Experiment 1–Flight Cylinder Data

## Analysis of Flight Cylinder Data: Overview

Reads in data on how many out of 10 navel orangeworm adults left a flight cylinder within 24 hours, creates a summary, and performs a 2-way analysis of Deviance with moth performance (y/n, with y as number leaving and n a the number of moths in the flight cylinder).

## Load data into the Global Environment (working memory)

library(readxl) # Read Excel files  
library(janitor) # Clean variable names   
df\_fltcyl <- read\_excel("Dataset.xlsx", sheet = "Flight\_ability\_assay")  
df\_fltcyl <- clean\_names(df\_fltcyl)  
df\_fltcyl

## # A tibble: 60 × 4  
## rep sex dose twentyfour\_out  
## <dbl> <chr> <dbl> <dbl>  
## 1 1 f 0 9  
## 2 1 f 100 9  
## 3 1 f 150 9  
## 4 1 f 200 9  
## 5 1 f 250 7  
## 6 1 f 300 10  
## 7 2 f 0 7  
## 8 2 f 100 8  
## 9 2 f 150 8  
## 10 2 f 200 9  
## # ℹ 50 more rows

## Get and export treatment means and SE

Will use dplyr to get a table of sample size, mean, and standard error by sex and radiation dose.

library(dplyr) # Easy and efficient data wrangling and summary  
library(FSA) # Provides an se() function for standard error  
tbl\_escapes <- df\_fltcyl %>%   
 group\_by(sex,dose) %>%   
 summarise(nObs = n(),  
 mn = mean(twentyfour\_out),  
 sem = se(twentyfour\_out))  
write.csv(tbl\_escapes,"tbl01\_flt\_cyl\_escapes.csv", row.names = F)  
tbl\_escapes

## # A tibble: 12 × 5  
## # Groups: sex [2]  
## sex dose nObs mn sem  
## <chr> <dbl> <int> <dbl> <dbl>  
## 1 f 0 5 8.4 0.6   
## 2 f 100 5 6.6 0.812  
## 3 f 150 5 7.8 0.374  
## 4 f 200 5 7.8 0.583  
## 5 f 250 5 7.4 0.510  
## 6 f 300 5 6.8 0.860  
## 7 m 0 5 8.8 0.583  
## 8 m 100 5 8 0.316  
## 9 m 150 5 8.8 0.2   
## 10 m 200 5 8.4 0.510  
## 11 m 250 5 8.6 0.245  
## 12 m 300 5 8.4 0.678

## Statistical Analysis

Will perform the Analysis of Deviance described above using the R-native glm() function. The output provides general information on degrees of freedom and significance of the main factors and interaction.

# Identify Sex and Dose as Factors  
df\_fltcyl$sex <- as.factor(df\_fltcyl$sex)  
df\_fltcyl$dose <- as.factor(df\_fltcyl$dose)  
  
# Contastant for number at risk  
df\_fltcyl$n <- 10  
df\_fltcyl <- df\_fltcyl %>% rename(y = twentyfour\_out)  
  
# Create parameter for non-event  
df\_fltcyl <- df\_fltcyl %>%   
 mutate(not\_y = n - y)  
  
# Fit a logistic regression model using glm with binomial family  
m1 <- glm(cbind(y,not\_y) ~ sex \* dose, data = df\_fltcyl, family = binomial)  
  
# Perform analysis of deviance using ANOVA for the GLM  
anova\_results <- anova(m1, test = "Chisq")  
  
# Print results  
print(anova\_results)

## Analysis of Deviance Table  
##   
## Model: binomial, link: logit  
##   
## Response: cbind(y, not\_y)  
##   
## Terms added sequentially (first to last)  
##   
##   
## Df Deviance Resid. Df Resid. Dev Pr(>Chi)   
## NULL 59 72.852   
## sex 1 10.0391 58 62.813 0.001533 \*\*  
## dose 5 6.9998 53 55.814 0.220656   
## sex:dose 5 0.9059 48 54.908 0.969792   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

The ‘car’ package provides an alternative Anova() function that provides type II degrees of freedom. This is often seen as preferable.

library(car)  
Anova(m1, type = "II")

## Analysis of Deviance Table (Type II tests)  
##   
## Response: cbind(y, not\_y)  
## LR Chisq Df Pr(>Chisq)   
## sex 10.1565 1 0.001438 \*\*  
## dose 6.9998 5 0.220656   
## sex:dose 0.9059 5 0.969792   
## ---  
## Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1