One-Way ANOVA Analysis: Fetal Health

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INTRODUCTION

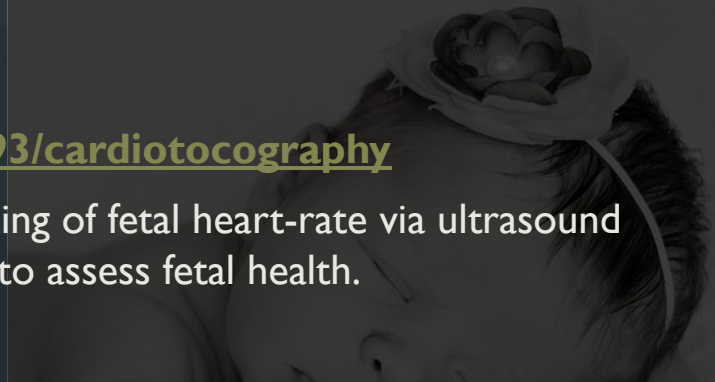
Dataset Original Source:

https://archive.ics.uci.edu/dataset/193/cardiotocography

Cardiotocography: Continuous recording of fetal heart-rate via ultrasound transducer placed on mothers abdomen to assess fetal health.

Main Objective:

Compare Parametric and Non Parametric One-Way Anova methods by performing both methods on the Fetal Health Dataset.



DATA Description

Search for Appropriate Variables for Anova

Original Numerical Variables: 12 measurements

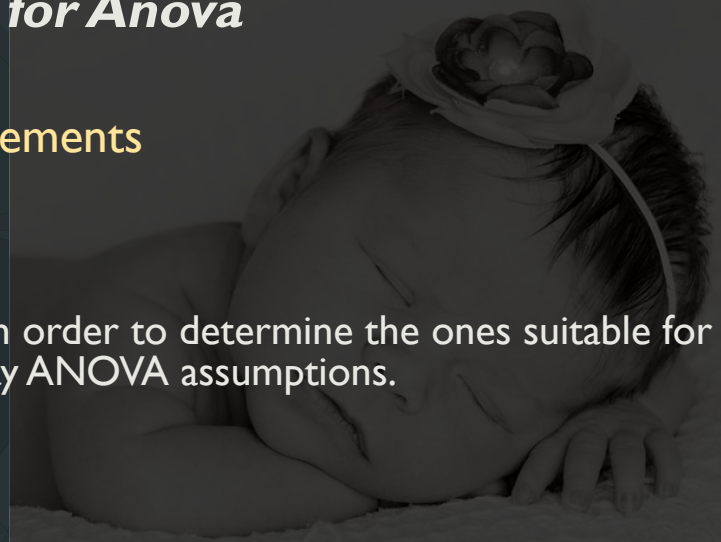
Number Observations: 2126

We screened several numerical variables in order to determine the ones suitable for our Analysis because it needed to pass one-way ANOVA assumptions.

Final Pick:

Factor Variable: Fetal Health

Numerical Variables Screening: Baseline.Value



VARIABLES Description:

Fetal Health:

Normal: Regular healthy fetus
Suspect: Needs additional examination
Pathological: Abnormal development

Baseline.Value:

Heart Rate (Number of heart beats per minute)

fetal_health	N	Mean	Sd	Min	Max
Normal	1655	131.9819	9.454513	106	160
Suspect	295	141.6847	7.889044	120	159
Pathological	176	131.6875	9.433016	110	152

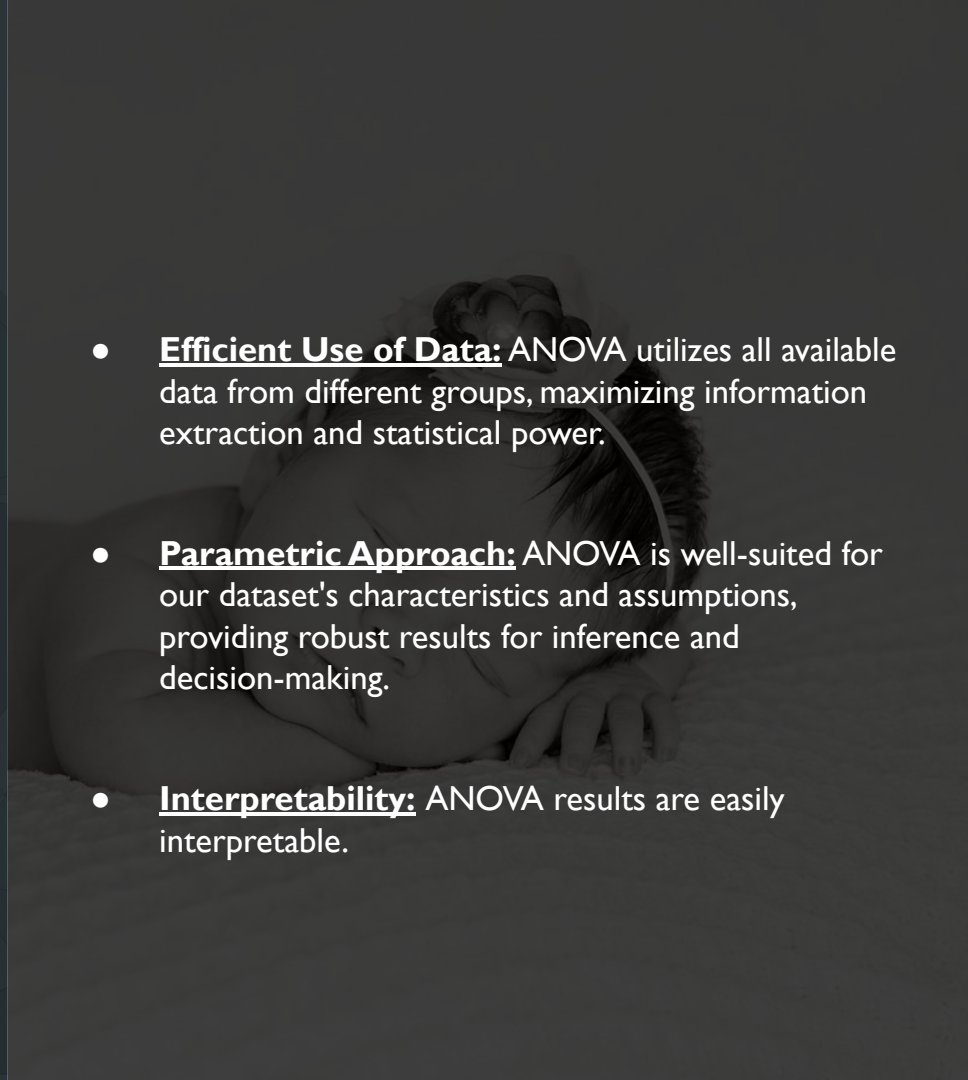
Hypothesis

Why we chose Anova for this problem ?

- **Comprehensive Analysis:**

  ANOVA allows simultaneous comparison of fetal health (via fetus heart rate) across multiple groups (classes), providing a holistic view of differences in health status.

- **Identifying Predictive Features:** ANOVA helps identify which features significantly impact fetal health classification, aiding in the development of effective predictive models.



- **Efficient Use of Data:** ANOVA utilizes all available data from different groups, maximizing information extraction and statistical power.

- **Parametric Approach:** ANOVA is well-suited for our dataset's characteristics and assumptions, providing robust results for inference and decision-making.

- **Interpretability:** ANOVA results are easily interpretable.

Hypothesis

$H_0 : \mu_N = \mu_P = \mu_S$

There is no significant difference in fetal health across different groups

$H_A : \mu_i \neq \mu_j$, where $i \neq j$

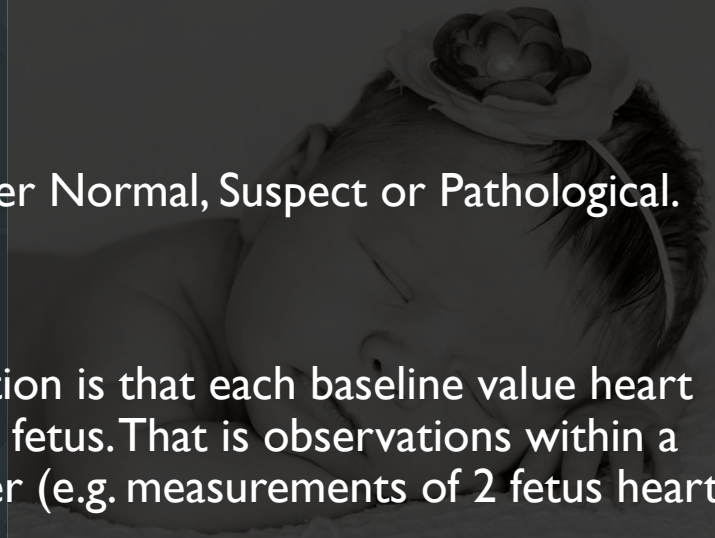
There is a significant difference in fetal health across at least one pair of groups (Normal, Suspect, Pathological).

Parametric ANOVA Assumptions

I) Independence :

- Independence Between:
  - Each observation belongs to either Normal, Suspect or Pathological.

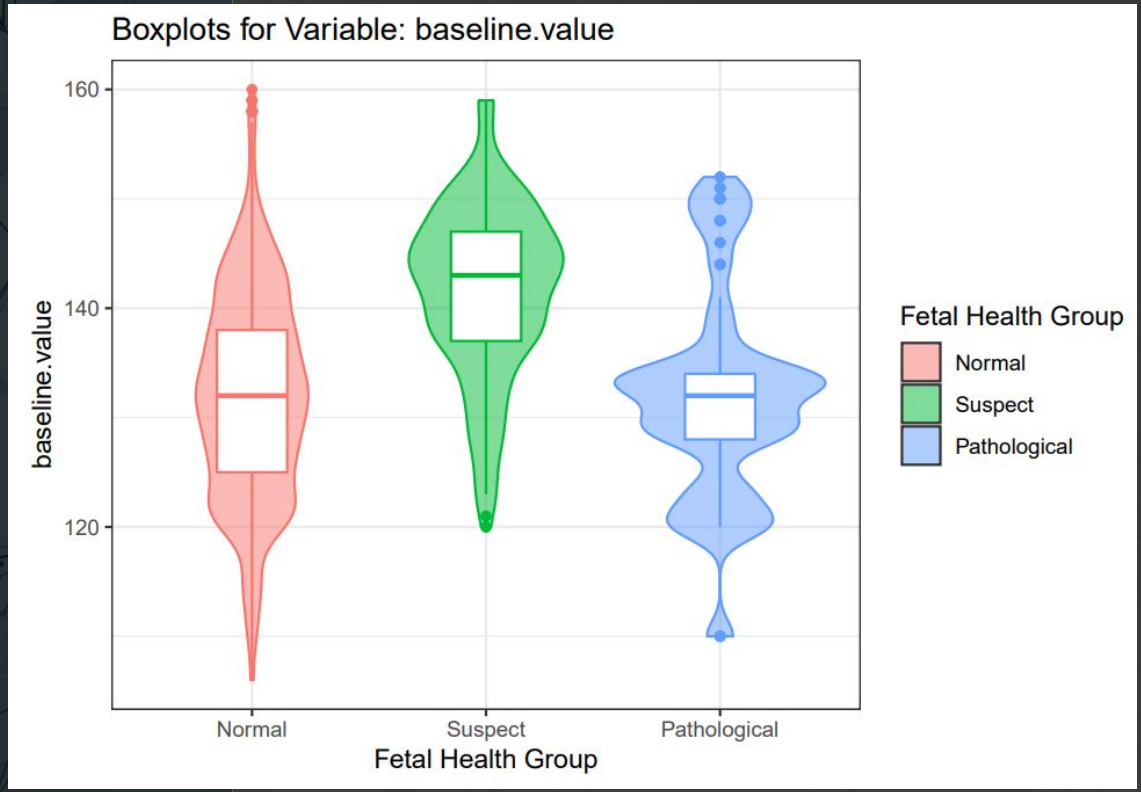
- Independence Within:
  - Within each Group , the assumption is that each baseline value heart rate observed belongs to a single fetus. That is observations within a group do not influence each other (e.g. measurements of 2 fetus heart rates in the same womb)



Parametric ANOVA Assumptions

2) Constant Variance :

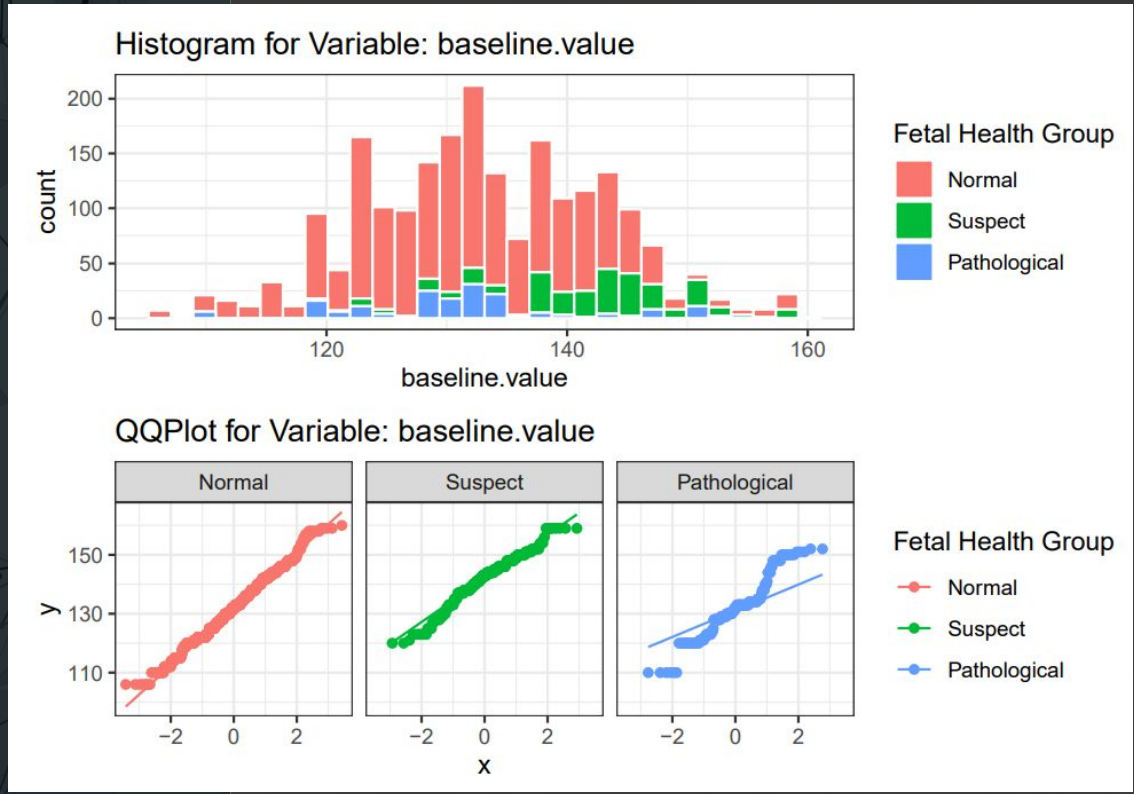
Based on the Boxplots we see that the Normal Group has a higher variance than the Suspect and Pathological Baseline Heart Rate Values.



Parametric ANOVA Assumptions

3) Normality :

Fetus in the Normal Group and the Suspect Group show a more normal , symmetrical distribution than the Pathological group.

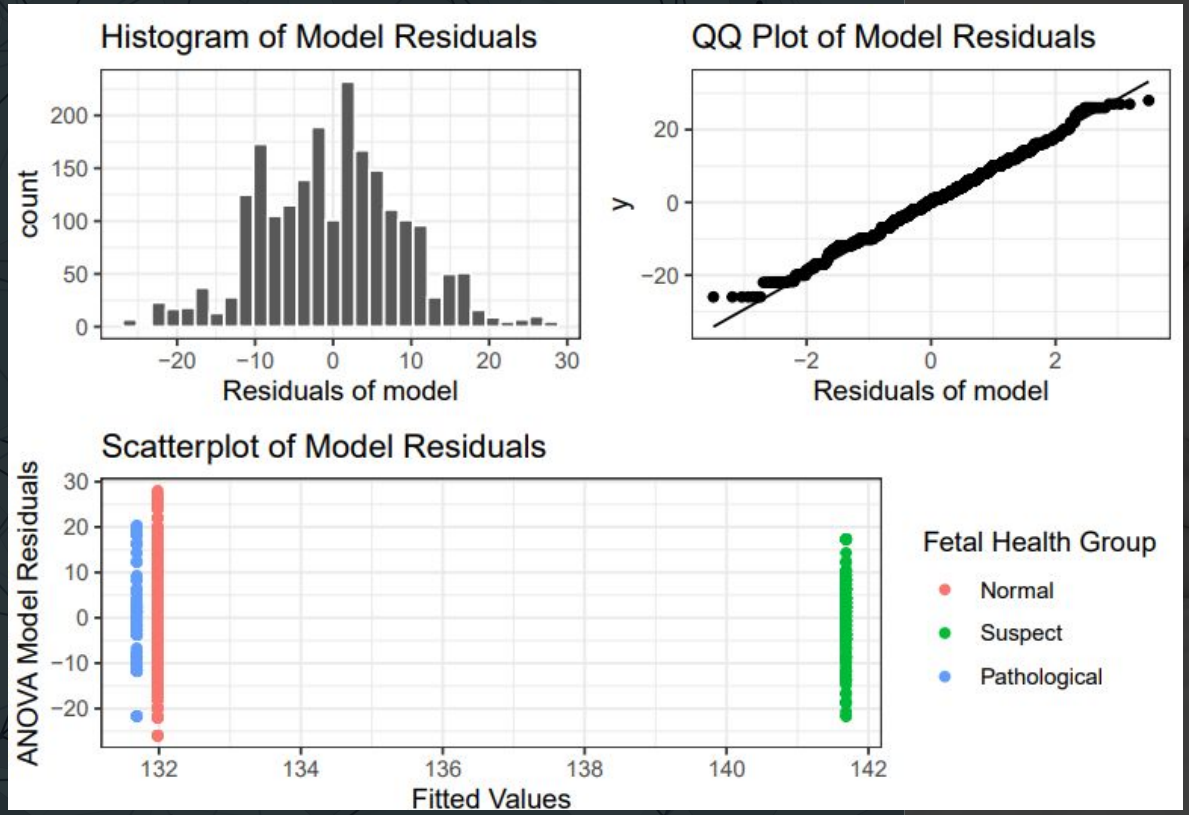


Model and Results of Anova

```
Analysis of Variance Table

Response: baseline.value
               Df Sum Sq Mean Sq F value    Pr(>F)
fetal_health    2  24073 12036.4  140.62 < 2.2e-16 ***
Residuals    2123 181717    85.6
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

- As the **p-value** is significant, we reject $\mathbf{H_0}$ and conclude that there is a significant difference in fetal health across at least one pair of groups (Normal, Suspect, Pathological).

Checking of Assumptions in Model



Anova Model Assumptions:

$\varepsilon \sim N(0,\sigma^2)$

1. **Histogram and QQ plot**
   Normality ✔

2. **Residuals vs fitted Values**
   Constant Variance ✖

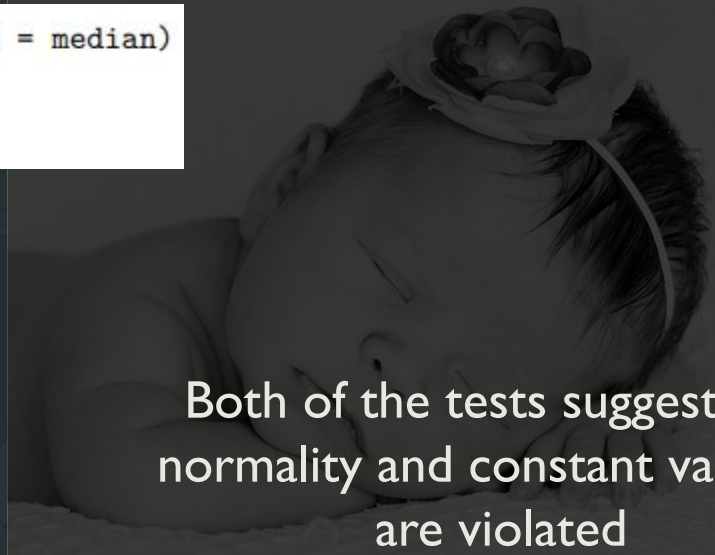
Checking of Assumptions in Model

Levene's Test - Variance

```
Levene's Test for Homogeneity of Variance (center = median)
        Df F value    Pr(>F)
group    2  9.3392 9.157e-05 ***
      2123
```

Shapiro-wilk Test - Normality

```
        Shapiro-Wilk normality test

data:  Norm$baseline.value
W = 0.99402, p-value = 3.21e-06


        Shapiro-Wilk normality test

data:  Sus$baseline.value
W = 0.97297, p-value = 2.341e-05


        Shapiro-Wilk normality test

data:  Path$baseline.value
W = 0.94487, p-value = 2.517e-06
```

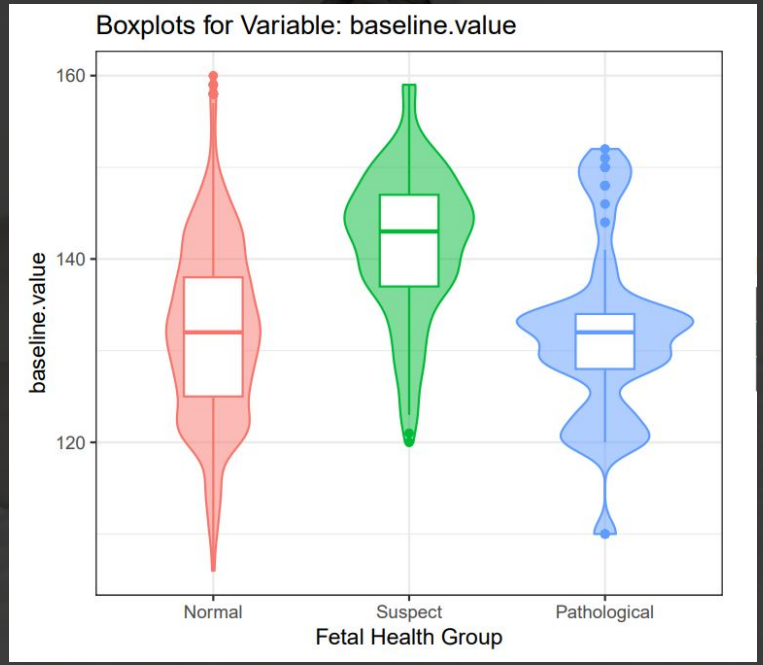


Both of the tests suggest that normality and constant variance are violated

Limitations with Parametric Anova

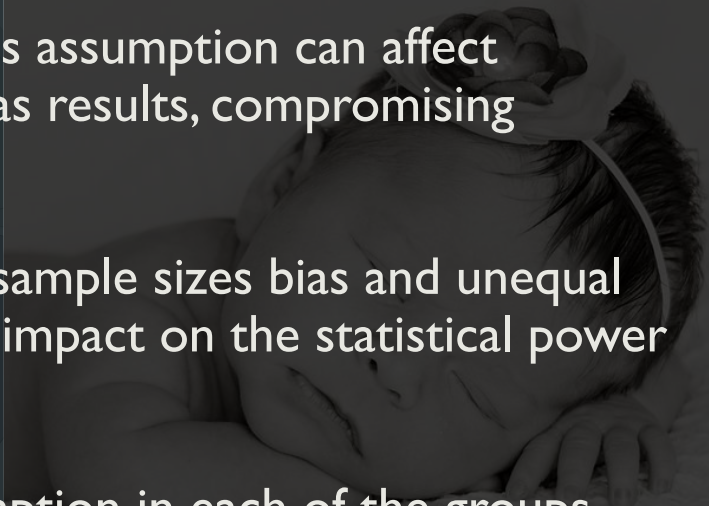
- **One-Way Anova Tests** only let you know that the groups are not equal to each other. We need separate post-hoc tests to check differences between each group.

```
  Tukey multiple comparisons of means
    95% family-wise confidence level

Fit: aov(formula = baseline.value ~ fetal_health, data = data)

$fetal_health
                           diff        lwr        upr     p adj
Suspect-Normal          9.7028727   8.331557 11.074188 0.000000
Pathological-Normal    -0.2943731  -2.014732  1.425986 0.915065
Pathological-Suspect   -9.9972458 -12.063926 -7.930566 0.000000
```



Limitations with Parametric Anova

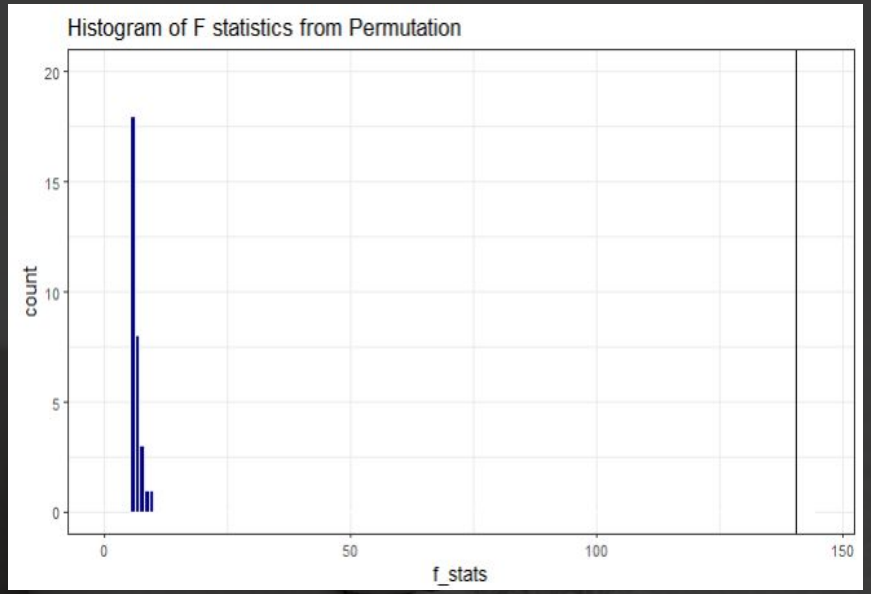
- **Unequal Variance:** Violating this assumption can affect standard error estimation and bias results, compromising reliability.
- **Unbalanced Design:** Unequal sample sizes bias and unequal variance can have an even bigger impact on the statistical power and F-statistic accuracy.
- **Normality:** Violating this assumption in each of the groups may lead to a less powerful test than a permutation test.



Permutation Anova Test

```
observed <- anova(model)$F[1]
n <- length(data$baseline.value)
N <- 5000
f_stats <-numeric(N)

for(i in 1:N)
  {
  index <- sample(n, replace = FALSE)
  perm_sample <- data$baseline.value[index]
  f_stats[i] <- anova(aov(perm_sample ~
fetal_health, data=data))$F[1]
  }

pval <- (sum(f_stats >= observed)+1)/(N+1)
```

P value: 0.00019996




```
PT = pairwisePermutationTest(
        baseline.value ~ fetal_health,
        data = data,
        method="fdr")
```

(from R package "rcompanion")

Comparison	Stat	p.value	p.adjust
Normal - Suspect = 0	-15.56	1.333e-54	0.0000
Normal - Pathological = 0	0.3929	0.6944	0.6944
Suspect - Pathological = 0	10.74	0	0.0000

Comparison of Parametric vs Non-Parametric

Parametric Results

```
Analysis of Variance Table

Response: baseline.value
               Df Sum Sq Mean Sq F value    Pr(>F)
fetal_health    2  24073 12036.4  140.62 < 2.2e-16 ***
Residuals    2123 181717    85.6
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Non Parametric Results

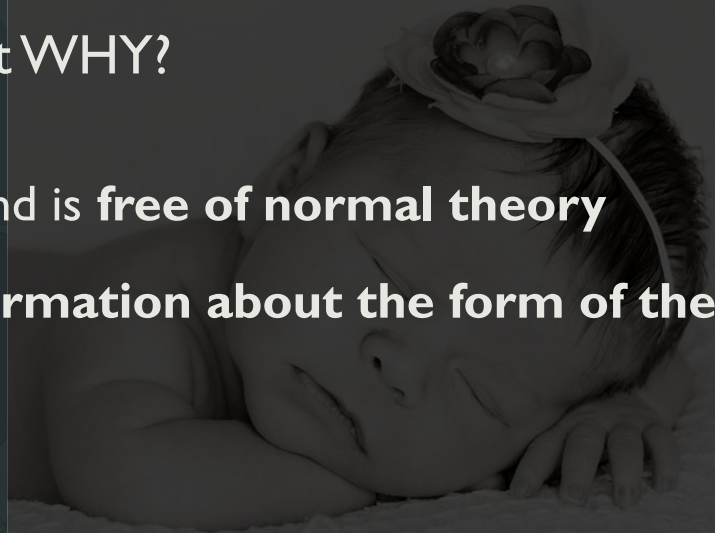
```
observed <- anova(model)$F[1]
n <- length(data$baseline.value)
N <- 5000
f_stats <-numeric(N)

for(i in 1:N)
  {
  index <- sample(n, replace = FALSE)
  perm_sample <-
data$baseline.value[index]
  f_stats[i] <- anova(aov(perm_sample ~
fetal_health, data=data))$F[1]
  }


pval <- (sum(f_stats >=
observed)+1)/(N+1)
```

P value: 0.00019996

Conclusion: which one to chose? And why?

Non-parametric Approach. But WHY?

- Uses distributional information and is **free of normal theory assumptions**.
- Bootstrap approach **retains information about the form of the original sample**.



Any Questions?

Thank you!!