

One-way ANOVA Practical Report – Baseline Value by Fetal Health

1. Objective

To test whether the mean baseline_value differs among the three fetal_health groups (Normal, Suspect, Pathological).

2. Hypotheses

- **Null Hypothesis (H_0):** Mean baseline_value is the same across all fetal_health groups.
 $H_0: \mu_1 = \mu_2 = \mu_3$
 - **Alternative Hypothesis (H_1):** At least one group has a different mean.
 H_1 : At least one μ_i is different
-

3. Assumption Checks

3.1 Homogeneity of Variances (Levene's Test)

Test	F-value	p-value	Decision
Levene	9.3392	9.157×10^{-5}	Variances are not equal

Interpretation: The assumption of equal variances is violated. ANOVA is still robust for large sample sizes, but caution is advised.

3.2 Normality of Residuals (Shapiro-Wilk Test)

Test	W	p-value	Decision
Shapiro-Wilk	0.99624	3.807×10^{-5}	Residuals are not perfectly normal

Interpretation: Residuals deviate slightly from normality. Given the large sample size ($n = 2126$), ANOVA results are considered reliable.

Name :- Priya Gupta

Roll no. :- S081

Sheth L.U.J & Sir M.V. college

4. ANOVA Results

Source	Df	Sum Sq	Mean Sq	F value	Pr(>F)
fetal_health	2	24073	12036	140.6	< 2e-16 ***
Residuals	2123	181717	86	-	-

Interpretation: The p-value < 0.05 indicates that there is a **statistically significant difference** in baseline values between at least two fetal_health groups. Therefore, we reject H_0 .

5. Post-hoc Analysis (Tukey HSD)

Comparison	Mean Difference	95% CI	p-value	Significance
2 – 1	9.7029	8.3316, 11.0742	0.0000	Yes
3 – 1	-0.2944	-2.0147, 1.4260	0.9151	No
3 – 2	-9.9972	-12.0639, -7.9306	0.0000	Yes

Interpretation of post-hoc results:

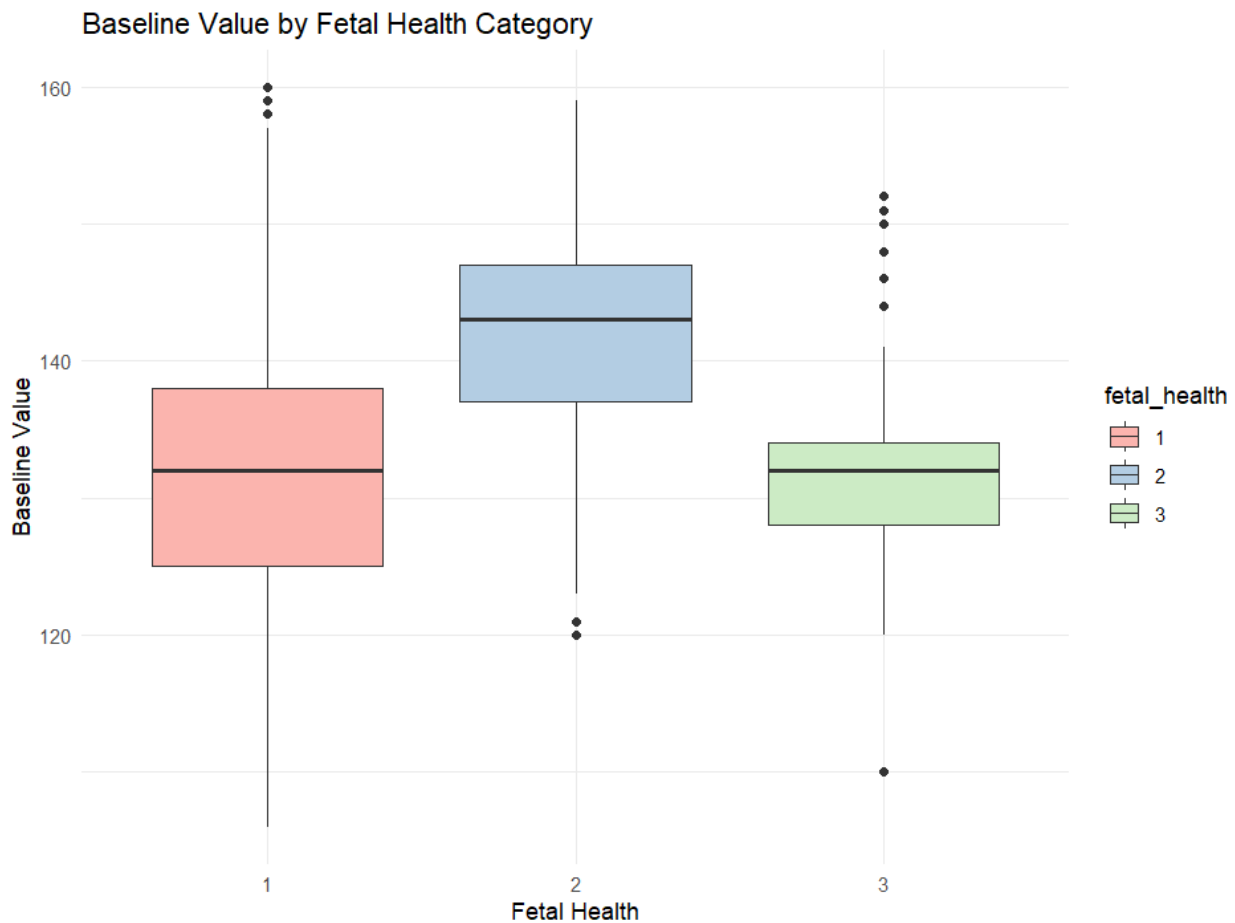
- Group 2 (Suspect) has significantly higher baseline values than Group 1 (Normal).
 - Group 3 (Pathological) is **not significantly different** from Group 1 (Normal).
 - Group 3 (Pathological) has significantly lower baseline values than Group 2 (Suspect).
-

Name :- Priya Gupta

Roll no. :- S081

6. Visualization

- Boxplot of Baseline Value by Fetal Health



- ANOVA and TukeyHSD output screenshots

```
>
> # Perform ANOVA
> summary(anova_model)
              Df Sum Sq Mean Sq F value Pr(>F)
fetal_health    2  24073   12036   140.6 <2e-16 ***
Residuals    2123 181717      86
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

```
<
> # Post-hoc analysis
> TukeyHSD(anova_model)
Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = baseline_value ~ fetal_health, data = df)

$fetal_health
      diff      lwr      upr    p adj
2-1  9.7028727  8.331557 11.074188 0.000000
3-1 -0.2943731 -2.014732  1.425986 0.915065
3-2 -9.9972458 -12.063926 -7.930566 0.000000
```

Name :- Priya Gupta

Roll no. :- S081

Interpretation from Boxplot:

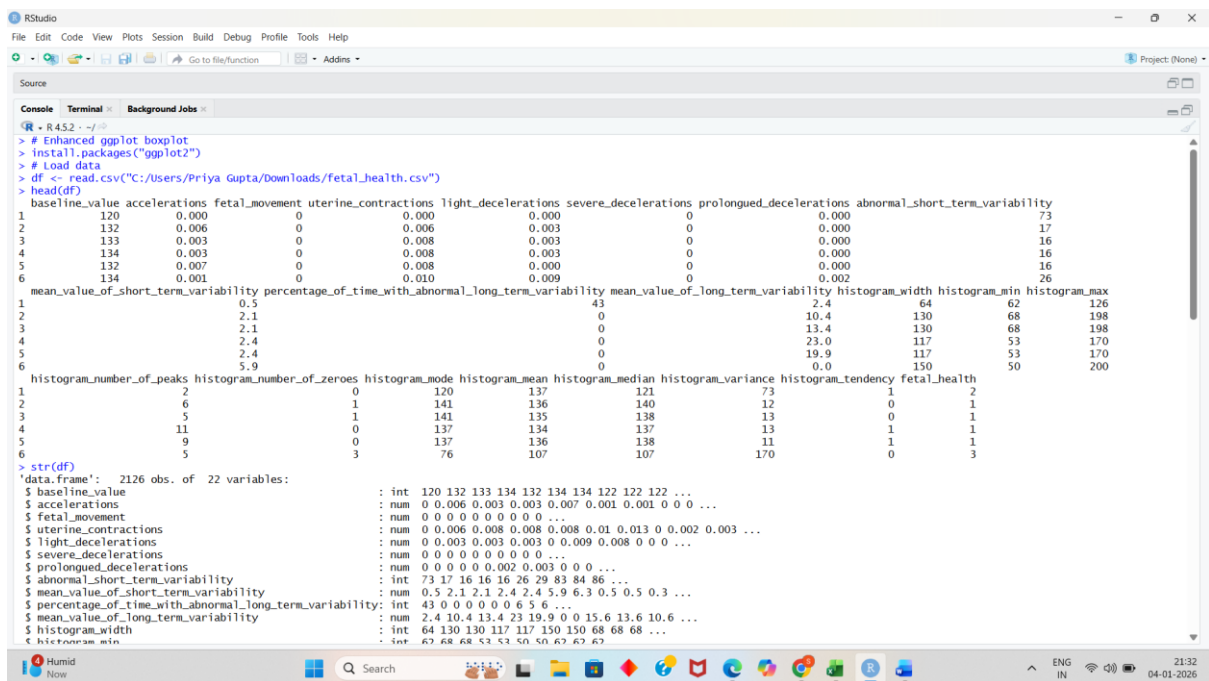
- Group 2 (Suspect) shows a higher median baseline value.
- Group 3 (Pathological) overlaps with Group 1 (Normal).
- Visual observation aligns with the TukeyHSD findings.

7. Conclusion

The analysis confirms that **baseline_value differs significantly across fetal health categories**, mainly due to elevated values in the Suspect group (Group 2). The results are consistent across ANOVA and post-hoc TukeyHSD tests, and the boxplot visually demonstrates these differences.

Note: Minor violations of ANOVA assumptions (normality and homogeneity of variances) exist, but given the **large sample size (n = 2126)**, the results are still reliable.

Screenshots



```
RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function Addins Project: (None)

Source
Console Terminal Background Jobs

> # Enhanced ggplot boxplot
> install.packages("ggplot2")
> # Load data
> df <- read.csv("C:/Users/Priya Gupta/Downloads/fetal_health.csv")
> head(df)
  baseline_value accelerations fetal_movement uterine_contractions light_decelerations severe_decelerations prolonged_decelerations abnormal_short_term_variability
1          120          0.000              0              0.000              0.000              0              0.000              0.000              73
2          132          0.006              0              0.006              0.003              0              0.000              0.000              17
3          133          0.003              0              0.008              0.003              0              0.000              0.000              16
4          134          0.003              0              0.008              0.003              0              0.000              0.000              16
5          132          0.007              0              0.008              0.000              0              0.000              0.000              16
6          134          0.001              0              0.010              0.009              0              0.002              0.000              26
  mean_value_of_short_term_variability percentage_of_time_with_abnormal_long_term_variability mean_value_of_long_term_variability histogram_width histogram_min histogram_max
1              0.5                        43                        2.4              64              62              126
2              2.1                        0                        10.4             130              68              198
3              2.1                        0                        13.4             130              68              198
4              2.4                        0                        23.0             117              53              170
5              2.4                        0                        19.9             117              53              170
6              5.9                        0                        0.0              150              50              200
  histogram_number_of_peaks histogram_number_of_zeroes histogram_mode histogram_mean histogram_median histogram_variance histogram_tendency fetal_health
1              2              0              120              137              121              73              1              2
2              6              1              141              136              140              12              0              1
3              5              1              141              135              138              13              0              1
4              11             0              137              134              137              13              1              1
5              9              0              137              136              138              11              1              1
6              5              3              76              107              107              170              0              3

> str(df)
'data.frame':   2126 obs. of  22 variables:
 $ baseline_value      : int  120 132 133 134 132 134 134 122 122 122 ...
 $ accelerations        : num  0 0.006 0.003 0.003 0.007 0.001 0.001 0 0 0 ...
 $ fetal_movement       : num  0 0 0 0 0 0 0 0 0 0 ...
 $ uterine_contractions : num  0 0.006 0.008 0.008 0.008 0.01 0.013 0 0.002 0.003 ...
 $ light_decelerations  : num  0 0.003 0.003 0.003 0 0.009 0.008 0 0 0 ...
 $ severe_decelerations : num  0 0 0 0 0 0 0 0 0 0 ...
 $ prolonged_decelerations : num  0 0 0 0 0 0.002 0.003 0 0 0 ...
 $ abnormal_short_term_variability : int  73 17 16 16 16 26 29 83 84 86 ...
 $ mean_value_of_short_term_variability : num  0.5 2.1 2.1 2.4 2.4 5.9 6.3 0.5 0.5 0.3 ...
 $ percentage_of_time_with_abnormal_long_term_variability: int  43 0 0 0 0 0 0 6 5 6 ...
 $ mean_value_of_long_term_variability : num  2.4 10.4 13.4 23 19.9 0 0 15.6 13.6 10.6 ...
 $ histogram_width      : int  64 130 130 117 117 150 150 68 68 68 ...
 $ histogram_min        : int  62 68 68 53 53 50 50 62 62 62 ...
 $ histogram_max        : int  126 198 198 170 170 200 200 170 170 170 ...
```

Sheth L.U.J & Sir M.V. college

```
RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function Addins Project: (None)

Source
Console Terminal Background Jobs

R v4.5.2 ~ ~/R
$ histogram_min : int 62 68 68 53 53 50 50 62 62 ...
$ histogram_max : int 126 198 198 170 170 200 200 130 130 ...
$ histogram_number_of_peaks : int 2 6 5 11 9 5 6 0 0 1 ...
$ histogram_number_of_zeroes : int 0 1 1 0 0 3 3 0 0 0 ...
$ histogram_mode : int 120 141 141 137 137 76 71 122 122 122 ...
$ histogram_mean : int 137 136 135 134 136 107 107 122 122 122 ...
$ histogram_median : int 121 140 138 137 138 107 106 123 123 123 ...
$ histogram_variance : int 73 12 13 13 11 170 215 3 3 1 ...
$ histogram_tendency : int 1 0 0 1 1 0 0 1 1 1 ...
$ fetal_health : int 2 1 1 1 1 3 3 3 3 3 ...

>
> # Convert fetal_health to factor
> df$fetal_health <- as.factor(df$fetal_health)
> str(df$fetal_health)
Factor w/ 3 levels "1","2","3": 2 1 1 1 1 3 3 3 3 3 ...
>
> # Check ANOVA assumptions
> anova_model <- aov(baseline_value ~ fetal_health, data = df)
>
> # Normality of residuals
> res <- residuals(anova_model)
> shapiro.test(res)

Shapiro-Wilk normality test

data: res
W = 0.99624, p-value = 3.807e-05

>
> # Homogeneity of variance
> #install.packages("car")
> library(car)
> leveneTest(baseline_value ~ fetal_health, data = df)
Levene's Test For Homogeneity of Variance (center = median)
Df F value Pr(>F)
group 2 9.3392 9.157e-05 ***
2123
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> # Perform ANOVA
```

```
RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function Addins Project: (None)

Source
Console Terminal Background Jobs

R v4.5.2 ~ ~/R
Df F value Pr(>F)
group 2 9.3392 9.157e-05 ***
2123
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> # Perform ANOVA
> summary(anova_model)

Df Sum Sq Mean Sq F value Pr(>F)
fetal_health 2 24073 12036 140.6 <2e-16 ***
Residuals 2123 181717 86
---
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

>
> # Post-hoc analysis
> TukeyHSD(anova_model)
Tukey multiple comparisons of means
95% family-wise confidence level

Fit: aov(formula = baseline_value ~ fetal_health, data = df)

$fetal_health
      diff      lwr      upr    p.adj
2-1  9.7028727  8.331357 11.074188 0.000000
3-1 -0.2943731 -2.014732  1.425986 0.915065
3-2 -9.9972458 -12.063926 -7.930566 0.000000

>
>
> # Enhanced ggplot boxplot
> #install.packages("ggplot2")
> library(ggplot2)
> ggplot(df, aes(x = fetal_health, y = baseline_value, fill = fetal_health)) +
+   geom_boxplot() +
+   theme_minimal() +
+   labs(title = "Baseline Value by Fetal Health Category",
+        x = "Fetal Health", y = "Baseline Value") +
+   scale_fill_brewer(palette = "Pastel1")
>
```

Name :- Priya Gupta
Roll no. :- S081