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Week 8:

Regression Model:

- a) Import a data from web storage. Name the dataset and now do Logistic Regression to find out relation between variables that are affecting the admission of a student in an institute based on his or her GRE score, GPA obtained and rank of the student. Also check the model is fit or not. Require (foreign), require (MASS).
- b) Apply regression Model to predict the data on any dataset.

Program:

```
A) data <- read.csv("D:/5d8_r/Admission_Predict.csv")  
head(data,n=3)  
summary(data)  
  
data$Admission <- ifelse(data$Chance.of.Admit >= 0.75, 1, 0)  
  
model <- glm(Admission ~ GRE.Score + CGPA, data = data, family = binomial)  
summary(model)  
  
pseudo_r2 <- 1 - (model$deviance / model>null.deviance)  
cat("Pseudo R-squared:", pseudo_r2, "\n")  
  
predicted_probs <- predict(model, type = "response")  
predicted_class <- ifelse(predicted_probs >= 0.5, 1, 0)  
  
conf_matrix <- table(Predicted = predicted_class, Actual = data$Admission)  
print(conf_matrix)  
  
accuracy <- sum(diag(conf_matrix)) / sum(conf_matrix)  
cat("Accuracy:", round(accuracy, 4), "\n")
```

Output:

Serial.No.	GRE.Score	TOEFL.Score	University.Rating	SOP	LOR	CGPA	Research	Chance.of.Admit
1	1	337	118	4 4.5	4.5	9.65	1	0.92
2	2	324	107	4 4.0	4.5	8.87	1	0.76
3	3	316	104	3 3.0	3.5	8.00	1	0.72

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Call:

```
glm(formula = Admission ~ GRE.Score + CGPA, family = binomial,  
    data = data)
```

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept)	-70.82714	8.32195	-8.511 <2e-16 ***
GRE.Score	0.09199	0.02762	3.330 0.000868 ***
CGPA	4.78748	0.68169	7.023 2.17e-12 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 550.51 on 399 degrees of freedom

Residual deviance: 226.07 on 397 degrees of freedom

AIC: 232.07

Pseudo R-squared: 0.5893459

Actual

Predicted	0	1
0	196	26
1	24	154

Accuracy: 0.875

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B) require(MASS)

data(mtcars)

head(mtcars)

linear_model <- lm(mpg ~ hp + wt, data = mtcars)

summary(linear_model)

predicted_mpg <- predict(linear_model, mtcars)

data.frame(Actual = mtcars\$mpg, Predicted = round(predicted_mpg, 2))

plot(mtcars\$mpg, predicted_mpg,

 xlab = "Actual MPG", ylab = "Predicted MPG",

 main = "Actual vs Predicted MPG", pch = 19, col = "blue")

abline(0, 1, col = "red", lwd = 2)

SSE <- sum((mtcars\$mpg - predicted_mpg)^2)

SST <- sum((mtcars\$mpg - mean(mtcars\$mpg))^2)

R2 <- 1 - (SSE / SST)

cat("Model R-squared:", round(R2, 3))

Output:

mpg cyl disp hp drat wt qsec vs am gear carb
Mazda RX4 21.0 6 160 110 3.90 2.620 16.46 0 1 4 4
Mazda RX4 Wag 21.0 6 160 110 3.90 2.875 17.02 0 1 4 4
Datsun 710 22.8 4 108 93 3.85 2.320 18.61 1 1 4 1
Hornet 4 Drive 21.4 6 258 110 3.08 3.215 19.44 1 0 3 1
Hornet Sportabout 18.7 8 360 175 3.15 3.440 17.02 0 0 3 2
Valiant 18.1 6 225 105 2.76 3.460 20.22 1 0 3 1

Actual Predicted

Mazda RX4 21.0 23.57

Mazda RX4 Wag 21.0 22.58

Datsun 710 22.8 25.28

Hornet 4 Drive 21.4 21.27

Hornet Sportabout 18.7 18.33

Call:

lm(formula = mpg ~ hp + wt, data = mtcars)

Residuals:

Min 1Q Median 3Q Max

-3.941 -1.600 -0.182 1.050 5.854

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Coefficients:

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

(Intercept)	37.22727	1.59879	23.285 < 2e-16 ***
hp	-0.03177	0.00903	-3.519 0.00145 **
wt	-3.87783	0.63273	-6.129 1.12e-06 ***

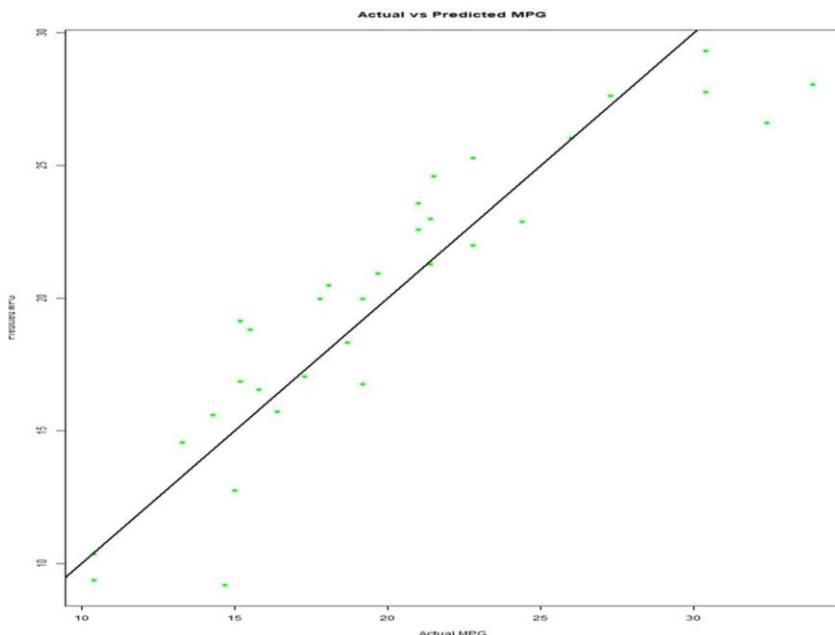
Signif. codes: 0 '****' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.593 on 29 degrees of freedom

Multiple R-squared: 0.8268, Adjusted R-squared: 0.8148

F-statistic: 69.21 on 2 and 29 DF, p-value: 9.109e-12

Model R-squared: 0.827



TITLE:**DATE:****PAGE NO:****Week 9:****Multiple Regression Model:**

- a) Develop Multiple Regression model for any dataset.
- b) Apply Multiple Regression Model to predict the data on any dataset.

Program:

```
A) library(MASS)      # Contains Boston

dataset library(caret) # For data partitioning

library(ggplot2) # For visualization

data("Boston")

head(Boston)

set.seed(123)

trainIndex <- createDataPartition(Boston$medv, p = 0.8, list = FALSE)

trainData <- Boston[trainIndex, ]

testData <- Boston[-trainIndex, ]

lm_model <- lm(medv ~ ., data = trainData)

summary(lm_model)

predictions <- predict(lm_model, newdata = testData)

rmse <- sqrt(mean((predictions - testData$medv)^2))

cat("RMSE: ", rmse)

ggplot(data.frame(Actual = testData$medv, Predicted = predictions), aes(x = Actual, y = Predicted)) +
  geom_point(color = "blue") +
  geom_abline(slope = 1, intercept = 0, linetype = "dashed", color = "red") +
  labs(title = "Actual vs Predicted: Boston Housing Prices",
       x = "Actual Median Value of Homes ($1000s)",
       y = "Predicted Median Value of Homes ($1000s)")

par(mfrow = c(2, 2))

plot(lm_model)
```

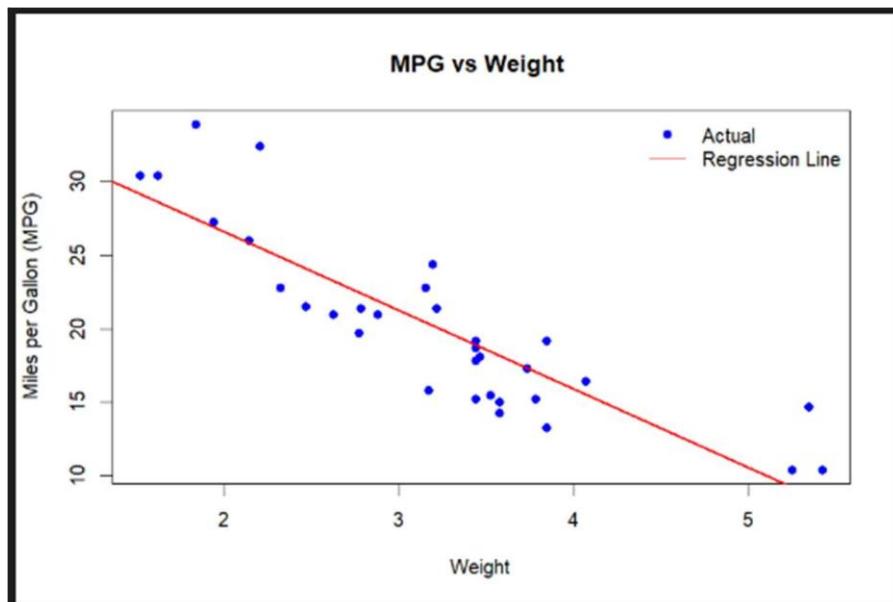
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Output:

```
crim zn indus chas nox rm age dis rad tax ptratio black lstat medv
1 0.00632 18 2.31 0 0.538 6.575 65.2 4.0900 1 296 15.3 396.90 4.98 24.0
2 0.02731 0 7.07 0 0.469 6.421 78.9 4.9671 2 242 17.8 396.90 9.14 21.6
3 0.02729 0 7.07 0 0.469 7.185 61.1 4.9671 2 242 17.8 392.83 4.03 34.7
4 0.03237 0 2.18 0 0.458 6.998 45.8 6.0622 3 222 18.7 394.63 2.94 33.4
5 0.06905 0 2.18 0 0.458 7.147 54.2 6.0622 3 222 18.7 396.90 5.33 36.2
6 0.02985 0 2.18 0 0.458 6.430 58.7 6.0622 3 222 18.7 394.12 5.21 28.7
RMSE: 4.588948
```



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```
B) install.packages("caret")  
install.packages("ggplot2")  
library(caret)  
library(ggplot2)  
data("mtcars")  
head(mtcars)  
set.seed(123)  
  
trainIndex <- createDataPartition(mtcars$mpg, p = 0.8, list = FALSE)  
  
trainData <- mtcars[trainIndex, ]  
  
testData <- mtcars[-trainIndex, ]  
  
cat("Dimensions of trainData:", dim(trainData), "\n")  
cat("Dimensions of testData:", dim(testData), "\n")  
  
lm_model_mtcars <- lm(mpg ~ cyl + disp + hp + wt + qsec + drat + vs + am + gear + carb, data = trainData)  
  
summary(lm_model_mtcars)  
  
predictions_mtcars <- predict(lm_model_mtcars, newdata = testData)  
  
cat("Length of predictions:", length(predictions_mtcars), "\n")  
cat("Length of testData$mpg:", length(testData$mpg), "\n")  
  
rmse_mtcars <- sqrt(mean((predictions_mtcars - testData$mpg)^2))  
cat("RMSE: ", rmse_mtcars, "\n")  
  
comparison_data <- data.frame(Actual = testData$mpg, Predicted = predictions_mtcars)
```

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OUTPUT:

```
mpg cyl disp hp drat wt qsec vs am gear carb
Mazda RX4     21.0   6 160 110 3.90 2.620 16.46  0  1   4   4
Mazda RX4 Wag  21.0   6 160 110 3.90 2.875 17.02  0  1   4   4
Datsun 710    22.8   4 108  93 3.85 2.320 18.61  1  1   4   1
Hornet 4 Drive 21.4   6 258 110 3.08 3.215 19.44  1  0   3   1
Hornet Sportabout 18.7   8 360 175 3.15 3.440 17.02  0  0   3   2
Valiant      18.1   6 225 105 2.76 3.460 20.22  1  0   3   1
RMSE: 4.808981>
```

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Week 10:

Classification Model:

- a) Install relevant package for classification.**
- b) Implement and evaluate the performance of various classifiers with different datasets.**

PROGRAMS:

```
a) install.packages("caret")      # For building and evaluating classification models  
install.packages("e1071")        # For SVM and Naive Bayes  
install.packages("randomForest") # For Random Forest classifier  
install.packages("nnet")         # For Neural Network classifier  
install.packages("rpart")        # For Decision Tree classifier  
install.packages("ggplot2")       # For data visualization  
  
library(caret)  
  
library(e1071)  
  
library(randomForest)  
  
library(nnet)  
  
library(rpart)  
  
library(ggplot2)  
  
data(iris)  
  
set.seed(123)  
  
trainIndex <- createDataPartition(iris$Species, p = 0.8, list = FALSE)  
  
trainData <- iris[trainIndex, ]  
  
testData <- iris[-trainIndex, ]  
  
model <- randomForest(Species ~ ., data = trainData, ntree = 100)  
  
predictions <- predict(model, testData)  
  
confusionMatrix(predictions, testData$Species)
```

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OUTPUT:

Confusion Matrix and Statistics

Reference				
Prediction	setosa	versicolor	virginica	
setosa	10	0	0	
versicolor	0	10	1	
virginica	0	0	9	

Overall Statistics

Accuracy : 0.9667

95% CI : (0.8278, 0.9992)

No Information Rate : 0.3333

P-Value [Acc > NIR] : 2.963e-13

Kappa : 0.95

Mcnemar's Test P-Value : NA

Statistics by Class:

	Class: setosa	Class: versicolor	Class: virginica
Sensitivity	1.0000	1.0000	0.9000
Specificity	1.0000	0.9500	1.0000
Pos Pred Value	1.0000	0.9091	1.0000
Neg Pred Value	1.0000	1.0000	0.9524
Prevalence	0.3333	0.3333	0.3333
Detection Rate	0.3333	0.3333	0.3000
Detection Prevalence	0.3333	0.3667	0.3000
Balanced Accuracy	1.0000	0.9750	0.9500

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B)

```

library(caret)
library(e1071)
data(iris)
set.seed(123)

trainIndex <- createDataPartition(iris$Species, p = 0.8, list = FALSE)

trainData <- iris[trainIndex, ]
testData <- iris[-trainIndex, ]

svm_model <- svm(Species ~ ., data = trainData, kernel = "linear") # Linear kernel

svm_predictions <- predict(svm_model, testData)

confusionMatrix(svm_predictions, testData$Species)

```

OUTPUT:

Confusion Matrix and Statistics

Reference
Prediction setosa versicolor virginica
setosa 10 0 0
versicolor 0 10 1
virginica 0 0 9

Overall Statistics

Accuracy : 0.9667
95% CI : (0.8278, 0.9992)

No Information Rate : 0.3333
P-Value [Acc > NIR] : 2.963e-13

Kappa : 0.95

McNemar's Test P-Value : NA

Statistics by Class:

	Class: setosa	Class: versicolor	Class: virginica
Sensitivity	1.0000	1.0000	0.9000
Specificity	1.0000	0.9500	1.0000
Pos Pred Value	1.0000	0.9091	1.0000
Neg Pred Value	1.0000	1.0000	0.9524
Prevalence	0.3333	0.3333	0.3333
Detection Rate	0.3333	0.3333	0.3000
Detection Prevalence	0.3333	0.3667	0.3000
Balanced Accuracy	1.0000	0.9750	0.9500

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Week 11:

Clustering Model:

a) Clustering algorithms for unsupervised classification.

b) Plot the cluster data using R visualizations.

a) Clustering algorithms for unsupervised classification.

```
library(caret)
```

```
library(ggplot2)
```

```
library(dplyr)
```

```
data <- iris
```

```
ggplot(data, aes(Sepal.Length, Sepal.Width, color = Species)) +
```

```
  geom_point() +
```

```
  ggtitle("Original Iris Data (Sepal Length vs Sepal Width)") +
```

```
  theme_minimal()
```

```
data <- data[, -5]
```

```
scal <- scale(data)
```

```
maximum <- 10
```

```
wss <- sapply(1:maximum, function(k) {
```

```
  kmeans(scal, k, nstart = 50, iter.max = 15)$tot.withinss
```

```
}
```

```
plot(1:maximum, wss, type = "b", xlab = "Number of Clusters (k)", ylab = "Within-cluster Sum of Squares (WSS)")
```

```
abline(v = 3, col = "red", lty = 2) # The elbow at k = 3 is usually optimal
```

```
km <- kmeans(scal, centers = 3, iter.max = 50)
```

```
print(km)
```

```
data$cluster <- as.factor(km$cluster)
```

```
ggplot(data, aes(Sepal.Length, Sepal.Width, color = cluster)) +
```

```
  geom_point() +
```

```
  ggtitle("K-Means Clustering (k = 3)") +
```

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output:

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

Cluster means:

```

Sepal.Length Sepal.Width Petal.Length Petal.Width
1 -1.01119138 0.85041372 -1.3006301 -1.2507035
2 -0.05005221 -0.88042696 0.3465767 0.2805873
3 1.13217737 0.08812645 0.9928284 1.0141287

```

Clustering vector:

Within cluster sum of squares by cluster:

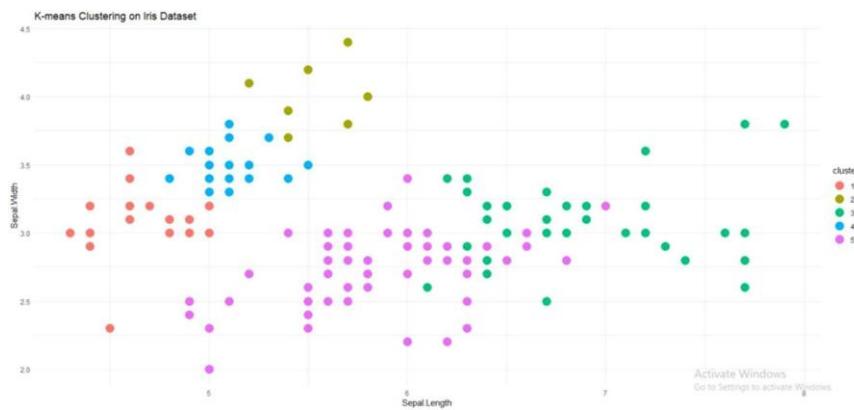
[1] 47.35062 44.08754 47.45019
 (between_SS / total_SS = 76.7 %)

Available components:

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

Cluster vs Species Table:

	setosa	versicolor	virginica
1	50	0	0
2	0	39	14
3	0	11	36



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```

library(ggplot2)
library(dplyr)
library(cluster)
data("trees")
head(trees)

tree_data <- trees[, -3]

scaled_data <- scale(tree_data)

dist_matrix <- dist(scaled_data, method = "euclidean")

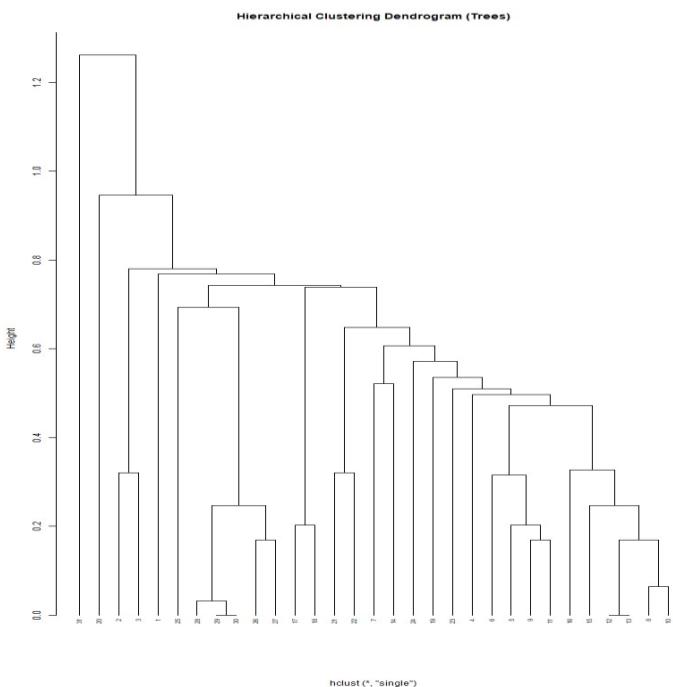
hclust_result <- hclust(dist_matrix, method = "single")

plot(hclust_result, main = "Dendrogram using Single Linkage (Tree Dataset)",

xlab = "", ylab = "Height", sub = "",

cex = 0.7, hang = -1) # 'cex' for label size and 'hang' for clarity of tree

```

Output

b) Plot the cluster data using r visualization

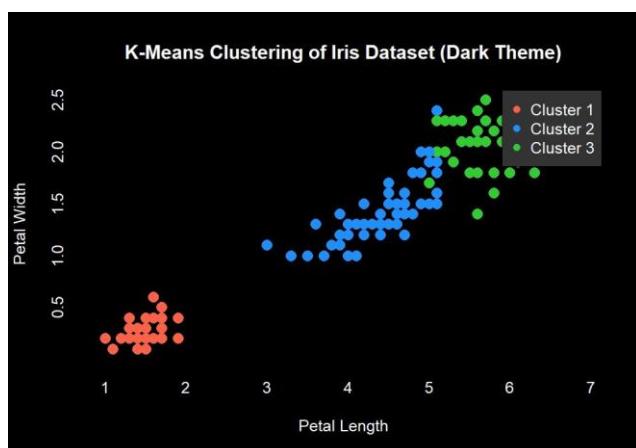
```

library(ggplot2)
library(dplyr)
data(iris)
iris_data <- iris[, -5]
scaled_data <- scale(iris_data)
set.seed(123) # For reproducibility
kmeans_result <- kmeans(scaled_data, centers = 3, nstart = 25)
iris$Cluster <- as.factor(kmeans_result$cluster)
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster)) +
  geom_point(size = 4) + ggtitle("Clustering of Iris Dataset using K-means") + theme_minimal() + xlab("Sepal Length") + ylab("Sepal Width") + scale_color_manual(values = c("red", "blue", "green")) # Customize colors
cluster_centers <- as.data.frame(kmeans_result$centers)
cluster_centers$Cluster <- as.factor(1:3)
ggplot(iris, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster)) + geom_point(size = 4) + geom_point(data = cluster_centers, aes(x = Sepal.Length, y = Sepal.Width, color = Cluster), shape = 8, size = 6, show.legend = FALSE) +
  ggtitle("Clustering of Iris Dataset with K-means (Cluster Centers)") + theme_minimal() + xlab("Sepal Length") +
  ylab("Sepal Width") + scale_color_manual(values = c("red", "blue", "green"))

```

output:

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



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