DSA 8020 R Lab 7: Completely Randomized Designs

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Contents

The dataset `PlantGrowth` contains results from an experiment comparing yields (measured by the dried weight of plants) obtained under a control condition and two different treatment conditions.

Data Source: Dobson, A. J. (1983) *An Introduction to Statistical Modelling.* London: Chapman and Hall.

Let's load the data first:

Code:

```
data(PlantGrowth)
str(PlantGrowth)
```

```
## 'data.frame':   30 obs. of  2 variables:
##  $ weight: num  4.17 5.58 5.18 6.11 4.5 4.61 5.17 4.53 5.33 5.14 ...
##  $ group : Factor w/ 3 levels "ctrl","trt1",..: 1 1 1 1 1 1 1 1 1 1 ...
```

1. Compute the treatment means and standard deviations

Treatmeant means:

Code:

```
(means <- tapply(PlantGrowth$weight, PlantGrowth$group, mean))
```

```
##  ctrl  trt1  trt2
## 5.032 4.661 5.526
```

Treatmeant Standard Deviations:
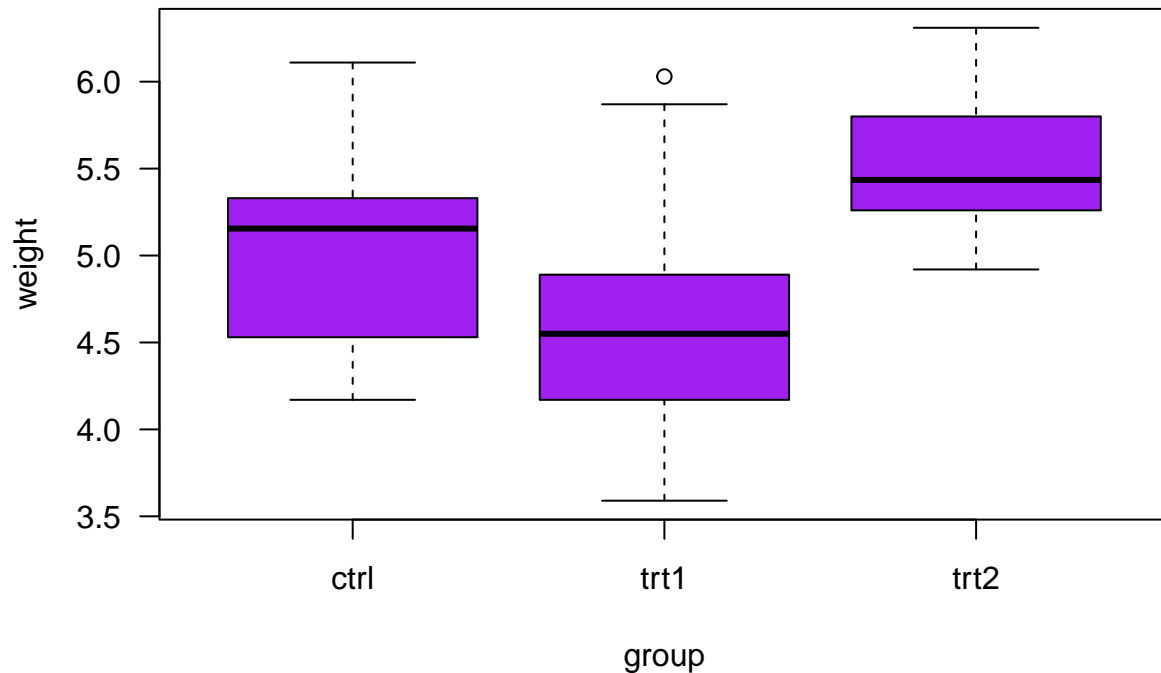
Code:

```
(sd <- tapply(PlantGrowth$weight, PlantGrowth$group, sd))
```

```
##      ctrl      trt1      trt2
## 0.5830914 0.7936757 0.4425733
```

2. Make side-by-side boxplots by treatment

Code:

```
boxplot(weight ~ group, data = PlantGrowth, las = 1, col = "purple")
```


3. Write down the effects model and explain each term in the model, including the model assumptions regarding the random error.

Answer:

The effects model for this analysis is given by $y_{ij} = \mu + \alpha_i + \epsilon_{ij}$, where μ represents the overall mean, α_i denotes the effect of the ith treatment, and ϵ_{ij} is the independent random error term. The random errors ϵ_{ij} are assumed to follow a normal distribution with a mean of zero and variance σ^2, i.e., $\epsilon_{ij} \sim N(0, \sigma^2)$. This model accounts for variations due to treatment effects while incorporating random errors to reflect natural variability in the data.

4. Perform an overall F-test using ANOVA. State the hypotheses, p-value, decision, and conclusion.

Code:

```
AOV <- aov(weight ~ group, data = PlantGrowth)
summary(AOV)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## group        2  3.766  1.8832   4.846 0.0159 *
## Residuals   27 10.492  0.3886
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Answer:

The null hypothesis (H_0) states that all treatment effects are equal, meaning $\alpha_1 = \alpha_2 = \alpha_3 = 0$, while the alternative hypothesis (H_a) suggests that at least one of the treatment effects is different from zero. The calculated p-value is 0.0159, which is less than the significance level of 0.05. Since the p-value falls below this threshold, we reject the null hypothesis. This leads us to conclude that there is sufficient statistical evidence to suggest that the yield is significantly affected by the treatment conditions at the 0.05 significance level.

5. Conduct pairwise comparisons using Tukey's HSD procedure. Interpret the results.

Code:

```
(HSD <- TukeyHSD(AOV, conf.level= 0.95))
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = weight ~ group, data = PlantGrowth)
##
## $group
##             diff        lwr       upr       p adj
## trt1-ctrl -0.371 -1.0622161 0.3202161 0.3908711
## trt2-ctrl  0.494 -0.1972161 1.1852161 0.1979960
## trt2-trt1  0.865  0.1737839 1.5562161 0.0120064
```

Answer:

To assess which treatment groups differ significantly from each other, we apply Tukey's Honest Significant Difference (HSD) test. This method controls the family-wise error rate and is particularly useful for multiple comparisons following an ANOVA.

The results show the following comparisons:

- **trt1 vs. ctrl**: The mean difference is -0.371, with a confidence interval ranging from -1.062 to 0.320. The adjusted p-value is 0.3909, which is greater than 0.05. This indicates that the difference between the control group and treatment 1 is not statistically significant.
- **trt2 vs. ctrl**: The mean difference is 0.494, with a confidence interval of -0.197 to 1.185. The adjusted p-value is 0.1980, which is also greater than 0.05. This suggests that the difference between the control group and treatment 2 is not statistically significant.
- **trt2 vs. trt1**: The mean difference is 0.865, with a confidence interval from 0.174 to 1.556. The adjusted p-value is 0.0120, which is less than 0.05, indicating a statistically significant difference between treatment 1 and treatment 2.

From these results, we conclude that only the comparison between treatment 1 and treatment 2 shows a statistically significant difference in yield, while the other pairwise comparisons do not indicate significant differences.

6. Use a QQ plot to examine the normality assumption of the error.

Code:

```
qqnorm(AOV$resid, cex = 0.8, las = 1, pch = 16)
qqline(AOV$resid, col = "orange", lwd = 1.5)
```
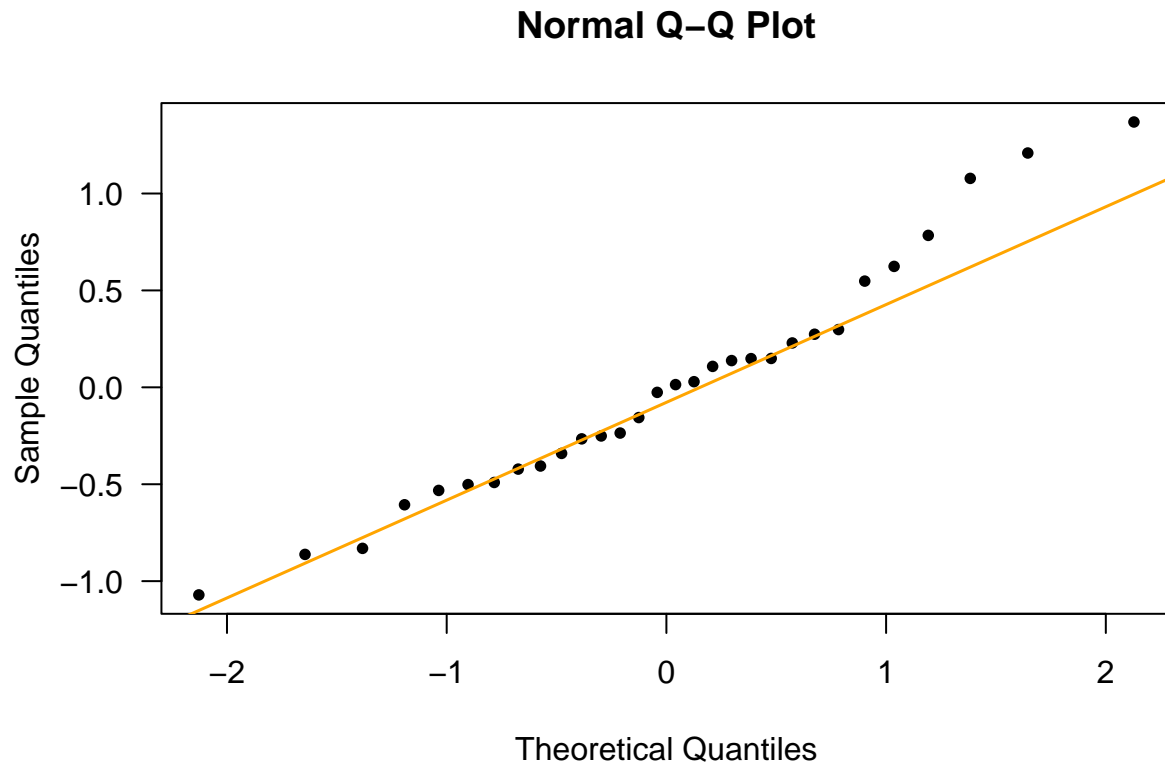
Normal Q–Q Plot

Answer:

A **quantile-quantile (QQ) plot** is used to assess whether the residuals follow a normal distribution, which is a key assumption of ANOVA.

By plotting the theoretical quantiles against the sample quantiles, we can visually inspect the normality of the residuals. If the residuals follow a normal distribution, the points should closely align along the 45-degree reference line.

In our QQ plot, the residuals approximately follow a straight line, with only slight deviations at the tails. This suggests that the assumption of normality is reasonably met, and no major violations of normality are evident.

7. Make a residual plot to assess the equal variance assumption.

Code:

```
plot(AOV$fitted, AOV$resid, las = 1, xlab = "Fitted Values", ylab = "Residual Values", cex = 0.75, pch =
abline(h = 0)
```
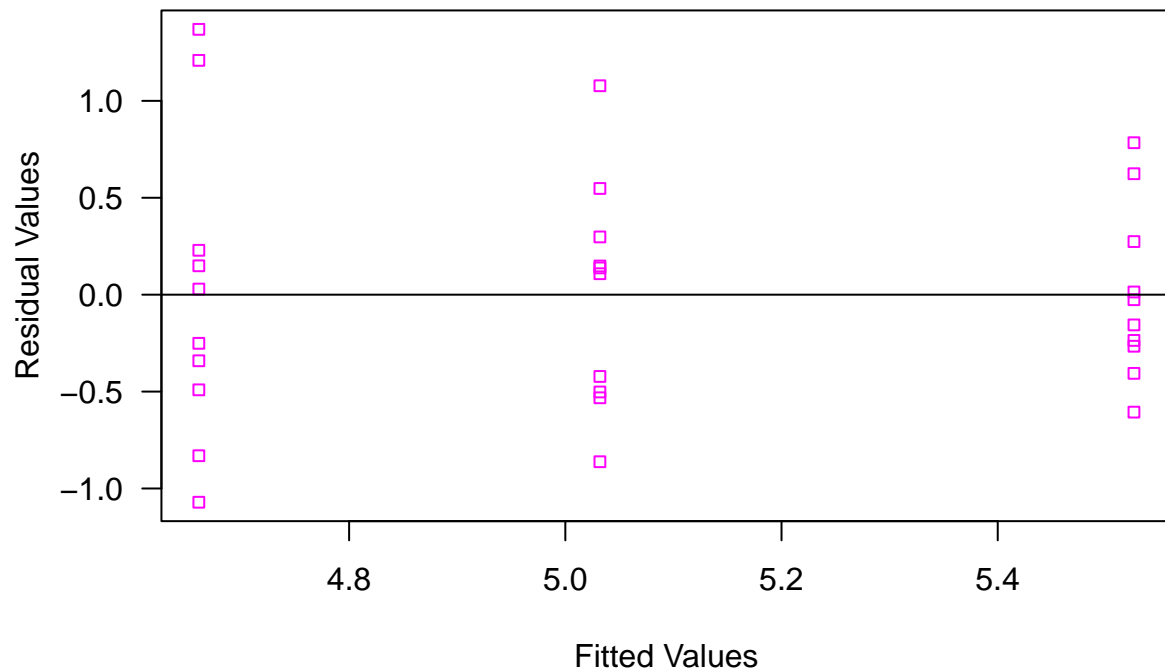
Answer:

A **residual plot** is used to check for homoscedasticity, meaning that the variance of residuals should be constant across different levels of fitted values. This is an important assumption in ANOVA.

In our residual plot, we observe that the variance of residuals appears to increase as fitted values decrease. Specifically, for smaller fitted values, there is greater variability in residuals, which suggests potential heteroscedasticity. Ideally, the points should be randomly scattered with no clear pattern and consistent spread.

Since some variation in spread is observed, this could indicate that the assumption of equal variance is not perfectly met, warranting further validation through statistical tests such as Levene's test.

8. Perform a Levene's test for equal variance.s

Code:

```
library(car)
```

```
## Warning: package 'car' was built under R version 4.4.2
```

```
## Loading required package: carData
```

```
## Warning: package 'carData' was built under R version 4.4.2
```

```
leveneTest(PlantGrowth$weight, PlantGrowth$group)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  2  1.1192 0.3412
##       27
```

```
med <- with(PlantGrowth, tapply(weight, group, median))
wt <- with(PlantGrowth, abs(weight - med[group]))
anova(lm(wt ~ group, PlantGrowth))
```

```
## Analysis of Variance Table
##
## Response: wt
##           Df Sum Sq Mean Sq F value Pr(>F)
## group      2 0.3495 0.17476  1.1192 0.3412
## Residuals 27 4.2161 0.15615
```

Answer:

To formally test the assumption of equal variances across groups, we perform **Levene's test**, which assesses whether the variance of residuals is constant across different treatment groups.

The test yields a p-value of **0.3412**, which is greater than the significance level of 0.05. Since the p-value is not low enough to reject the null hypothesis, we fail to find sufficient evidence against the assumption of homogeneity of variances.

Thus, based on Levene's test, we conclude that the variance among the groups does not significantly differ, and the assumption of equal variances is reasonable.