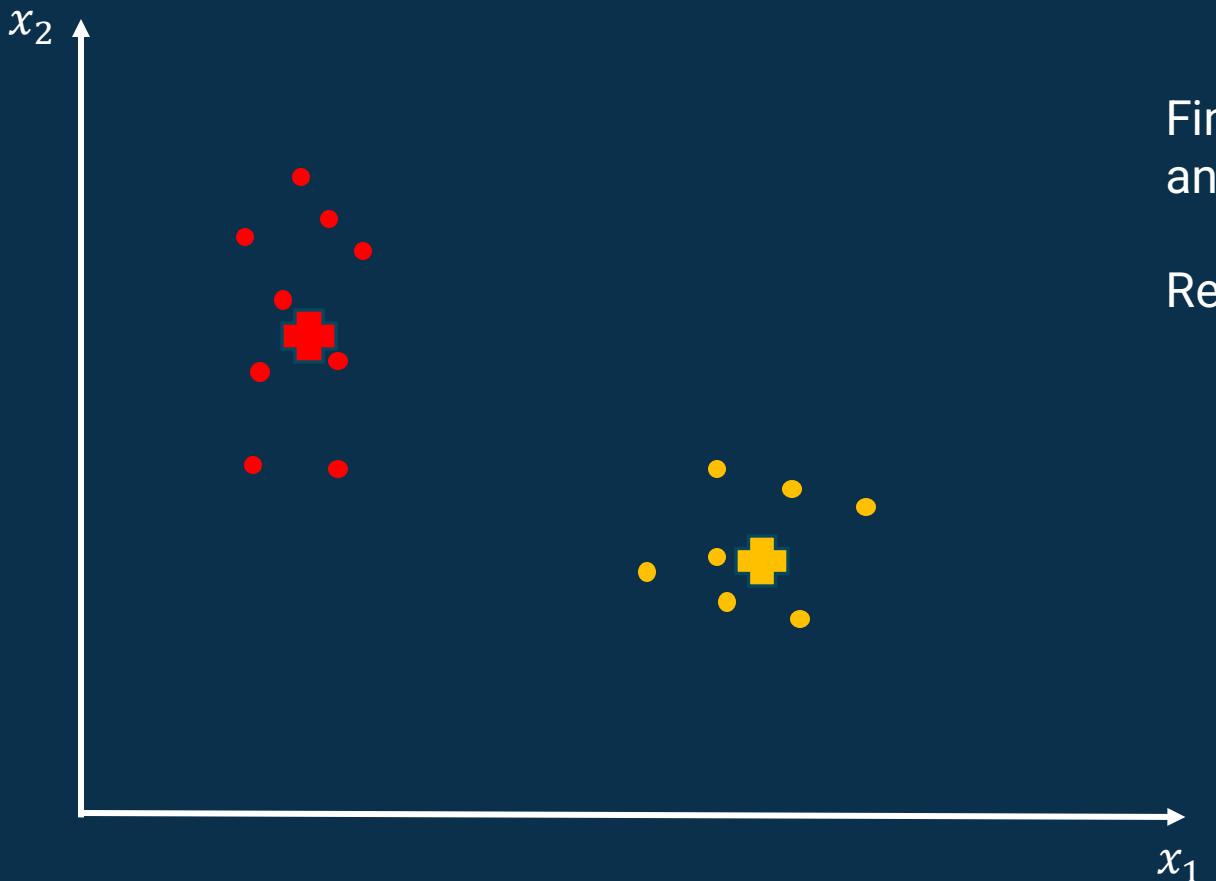


Now update the center of  
the centroids



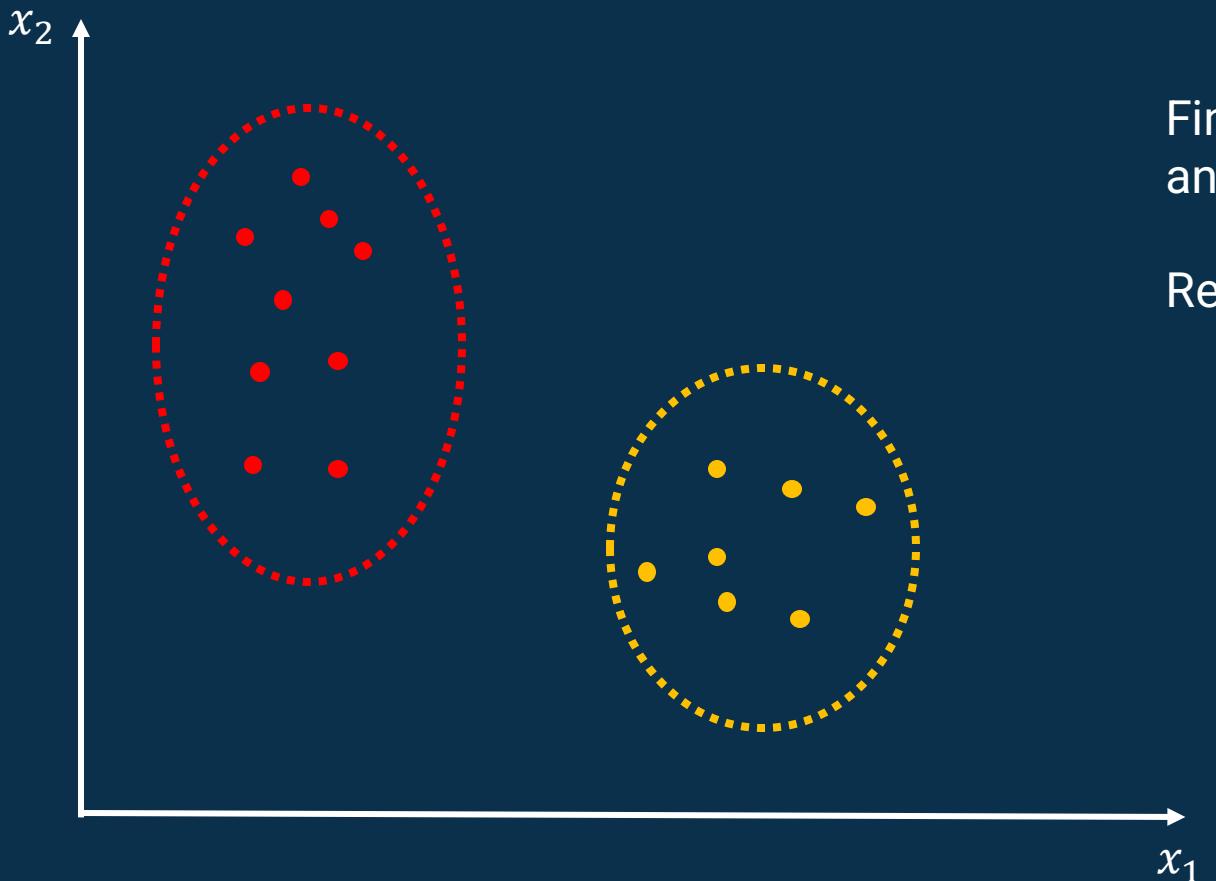
Find the closest points  
and update the centroid

Repeat the process



Find the closest points  
and update the centroid

Repeat the process



Find the closest points  
and update the centroid

Repeat the process

# K-Means Clustering

```
set.seed(123)

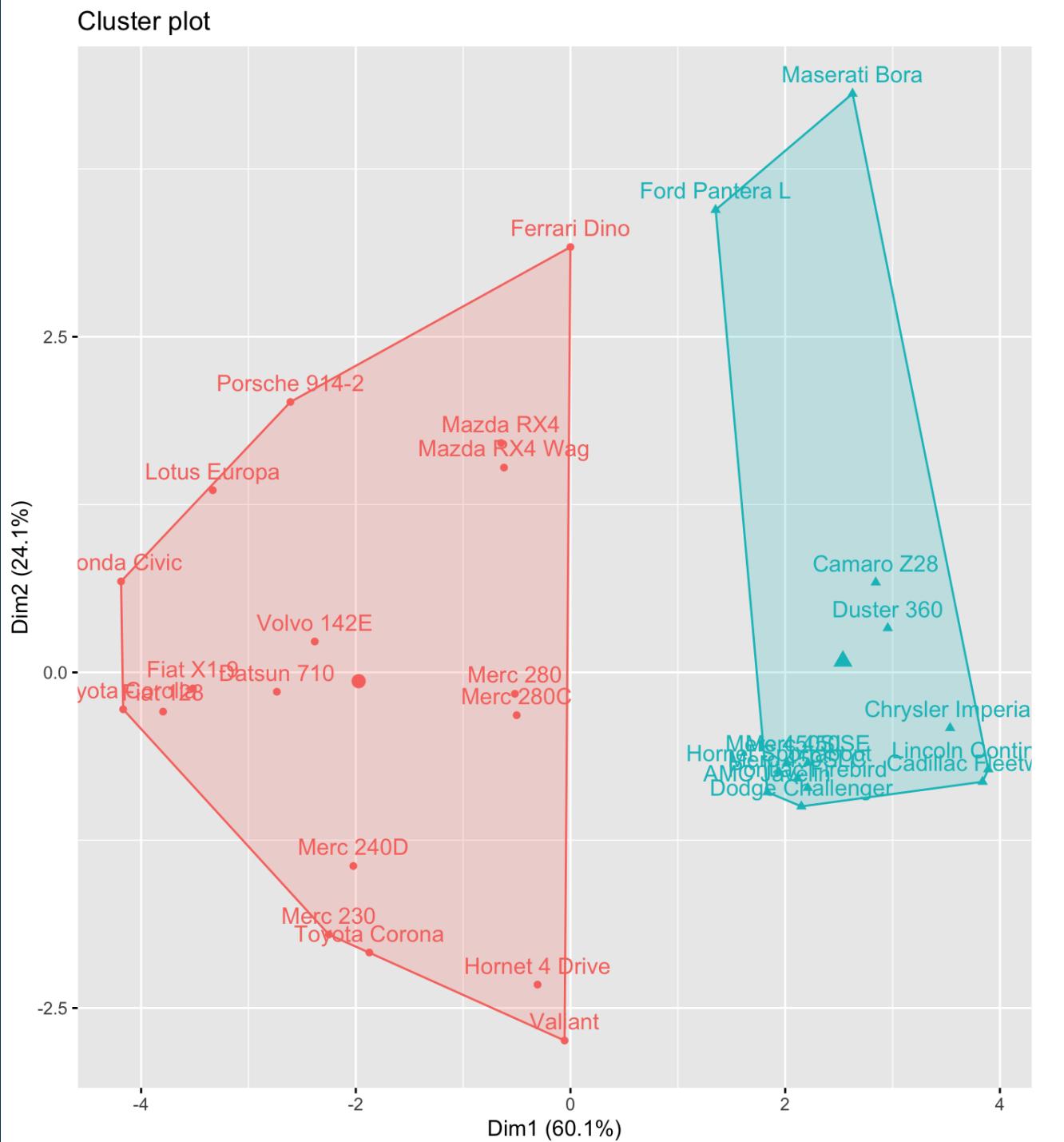
k_means_clustering <- kmeans(mtcars, centers = 2)

print(k_means_clustering$cluster)
```

Mazda RX4	Mazda RX4 Wag	Datsun 710	Hornet 4 Drive	Hornet Sportabout	Valiant	Duster 360
1	1	1	1	2	1	2
Merc 240D	Merc 230	Merc 280	Merc 280C	Merc 450SE	Merc 450SL	Merc 450SLC
1	1	1	1	2	2	2
Cadillac Fleetwood	Lincoln Continental	Chrysler Imperial	Fiat 128	Honda Civic	Toyota Corolla	Toyota Corona
2	2	2	1	1	1	1
Dodge Challenger	AMC Javelin	Camaro Z28	Pontiac Firebird	Fiat X1-9	Porsche 914-2	Lotus Europa
2	2	2	2	1	1	1
Ford Pantera L	Ferrari Dino	Maserati Bora	Volvo 142E			
2	1	2	1			

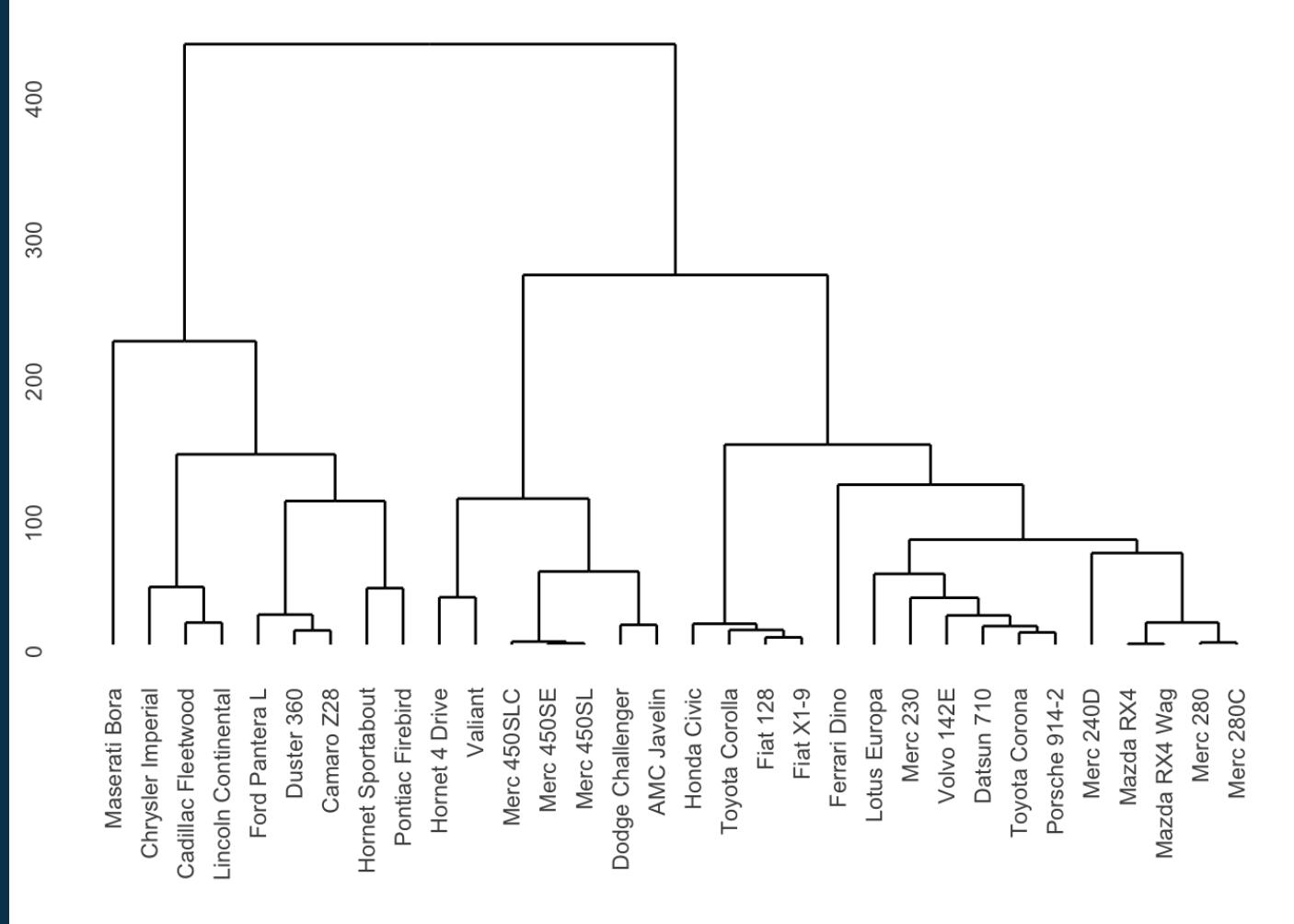
# Plot K-Means Clustering

```
library(factoextra)  
  
fviz_cluster(k_means_clustering,  
             data = mtcars)
```



# Hierarchical Clustering

```
library(ggdendro)
set.seed(123)
mtcars_distance = dist(mtcars, method = 'euclidean')
h_clustering = hclust(mtcars_distance)
ggdendrogram(h_clustering)
```

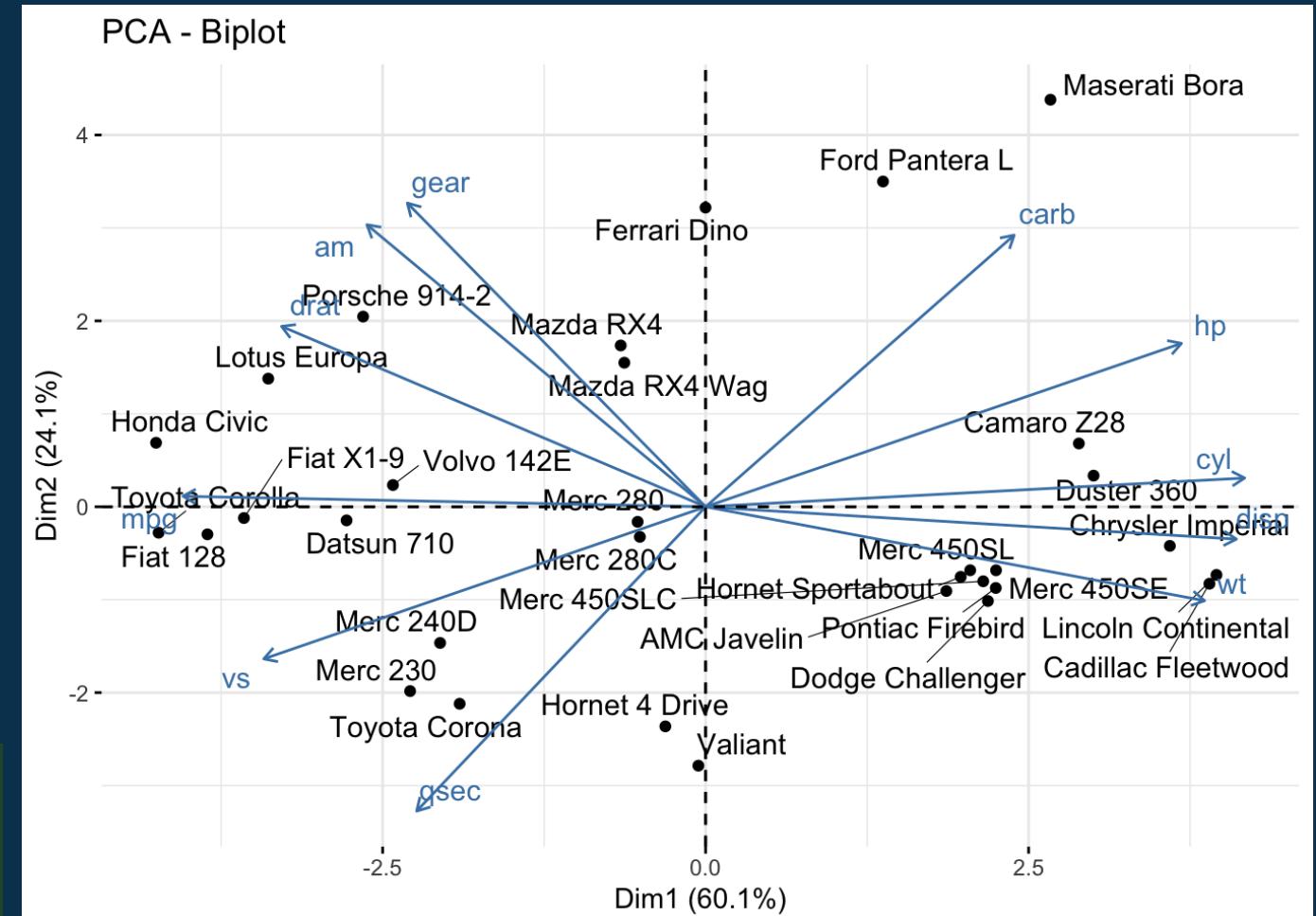


# Principal Component Analysis Biplot

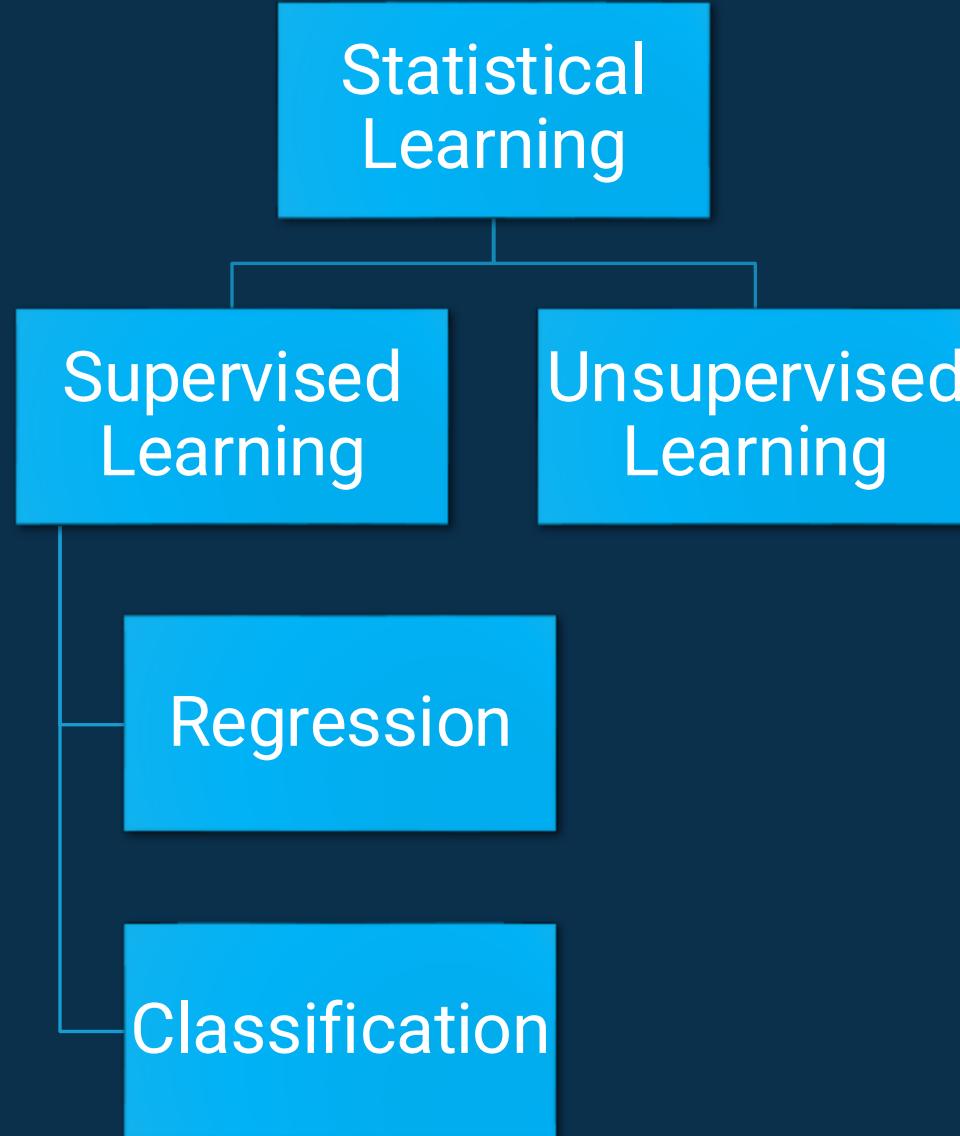
```
library(FactoMineR)
```

```
pca_mtcars <- PCA(mtcars, graph = FALSE)
```

```
fviz_pca_biplot(pca_mtcars, repel = TRUE)
```



PCA Biplot can be used to understand  
the correlation structure of the  
variables



Thank you!