



SYMBIOSIS INSTITUTE OF TECHNOLOGY, PUNE

Symbiosis International (Deemed University)

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Founder: Prof. Dr. S. B. Mujumdar, M. Sc., Ph. D. (Awarded Padma Bhushan and Padma Shri by President of India)

Assignment No. 06

Subject:

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Branch	CS
Class	A
Academic Year & Semester	2023-24 _ 7th semester
Date of Performance	28th August
Title of Lab Assignment	REGRESSION MODEL

Theory: Import a data from web storage. Name the dataset and now do Logistic Regression to find out the relationship between variables that are affecting the admission of a student to an institute based on his or her GRE score, GPA obtained, and rank of the student. Also check the model is fit or not.

Use different datasets from an online repository to develop a logistic regression model.

Also, check if the model fits or not. Require (foreign), require (MASS).

The logistic regression model predicts the probability of a binary outcome (e.g., admission) based on one or more predictor variables (e.g., GRE score, GPA, rank).

In the provided dataset, the column names are in lowercase, so the formula is adjusted to admit ~ gre + gpa + rank. The glm function with family = "binomial" is used to fit the logistic regression model in R.

Answer:

```
# Load necessary libraries
library(foreign)
library(MASS)
```

```
# Import the dataset
data <- read.csv("https://figshare.com/ndownloader/files/34757857")
```

```

# Check foí missing values
pínt(sum(is.na(data)))

# Handle missing values if any (you can use mean imputation oí otheí methods)
data[is.na(data)] <- mean(data, na.rm = TRUE)

# Display covariance and correlation
pínt(cov(data))
pínt(cor(data))

# Check the names of the columns in the dataset
pínt(names(data))

# Peíom logistic regression using the MASS function
logit_model <- glm(admit ~ gíe + gpa + íank, data = data, family = "binomial")

# Display the summary of the model
summary(logit_model)

# Check the goodness of fit
anova(logit_model, test="Chisq")

# Plot the graph foí the model
plot(logit_model)

```

Output:

Answer:

a.

```

> # Load necessary libraries
> library(foreign)
> library(MASS)
>
> # Import the dataset
> data <- read.csv("https://figshare.com/downloads/files/34757857")
>
> # Check for missing values
> pínt(sum(is.na(data)))
[1] 0
>
> # Handle missing values if any (you can use mean imputation oí otheí methods)
> data[is.na(data)] <- mean(data, na.rm = TRUE)
>
> # Display covariance and correlation
> pínt(cov(data))
      admit     gíe      gpa     íank
admit  0.21723684  9.930075  0.03161078 -0.10675439
gíe    9.93007519 13344.070175 16.89300251 -13.46817043
gpa   0.03161078  16.893003  0.14483107 -0.02065313
íank -0.10675439 -13.468170 -0.02065313  0.89200501

```

```

> print(coi(data))
  admit  gie  gpa  iank
admit 1.0000000 0.1844343 0.17821225 -0.24251318
gie  0.1844343 1.0000000 0.38426588 -0.12344707
gpa  0.1782123 0.3842659 1.00000000 -0.05746077
iank -0.2425132 -0.1234471 -0.05746077 1.00000000
>
> # Check the names of the columns in the dataset
> print(names(data))
[1] "admit" "gie" "gpa" "iank"
>
> # Peífoím logistic régression using the MASS function
> logit_model <- glm(admit ~ gie + gpa + iank, data = data, family = "binomial")
>
> # Display the summary of the model
> summary(logit_model)
Call:
glm(formula = admit ~ gie + gpa + iank, family = "binomial",
     data = data)


```

Coefficients:

	Estimate	Std. Error	t value	P(> t)
(Intercept)	-3.449548	1.132846	-3.045	0.00233 **
gie	0.002294	0.001092	2.101	0.03564 *
gpa	0.777014	0.327484	2.373	0.01766 *
iank	-0.560031	0.127137	-4.405	1.06e-05 ***

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 499.98 on 399 degrees of freedom
 Residual deviance: 459.44 on 396 degrees of freedom
 AIC: 467.44

Number of Fisher Scoring iterations: 4

```

>
> # Check the goodness of fit
> anova(logit_model, test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: admit

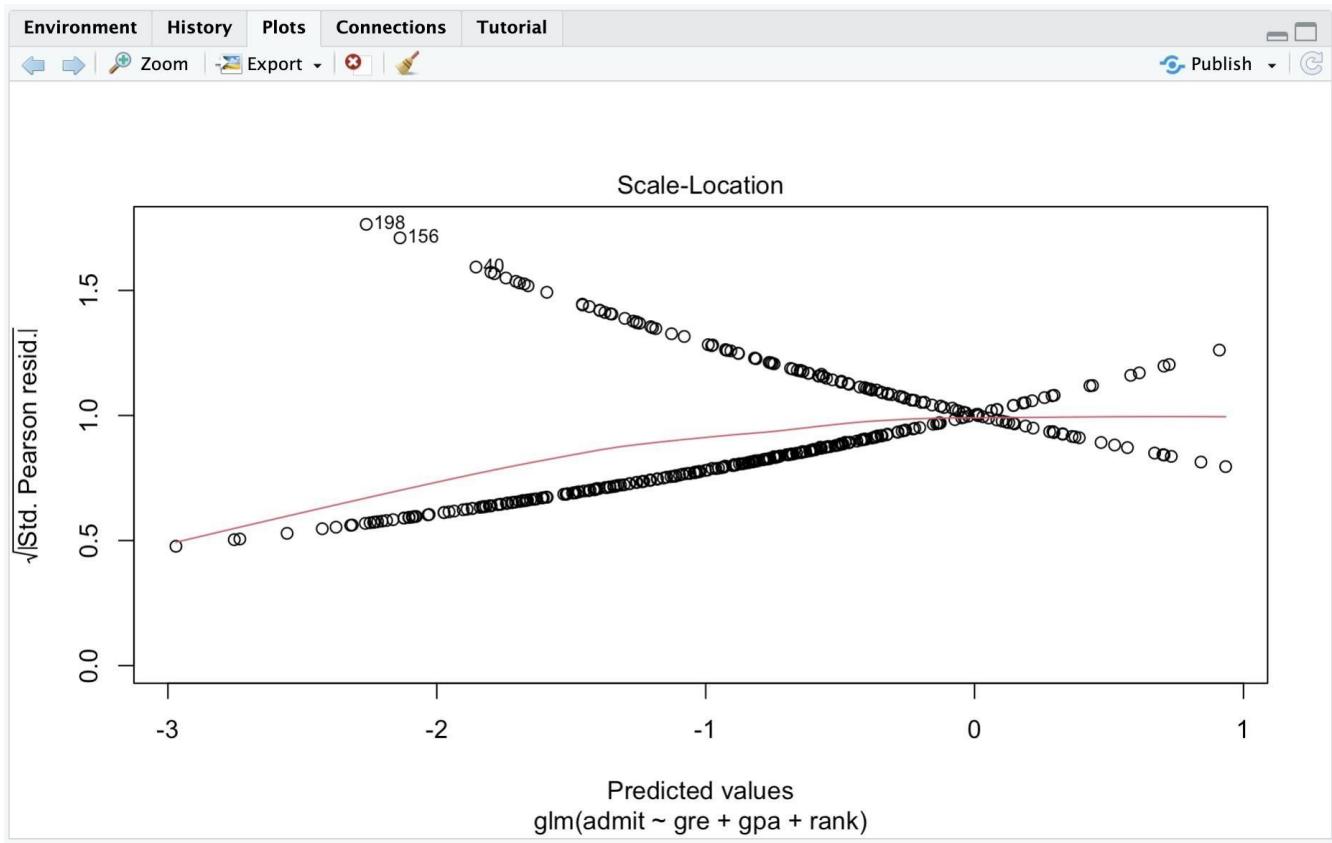
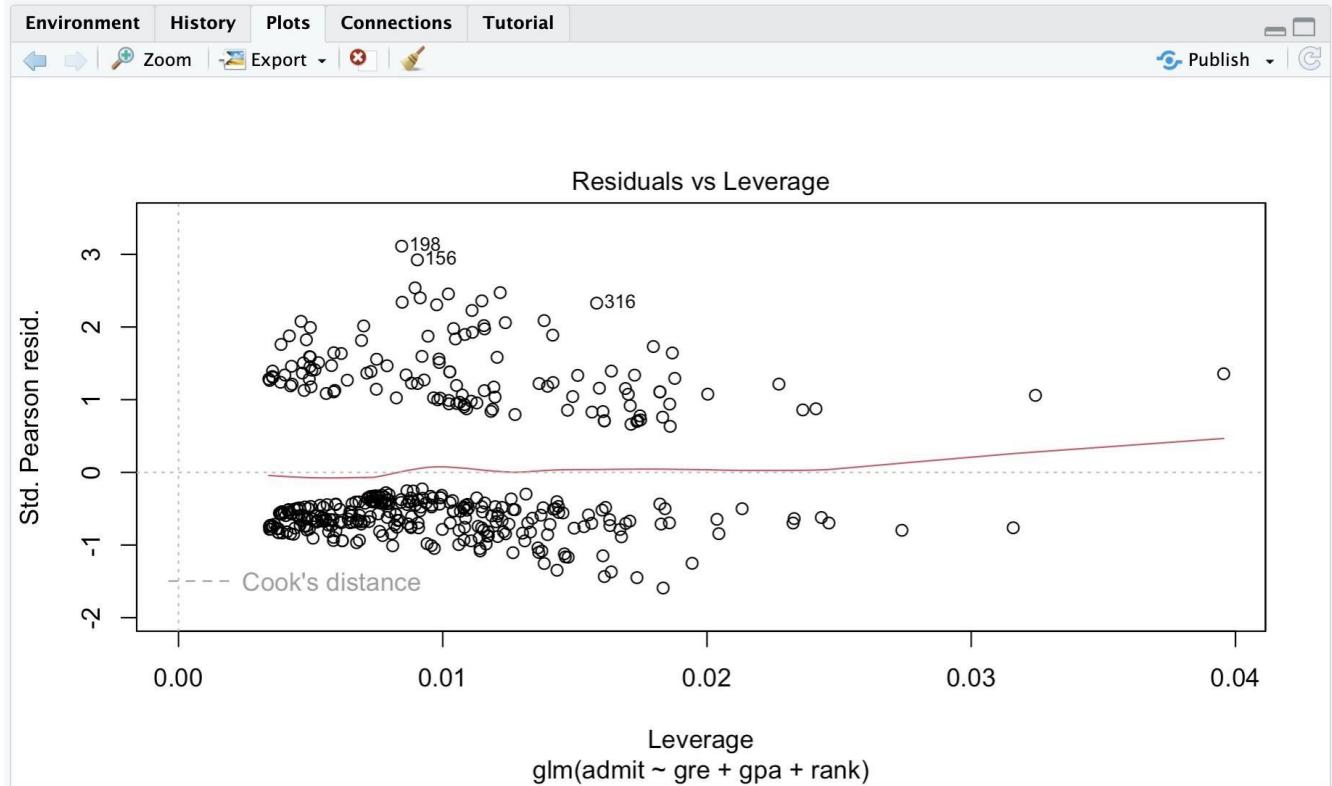
Terms added sequentially (first to last)

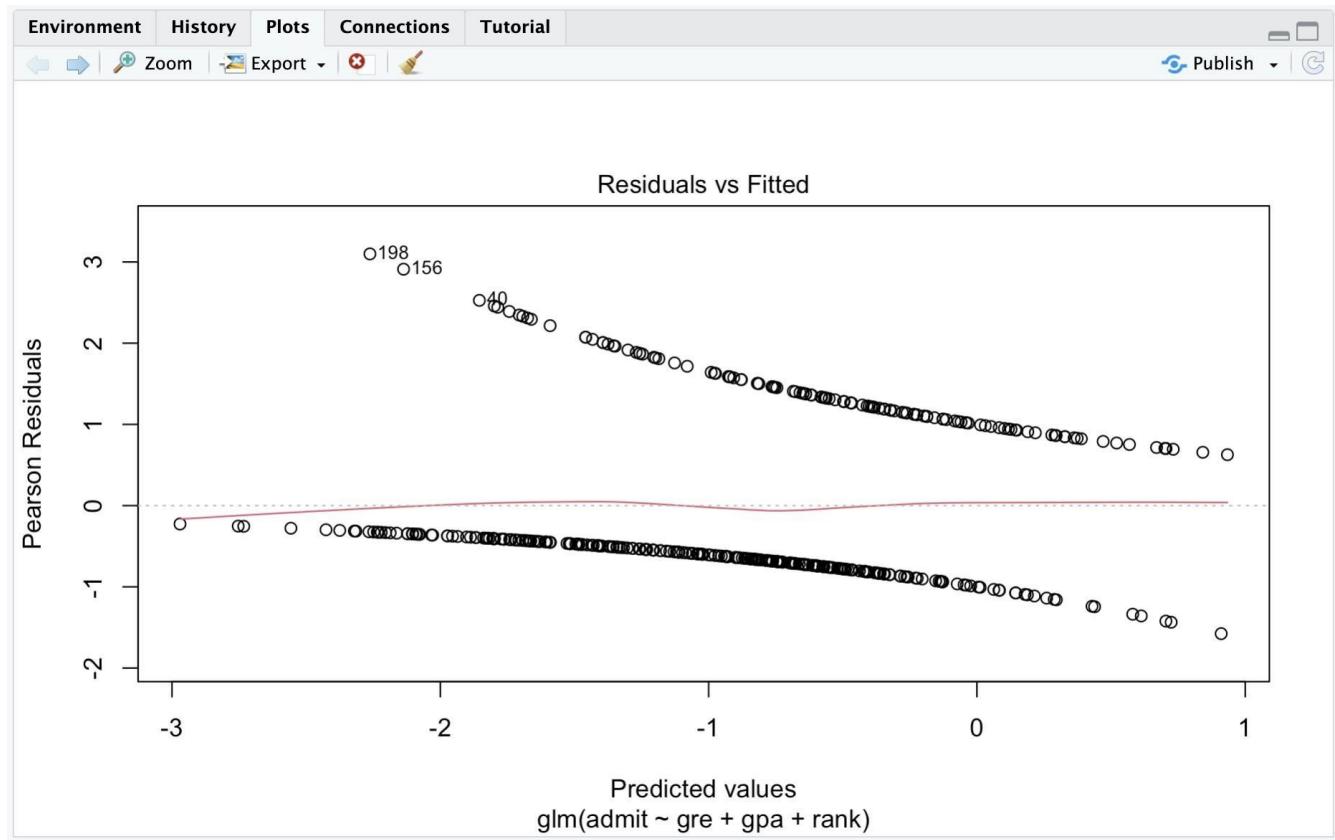
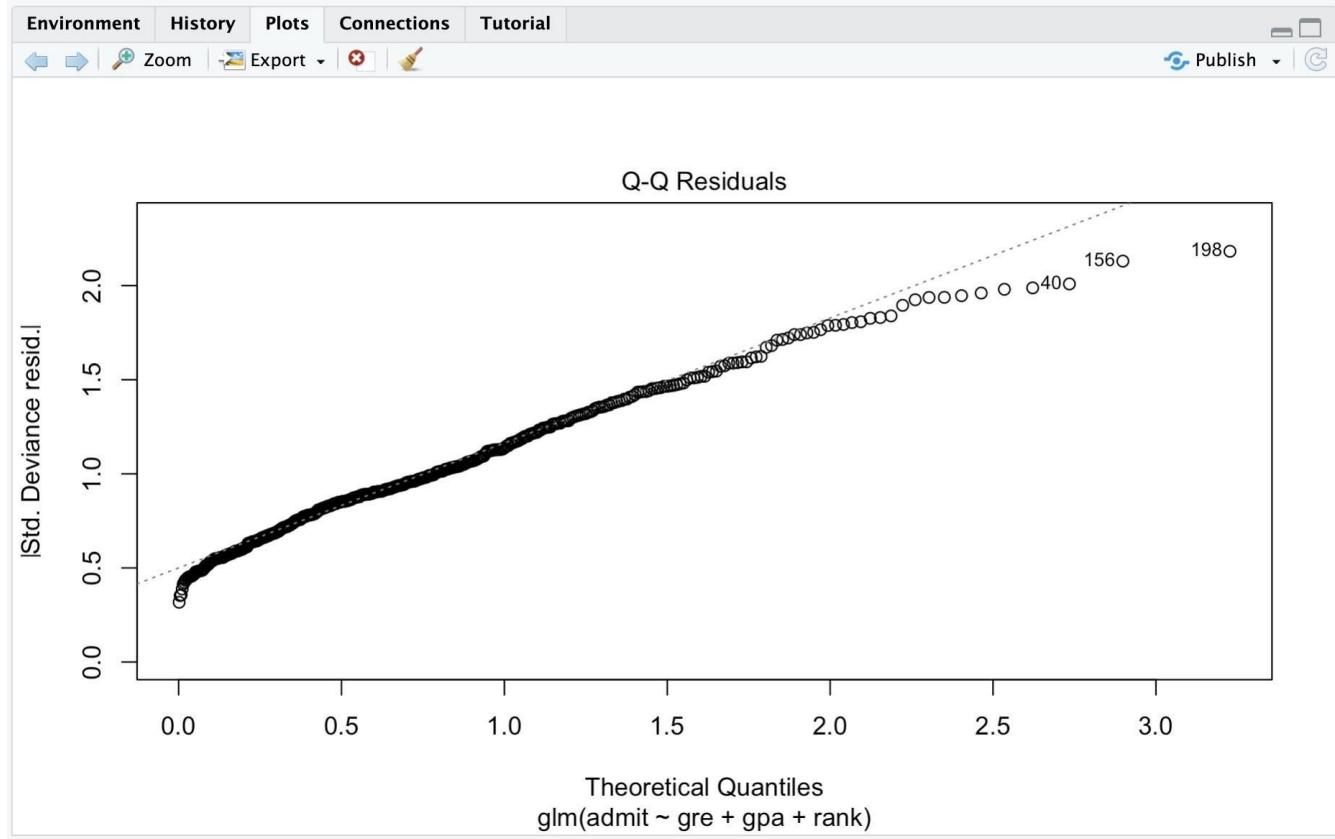
	Df	Deviance	Resid. Df	Resid. Dev	P(>Chi)
NULL	399	499.98			
gie	1	13.9204	398	486.06	0.0001907 ***
gpa	1	5.7122	397	480.34	0.0168478 *
iank	1	20.9022	396	459.44	4.833e-06 ***

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

```

>
> # Plot the graph for the model
> plot(logit_model)
```





The screenshot shows the RStudio interface with the following components:

- Code Editor:** An R script titled "Assignment4(EL).R" containing code to load libraries, import a dataset, handle missing values, display covariance and correlation, perform logistic regression, and check the goodness of fit.
- Console:** Output from the R session showing model coefficients, significance codes, dispersion parameters, null and residual deviance, AIC, Fisher Scoring iterations, and an analysis of deviance table.
- Plots:** A scatter plot titled "Residuals vs Leverage" for the logistic regression model. The y-axis is "Std. Pearson resid." ranging from -2 to 2, and the x-axis is "Leverage" ranging from 0.00 to 0.04. A red horizontal line at 0 represents the residuals, and a dashed red line represents Cook's distance. Two specific points are labeled: 01956 and 0316.
- Environment:** Shows the current environment variables.
- Help:** Standard RStudio help menu.

Conclusion: In conclusion, logistic regression is a powerful statistical method used to model and analyze datasets in which the outcome is binary. For the provided dataset, the probability of a student's admission is predicted based on their GRE score, GPA, and rank. Proper understanding and interpretation of the dataset's column names and structure are crucial for accurate model formulation. Using R's `glm` function with the appropriate formula and family setting ensures a correct fit for the data, enabling meaningful insights and predictions.

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