STAT 8020 R Session 8: Replication, Blocking, and Randomization

Whitney Huang, Clemson University

Contents

Objective . . . 1
Experimental Scenario . . . 1
Load Necessary Libraries . . . 1
Step 1: Experimental Design . . . 2
  1.1 Define Factors and Levels . . . 2
  1.2 Randomization . . . 2
Step 2: Data Collection . . . 2
  2.1 Experiment configuration . . . 2
  2.2 Simulating Flight Time Data . . . 3
Step 3: Summarizing and Visualizing the Data . . . 3
Step 4: Analyze the Data . . . 5
  4.1 Perform ANOVA to Assess Treatment and Block Effects . . . 5
  4.2 Interpretation . . . 6
Conclusion . . . 6

Objective

This `R` session demonstrates the principles of *replication*, *blocking*, and *randomization* in the design and analysis of experiments. By the end of this exercise, you should understand:

- The role of *randomization* in ensuring unbiased results.
- Why *replication* is crucial for estimating variability.
- How *blocking* helps reduce confounding variables.

Experimental Scenario

In this experiment, we will use **paper helicopters** to study the effect of two **helicopter wing lengths** on **flight time (seconds)**. The experiments are performed by **different experimenters**, which introduces a potential blocking factor.

Load Necessary Libraries

```
library(dplyr)
library(ggplot2)
```

Step 1: Experimental Design

1.1 Define Factors and Levels

- *Treatment:* Wing length ("Short", 5 cm or "Long", 10 cm)
- *Blocking Factor:* Experimenter (1 or 2)
- *Response Variable:* Flight time (seconds)

Each treatment level will be **replicated** 10 times. Moreover, we will **block** the experiment by assigning a single experimenter to test all treatment levels within a block to control for variability due to individual differences in timing.

1.2 Randomization

To minimize bias, we will **randomize** the order of helicopter drops.

Step 2: Data Collection

2.1 Experiment configuration

```
n_rep <- 10
treatment <- rep(c("Short", "Long"), each = n_rep)
block <- rep(c("Experimenter 1", "Experimenter 2"), times = n_rep)
cbind(treatment, block)
```

```
##       treatment block
##  [1,] "Short"   "Experimenter 1"
##  [2,] "Short"   "Experimenter 2"
##  [3,] "Short"   "Experimenter 1"
##  [4,] "Short"   "Experimenter 2"
##  [5,] "Short"   "Experimenter 1"
##  [6,] "Short"   "Experimenter 2"
##  [7,] "Short"   "Experimenter 1"
##  [8,] "Short"   "Experimenter 2"
##  [9,] "Short"   "Experimenter 1"
## [10,] "Short"   "Experimenter 2"
## [11,] "Long"    "Experimenter 1"
## [12,] "Long"    "Experimenter 2"
## [13,] "Long"    "Experimenter 1"
## [14,] "Long"    "Experimenter 2"
## [15,] "Long"    "Experimenter 1"
## [16,] "Long"    "Experimenter 2"
## [17,] "Long"    "Experimenter 1"
## [18,] "Long"    "Experimenter 2"
## [19,] "Long"    "Experimenter 1"
## [20,] "Long"    "Experimenter 2"
```

2.2 Simulating Flight Time Data

For demonstration, we simulate flight times assuming variability:

- Short wings: $\mu = 2.6$ sec, sd $= \sqrt{\text{Var}} = 0.5$ sec
- Long wings: $\mu = 3.2$ sec, sd $= \sqrt{\text{Var}} = 0.6$ sec

Additionally, we assume there is a measurement error for experimenters, with the first experiment tending to underestimate ($\mu =$ -0.3 sec) while the second overestimates ($\mu = 0.3$ sec). Finally, we assume there is an order effect that negatively biases the flight time over runs (and therefore, it is important to randomize the runs to mitigate such a bias).

```
set.seed(123)  # For reproducibility
n <- length(treatment)
effect <- c(rnorm(n_rep, mean = 2.6, sd = 0.5),  # Short
            rnorm(n_rep, mean = 3.2, sd = 0.6))  # Long
experimenter <- rnorm(n, mean = rep(c(-0.3, 0.3), n_rep), sd = 0.1)
order <- seq(0.5, -0.5, len = n)
time1 <- effect + experimenter + order
# Randomize the order
run_order <- sample(n)
time2 <- effect + experimenter + order[run_order]

data1 <- data.frame(Treatment = treatment, Block = block, Response = time1)
data2 <- data.frame(Treatment = treatment, Block = block, Response = time2)
```

Step 3: Summarizing and Visualizing the Data

Without and with randomization

```
tapply(data1$Response, list(data1$Treatment, data1$Block), mean)
```

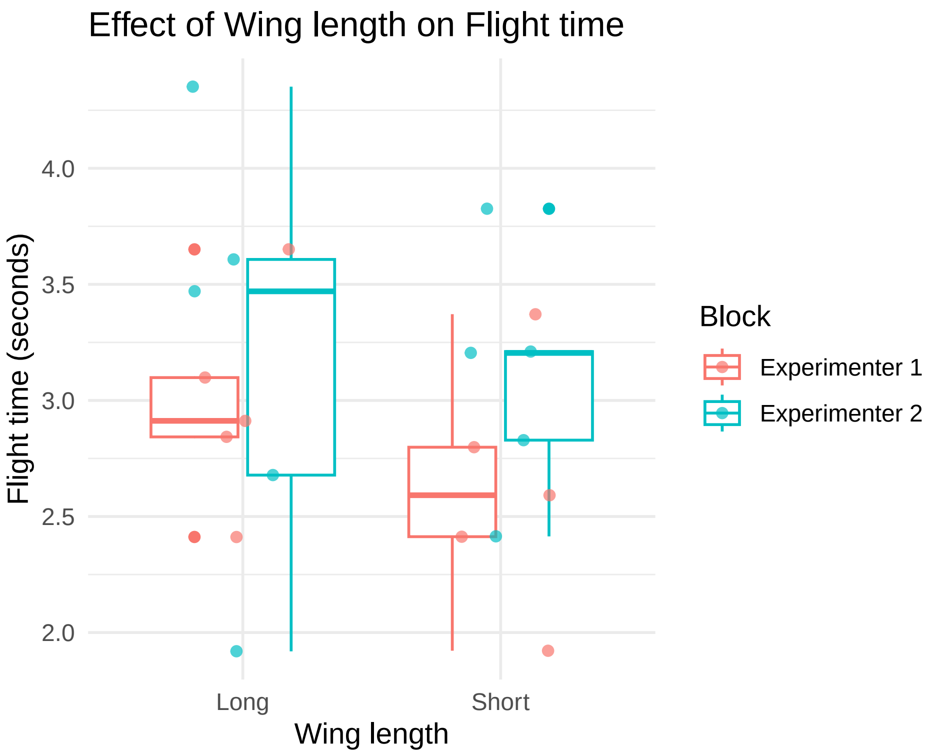
```
##       Experimenter 1 Experimenter 2
## Long        2.983167       3.205273
## Short       2.619248       3.096782
```

```
tapply(data2$Response, list(data2$Treatment, data2$Block), mean)
```

```
##       Experimenter 1 Experimenter 2
## Long        3.351588       3.300010
## Short       2.198195       3.054677
```

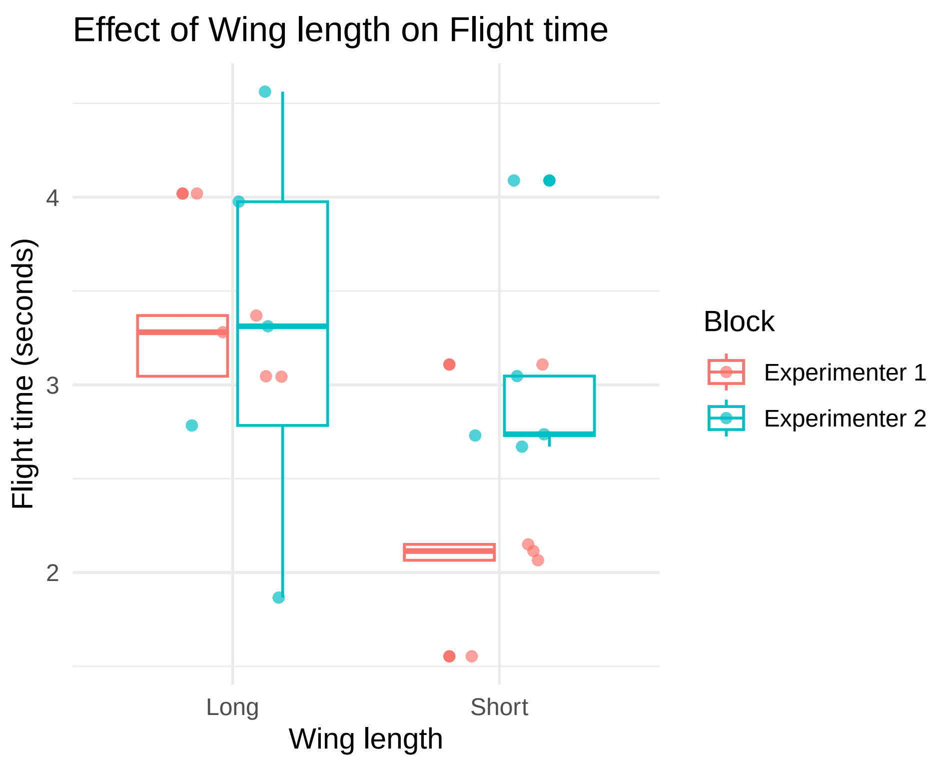
Without randomization

```
ggplot(data1, aes(x = Treatment, y = Response, color = Block)) +
  geom_boxplot() +
  geom_jitter(width = 0.2, alpha = 0.7) +
  theme_minimal() +
  labs(title = "Effect of Wing length on Flight time",
       x = "Wing length",
       y = "Flight time (seconds)")
```



With randomization

```
ggplot(data2, aes(x = Treatment, y = Response, color = Block)) +
  geom_boxplot() +
  geom_jitter(width = 0.2, alpha = 0.7) +
  theme_minimal() +
  labs(title = "Effect of Wing length on Flight time",
       x = "Wing length",
       y = "Flight time (seconds)")
```



Step 4: Analyze the Data

4.1 Perform ANOVA to Assess Treatment and Block Effects

Model 1: did not account for the block effect and was not randomized to eliminate the run order bias

```
model1 <- aov(Response ~ Treatment, data = data1)
summary(model1)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Treatment    1  0.279  0.2790   0.697  0.415
## Residuals   18  7.202  0.4001
```

```
coef(model1)
```

```
##   (Intercept) TreatmentShort
##     3.0942197     -0.2362049
```

Model 2: did not account for the block effect but was randomized to eliminate run order bias

```
model2 <- aov(Response ~ Treatment, data = data2)
summary(model2)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Treatment    1  2.446  2.4455   4.611 0.0456 *
## Residuals   18  9.546  0.5303
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
coef(model2)
```

```
##   (Intercept) TreatmentShort
##     3.3257987     -0.6993628
```

Model 3: did account for the block effect but was not randomized to eliminate the run order bias

```r
model3 <- aov(Response ~ Treatment + Block, data = data1)
summary(model3)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Treatment    1  0.279  0.2790   0.720  0.408
## Block        1  0.612  0.6119   1.578  0.226
## Residuals   17  6.591  0.3877
```

```r
coef(model3)
```

```
##         (Intercept)      TreatmentShort BlockExperimenter 2
##           2.9193096          -0.2362049           0.3498202
```

Model 4: did account for the block effect and was randomized to eliminate the run order bias

```r
model4 <- aov(Response ~ Treatment + Block, data = data2)
summary(model4)
```

```
##             Df Sum Sq Mean Sq F value Pr(>F)
## Treatment    1  2.446  2.4455   4.759 0.0435 *
## Block        1  0.810  0.8098   1.576 0.2263
## Residuals   17  8.736  0.5139
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
coef(model4)
```

```
##         (Intercept)      TreatmentShort BlockExperimenter 2
##           3.1245728          -0.6993628           0.4024518
```

4.2 Interpretation

- *Replication* ensures that variability can be measured within treatments.
- *Blocking* accounts for the effect of different experimenters.
- *Randomization* prevents systematic biases in treatment allocation.

Therefore, model 4 is the preferred model because it includes blocking and uses randomized run order.

Conclusion

By conducting this experiment with proper replication, blocking, and randomization, we ensure a robust and reliable analysis of treatment effects. The ANOVA results indicate whether wing length significantly affects flight time while controlling for experimenter variation.