Experiment 2 – Mating

## Overview

For experiment 2, males and females were exposed to 0, 100, 200, 300, or 400 Gy x-ray and placed overnight in a 30 ml plastic cup with a non-exposed moth of the opposite sex for an opportunity to mate. Afterward the females was isolated and place in an oviposition jar until death. After death the female was detected to determine if there was a spermatophore, indicating successful mating.

library(readxl)  
df\_mating <- read\_excel("Dataset.xlsx", sheet = "Mating\_400Gy")  
df\_mating

## # A tibble: 92 × 5  
## rep FemID sex dose mate   
## <chr> <chr> <chr> <dbl> <chr>  
## 1 c C1 female 0 No   
## 2 c C2 female 0 Yes   
## 3 c C5 female 0 Yes   
## 4 e E1 female 0 Yes   
## 5 e E2 female 0 Yes   
## 6 e E3 female 0 Yes   
## 7 e E4 female 0 Yes   
## 8 e E5 female 0 Yes   
## 9 c C10 female 100 No   
## 10 c C8 female 100 No   
## # ℹ 82 more rows

## Summary of mating success

Obtain a table indicated number and percent of moths mated.

library(dplyr)  
tbl\_mating <- df\_mating %>%   
 group\_by(sex,dose) %>%   
 summarise(nMated = sum(mate == "Yes"),  
 nNot = sum(mate == "No"),  
 nTotal = sum(!is.na(mate)),  
 prop\_mated = nMated/nTotal)  
write.csv(tbl\_mating,"expt2\_mating\_summary.csv",row.names = F)  
tbl\_mating

## # A tibble: 10 × 6  
## # Groups: sex [2]  
## sex dose nMated nNot nTotal prop\_mated  
## <chr> <dbl> <int> <int> <int> <dbl>  
## 1 female 0 7 1 8 0.875  
## 2 female 100 4 3 7 0.571  
## 3 female 200 9 1 10 0.9   
## 4 female 300 8 1 9 0.889  
## 5 female 400 9 1 10 0.9   
## 6 male 0 9 0 9 1   
## 7 male 100 7 3 10 0.7   
## 8 male 200 5 5 10 0.5   
## 9 male 300 7 2 9 0.778  
## 10 male 400 9 1 10 0.9

## Data Analysis

Examine whether there are signficant differenct due to sex or irradiation using a GLM binomial model with both categories categorical.

# rename variables for ease of use in formula  
tbl\_mating2 <- tbl\_mating %>%   
 rename(y = nMated,  
 n = nTotal)  
  
# Make dose a categorical variable  
tbl\_mating2$dose <- as.factor(tbl\_mating2$dose)  
  
# Fit a logistic regression model using glm with binomial family  
m1 <- glm(cbind(y,n) ~ sex + dose, data = tbl\_mating2, family = binomial)  
  
# Examine model summary for sake of completeness  
summary(m1)

##   
## Call:  
## glm(formula = cbind(y, n) ~ sex + dose, family = binomial, data = tbl\_mating2)  
##   
## Coefficients:  
## Estimate Std. Error z value Pr(>|z|)  
## (Intercept) -0.01438 0.38838 -0.037 0.970  
## sexmale -0.08484 0.31502 -0.269 0.788  
## dose100 -0.36962 0.52106 -0.709 0.478  
## dose200 -0.30503 0.49397 -0.618 0.537  
## dose300 -0.12689 0.49400 -0.257 0.797  
## dose400 -0.04861 0.47664 -0.102 0.919  
##   
## (Dispersion parameter for binomial family taken to be 1)  
##   
## Null deviance: 1.63837 on 9 degrees of freedom  
## Residual deviance: 0.75263 on 4 degrees of freedom  
## AIC: 45.308  
##   
## Number of Fisher Scoring iterations: 3

Using Deviance residual chi-square and df to check model fit

pchisq(0.75263, df = 4, lower.tail = F)

## [1] 0.9446835

Get type II Analysis of Deviance

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

## Analysis of Deviance Table (Type II tests)  
##   
## Response: cbind(y, n)  
## LR Chisq Df Pr(>Chisq)  
## sex 0.07254 1 0.7877  
## dose 0.80817 4 0.9374