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Question 1

1. $\chi = \mathbb{R}$ and dimension of $\mathbb{R} = 1$

2. Output space, $\Upsilon = \mathbb{R}$ and dimension of $\mathbb{R} = 1$.

3. $\mathbf{x} \in \mathbb{R}^{n \times 1}$ and dimension is $n \times 1$

4. $\mathbf{y} \in \mathbb{R}^{n \times 1}$ and dimension is $n \times 1$

5. $P(Y_i|X_i = x_i)$ $\mathbf{y}_i = f(\mathbf{x}_i) + \epsilon, \forall_i \sim N(\theta_i x_i, \sigma^2)$ The distribution of $P(\mathbf{y}|\mathbf{x} = x)$ is $N \sim (\mathbf{x}\theta, \sigma^2)$.

6. $\mathbf{y}_i = f(\mathbf{x}_i) + \epsilon_i$ $\mathbf{y}_i = \theta \mathbf{x}_1 + \epsilon_i$ with $\epsilon_1 \sim N(0, \sigma^2), \forall_1 = 1, \dots, n$, Which is a Homoscedastic Gaussian noise model

7. Regression because the output space is continuous.

8. $\frac{\partial SSE_n(a)}{\partial a}$

$$SSE_n(a) = (\mathbf{y} - a\mathbf{x})^T (\mathbf{y} - a\mathbf{x})$$

$$= \mathbf{y}^T \mathbf{y} - \mathbf{y}^T \mathbf{x} a - (\mathbf{x}a)^T \mathbf{y} + (ax)^T \mathbf{x} a$$

$$\frac{\partial SSE_n(a)}{\partial a} = a(\mathbf{x}^T \mathbf{x}) - \mathbf{x}^T \mathbf{y}$$

9. $\frac{\partial SSE_n(a)}{\partial a}$

$$\frac{\partial SSE_n(a)}{\partial a} = a(\mathbf{x}^T \mathbf{x}) - \mathbf{x}^T \mathbf{y} = 0$$
$$(\mathbf{x}^T \mathbf{x})a = \mathbf{x}^T \mathbf{y}$$
$$a = \frac{\mathbf{x}^T \mathbf{y}}{\mathbf{x}^T \mathbf{x}}$$
$$\theta = \frac{\mathbf{x}^T \mathbf{y}}{\mathbf{x}^T \mathbf{x}}$$

10.

$$\mathbb{E}(\hat{\theta}) = (\mathbf{x}^T \mathbf{x})^{-1} \mathbf{x}^T \mathbb{E}(\mathbf{y})$$

$$= (\mathbf{x}^T \mathbf{x})^{-1} \mathbf{x}^T \mathbb{E}(\mathbf{x}\theta + \epsilon)$$

$$= (\mathbf{x}^T \mathbf{x})^{-1} \mathbf{x}^T \mathbf{x}\theta$$

$$= \theta$$

11.

$$V(\theta) = (\mathbf{x}^T \mathbf{x})^{-1} \mathbf{x}^T V ar(\mathbf{y}) \mathbf{x} (\mathbf{x}^T \mathbf{x})^{-1}$$
$$= (\mathbf{x}^T \mathbf{x})^{-1} \mathbf{x} \sigma^2 I_n \mathbf{x} (\mathbf{x}^T \mathbf{x})^{-1}$$
$$= \sigma^2 (\mathbf{x}^T \mathbf{x})^{-1}$$

12.

$$\mathbb{E}(Y_i|X_i) = \mathbb{E}(\theta\mathbf{x}_1 + \epsilon)$$

$$= \theta \mathbb{E}(\mathbf{x}_i) + \mathbb{E}(\epsilon_i) X_i \in \mathbb{R} \text{ and } \epsilon_i \sim N(0, \sigma^2).$$

$$= \theta\mathbf{x}_i$$

$$\mathbb{E}(\mathbf{y}|\mathbf{x}) = \theta\mathbf{x}, \mathbf{x} \in \mathbb{R}^{n \times 1}, \theta \in \mathbb{R}$$

13.

$$\mathbf{y} = f(\mathbf{x}) + \epsilon$$
$$\mathbf{y} = \theta \mathbf{x} + \epsilon, \quad \epsilon \sim N(0, \sigma_I^2)$$

14.

$$\mathbf{y} = \theta \mathbf{x} + \epsilon$$

$$\hat{\mathbf{y}} = \theta \mathbf{x}$$

$$= \mathbf{x}((\mathbf{x}^T \mathbf{x})^{-1} \mathbf{x}^T \mathbf{y})$$

15

$$V(Y_i|X_i) = V(f(\mathbf{x}_i) + \epsilon_i)$$

$$= Vf(\mathbf{x}_i) + V(\epsilon_i)$$

$$= \sigma^2$$

$$V(\mathbf{y}|\mathbf{x}) = V(f(\mathbf{x}) + \epsilon)$$

$$= Vf(\mathbf{x}) + V(\epsilon)$$

$$= \sigma^2 I_n$$

$$\mathbb{E}(\hat{Y}_i|X_i) = \mathbb{E}(\mathbf{x}^T\mathbf{x})^{-1}\mathbf{x}^T\mathbf{y}\mathbf{x}_i)$$

$$= \mathbf{x}_i((\mathbf{x}^T\mathbf{x})^{-1}\mathbf{x}^T\mathbb{E}(\theta\mathbf{x} + (\epsilon))$$

$$= \theta\mathbf{x}_i$$

$$\mathbb{V}(\hat{Y}_i|X_i) = \mathbb{V}(\mathbf{x}^T\mathbf{x})^{-1}\mathbf{x}^T\mathbf{y}\mathbf{x}_i)
= \mathbb{V}(\mathbf{x}_i(\mathbf{x}^T\mathbf{x})^{-1}\mathbf{x}^T\epsilon)
= \mathbf{x}_i^2\sigma^2(\mathbf{x}^T\mathbf{x})^{-1}
\mathbb{V}(\hat{\mathbf{y}}|\mathbf{x}) = (\mathbf{x}^T\mathbf{x})\sigma^2(\mathbf{x}^T\mathbf{x})^{-1}
= \sigma^2.$$

$$\begin{split} \mathbb{E}(\theta &= \theta \\ \mathbb{V}(\theta) &= \sigma^2(\mathbf{x}^T\mathbf{x})^{-1} \\ &\quad \theta \sim N(\theta, \sigma^2(\mathbf{x}^T\mathbf{x})^{-1}) \end{split}$$

$$\mathbf{y}_{i} | \mathbf{x}_{i} \sim N(\theta \mathbf{x}_{i}, \mathbf{x}_{i}^{2} \sigma^{2} (\mathbf{x}^{T} \mathbf{x})^{-1})$$
$$\mathbf{y}_{i} | \mathbf{x}_{i} \sim N(\theta \mathbf{x}, \sigma^{2} I_{n})$$

$$\hat{\sigma}^2 = \frac{SSE}{n-p-1} = \sum_{i=1}^n \frac{(\mathbf{y}_i - \hat{\mathbf{y}_i})^2}{n-p-1}$$

Question 2

1. Thid data is obtained from a DNA microarray survey. The goal is to use different DNA gene expression to predict if one has prostrate cancer or not.

A set of 500 different DNA gene combination were used to model if one has a probability of having prostrate cancer. Y is the response variable, 0 means that one has no prostrate cancer and 1 means one has prostrate cancer. All other 500 are different DNA gene combination to explain Y.

2. We plot barplot of the response variable.

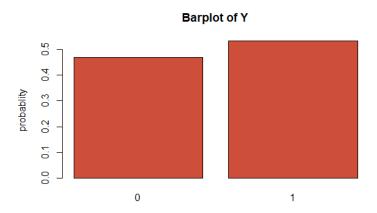


Figure 1: histogram

The probability of response is almost equal, that response 0 and response 1 is approximately 0.5.

- 3. We can make some the following comments about the data set. The dimension of input space χ is 500, n, the sample size is 79. n is small and p is large i.e p>>>n, this implies that we have a high dimensional data. This is called poverty in data.
- 4. We carry out missing value analysis and find out that our data has no missing values. The we randomly select variables and draw some descriptive statistics; we can visualize our data graphically

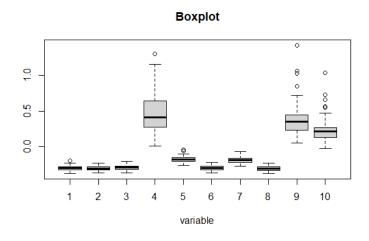


Figure 2: boxplot

Some variables e.g variable 9 and 10 show existence of outliers in our data set The measurement scales are different, some variables are taking negative values. This implies that our data set is non homogeneous.

The median values is very different across most of the variables and some of the median assumes negative values.

The spread from the median in some of variables is different e.g in variables 4, 9 and 10 the variance is large, while some variables like variables 1, 2, 3 show almost the same spread from the median.

Some variables like variable 1, variable 2, variable 3 have median at the center, this shows that they follow a normal distribution, while other variables like variable 4 and variable 10 do not follow a normal distribution.

Y X20	6212_at X20	7075_at X21	.5872_at X20	1876_at
Min. :0.0000	Min. $:-0.27572$	Min. :-0.3700	Min. :-0.3745	Min. :-C
1st Qu.:0.0000	1st Qu.:-0.22092	1st Qu.:-0.3189	1st Qu.:-0.3273	1st Qu.: 0
Median :1.0000	Median :-0.19108	Median :-0.2912	Median :-0.3019	Median : C
Mean :0.5316	Mean :-0.18635	Mean :-0.2945	Mean :-0.3027	Mean : C
3rd Qu.:1.0000	3rd Qu.:-0.16036	3rd Qu.:-0.2733	3rd Qu.:-0.2783	3rd Qu.: 0
Max. :1.0000	Max. : -0.07154	Max. : -0.2076	Max. : -0.1972	Max. : 1
X211935_at	X206788_s_at	X216441_at	X209290_s_at	X219877
Min. :0.04825	Min. :-0.26716	Min. :-0.3771	Min. :0.00699	Min. :-
1st Qu.:0.22764	1st Qu.:-0.20338	1st Qu.:-0.3304	1st Qu.:0.27076	1st Qu.:-
Median :0.35430	Median :-0.18122	Median :-0.3080	Median :0.40936	Median :-
Mean :0.37536	Mean :-0.17665	Mean :-0.3074	Mean :0.46183	Mean :-
3rd Qu.:0.44529	3rd Qu.:-0.15582	3rd Qu.:-0.2827	3rd Qu.:0.64654	3rd Qu.:-
Max. :1.42433	Max. : -0.03853	Max. :-0.2293	Max. :1.30156	Max. :-

From the above summary statistics we can conclude that;

The mean value of most variables lies between negative -1 and 1. This is also true to the median value.

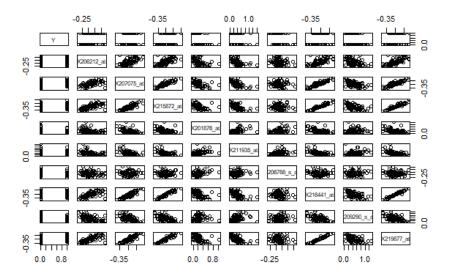


Figure 3: scatter plot

From the above scatter plot, the explanatory variables very weak or no linear relation

with the response variable y. The variables indicate strong linear relationship among themselves, this is what we refer to as multicollinearity in data.

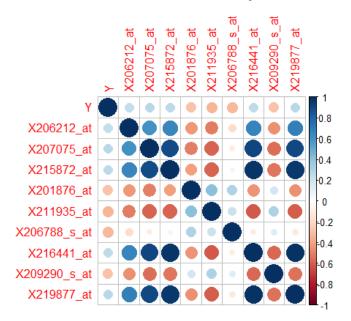


Figure 4: corrplot

The cor plot visualizes the very weak linear relationship between the explanatory variables and the response variables y.

Question 3

1.

$$\mathbf{X}^T \mathbf{X} = \begin{bmatrix} 1 & -2 & 4 \\ -2 & 1 & 1 \end{bmatrix} \begin{bmatrix} 1 & -2 \\ -2 & 1 \\ 4 & 1 \end{bmatrix} = \begin{bmatrix} 21 & 0 \\ 0 & 6 \end{bmatrix}$$

2. $\mathbf{X}^T \mathbf{X} \in \mathbb{R}^{2 \times 2}$ and the shape is 2×2

3.

$$(\mathbf{X}^T\mathbf{X})^{-1} = \frac{1}{26} \begin{bmatrix} 21 & 0\\ 0 & 6 \end{bmatrix}$$

4.

$$\hat{\theta} = \frac{1}{26} \begin{bmatrix} 21 & 0 \\ 0 & 6 \end{bmatrix} \begin{bmatrix} 1 & -2 & 4 \\ -2 & 1 & 1 \end{bmatrix} \begin{bmatrix} -5 \\ 4 \\ -3 \end{bmatrix} = \begin{bmatrix} -1.19 \\ 1.83 \end{bmatrix}$$

5.

$$\hat{\mathbf{Y}} = \mathbf{X}\hat{\boldsymbol{\theta}} \\
= \begin{bmatrix} 1 & -2 \\ -2 & 1 \\ 4 & 1 \end{bmatrix} \begin{bmatrix} -1.19 \\ 1.83 \end{bmatrix} = \begin{bmatrix} -4.86 \\ 4.21 \\ -2.92 \end{bmatrix}$$

6.

$$\mathbf{e} = \mathbf{Y} - \hat{\mathbf{Y}} = \begin{bmatrix} -0.143 \\ -0.214 \\ -0.071 \end{bmatrix}$$

7.

$$SSE(\hat{\theta}) = \sum_{i=1}^{n} (\mathbf{Y}_i - \hat{\mathbf{Y}}_i)^2$$

$$= (-5 + 4.86)^2 + (4 - 4.21)^2 + (-3 + 2.92)^2$$

$$= 0.0701$$

8.

$$\frac{SSE(\hat{\theta})}{n-2} = \frac{0.0701}{1}$$
$$= 0.0701$$

9.

$$\hat{\sigma^2}(\mathbf{X}^T\mathbf{X})^{-1} = \begin{bmatrix} 0.0033 & 0.0000 \\ 0.0000 & 0.0117 \end{bmatrix}$$

10.

$$(\mathbf{X}^T \mathbf{X}) = \begin{bmatrix} 1 & 2 \\ -2 & 1 \end{bmatrix} \begin{bmatrix} 1 & -2 \\ -2 & 1 \end{bmatrix} = \begin{bmatrix} 5 & 0 \\ 0 & 5 \end{bmatrix} = 5 \begin{bmatrix} 1 & 0 \\ 0 & 1 \end{bmatrix}$$

Question 4

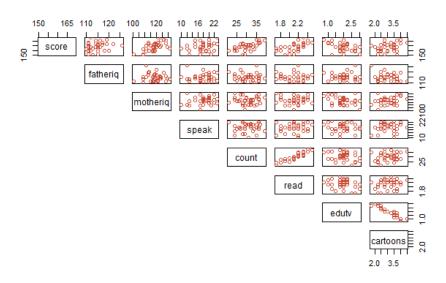


Figure 5: Scatterplot

- 1. From the above upper triangular pairwise scatterplot for this data, the explanatory variables which have the strongest linear relationship with the response are **motheriq**, **read** and **count**. You cannot tell from this plot the strongest related of all predictor variables.
- 2. score fatheriq motheriq edutv cartoons speak count read score 1.0000 0.1881 0.5712 0.2679 0.5442 0.5252 -0.3703 0.2451 fatheriq 0.1881 1.0000 -0.0248 -0.0305 -0.0750 -0.0682 0.1162 -0.2484motheriq 0.5712 -0.0248 1.0000 0.0722 0.0243 -0.0430 -0.3300 0.3384 -0.0305 1.0000 0.1851 -0.1545 speak 0.2679 0.0722 0.0595 0.1094 count 0.5442 -0.07500.0243 0.0595 1.0000 0.9103 - 0.21570.1549 0.5252 -0.0682 -0.0430 0.1851 0.9103 1.0000 -0.1666 read 0.1257 -0.37030.1162 -0.3300 -0.1545 -0.2157 -0.1666 1.0000 -0.9234edutv 0.2451 -0.24840.3384 0.1094 0.1549 0.1257 -0.9234 1.0000 cartoons

From the correlation matrix above, among all explanatory variables **motheriq** has the strongest linear relationship with the response, count. The coefficient of correlation between **motheriq** and response variable **score** is 0.57. This is moderate linear relationship.

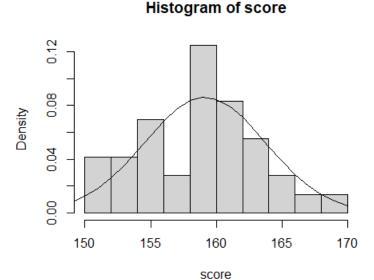


Figure 6: histogram

- 3. From the above histogram, the response variable follows a normal distribution. We can test the normality by using Shapiro test.

 Shapiro test of normality, the null hypothesis is, the null hypothesis is the data follow a normal distribution, and the alternative hypothesis is that the data is not normally distributed. From Shapiro test of normality the p-value is 0.76, this shows that the response variable follows a normal distribution.
- 4. We perform simple linear regression using **motheriq**, because its most important predictor variable.

Residual standard error: 3.856 on 34 degrees of freedom Multiple R-squared: 0.3263, Adjusted R-squared: 0.3065 F-statistic: 16.47 on 1 and 34 DF, p-value: 0.000274

Our regression model is given by:

$$\hat{\mathbf{y}} = 0.04066 \, \mathbf{motheriq} + 111.09$$

Where $\hat{\mathbf{y}}$ is the predicted **score**

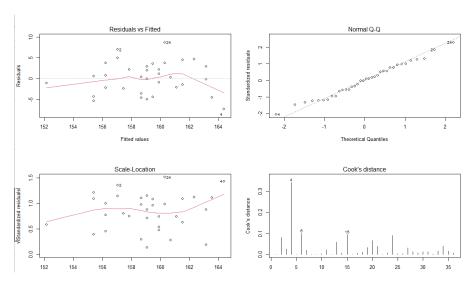


Figure 7: Residual analysis

5. **Linear association** - The first plot from left is a plot of residuals against fitted values, it shows residuals are not random. The assumption of linear association does not hold.

Normality- for the assumption of normality to be true, the residuals should follow a straight line, from our second plot most data points follow a straight line which show that the residues are normally distributed, consequently the assumption of normality holds.

Homoskedasticity - for this assumption, we expect that the residuals to have a constant variance, from our third plot the residues have a same variance. Homoskedasticity assumption is not violated.

Check for outliers - we observe from our fourth plot that are significant outliers in our data. The outliers need to be investigated and a decision reached whether to remove or retail them in our data.

Consequently the assumption of linear association and present of outliers affect the

suitability and quality of our model. Our model is not the best and should be improved.

6.

$$\hat{y} = 0.04066 \, \text{motheriq} + 111.09$$

For every unit increase in **motheriq**, the expected **score** increase by 0.4066.

From the R output, the fitted **score** for **motheriq** of 100 is 151.75. The confidence interval (147.83,155.67) is the range of true value of **score** at 95% confidence interval according to our model.

The fitted **score** for **motheriq** remains the same at 151.75. The predicted interval is (142.9896, 160.515). This means, according to our model 95% of children with a **motheriq** of 100 have a score between 142.98 and 160.52.

We can also plot confidence interval;

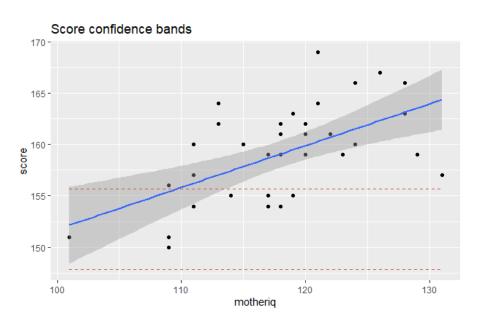


Figure 8: confidence bands

8. The multiple linear regression indicates that among all explanatory variables only **motheriq**, which is significant to our model, with a p-value of < 0.001. The predicted bands can plotted as below;

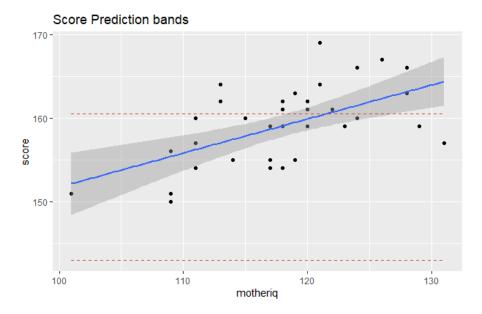


Figure 9: predicted bands

Coefficients:

Estimate Std. Error t value Pr(>|t|) 3.143 0.00393 ** (Intercept) 75.50849 24.02618 fatheriq 0.25249 0.13756 1.835 0.07707 . 0.07291 5.488 7.33e-06 *** motheriq 0.40007 speak 0.18764 0.14767 1.271 0.21429 count 0.20649 0.26631 0.775 0.44462 7.54405 read 5.58640 1.350 0.18769 edutv -4.20244 2.24503 -1.872 0.07170 . -3.33899 2.01808 -1.655 0.10919 cartoons

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

Residual standard error: 2.591 on 28 degrees of freedom Multiple R-squared: 0.7496, Adjusted R-squared: 0.687 F-statistic: 11.97 on 7 and 28 DF, p-value: 5.803e-07

Our multiple regression model is given by;

 \hat{y} =0.252 fatheriq + 0.4000 motheriq + 0.188 speak + 0.206 count +7.54 read - 4.202 eduty - 3.339 cartoons.

 \hat{y} is the predicted score.