

Investigating the foraging, guarding and drifting behaviors of commercial *Bombus terrestris*
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Supplementary Information 4: R Code

```
### PACKAGES ###
```

```
library(lme4)
```

```
library(lmerTest)
```

```
library(boot)
```

```
library(MuMIn)
```

```
library(ggplot2)
```

```
library(cowplot)
```

```
library(tidyverse)
```

```
### DATA ###
```

```
## 1.
```

```
bees <- read.csv(file.choose())
```

```
# file: "bee_behaviour.csv"
```

```
bees$bee<-factor(bees$bee)
```

```
bees$colony<-factor(bees$colony)
```

```
bees$switched<-factor(bees$switched)
```

```
bees$stole<-factor(bees$stole)
```

```
bees$visit<-factor(bees$visit)
```

```
bees$guard<-factor(bees$guard)
```

```
bees$site<-factor(bees$site)
```

```
## Subsets
```

```
# Foraging bees
```

```
foragers <- subset(bees, mean_forage_time > 0)
```

```
# Guarding bees
```

```
guards <- subset(bees, guard==1)
```

```
# Bees with thorax measurement
```

```
thorax <- subset(bees, thorax > 0)
```

```
# Foragers with thorax measurement
```

```
foragersT <- subset(foragers, thorax > 0)
```

```
# Guards with thorax measurement
```

```
guardsT <- subset(guards, thorax > 0)
```

```
# Bees at Gipps
```

```
beesG <- subset(bees, site==1)
```

```
# Foragers at Gipps
```

```
foragersG <- subset(foragers, site==1)
```

```
# Bees with thorax measurement at Gipps
```

```
thoraxG <- subset(beesG, thorax > 1)
```

```
## 2.
```

```
days <- read.csv(file.choose())
```

```
# File: "foraging_days.csv"
```

```
days$site <- factor(days$site)
```

```
days$colony <- factor(days$colony)
```

```
days$guard <- factor(days$guard)
```

```
## Subsets
```

```
foragerdays <- subset(days, mean_forage_time > 0)
```

```
### MODELLING ###
```

```
## 1. Longevity and Mean foraging time
```

```
# Preliminary plots
```

```
ggplot(data=foragers,  
        aes(x = mean_forage_time, y = longevity,  
            colour = site)) +  
  geom_point()+  
  stat_smooth(method = "lm")
```

```
ggplot(data=foragers,  
        aes(x = mean_forage_time, y = longevity))+  
  geom_point(aes(colour = site))+  
  stat_smooth(method = "lm")
```

```
# Model selection using AICc
```

```
m1 <- lmer(longevity ~ site*mean_forage_time + thorax + guard +(1|colony), data = foragers)
```

```
m2 <- lmer(longevity ~ site*mean_forage_time + thorax +(1|colony), data = foragers)
```

```
AICc(m1,m2)
```

```
# keep m1
```

```
m3 <- lmer(longevity ~ site*mean_forage_time + guard +(1|colony), data = foragers)
```

```
AICc(m1,m3)
```

```
# keep m1
```

```
m4 <- lmer(longevity ~ mean_forage_time + site + thorax + guard +(1|colony), data = foragers)
```

```
AICc(m1,m4)
```

```
# keep m1
```

```
m1 <- lmer(longevity ~ site*mean_forage_time + thorax + guard +(1|colony), data = foragers)
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))

sresid <- resid(m1, type = "pearson")

hist(sresid)

fits <- fitted(m1)

plot(sresid ~ fits)

qqnorm(resid(m1))

qqline(resid(m1))
```

```
## Square root transformation
```

```
m1 <- lmer(sqrt(longevity) ~ site*mean_forage_time + thorax + guard +(1|colony), data = foragers)

m2 <- lmer(sqrt(longevity) ~ site*mean_forage_time + thorax +(1|colony), data = foragers)

AICc(m1,m2)

# keep m1
```

```
m3 <- lmer(sqrt(longevity) ~ site*mean_forage_time + guard +(1|colony), data = foragers)

AICc(m1,m3)

# keep m1
```

```
m4 <- lmer(sqrt(longevity) ~ mean_forage_time + site + thorax + guard +(1|colony), data = foragers)

AICc(m1,m4)

# keep m4
```

```
# Check assumptions
```

```
par(mfrow=c(1,3))

sresid <- resid(m4, type = "pearson")

hist(sresid)

fits <- fitted(m4)

plot(sresid ~ fits)

qqnorm(resid(m4))

qqline(resid(m4))
```

```
# Final Model
```

```
model1 <- lmer(sqrt(longevity) ~ mean_forage_time + site + thorax + guard +(1|colony), data = foragers)
```

```
summary(model1, ddf="Kenward-Roger")
```

```
## 2. Longevity and Foraging Trips/day
```

```
# Preliminary plots
```

```
ggplot(data=bees,  
       aes(x = forage_days, y = longevity,  
           colour = site)) +  
  geom_point()+  
  stat_smooth(method = "lm")
```

```
ggplot(data=bees,  
       aes(x = forage_days, y = longevity))+  
  geom_point(aes(colour = site))+  
  stat_smooth(method = "lm")
```

```
# Model selection using AICc
```

```
m1 <- lmer(longevity ~ site*forage_days + thorax + guard +(1|colony), data = foragers)
```

```
m2 <- lmer(longevity ~ site*forage_days + thorax +(1|colony), data = foragers)
```

```
AICc(m1,m2)
```

```
# keep m1
```

```
m3 <- lmer(longevity ~ site*forage_days + guard +(1|colony), data = foragers)
```

```
AICc(m1,m3)
```

```
# keep m1
```

```
m4 <- lmer(longevity ~ forage_days + site + thorax + guard +(1|colony), data = foragers)
```

```
AICc(m1,m4)
```

```
# keep m4
```

```
# Square root transformation
```

```
m5 <- lmer(sqrt(longevity) ~ forage_days + site + thorax + guard +(1|colony), data = foragers)
```

```
# Check assumptions
```

```
par(mfrow=c(1,3))
```

```
sresid <- resid(m5, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m5)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m5))
```

```
qqline(resid(m5))
```

```
# Final Model
```

```
model2 <- lmer(sqrt(longevity) ~ forage_days + site + thorax + guard +(1|colony), data = foragers)
```

```
summary(m4, ddf="Kenward-Roger")
```

```
## 3. Mean Foraging Time and Thorax
```

```
# Preliminary plots
```

```
ggplot(data=foragersT,
```

```
  aes(x = thorax, y = mean_forage_time,
```

```
      colour = site)) +
```

```
  geom_point()+
```

```
  stat_smooth(method = "lm"))
```

```
ggplot(data=foragersT,
```

```
  aes(x = thorax, y = mean_forage_time))+
```

```
  geom_point(aes(colour = site))+
```

```
  stat_smooth(method = "lm"))
```

```

# Model selection using AICc

m1 <- lmer(mean_forage_time ~ site*thorax + longevity + forage_days + guard + (1|colony), data = foragersT)

m2 <- lmer(mean_forage_time ~ site*thorax + longevity + forage_days + (1|colony), data = foragersT)

AICc(m1,m2)

# keep m2


m3 <- lmer(mean_forage_time ~ site*thorax + longevity + (1|colony), data = foragersT)

AICc(m2,m3)

# keep m2


m4 <- lmer(mean_forage_time ~ site*thorax + forage_days + (1|colony), data = foragersT)

AICc(m2,m4)

# keep m4


m5 <- lmer(mean_forage_time ~ thorax + site + forage_days + (1|colony), data = foragersT)

AICc(m4,m5)

# keep m4


# Check assumptions

par(mfrow=c(2,3))

sresid <- resid(m4, type = "pearson")

hist(sresid)

fits <- fitted(m4)

plot(sresid ~ fits)

qqnorm(resid(m4))

qqline(resid(m4))


## Square root transformation

m5 <- lmer(sqrt(mean_forage_time) ~ site*thorax + forage_days + (1|colony), data = foragersT)

```

```

# Check assumptions

sresid <- resid(m5, type = "pearson")

hist(sresid)

fits <- fitted(m5)

plot(sresid ~ fits)

qqnorm(resid(m5))

qqline(resid(m5))


# Final Model

model3 <- lmer(sqrt(mean_forage_time) ~ site*thorax + forage_days
+ (1|colony), data = foragersT)

summary(model3, ddf="Kenward-Roger")

```

4. Foraging Trips/day and Thorax

Preliminary plots

```

ggplot(data=foragersT,
       aes(x = thorax, y = forage_days,
           colour = site)) +
  geom_point()+
  stat_smooth(method = "lm")

```

```

ggplot(data=foragersT,
       aes(x = thorax, y = forage_days))+
  geom_point(aes(colour = site))+
  stat_smooth(method = "lm")

```

Model selection using AICc

```

m1 <- lmer(forage_days ~ site*thorax + longevity + mean_forage_time + guard + (1|colony), data = foragersT)

m2 <- lmer(forage_days ~ site*thorax + longevity + mean_forage_time + (1|colony), data = foragersT)

AICc(m1,m2)

```

```
# keep m1
```

```
m3 <- lmer(forage_days ~ site*thorax + longevity + guard + (1|colony), data = foragersT)
```

```
AICc(m1,m3)
```

```
# keep m1
```

```
m4 <- lmer(forage_days ~ site*thorax + mean_forage_time + guard + (1|colony), data = foragersT)
```

```
AICc(m1,m4)
```

```
# keep m4
```

```
m5 <- lmer(forage_days ~ thorax + site + mean_forage_time + guard + (1|colony), data = foragersT)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m4 <- lmer(forage_days ~ site*thorax + mean_forage_time + guard + (1|colony), data = foragersT)
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m4, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4))
```

```
qqline(resid(m4))
```

```
## Square root transformation
```

```
m1 <- lmer(sqrt(forage_days) ~ site*thorax + longevity + mean_forage_time + guard + (1|colony), data =  
foragersT)
```

```
m2 <- lmer(sqrt(forage_days) ~ site*thorax + longevity + mean_forage_time + (1|colony), data = foragersT)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(sqrt(forage_days) ~ site*thorax + longevity + (1|colony), data = foragersT)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(sqrt(forage_days) ~ site*thorax + mean_forage_time + (1|colony), data = foragersT)
```

```
AICc(m3,m4)
```

```
# keep m4
```

```
m5 <- lmer(sqrt(forage_days) ~ thorax + site + mean_forage_time + (1|colony), data = foragersT)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m4 <- lmer(sqrt(forage_days) ~ site*thorax + mean_forage_time + (1|colony), data = foragersT)
```

```
# Check assumptions
```

```
sresid <- resid(m4, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4))
```

```
qqline(resid(m4))
```

```
# Final Model
```

```
model4 <- lmer(sqrt(forage_days) ~ site*thorax + mean_forage_time + (1|colony), data = foragersT)
```

```
summary(model4, ddf="Kenward-Roger")
```

```
## 5. Mean Foraging Time and Day
```

```
# Preliminary plots
```

```
ggplot(data=foragerdays,  
       aes(x = day, y = mean_forage_time,  
           colour = site)) +  
  geom_point()+  
  stat_smooth(method = "lm")
```

```
ggplot(data=foragerdays,  
       aes(x = day, y = mean_forage_time,  
           colour = site)) +  
  geom_point()+  
  stat_smooth(method = "lm")+  
  facet_grid(. ~ site)
```

```
ggplot(data=foragerdays,  
       aes(x = day, y = mean_forage_time))+  
  geom_point(aes(colour = site))+  
  stat_smooth(method = "lm")
```

Model selection using AICc

```
m1 <- lmer(mean_forage_time ~ day + site + colony + thorax + longevity + (1|bee), data = foragerdays)
```

```
m2 <- lmer(mean_forage_time ~ day + site + colony + thorax + (1|bee), data = foragerdays)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(mean_forage_time ~ day + site + colony + (1|bee), data = foragerdays)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(mean_forage_time ~ colony*day + site + thorax + (1|bee), data = foragerdays)
```

```
AICc(m2,m4)
```

```
# keep m2
```

```
m5 <- lmer(mean_forage_time ~ site*day + colony + thorax + (1|bee), data = foragerdays)
```

```
AICc(m2,m5)
```

```
# keep m2
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m2, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m2)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m2))
```

```
qqline(resid(m2))
```

```
# Log transformation
```

```
m2a <- lmer(log(mean_forage_time) ~ day + site + colony + thorax + (1|bee), data = foragerdays)
```

```
# Check assumptions
```

```
sresid <- resid(m2a, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m2a)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m2a))
```

```
qqline(resid(m2a))
```

```
# Final Model
```

```
model5 <- lmer(log(mean_forage_time) ~ day + site + colony + thorax + (1|bee), data = foragerdays)
```

```
summary(model5, ddf="Kenward-Roger")
```

```
## 6. Mean Foraging Trips/day and Day
```

```
# Preliminary plots
```

```
ggplot(data=foragerdays,  
       aes(x = day, y = forage_days,  
           colour = site)) +  
  geom_point()+  
  stat_smooth(method = "lm")
```

```
ggplot(data=foragerdays,  
       aes(x = day, y = forage_days,  
           colour = site)) +  
  geom_point()+  
  stat_smooth(method = "lm")+  
  facet_grid(. ~ site)
```

```
ggplot(data=foragerdays,  
       aes(x = day, y = forage_days))+  
  geom_point(aes(colour = site))+  
  stat_smooth(method = "lm")
```

```
# Model selection using AICc
```

```
m1 <- lmer(forage_days ~ site*day + thorax + colony + longevity + mean_forage_time + guard + (1|bee), data  
= foragerdays)
```

```
m2 <- lmer(forage_days ~ site*day + thorax + colony + longevity + mean_forage_time + (1|bee), data =  
foragerdays)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(forage_days ~ site*day + thorax + colony + longevity + (1|bee), data = foragerdays)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(forage_days ~ site*day + thorax + colony + mean_forage_time + (1|bee), data = foragerdays)
```

```
AICc(m2,m4)
```

```
# keep m4
```

```
m5 <- lmer(forage_days ~ site*day + thorax + mean_forage_time + (1|bee), data = foragerdays)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m6 <- lmer(forage_days ~ site*day + colony + mean_forage_time + (1|bee), data = foragerdays)
```

```
AICc(m4,m6)
```

```
# keep m4
```

```
m7 <- lmer(forage_days ~ day + site + thorax + colony + mean_forage_time + (1|bee), data = foragerdays)
```

```
AICc(m4,m7)
```

```
# keep m4
```

```
# Check assumptions
```

```
sresid <- resid(m4, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4))
```

```
qqline(resid(m4))
```

```
# Final Model
```

```
model6 <- lmer(forage_days ~ site*day + thorax + colony + mean_forage_time + (1|bee), data = foragerdays)
```

```
summary(model6, ddf="Kenward-Roger")
```

```
## 7. Longevity and Guarding
```

```
# Preliminary plots
```

```
gplot(data=bees,  
      aes(x = guard, y = longevity)) +  
      geom_boxplot()+  
stat_summary(fun.y = "mean",  
            geom = "point",  
            shape = 5, size = 3)
```

```
ggplot(data=bees,  
      aes(x = guard, y = longevity)) +  
      geom_boxplot()+  
      facet_grid(. ~ site)+  
stat_summary(fun.y = "mean",  
            geom = "point",  
            shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(longevity ~ site*guard + thorax + mean_forage_time + forage_days + (1|colony), data = bees)
```

```
m2 <- lmer(longevity ~ site*guard + thorax + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m1,m2)
```

```
## keep m2
```

```
m3 <- lmer(longevity ~ site*guard + thorax + (1|colony), data = bees)
```

```
AICc(m2,m3)
```

```
## keep m2
```

```
m4 <- lmer(longevity ~ site*guard + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m2,m4)
```

```
## keep m2
```

```
m5 <- lmer(longevity ~ guard + site + thorax + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m2,m5)
```

```
## keep m2
```

```
m2 <- lmer(longevity ~ site*guard + thorax + mean_forage_time + (1|colony), data = bees)
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m2, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m2)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m2))
```

```
qqline(resid(m2))
```

```
## Square root transformation
```

```
m1 <- lmer(sqrt(longevity) ~ site*guard + thorax + mean_forage_time + forage_days + (1|colony), data = bees)
```

```
m2 <- lmer(sqrt(longevity) ~ site*guard + thorax + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m1,m2)
```

```
## keep m2
```

```
m3 <- lmer(sqrt(longevity) ~ site*guard + thorax + (1|colony), data = bees)
```

```
AICc(m2,m3)
```

```
## keep m3
```

```
m4 <- lmer(sqrt(longevity) ~ site*guard + (1|colony), data = bees)
```

```
AICc(m3,m4)
```

```
## keep m3
```

```
m5 <- lmer(sqrt(longevity) ~ guard + site + thorax + (1|colony), data = bees)
```

```
AICc(m3,m5)
```

```
## keep m5
```

```
m5 <- lmer(sqrt(longevity) ~ guard + site + thorax + (1|colony), data = bees)
```

```
# Check assumptions
```

```
sresid <- resid(m5, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m5)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m5))
```

```
qqline(resid(m5))
```

```
# Final Model
```

```
model7 <- lmer(sqrt(longevity) ~ guard + site + thorax + (1|colony), data = bees)
```

```
summary(model7, ddf="Kenward-Roger")
```

```
## 8. Mean foraging time and Guarding
```

```
# Preliminary plots
```

```
ggplot(data=foragers,
```

```
  aes(x = guard, y = mean_forage_time)) +
```

```
  geom_boxplot()+
```

```
stat_summary(fun.y = "mean",
```

```
  geom = "point",
```

```
  shape = 5, size = 3)
```

```
ggplot(data=foragers,
```

```
  aes(x = guard, y = mean_forage_time)) +
```

```
  geom_boxplot()+
```

```

    facet_grid(. ~ site)+
stat_summary(fun.y = "mean",
    geom = "point",
    shape = 5, size = 3)

# Model selection using AICc
m1 <- lmer(mean_forage_time ~ site*guard + longevity + thorax + forage_days + (1|colony), data = foragers)
m2 <- lmer(mean_forage_time ~ site*guard + longevity + thorax + (1|colony), data = foragers)
AICc(m1,m2)
# keep m1

m3 <- lmer(mean_forage_time ~ site*guard + longevity + forage_days + (1|colony), data = foragers)
AICc(m1,m3)
# keep m1

m4 <- lmer(mean_forage_time ~ site*guard + thorax + forage_days + (1|colony), data = foragers)
AICc(m1,m4)
# keep m4

m5 <- lmer(mean_forage_time ~ guard + site + thorax + forage_days + (1|colony), data = foragers)
AICc(m4,m5)
# keep m5

m5 <- lmer(mean_forage_time ~ guard + site + thorax + forage_days + (1|colony), data = foragers)

# Check assumptions
par(mfrow=c(2,3))
sresid <- resid(m5, type = "pearson")
hist(sresid)

```

```

fits <- fitted(m5)

plot(sresid ~ fits)

qqnorm(resid(m5))

qqline(resid(m5))

# Square root transformation

m1 <- lmer(sqrt(mean_forage_time) ~ site*guard + longevity + thorax + forage_days + (1|colony), data =
foragers)

m2 <- lmer(sqrt(mean_forage_time) ~ site*guard + longevity + thorax + (1|colony), data = foragers)

AICc(m1,m2)

# keep m1

m3 <- lmer(sqrt(mean_forage_time) ~ site*guard + longevity + forage_days + (1|colony), data = foragers)

AICc(m1,m3)

# keep m3

m4 <- lmer(sqrt(mean_forage_time) ~ site*guard + forage_days + (1|colony), data = foragers)

AICc(m3,m4)

# keep m4

m5 <- lmer(sqrt(mean_forage_time) ~ guard + site + forage_days + (1|colony), data = foragers)

AICc(m4,m5)

# keep m5

m5 <- lmer(sqrt(mean_forage_time) ~ guard + site + forage_days + (1|colony), data = foragers)

# Check assumptions

sresid <- resid(m5, type = "pearson")

hist(sresid)

```

```
fits <- fitted(m5)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m5))
```

```
qqline(resid(m5))
```

```
# Final Model
```

```
model8 <- lmer(sqrt(mean_forage_time) ~ guard + site + forage_days + (1|colony), data = foragers)
```

```
summary(model8,ddf="Kenward-Roger")
```

```
## 9. Foraging trips/day and Guarding
```

```
# Preliminary plots
```

```
ggplot(data=foragers,
```

```
  aes(x = guard, y = forage_days)) +
```

```
  geom_boxplot()+
```

```
stat_summary(fun.y = "mean",
```

```
  geom = "point",
```

```
  shape = 5, size = 3)
```

```
ggplot(data=foragers,
```

```
  aes(x = guard, y = forage_days)) +
```

```
  geom_boxplot()+
```

```
  facet_grid(. ~ site)+
```

```
stat_summary(fun = "mean",
```

```
  geom = "point",
```

```
  shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(forage_days ~ site*guard + longevity + thorax + mean_forage_time + (1|colony), data = foragers)
```

```
m2 <- lmer(forage_days ~ site*guard + longevity + thorax + (1|colony), data = foragers)
```

```
AICc(m1,m2)
```

```
# keep m1
```

```
m3 <- lmer(forage_days ~ site*guard + longevity + mean_forage_time + (1|colony), data = foragers)
```

```
AICc(m1,m3)
```

```
# keep m1
```

```
m4 <- lmer(forage_days ~ site*guard + thorax + mean_forage_time + (1|colony), data = foragers)
```

```
AICc(m1,m4)
```

```
# keep m4
```

```
m5 <- lmer(forage_days ~ site*guard + mean_forage_time + (1|colony), data = foragers)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m6 <- lmer(forage_days ~ guard + site + thorax + mean_forage_time + (1|colony), data = foragers)
```

```
AICc(m4,m6)
```

```
# keep m4
```

```
m4 <- lmer(forage_days ~ site*guard + thorax + mean_forage_time + (1|colony), data = foragers)
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m4, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4))
```

```
qqline(resid(m4))
```

```
# Square root transformation
```

```
m4a <- lmer(sqrt(forage_days) ~ site*guard + thorax + mean_forage_time + (1|colony), data = foragers)
```

```
# Check assumptions
```

```
sresid <- resid(m4a, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4a)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4a))
```

```
qqline(resid(m4a))
```

```
# Final Model
```

```
model9 <- lmer(sqrt(forage_days) ~ site*guard + thorax + mean_forage_time + (1|colony), data = foragers)
```

```
summary(model9, ddf="Kenward-Roger")
```

```
## 10. Mean guarding time and Thorax
```

```
# Preliminary plots
```

```
ggplot(data=guards,
```

```
  aes(x = thorax, y = mean_guard_time,
```

```
      colour = site)) +
```

```
  geom_point()+
```

```
  stat_smooth(method = "lm"))
```

```
ggplot(data=guards,
```

```
  aes(x = thorax, y = mean_guard_time))+
```

```
  geom_point(aes(colour = site))+
```

```
  stat_smooth(method = "lm"))
```

```
# Preliminary plots with outlier removed
```

```
ggplot(data=guards2,
```

```
aes(x = thorax, y = mean_guard_time,  
     colour = site)) +  
geom_point()+  
stat_smooth(method = "lm")
```

```
ggplot(data=guards2,  
       aes(x = thorax, y = mean_guard_time))+  
geom_point(aes(colour = site))+  
stat_smooth(method = "lm")
```

```
# Model selection using AICc
```

```
m1 <- lm(mean_guard_time ~ site*thorax + colony + longevity + forage_days+ mean_forage_time, data =  
guardsT)
```

```
m2 <- lm(mean_guard_time ~ site*thorax + colony + longevity + forage_days, data = guardsT)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lm(mean_guard_time ~ site*thorax + colony + longevity, data = guardsT)
```

```
AICc(m2,m3)
```

```
# keep m3
```

```
m4 <- lm(mean_guard_time ~ site*thorax + colony , data = guardsT)
```

```
AICc(m3,m4)
```

```
# keep m4
```

```
m5 <- lm(mean_guard_time ~ thorax + site + colony , data = guardsT)
```

```
AICc(m4,m5)
```

```
# keep m5
```

```
# Check assumptions
```

```

par(mfrow=c(2,2))

plot(m5)

# Remove outlier

guards2 <- subset(guardsT, mean_guard_time < 0.9)

# Check assumptions

m5 <- lm(mean_guard_time ~ thorax + site + colony , data = guards2)

plot(m5)


# Final Model

model10 <- lm(mean_guard_time ~ thorax + site + colony, data = guards2)

summary(model10)


## 11. Mean foraging time and Mean guarding time

# Preliminary plots

ggplot(data=guards,
       aes(x = mean_guard_time, y = mean_forage_time,
           colour = site)) +
  geom_point()+
  stat_smooth(method = "lm")


ggplot(data=guards,
       aes(x = mean_guard_time, y = mean_forage_time))+
  geom_point(aes(colour = site))+
  stat_smooth(method = "lm")


# Model selection using AICc

m1 <- lm(mean_forage_time ~ site*mean_guard_time + colony + longevity + thorax + forage_days, data =
guards)

m2 <- lm(mean_forage_time ~ site*mean_guard_time + colony + longevity + thorax , data = guards)

AICc(m1,m2)

```

```
# keep m2
```

```
m3 <- lm(mean_forage_time ~ site*mean_guard_time + colony + longevity , data = guards)
```

```
AICc(m2,m3)
```

```
# keep m3
```

```
m4 <- lm(mean_forage_time ~ site*mean_guard_time + colony , data = guards)
```

```
AICc(m3,m4)
```

```
# keep m4
```

```
m5 <- lm(mean_forage_time ~ mean_guard_time + site + colony, data = guards)
```

```
AICc(m4,m5)
```

```
# keep m5
```

```
# Check assumptions
```

```
par(mfrow=c(2,2))
```

```
plot(m5)
```

```
# Final Model
```

```
model11 <- lm(mean_forage_time ~ mean_guard_time + site + colony, data = guards)
```

```
summary(model11)
```

```
## 12. Foraging trips/day and Mean guarding time
```

```
# Preliminary plots
```

```
ggplot(data=guards,
```

```
  aes(x = mean_guard_time, y = forage_days,
```

```
      colour = site)) +
```

```
  geom_point()+
```

```
  stat_smooth(method = "lm")
```

```
ggplot(data=guards,  
       aes(x = mean_guard_time, y = forage_days))+  
  geom_point(aes(colour = site))+  
  stat_smooth(method = "lm")
```

```
# Model selection using AICc
```

```
m1 <- lm(forage_days ~ site*mean_guard_time + colony + longevity + thorax + mean_forage_time, data =  
guards)
```

```
m2 <- lm(forage_days ~ site*mean_guard_time + colony + longevity + thorax , data = guards)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lm(forage_days ~ site*mean_guard_time + colony + longevity , data = guards)
```

```
AICc(m2,m3)
```

```
# keep m3
```

```
m4 <- lm(forage_days ~ site*mean_guard_time + colony , data = guards)
```

```
AICc(m3,m4)
```

```
# keep m4
```

```
m5 <- lm(forage_days ~ mean_guard_time + site + colony , data = guards)
```

```
AICc(m4,m5)
```

```
# keep m5
```

```
# Check assumptions
```

```
par(mfrow=c(2,2))
```

```
plot(m5)
```

```
# Square root transformation
```

```
m5a <- lm(sqrt(forage_days) ~ mean_guard_time + site + colony , data = guards)
```

```
plot(m5a)
```

```
# Final Model
```

```
model12 <- lm(sqrt(forage_days) ~ mean_guard_time + site + colony , data = guards)
```

```
summary(model12)
```

```
## 13. Guarding and Thorax
```

```
# Preliminary plots
```

```
ggplot(data=thorax,  
       aes(x = guard, y = thorax)) +  
  geom_boxplot()+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
ggplot(data=thorax,  
       aes(x = guard, y = thorax)) +  
  geom_boxplot()+  
  facet_grid(. ~ site)+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- glm(guard ~ thorax*colony + longevity + forage_days + mean_forage_time, family = binomial  
(link="cloglog"), data=thorax)
```

```
m2 <- glm(guard ~ thorax*colony + longevity + forage_days, family = binomial (link="cloglog"), data=thorax)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- glm(guard ~ thorax*colony + longevity, family = binomial (link="cloglog"), data=thorax)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- glm(guard ~ thorax*colony + forage_days, family = binomial (link="cloglog"), data=thorax)
```

```
AICc(m2,m4)
```

```
# keep m2
```

```
m5 <- glm(guard ~ thorax + colony + longevity + forage_days, family = binomial (link="cloglog"),  
data=thorax)
```

```
AICc(m2,m5)
```

```
# keep m5
```

```
# Check assumptions
```

```
glm.diag.plots(m5)
```

```
# Remove outliers
```

```
row.names(thorax) <- 1:nrow(thorax)
```

```
thorax2 <- thorax[-c(68,70,80),]
```

```
m5a <- glm(guard ~ thorax + colony + longevity + forage_days, family = binomial (link="cloglog"),  
data=thorax2)
```

```
# Check assumptions
```

```
glm.diag.plots(m5a)
```

```
devresid <- resid(m5a, type="deviance")
```

```
hist(devresid)
```

```
# Final Model
```

```
model13 <- glm(guard ~ thorax + colony + longevity + forage_days, family = binomial (link="cloglog"),  
data=thorax2)
```

```
summary(model13)
```

```
## 14. Longevity and Stealing (all bees)
```

```
# Preliminary plots
```

```
ggplot(data=bees,  
       aes(x = stole, y = longevity)) +  
  geom_boxplot()+  
stat_summary(fun.y = "mean",  
            geom = "point",  
            shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(longevity ~ stole + site + thorax + mean_forage_time + forage_days + guard + (1|colony), data =  
bees)
```

```
m2 <- lmer(longevity ~ stole + site + thorax + mean_forage_time + forage_days +(1|colony), data = bees)
```

```
AICc(m1,m2)
```

```
# keep m1
```

```
m3 <- lmer(longevity ~ stole + site + thorax + mean_forage_time + guard + (1|colony), data = bees)
```

```
AICc(m1,m3)
```

```
# keep m3
```

```
m4 <- lmer(longevity ~ stole + site + thorax + guard + (1|colony), data = bees)
```

```
AICc(m3,m4)
```

```
# keep m4
```

```
m5 <- lmer(longevity ~ stole + site + guard + (1|colony), data = bees)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m6 <- lmer(longevity ~ site*stole + thorax + guard + (1|colony), data = bees)
```

```
AICc(m4,m6)
```

```
# keep m4
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m4, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4))
```

```
qqline(resid(m4))
```

```
# Square root transformation
```

```
m4a <- lmer(sqrt(longevity) ~ stole + site + thorax + guard + (1|colony), data = bees)
```

```
# Check assumptions
```

```
sresid <- resid(m4a, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4a)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4a))
```

```
qqline(resid(m4a))
```

```
# Final Model
```

```
model14 <- lmer(sqrt(longevity) ~ stole + site + thorax + guard + (1|colony), data = bees)
```

```
summary(model14, ddf="Kenward-Roger")
```

```
## 15. Mean foraging time and Stealing (all bees)
```

```
# Preliminary plots
```

```
plot(data=foragers,  
      aes(x = stole, y = mean_forage_time)) +  
      geom_boxplot()+  
      stat_summary(fun.y = "mean",  
                    geom = "point",  
                    shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(mean_forage_time ~ stole + site + longevity + thorax + forage_days + guard + (1|colony), data =  
foragers)
```

```
m2 <- lmer(mean_forage_time ~ stole + site + longevity + thorax + forage_days + (1|colony), data = foragers)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(mean_forage_time ~ stole + site + longevity + thorax + (1|colony), data = foragers)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(mean_forage_time ~ stole + site + longevity + forage_days + (1|colony), data = foragers)
```

```
AICc(m2,m4)
```

```
# keep m2
```

```
m5 <- lmer(mean_forage_time ~ stole + site + thorax + forage_days + (1|colony), data = foragers)
```

```
AICc(m2,m5)
```

```
# keep m5
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m5, type = "pearson")
```

```

hist(sresid)

fits <- fitted(m5)

plot(sresid ~ fits)

qqnorm(resid(m5))

qqline(resid(m5))


# Final Model

model15 <- lmer(mean_forage_time ~ stole + site + thorax + forage_days + (1|colony), data = foragers)

summary(model15, ddf="Kenward-Roger")


## 16. Foraging trips/day and Stealing (all bees)

# Preliminary plots

ggplot(data=foragers,
       aes(x = stole, y = forage_days)) +
  geom_boxplot()+
  stat_summary(fun.y = "mean",
              geom = "point",
              shape = 5, size = 3)


# Model selection using AICc

m1 <- lmer(forage_days ~ stole + site + longevity + thorax + mean_forage_time + guard + (1|colony), data =
foragers)

m2 <- lmer(forage_days ~ stole + site + longevity + thorax + mean_forage_time + (1|colony), data = foragers)

AICc(m1,m2)

# keep m1


m3 <- lmer(forage_days ~ stole + site + longevity + thorax + guard + (1|colony), data = foragers)

AICc(m1,m3)

# keep m1

```

```
m4 <- lmer(forage_days ~ stole + site + longevity + mean_forage_time + guard + (1|colony), data = foragers)
```

```
AICc(m1,m4)
```

```
# keep m1
```

```
m5 <- lmer(forage_days ~ stole + site + thorax + mean_forage_time + guard + (1|colony), data = foragers)
```

```
AICc(m1,m5)
```

```
# keep m5
```

```
# Model assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m5, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m5)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m5))
```

```
qqline(resid(m5))
```

```
# Final Model
```

```
model16 <- lmer(forage_days ~ stole + site + thorax + mean_forage_time + guard + (1|colony), data = foragers)
```

```
summary(model16, ddf="Kenward-Roger")
```

```
## 17. Longevity and Stealing (Gipps)
```

```
# Preliminary plots
```

```
ggplot(data=beesG,
```

```
  aes(x = stole, y = longevity)) +
```

```
  geom_boxplot()+
```

```
  stat_summary(fun.y = "mean",
```

```
  geom = "point",
```

```
  shape = 5, size = 3)
```

```
# Model selection using AICc

m1 <- lm(longevity ~ stole + colony + thorax + mean_forage_time + forage_days + guard, data = beesG)

m2 <- lm(longevity ~ stole + colony + thorax + mean_forage_time + forage_days, data = beesG)

AICc(m1,m2)

# keep m2


m3 <- lm(longevity ~ stole + colony + thorax + mean_forage_time, data = beesG)

AICc(m2,m3)

# keep m3


m4 <- lm(longevity ~ stole + colony + thorax , data = beesG)

AICc(m3,m4)

# keep m4


m5 <- lm(longevity ~ stole + colony , data = beesG)

AICc(m4,m5)

# keep m4


m6 <- lm(longevity ~ stole + thorax , data = beesG)

AICc(m4,m6)

# keep m4


m7 <- lm(longevity ~ colony*stole +thorax , data = beesG)

AICc(m4,m7)

# keep m4


# Check assumptions

plot(m4)


# Square root transformation
```

```
m4a <- lm(sqrt(longevity) ~ stole + colony + thorax , data = beesG)
```

```
# Check assumptions
```

```
plot(m4a)
```

```
# Final Model
```

```
model17 <- lm(sqrt(longevity) ~ stole + colony + thorax , data = beesG)
```

```
summary(model17)
```

```
## 18. Mean foraging time and Stealing (Gipps)
```

```
# Preliminary plots
```

```
ggplot(data=foragersG,  
       aes(x = stole, y = mean_forage_time)) +  
  geom_boxplot()+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lm(mean_forage_time ~ stole + colony + longevity + thorax + forage_days + guard , data = foragersG)
```

```
m2 <- lm(mean_forage_time ~ stole + colony + longevity + thorax + forage_days, data = foragersG)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lm(mean_forage_time ~ stole + colony + longevity + thorax , data = foragersG)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lm(mean_forage_time ~ stole + colony + longevity+ forage_days, data = foragersG)
```

```
AICc(m2,m4)
```

```
# keep m2
```

```

m5 <- lm(mean_forage_time ~ stole + colony + thorax + forage_days, data = foragersG)

AICc(m2,m5)

# keep m2


m6 <- lm(mean_forage_time ~ colony*stole + longevity + thorax + forage_days, data = foragersG)

AICc(m2,m6)

# keep m2


# Check assumptions

par(mfrow=c(2,2))

plot(m2)


# Log transformation

m2a <- lm(log(mean_forage_time) ~ stole + colony + longevity + thorax + forage_days, data = foragersG)

# Check assumptions

plot(m2a)


# Remove outliers

foragersG2 <- subset(foragersG, bee != "7B 17 66 01 0B 00 12 E0" & bee != "7A 17 66 01 0B 00 12 E0" & bee
!= "8D 17 66 01 0B 00 12 E0")


model2b <- lm(log(mean_forage_time) ~ stole + colony + longevity + thorax + forage_days, data = foragersG2)

# Check assumptions

plot(model2b)

# Final Model

model18 <- lm(log(mean_forage_time) ~ stole + colony + longevity + thorax + forage_days, data = foragersG2)

summary(model18)

```

```
## 19. Foraging trips/day and Stealing (Gipps)
```

```
# Preliminary plots
```

```
ggplot(data=foragersG,  
       aes(x = stole, y = forage_days)) +  
  geom_boxplot()+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
ggplot(data=foragersG,  
       aes(x = stole, y = forage_days)) +  
  geom_boxplot()+  
  facet_grid(. ~ colony)+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lm(forage_days ~ stole + colony + longevity + thorax + mean_forage_time + guard, data = foragersG)
```

```
m2 <- lm(forage_days ~ stole + colony + longevity + thorax + mean_forage_time , data = foragersG)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lm(forage_days ~ stole + colony + longevity + thorax , data = foragersG)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lm(forage_days ~ stole + colony + longevity + mean_forage_time , data = foragersG)
```

```
AICc(m2,m4)
```

```
# keep m2
```

```
m5 <- lm(forage_days ~ stole + colony + thorax + mean_forage_time , data = foragersG)
```

```
AICc(m2,m5)
```

```
# keep m2
```

```
m6 <- lm(forage_days ~ stole + longevity + thorax + mean_forage_time , data = foragersG)
```

```
AICc(m2,m6)
```

```
# keep m2
```

```
m7 <- lm(forage_days ~ colony*stole + longevity + thorax + mean_forage_time , data = foragersG)
```

```
AICc(m2,m7)
```

```
# keep m2
```

```
# Check assumptions
```

```
plot(m2)
```

```
# Square root transformation
```

```
m2a <- lm(sqrt(forage_days) ~ stole + colony + longevity + thorax + mean_forage_time , data = foragersG)
```

```
# Check assumptions
```

```
par(mfrow=c(2,2))
```

```
plot(m2a)
```

```
# Final Model
```

```
model19 <- lm(sqrt(forage_days) ~ stole + colony + longevity + thorax + mean_forage_time , data = foragersG)
```

```
summary(model19)
```

```
## 20. Stealing and Thorax (all bees)
```

```
# Preliminary plots
```

```
ggplot(data=thorax,  
       aes(x = stole, y = thorax)) +  
  geom_boxplot()+  
  stat_summary(fun = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- glm(stole ~ thorax + colony + forage_days + longevity + mean_forage_time ,family = binomial  
(link="cloglog"), data=thorax)
```

```
m2 <- glm(stole ~ thorax + colony + forage_days + longevity ,family = binomial (link="cloglog"), data=thorax)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- glm(stole ~ thorax + colony + forage_days,family = binomial (link="cloglog"), data=thorax)
```

```
AICc(m2,m3)
```

```
# keep m3
```

```
m4 <- glm(stole ~ thorax + colony,family = binomial (link="cloglog"), data=thorax)
```

```
AICc(m3,m4)
```

```
# keep m4 (m3 errors)
```

```
# Check assumptions
```

```
glm.diag.plots(m4)
```

```
devresid <- resid(m4, type="deviance")
```

```
hist(devresid)
```

```
# Final Model
```

```
model20 <- glm(stole ~ thorax + colony,family = binomial (link="cloglog"), data=thorax)
```

```
summary(model20)
```

```
## 21. Stealing and Thorax (Gipps)
```

```
# Preliminary plots
```

```
ggplot(data=thoraxG,  
       aes(x = stole, y = thorax)) +  
  geom_boxplot()+  
  stat_summary(fun = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- glm(stole ~ thorax + colony + mean_forage_time + forage_days + longevity,family = binomial  
(link="cloglog"), data=thoraxG)
```

```
m2 <- glm(stole ~ thorax + colony + mean_forage_time + forage_days,family = binomial (link="cloglog"),  
data=thoraxG)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- glm(stole ~ thorax + colony + mean_forage_time ,family = binomial (link="cloglog"), data=thoraxG)
```

```
AICc(m2,m3)
```

```
# keep m3 (m2 error)
```

```
m4 <- glm(stole ~ thorax + colony ,family = binomial (link="cloglog"), data=thoraxG)
```

```
AICc(m3,m4)
```

```
# keep m4
```

```
# Check assumptions
```

```
glm.diag.plots(m4)
```

```
devresid <- resid(m4, type="deviance")
```

```
hist(devresid)
```

```
# Final Model
```

```
model21 <- glm(stole ~ thorax + colony,family = binomial (link="cloglog"), data=thoraxG)
```

```
summary(model21)
```

```
## 22. Longevity and Switched colony
```

```
# Preliminary plots
```

```
ggplot(data=bees,  
       aes(x = switched, y = longevity)) +  
  geom_boxplot()+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
ggplot(data=bees,  
       aes(x = switched, y = longevity)) +  
  geom_boxplot()+  
  facet_grid(. ~ site)+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(longevity ~ site*switched + thorax + mean_forage_time + forage_days+ (1|colony), data = bees)
```

```
m2 <- lmer(longevity ~ site*switched + thorax + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(longevity ~ site*switched + thorax + (1|colony), data = bees)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(longevity ~ site*switched + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m2,m4)
```

```
# keep m2
```

```
m5 <- lmer(longevity ~ switched + site + thorax + mean_forage_time + (1|colony), data = bees)
```

```
AICc(m2,m5)
```

```
# keep m2
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m2, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m2)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m2))
```

```
qqline(resid(m2))
```

```
# Square root transformation
```

```
m2a <- lmer(sqrt(longevity) ~ site*switched + thorax + mean_forage_time + (1|colony), data = bees)
```

```
# Check assumptions
```

```
sresid <- resid(m2a, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m2a)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m2a))
```

```
qqline(resid(m2a))
```

```
# Final Model
```

```
model22 <- lmer(sqrt(longevity) ~ site*switched + thorax + mean_forage_time + (1|colony), data = bees)
```

```
## 23. Mean foraging time and Switched colony
```

```
# Preliminary plots
```

```
ggplot(data=foragers,  
       aes(x = switched, y = mean_forage_time)) +  
  geom_boxplot()+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
ggplot(data=foragers,  
       aes(x = switched, y = mean_forage_time)) +  
  geom_boxplot()+  
  facet_grid(. ~ site)+  
  stat_summary(fun.y = "mean",  
              geom = "point",  
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(mean_forage_time ~ site*switched + thorax + longevity + forage_days + guard + (1|colony),  
data=foragers)
```

```
m2 <- lmer(mean_forage_time ~ site*switched + thorax + longevity + forage_days + (1|colony), data=foragers)  
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(mean_forage_time ~ site*switched + thorax + longevity + (1|colony), data=foragers)  
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(mean_forage_time ~ site*switched + thorax + forage_days + (1|colony), data=foragers)
```

```
AICc(m2,m4)
```

```
# keep m4
```

```
m5 <- lmer(mean_forage_time ~ site*switched + forage_days + (1|colony), data=foragers)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m6 <- lmer(mean_forage_time ~ switched + site + thorax + forage_days + (1|colony), data=foragers)
```

```
AICc(m4,m6)
```

```
# keep m6
```

```
# Check assumptions
```

```
par(mfrow=c(3,3))
```

```
sresid <- resid(m6, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m6)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m6))
```

```
qqline(resid(m6))
```

```
# Square root transformation
```

```
m1 <- lmer(sqrt(mean_forage_time) ~ site*switched + thorax + longevity + forage_days + guard + (1|colony),  
data=foragers)
```

```
m2 <- lmer(sqrt(mean_forage_time) ~ site*switched + thorax + longevity + forage_days + (1|colony),  
data=foragers)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(sqrt(mean_forage_time) ~ site*switched + thorax + forage_days + (1|colony), data=foragers)
```

```
AICc(m2,m3)
```

```

# keep m3

m4 <- lmer(sqrt(mean_forage_time) ~ site*switched + forage_days + (1|colony), data=foragers)

AICc(m3,m4)

# keep m4

m5 <- lmer(sqrt(mean_forage_time) ~ switched + site + forage_days + (1|colony), data=foragers)

AICc(m4,m5)

# keep m5

m5 <- lmer(sqrt(mean_forage_time) ~ switched + site + forage_days + (1|colony), data=foragers)

# Check assumptions

sresid <- resid(m5, type = "pearson")

hist(sresid)

fits <- fitted(m5)

plot(sresid ~ fits)

qqnorm(resid(m5))

qqline(resid(m5))

# Final Model

model23 <- lmer(sqrt(mean_forage_time) ~ switched + site + forage_days + (1|colony), data=foragers)

summary(model23, ddf="Kenward-Roger")

## 24. Foraging trips/day and Switched colony

# Preliminary plots

ggplot(data=bees,

       aes(x = switched, y = forage_days)) +

  geom_boxplot()+

  stat_summary(fun.y = "mean",

```

```
geom = "point",  
shape = 5, size = 3)
```

```
ggplot(data=bees,  
aes(x = switched, y = forage_days)) +  
geom_boxplot()+  
facet_grid(. ~ site)+  
stat_summary(fun.y = "mean",  
geom = "point",  
shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- lmer(forage_days ~ site*switched + thorax + longevity + mean_forage_time + guard + (1|colony),  
data=foragers)
```

```
m2 <- lmer(forage_days ~ site*switched + thorax + longevity + mean_forage_time + (1|colony), data=foragers)
```

```
AICc(m1,m2)
```

```
# keep m1
```

```
m3 <- lmer(forage_days ~ site*switched + thorax + longevity + guard + (1|colony), data=foragers)
```

```
AICc(m1,m3)
```

```
# keep m1
```

```
m4 <- lmer(forage_days ~ site*switched + thorax + mean_forage_time + guard + (1|colony), data=foragers)
```

```
AICc(m1,m4)
```

```
# keep m4
```

```
m5 <- lmer(forage_days ~ site*switched + mean_forage_time + guard + (1|colony), data=foragers)
```

```
AICc(m4,m5)
```

```
# keep m4
```

```
m6 <- lmer(forage_days ~ switched + site + thorax + mean_forage_time + guard + (1|colony), data=foragers)
```

```
AICc(m4,m6)
```

```
# keep m4
```

```
m4 <- lmer(forage_days ~ site*switched + thorax + mean_forage_time + guard + (1|colony), data=foragers)
```

```
# Check assumptions
```

```
par(mfrow=c(2,3))
```

```
sresid <- resid(m4, type = "pearson")
```

```
hist(sresid)
```

```
fits <- fitted(m4)
```

```
plot(sresid ~ fits)
```

```
qqnorm(resid(m4))
```

```
qqline(resid(m4))
```

```
# Square root transformation
```

```
m1 <- lmer(sqrt(forage_days) ~ site*switched + thorax + longevity + mean_forage_time + guard + (1|colony),  
data=foragers)
```

```
m2 <- lmer(sqrt(forage_days) ~ site*switched + thorax + longevity + mean_forage_time + (1|colony),  
data=foragers)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- lmer(sqrt(forage_days) ~ site*switched + thorax + longevity + (1|colony), data=foragers)
```

```
AICc(m2,m3)
```

```
# keep m2
```

```
m4 <- lmer(sqrt(forage_days) ~ site*switched + thorax + mean_forage_time + (1|colony), data=foragers)
```

```
AICc(m2,m4)
```

```
# keep m4
```

```

m5 <- lmer(sqrt(forage_days) ~ site*switched + mean_forage_time + (1|colony), data=foragers)

AICc(m4,m5)

# keep m4


m6 <- lmer(sqrt(forage_days) ~ switched + site + thorax + mean_forage_time + (1|colony), data=foragers)

AICc(m4,m6)

# keep m6


# Check assumptions

sresid <- resid(m6, type = "pearson")

hist(sresid)

fits <- fitted(m6)

plot(sresid ~ fits)

qqnorm(resid(m6))

qqline(resid(m6))


# Final Model

model24 <- lmer(sqrt(forage_days) ~ switched + site + thorax + mean_forage_time + (1|colony), data=foragers)

summary(model24)


## 25. Switched colony and Thorax

# Preliminary plots

ggplot(data=thorax,

      aes(x = switched, y = thorax)) +

      geom_boxplot()+

      stat_summary(fun = "mean",

      geom = "point",

      shape = 5, size = 3)

```

```
ggplot(data=thorax,
       aes(x = switched, y = thorax)) +
  geom_boxplot()+
  facet_grid(. ~ site)+
  stat_summary(fun = "mean",
              geom = "point",
              shape = 5, size = 3)
```

```
# Model selection using AICc
```

```
m1 <- glmer(switched ~ thorax + longevity + mean_forage_time + forage_days + (1|colony), family = binomial
(link="cloglog"), data = thorax)
```

```
m2 <- glmer(switched ~ thorax + longevity + mean_forage_time + (1|colony), family = binomial
(link="cloglog"), data = thorax)
```

```
AICc(m1,m2)
```

```
# keep m2
```

```
m3 <- glmer(switched ~ thorax + longevity + (1|colony), family = binomial (link="cloglog"), data = thorax)
```

```
AICc(m2,m3)
```

```
# keep m3
```

```
# Check assumptions
```

```
devresid <- resid(model25, type="deviance")
```

```
hist(devresid)
```

```
# Final Model
```

```
model25 <- glmer(switched ~ thorax + longevity + (1|colony), family = binomial (link="cloglog"), data =
thorax)
```

```
### MAIN PLOTS ###
```

```
## 1. Guarding and Longevity
```

```
bees_summary1 <- bees %>%
```

```

group_by(guard) %>%

summarise(mlongev = mean(longevity),

          sd_mlongev = sd(longevity),

          n_mlongev = n(),

          SE_mlongev = sd(longevity)/sqrt(n()))

p1 <- ggplot(bees_summary1, aes(guard, mlongev)) +

  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"), width=0.8)+

  geom_errorbar(aes(ymin = mlongev - sd_mlongev,

                    ymax = mlongev + sd_mlongev), width=0.2)+

  theme_bw()+

  labs(x="", y="Mean Longevity (days)")+

  scale_x_discrete(labels=c("Not Guards", "Guards"))+

  scale_y_continuous(limits=c(0,30.3), expand = c(0, 0))+

  theme(axis.text=element_text(size=22),

        axis.title=element_text(size=22))

```

2. Guarding and No. foraging trips

```

bees_summary2 <- bees %>%

  group_by(guard) %>%

  summarise(mtrips = mean(forage_days),

            sd_mtrips = sd(forage_days),

            n_mtrips = n(),

            SE_mtrips = sd(forage_days)/sqrt(n()))

p2 <- ggplot(bees_summary2, aes(guard, mtrips, fill=c("steelblue1", "tomato1"))) +

  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"), width=0.8)+

  geom_errorbar(aes(ymin = mtrips - sd_mtrips,

                    ymax = mtrips + sd_mtrips), width=0.2)+

  theme_bw()+

```

```

labs(x="",y="Mean No. Foraging Trips per Day")+
scale_x_discrete(labels=c("Not Guards", "Guards"))+
scale_y_continuous(limits=c(0,15.3),expand = c(0, 0))+
theme(axis.text=element_text(size=22),
axis.title=element_text(size=22))

```

```

plot_grid(p1, p2, labels=c("a", "b"),label_size = 20, hjust = -0.3, ncol = 2, nrow = 1)

```

3. Gipps stealing and Mean foraging

```

bees_summary3 <- foragersG %>%
  group_by(stole) %>%
  summarise(mforage = mean(mean_forage_time),
            sd_mforage = sd(mean_forage_time),
            n_mforage = n(),
            SE_mforage = sd(mean_forage_time)/sqrt(n()))

```

```

p3 <- ggplot(bees_summary3, aes(stole, mforage, fill=c("steelblue1","tomato1")))+
  geom_col(show.legend = FALSE, fill=c("skyblue1","steelblue4"),width=0.8)+
  geom_errorbar(aes(ymin = mforage - sd_mforage,
ymax = mforage + sd_mforage), width=0.2)+
  theme_bw()+
  labs(x="",y="Mean Length of Foraging Trip (hrs)")+
  scale_x_discrete(labels=c("Not Stealing", "Stealing"))+
  scale_y_continuous(limits=c(0,2.04),expand = c(0, 0))+
  theme(axis.text=element_text(size=22),
axis.title=element_text(size=22))

```

4. Gipps stealing and No. foraging trips

```

bees_summary4 <- beesG %>%
  group_by(stole) %>%

```

```

summarise(mtrips = mean(forage_days),

          sd_mtrips = sd(forage_days),

          n_mtrips = n(),

          SE_mtrips = sd(forage_days)/sqrt(n()))

p4 <- ggplot(bees_summary4, aes(stole, mtrips, fill=c("steelblue1","tomato1"))) +

  geom_col(show.legend = FALSE, fill=c("skyblue1","steelblue4"),width=0.8)+

  geom_errorbar(aes(ymin = mtrips - sd_mtrips,

ymax = mtrips + sd_mtrips), width=0.2)+

  theme_bw()+

  labs(x="",y="Mean No. Foraging Trips per Day")+

  scale_x_discrete(labels=c("Not Stealing", "Stealing"))+

  scale_y_continuous(limits=c(0,15.3),expand = c(0, 0))+

  theme(axis.text=element_text(size=22),

        axis.title=element_text(size=22))

plot_grid(p3, p4, labels=c("a)", "b)"),label_size = 20, hjust = -0.3, ncol = 2, nrow = 1)

```

APPENDIX PLOTS

1. Guarding and Thorax

```

bees_summary5 <- thorax %>%

  group_by(guard) %>%

  summarise(mthorax = mean(thorax),

            sd_mthorax = sd(thorax),

            n_mthorax = n(),

            SE_mthorax = sd(thorax)/sqrt(n()))

p5 <- ggplot(bees_summary5, aes(guard, mthorax)) +

  geom_col(show.legend = FALSE, fill=c("skyblue1","steelblue4"),width=0.8)+

  geom_errorbar(aes(ymin = mthorax - sd_mthorax,

```

```

ymax = mthorax + sd_mthorax), width=0.2)+
theme_bw()+
labs(x="",y="Mean Thorax Width (mm)")+
scale_x_discrete(labels=c("Not Guards", "Guards"))+
scale_y_continuous(limits=c(0,8.1),expand = c(0, 0))+
theme(axis.text=element_text(size=22),
axis.title=element_text(size=22))

```

2. Guarding and Mean Foraging time

```

bees_summary6 <- foragers %>%
  group_by(guard) %>%
  summarise(mforage = mean(mean_forage_time),
            sd_mforage = sd(mean_forage_time),
            n_mforage = n(),
            SE_mforage = sd(mean_forage_time)/sqrt(n()))

p6 <- ggplot(bees_summary6, aes(guard, mforage, fill=c("steelblue1","tomato1")) +
  geom_col(show.legend = FALSE, fill=c("skyblue1","steelblue4"),width=0.8)+
  geom_errorbar(aes(ymin = mforage - sd_mforage,
ymax = mforage + sd_mforage), width=0.2)+
  theme_bw()+
  labs(x="",y="Mean Length of Foraging Trip (hrs)")+
  scale_x_discrete(labels=c("Not Guards", "Guards"))+
  scale_y_continuous(limits=c(0,2.04),expand = c(0, 0))+
  theme(axis.text=element_text(size=22),
axis.title=element_text(size=22))

```

```

plot_grid(p5, p6, labels=c("a)", "b)"),label_size = 20, hjust = -0.3, ncol = 2, nrow = 1)

```

3. Gipps Stealing and Thorax

```

bees_summary7 <- thoraxG %>%

  group_by(stole) %>%

  summarise(mthorax = mean(thorax),

            sd_mthorax = sd(thorax),

            n_mthorax = n(),

            SE_mthorax = sd(thorax)/sqrt(n()))

p7 <- ggplot(bees_summary7, aes(stole, mthorax)) +

  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"),width=0.8)+

  geom_errorbar(aes(ymin = mthorax - sd_mthorax,

ymax = mthorax + sd_mthorax), width=0.2)+

  theme_bw()+

  labs(x="",y="Mean Thorax Width (mm)")+

  scale_x_discrete(labels=c("Not Stealing", "Stealing"))+

  scale_y_continuous(limits=c(0,8.1),expand = c(0, 0))+

  theme(axis.text=element_text(size=22),

axis.title=element_text(size=22))

```

4. Gipps Stealing and Longevity

```

bees_summary8 <- beesG %>%

  group_by(stole) %>%

  summarise(mlongev = mean(longevity),

            sd_mlongev = sd(longevity),

            n_mlongev = n(),

            SE_mlongev = sd(longevity)/sqrt(n()))

p8 <- ggplot(bees_summary8, aes(stole, mlongev)) +

  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"),width=0.8)+

  geom_errorbar(aes(ymin = mlongev - sd_mlongev,

ymax = mlongev + sd_mlongev), width=0.2)+

```

```

theme_bw()+

labs(x="",y="Mean Longevity (days)")+

scale_x_discrete(labels=c("Not Stealing", "Stealing"))+

scale_y_continuous(limits=c(0,30.3),expand = c(0, 0))+

theme(axis.text=element_text(size=22),

axis.title=element_text(size=22))

```

```

plot_grid(p7, p8, labels=c("a", "b"),label_size = 20, hjust = -0.3, ncol = 2, nrow = 1)

```

5. Switching and Thorax

```

bees_summary9 <- thorax %>%

  group_by(switched) %>%

  summarise(mthorax = mean(thorax),

            sd_mthorax = sd(thorax),

            n_mthorax = n(),

            SE_mthorax = sd(thorax)/sqrt(n()))

```

```

p9 <- ggplot(bees_summary9, aes(switched, mthorax)) +

  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"),width=0.8)+

  geom_errorbar(aes(ymin = mthorax - sd_mthorax,

ymax = mthorax + sd_mthorax), width=0.2)+

  theme_bw()+

  labs(x="",y="Mean Thorax Width (mm)")+

  scale_x_discrete(labels=c("Stayed", "Switched"))+

  scale_y_continuous(limits=c(0,8.1),expand = c(0, 0))+

  theme(axis.text=element_text(size=15.4),

axis.title=element_text(size=15.4))

```

6. Switching and Longevity

```

bees_summary10 <- bees %>%

```

```

group_by(switched) %>%
summarise(mlongev = mean(longevity),
          sd_mlongev = sd(longevity),
          n_mlongev = n(),
          SE_mlongev = sd(longevity)/sqrt(n()))

p10 <- ggplot(bees_summary10, aes(switched, mlongev)) +
  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"), width=0.8)+
  geom_errorbar(aes(ymin = mlongev - sd_mlongev,
                    ymax = mlongev + sd_mlongev), width=0.2)+
  theme_bw()+
  labs(x="", y="Mean Longevity (days)")+
  scale_x_discrete(labels=c("Stayed", "Switched"))+
  scale_y_continuous(limits=c(0,25.3), expand = c(0, 0))+
  theme(axis.text=element_text(size=15.4),
        axis.title=element_text(size=15.4))

## 7. Switching and Mean foraging time

bees_summary11 <- foragers %>%
  group_by(switched) %>%
  summarise(mforage = mean(mean_forage_time),
            sd_mforage = sd(mean_forage_time),
            n_mforage = n(),
            SE_mforage = sd(mean_forage_time)/sqrt(n()))

p11 <- ggplot(bees_summary11, aes(switched, mforage, fill=c("steelblue1", "tomato1"))) +
  geom_col(show.legend = FALSE, fill=c("skyblue1", "steelblue4"), width=0.8)+
  geom_errorbar(aes(ymin = mforage - sd_mforage,
                    ymax = mforage + sd_mforage), width=0.2)+

```

```

theme_bw()+

labs(x="",y="Mean Length of Foraging
Trip (hrs)")+

scale_x_discrete(labels=c("Stayed", "Switched"))+

scale_y_continuous(limits=c(0,2.04),expand = c(0, 0))+

theme(axis.text=element_text(size=15.4),

axis.title=element_text(size=15.4))

```

8. Switching and No. foraging trips

```

bees_summary12 <- bees %>%

  group_by(switched) %>%

  summarise(mtrips = mean(forage_days),

            sd_mtrips = sd(forage_days),

            n_mtrips = n(),

            SE_mtrips = sd(forage_days)/sqrt(n()))

p12 <- ggplot(bees_summary12, aes(switched, mtrips, fill=c("steelblue1","tomato1"))) +

  geom_col(show.legend = FALSE, fill=c("skyblue1","steelblue4"),width=0.8)+

  geom_errorbar(aes(ymin = mtrips - sd_mtrips,

ymax = mtrips + sd_mtrips), width=0.2)+

  theme_bw()+

  labs(x="",y="Mean No. Foraging Trips
per Day")+

  scale_x_discrete(labels=c("Stayed", "Switched"))+

  scale_y_continuous(limits=c(0,15.3),expand = c(0, 0))+

  theme(axis.text=element_text(size=15.4),

axis.title=element_text(size=15.4))

```

```

plot_grid(p9, p10, p11, p12, labels=c("a)", "b)", "c)", "d)"),label_size = 14, vjust = 0.9,hjust = -0.3, ncol = 2,
nrow = 2)

```