Code for 'Carry-over effects of larval microclimate on the transmission potential of a mosquito-borne pathogen' (Evans et al. 2017)

Michelle Evans

This document contains the code for the analysis of mosquito population and infection data in 'Carry-over effects of larval microclimate on the transmission potential of a mosquito-borne pathogen' (Evans et al. 2017).

Paper Citation:

Evans MV, Shiau JC, Solano N, Brindley MA, Drake JM, Murdock, CC. 2017. Carry-over effects of larval microclimate on the transmission potential of a mosquito-borne pathogen.

Set-Up

NOTE: Working directory should be set to source file location.

```
library(xtable)
library(tidyr)
library(ggplot2)
library(lme4) #mixed models
library(broom) #easy model comparison
library(MuMIn)
library(car)
library(MASS)
library(gridExtra) #for facet grids later
library(cowplot)
library(caret)
library(ggthemes)
library(dplyr)
library(multcomp)

colR <- "dodgerblue"
colS <- "gray60"
colU <- "maroon"

axisColor <- errorColor <- "gray40"
```

Data Loading and Formatting

Load and format infection data:

```
formatData <- function(month){
  #' format infection data
  #' @params month (ie. "august")
  #' @returns dataframe of properly formatted data
  #adjust wingLength
  monthDf <- read.csv(paste0("../data/infections/raw/", month,"Dengue.csv"))
```

```
  #convert wingLength and drop extra columns
  monthDf$Wing <- monthDf$WingLength*monthDf$conversion..mm.bar.
  monthDf <- dplyr::select(monthDf, -WingLength, -conversion..mm.bar.)

  #dpi as factor
  monthDf$DPI <- as.factor(monthDf$DPI)

  #add in class and site
  monthDf$site <- as.factor(substr(as.character(monthDf$Individual), 1, 2))
  monthDf$class <- NULL
  for (i in 1:nrow(monthDf)){
    if (substr(monthDf$site[i], 1,1)=="R"){
    monthDf$class[i] <- "Rural"
    } else if (substr(monthDf$site[i], 1,1)=="S"){
    monthDf$class[i] <- "Suburban"
    } else if (substr(monthDf$site[i], 1,1)=="U"){
    monthDf$class[i] <- "Urban"
    }
  }
  monthDf$class <- as.factor(monthDf$class)

  #convert Y and N to 1 and 0 for statistics
  levels(monthDf$Body) <- c("NA", 0, 1)
  monthDf$Body <- as.numeric(as.character(monthDf$Body))
  levels(monthDf$Saliva) <- c("NA", 0, 1)
  monthDf$Saliva <- as.numeric(as.character(monthDf$Saliva))
  # august had no contaminated heads, so different corrections
  if (month=="august"){
    levels(monthDf$Head) <- c(0, 1)
  } else levels(monthDf$Head) <- c("NA",0, 1)
  monthDf$Head <- as.numeric(as.character(monthDf$Head))

  ##Fix false negatievs
  #adjust so that if saliva is positive, so is head
  #ddjust so that is head is positive, so is body
  monthDf$Head[monthDf$Saliva>0] <- 1
  monthDf$Body[monthDf$Head>0] <- 1

  return(monthDf)
}

august <- formatData("august")
oct <- formatData("october")
seasons <- rbind(august,oct)
seasons$block <- as.factor(c(rep("summer", nrow(august)), rep("fall", nrow(oct))))

seasonSumm <- seasons %>%
  filter(DPI==21) %>%
  #drop individual
  dplyr::select(-Individual, -site, -Wing, -DPI) %>%
  group_by(block, class) %>%
  summarise_all(funs(mean(.,na.rm=T),sd(.,na.rm=T),se=(sd(., na.rm=T)/sqrt(n())))) %>%
  ungroup()
```

Load and format microclimate data

```
climate <- read.csv('../data/microclimate/clean/2016TrialsAdult.csv')[,-1]
#toss out ridiculous levels
climate <- climate[climate$Temp<75,]
#format date
climate$Date <- strptime(climate$Date, format="%Y-%m-%d %H:%M:%S")
#draw out day
climate$Day <- as.Date(climate$Date)

# add tray id to climate data
trayID <- read.csv("../data/microclimate/trayLoggerID.csv") #read in IDs
climate <- merge(climate, trayID, by="Pot_ID")

#fix duplicates for R1T1
climate <- unique(climate)

#U2T2 and U1T2 are missing data
# range(climate[climate$Tray_ID=="U2T2", 'Date'])
# range(climate[climate$Tray_ID=="U1T2", 'Date'])

#drop U2T2 becuase it only has data until August 5th
inds <- which(climate$Tray_ID=="U2T2")
climate <- climate[-inds,]
rm(inds)

#U2T4 wasn't working right, reporting temps above 40C in October
inds <- which(climate$Tray_ID=="U2T4")
climate <- climate[-inds,]
rm(inds)
```

Load and format emergence data

```
augEmerg <- read.csv("../data/emergence/raw/AugustEmergence.csv")
augEmerg$block <- as.factor("summer")
octEmerg <- read.csv("../data/emergence/raw/OctoberEmergence.csv")
octEmerg$block <- as.factor("fall")

allEmerg <- rbind(augEmerg, octEmerg)
```

Subset and standardize emergence data to be used with infections (i.e. weight by number of days mosquitoes were in larval environment)

```
#filter out only days when infected mosquitoes were in the trays
octInf <- octEmerg %>%
  filter(Sex=="F") %>%
  filter((Site_Code %in% c("U3", "R3") & Day <= 21) |
           (Site_Code %in% c("U2", "U1", "S3") & Day <= 20) |
           (Site_Code %in% c("S1", "S2", "R1", "R2") & Day <= 24))

augInf <- augEmerg %>%
  filter(Sex=="F") %>%
    filter((Site_Code %in% c("U2", "U1", "S3", "R1") & Day <= 14) |
           (Site_Code %in% c("S1", "S2", "R2", "R3", "U3") & Day <= 17))
```

```
octClim <- climate %>%
  dplyr::select(-Date) %>%
  filter(Day >= as.Date("2016-09-26","%Y-%m-%d")) %>%
  #filter out appropriate days
  filter((Site_ID %in% c("U3", "R3") & Day <= "2016-10-21") |
           (Site_ID %in% c("U2", "U1", "S3") & Day <= "2016-10-20") |
           (Site_ID %in% c("S1", "S2", "R1", "R2") & Day <= "2016-10-24")) %>%
  dplyr::select(-Site_ID, -Pot_ID, -Class) %>%
  #get daily averages by Tray
  group_by(Tray_ID, Day) %>%
  summarise_all(funs(mean(., na.rm=T), min(., na.rm=T), max(., na.rm=T))) %>%
  #calculate DTR
  mutate(DTR=Temp_max-Temp_min) %>%
  #get overall average over study period per tray (average daily values)
  ungroup() %>%
  dplyr::select(-Day) %>%
  group_by(Tray_ID) %>%
  summarise_all(funs(mean))

##new method of weighting climate by expanded infection
octInfExp <- octInf[rep(seq.int(1,nrow(octInf)), octInf$Num_Emerge),]
test <- merge(octInfExp, octClim, by.x="Tray_Code", by.y="Tray_ID", all.x=T)

octEnvVar <- test %>%
  dplyr::select(-Tray_Code,-Site, -Tray, - Class, - Month, - Day, - Exp_Day, - Sex, -Num_Emerge) %>%
  group_by(block,Site_Code) %>%
  summarise_all(funs(mean(.,na.rm=T),se=(sd(., na.rm=T)/sqrt(n()))))


rm(test) #clear unused temporary dataframe
```

```
##repeat above for August
augClim <- climate %>%
  dplyr::select(-Date) %>%
  filter(Day >= as.Date("2016-08-01","%Y-%m-%d")) %>%
    filter((Site_ID %in% c("U2", "U1", "S3", "R1") & Day <= "2016-08-14") |
           (Site_ID %in% c("S1", "S2", "R2", "R3", "U3") & Day <= "2016-08-17")) %>%
  dplyr::select(-Site_ID, -Pot_ID, -Class) %>%
  #get daily averages by Tray
  group_by(Tray_ID, Day) %>%
  summarise_all(funs(mean(., na.rm=T), min(., na.rm=T), max(., na.rm=T))) %>%
  #calculate DTR
  mutate(DTR=Temp_max-Temp_min) %>%
  #get overall average over study period per tray (average daily values)
  ungroup() %>%
  dplyr::select(-Day) %>%
  group_by(Tray_ID) %>%
  summarise_all(funs(mean))

##new method of weighting climate by expanded infection
augInfExp <- augInf[rep(seq.int(1,nrow(augInf)), augInf$Num_Emerge),]
test <- merge(augInfExp, augClim, by.x="Tray_Code", by.y="Tray_ID", all.x=T)

augEnvVar <- test %>%
```

```
  dplyr::select(-Tray_Code,-Site, -Tray, - Class, - Month, - Day, - Exp_Day, - Sex, -Num_Emerge) %>%
  group_by(block,Site_Code) %>%
  summarise_all(funs(mean(.,na.rm=T),se=(sd(., na.rm=T)/sqrt(n()))))

rm(test)
```

```
#merge the summer and fall into one dataframe
oct$block <- as.factor("fall")
august$block <- as.factor("summer")
seasonInf <- merge(rbind(oct, august[august$DPI=="21",]), rbind(augEnvVar,octEnvVar), by.x=c("block", "s
```

Infection Dynamics

Infection by Class and Season

Make data long

```
infLong <- seasonInf %>%
  gather(type, infection, Body:Saliva) %>%
  dplyr::select(block, class, site, Individual, type, infection) %>%
  dplyr::group_by(block, class, type, site) %>%
  summarise(mean.inf=mean(infection, na.rm=T), sampleSize=sum(!is.na(infection)), positive=sum(infection
  group_by(block, class, type) %>%
  summarise(se.inf=sd(mean.inf, na.rm=T)/n(), mean.inf=mean(mean.inf), samples=sum(sampleSize), positive
  ungroup() %>%
  mutate(stripLabel=case_when(
    type=="Body" ~ "Infected",
    type=="Head" ~ "Disseminated",
    type=="Saliva" ~ "Infectious"
  ))
infLong$sampleLab <- paste0(infLong$positives, "(", infLong$samples, ")")
```

Figure 4.

```
#pdf(file="figures/forMS/landclassXseasonInfection.pdf", width = 4, height=7,  family="sans")

ggplot(data=infLong[order(infLong$block, decreasing=F),], aes(x=class, group=block))+
  geom_bar(stat="identity", aes(y=mean.inf, alpha=block, fill=class, color=factor(class)), position=posi
  #geom_text(aes(label=sampleLab, y=mean.inf), vjust=-2, color="black", position=position_dodge(width=-
  facet_wrap(~factor(stripLabel, levels=c("Infected", "Disseminated", "Infectious")), nrow=3, dir="v", s
  scale_y_continuous(breaks=c(0,0.5,1), minor_breaks = c(0.25, 0.75), labels=c("0%", "50%", "100%"), lim
  #ylim(0,1)+
  scale_fill_manual(values=c(colR, colS, colU))+
  scale_color_manual(values=c(colR, colS, colU))+
  scale_alpha_discrete(range=c(0,1), name="Season", labels=c("Fall", "Summer"))+
  geom_errorbar(aes(ymin=mean.inf-se.inf, ymax=mean.inf+se.inf), width=0.2, color=errorColor, position =
  xlab("Land Class") +
  ylab("Percent Positive") +
  guides(fill=F, color= F,
         alpha=guide_legend(override.aes=list(color=axisColor), reverse=T)) +
  theme_fivethirtyeight() +
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
```

```
        legend.key = element_blank(),
        panel.grid.major.x = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        axis.title = element_text(),
        axis.title.x = element_text(),
        axis.title.y=element_text(),
        #strip.background = element_blank(),
        strip.text.x = element_text(size=12),
        axis.line=element_line(color=axisColor, size=0.5),
        panel.grid = element_blank(),
        axis.text.y=element_text(size=12),
        axis.text.x=element_text(size=12))

#dev.off()
```

Statistics on infection by season and land class

Body model selection

```
#create all the models
m0 <- glmer(Body~1 + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m1 <- glmer(Body~block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m2 <- glmer(Body~class +  (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m3 <- glmer(Body~class + block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m4 <- glmer(Body~class*block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))

modelSums <- do.call(rbind, lapply(list(m0,m1,m2,m3, m4), broom::glance)) #m3 is best

AICc(m0,m1,m2,m3,m4) #still 3
```

```
##    df     AICc
## m0  2 435.5883
## m1  3 426.0884
## m2  4 428.7311
## m3  5 417.7706
## m4  7 419.9622
```

```
Weights(AICc(m0,m1,m2,m3,m4))
```

```
## [1] 9.982942e-05 1.153806e-02 3.078070e-03 7.384377e-01 2.468464e-01
```

```
#create all the models
m0 <- glmer(Head~1 + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
```

```
m1 <- glmer(Head~block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m2 <- glmer(Head~class +  (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m3 <- glmer(Head~class + block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m4 <- glmer(Head~class*block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))

modelSums <- do.call(rbind, lapply(list(m0,m1,m2,m3, m4), broom::glance)) #model 3 is best

AICc(m0,m1,m2,m3,m4)
```

```
##    df     AICc
## m0  2 431.6814
## m1  3 419.6907
## m2  4 427.6540
## m3  5 414.1413
## m4  7 417.3718
```

```
tidy(m3)
```

```
##                   term      estimate std.error statistic      p.value group
## 1          (Intercept)  2.817563e-01 0.2342544  1.202779 0.2290617845 fixed
## 2        classSuburban  3.523897e-01 0.2867938  1.228721 0.2191763368 fixed
## 3           classUrban -7.675402e-01 0.2933131 -2.616795 0.0088759581 fixed
## 4          blocksummer -9.375460e-01 0.2416696 -3.879454 0.0001046913 fixed
## 5 sd_(Intercept).site  2.255814e-07        NA        NA           NA  site
```

```
#create all the models
m0 <- glmer(Saliva~1 + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m1 <- glmer(Saliva~block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m2 <- glmer(Saliva~class +  (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m3 <- glmer(Saliva~class + block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m4 <- glmer(Saliva~class*block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
m5 <- glmer(Saliva~ 1 + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit")) #null model

modelSums <- do.call(rbind, lapply(list(m0, m1,m2,m3, m4, m5), broom::glance)) #model 1 is best (basica
```

```r
AICc(m0, m1,m2,m3,m4, m5) #model 1
```

```
##    df     AICc
## m0  2 216.2245
## m1  3 214.1310
## m2  4 219.1221
## m3  5 217.1499
## m4  7 221.0126
## m5  2 216.2245
```

```r
tidy(m1)
```

```
##                  term   estimate std.error statistic      p.value group
## 1         (Intercept) -2.6473436 0.3430712 -7.716600 1.194739e-14 fixed
## 2         blocksummer  0.7827283 0.3988372  1.962526 4.970127e-02 fixed
## 3 sd_(Intercept).site  0.1700891        NA        NA           NA  site
```

```r
mixModelseasonsBody21 <- lme4::glmer(Body~class + block + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
summary(mixModelseasonsBody21)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: Body ~ class + block + (1 | site)
##    Data: seasons[seasons$DPI == "21", ]
##
##      AIC      BIC   logLik deviance df.resid
##    417.6    436.4   -203.8    407.6      311
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5779 -0.8367 -0.5458  0.9716  1.8323
##
## Random effects:
##  Groups Name        Variance  Std.Dev.
##  site   (Intercept) 6.524e-15 8.077e-08
## Number of obs: 316, groups:  site, 9
##
## Fixed effects:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)     0.4917     0.2368   2.077 0.037846 *
## classSuburban   0.4205     0.2886   1.457 0.145130
## classUrban     -0.8483     0.2892  -2.933 0.003360 **
## blocksummer    -0.8546     0.2407  -3.551 0.000384 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) clssSb clssUr
## classSubrbn -0.540
## classUrban  -0.644  0.464
## blocksummer -0.544 -0.069  0.123
```

```r
tidy(mixModelseasonsBody21)
```

```
##                   term      estimate std.error statistic      p.value group
## 1          (Intercept)  4.917107e-01 0.2367960  2.076517 0.0378462050 fixed
## 2        classSuburban  4.205379e-01 0.2886423  1.456952 0.1451296729 fixed
## 3           classUrban -8.482715e-01 0.2892454 -2.932706 0.0033602215 fixed
## 4          blocksummer -8.546034e-01 0.2406755 -3.550854 0.0003839835 fixed
## 5 sd_(Intercept).site  8.076923e-08        NA        NA           NA  site
```

```r
car::Anova(mixModelseasonsBody21) #Wald test
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Body
##        Chisq Df Pr(>Chisq)
## class 18.733  2  8.553e-05 ***
## block 12.609  1   0.000384 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#confint(mixModelseasonsBody21) #profiled confidence interval
drop1(mixModelseasonsBody21, test="Chisq") #Likelihood ratio test
```

```
## Single term deletions
##
## Model:
## Body ~ class + block + (1 | site)
##        Df    AIC    LRT   Pr(Chi)
## <none>    417.58
## class   2 426.01 12.434 0.0019948 **
## block   1 428.60 13.025 0.0003073 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
summary(multcomp::glht(mixModelseasonsBody21, linfct = multcomp::mcp(class = "Tukey"), test = multcomp:
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Body ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                         Estimate Std. Error z value Pr(>|z|)
## Suburban - Rural == 0     0.4205     0.2886   1.457  0.31174
## Urban - Rural == 0       -0.8483     0.2892  -2.933  0.00931 **
## Urban - Suburban == 0    -1.2688     0.2990  -4.243  < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
summary(multcomp::glht(mixModelseasonsBody21, linfct = multcomp::mcp(block = "Tukey"), test = multcomp:
```

```
##
```

```
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Body ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                    Estimate Std. Error z value Pr(>|z|)
## summer - fall == 0  -0.8546     0.2407  -3.551 0.000384 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
mixModelseasonsHead21 <- lme4::glmer(Head~class + block  + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
tidy(mixModelseasonsHead21)
```

```
##                  term      estimate std.error statistic      p.value group
## 1         (Intercept)  2.817563e-01 0.2342544  1.202779 0.2290617845 fixed
## 2       classSuburban  3.523897e-01 0.2867938  1.228721 0.2191763368 fixed
## 3          classUrban -7.675402e-01 0.2933131 -2.616795 0.0088759581 fixed
## 4         blocksummer -9.375460e-01 0.2416696 -3.879454 0.0001046913 fixed
## 5 sd_(Intercept).site  2.255814e-07        NA        NA           NA  site
```

```
car::Anova(mixModelseasonsHead21) #Wald test
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Head
##        Chisq Df Pr(>Chisq)
## class 14.208  2  0.0008220 ***
## block 15.050  1  0.0001047 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#confint(mixModelseasonsHead21) #profiled confidence interval
drop1(mixModelseasonsHead21, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Head ~ class + block + (1 | site)
##        Df    AIC     LRT  Pr(Chi)
## <none>    413.95
## class   2 419.61  9.6653 0.007966 **
## block   1 427.53 15.5772 7.92e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(multcomp::glht(mixModelseasonsHead21, linfct = multcomp::mcp(class = "Tukey"), test = multcomp:
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
```

```
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Head ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                        Estimate Std. Error z value Pr(>|z|)
## Suburban - Rural == 0    0.3524     0.2868   1.229    0.436
## Urban - Rural == 0      -0.7675     0.2933  -2.617    0.024 *
## Urban - Suburban == 0   -1.1199     0.3031  -3.695   <0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
summary(multcomp::glht(mixModelseasonsHead21, linfct = multcomp::mcp(block = "Tukey"), test = multcomp:
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Head ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                     Estimate Std. Error z value Pr(>|z|)
## summer - fall == 0   -0.9375     0.2417  -3.879 0.000105 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
mixModelseasonsSaliva21 <- lme4::glmer(Saliva~block  + (1|site),
                          data=seasons[seasons$DPI=="21",],
                          family=binomial(link="logit"))
tidy(mixModelseasonsSaliva21) #z-test
```

```
##                   term   estimate std.error statistic      p.value group
## 1          (Intercept) -2.6473436 0.3430712 -7.716600 1.194739e-14 fixed
## 2          blocksummer  0.7827283 0.3988372  1.962526 4.970127e-02 fixed
## 3 sd_(Intercept).site  0.1700891        NA        NA           NA  site
```

```
car::Anova((mixModelseasonsSaliva21)) #Wald test
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Saliva
##        Chisq Df Pr(>Chisq)
## block 3.8515  1     0.0497 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
confint(mixModelseasonsSaliva21) #profiled confidence interval
```

```
##                   2.5 %     97.5 %
## .sig01       0.00000000  0.8214351
```

```
## (Intercept) -3.41631136 -2.0450739
## blocksummer  0.02729408  1.6074316
```

```
drop1(mixModelseasonsSaliva21, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Saliva ~ block + (1 | site)
##        Df    AIC    LRT Pr(Chi)
## <none>    214.06
## block   1 216.19 4.1318 0.04208 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#pairwise comparison
summary(multcomp::glht(mixModelseasonsSaliva21, linfct = multcomp::mcp(block = "Tukey"), test = multcomp
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Saliva ~ block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                    Estimate Std. Error z value Pr(>|z|)
## summer - fall == 0   0.7827     0.3988   1.963   0.0497 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Infection Efficiency

Format data for infection efficiency

```
bodyEff <- seasons %>%
  filter(DPI==21) %>%
  #drop individual
  dplyr::select(-Individual, -site, -Wing, -DPI, -Head, -Saliva) %>%
  group_by(block, class) %>%
  summarise(bodyMean=mean(Body,na.rm=T), bodySE=(sd(Body, na.rm=T)/sqrt(n()))) %>%
  ungroup()

headEff <- seasons %>%
  filter(DPI==21) %>%
  filter(Body==1) %>%
  #drop individual
  dplyr::select(-Individual, -site, -Wing, -DPI, -Body, -Saliva) %>%
  group_by(block, class) %>%
  summarise(headMean=mean(Head,na.rm=T),headSE=(sd(Head, na.rm=T)/sqrt(n()))) %>%
  ungroup()
```

```
salEff <-  seasons %>%
  filter(DPI==21) %>%
  filter(Head==1) %>%
  #drop individual
  dplyr::select(-Individual, -site, -Wing, -DPI, -Head, -Body) %>%
  group_by(block, class) %>%
  summarise(salMean=mean(Saliva,na.rm=T),salSE=(sd(Saliva, na.rm=T)/sqrt(n()))) %>%
  ungroup()

#group together
allEff <- full_join(bodyEff, headEff, by=c("block", "class"))
allEff <- full_join(allEff, salEff, by=c("block", "class"))

meltMean <- allEff %>%
  select(block, class, contains("Mean")) %>%
  gather(key=variable, value=mean, -block, -class)

meltMean$type <- rep(c("Body", "Head", "Saliva"), each=6)

meltSE <- allEff %>%
  select(block, class, contains("SE")) %>%
  gather(variable, SE, -block, -class)

meltSE$type <- rep(c("Body", "Head", "Saliva"), each=6)

meltAll <- full_join(meltMean, meltSE, by=c("class", "block", "type")) %>%
  select(-variable.x, -variable.y)
```

Plot of infection efficiency.

```
#supplemental plot
ggplot(data=meltAll[order(meltAll$block, decreasing=F),], aes(x=class, group=block))+
  geom_bar(stat="identity", aes(y=mean, alpha=factor(block), fill=factor(class)), color="gray20", positi
  facet_wrap(~type, nrow=3, dir="v") +
  scale_fill_manual(values=c(colR, colS, colU))+
  scale_alpha_discrete(range=c(1,0.3), name="Season", labels=c("Fall", "Summer"), guide=guide_legend(re
  geom_errorbar(aes(ymin=mean-SE, ymax=mean+SE), width=0.2, color="gray20", position =position_dodge(-0
  theme_base() +
  xlab("Land Class") +
  ylab("Infection Efficiency") +
  guides(fill=F)
  #theme(legend.title=element_text("Season"))
```

Model Selection (Body is same as initial infection)

```
#create all the models
m1 <- glmer(Head~block + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m2 <- glmer(Head~class +  (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m3 <- glmer(Head~class + block + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
```

```r
m4 <- glmer(Head~class*block + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m5 <- glmer(Head~class*(1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4, m5), broom::glance)) #model 1 is best

AICc(m1,m2,m3,m4, m5)
```

```
##    df     AICc
## m1  3 106.3355
## m2  4 109.4356
## m3  5 110.3993
## m4  7 108.9752
## m5  4 109.4356
```

```r
tidy(m1)
```

```
##                   term   estimate std.error statistic      p.value group
## 1          (Intercept)  2.3978953 0.3947713  6.074137 1.246562e-09 fixed
## 2          blocksummer -0.5877867 0.5339828 -1.100760 2.710013e-01 fixed
## 3 sd_(Intercept).site  0.0000000        NA        NA           NA  site
```

```r
#create all the models
m1 <- glmer(Saliva~block + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m2 <- glmer(Saliva~class +  (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m3 <- glmer(Saliva~class + block + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m4 <- glmer(Saliva~class*block + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
m5 <- glmer(Saliva~class*(1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4, m5), broom::glance)) #between 1 and 3

AICc(m1,m2,m3,m4, m5)
```

```
##    df     AICc
## m1  3 150.9633
## m2  4 162.7401
## m3  5 150.3630
## m4  7 153.2814
## m5  4 162.7401
```

```r
tidy(m1)
```

```
##                   term   estimate std.error statistic      p.value group
```

```
## 1         (Intercept) -2.0361094 0.3666955 -5.552589 2.814701e-08 fixed
## 2         blocksummer  1.4633691 0.4480834  3.265841 1.091397e-03 fixed
## 3 sd_(Intercept).site  0.2624814        NA        NA           NA  site
```

```
tidy(m3)
```

```
##                  term   estimate std.error  statistic      p.value group
## 1         (Intercept) -2.5015553 0.4924147 -5.0801796 3.770782e-07 fixed
## 2       classSuburban  0.1556519 0.5058740  0.3076891 7.583189e-01 fixed
## 3          classUrban  1.1685198 0.5635947  2.0733338 3.814123e-02 fixed
## 4         blocksummer  1.6490627 0.4616055  3.5724499 3.536572e-04 fixed
## 5 sd_(Intercept).site  0.0000000        NA         NA           NA  site
```

```
#model
mixModelseasonsBody21 <- lme4::glmer(Body~class + block + (1|site),
                         data=seasons[seasons$DPI=="21",],
                         family=binomial(link="logit"))
tidy(mixModelseasonsBody21)
```

```
##                  term      estimate std.error statistic      p.value group
## 1         (Intercept)  4.917107e-01 0.2367960  2.076517 0.0378462050 fixed
## 2       classSuburban  4.205379e-01 0.2886423  1.456952 0.1451296729 fixed
## 3          classUrban -8.482715e-01 0.2892454 -2.932706 0.0033602215 fixed
## 4         blocksummer -8.546034e-01 0.2406755 -3.550854 0.0003839835 fixed
## 5 sd_(Intercept).site  8.076923e-08        NA        NA           NA  site
```

```
car::Anova(mixModelseasonsBody21)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Body
##        Chisq Df Pr(>Chisq)
## class 18.733  2  8.553e-05 ***
## block 12.609  1   0.000384 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(multcomp::glht(mixModelseasonsBody21, linfct = multcomp::mcp(class = "Tukey"), test = multcomp:
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Body ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                         Estimate Std. Error z value Pr(>|z|)
## Suburban - Rural == 0     0.4205     0.2886   1.457  0.31181
## Urban - Rural == 0       -0.8483     0.2892  -2.933  0.00973 **
## Urban - Suburban == 0    -1.2688     0.2990  -4.243  < 0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
summary(multcomp::glht(mixModelseasonsBody21, linfct = multcomp::mcp(block = "Tukey"), test = multcomp:
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Body ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21", ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                    Estimate Std. Error z value Pr(>|z|)
## summer - fall == 0  -0.8546     0.2407  -3.551 0.000384 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
mixModelseasonsHead21 <- lme4::glmer(Head~block  + (1|site),
                          data=seasons[seasons$DPI=="21" & seasons$Body==1,],
                          family=binomial(link="logit"))
tidy(mixModelseasonsHead21)
```

```
##                 term   estimate std.error statistic      p.value group
## 1        (Intercept)  2.3978953 0.3947713  6.074137 1.246562e-09 fixed
## 2        blocksummer -0.5877867 0.5339828 -1.100760 2.710013e-01 fixed
## 3 sd_(Intercept).site  0.0000000        NA        NA           NA  site
```

```r
car::Anova(mixModelseasonsHead21) #no effect
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Head
##        Chisq Df Pr(>Chisq)
## block 1.2117  1      0.271
```

```r
drop1(mixModelseasonsHead21, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Head ~ block + (1 | site)
##        Df    AIC    LRT Pr(Chi)
## <none>    106.17
## block   1 105.39 1.2235  0.2687
```

```r
summary(multcomp::glht(mixModelseasonsHead21, linfct = multcomp::mcp(block = "Tukey"), test = multcomp:
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Head ~ block + (1 | site), data = seasons[seasons$DPI ==
##     "21" & seasons$Body == 1, ], family = binomial(link = "logit"))
##
```

```
## Linear Hypotheses:
##                      Estimate Std. Error z value Pr(>|z|)
## summer - fall == 0  -0.5878     0.5340  -1.101    0.271
## (Adjusted p values reported -- single-step method)
```

```
mixModelseasonsSaliva21 <- lme4::glmer(Saliva~class + block  + (1|site),
                           data=seasons[seasons$DPI=="21" & seasons$Head==1,],
                           family=binomial(link="logit"))
tidy(mixModelseasonsSaliva21)
```

```
##                   term      estimate std.error  statistic      p.value
## 1          (Intercept) -2.378555e+00 0.4916104 -4.8382922 1.309595e-06
## 2        classSuburban  2.621010e-01 0.5198468  0.5041889 6.141286e-01
## 3           classUrban  1.122170e+00 0.5732326  1.9576171 5.027495e-02
## 4          blocksummer  1.714163e+00 0.4638138  3.6957993 2.191961e-04
## 5 sd_(Intercept).site  2.523364e-08        NA         NA           NA
##   group
## 1 fixed
## 2 fixed
## 3 fixed
## 4 fixed
## 5  site
```

```
car::Anova((mixModelseasonsSaliva21)) #only block is significant
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Saliva
##         Chisq Df Pr(>Chisq)
## class  4.1137  2  0.1278553
## block 13.6589  1  0.0002192 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
drop1(mixModelseasonsSaliva21, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Saliva ~ class + block + (1 | site)
##        Df    AIC     LRT   Pr(Chi)
## <none>    139.79
## class   2 139.95  4.1567    0.1251
## block   1 153.23 15.4317 8.554e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
summary(multcomp::glht(mixModelseasonsSaliva21, linfct = multcomp::mcp(class = "Tukey"), test = multcomp
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Saliva ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21" & seasons$Head == 1, ], family = binomial(link = "logit"))
```

```
##
## Linear Hypotheses:
##                          Estimate Std. Error z value Pr(>|z|)
## Suburban - Rural == 0    0.2621     0.5198   0.504    0.869
## Urban - Rural == 0       1.1222     0.5732   1.958    0.123
## Urban - Suburban == 0    0.8601     0.5521   1.558    0.264
## (Adjusted p values reported -- single-step method)
```

```
summary(multcomp::glht(mixModelseasonsSaliva21, linfct = multcomp::mcp(block = "Tukey"), test = multcomp
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lme4::glmer(formula = Saliva ~ class + block + (1 | site), data = seasons[seasons$DPI ==
##     "21" & seasons$Head == 1, ], family = binomial(link = "logit"))
##
## Linear Hypotheses:
##                       Estimate Std. Error z value Pr(>|z|)
## summer - fall == 0   1.7142     0.4638   3.696 0.000219 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Infection and Microclimate

```
seasonSite <- seasons %>%
  filter(DPI=="21") %>%
  dplyr::select(-Individual, -DPI, - Wing) %>%
  dplyr::group_by(block, class, site) %>%
  summarise_all(funs(mean(.,na.rm=T), se=(sd(., na.rm=T)/sqrt(n()))))

#group with temperature data
seasonInfSite <- merge(seasonSite, rbind(augEnvVar,octEnvVar), by.x=c("block", "site"), by.y=c("block",

# inspect variable correlations
# cor(seasonInfSite[,10:18])
```

```
respV <- "Body_mean"
predVs <- c("Temp_mean_mean","RH_mean_mean", "DTR_mean", "Temp_min_mean", "RH_min_mean", "Temp_max_mean

myCols <- c(respV, predVs, "block","class", "site")
modDF <- seasonInfSite %>%
  dplyr::select(one_of(myCols))
modDF <- na.omit(modDF)

#model selection for initial variable (bc of high correlation)
m1 <- glm(Body_mean ~ Temp_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m2 <- glm(Body_mean ~ RH_mean_mean,
          data=modDF,
```

```r
          family=gaussian(link="log"))
m3 <- glm(Body_mean ~ DTR_mean,
          data=modDF,
          family=gaussian(link="log"))
m4 <- glm(Body_mean ~ Temp_min_mean,
          data=modDF,
          family=gaussian(link="log"))
m5 <- glm(Body_mean ~ Temp_max_mean,
          data=modDF,
          family=gaussian(link="log"))
m6 <- glm(Body_mean ~ RH_min_mean,
          data=modDF,
          family=gaussian(link="log"))
m7 <- glm(Body_mean ~ RH_max_mean,
          data=modDF,
          family=gaussian(link="log"))

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4, m5, m6, m7), broom::glance)) #1 seems best

AICc(m1,m2,m3, m4, m5, m6, m7)
```

```
##    df       AICc
## m1  3 -9.0569871
## m2  3 -0.5439088
## m3  3 -6.7374663
## m4  3 -8.0859090
## m5  3 -6.4929200
## m6  3 -2.3719484
## m7  3 -1.1379604
```

```r
tidy(m1)
```

```
##            term    estimate  std.error statistic     p.value
## 1   (Intercept)  0.95866798 0.53632500  1.787476 0.092815805
## 2 Temp_mean_mean -0.07494337 0.02488645 -3.011412 0.008279968
```

```r
#find covariates that aren't correlated
covars <- data.frame(cor(seasonInfSite[,10:18]))
rownames(covars[abs(covars$Temp_mean_mean)<0.8,]) #only RH_mean and RH_max
```

```
## [1] "RH_mean_mean" "RH_max_mean"  "Temp_mean_se" "RH_mean_se"
```

```r
#model selection
m1 <- glm(Body_mean ~ Temp_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m2 <- glm(Body_mean ~ RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))

m3 <- glm(Body_mean ~ Temp_mean_mean+RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m4 <- glm(Body_mean ~ Temp_mean_mean*RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
```

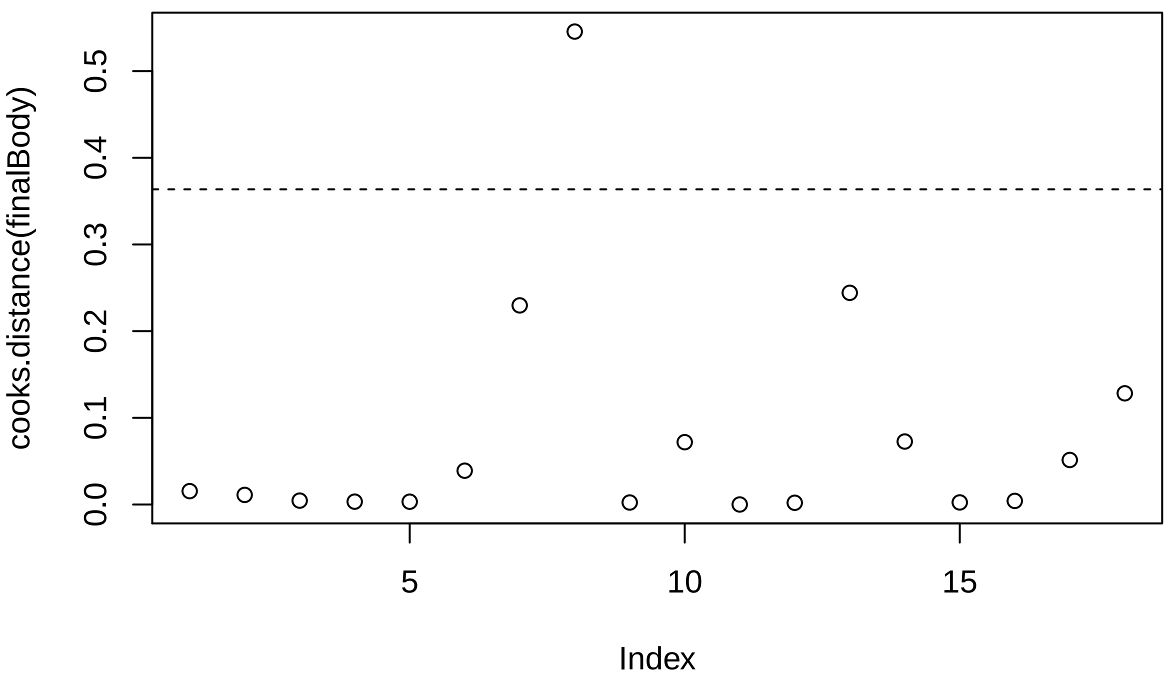
```r
modelSums <- do.call(rbind, lapply(list(m1,m2, m3, m4), broom::glance)) #3 seems best

AICc(m1,m2, m3, m4)
```

```
##    df        AICc
## m1  3  -9.0569871
## m2  3  -0.5439088
## m3  4 -12.8120279
## m4  5  -9.0366850
```

```r
tidy(m3)
```

```
##             term    estimate  std.error statistic      p.value
## 1    (Intercept) -1.02698904 0.88089922 -1.165842 0.2618821166
## 2 Temp_mean_mean -0.12883362 0.03098415 -4.158050 0.0008413049
## 3   RH_mean_mean  0.03760852 0.01518724  2.476323 0.0256769139
```

```r
finalBody <- glm(Body_mean ~ Temp_mean_mean+RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
plot(cooks.distance(finalBody))
abline(h=4/length(modDF), lty=2)
```




```r
car::Anova(finalBody)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Body_mean
##                LR Chisq Df Pr(>Chisq)
## Temp_mean_mean  20.7454  1  5.246e-06 ***
## RH_mean_mean     7.2752  1   0.006991 **
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#confint(finalBody)
tidy(finalBody)
```

```
##            term    estimate  std.error statistic      p.value
## 1   (Intercept) -1.02698904 0.88089922 -1.165842 0.2618821166
## 2 Temp_mean_mean -0.12883362 0.03098415 -4.158050 0.0008413049
## 3   RH_mean_mean  0.03760852 0.01518724  2.476323 0.0256769139
```

```r
drop1(finalBody, test="F")
```

```
## Single term deletions
##
## Model:
## Body_mean ~ Temp_mean_mean + RH_mean_mean
##                Df Deviance      AIC F value    Pr(>F)
## <none>              0.27952 -15.8890
## Temp_mean_mean  1  0.66611  -2.2582 20.7455 0.0003796 ***
## RH_mean_mean    1  0.41510 -10.7713  7.2753 0.0165491 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
vif(finalBody)
```

```
## Temp_mean_mean   RH_mean_mean
##       2.500624       2.500624
```

```r
sqrt(vif(finalBody))>2
```

```
## Temp_mean_mean   RH_mean_mean
##          FALSE          FALSE
```

```r
respV <- "Head_mean"
predVs <- c("Temp_mean_mean","RH_mean_mean", "DTR_mean", "Temp_min_mean", "RH_min_mean", "Temp_max_mean

myCols <- c(respV, predVs, "block","class", "site")
modDF <- seasonInfSite %>%
  dplyr::select(one_of(myCols))
modDF <- na.omit(modDF)

#model selection for initial variable (bc of high correlation)
m1 <- glm(Head_mean ~ Temp_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m2 <- glm(Head_mean ~ RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m3 <- glm(Head_mean ~ DTR_mean,
          data=modDF,
          family=gaussian(link="log"))
m4 <- glm(Head_mean ~ Temp_min_mean,
          data=modDF,
          family=gaussian(link="log"))
m5 <- glm(Head_mean ~ Temp_max_mean,
          data=modDF,
          family=gaussian(link="log"))
```

```r
m6 <- glm(Head_mean ~ RH_min_mean,
          data=modDF,
          family=gaussian(link="log"))
m7 <- glm(Head_mean ~ RH_max_mean,
          data=modDF,
          family=gaussian(link="log"))

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4, m5, m6, m7), broom::glance)) #1 seems best
tidy(m1)
```

```
##              term    estimate  std.error statistic     p.value
## 1    (Intercept)  1.24680019 0.59855991  2.083000 0.053652279
## 2 Temp_mean_mean -0.09311821 0.02822372 -3.299289 0.004526073
```

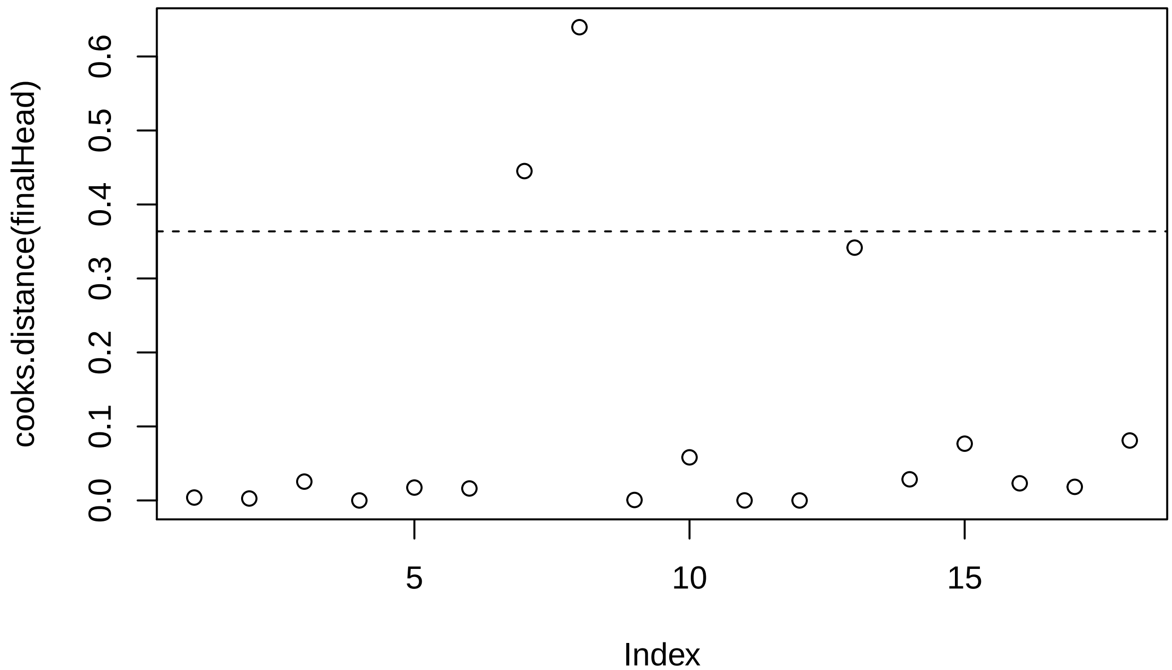
```r
#model selection
m1 <- glm(Head_mean ~ Temp_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m2 <- glm(Head_mean ~ RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))

m3 <- glm(Head_mean ~ Temp_mean_mean+RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))
m4 <- glm(Head_mean ~ Temp_mean_mean*RH_mean_mean,
          data=modDF,
          family=gaussian(link="log"))

modelSums <- do.call(rbind, lapply(list(m1,m2, m3, m4), broom::glance)) #3 seems best

AICc(m1,m2, m3, m4)
```

```
##    df         AICc
## m1  3  -9.81626751
## m2  3   0.06694249
## m3  4 -12.42640583
## m4  5  -8.51958039
```

```r
tidy(m3)
```

```
##              term    estimate  std.error  statistic      p.value
## 1    (Intercept) -0.76290213 1.00469599 -0.7593363 0.4594190579
## 2 Temp_mean_mean -0.14570591 0.03490278 -4.1746212 0.0008135761
## 3   RH_mean_mean  0.03758149 0.01708945  2.1991047 0.0439706330
```

```r
finalHead <- glm(Head_mean ~ Temp_mean_mean+RH_mean_mean,
          data=modDF,
          family=gaussian)

plot(cooks.distance(finalHead))
abline(h=4/length(modDF), lty=2)
```




```r
car::Anova(finalHead)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Head_mean
##                LR Chisq Df Pr(>Chisq)
## Temp_mean_mean  23.2199  1  1.445e-06 ***
## RH_mean_mean     7.3387  1   0.006749 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#confint(finalHead)
drop1(finalHead, test="F")
```

```
## Single term deletions
##
## Model:
## Head_mean ~ Temp_mean_mean + RH_mean_mean
##                Df Deviance      AIC F value    Pr(>F)
## <none>             0.26932 -16.5584
## Temp_mean_mean  1  0.68622  -1.7229 23.2199 0.0002255 ***
## RH_mean_mean    1  0.40108 -11.3895  7.3387 0.0161642 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
tidy(finalHead)
```

```
##             term    estimate  std.error statistic      p.value
## 1    (Intercept)  0.59188906 0.35139747  1.684386 0.1127946327
## 2 Temp_mean_mean -0.06672422 0.01384692 -4.818705 0.0002254676
## 3   RH_mean_mean  0.01603968 0.00592088  2.709003 0.0161642326
```

```r
respV <- "Saliva_mean"
predVs <- c("Temp_mean_mean","RH_mean_mean", "DTR_mean", "Temp_min_mean", "RH_min_mean", "Temp_max_mean
```

```
myCols <- c(respV, predVs, "block","class", "site")
modDF <- seasonInfSite %>%
  dplyr::select(one_of(myCols))
modDF <- na.omit(modDF)

#model selection for initial variable (bc of high correlation)
m1 <- glm(Saliva_mean ~ Temp_mean_mean,
          data=modDF,
          family=gaussian)
m2 <- glm(Saliva_mean ~ RH_mean_mean,
          data=modDF,
          family=gaussian)
m3 <- glm(Saliva_mean ~ DTR_mean,
          data=modDF,
          family=gaussian)
m4 <- glm(Saliva_mean ~ Temp_min_mean,
          data=modDF,
          family=gaussian)
m5 <- glm(Saliva_mean ~ Temp_max_mean,
          data=modDF,
          family=gaussian)
m6 <- glm(Saliva_mean ~ RH_min_mean,
          data=modDF,
          family=gaussian)
m7 <- glm(Saliva_mean ~ RH_max_mean,
          data=modDF,
          family=gaussian)

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4, m5, m6, m7), broom::glance)) #2 seems best, but t
tidy(m2)
```

```
##           term   estimate   std.error statistic    p.value
## 1  (Intercept) -0.2856187 0.222758502 -1.282190 0.21804309
## 2 RH_mean_mean  0.0045945 0.002597975  1.768493 0.09603649
```

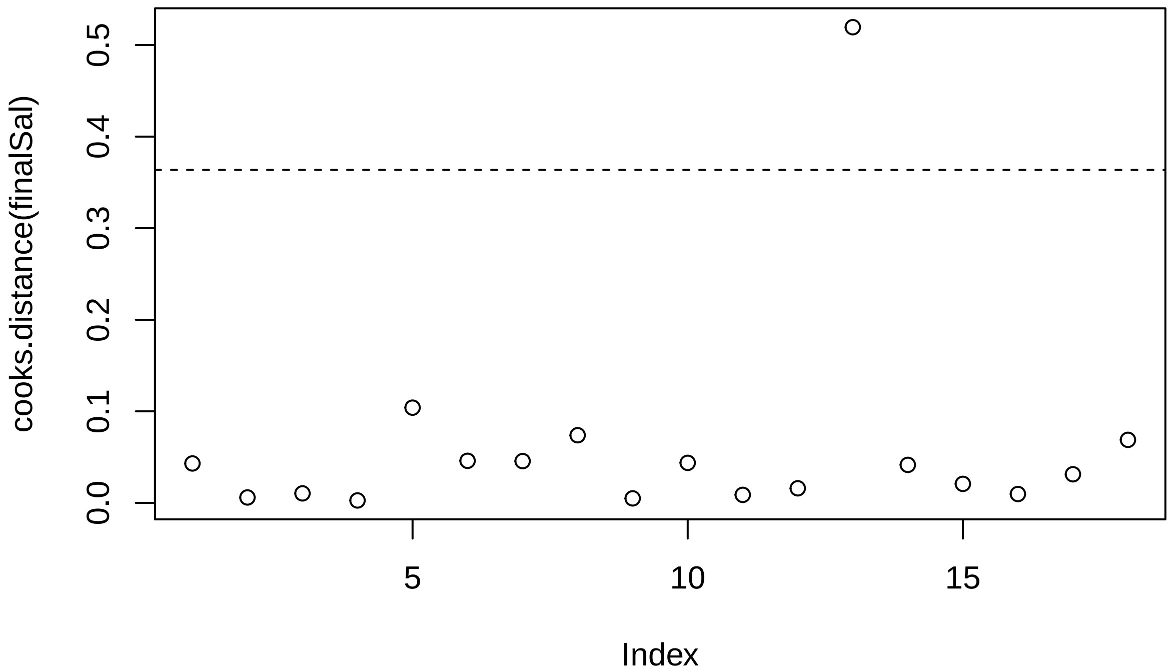
```
#model selection
m1 <- glm(Saliva_mean ~ Temp_mean_mean,
          data=modDF,
          family=gaussian)
m2 <- glm(Saliva_mean ~ RH_mean_mean,
          data=modDF,
          family=gaussian)

m3 <- glm(Saliva_mean ~ Temp_mean_mean+RH_mean_mean,
          data=modDF,
          family=gaussian)
m4 <- glm(Saliva_mean ~ Temp_mean_mean*RH_mean_mean,
          data=modDF,
          family=gaussian)

modelSums <- do.call(rbind, lapply(list(m1,m2, m3, m4), broom::glance)) #2 seems best

AICc(m1,m2, m3, m4)
```

```
##    df      AICc
## m1  3 -29.49212
## m2  3 -31.70849
## m3  4 -28.52592
## m4  5 -24.73537
```

```r
tidy(m2)
```

```
##          term   estimate   std.error statistic    p.value
## 1  (Intercept) -0.2856187 0.222758502 -1.282190 0.21804309
## 2 RH_mean_mean  0.0045945 0.002597975  1.768493 0.09603649
```

```r
finalSal <- glm(Saliva_mean ~ RH_mean_mean,
                data=modDF,
                family=gaussian)

plot(cooks.distance(finalSal))
abline(h=4/length(modDF), lty=2)
```




```r
car::Anova(finalSal)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: Saliva_mean
##              LR Chisq Df Pr(>Chisq)
## RH_mean_mean   3.1276  1    0.07698 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#confint(finalSal)
drop1(finalSal, test="F")
```

```
## Single term deletions
##
## Model:
```

```
## Saliva_mean ~ RH_mean_mean
##              Df Deviance     AIC F value  Pr(>F)
## <none>            0.11793 -33.423
## RH_mean_mean  1   0.14098 -32.209  3.1276 0.09604 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
tidy(finalSal)
```

```
##           term   estimate   std.error statistic    p.value
## 1  (Intercept) -0.2856187 0.222758502 -1.282190 0.21804309
## 2 RH_mean_mean  0.0045945 0.002597975  1.768493 0.09603649
```

Infection and Body Size

Body Infection

```r
bodyWingDF <- seasonInf %>%
  dplyr::select(Body, Wing, site, block, class) %>%
  filter(!is.na(Body)) %>%
  filter(!is.na(Wing))


bodyWing <- glmer(Body~Wing + (1|site),
                          data=bodyWingDF,
                          family=binomial(link="logit"))

tidy(bodyWing)
```

```
##                   term   estimate std.error statistic    p.value group
## 1          (Intercept)  4.9878964 2.3128770  2.156577 0.03103867 fixed
## 2                 Wing -2.0232763 0.9260367 -2.184877 0.02889787 fixed
## 3 sd_(Intercept).site  0.2128793        NA        NA         NA  site
```

```r
summary(bodyWing)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: Body ~ Wing + (1 | site)
##    Data: bodyWingDF
##
##      AIC      BIC   logLik deviance df.resid
##    399.5    410.5   -196.8    393.5      286
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5784 -0.9612 -0.6971  0.9858  1.5234
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  site   (Intercept) 0.04532  0.2129
## Number of obs: 289, groups:  site, 9
##
```

```
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)    4.988      2.313   2.157   0.0310 *
## Wing          -2.023      0.926  -2.185   0.0289 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr)
## Wing -0.998
```

```r
Anova(bodyWing)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Body
##       Chisq Df Pr(>Chisq)
## Wing 4.7737  1     0.0289 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
drop1(bodyWing, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Body ~ Wing + (1 | site)
##        Df    AIC    LRT Pr(Chi)
## <none>    399.51
## Wing    1 402.21 4.6937 0.03027 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Head Infection

```r
headWingDF <- seasonInf %>%
  dplyr::select(Head, Wing, site, block, class) %>%
  filter(!is.na(Head)) %>%
  filter(!is.na(Wing))


headWing <- glmer(Head~Wing + (1|site),
                          data=headWingDF,
                          family=binomial(link="logit"))
# headWing <- lmer(Wing~Head + (1|site),
#                            data=headWingDF) #this tests if the wing length is significantly different
tidy(headWing)
```

```
##                   term   estimate std.error statistic    p.value group
## 1          (Intercept)  3.9718215 2.3146765  1.715929 0.08617496 fixed
## 2                 Wing -1.7142078 0.9275247 -1.848153 0.06458016 fixed
## 3 sd_(Intercept).site  0.1861565        NA        NA         NA  site
```

```r
Anova(headWing)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Head
##       Chisq Df Pr(>Chisq)
## Wing 3.4157  1    0.06458 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
drop1(headWing, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Head ~ Wing + (1 | site)
##        Df    AIC    LRT Pr(Chi)
## <none>    396.88
## Wing    1 398.18 3.3029 0.06916 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Saliva Infection

```
salWingDF <- seasonInf %>%
  dplyr::select(Saliva, Wing, site, block, class) %>%
  filter(!is.na(Saliva)) %>%
  filter(!is.na(Wing))


salWing <- glmer(Saliva~Wing + (1|site),
                          data=salWingDF,
                          family=binomial(link="logit"))
summary(salWing)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: binomial  ( logit )
## Formula: Saliva ~ Wing + (1 | site)
##    Data: salWingDF
##
##      AIC      BIC   logLik deviance df.resid
##    194.7    205.7    -94.4    188.7      288
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -0.3494 -0.3369 -0.3324 -0.3267  3.1482
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  site   (Intercept) 0        0
## Number of obs: 291, groups:  site, 9
##
## Fixed effects:
##             Estimate Std. Error z value Pr(>|z|)
## (Intercept)  -2.9552     3.5124  -0.841     0.40
```

```
## Wing          0.3021     1.4033   0.215     0.83
##
## Correlation of Fixed Effects:
##      (Intr)
## Wing -0.998
```

```
tidy(salWing)
```

```
##                  term   estimate std.error  statistic   p.value group
## 1         (Intercept) -2.9551864  3.512354 -0.8413692 0.4001411 fixed
## 2                Wing  0.3020559  1.403287  0.2152488 0.8295734 fixed
## 3 sd_(Intercept).site  0.0000000        NA         NA        NA  site
```

```
Anova(salWing)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: Saliva
##       Chisq Df Pr(>Chisq)
## Wing 0.0463  1     0.8296
```

```
drop1(salWing, test="Chisq")
```

```
## Single term deletions
##
## Model:
## Saliva ~ Wing + (1 | site)
##        Df    AIC      LRT Pr(Chi)
## <none>    194.71
## Wing    1 192.76 0.046633   0.829
```

Direct Effects

Data Format and Loading

```
emergAug <- read.csv("../data/emergence/raw/AugustEmergence.csv")
emergAug$block <- "summer"

emergOct <- read.csv("../data/emergence/raw/OctoberEmergence.csv")
emergOct$block <- "fall"
#drop U3T1 in fall because it was eaten by ants
emergOct <- filter(emergOct, Tray_Code!="U3T1")
emergOct <- filter(emergOct, Tray_Code!="S1T3") #dumped
emergOct <- filter(emergOct, Tray_Code!="U1T4") #dumped

emergAll <- rbind(emergOct, emergAug)
#expand so each mosquito gets one row
emergExp <- emergAll[rep(seq.int(1,nrow(emergAll)), emergAll$Num_Emerge),
                      c(11, 2,4,5,6:9)]
#sum(emergAll$Num_Emerge)==nrow(emergExp) #quick check this worked
emergTray <- emergExp %>%
  filter(Sex=="F") %>%
  mutate(devRate=1/Exp_Day) %>%
  group_by(Tray_Code, Site_Code, Class, block) %>%
```

```r
  summarise(devRate=mean(devRate, na.rm=T)) %>%
  ungroup() %>%
  mutate(block=case_when(
    block=="summer" ~ "Summer",
    block=="fall"   ~ "Fall"
  ))
emergTray$block <- factor(emergTray$block, levels=c("Summer", "Fall"))

#get survival per tray
survSumm <- emergExp %>%
  filter(Sex=="F") %>%
  group_by(block, Tray_Code) %>%
  dplyr::mutate(percSurv=n()) %>%
  ungroup() %>%
  dplyr::select(block, Class, Site_Code, Tray_Code, percSurv)
survSumm <- unique(survSumm)
```

```r
fillIn <- function(df, endDay, totalMosq=50){
  #' Fill In Emergence Dates
  #' this function fills in for those mosquitoes that did not emerge so we do not have data for, it giv
  #' @param df the data frame you wish to fill in, in our case by pot
  #' @param endDay the last day of emergence
  #' @param totalMosq estimated starting number of mosquitoes per pot
  #' @returns dataframe with census data filled in for mosquitoes that did not emerge
  toRep <- df[1,]
  toRep$Exp_Day <- endDay
  toRep$event <- 0
  if(nrow(df)<totalMosq){
    toAdd <- toRep[rep(1, (totalMosq-nrow(df))),]
    allTest <- rbind(df, toAdd)
  } else {
    toAdd <- NA
    allTest <- NA
  }
  return(allTest)
}
```

```r
applyFill <- function(season, allData=emergExp){
  #' Apply FillIn function
  #' @param season "fall" or "summer"
  #' @param allData full dataframe with row for each mosquito that emerged
  #' @returns censused data for the full season
  tempList <- list()
  tempDF <- allData
  tempDF <- tempDF[tempDF$Sex=="F",]
  tempDF <- tempDF[tempDF$block==season,]
  tempDF$event <- 1 #add emergence event
  for (i in 1:length(unique(tempDF$Tray_Code))){
    df <- tempDF[tempDF$Tray_Code==unique(tempDF$Tray_Code)[i],]
    endDay <- max(tempDF$Exp_Day)
    tempList[[i]] <- fillIn(df=df, endDay=endDay)
  }
  allSurv <- do.call(rbind.data.frame, tempList)
  return(allSurv)
```

```
}
```

```
summerSurv <- applyFill(season="summer")
fallSurv <- applyFill(season="fall")
allSurv <- rbind(summerSurv, fallSurv)

survTray <- allSurv %>%
  filter(Sex=="F") %>%
  group_by(Tray_Code, Site_Code, Class, block) %>%
  summarise(survival=mean(event))
survTray$block[survTray$block=="summer"] <- "Summer"
survTray$block[survTray$block=="fall"] <- "Fall"
survTray$block <- factor(survTray$block, levels=c("Summer", "Fall"))
```

Tie in tray-level climate data:

```
allClim <- rbind(augClim, octClim)
allClim$block <- factor(rep(c("Summer", "Fall"), each=34), levels=c("Summer", "Fall"))
survClim <- merge(survTray, allClim, by.x=c("block","Tray_Code"), by.y=c("block","Tray_ID"))

emergClim <- merge(emergTray, allClim, by.x=c("block","Tray_Code"), by.y=c("block","Tray_ID"))
```

Survival

Class x Season

```
#model selection by AIC and logLik
m1 <- glmer(survival ~ block + (1|Site_Code),
                   data=survTray,
                 family=gaussian(link="logit"))

m2 <- glmer(survival ~ Class + (1|Site_Code),
                   data=survTray,
                 family=gaussian(link="logit"))

m3 <- glmer(survival ~ Class + block + (1|Site_Code),
                   data=survTray,
                 family=gaussian(link="logit"))

m4 <- glmer(survival ~ Class * block + (1|Site_Code),
                   data=survTray,
                 family=gaussian(link="logit"))

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4), broom::glance))
modelSums #m1 is best, but near m3 & m4
```

```
##       sigma    logLik       AIC       BIC deviance df.residual
## 1 0.1658887 23.119655 -38.23931 -29.42054 1.693916          63
## 2 0.2422129 -1.621092  13.24218  24.26565 3.848056          62
## 3 0.1658848 23.140524 -34.28105 -21.05289 1.693094          61
## 4 0.1593213 25.878542 -35.75708 -18.11954 1.558505          59
```

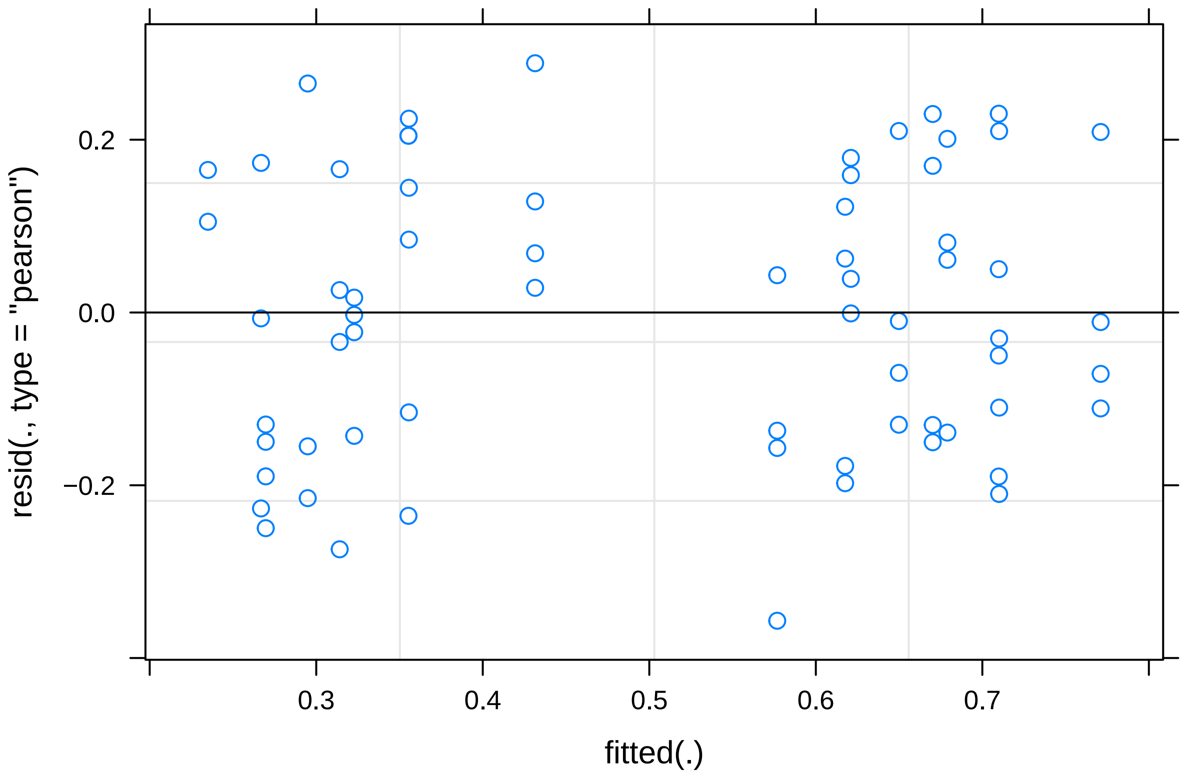
```
AICc(m1,m2,m3, m4) #still m1
```

```
##    df      AICc
## m1  4 -37.59415
## m2  5  14.22579
## m3  6 -32.88105
## m4  8 -33.27433
```

```
SurvModSeason <- glmer(survival ~ block + (1|Site_Code),
                   data=survTray,
                 family=gaussian(link="logit"))

summary(SurvModSeason)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: gaussian  ( logit )
## Formula: survival ~ block + (1 | Site_Code)
##    Data: survTray
##
##      AIC      BIC   logLik deviance df.resid
##    -38.2    -29.4     23.1    -46.2       63
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.15106 -0.83144 -0.01688  0.91427  1.73948
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Site_Code (Intercept) 0.10886  0.3299
##  Residual              0.02752  0.1659
## Number of obs: 67, groups:  Site_Code, 9
##
## Fixed effects:
##             Estimate Std. Error t value Pr(>|z|)
## (Intercept)   0.7042     0.2288   3.078  0.00208 **
## blockFall    -1.4902     0.1917  -7.775 7.55e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr)
## blockFall -0.381
```

```
modResults <- tidy(SurvModSeason)
plot(SurvModSeason)
```




```
car::Anova(SurvModSeason)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: survival
##        Chisq Df Pr(>Chisq)
## block 60.45  1  7.549e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#pairwise
survPair <- pairs(lsmeans::lsmeans(SurvModSeason, ~block))
survPair
```

```
##  contrast      estimate        SE df z.ratio p.value
##  Summer - Fall 1.490186 0.1916654 NA   7.775  <.0001
##
## Results are given on the log odds ratio (not the response) scale.
```

```
#coefficients
boot::inv.logit(modResults$estimate[1]) #fall
```

```
## [1] 0.6691121
```

```
boot::inv.logit(modResults$estimate[1]+modResults$estimate[2]) #summer
```

```
## [1] 0.3130252
```

Microclimate

Model selection

```r
respV <- "survival"
predVs <- c("Temp_mean","RH_mean", "DTR", "Temp_min", "RH_min", "Temp_max", "RH_max")

myCols <- c(respV, predVs, "block","Class", "Site_Code")
modDF <- survClim %>%
  dplyr::select(one_of(myCols))
modDF <- na.omit(modDF)

#model selection for initial variable

m1 <- lmer(survival~Temp_mean + (1|Site_Code),
           data=modDF)

m2 <- lmer(survival~RH_mean + (1|Site_Code),
           data=modDF)

m3 <- lmer(survival~DTR + (1|Site_Code),
           data=modDF)

m4 <- lmer(survival~Temp_min + (1|Site_Code),
           data=modDF)

m5 <- lmer(survival~RH_min + (1|Site_Code),
           data=modDF)

m6 <- lmer(survival~Temp_max + (1|Site_Code),
           data=modDF)

m7 <- lmer(survival~RH_max + (1|Site_Code),
           data=modDF)

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4, m5, m6, m7), broom::glance))
modelSums #m1 or m4
```

```
##       sigma    logLik        AIC        BIC   deviance df.residual
## 1 0.1621684 15.571069 -23.142137 -14.569598 -44.577817          59
## 2 0.1837171  4.483259  -0.966518   7.606021 -22.715586          59
## 3 0.1775250 10.431923 -12.863847  -4.291308 -33.640148          59
## 4 0.1627902 15.193627 -22.387254 -13.814715 -44.485120          59
## 5 0.1794725  7.550733  -7.101467   1.471072 -30.579517          59
## 6 0.1864933  7.270278  -6.540555   2.031984 -26.644909          59
## 7 0.2517561 -8.273081  24.546163  33.118702   4.570757          59
```

```r
Weights(AICc(m1,m2,m3, m4, m5, m6, m7))
```

```
## [1] 5.909927e-01 9.040816e-06 3.464812e-03 4.051924e-01 1.942651e-04
## [6] 1.467555e-04 2.607350e-11
```

```r
tidy(m1)
```

```
##                       term    estimate   std.error statistic     group
## 1              (Intercept) -0.74564962 0.145368674 -5.129369     fixed
## 2                Temp_mean  0.05430927 0.006132529  8.855935     fixed
## 3 sd_(Intercept).Site_Code  0.07289187          NA        NA Site_Code
## 4  sd_Observation.Residual  0.16216844          NA        NA  Residual
```

```r
#find covariates that aren't correlated
covars <- data.frame(cor(survClim[,6:12]))
rownames(covars[abs(covars$Temp_mean)<0.8,]) #only RH_mean and RH_max
```

```
## [1] "RH_mean" "RH_max"
```

```r
#model selection
m1 <- lmer(survival~Temp_mean + (1|Site_Code),
           data=modDF)

m2 <- lmer(survival~Temp_mean + RH_mean + (1|Site_Code),
           data=modDF)

m3 <- lmer(survival~Temp_mean * RH_mean + (1|Site_Code),
           data=modDF)

m4 <- lmer(survival~RH_mean + (1|Site_Code),
           data=modDF)

modelSums <- do.call(rbind, lapply(list(m1,m2, m3, m4), broom::glance)) #1 seems best
modelSums
```

```
##       sigma    logLik         AIC        BIC  deviance df.residual
## 1 0.1621684 15.571069 -23.1421372 -14.569598 -44.57782          59
## 2 0.1627397 11.266002 -12.5320031  -1.816329 -44.61667          58
## 3 0.1641516  6.089038  -0.1780767  12.680732 -44.92508          57
## 4 0.1837171  4.483259  -0.9665180   7.606021 -22.71559          59
```

```r
AICc(m1,m2, m3, m4)
```

```
##    df        AICc
## m1  4 -22.4524820
## m2  5 -11.4793715
## m3  6   1.3219233
## m4  4  -0.2768628
```

```r
tidy(m1)
```

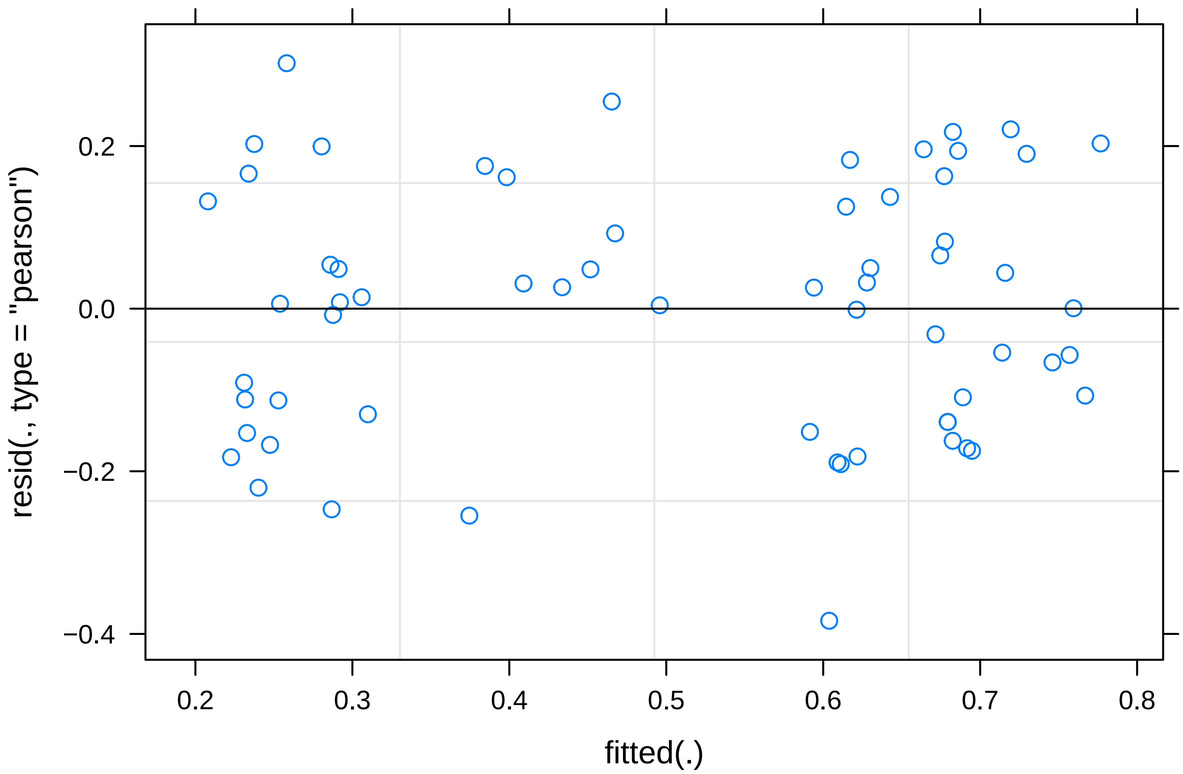
```
##                       term    estimate   std.error statistic     group
## 1              (Intercept) -0.74564962 0.145368674 -5.129369     fixed
## 2                Temp_mean  0.05430927 0.006132529  8.855935     fixed
## 3 sd_(Intercept).Site_Code  0.07289187          NA        NA Site_Code
## 4  sd_Observation.Residual  0.16216844          NA        NA  Residual
```

```r
survModClim <- glmer(survival~Temp_mean+(1|Site_Code),
                     data=survClim,
                     family=gaussian("logit"))

summary(survModClim)
```

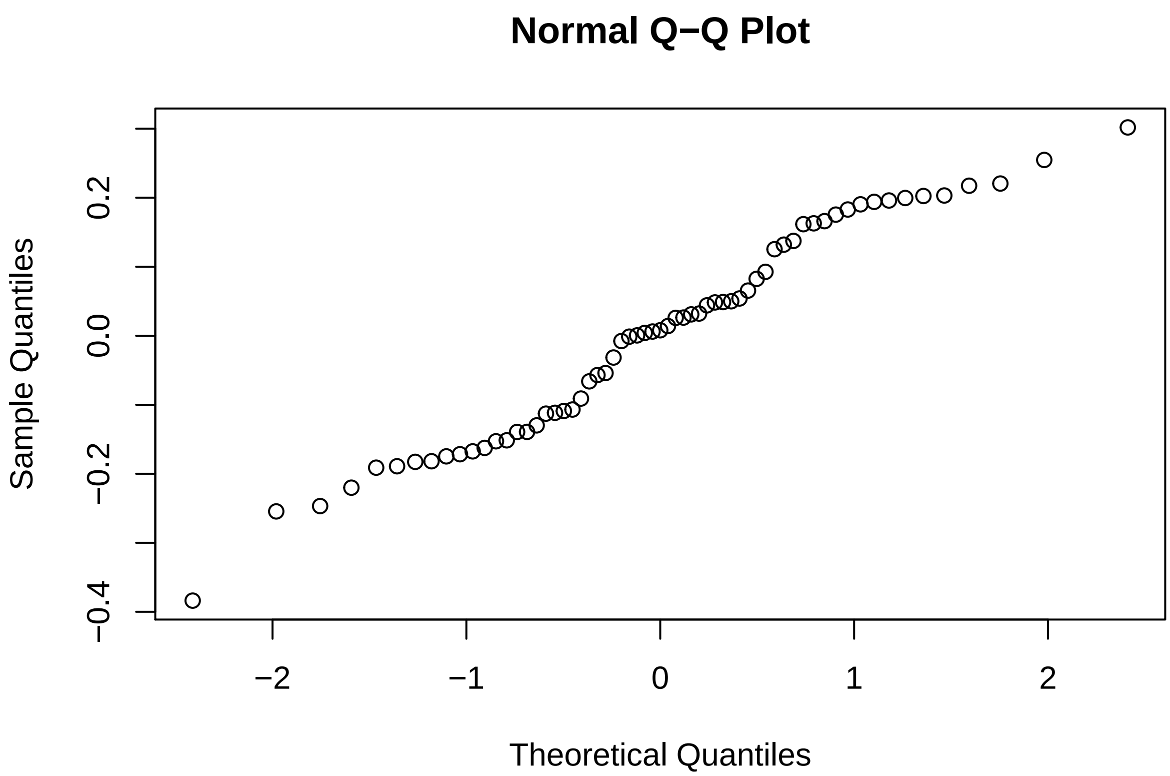
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: gaussian  ( logit )
## Formula: survival ~ Temp_mean + (1 | Site_Code)
##    Data: survClim
##
##      AIC      BIC   logLik deviance df.resid
```

```
##     -40.2    -31.6     24.1    -48.2       59
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.40767 -0.84428  0.04972  0.84500  1.89339
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Site_Code (Intercept) 0.11266  0.3357
##  Residual              0.02542  0.1594
## Number of obs: 63, groups:  Site_Code, 9
##
## Fixed effects:
##             Estimate Std. Error t value Pr(>|z|)
## (Intercept) -5.53248    0.73027  -7.576 3.57e-14 ***
## Temp_mean    0.23995    0.02966   8.089 6.02e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##           (Intr)
## Temp_mean -0.956
```

```r
modResults <- tidy(survModClim)

plot(survModClim)
```




```r
qqnorm(resid(survModClim))
```




```
#coefficients
modResults$estimate[2] #temp coefficient
```

```
## [1] 0.2399536
```

Emergence

Class x Season

Model Selection

```
#model selection
m0 <- lmer(devRate ~ 1 + (1|Site_Code),
           data=emergTray)
m1 <- lmer(devRate ~ Class +(1|Site_Code),
                   data=emergTray)

m2 <- lmer(devRate ~ block +(1|Site_Code),
                   data=emergTray)

m3 <- lmer(devRate ~ Class * block +(1|Site_Code),
                   data=emergTray)

m4 <- lmer(devRate ~ Class + block +(1|Site_Code),
                   data=emergTray)

modelSums <- do.call(rbind, lapply(list(m0, m1,m2,m3, m4), broom::glance))
modelSums #m2 is best
```

```
##          sigma    logLik       AIC       BIC   deviance df.residual
```

```
## 1 0.019849282 162.9405 -319.8810 -313.2669 -336.0945          64
## 2 0.019767728 155.6473 -301.2945 -290.2711 -338.7079          62
## 3 0.006157888 228.8366 -449.6732 -440.8544 -479.8224          63
## 4 0.006095069 213.1806 -410.3611 -392.7236 -487.0683          59
## 5 0.006160639 221.1502 -430.3004 -417.0723 -483.8547          61
```

```
AICc(m0, m1,m2,m3, m4) #still m2
```

```
##    df      AICc
## m0  3 -319.5000
## m1  5 -300.3109
## m2  4 -449.0280
## m3  8 -407.8784
## m4  6 -428.9004
```

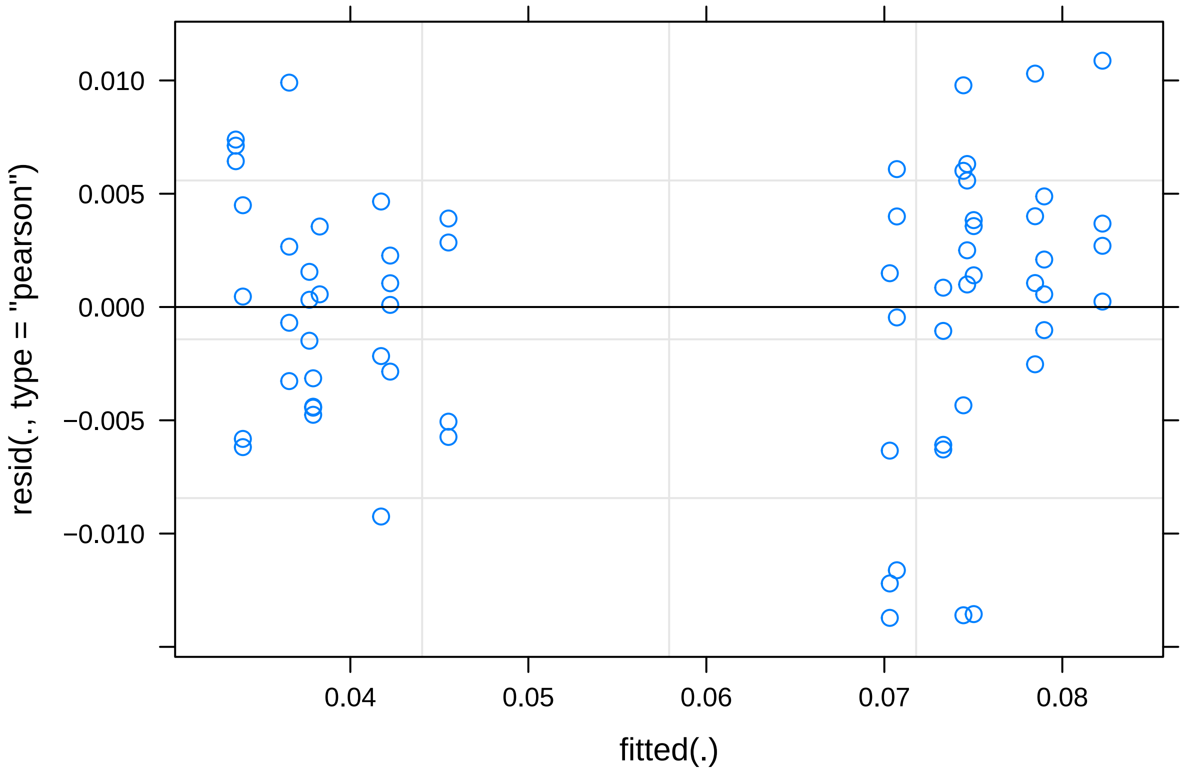
```
mixEmergeTray <- lmer(devRate ~ block +(1|Site_Code),
                   data=emergTray)

summary(mixEmergeTray)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: devRate ~ block + (1 | Site_Code)
##    Data: emergTray
##
## REML criterion at convergence: -457.7
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2281 -0.6178  0.1385  0.6286  1.7654
##
## Random effects:
##  Groups    Name        Variance  Std.Dev.
##  Site_Code (Intercept) 1.947e-05 0.004412
##  Residual              3.792e-05 0.006158
## Number of obs: 67, groups:  Site_Code, 9
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.075350   0.001793   42.02
## blockFall   -0.036743   0.001515  -24.25
##
## Correlation of Fixed Effects:
##           (Intr)
## blockFall -0.388
```

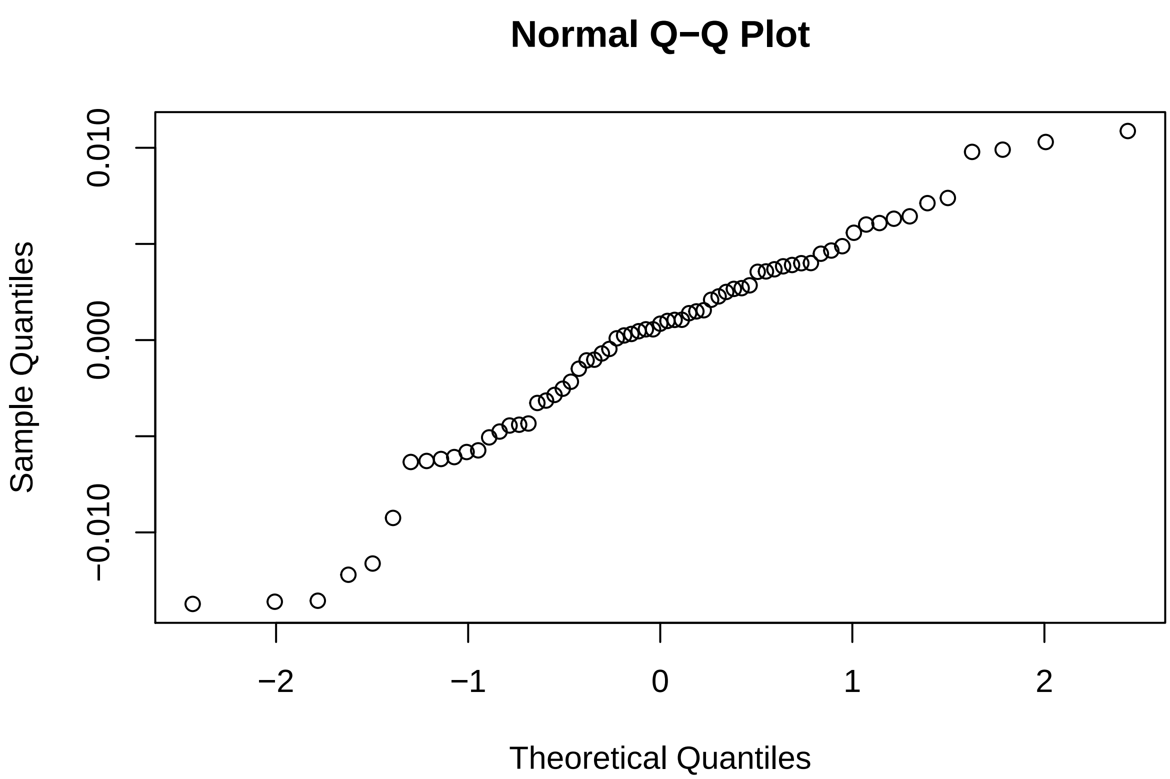
```
tidy(mixEmergeTray)
```

```
##                        term     estimate   std.error statistic     group
## 1               (Intercept)  0.075350056 0.001793406  42.01506     fixed
## 2                 blockFall -0.036742816 0.001515196 -24.24955     fixed
## 3 sd_(Intercept).Site_Code  0.004412125          NA        NA Site_Code
## 4  sd_Observation.Residual  0.006157888          NA        NA  Residual
```

```r
plot(mixEmergeTray)
```




```r
qqnorm(resid(mixEmergeTray))
```



```r
#confint(mixEmerge)
Anova(mixEmergeTray)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: devRate
##        Chisq Df Pr(>Chisq)
## block 588.04  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#pairwise
summary(multcomp::glht(mixEmergeTray, linfct = multcomp::mcp(block = "Tukey"), test = adjusted("holm")))
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lmer(formula = devRate ~ block + (1 | Site_Code), data = emergTray)
##
## Linear Hypotheses:
##                       Estimate Std. Error z value Pr(>|z|)
## Fall - Summer == 0 -0.036743   0.001515  -24.25   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

Microclimate

Model Selection:

```r
respV <- "devRate"
predVs <- c("Temp_mean","RH_mean", "DTR", "Temp_min", "RH_min", "Temp_max", "RH_max")

myCols <- c(respV, predVs, "block","Class", "Site_Code")
modDF <- emergClim %>%
  dplyr::select(one_of(myCols))
modDF <- na.omit(modDF)

#model selection for initial variable
m0 <- lmer(devRate~1 + (1|Site_Code),
           data=modDF)

m1 <- lmer(devRate~Temp_mean + (1|Site_Code),
           data=modDF)

m2 <- lmer(devRate~RH_mean + (1|Site_Code),
           data=modDF)

m3 <- lmer(devRate~DTR + (1|Site_Code),
           data=modDF)
```

```r
m4 <- lmer(devRate~Temp_min + (1|Site_Code),
           data=modDF)

m5 <- lmer(devRate~RH_min + (1|Site_Code),
           data=modDF)

m6 <- lmer(devRate~Temp_max + (1|Site_Code),
           data=modDF)

m7 <- lmer(devRate~RH_max + (1|Site_Code),
           data=modDF)

modelSums <- do.call(rbind, lapply(list(m0, m1,m2,m3, m4, m5, m6, m7), broom::glance))
modelSums #m1 or m4
```

```
##         sigma   logLik       AIC       BIC  deviance df.residual
## 1 0.019768076 153.2228 -300.4457 -294.0163 -316.6063          60
## 2 0.007165630 209.3282 -410.6565 -402.0840 -445.4920          59
## 3 0.009061652 183.4426 -358.8852 -350.3127 -391.4812          59
## 4 0.010435571 183.4782 -358.9563 -350.3838 -391.1167          59
## 5 0.006977285 209.7237 -411.4474 -402.8749 -446.7692          59
## 6 0.010041227 181.0941 -354.1882 -345.6156 -388.6008          59
## 7 0.010883466 180.9413 -353.8826 -345.3101 -385.4466          59
## 8 0.019655919 147.9562 -287.9124 -279.3398 -318.3476          59
```

```r
MuMIn::AICc(m0, m1,m2,m3, m4, m5, m6, m7)
```

```
##    df      AICc
## m0  3 -300.0389
## m1  4 -409.9668
## m2  4 -358.1956
## m3  4 -358.2666
## m4  4 -410.7577
## m5  4 -353.4985
## m6  4 -353.1930
## m7  4 -287.2227
```

```r
tidy(m1)
```

```
##                      term      estimate    std.error statistic     group
## 1             (Intercept) -6.667066e-02 0.0062175042 -10.72306     fixed
## 2               Temp_mean  5.405793e-03 0.0002666941  20.26964     fixed
## 3 sd_(Intercept).Site_Code  3.571659e-10           NA        NA Site_Code
## 4  sd_Observation.Residual  7.165630e-03           NA        NA  Residual
```

```r
#find covariates that aren't correlated
covars <- data.frame(cor(modDF[,2:7]))
rownames(covars[abs(covars$Temp_mean)<0.8,]) #mean RH
```

```
## [1] "RH_mean"
```

```r
#model selection
m1 <- lmer(devRate~Temp_mean + (1|Site_Code),
           data=modDF)

m2 <- lmer(devRate~Temp_mean + RH_mean + (1|Site_Code),
```

```r
          data=modDF)

m3 <- lmer(devRate~Temp_mean * RH_mean + (1|Site_Code),
          data=modDF)

m4 <- lmer(devRate~ RH_mean + (1|Site_Code),
          data=modDF)

modelSums <- do.call(rbind, lapply(list(m1,m2, m3, m4), broom::glance)) #1 seems best
modelSums
```

```
##         sigma   logLik       AIC       BIC  deviance df.residual
## 1 0.007165630 209.3282 -410.6565 -402.0840 -445.4920          59
## 2 0.007155482 201.8216 -393.6431 -382.9275 -445.8598          58
## 3 0.007115474 193.9168 -375.8336 -362.9748 -446.9274          57
## 4 0.009061652 183.4426 -358.8852 -350.3127 -391.4812          59
```

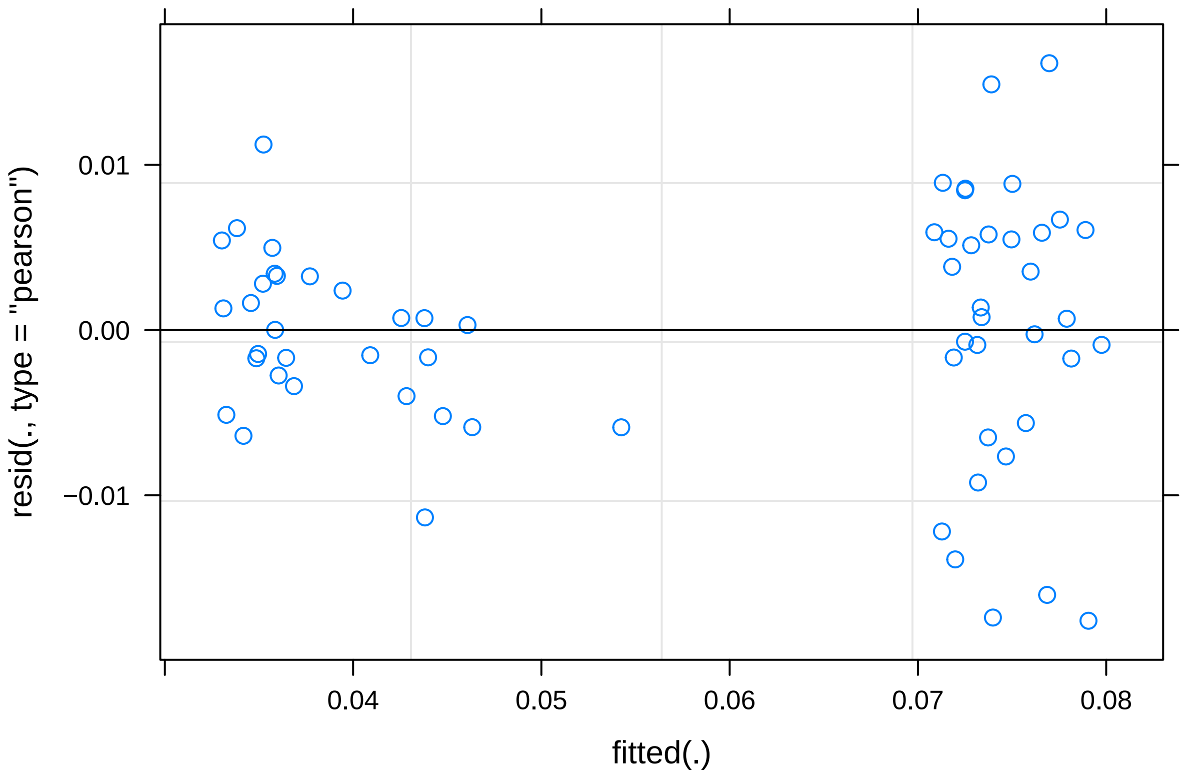
```r
AICc(m1,m2, m3, m4)
```

```
##    df      AICc
## m1  4 -409.9668
## m2  5 -392.5905
## m3  6 -374.3336
## m4  4 -358.1956
```

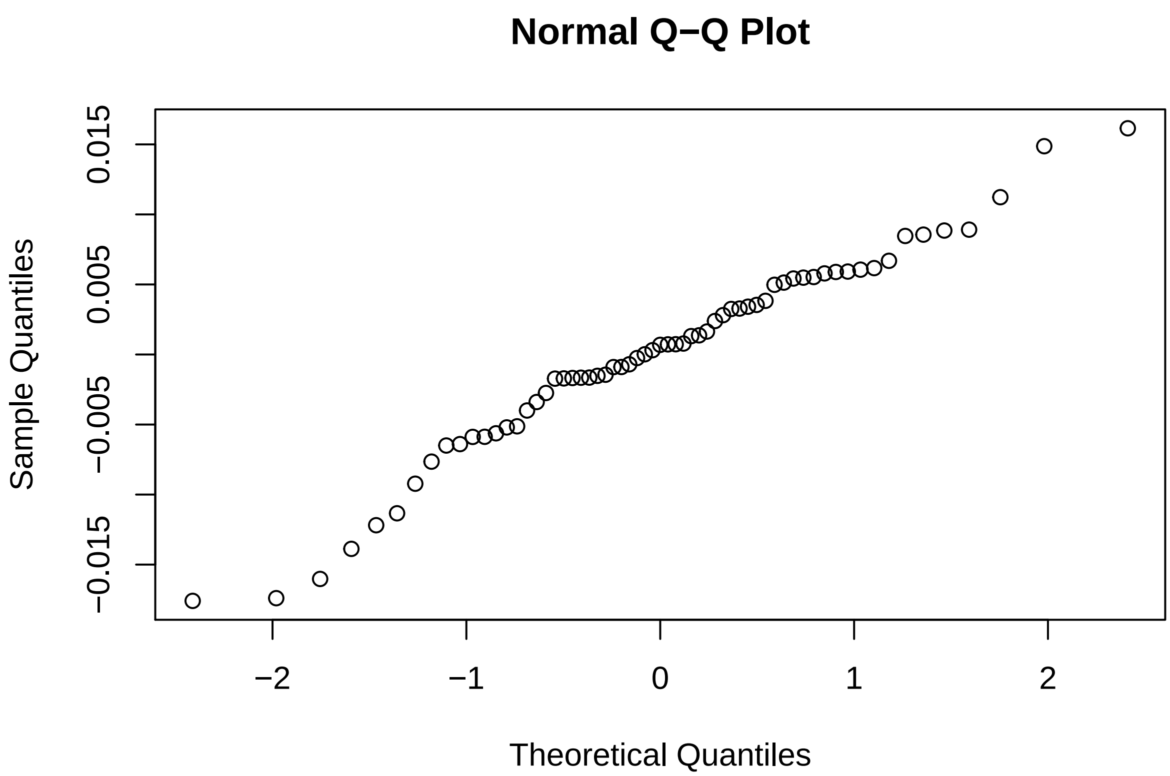
```r
tidy(m1)
```

```
##                       term      estimate    std.error statistic     group
## 1              (Intercept) -6.667066e-02 0.0062175042 -10.72306     fixed
## 2                Temp_mean  5.405793e-03 0.0002666941  20.26964     fixed
## 3 sd_(Intercept).Site_Code  3.571659e-10           NA        NA Site_Code
## 4  sd_Observation.Residual  7.165630e-03           NA        NA  Residual
```

```r
devClimMod <- lmer(devRate~Temp_mean +(1|Site_Code),
                    data=emergClim)

plot(devClimMod)
```




```r
qqnorm(resid(devClimMod))
```




```r
summary(devClimMod)
```

```
## Linear mixed model fit by REML ['lmerMod']
```

```
## Formula: devRate ~ Temp_mean + (1 | Site_Code)
##    Data: emergClim
##
## REML criterion at convergence: -418.7
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.45479 -0.51575  0.09618  0.73667  2.25385
##
## Random effects:
##  Groups    Name        Variance  Std.Dev.
##  Site_Code (Intercept) 1.276e-19 3.572e-10
##  Residual              5.135e-05 7.166e-03
## Number of obs: 63, groups:  Site_Code, 9
##
## Fixed effects:
##               Estimate Std. Error t value
## (Intercept) -0.0666707  0.0062175  -10.72
## Temp_mean    0.0054058  0.0002667   20.27
##
## Correlation of Fixed Effects:
##           (Intr)
## Temp_mean -0.989
```

```
modResults <- tidy(devClimMod)
#coefficients
modResults$estimate[2] #temp coefficient
```

```
## [1] 0.005405793
```

Indirect Effects

Uninfected Body Size

Load body size data:

```
augWing <- read.csv("../data/emergence/raw/AugustWingLength.csv", stringsAsFactors = F)
octWing <- read.csv("../data/emergence/raw/OctoberWingLength.csv",  stringsAsFactors = F)



#convert to mm & clean
augWing$mm <- augWing$Bars*augWing$Conversion.mm.bars.
octWing$mm <- octWing$Bars*octWing$Conversion.bars.mm.

octWing$site <- as.factor(substr(as.character(octWing$TrayCode), 1, 2))
augWing$site <- as.factor(substr(as.character(augWing$TrayCode), 1, 2))

getClass <- function(monthDf){
  monthDf$class <- NULL
  for (i in 1:nrow(monthDf)){
    if (substr(monthDf$site[i], 1,1)=="R"){
    monthDf$class[i] <- "Rural"
    }
```

```r
    if (substr(monthDf$site[i], 1,1)=="S"){
    monthDf$class[i] <- "Suburban"
    }
    if (substr(monthDf$site[i], 1,1)=="U"){
    monthDf$class[i] <- "Urban"
    }
  }
  monthDf$class <- as.factor(monthDf$class)
  return(monthDf)
}

augWing <- getClass(augWing)
octWing <- getClass(octWing)

octWing$block <- "Fall"
augWing$block <- "Summer"

augWing$Date <- as.Date(as.character(augWing$Date), format="%m/%d/%Y")
octWing$Date <- as.Date(as.character(octWing$Date), format="%m/%d/%Y")

#add day of experiment
augWing$Exp_Day <- as.numeric(augWing$Date-as.Date("2016-08-01", format="%Y-%m-%d"))
octWing$Exp_Day <- as.numeric(octWing$Date-as.Date("2016-09-26", format="%Y-%m-%d"))

#rename traycode column to match
colnames(augWing)[1] <- "Tray_Code"
colnames(octWing)[1] <- "Tray_Code"

#combine
fallWing <- octWing %>%
  dplyr::select(block, class, Site_Code=site, Tray_Code, Exp_Day, mm)

summerWing <- augWing %>%
  dplyr::select(block, class, Site_Code=site, Tray_Code, Exp_Day, mm)

allWing <- rbind(summerWing, fallWing)
allWing$block<- factor(allWing$block, levels=c("Summer", "Fall"))

#drop outlier in S2 (wing size =1.56 mm)
allWing <- allWing %>%
  filter(mm>1.6)
```

Land Class x Season

Model Selection

```r
#model selection by AIC and logLik
m0 <- lmer(mm~1 + (1|Site_Code),
           data=allWing)
m1 <- lmer(mm ~ block + (1|Site_Code),
                   data=allWing)

m2 <- lmer(mm ~ class + (1|Site_Code),
```

```
                   data=allWing)

m3 <- lmer(mm ~ class + block + (1|Site_Code),
                   data=allWing)

m4 <- lmer(mm ~ class*block + (1|Site_Code),
                   data=allWing)

modelSums <- do.call(rbind, lapply(list(m0,m1,m2,m3, m4), broom::glance))
modelSums #m0 is best
```

```
##       sigma   logLik       AIC       BIC  deviance df.residual
## 1 0.1782356 80.15274 -154.3055 -143.2243 -165.6758         294
## 2 0.1776557 78.44084 -148.8817 -134.1067 -167.9672         293
## 3 0.1782550 76.79547 -143.5909 -125.1223 -165.8069         292
## 4 0.1776747 75.26388 -138.5278 -116.3654 -168.4225         291
## 5 0.1741417 78.38996 -140.7799 -111.2301 -183.3942         289
```

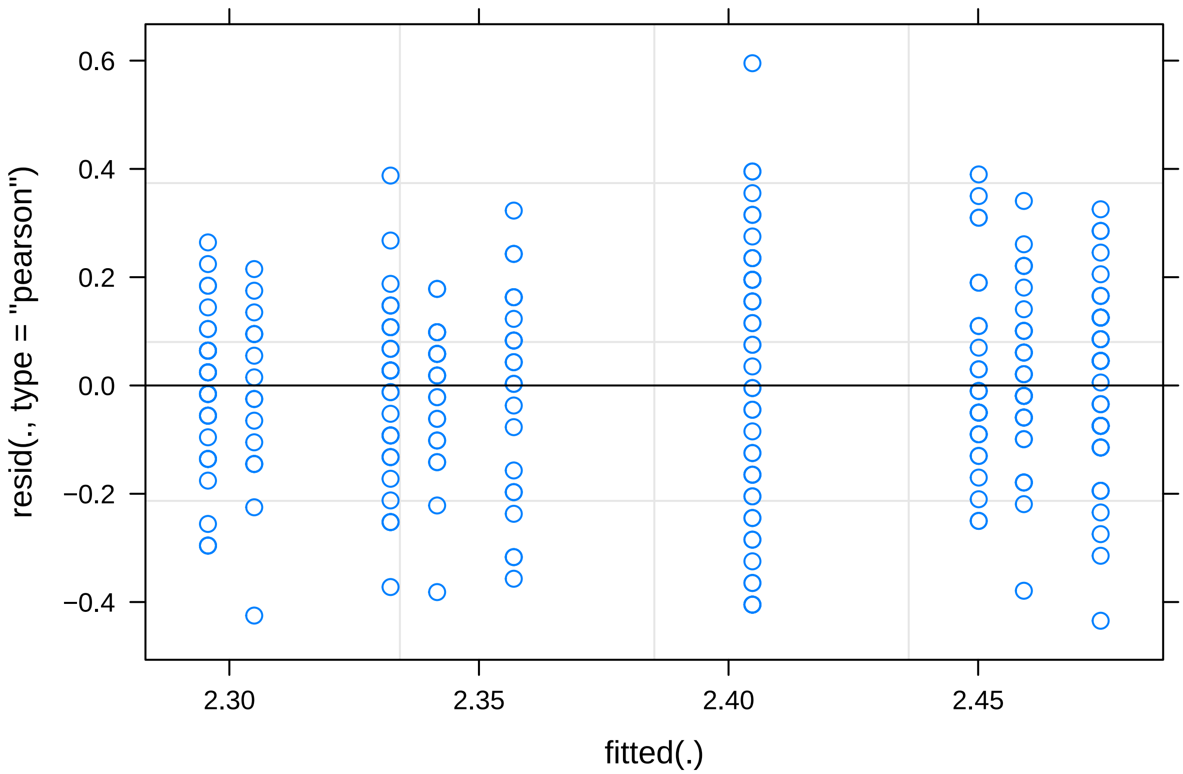
```
AICc(m0, m1,m2,m3, m4) #still m0
```

```
##    df      AICc
## m0  3 -154.2236
## m1  4 -148.7447
## m2  5 -143.3848
## m3  6 -138.2381
## m4  8 -140.2799
```

```
wingMod <- lmer(mm~1 +(1|Site_Code),
                data=allWing)
summary(wingMod)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mm ~ 1 + (1 | Site_Code)
##    Data: allWing
##
## REML criterion at convergence: -160.3
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.4380 -0.6426  0.1031  0.6165  3.3395
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Site_Code (Intercept) 0.005613 0.07492
##  Residual              0.031768 0.17824
## Number of obs: 297, groups:  Site_Code, 9
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept)  2.38002    0.02724   87.39
```

```
plot(wingMod)
```



Microclimate

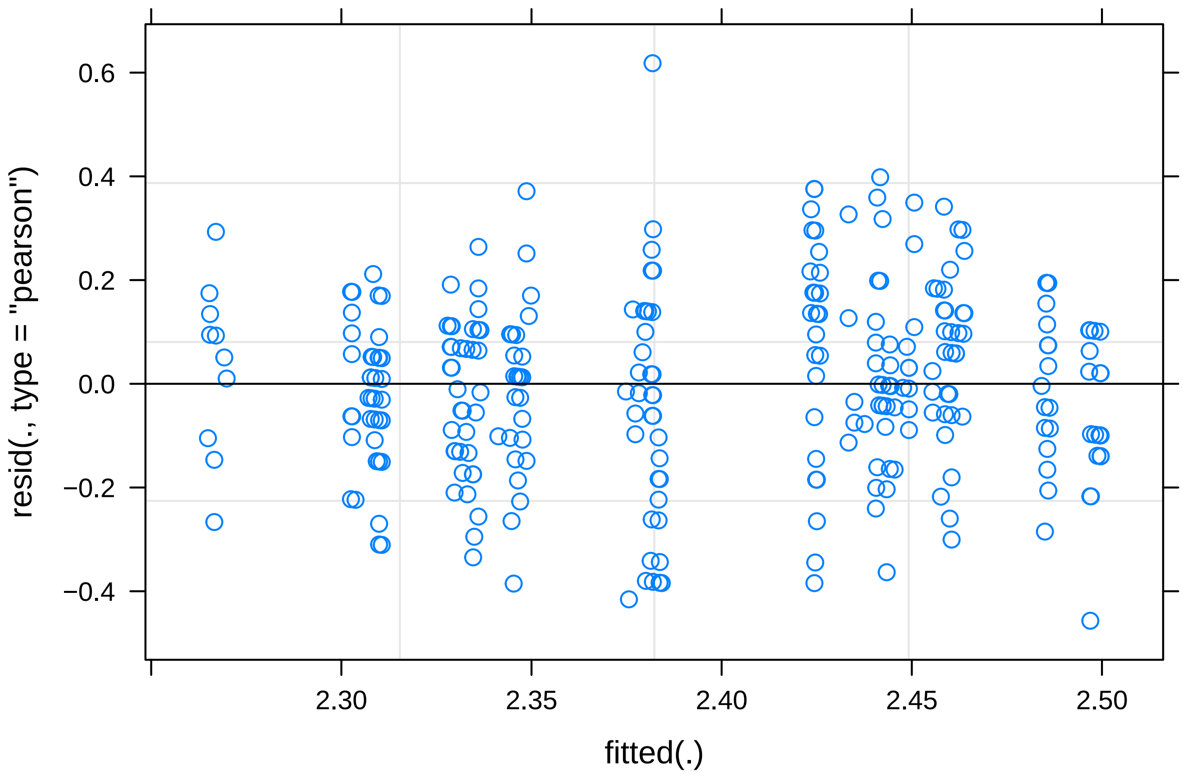
Load Data:

```
climate <- read.csv(file='../data/microclimate/clean/2016TrialsAdultCleaned.csv', stringsAsFactors = F)

climate$Day <- as.Date(climate$Day, format="%Y-%m-%d")
climate$Site_Code <- as.factor(climate$Site_ID)
climate$Tray_Code <- as.factor(climate$Tray_ID)

getClimate <- function(indMosq, climateDF=climate, season){
  #' This is a function to apply over the rows of the octWing and augWing data frames. Must have climat

  #' @param indMosq row of the dataframe for each individual mosquito
  #' @param climateDF the dataframe containing climate data every 10 minutes
  #' @param season, either "summer" or "fall"
  #' @returns formatted data with climate and winglength for the individual mosquito


  #get date range
  startDate <- ifelse(season=="Summer", "2016-08-01", "2016-09-26")
  startDate <- as.Date(startDate, format="%Y-%m-%d")
  endDate <- indMosq$Date

  #subset temperature data
  try(climSubset <- climateDF %>%
    filter(Tray_Code==as.character(indMosq$Tray_Code)) %>%
    filter(Day>startDate & Day<endDate),
```

```
    silent=T)

  #now take mean temperature
  tempMean <- climSubset %>%
    summarise(Tmean=mean(Temp, na.rm=T))

  # if (nrow(climSubset)<1000){
  #   climSubset <- climate %>%
  #     filter(Site_ID==indMosq$site) %>%
  #     filter(Day>startDate & Day<endDate)
  # }

  #merge this all together
  #mosqFormat <- cbind(indMosq[,c('block','class','site','Tray_ID','Exp_Day', 'mm')], Tmean=tempMean$Tm

  return(tempMean$Tmean)
}

augWing$Temp <- NA
for(i in 1:nrow(augWing)){
  indMosq <- augWing[i,]
  augWing$Temp[i] <- getClimate(indMosq, season="Summer")
}

octWing$Temp <- NA
for(i in 1:nrow(octWing)){
  indMosq <- octWing[i,]
  octWing$Temp[i] <- getClimate(indMosq, season="Fall")
}

#combine
fallWing <- octWing %>%
  dplyr::select(block, class, Site_Code=site, Tray_Code, Exp_Day, mm, Temp)

summerWing <- augWing %>%
    dplyr::select(block, class, Site_Code=site, Tray_Code, Exp_Day, mm, Temp)

allWing <- rbind(summerWing, fallWing)
allWing$block<- factor(allWing$block, levels=c("Summer", "Fall"))

#drop outlier in S2 (wing size =1.56 mm)
allWing <- allWing %>%
  filter(mm>1.6)
```

Statistics:

```
wingModTemp <- lmer(mm~Temp+(1|Site_Code),
                    data=allWing)
plot(wingModTemp)
```




```r
summary(wingModTemp)
```

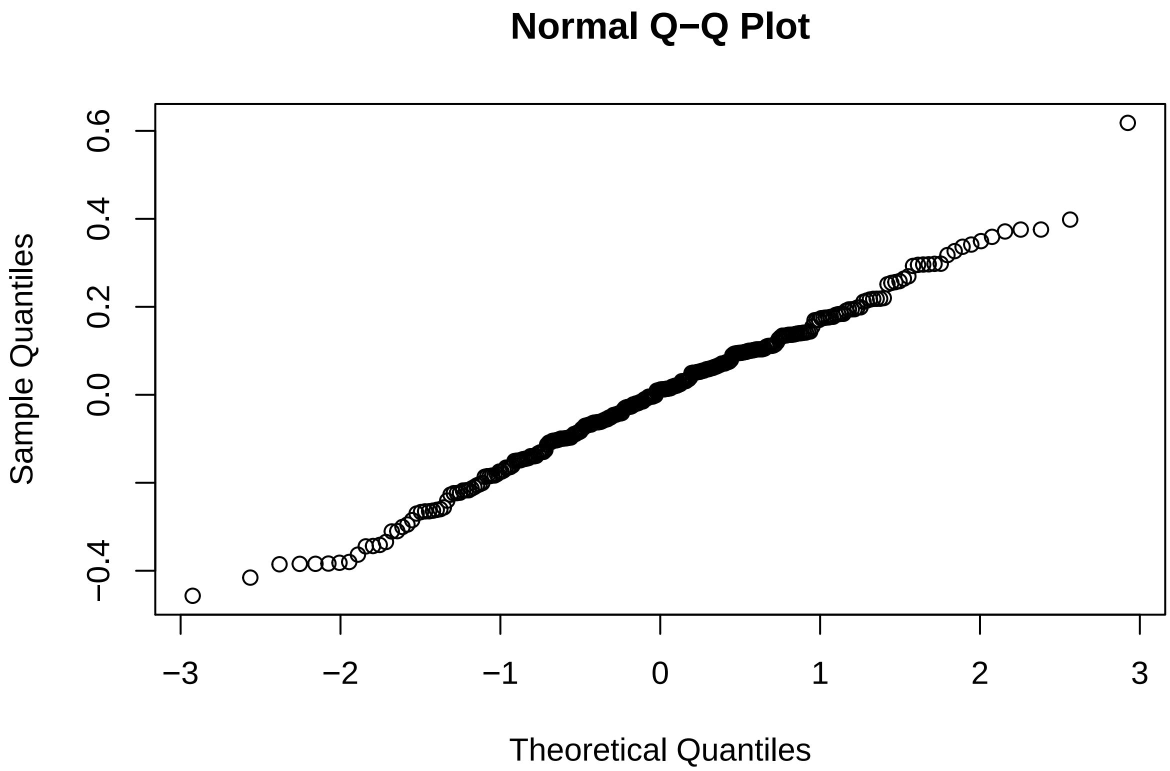
```
## Linear mixed model fit by REML ['lmerMod']
## Formula: mm ~ Temp + (1 | Site_Code)
##    Data: allWing
##
## REML criterion at convergence: -151.5
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.5796 -0.5915  0.0659  0.6242  3.4898
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Site_Code (Intercept) 0.005402 0.0735
##  Residual              0.031376 0.1771
## Number of obs: 290, groups:  Site_Code, 9
##
## Fixed effects:
##             Estimate Std. Error t value
## (Intercept) 2.253964   0.074292  30.339
## Temp        0.005917   0.003142   1.883
##
## Correlation of Fixed Effects:
##      (Intr)
## Temp -0.932
```

```r
confint(wingModTemp) #no effect of temperature
```

```
##                        2.5 %     97.5 %
```

```
## .sig01        0.0397126866 0.12624823
## .sigma        0.1631525337 0.19248521
## (Intercept)  2.1094289217 2.40017384
## Temp        -0.0003154784 0.01203926
```

```r
qqnorm(resid(wingModTemp))
```



Growth Rate

```r
#calculate means per Exp_Day and Tray
growthWing <- allWing %>%
  dplyr::group_by(block,class,Site_Code,Tray_Code, Exp_Day) %>%
  dplyr::summarise(meanWing=mean(mm, na.rm=T)) %>%
  dplyr::ungroup()

growthWing$class <- tolower(growthWing$class)

#merge with emergence data
allEmerg$class <- allEmerg$Class
levels(allEmerg$class) <- c("Rural", "Suburban", "Urban")
levels(allEmerg$block) <- c("Summer", "Fall")
growthDF <- merge(allEmerg, growthWing, by=c("block", "class", "Site_Code", "Tray_Code", "Exp_Day"), al

trayMeans <- allWing %>%
  dplyr::group_by(block, Tray_Code) %>%
  dplyr::summarise(meanWing=mean(mm, na.rm=T))

#fill in missing with mean of tray during that block
```

```
for (i in 1:nrow(growthDF)){
  if (is.na(growthDF$meanWing[i])){
    temp <- trayMeans$meanWing[trayMeans$block==growthDF$block[i] & trayMeans$Tray_Code==growthDF$Tray_C
    if (length(temp)==0) next
    growthDF$meanWing[i] <- temp
  } else next
}

#some trays had no mosquitoes emerge that weren't infected, so we take the site level mean for them

siteMeans <- allWing %>%
  dplyr::group_by(Site_Code, block) %>%
  dplyr::summarise(meanWing=mean(mm, na.rm=T))

for (i in 1:nrow(growthDF)){
  if (is.na(growthDF$meanWing[i])){
    temp <- siteMeans$meanWing[siteMeans$block==growthDF$block[i] & siteMeans$Site_Code==growthDF$Site_C
    if (length(temp)==0) next
    growthDF$meanWing[i] <- temp
  } else next
}
```

```
growthDF$Fwx <- -121.240 + (78.02 * growthDF$meanWing)
growthDF$AxFwx <- growthDF$Num_Emerge*growthDF$Fwx
growthDF$xAxFwx <- growthDF$Exp_Day*growthDF$AxFwx

#get sum per day
growthDF2 <- growthDF %>%
  dplyr::group_by(block, Tray_Code, class, Site_Code) %>%
  dplyr::summarise(xAxFwx = sum(xAxFwx), AxFwx=sum(AxFwx))

growthDF2 <- growthDF2 %>%
  mutate(r=(log((1/50)*AxFwx))/(14+(xAxFwx/AxFwx))) %>%
  ungroup()
```

Plot

```
levels(emergTray$block) <- c("Summer", "Fall")
levels(emergTray$Class) <- c("Rural", "Suburban", "Urban")

levels(survTray$block) <- c("Summer", "Fall")
levels(survTray$Class) <- c("Rural", "Suburban", "Urban")
```

Figure 3.

```
#png(file="figures/forMS/survEmergeGrowth.png", width = 4, height=7, units="in", res=500, family="sans"

survPlot <- ggplot(data=survTray, aes(x=Class, y=(survival*100)))+
  geom_boxplot(aes(fill=Class), width=0.4)+
  scale_fill_manual(values=c(colR, colS, colU), labels=c("Rural", "Suburban", "Urban"))+
  facet_wrap(~block, ncol=2)+
  ylab("Percent Survival")+
  theme_fivethirtyeight() +
```

```
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
        legend.key = element_blank(),
        panel.grid.major.x = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        axis.title = element_text(),
        axis.title.x = element_text(),
        axis.title.y=element_text(),
        #strip.background = element_blank(),
        strip.text.x = element_text(size=12),
        axis.line=element_line(color=axisColor, size=0.5),
        panel.grid = element_blank(),
        axis.text.y=element_text(size=12),
        axis.text.x=element_text(size=12))+
  theme(axis.title.x = element_blank(),
        axis.text.x = element_blank(),
        axis.title.y= element_text(size=10),
        strip.text = element_text(size=10))+
  theme(legend.position="none")

#Emergence Plot
emergePlot <- ggplot(emergTray, aes(x=Class, y=devRate))+
  geom_boxplot(aes(fill=Class), width=0.4)+
  scale_fill_manual(values=c(colR, colS, colU), labels=c("Rural", "Suburban", "Urban"))+
  facet_wrap(~block, ncol=2)+
  ylab("Development Rate")+
   theme_fivethirtyeight() +
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
        legend.key = element_blank(),
        panel.grid.major.x = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        axis.title = element_text(),
        axis.title.x = element_text(),
        axis.title.y=element_text(),
        #strip.background = element_blank(),
        strip.text.x = element_text(size=12),
        axis.line=element_line(color=axisColor, size=0.5),
        panel.grid = element_blank(),
        axis.text.y=element_text(size=12),
        axis.text.x=element_text(size=12))+
  theme(legend.position="none") +
  theme(strip.background = element_blank(),
  strip.text.x = element_blank()) +
  theme(axis.title.x = element_blank(),
        axis.text.x = element_blank(),
        axis.title.y= element_text(size=10))

growthPlot <- ggplot(data=growthDF2, aes(x=class, y=r))+
  geom_boxplot(aes(fill=class), width=0.4)+
  scale_fill_manual(values=c(colR, colS, colU), labels=c("Rural", "Suburban", "Urban"))+
  facet_wrap(~block, ncol=2)+
   theme_fivethirtyeight() +
```

```
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
        legend.key = element_blank(),
        panel.grid.major.x = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        axis.title = element_text(),
        axis.title.x = element_text(),
        axis.title.y=element_text(),
        #strip.background = element_blank(),
        strip.text.x = element_text(size=12),
        axis.line=element_line(color=axisColor, size=0.5),
        panel.grid = element_blank(),
        axis.text.y=element_text(size=12),
        axis.text.x=element_text(size=12))+
  theme(legend.position="none") +
  theme(strip.background = element_blank(),
  strip.text.x = element_blank()) +
  ylab("Per Capita Growth\nRate (r')")+
  xlab("Land Class") +
  theme(axis.text.x = element_text(size=10)) +
  theme(axis.title = element_text(size=12),
        axis.title.y= element_text(size=10))

plot_grid(survPlot, emergePlot, growthPlot,
          labels=c("A", "B", "C"),
          nrow=3,
          align='v')

#dev.off()
```

Statistics

Season x Land Class

Model Selection

```
#model selection by AIC and logLik
m1 <- lmer(r ~ block + (1|Site_Code),
                   data=growthDF2)

m2 <- lmer(r ~ class + (1|Site_Code),
                   data=growthDF2)

m3 <- lmer(r ~ block + class + (1|Site_Code),
                   data=growthDF2)

m4 <- lmer(r ~ block*class + (1|Site_Code),
                   data=growthDF2)

modelSums <- do.call(rbind, lapply(list(m1,m2,m3, m4), broom::glance))
modelSums #m1 is best
```

```
##          sigma    logLik       AIC       BIC  deviance df.residual
```

```
## 1 0.02317469 150.8876 -293.7752 -284.7812 -319.0258          66
## 2 0.04934191 101.7433 -193.4867 -182.2442 -225.4769          65
## 3 0.02317408 144.3205 -276.6410 -263.1500 -319.4812          64
## 4 0.02304346 138.7162 -261.4324 -243.4445 -322.2346          62
```

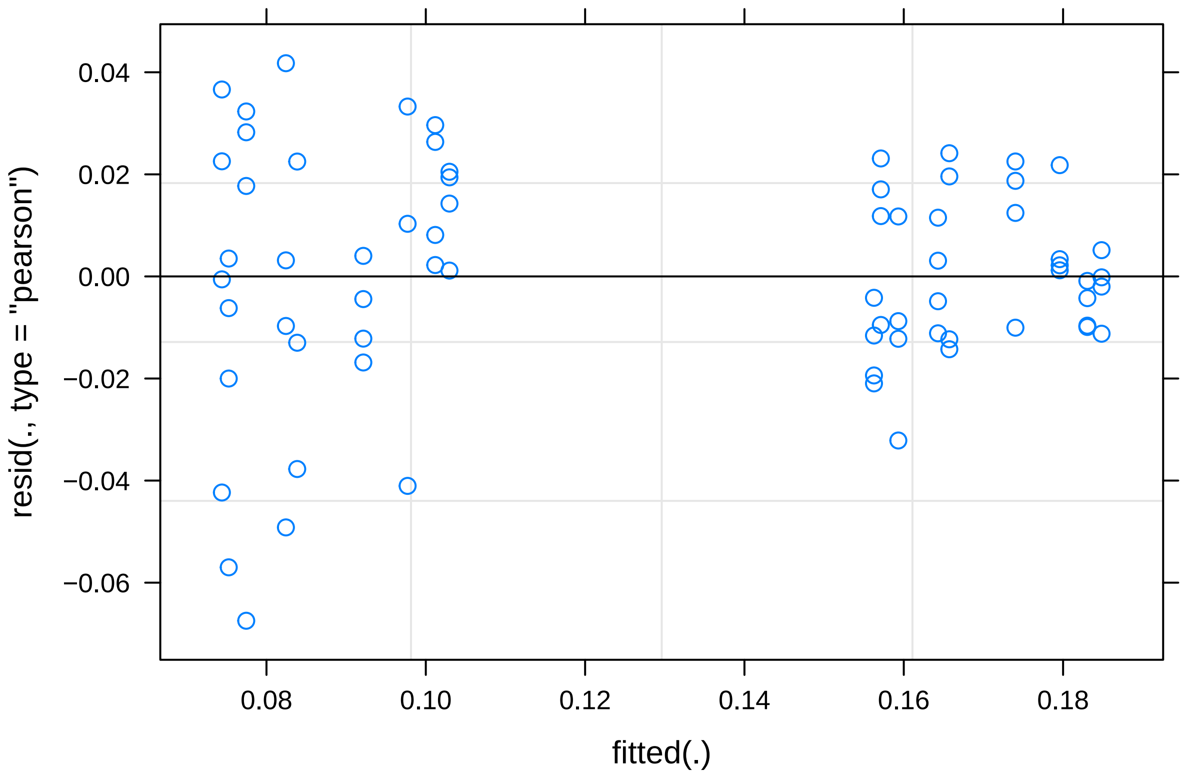
```r
AICc(m1,m2,m3, m4) #still m1
```

```
##    df      AICc
## m1  4 -293.1598
## m2  5 -192.5492
## m3  6 -275.3076
## m4  8 -259.0718
```

```r
growthModSeason <- lmer(r~ block+ (1|Site_Code),
                        data=growthDF2)

summary(growthModSeason)
```

```
## Linear mixed model fit by REML ['lmerMod']
## Formula: r ~ block + (1 | Site_Code)
##    Data: growthDF2
##
## REML criterion at convergence: -301.8
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.91104 -0.48351  0.05068  0.75767  1.80245
##
## Random effects:
##  Groups    Name        Variance  Std.Dev.
##  Site_Code (Intercept) 0.0001764 0.01328
##  Residual              0.0005371 0.02317
## Number of obs: 70, groups:  Site_Code, 9
##
## Fixed effects:
##              Estimate Std. Error t value
## (Intercept)  0.169354   0.005876   28.82
## blockFall   -0.081859   0.005548  -14.75
##
## Correlation of Fixed Effects:
##           (Intr)
## blockFall -0.458
```

```r
plot(growthModSeason)
```




```
tidy(growthModSeason)
```

```
##                        term     estimate    std.error statistic     group
## 1               (Intercept)  0.16935442 0.005875706  28.82282     fixed
## 2                 blockFall -0.08185939 0.005548448 -14.75356     fixed
## 3 sd_(Intercept).Site_Code  0.01328340          NA        NA Site_Code
## 4  sd_Observation.Residual  0.02317469          NA        NA  Residual
```

```
car::Anova(growthModSeason) #Wald test
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: r
##        Chisq Df Pr(>Chisq)
## block 217.67  1  < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

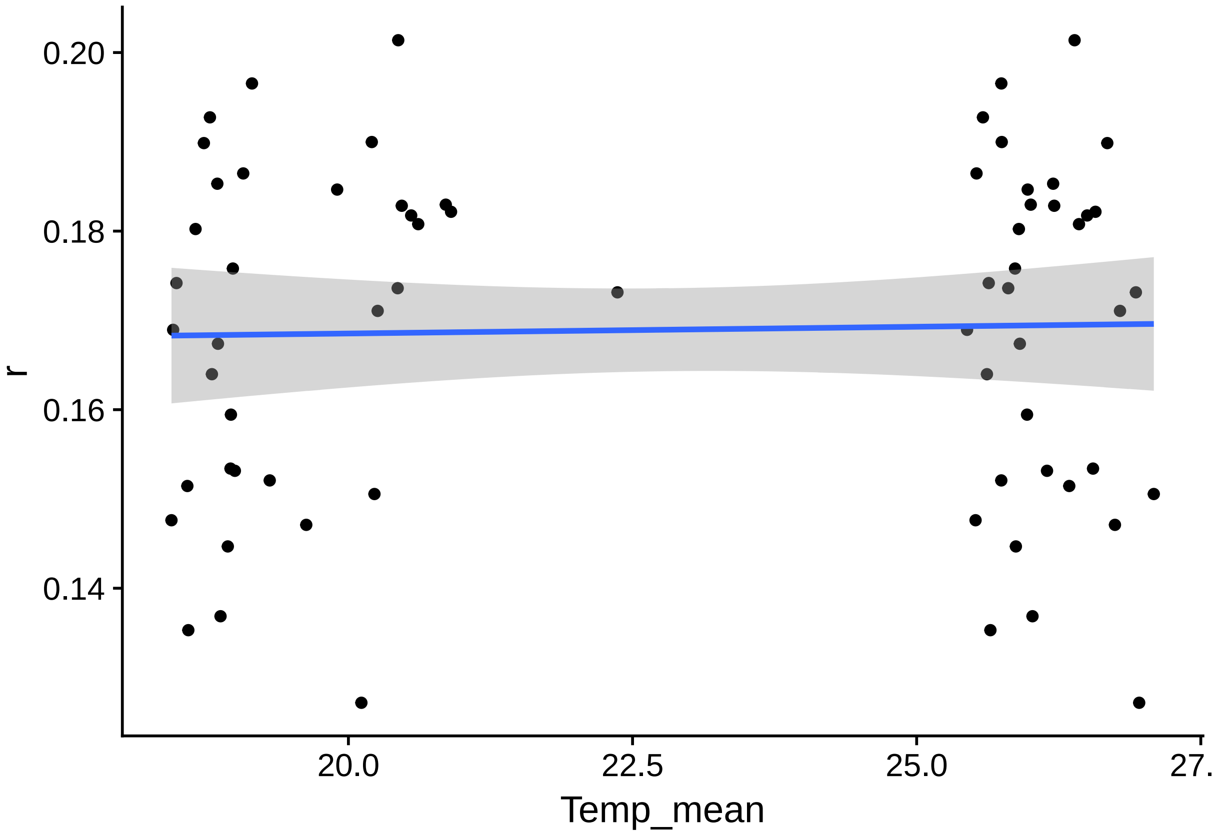
```
confint(growthModSeason) #profiled confidence interval
```

```
##                    2.5 %      97.5 %
## .sig01       0.005098632  0.02410232
## .sigma       0.019439256  0.02774893
## (Intercept)  0.157555871  0.18115298
## blockFall   -0.092829521 -0.07091747
```

Microclimate

```
levels(allClim$block) <- factor(as.character(allClim$block), levels=c("Summer", "Fall"))
#get temperature data
```

```r
growthTemp <- merge(growthDF2, allClim, by.x=c("block","Tray_Code"), by.y=c("block", "Tray_ID"))
ggplot(data=growthTemp, aes(x=Temp_mean, y=r))+
  geom_point()+
  geom_smooth(method="lm")
```




```r
growthTempMod <- lm(r~Temp_mean,
                    data=growthTemp)
summary(growthTempMod)
```

```
##
## Call:
## lm(formula = r ~ Temp_mean, data = growthTemp)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.042414 -0.016481  0.004224  0.014253  0.032784
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.1655056  0.0158639   10.43 1.34e-15 ***
## Temp_mean   0.0001513  0.0006878    0.22    0.827
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01919 on 66 degrees of freedom
## Multiple R-squared:  0.0007328,  Adjusted R-squared:  -0.01441
## F-statistic: 0.0484 on 1 and 66 DF,  p-value: 0.8266
```

```
anova(growthTempMod)
```

```
## Analysis of Variance Table
##
## Response: r
##           Df    Sum Sq   Mean Sq F value Pr(>F)
## Temp_mean  1 0.0000178 1.782e-05  0.0484 0.8266
## Residuals 66 0.0243013 3.682e-04
```

Vectorial Capacity

```
climS <- climate[climate$Day >="2016-08-01" & climate$Day <="2016-09-03",]
climS$Block <- "summer"

climF <- climate[climate$Day >="2016-09-26" & climate$Day <="2016-11-08",]
climF$Block <- "fall"

#bind back together
climAll <- rbind(climS, climF)
climAll$Date <- as.POSIXct(climAll$Date)
climAll$Hour <- lubridate::hour(climAll$Date)

parameters <- dplyr::select(climAll, Block, Class, Site_ID, Tray_ID, Temp, Day, Hour)
```

Calculated set at 27C constant (x=27):

Briere: y ~ a * x * (x - t0) * (tmax - x)^(1/2) Quad: y ~ a * (x-t0) * (x-Tmax)

```
parameters <- unique(dplyr::select(climAll, Block, Class, Site_ID))
#a -- bite rate
parameters$a <- ((1.93/10000)*27*(27-10.25)*((38.32-27)^0.5))
#adjust negatives
parameters$a[parameters$a<0] <- 0
parameters$a[is.na(parameters$a)] <- 0

# PDR - parasite development rate
parameters$PDR <- ((1.09/10000)*27*(27-10.39)*((43.05-27)^0.5))
#adjust negatives
parameters$PDR[parameters$PDR<0] <- 0
parameters$PDR[is.na(parameters$PDR)] <- 0

# lf - mosquito lifespan
parameters$lf <- -1.43*(27- 13.41)*(27-31.51)
#adjust for zeros
parameters$lf[parameters$lf<0] <- 0
parameters$lf[is.na(parameters$lf)] <- 0

# we will then calculate the mean and se for these parameters per site and hour, then sum them up for a
library(dplyr)

paramRate <- parameters

paramRate <- dplyr::rename(paramRate, Site_Code=Site_ID)
```

```
paramRate <- dplyr::rename(paramRate, block=Block)

## u - daily probability of mosquito mortality
paramRate$mu <- 1/paramRate$lf

paramRate$block <- tolower(paramRate$block)
paramRate$Class <- tolower(paramRate$Class)

paramRateOld <- paramRate
```

Combine with field measured fecundity, survival, development rate and vector competence:

```
#EFD: from wing length
EFD  <- allWing %>%
  group_by(block, Class=class, Site_Code) %>%
  dplyr::summarise(wingL=mean(mm, na.rm=T)) %>%
  ungroup() %>%
  mutate(fecundity=-121.240 + (78.02*wingL))
EFD$block <- tolower(EFD$block)
EFD$Class <- tolower(EFD$Class)

#pEA: larval survival
pEA <- survSumm %>%
  group_by(block, Class, Site_Code) %>%
  dplyr::summarise(pEA=mean((percSurv/50), na.rm=T))
pEA$block <- tolower(pEA$block)
pEA$Class <- tolower(pEA$Class)

#MDR: emergence rate (day^-1)
MDR <- emergTray %>%
  group_by(block, Class, Site_Code) %>%
  dplyr::summarise(MDR=mean(devRate, na.rm=T))
MDR$block <- tolower(MDR$block)
MDR$Class <- tolower(MDR$Class)

#bc
bc <- seasonInfSite %>%
  dplyr::select(block, Class=class, Site_Code=site, bc=Saliva_mean)
bc$block <- tolower(bc$block)
bc$Class <- tolower(bc$Class)
```

Merge traits together

```
paramRate <- full_join(paramRate, EFD, by=c("block", "Class", "Site_Code"))
paramRate <- full_join(paramRate, pEA, by=c("block", "Class", "Site_Code"))
paramRate <- full_join(paramRate, MDR, by=c("block", "Class", "Site_Code"))
paramRate <- full_join(paramRate, bc, by=c("block", "Class", "Site_Code"))
```

Calculate EFD

```
paramRate$EFD <- paramRate$fecundity*paramRate$a
```

Calcuate VC w/o carry-over effects

```
paramNoCOE <- dplyr::select(climAll, Block, Class, Site_ID, Tray_ID, Temp, Day, Hour)
```

```
#based on model
paramNoCOE$fecundity2 <- ((4.88/100)*27*(27-8.02)*((35.65-27)^0.5))/24
paramNoCOE$fecundity2[paramNoCOE$fecundity2<0] <- 0
paramNoCOE$fecundity2[is.na(paramNoCOE$fecundity2)] <- 0

paramNoCOE$bc2 <- (((7.35/10000)*27*(27-15.84)*((36.40-27)^0.5)) * ((4.39/10000)*27*(27-3.62)*((36.82-2
paramNoCOE$bc2[paramNoCOE$bc2<0] <- 0
paramNoCOE$bc2[is.na(paramNoCOE$bc2)] <- 0


#take mean of each hour and sum up
library(dplyr)
paramRateNoCOE <- paramNoCOE %>%
  group_by(Block, Class, Site_ID, Hour) %>%
  dplyr::select(-Temp, -Day, -Tray_ID) %>%
  summarise_all(funs(mean(.,na.rm=T))) %>%
  ungroup() %>%
  group_by(Block, Class, Site_ID) %>%
  summarise_all(funs(sum)) %>%
  ungroup()

paramRateNoCOE <- dplyr::rename(paramRateNoCOE, Site_Code=Site_ID)
paramRateNoCOE <- dplyr::rename(paramRateNoCOE, block=Block)

paramRateNoCOE$Class <- tolower(paramRateNoCOE$Class)
```

Merge w/ and w/o carry-over effects together

```
paramAll <- full_join(paramRate, paramRateNoCOE, by=c("block", "Class", "Site_Code"))

#calculate EFD
paramAll$EFD2 <- paramAll$fecundity2*paramAll$a
```

Calculate VC from traits (VCnoCOE is w/o carry-over)

```
paramAll <- mutate(paramAll,
                   VC=((a^2)*bc*(exp(-mu/PDR))*EFD*pEA*(MDR^2))/((mu^2)))

paramAll <- mutate(paramAll,
                  VCnoCOE=(((a^2)*bc2*(exp(-mu/PDR))*EFD2*pEA*(MDR^2))/((mu^2))))
```

Plot

Figure 5.

```
siteTemps <- dplyr::select(seasonInfSite, block, site, class, Temp_mean_mean)
levels(paramAll$Class) <- c("Rural", "Suburban", "Urban")
VCplot <- merge(paramAll, siteTemps, by.x=c("block", "Site_Code"), by.y=c("block", "site"))
VCplot <- VCplot %>%
  dplyr::select(block, Class, Site_Code, VC, VCnoCOE, Temp_mean_mean) %>%
  mutate(VCdiff=(VC-VCnoCOE)/VCnoCOE*100)
VCplot$block <- factor(VCplot$block, levels=c("summer", "fall"))
```

```
#pdf(file="figures/forMS/VCxTemp.pdf", width = 4, height=4, family="sans")
```

```r
VCxTempPlot <- ggplot(data=VCplot, aes(x=Temp_mean_mean))+
  geom_smooth(aes(y=VC, color="WithCOE"), method="lm", show.legend=F)+
  geom_smooth(aes(y=VCnoCOE, color="WithoutCOE"),  method="lm", show.legend=F)+
  geom_smooth(aes(y=VC, color="WithCOE"), method="lm", fill=NA)+
  geom_smooth(aes(y=VCnoCOE, color="WithoutCOE"),  method="lm", fill=NA)+
  geom_point(aes(y=VC, color="WithCOE")) +
  geom_point(aes(y=VCnoCOE, color="WithoutCOE"))+
  coord_cartesian(ylim=c(0,40))+
  theme_fivethirtyeight()+
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
        legend.key = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        legend.position="bottom",
        legend.direction="horizontal",
        axis.title = element_text(),
        legend.text=element_text(size=8),
        legend.title = element_text(size=10),
        axis.line=element_line(color="gray40", size=0.5),
        panel.grid = element_blank())+
  guides(colour=guide_legend(title.position="top", title.hjust=0.5))+
  xlab("Temperature (C)")+
  ylab("Vectorial Capacity")+
  scale_colour_manual(name="Calcuation Type",
                      #values=c(WithCOE="#af8dc3", WithoutCOE="#7fbf7b"),
                      values=c(WithCOE="black", WithoutCOE="gray55"),
                      labels=c("With COEs", "Without COEs"))
#dev.off()
```

```r
#get mean and se summary
VCplotsumm <- VCplot %>%
  dplyr::select(-Site_Code) %>%
  gather(calc, value, VC, VCnoCOE, VCdiff) %>%
  group_by(block, Class, calc) %>%
  dplyr::summarise_all(funs(mean=mean(., na.rm=T), se=sd(.)/sqrt(n()))) %>%
  ungroup()
#add in facet labels
VCplotsumm$labels <- case_when(
  VCplotsumm$calc=="VC" ~ "With COEs" ,
  VCplotsumm$calc=="VCnoCOE" ~ "No COEs",
  VCplotsumm$calc=="VCdiff" ~ "Difference due to COEs"
)
VCplotsumm$labels <- factor(VCplotsumm$labels, levels=c("No COEs", "With COEs", "Difference due to COEs
#order factor
VCplotsumm$calc <- factor(VCplotsumm$calc, levels=c("VCnoCOE", "VC", "VCdiff"))
```

```r
noCOEplot <- ggplot(data=VCplotsumm[VCplotsumm$labels=="No COEs",], aes(x=factor(Class), group=block)) +
  geom_bar(stat='identity',
           aes(y=value_mean, fill=Class, alpha=block, color=Class),
           position=position_dodge(0.9),
           width=0.7) +
  geom_errorbar(aes(ymin=value_mean-value_se, ymax=value_mean+value_se),
                position=position_dodge(0.9),
                width=0.4,
```

```
                color=errorColor)+
  ylim(0,50)+
  #facet_wrap(~labels, nrow=3) +
  #theme_fivethirtyeight() +
  ylab("Vectorial Capacity")+
  xlab("Land Class")+
  #theme_fivethirtyeight() +
  scale_x_discrete(labels=c("Rural", "Suburban", "Urban"))+
  scale_fill_manual(values=c(colR, colS, colU),
                    labels=c("Rural", "Suburban", "Urban")) +
  scale_color_manual(values=c(colR, colS, colU))+
  scale_alpha_discrete(range=c(1,0),
                       name="Season",
                       guide=guide_legend(),
                       labels=c("Summer", "Fall"))+
  #geom_hline(aes(yintercept=0))+
  guides(fill=F, alpha=F, color=F)+
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
        legend.key = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        legend.position="right",
        axis.title.y=element_text(size=12),
        axis.title.x = element_blank(),
        axis.text.x = element_text(size=10),
        legend.text=element_text(size=6),
        legend.title = element_text(size=8),
        legend.key.size = unit(0.1, "in"),
        legend.direction = "vertical",
        legend.box = "vertical",
        panel.grid.major.x = element_blank(),
        panel.grid.major=element_blank(),
        strip.background = element_blank(),
        axis.ticks=element_blank(),
        axis.line=element_line(color=axisColor)) +
 theme(strip.text.x = element_text()) #this has to be seperate for some reason?


withCOEplot <- ggplot(data=VCplotsumm[VCplotsumm$labels=="With COEs",], aes(x=factor(Class), group=bloc
  geom_bar(stat='identity',
           aes(y=value_mean, fill=Class, alpha=block, color=Class),
           position=position_dodge(0.9),
           width=0.7) +
  geom_errorbar(aes(ymin=value_mean-value_se, ymax=value_mean+value_se),
                position=position_dodge(0.9),
                width=0.4,
                color=errorColor)+
  ylim(0,50)+
  #facet_wrap(~labels, nrow=3) +
  ylab("Vectorial Capacity")+
  xlab("Land Class")+
  #theme_fivethirtyeight() +
  scale_x_discrete(labels=c("Rural", "Suburban", "Urban"))+
```

```
  scale_fill_manual(values=c(colR, colS, colU),
                    labels=c("Rural", "Suburban", "Urban")) +
  scale_color_manual(values=c(colR, colS, colU))+
  scale_alpha_discrete(range=c(1,0),
                       name="Season",
                       guide=guide_legend(),
                       labels=c("Summer", "Fall"))+
  #geom_hline(aes(yintercept=0))+
  guides(color=F, fill=F, alpha=F)+
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
        legend.key = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        legend.position="right",
        axis.title.y=element_text(size=12),
        axis.title.x = element_blank(),
        axis.text.x = element_text(size=10),
        legend.text=element_text(size=6),
        legend.title = element_text(size=8),
        legend.key.size = unit(0.1, "in"),
        legend.direction = "vertical",
        legend.box = "vertical",
        panel.grid.major.x = element_blank(),
        panel.grid.major=element_blank(),
        strip.background = element_blank(),
        axis.line = element_line(color=axisColor),
        axis.ticks=element_blank()) +
 theme(strip.text.x = element_text()) #this has to be seperate for some reason?

diffPlot <- ggplot(data=VCplotsumm[VCplotsumm$labels=="Difference due to COEs",], aes(x=factor(Class),
  geom_bar(stat='identity',
           aes(y=value_mean, fill=Class, alpha=block, color=Class),
           position=position_dodge(0.9),
           width=0.7) +
  geom_errorbar(aes(ymin=value_mean-value_se, ymax=value_mean+value_se),
                position=position_dodge(0.9),
                width=0.4,
                color=errorColor)+
  #theme_fivethirtyeight() +
  ylab("Change in VC") +
  xlab("Land Class") +
  scale_x_discrete(labels=c("Rural", "Suburban", "Urban"))+
  scale_fill_manual(values=c(colR, colS, colU),
                    labels=c("Rural", "Suburban", "Urban")) +
  scale_color_manual(values=c(colR, colS, colU))+
  scale_alpha_discrete(range=c(1,0),
                       name="Season",
                       guide=guide_legend(),
                       labels=c("Summer", "Fall"))+
  geom_hline(aes(yintercept=0))+
  guides(color=F, alpha=guide_legend(override.aes=list(color=axisColor)))+
  theme(panel.background = element_rect(fill = "transparent", colour = NA),
        plot.background = element_rect(fill = "transparent", colour = NA),
```

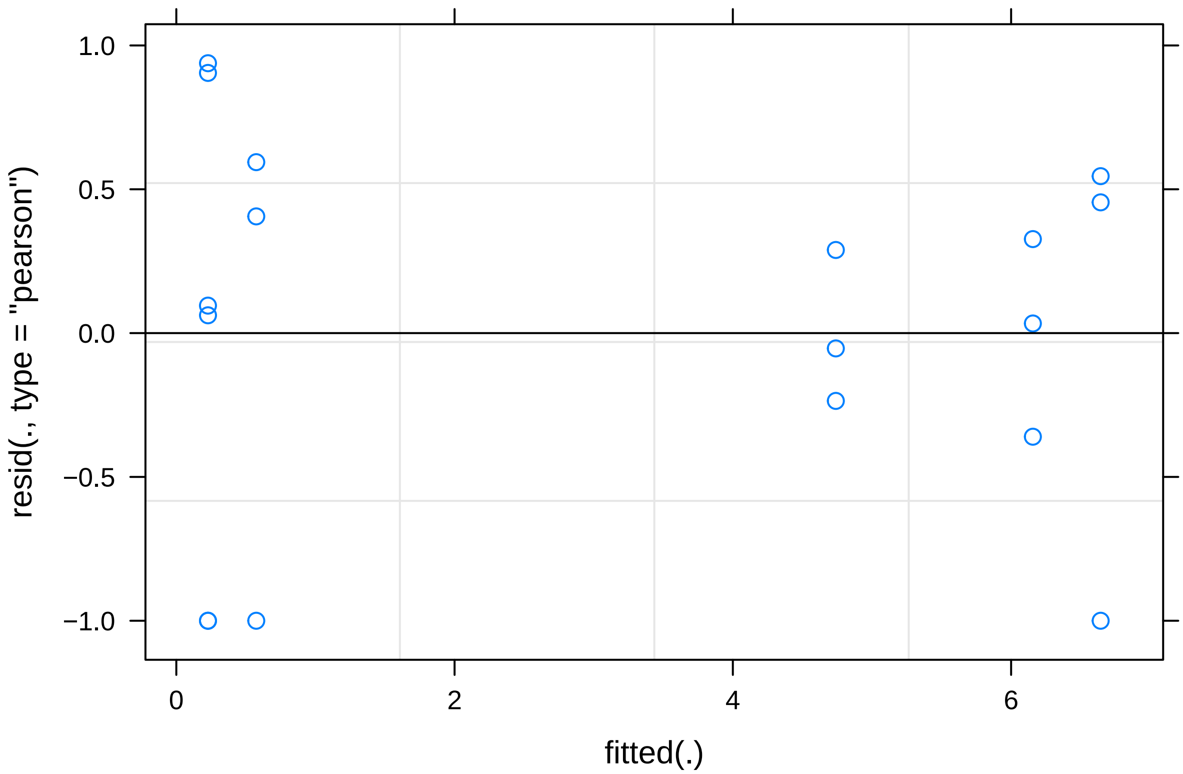
```
        legend.key = element_blank(),
        legend.background = element_rect(fill = "transparent", colour = NA),
        legend.position="bottom",
        axis.title.y = element_text(size=12),
        axis.title.x = element_text(size=12),
        axis.text.x = element_text(size=10),
        legend.text=element_text(size=8),
        legend.title = element_text(size=12),
        legend.key.size = unit(0.1, "in"),
        legend.direction = "horizontal",
        legend.box = "vertical",
        panel.grid.major.x = element_blank(),
        panel.grid.major=element_blank(),
        strip.background = element_blank(),
        axis.ticks=element_blank(),
        axis.line = element_line(color=axisColor)) +
 theme(strip.text.x = element_text()) #this has to be seperate for some reason?
```

Use cowplot to combine the three bar graphs and VC over temp chart.

```
#pdf(file="figures/forMS/VCPlot.pdf", width = 10, height=7, family="sans")

ggdraw()+
  draw_plot(VCxTempPlot, x=0, y=0, width=0.7, height=1)+
  draw_plot(noCOEplot, x=0.7, y=0.72, width=0.3, height=0.28)+
  draw_plot(withCOEplot, x=0.7, y=0.44, width=0.3, height=0.28)+
  draw_plot(diffPlot, x=0.685, y=0, width=0.3, height=0.44)+
  draw_plot_label(label=c("A", "B", "C", "D"),
                  x=c(0,0.67,0.67,0.67),
                  y=c(1,1,0.72,0.44))
#dev.off()
```

Statistics

```
VCplot$VCforStats <- VCplot$VC+0.000000001
VCplot$VCforStatsnoCOE <- VCplot$VCnoCOE+0.000000001
VCclass <- glmer(VCforStats~Class*block+ (1|Site_Code),
                 data=VCplot,
                family=Gamma())

plot(VCclass)
```




```r
summary(VCclass)
```

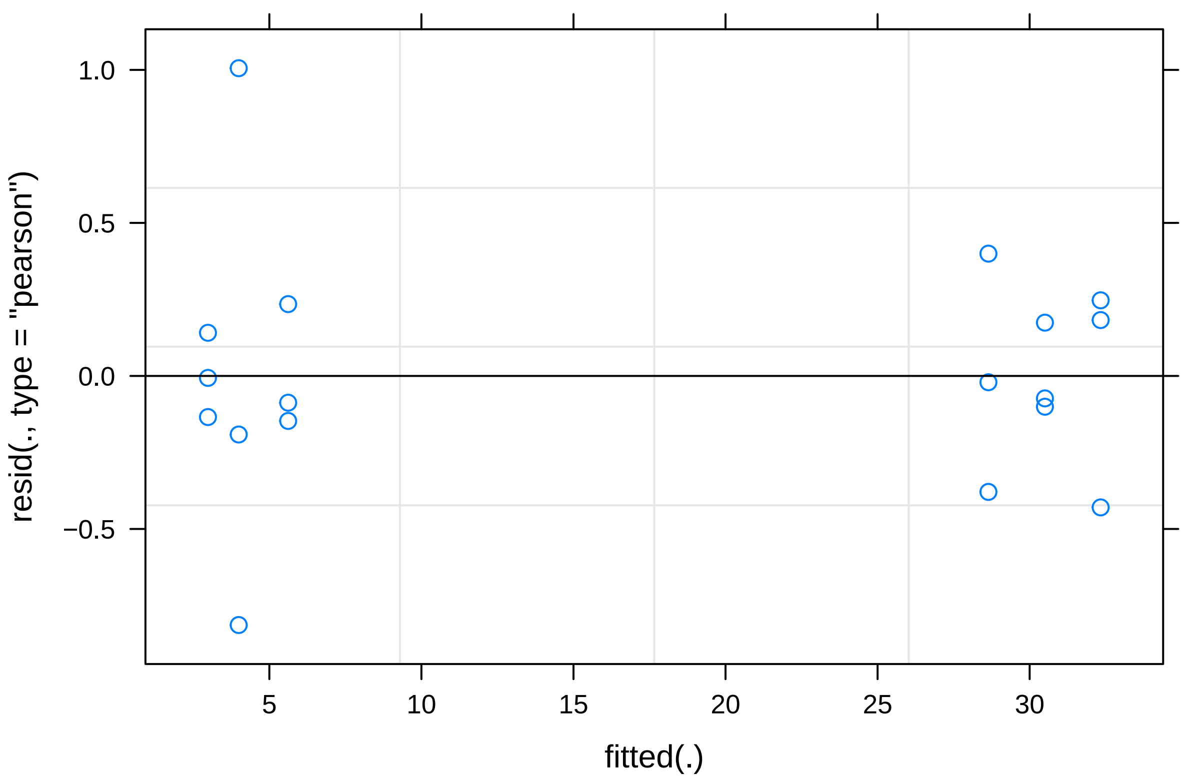
```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Gamma  ( inverse )
## Formula: VCforStats ~ Class * block + (1 | Site_Code)
##    Data: VCplot
##
##      AIC      BIC   logLik deviance df.resid
##    -21.3    -14.2     18.6    -37.3       10
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -1.5908 -0.5236  0.1252  0.7036  1.4925
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Site_Code (Intercept) 0.0000   0.0000
##  Residual              0.3951   0.6286
## Number of obs: 18, groups:  Site_Code, 9
##
## Fixed effects:
##                         Estimate Std. Error t value Pr(>|z|)
## (Intercept)              0.21097    0.28460   0.741    0.459
## Classsuburban           -0.04853    0.35919  -0.135    0.893
## Classurban              -0.06044    0.34962  -0.173    0.863
## blockfall                4.18018    5.93087   0.705    0.481
## Classsuburban:blockfall  0.05330    8.39037   0.006    0.995
## Classurban:blockfall    -2.59022    6.38198  -0.406    0.685
```

```
##
## Correlation of Fixed Effects:
##              (Intr) Clsssb Clssrb blckfl Clsss:
## Classsubrbn -0.792
## Classurban  -0.814  0.645
## blockfall   -0.048  0.038  0.039
## Clsssbrbn:b  0.034 -0.043 -0.028 -0.707
## Clssrbn:blc  0.045 -0.035 -0.055 -0.929  0.657
```

```
car::Anova(VCclass)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: VCforStats
##               Chisq Df Pr(>Chisq)
## Class        0.0400  2     0.9802
## block        1.1650  1     0.2804
## Class:block 0.2958  2     0.8625
```

```
VCclassnoCOE <- glmer(VCforStatsnoCOE~Class*block+ (1|Site_Code),
                 data=VCplot,
                family=Gamma())

plot(VCclassnoCOE)
```




```
summary(VCclassnoCOE)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: Gamma  ( inverse )
## Formula: VCforStatsnoCOE ~ Class * block + (1 | Site_Code)
```

```
##    Data: VCplot
##
##      AIC      BIC   logLik deviance df.resid
##    122.2    129.3    -53.1    106.2       10
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.2014 -0.3893 -0.1272  0.4879  2.7192
##
## Random effects:
##  Groups    Name        Variance Std.Dev.
##  Site_Code (Intercept) 0.0000   0.0000
##  Residual              0.1367   0.3697
## Number of obs: 18, groups:  Site_Code, 9
##
## Fixed effects:
##                            Estimate Std. Error t value Pr(>|z|)
## (Intercept)                0.032784   0.007897   4.152  3.3e-05 ***
## Classsuburban              0.002126   0.011536   0.184 0.853751
## Classurban                -0.001858   0.010856  -0.171 0.864088
## blockfall                  0.302685   0.081193   3.728 0.000193 ***
## Classsuburban:blockfall -0.087132   0.101503  -0.858 0.390666
## Classurban:blockfall    -0.155630   0.092118  -1.689 0.091132 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) Clsssb Clssrb blckfl Clsss:
## Classsubrbn -0.685
## Classurban  -0.727  0.498
## blockfall   -0.097  0.067  0.071
## Clsssbrbn:b  0.078 -0.114 -0.057 -0.800
## Clssrbn:blc  0.086 -0.059 -0.118 -0.881  0.705
```

```r
car::Anova(VCclassnoCOE)
```

```
## Analysis of Deviance Table (Type II Wald chisquare tests)
##
## Response: VCforStatsnoCOE
##               Chisq Df Pr(>Chisq)
## Class        0.2985  2     0.8614
## block       34.7659  1  3.718e-09 ***
## Class:block  3.0744  2     0.2150
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#make long for comparison of with and without carry-over
VClong <- VCplot %>%
  gather(COE, value, VC, VCnoCOE)

VCtemp <- lm(value~Temp_mean_mean*COE, data=VClong)
#plot(VCtemp)
summary(VCtemp)
```

```
##
## Call:
```

```
## lm(formula = value ~ Temp_mean_mean * COE, data = VClong)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -14.3372  -1.3931   0.4208   1.1874  10.8765
##
## Coefficients:
##                            Estimate Std. Error t value Pr(>|t|)
## (Intercept)                -15.2797     8.1697  -1.870   0.0706 .
## Temp_mean_mean               0.8017     0.3527   2.273   0.0299 *
## COEVCnoCOE                 -57.0284    11.5537  -4.936 2.39e-05 ***
## Temp_mean_mean:COEVCnoCOE    3.1099     0.4988   6.234 5.52e-07 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 4.984 on 32 degrees of freedom
## Multiple R-squared:  0.8631, Adjusted R-squared:  0.8502
## F-statistic: 67.24 on 3 and 32 DF,  p-value: 6.578e-14
```

```
## Vectorial Capacity (w carry over) across Temp
VCtempCOE <- lm(VCforStats~Temp_mean_mean, data=VCplot)
#plot(VCtempCOE)
summary(VCtempCOE)
```

```
##
## Call:
## lm(formula = VCforStats ~ Temp_mean_mean, data = VCplot)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -6.2585 -1.3362  0.2381  0.8065  4.4154
##
## Coefficients:
##                 Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -15.2797     3.9592  -3.859 0.001388 **
## Temp_mean_mean   0.8017     0.1709   4.690 0.000246 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.415 on 16 degrees of freedom
## Multiple R-squared:  0.5789, Adjusted R-squared:  0.5526
## F-statistic: 21.99 on 1 and 16 DF,  p-value: 0.000246
```