

Padula_2025_Wing_Diff_Analysis

Sara Padula

2025-03-13

Load Libraries

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'  
  
## The following objects are masked from 'package:stats':  
##  
##   filter, lag  
  
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.4.3
```

```
library(cowplot)  
library(lme4)
```

```
## Warning: package 'lme4' was built under R version 4.4.3
```

```
## Loading required package: Matrix
```

```
library(lmerTest)
```

```
##  
## Attaching package: 'lmerTest'  
  
## The following object is masked from 'package:lme4':  
##  
##   lmer  
  
## The following object is masked from 'package:stats':  
##  
##   step
```

```
library(DHARMa)
```

```
## This is DHARMa 0.4.7. For overview type '?DHARMa'. For recent changes, type news(package = 'DHARMa')
```

```
library(glmmTMB)
```

```
## Warning: package 'glmmTMB' was built under R version 4.4.3
```

```
library(car)
```

```
## Loading required package: carData
```

```
##
```

```
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      recode
```

```
library(emmeans)
```

```
## Warning: package 'emmeans' was built under R version 4.4.3
```

```
## Welcome to emmeans.
```

```
## Caution: You lose important information if you filter this package's results.
```

```
## See '? untidy'
```

```
library(ggpubr)
```

```
## Warning: package 'ggpubr' was built under R version 4.4.3
```

```
##
```

```
## Attaching package: 'ggpubr'
```

```
## The following object is masked from 'package:cowplot':
```

```
##
```

```
##      get_legend
```

```
library(ggdist)
```

```
## Warning: package 'ggdist' was built under R version 4.4.3
```

```
library(patchwork)
```

```
## Warning: package 'patchwork' was built under R version 4.4.3
```

```
##
## Attaching package: 'patchwork'

## The following object is masked from 'package:cowplot':
##
## align_plots

library(ggeffects)

## Warning: package 'ggeffects' was built under R version 4.4.3

##
## Attaching package: 'ggeffects'

## The following object is masked from 'package:cowplot':
##
## get_title
```

Load data

```
#Loading data
breed <- read.csv("paired_SMI.csv")

## Scaling elevation variable for each species
breedMOCH <- breed %>%
  filter(Species == "MOCH") %>%
  mutate(scale_ele = scale(Elevation))

breedBCCH <- breed %>%
  filter(Species == "BCCH") %>%
  filter(Elevation < 2000) %>%
  mutate(scale_ele = scale(Elevation))

breed <- rbind(breedMOCH, breedBCCH)

#What is the sample size and mean wing difference in...

#MOCH?
nrow(breedMOCH)
```

```
## [1] 81
```

```
mean(breedMOCH$Wing_Difference)
```

```
## [1] 3.407407
```

```
#BCCH?
nrow(breedBCCH)
```

```
## [1] 63
```

```
mean(breedBCCH$Wing_Difference)
```

```
## [1] 3.301587
```

Breeding Success Analysis – Numerical wing difference variable

```
#first egg, removing blank values  
breed.fe <- breed %>% filter(!is.na(First.Egg))  
sum(breed.fe$Species == "MOCH")
```

```
## [1] 73
```

```
sum(breed.fe$Species == "BCCH")
```

```
## [1] 50
```

```
#clutch size, removing blank values  
breed.cs <- breed %>% filter(!is.na(Egg_Number))  
sum(breed.cs$Species == "MOCH")
```

```
## [1] 80
```

```
sum(breed.cs$Species == "BCCH")
```

```
## [1] 59
```

```
#brood size, removing blank values  
breed.bs <- breed %>% filter(!is.na(Nestling_Number))  
sum(breed.bs$Species == "MOCH")
```

```
## [1] 80
```

```
sum(breed.bs$Species == "BCCH")
```

```
## [1] 59
```

```
#nestling size, removing blank values  
breed.mm <- breed %>% filter(!is.na(Avg_Nestling_Weight))  
sum(breed.mm$Species == "MOCH")
```

```
## [1] 78
```

```
sum(breed.mm$Species == "BCCH")
```

```
## [1] 51
```

```
#Female SMI, removing blank values
breed.fs <- breed %>% filter(!is.na(Female_SMI))
sum(breed.fs$Species == "MOCH")
```

```
## [1] 79
```

```
sum(breed.fs$Species == "BCCH")
```

```
## [1] 63
```

```
#Male SMI, removing blank values
breed.ms <- breed %>% filter(!is.na(Male_SMI))
sum(breed.ms$Species == "MOCH")
```

```
## [1] 79
```

```
sum(breed.ms$Species == "BCCH")
```

```
## [1] 61
```

```
#Provisioning
breed.p <- breed %>% filter(!is.na(Provisioning))
sum(breed.p$Species == "MOCH")
```

```
## [1] 38
```

```
sum(breed.p$Species == "BCCH")
```

```
## [1] 48
```

Modeling date of first egg

```
# Add constant so log is defined (if needed)
min_FE <- min(breed.fe$First.Egg, na.rm = TRUE)
breed.fe$First.Egg_log <- log(breed.fe$First.Egg - min_FE + 1)

# Center the log-transformed First.Egg within Year × Elevation groups
breed.fe$First.Egg_log_Centered <- ave(breed.fe$First.Egg_log,
                                       interaction(breed.fe$Year, breed.fe$scale_ele),
                                       FUN = function(x) scale(x, center = TRUE, scale = FALSE))

## Model first egg #####
fe1 <- lmer(First.Egg_log_Centered ~ Wing_Difference*Species + scale_ele + (1|Year), data = breed.fe)

## boundary (singular) fit: see help('isSingular')
```

```
fe2 <- lmer(First.Egg_log_Centered ~ Species + scale_ele + (1|Year), data = breed.fe)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
anova(fe2, fe1) #wing difference doesn't significantly improve model fit
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breed.fe
```

```
## Models:
```

```
## fe2: First.Egg_log_Centered ~ Species + scale_ele + (1 | Year)
```

```
## fe1: First.Egg_log_Centered ~ Wing_Difference * Species + scale_ele + (1 | Year)
```

```
##      npar      AIC      BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
```

```
## fe2      5 -96.539 -82.478 53.269   -106.54
```

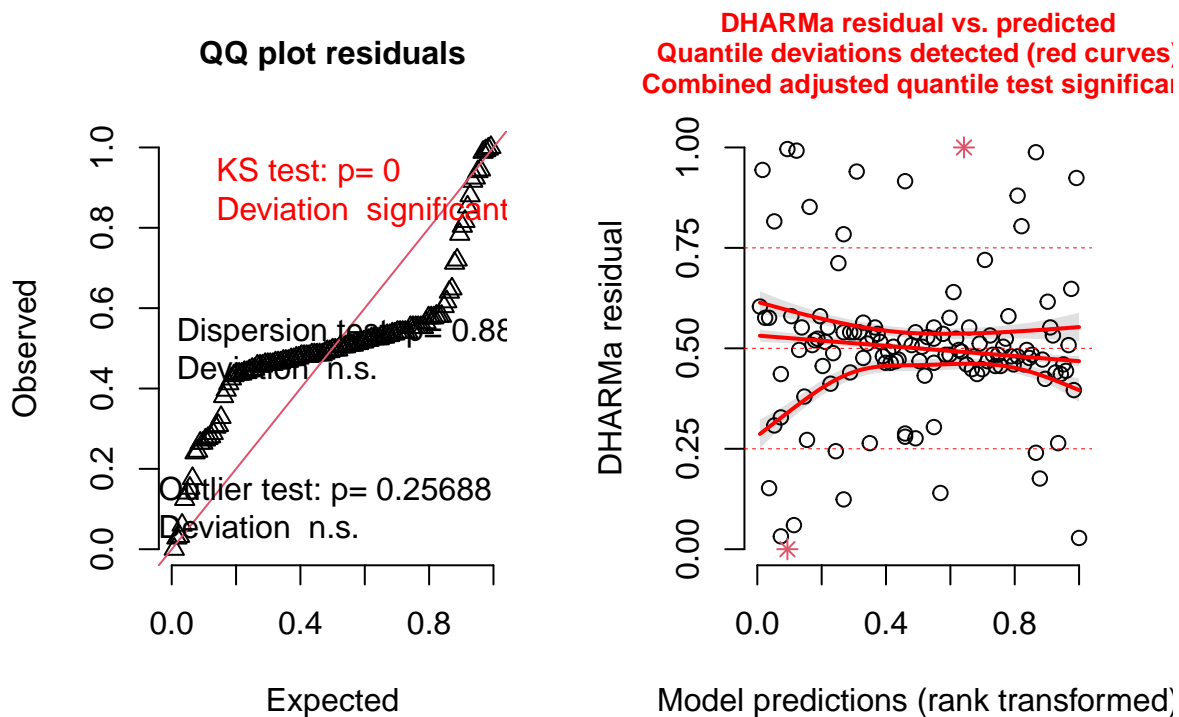
```
## fe1      7 -94.037 -74.352 54.019   -108.04 1.4987  2      0.4727
```

```
#Check residuals
```

```
fe1r = simulateResiduals(fe1)
```

```
plot(fe1r)
```

DHARMA residual



```
#quantile deviation
```

```
#wing diff doesnt improve fit and the model deviates, so we can confidently say that wing difference wi
```

```
summary(fe1) # species significant
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: First.Egg_log_Centered ~ Wing_Difference * Species + scale_ele +
## (1 | Year)
## Data: breed.fe
##
## REML criterion at convergence: -74.1
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -6.9665 -0.1209 -0.0144  0.0810  4.1056
##
## Random effects:
## Groups Name Variance Std.Dev.
## Year (Intercept) 1.103e-33 3.321e-17
## Residual 2.536e-02 1.592e-01
## Number of obs: 123, groups: Year, 6
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   -0.036157   0.039973 118.000000  -0.905   0.368
## Wing_Difference    0.009556   0.008715 118.000000   1.097   0.275
## SpeciesMOCH      0.022770   0.051686 118.000000   0.441   0.660
## scale_ele       0.001672   0.014782 118.000000   0.113   0.910
## Wing_Difference:SpeciesMOCH -0.005467   0.011994 118.000000  -0.456   0.649
##
## Correlation of Fixed Effects:
##              (Intr) Wng_Df SpMOCH scal_1
## Wing_Dffrnc -0.825
## SpeciesMOCH -0.773  0.637
## scale_ele -0.131  0.098  0.095
## Wng_D:SMOCH  0.598 -0.726 -0.822 -0.063
## optimizer (nlptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
mochFEp <- 0.675
```

```
bcchFEp <- 0.628
```

Modeling clutch size

```
cs1 <- glmmTMB(Egg_Number ~ Wing_Difference*Species, data =breed.cs,family = "genpois")
```

```
## Warning in (function (start, objective, gradient = NULL, hessian = NULL, :
## NA/NaN function evaluation
```

```
cs2 <- glmmTMB(Egg_Number ~ Species, data=breed.cs, family="genpois")
```

```
anova(cs1,cs2) # wing difference significantly improves model fit
```

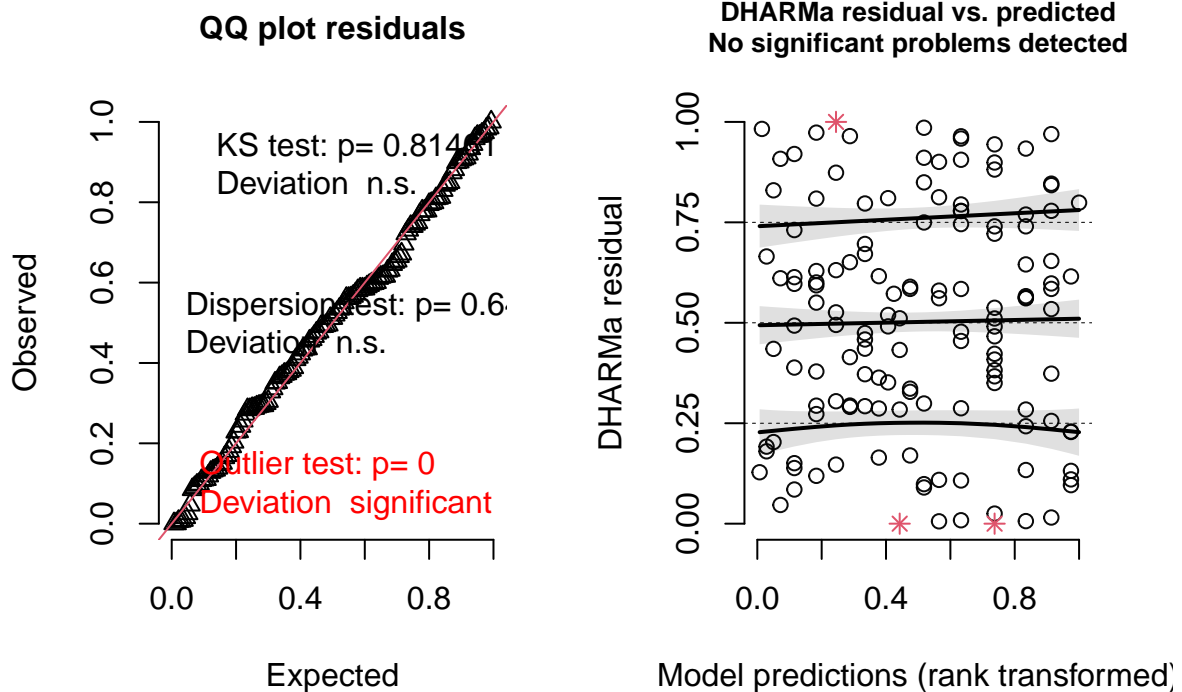
```
## Data: breed.cs
```

```
## Models:
## cs2: Egg_Number ~ Species, zi=~0, disp=~1
## cs1: Egg_Number ~ Wing_Difference * Species, zi=~0, disp=~1
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## cs2   3 455.86 464.66 -224.93  449.86
## cs1   5 453.77 468.44 -221.88  443.77 6.0932      2    0.04752 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#Check residuals
```

```
cs1r = simulateResiduals(cs1)
plot(cs1r)
```

DHARMA residual



```
#outliers significant on q-q plot
```

```
res <- cs1r$scaledResiduals
breed.cs$resid <- res
breed.cs[abs(res) > 2.5, ] # Inspect top outliers
```

```
## [1] Location      Nestbox      Species
## [4] Year          Male.Wing.Chord Male.Tarsus
## [7] Male.Bill     Male.Weight  Male.BillHead
## [10] Male.ID       Female.Wing.Chord Female.Tarsus
## [13] Female.Bill   Female.Weight Female.BillHead
## [16] Female.ID     Wing_Difference Tarsus_Difference
```



```
## [19] Bill_Difference      Weight_Difference      Wing_Difference_Category
## [22] BillHead_Difference   Egg_Number              Nestling_Number
## [25] Avg_Nestling_Weight   Egg_Nestling_Diff       Pair.ID
## [28] Avg.Wing              Avg.Tarsus              Avg.Weight
## [31] Avg.Nestling.Wing     Avg.Nestling.Tarsus     MaleBander
## [34] FemaleBander          Elevation               Male_SMI
## [37] Female_SMI            male.logwing            female.logwing
## [40] male.logmass          female.logmass          First.Egg
## [43] Provisioning          scale_ele               resid
## <0 rows> (or 0-length row.names)
```

```
#no evidence of true outliers, proceed with this model
```

```
summary(cs1) #species significant
```

```
## Family: genpois ( log )
## Formula:      Egg_Number ~ Wing_Difference * Species
## Data: breed.cs
##
##      AIC      BIC    logLik -2*log(L)  df.resid
##    453.8    468.4   -221.9    443.8      134
##
##
## Dispersion parameter for genpois family (): 0.222
##
## Conditional model:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.787206   0.036845  48.51 < 2e-16 ***
## Wing_Difference   -0.002147   0.008272  -0.26  0.795
## SpeciesMOCH        0.203787   0.050963   4.00 6.37e-05 ***
## Wing_Difference:SpeciesMOCH -0.020109   0.012246  -1.64  0.101
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mochCSp <- 0.101
```

```
bcchCSp <- 0.795
```

Modeling brood size

```
bs1 <- glmmTMB(Nestling_Number ~ Wing_Difference*Species + (1|Year), data = breed.bs, family="genpois")
```

```
## Warning in (function (start, objective, gradient = NULL, hessian = NULL, :
## NA/NaN function evaluation
```

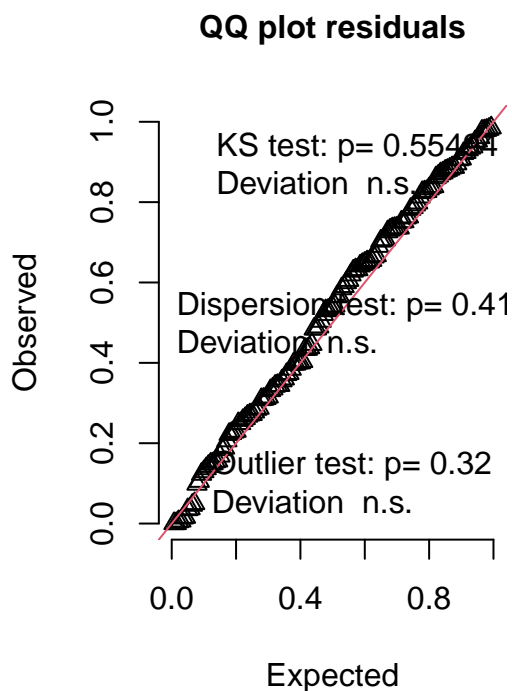
```
bs2 <- glmmTMB(Nestling_Number ~ Species + (1|Year), data = breed.bs, family = "genpois") #got error wh
```

```
anova(bs1,bs2) #wing difference significantly improves model fit
```

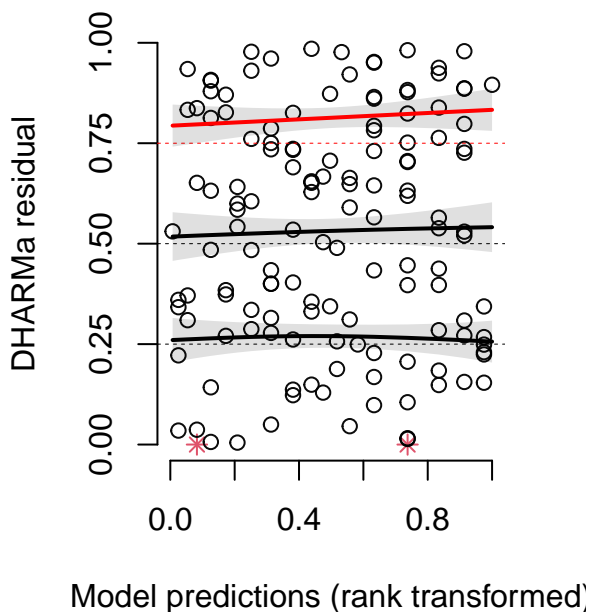
```
## Data: breed.bs
## Models:
## bs2: Nestling_Number ~ Species + (1 | Year), zi=~0, disp=~1
## bs1: Nestling_Number ~ Wing_Difference * Species + (1 | Year), zi=~0, disp=~1
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## bs2   4 541.25 552.99 -266.62  533.25
## bs1   6 532.42 550.03 -260.21  520.42 12.827    2  0.001639 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#check residuals
bs1r = simulateResiduals(bs1)
plot(bs1r)
```

DHARMA residual



DHARMA residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test n.s.



```
#look good
```

```
#Results
```

```
summary(bs1) #species and wing_difference*species significant
```

```
## Family: genpois ( log )
## Formula:      Nestling_Number ~ Wing_Difference * Species + (1 | Year)
## Data: breed.bs
##
##      AIC      BIC      logLik -2*log(L)  df.resid
## 532.4    550.0    -260.2    520.4      133
```

```
##
## Random effects:
##
## Conditional model:
##   Groups Name      Variance Std.Dev.
##   Year   (Intercept) 0.000934 0.03056
## Number of obs: 139, groups: Year, 6
##
## Dispersion parameter for genpois family (): 0.444
##
## Conditional model:
##
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      1.49324    0.06200  24.086 < 2e-16 ***
## Wing_Difference    0.01249    0.01344   0.929  0.35266
## SpeciesMOCH        0.37499    0.08216   4.564 5.01e-06 ***
## Wing_Difference:SpeciesMOCH -0.06374    0.01966  -3.243  0.00118 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mochBSp <- 0.00118
```

```
bcchBSp <- 0.353
```

Modeling average nestling mass

```
##Model nestling mass #####
mm1 <- lmer(Avg_Nestling_Weight ~ Wing_Difference*Species + Nestling_Number + (1|Year), data = breed.mm)
mm2 <- lmer(Avg_Nestling_Weight ~ Species + Nestling_Number + (1|Year), data = breed.mm)

anova(mm1, mm2) # wing difference significantly improves model fit
```

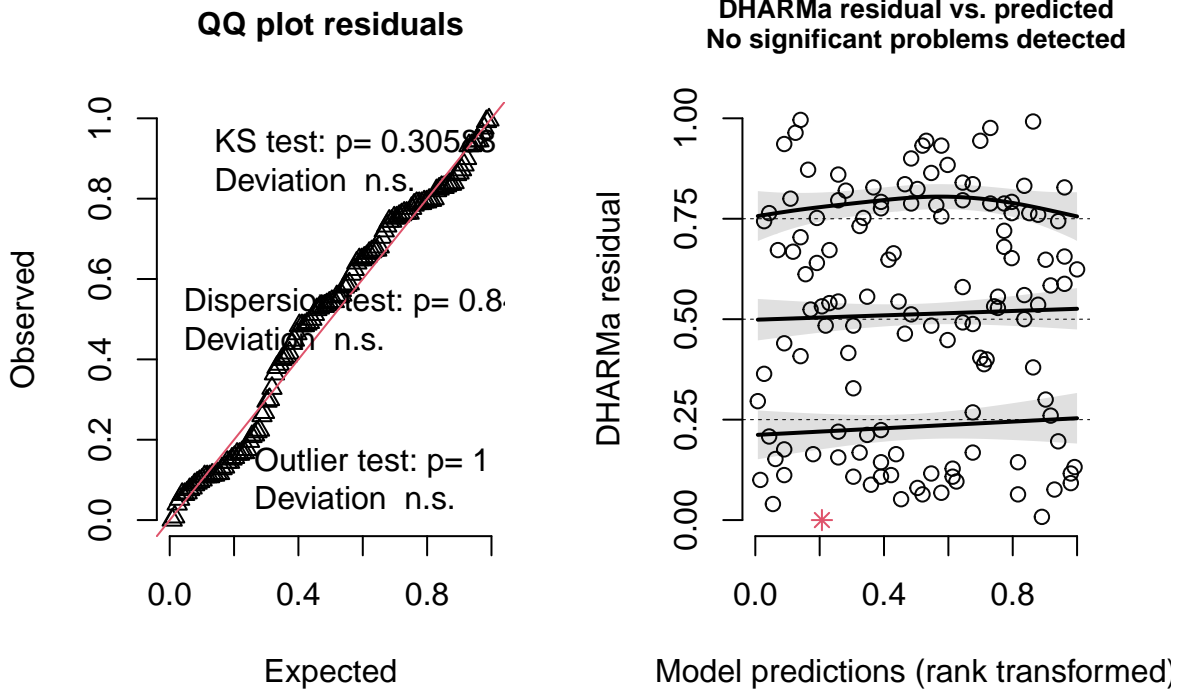
```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breed.mm
## Models:
## mm2: Avg_Nestling_Weight ~ Species + Nestling_Number + (1 | Year)
## mm1: Avg_Nestling_Weight ~ Wing_Difference * Species + Nestling_Number + (1 | Year)
##      npar    AIC    BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
## mm2     5 388.68 402.94 -189.34    378.68
## mm1     7 381.46 401.42 -183.73    367.46 11.218  2    0.003666 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#check residuals
mm1r = simulateResiduals(mm1)
plot(mm1r)
```

```
## Warning in newton(lsp = lsp, X = G$X, y = G$y, Eb = G$Eb, UrS = G$UrS, L = G$L,
## : Fitting terminated with step failure - check results carefully
```

DHARMA residual



#some deviation

#results

`summary(mm1)` *#wing_difference*species significant*

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Avg_Nestling_Weight ~ Wing_Difference * Species + Nestling_Number +
## (1 | Year)
## Data: breed.mm
##
## REML criterion at convergence: 382.3
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -2.7999 -0.8000  0.1289  0.7045  2.8708
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Year      (Intercept)  0.2652    0.5150
##   Residual                    0.9910    0.9955
## Number of obs: 128, groups: Year, 6
##
## Fixed effects:
##               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  10.355599   0.394462  35.934041  26.252  <2e-16
```

```
## Wing_Difference      0.015705    0.047756 120.278080    0.329    0.7428
## SpeciesMOCH          0.102748    0.321136 121.548860    0.320    0.7496
## Nestling_Number     -0.002022    0.059659 121.032995   -0.034    0.9730
## Wing_Difference:SpeciesMOCH  0.173507    0.073860 121.224225    2.349    0.0204
##
## (Intercept)          ***
## Wing_Difference
## SpeciesMOCH
## Nestling_Number
## Wing_Difference:SpeciesMOCH *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) Wng_Df SpMOCH Nstl_N
## Wing_Dffrnc -0.336
## SpeciesMOCH -0.077  0.466
## Nstlng_Nmbr -0.654 -0.059 -0.388
## Wng_D:SMOCH  0.049 -0.661 -0.784  0.304
```

```
mochMmp <- 0.0204
```

```
bcchMmp <- 0.7428
```

Modeling Female SMI

```
fs1 <- lmer(Female_SMI ~ Wing_Difference*Species + (1|Year), data = breed.fs)
fs2 <- lmer(Female_SMI ~ Species + (1|Year), data = breed.fs)
```

```
anova(fs1,fs2) # wing difference doesn't improve model fit
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breed.fs
```

```
## Models:
```

```
## fs2: Female_SMI ~ Species + (1 | Year)
```

```
## fs1: Female_SMI ~ Wing_Difference * Species + (1 | Year)
```

```
##      npar    AIC    BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
```

```
## fs2     4 379.10 390.93 -185.55    371.10
```

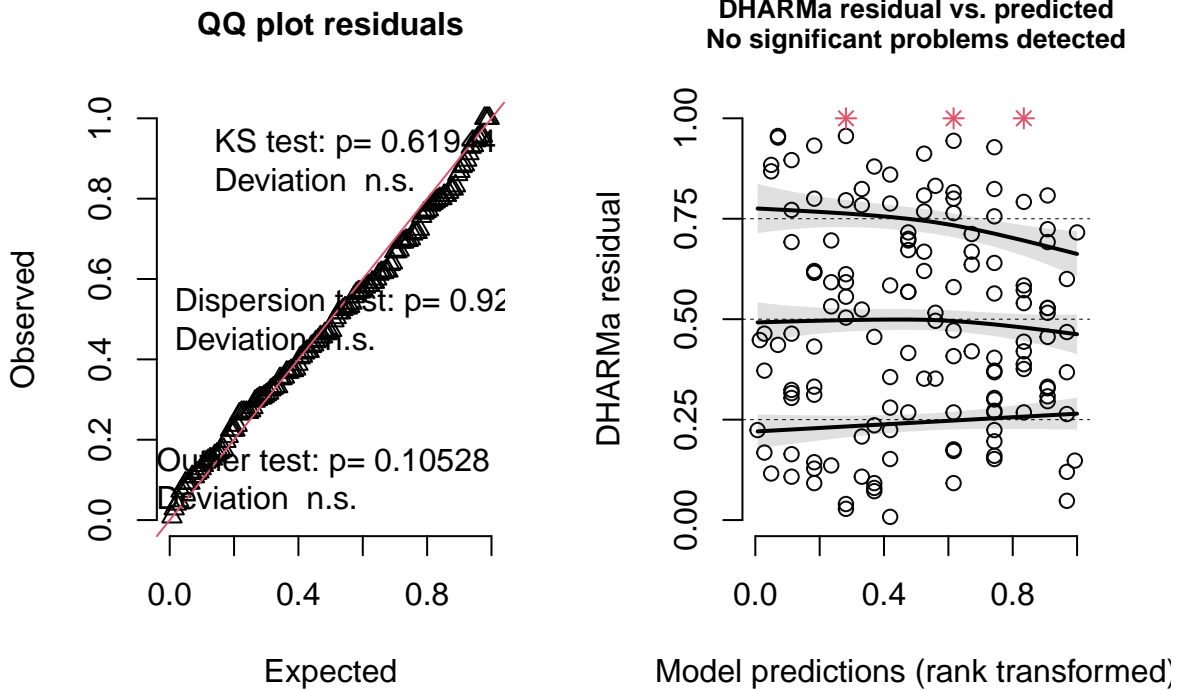
```
## fs1     6 382.46 400.19 -185.23    370.46 0.6461  2    0.7239
```

```
#check residuals
```

```
fs1r = simulateResiduals(fs1)
```

```
plot(fs1r)
```

DHARMA residual



#look okay

#results

*summary(fs1) #species*elevation significant, elevation almost significant*

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Female_SMI ~ Wing_Difference * Species + (1 | Year)
## Data: breed.fs
##
## REML criterion at convergence: 384.7
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -2.3909 -0.6279 -0.0641  0.5615  4.0482
##
## Random effects:
##   Groups Name          Variance Std.Dev.
##   Year    (Intercept)  0.00814  0.09022
##   Residual                0.81236  0.90131
## Number of obs: 142, groups: Year, 6
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)   1.143e+01  1.765e-01  3.965e+01  64.779  <2e-16
## Wing_Difference -2.262e-02  3.936e-02  1.377e+02  -0.575   0.566
```

```
## SpeciesMOCH          1.138e-01  2.527e-01  1.369e+02  0.450  0.653
## Wing_Difference:SpeciesMOCH -7.819e-04  5.959e-02  1.377e+02  -0.013  0.990
##
## (Intercept)          ***
## Wing_Difference
## SpeciesMOCH
## Wing_Difference:SpeciesMOCH
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##      (Intr) Wng_Df SpMOCH
## Wing_Dffrnc -0.734
## SpeciesMOCH -0.662  0.506
## Wng_D:SMOCH  0.484 -0.658 -0.792

mochFSp <- 0.990

bcchFSp <- 0.566
```

Modeling male SMI

```
ms1 <- lmer(Male_SMI ~ Wing_Difference*Species + (1|Year), data = breed.ms)
ms2 <- lmer(Male_SMI ~ Species + (1|Year), data = breed.ms)

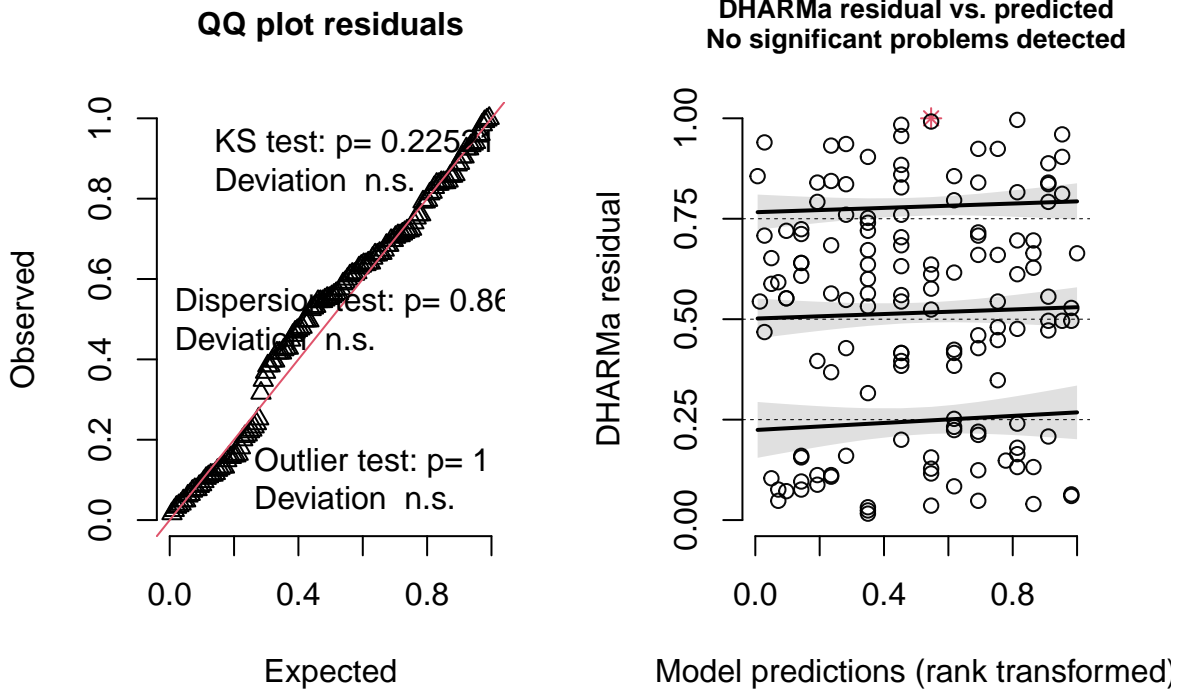
anova(ms1,ms2) #wing difference significantly improves model fit

## refitting model(s) with ML (instead of REML)

## Data: breed.ms
## Models:
## ms2: Male_SMI ~ Species + (1 | Year)
## ms1: Male_SMI ~ Wing_Difference * Species + (1 | Year)
##      npar    AIC    BIC  logLik -2*log(L)  Chisq Df Pr(>Chisq)
## ms2     4 319.52 331.29 -155.76    311.52
## ms1     6 315.34 332.99 -151.67    303.34 8.1789  2    0.01675 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

#check residuals
ms1r = simulateResiduals(ms1)
plot(ms1r)
```

DHARMA residual



#look good

#results

`summary(ms1)` *#wing_difference significant*

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Male_SMI ~ Wing_Difference * Species + (1 | Year)
## Data: breed.ms
##
## REML criterion at convergence: 319
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.28111 -0.85170  0.08054  0.57810  2.85026
##
## Random effects:
## Groups Name Variance Std.Dev.
## Year (Intercept) 0.01209 0.1099
## Residual 0.51728 0.7192
## Number of obs: 140, groups: Year, 6
##
## Fixed effects:
##              Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)  11.91983    0.14649  43.79162  81.368 < 2e-16 ***
## Wing_Difference -0.08832    0.03159 135.99021  -2.795  0.00593 **
```



```
## SpeciesMOCH          -0.31499    0.20366 135.83449  -1.547  0.12428
## Wing_Difference:SpeciesMOCH  0.07062    0.04794 135.50582   1.473  0.14301
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##          (Intr) Wng_Df SpMOCH
## Wing_Dffrnc -0.711
## SpeciesMOCH -0.642  0.500
## Wng_D:SMOCH  0.467 -0.655 -0.787
```

```
mochMSP <- 0.14301
```

```
bcchMSP <- 0.00593
```

Modeling provisioning rate

```
p1 <- lmer(Provisioning ~ Wing_Difference*Species + (1|Year), data = breed.p)
p2 <- lmer(Provisioning ~ Species + (1|Year), data = breed.p)
```

```
anova(p1,p2) #wing difference doesn't improve model fit
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breed.p
```

```
## Models:
```

```
## p2: Provisioning ~ Species + (1 | Year)
```

```
## p1: Provisioning ~ Wing_Difference * Species + (1 | Year)
```

```
##      npar    AIC    BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
```

```
## p2      4 601.70 611.51 -296.85    593.70
```

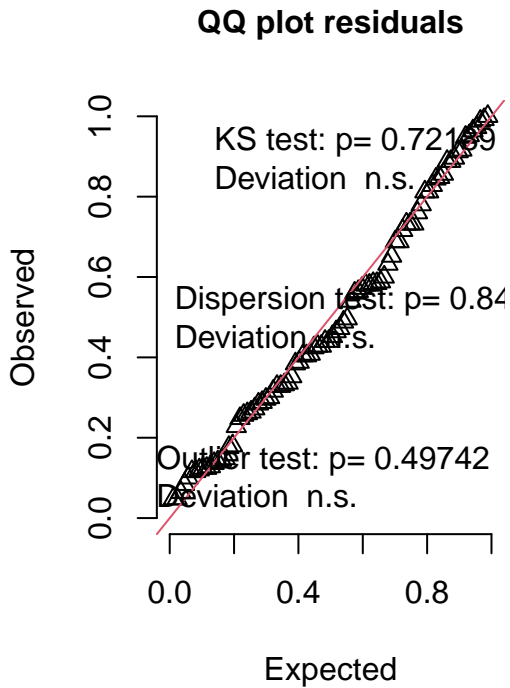
```
## p1      6 605.52 620.25 -296.76    593.52 0.1784  2    0.9147
```

```
#check residuals
```

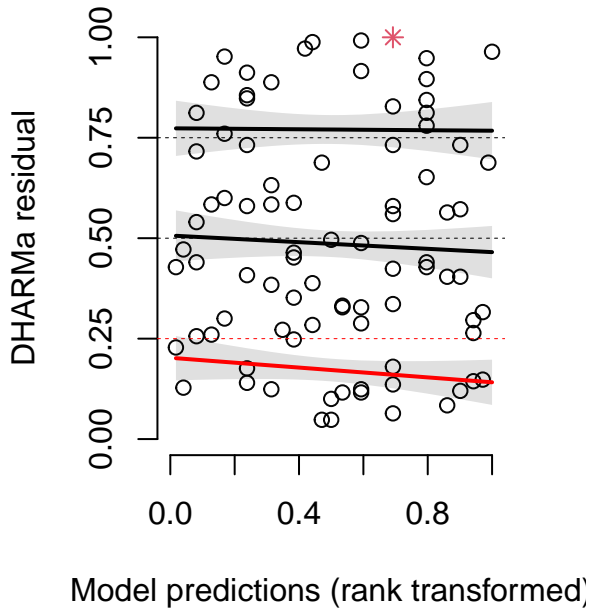
```
p1r = simulateResiduals(p1)
```

```
plot(p1r)
```

DHARMa residual



DHARMa residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



```
#quantile deviations
```

```
#results
```

```
summary(p1) #nothing significant
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Provisioning ~ Wing_Difference * Species + (1 | Year)
## Data: breed.p
##
## REML criterion at convergence: 588.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.8009 -0.6223 -0.1787  0.6160  3.2358
##
## Random effects:
## Groups Name Variance Std.Dev.
## Year (Intercept) 2.201 1.484
## Residual 59.491 7.713
## Number of obs: 86, groups: Year, 5
##
## Fixed effects:
##              Estimate Std. Error    df t value Pr(>|t|)
## (Intercept) 18.86580    1.89021 29.56625   9.981 5.6e-11 ***
## Wing_Difference -0.05069    0.37332 80.20824  -0.136 0.892
```

```
## SpeciesMOCH -0.25633 2.85599 80.14356 -0.090 0.929
## Wing_Difference:SpeciesMOCH -0.17497 0.64677 80.39404 -0.271 0.787
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Wng_Df SpMOCH
## Wing_Dffrnc -0.722
## SpeciesMOCH -0.577 0.484
## Wng_D:SMOCH 0.421 -0.577 -0.786
```

```
mochPp <- 0.787
```

```
bcchPp <- 0.892
```

Adjust the p-values to account for multiple comparisons

```
p_values <- c(mochFEp, bcchFEp, mochCSp, bcchCSp, mochBSp, bcchBSp, mochMMp, bcchMMp, mochFSp, bcchFSp,
p_adjusted <- p.adjust(p_values, method = "BH")
p_adjusted
```

```
## [1] 0.9275000 0.9275000 0.3535000 0.9275000 0.0165200 0.8236667 0.0952000
## [8] 0.9275000 0.9900000 0.9275000 0.4004280 0.0415100 0.9275000 0.9606154
```

Visualizing wing difference (numeric) predicting reproductive success variables.

```
# Use your fitted model with Wing_Difference
breed.fe$Species <- as.factor(breed.fe$Species)

fe1 <- lmer(First.Egg_log_Centered ~ Wing_Difference * Species + scale_ele + (1|Year), data = breed.fe)

## boundary (singular) fit: see help('isSingular')

# Generate predicted values over range of Wing_Difference for each species
preds_a <- ggpredict(fe1, terms = c("Wing_Difference", "Species"))

# Plot
a <- ggplot(preds_a, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "", y = "Pred. Scaled Date of First Egg", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2"))+
  theme_minimal()+
  theme(legend.position = "none")+
  theme(axis.title.y = element_text(size = 6))+
  theme(axis.text.y = element_text(size = 5))+
  theme(axis.text.x = element_text(size = 5))
```

```
## Warning: Using 'size' aesthetic for lines was deprecated in ggplot2 3.4.0.
```

```
## i Please use 'linewidth' instead.
## This warning is displayed once every 8 hours.
## Call 'lifecycle::last_lifecycle_warnings()' to see where this warning was
## generated.
```

```
# Use your fitted model with Wing_Difference
breed.cs$Species <- as.factor(breed.cs$Species)

cs1 <- glmmTMB(Egg_Number ~ Wing_Difference*Species, data =breed.cs,family = "genpois")
```

```
## Warning in (function (start, objective, gradient = NULL, hessian = NULL, :
## NA/NaN function evaluation
```

```
# Generate predicted values over range of Wing_Difference for each species
preds_b <- ggpredict(cs1, terms = c("Wing_Difference", "Species"))

b <- ggplot(preds_b, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "", y = "Pred. Clutch Size", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2"))+
  theme_minimal()+
  theme(legend.position = "none")+
  theme(axis.title.y = element_text(size = 6))+
  theme(axis.text.y = element_text(size = 5))+
  theme(axis.text.x = element_text(size = 5))
```

```
# Use your fitted model with Wing_Difference
breed.bs$Species <- as.factor(breed.bs$Species)
```

```
bs1 <- glmmTMB(Nestling_Number ~ Wing_Difference*Species, data =breed.bs,family = "genpois")
```

```
# Generate predicted values over range of Wing_Difference for each species
preds_c <- ggpredict(bs1, terms = c("Wing_Difference", "Species"))
```

```
c <- ggplot(preds_c, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "", y = "Pred. Brood Size", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2"))+
  theme_minimal()+
  theme(legend.position = "none")+
  theme(axis.title.y = element_text(size = 6))+
  theme(axis.text.y = element_text(size = 5))+
  theme(axis.text.x = element_text(size = 5))
```

```
breed.mm$Species <- as.factor(breed.mm$Species)
```

```
mm1 <- lmer(Avg_Nestling_Weight ~ Wing_Difference*Species + Nestling_Number + (1|Year), data = breed.mm)
```

```
# Generate predicted values over range of Wing_Difference for each species
```

```

preds_d <- ggpredict(bs1, terms = c("Wing_Difference", "Species"))

d <- ggplot(preds_d, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "", y = "Pred. Avg. Nestling Mass (g)", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2"))+
  theme_minimal()+
  theme(legend.position = "none")+
  theme(axis.title.y = element_text(size = 5))+
  theme(axis.text.y = element_text(size = 5))+
  theme(axis.text.x = element_text(size = 5))

breed.fs$Species <- as.factor(breed.fs$Species)

fs1 <- lmer(Female_SMI ~ Wing_Difference*Species + (1|Year), data = breed.fs)

# Generate predicted values over range of Wing_Difference for each species
preds_e <- ggpredict(fs1, terms = c("Wing_Difference", "Species"))

e <- ggplot(preds_e, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "", y = "Pred. Female Body Condition", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2"))+
  theme_minimal()+
  theme(legend.position = "none")+
  theme(axis.title.y = element_text(size = 5))+
  theme(axis.text.y = element_text(size = 5))+
  theme(axis.text.x = element_text(size = 5))

breed.ms$Species <- as.factor(breed.ms$Species)

ms1 <- lmer(Male_SMI ~ Wing_Difference*Species + (1|Year), data = breed.ms)

# Generate predicted values over range of Wing_Difference for each species
preds_f <- ggpredict(ms1, terms = c("Wing_Difference", "Species"))

f <- ggplot(preds_f, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "Wing Difference (mm)", y = "Pred. Male Body Condition", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2"))+
  theme_minimal()+
  theme(legend.position = "none")+
  theme(axis.title.y = element_text(size = 5))+
  theme(axis.text.y = element_text(size = 5))+
  theme(axis.text.x = element_text(size = 5))

breed.p$Species <- as.factor(breed.p$Species)

p1 <- lmer(Provisioning ~ Wing_Difference*Species + (1|Year), data = breed.p)

```

```

# Generate predicted values over range of Wing_Difference for each species
preds_g <- ggpredict(p1, terms = c("Wing_Difference", "Species"))

g <- ggplot(preds_g, aes(x = x, y = predicted, color = group)) +
  geom_line(size = 0.8) +
  geom_ribbon(aes(ymin = conf.low, ymax = conf.high, fill = group), alpha = 0.2, color = NA) +
  labs(x = "Wing Difference (mm)", y = "Pred. Provisioning Rate", color = "Species", fill = "Species") +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2")) +
  theme_minimal() +
  theme(legend.position = "none") +
  theme(axis.title.y = element_text(size = 5)) +
  theme(axis.text.y = element_text(size = 5)) +
  theme(axis.text.x = element_text(size = 5))

allLine <- (a + b + c)/(d + e + f + g)

ggsave("wingdiffRepVarPlot.png", plot = allLine, width = 6, height = 4, dpi = 300)

```

Does female wing length predict male wing length within pairs?

```

# Subset data by species
mochBreed <- subset(breed, Species == "MOCH")
bcchBreed <- subset(breed, Species == "BCCH")

### ---- MOCH: Does female wing predict male wing? ----

# Linear model
linM1 <- lmer(Male.Wing.Chord ~ Female.Wing.Chord + (1|Year), data = mochBreed)

# Summary of model
summary(linM1)

```

```

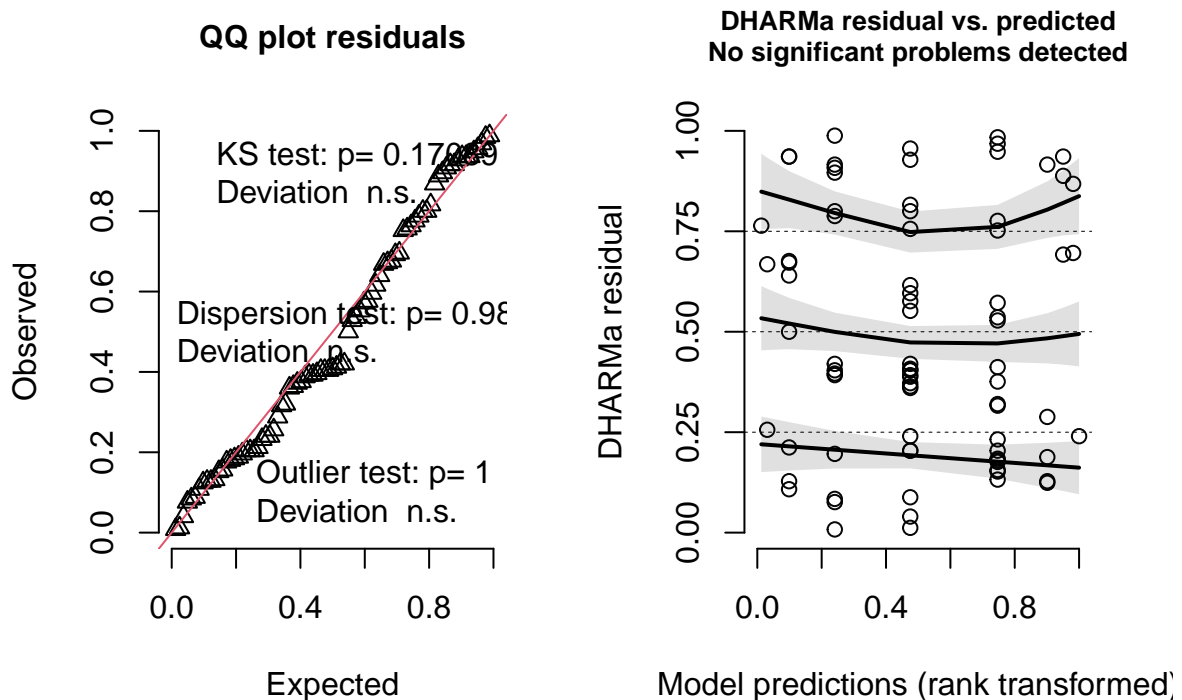
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Male.Wing.Chord ~ Female.Wing.Chord + (1 | Year)
## Data: mochBreed
##
## REML criterion at convergence: 326.9
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.5975 -0.6782 -0.1560  0.7051  1.9116
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Year      (Intercept) 0.2232   0.4724
##  Residual                 3.1355   1.7707
## Number of obs: 81, groups: Year, 6
##
## Fixed effects:

```

```
##               Estimate Std. Error      df t value Pr(>|t|)
## (Intercept)    59.5357     8.2396 78.3609   7.226 2.86e-10 ***
## Female.Wing.Chord  0.1519     0.1245 78.1504   1.220   0.226
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr)
## Fml.Wng.Chr -0.999

# Residual diagnostics
linM1_res <- simulateResiduals(linM1)
plot(linM1_res)
```

DHARMA residual



```
### ---- BCCH: Does female wing predict male wing? ----

# Linear model
linB1 <- lmer(Male.Wing.Chord ~ Female.Wing.Chord + (1|Year), data = bcchBreed)

# Summary of model
summary(linB1)

## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Male.Wing.Chord ~ Female.Wing.Chord + (1 | Year)
```

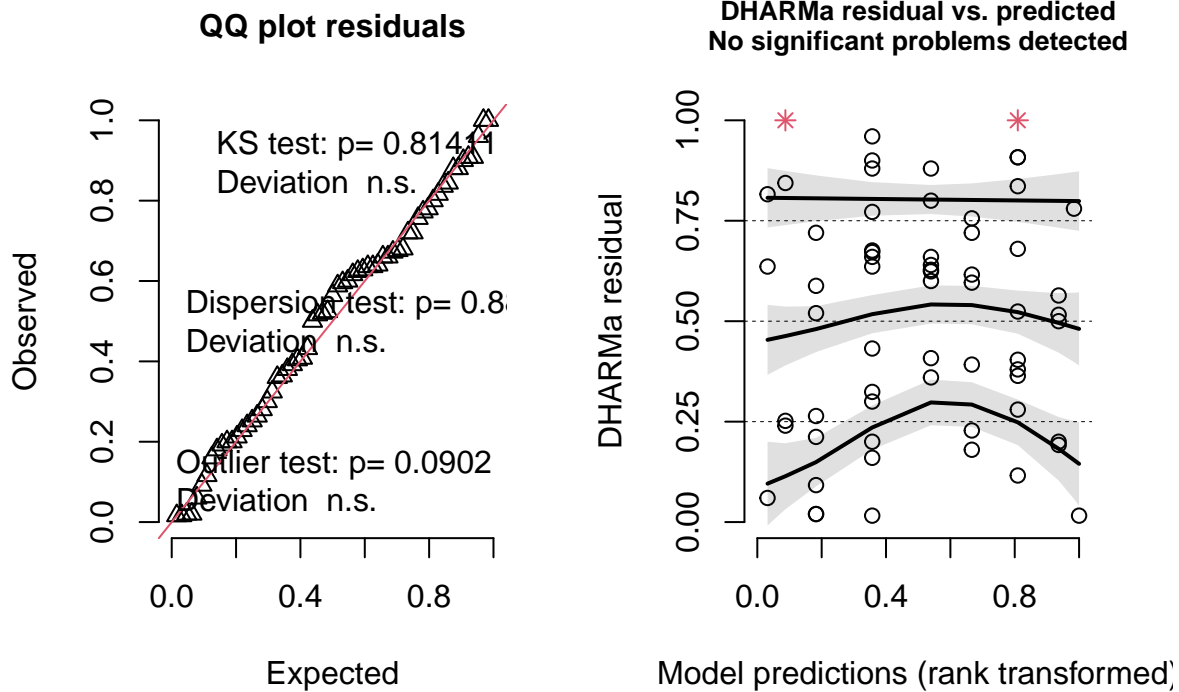
```

## Data: bcchBreed
##
## REML criterion at convergence: 289
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.31112 -0.70971  0.09945  0.54983  2.60580
##
## Random effects:
## Groups Name Variance Std.Dev.
## Year (Intercept) 0.08563 0.2926
## Residual 5.62933 2.3726
## Number of obs: 63, groups: Year, 6
##
## Fixed effects:
## Estimate Std. Error df t value Pr(>|t|)
## (Intercept) 53.9823 9.0203 60.9514 5.985 1.24e-07 ***
## Female.Wing.Chord 0.2081 0.1408 60.9211 1.478 0.145
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr)
## Fml.Wng.Chr -0.999

# Residual diagnostics
linB1_res <- simulateResiduals(linB1)
plot(linB1_res)

```


DHARMA residual



```
# Pearson's correlation for MOCH
moch_cor <- cor.test(mochBreed$Female.Wing.Chord, mochBreed$Male.Wing.Chord, method = "pearson")
print(moch_cor)
```

```
##
## Pearson's product-moment correlation
##
## data: mochBreed$Female.Wing.Chord and mochBreed$Male.Wing.Chord
## t = 1.2118, df = 79, p-value = 0.2292
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.08579094 0.34331188
## sample estimates:
## cor
## 0.135089
```

```
# Pearson's correlation for BCCH
bcch_cor <- cor.test(bcchBreed$Female.Wing.Chord, bcchBreed$Male.Wing.Chord, method = "pearson")
print(bcch_cor)
```

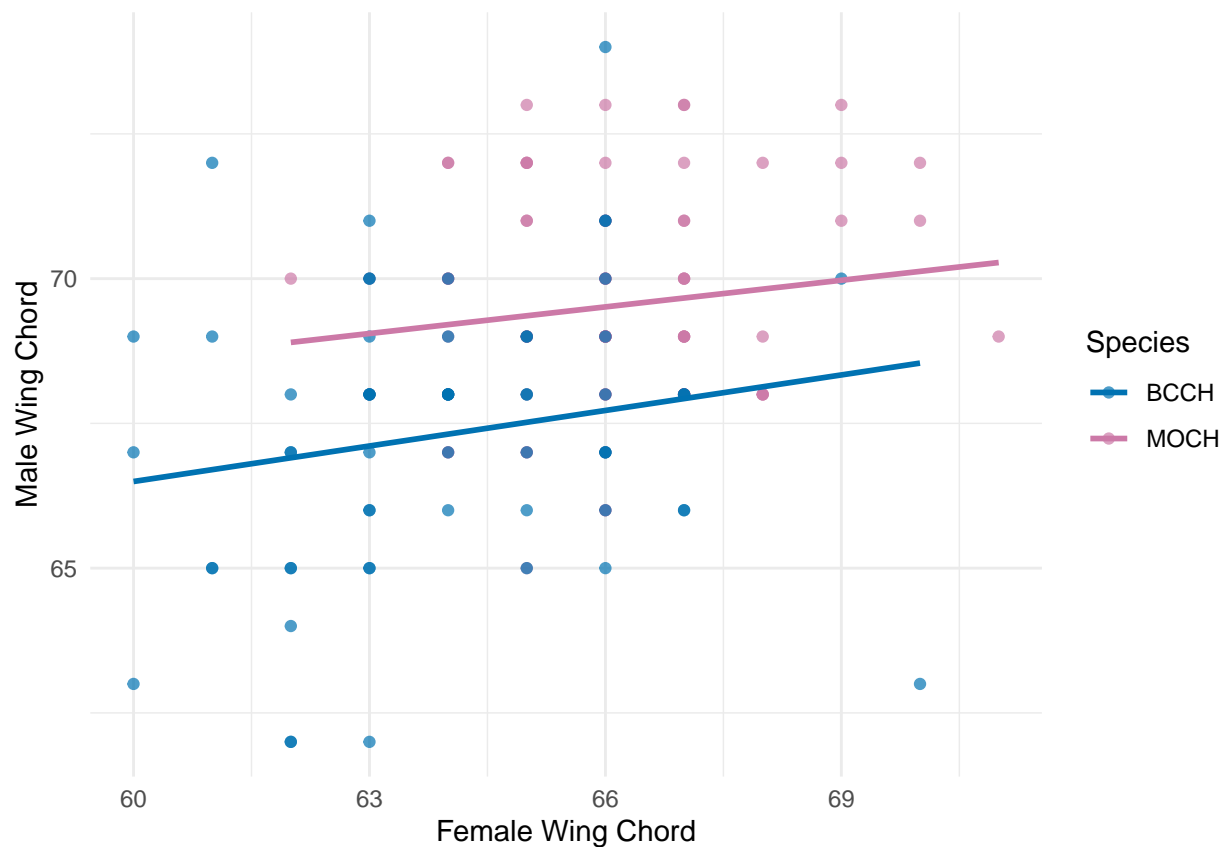
```
##
## Pearson's product-moment correlation
##
## data: bcchBreed$Female.Wing.Chord and bcchBreed$Male.Wing.Chord
## t = 1.451, df = 61, p-value = 0.1519
```

```
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
## -0.06819288 0.41178736
## sample estimates:
##      cor
## 0.1826583
```

Plot the linear models

```
ggplot(breed, aes(x = Female.Wing.Chord, y = Male.Wing.Chord, color = Species)) +
  geom_point(alpha = 0.7) +
  geom_smooth(method = "lm", se = FALSE) +
  scale_color_manual(values = c("MOCH" = "#cc79a7", "BCCH" = "#0072b2")) +
  labs(x = "Female Wing Chord", y = "Male Wing Chord") +
  theme_minimal()
```

```
## 'geom_smooth()' using formula = 'y ~ x'
```



Breeding Success Analysis – categorical wing difference (only male larger categories)

```
head(breed)
```

```
## Location Nestbox Species Year Male.Wing.Chord Male.Tarsus Male.Bill
## 1 BLD BLD-161 MOCH 2019 68 17.8 8.9
## 2 BLD BLD-334 MOCH 2019 71 18.6 8.8
## 3 BLD BLD-367 MOCH 2020 73 18.4 8.7
## 4 SGR SGR-236 MOCH 2020 71 19.5 8.8
## 5 MRS MRS-044 MOCH 2021 69 21.3 8.8
## 6 SGR SGR-137 MOCH 2021 69 22.4 8.9
## Male.Weight Male.BillHead Male.ID Female.Wing.Chord Female.Tarsus
## 1 12.0 29.5 283031951 67 18.0
## 2 12.0 30.6 283031954 65 19.3
## 3 11.0 29.1 283032093 67 18.5
## 4 12.0 29.6 283032100 69 19.6
## 5 11.5 29.5 291054241 66 21.3
## 6 NA 30.8 291053959 67 20.8
## Female.Bill Female.Weight Female.BillHead Female.ID Wing_Difference
## 1 9.5 11 29.7 283031952 1
## 2 8.7 9 29.0 209037443 6
## 3 8.8 12 29.6 283032092 6
## 4 9.2 11 30.1 283032099 2
## 5 9.9 11 30.4 291054242 3
## 6 8.6 NA 29.6 291053960 2
## Tarsus_Difference Bill_Difference Weight_Difference Wing_Difference_Category
## 1 -0.2 -0.6 1.0 Slightly
## 2 -0.7 0.1 3.0 Much
## 3 -0.1 -0.1 -1.0 Much
## 4 -0.1 -0.4 1.0 Slightly
## 5 0.0 -1.1 0.5 Slightly
## 6 1.6 0.3 NA Slightly
## BillHead_Difference Egg_Number Nestling_Number Avg_Nestling_Weight
## 1 -0.2 8 7 12.00
## 2 1.6 8 8 NA
## 3 -0.5 8 4 11.75
## 4 -0.5 8 8 10.88
## 5 -0.9 8 7 11.29
## 6 1.2 7 4 9.75
## Egg_Nestling_Diff Pair.ID Avg.Wing Avg.Tarsus Avg.Weight
## 1 1 283031951-283031952 67.5 17.90 11.50
## 2 0 283031954-209037443 68.0 18.95 10.50
## 3 4 283032093-283032092 70.0 18.45 11.50
## 4 0 283032100-283032099 70.0 19.55 11.50
## 5 1 291054241-291054242 67.5 21.30 11.25
## 6 3 291053959-291053960 68.0 21.60 0.00
## Avg.Nestling.Wing Avg.Nestling.Tarsus MaleBander FemaleBander Elevation
## 1 NA 17.94286 KCG KCG 1653.540
## 2 NA 19.98750 KCG KF 1691.640
## 3 NA 18.37500 KCG KCG 1798.320
## 4 NA 18.73750 KCG KCG 2491.740
## 5 30.71429 20.27143 ANT ANT 3060.192
```

```
## 6      25.00000      18.95000      ANT      ANT 2522.220
##  Male_SMI Female_SMI male.logwing female.logwing male.logmass female.logmass
## 1 11.97791 11.081054 4.219508 4.204693 2.484907 2.397895
## 2 11.66161 9.238249 4.262680 4.174387 2.484907 2.197225
## 3 10.50730 12.088423 4.290459 4.204693 2.397895 2.484907
## 4 11.66161 10.880837 4.262680 4.234107 2.484907 2.397895
## 5 11.37542 11.184835 4.234107 4.189655 2.442347 2.397895
## 6      NA      NA 4.234107 4.204693      NA      NA
##  First.Egg Provisioning scale_ele
## 1      120      20 -2.3925361
## 2      121      24 -2.2993401
## 3      126      12 -2.0383914
## 4      NA      16 -0.3422248
## 5      154      10 1.0482590
## 6      144      20 -0.2676680
```

```
breedCat <-breed[breed$Wing_Difference_Category %in% c("Much", "Slightly"), ]
```

```
#first egg, removing blank values
breedCat.fe <- breedCat %>% filter(!is.na(First.Egg))
sum(breedCat.fe$Species == "MOCH")
```

```
## [1] 66
```

```
sum(breedCat.fe$Species == "BCCH")
```

```
## [1] 45
```

```
#clutch size, removing blank values
breedCat.cs <- breedCat %>% filter(!is.na(Egg_Number))
sum(breedCat.cs$Species == "MOCH")
```

```
## [1] 73
```

```
sum(breedCat.cs$Species == "BCCH")
```

```
## [1] 50
```

```
#brood size, removing blank values
breedCat.bs <- breedCat %>% filter(!is.na(Nestling_Number))
sum(breedCat.bs$Species == "MOCH")
```

```
## [1] 73
```

```
sum(breedCat.bs$Species == "BCCH")
```

```
## [1] 50
```

```
#nestling size, removing blank values
breedCat.mm <- breedCat %>% filter(!is.na(Avg_Nestling_Weight))
sum(breedCat.mm$Species == "MOCH")
```

```
## [1] 71
```

```
sum(breedCat.mm$Species == "BCCH")
```

```
## [1] 43
```

```
#Female SMI, removing blank values
breedCat.fs <- breedCat %>% filter(!is.na(Female_SMI))
sum(breedCat.fs$Species == "MOCH")
```

```
## [1] 72
```

```
sum(breedCat.fs$Species == "BCCH")
```

```
## [1] 54
```

```
#Male SMI, removing blank values
breedCat.ms <- breedCat %>% filter(!is.na(Male_SMI))
sum(breedCat.ms$Species == "MOCH")
```

```
## [1] 72
```

```
sum(breedCat.ms$Species == "BCCH")
```

```
## [1] 52
```

```
#Provisioning
breedCat.p <- breedCat %>% filter(!is.na(Provisioning))
sum(breedCat.p$Species == "MOCH")
```

```
## [1] 34
```

```
sum(breedCat.p$Species == "BCCH")
```

```
## [1] 42
```

Modeling date of first egg

```

# Ensure elevation is numeric
breedCat.fe$scale_ele <- as.numeric(breedCat.fe$scale_ele)

# Center First.Egg within each Year x Elevation group
breedCat.fe$First.Egg_Centered <- ave(breedCat.fe$First.Egg,
                                     interaction(breedCat.fe$Year, breedCat.fe$scale_ele),
                                     FUN = function(x) scale(x, center = TRUE, scale = FALSE))

fec1 <- lmer(First.Egg_Centered ~ Wing_Difference_Category*Species + scale_ele + (1|Year), data = breedCat.fe)

## boundary (singular) fit: see help('isSingular')

fec2 <- lmer(First.Egg_Centered ~ Species + scale_ele + (1|Year), data = breedCat.fe)

## boundary (singular) fit: see help('isSingular')

anova(fec1,fec2) #wing difference doesnt improve model fit

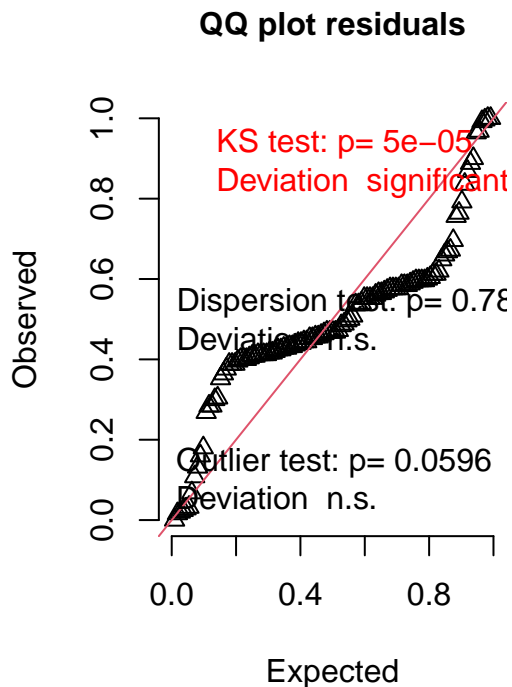
## refitting model(s) with ML (instead of REML)

## Data: breedCat.fe
## Models:
## fec2: First.Egg_Centered ~ Species + scale_ele + (1 | Year)
## fec1: First.Egg_Centered ~ Wing_Difference_Category * Species + scale_ele + (1 | Year)
##      npar    AIC    BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
## fec2     5 576.05 589.60 -283.03   566.05
## fec1     7 576.17 595.14 -281.09   562.17 3.8789  2    0.1438

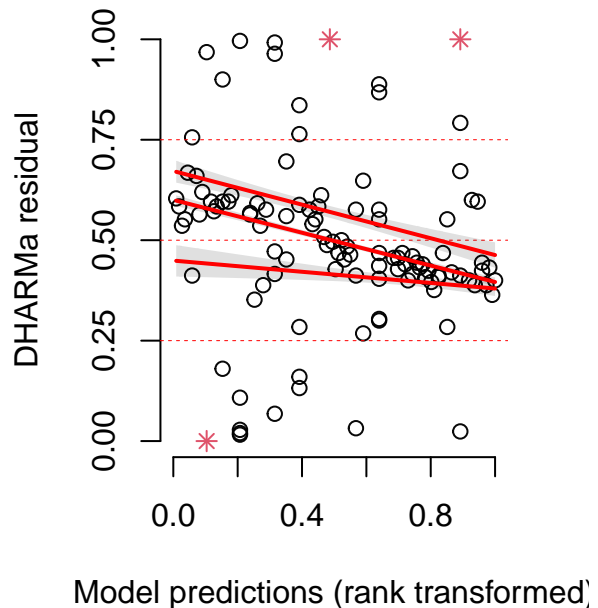
#Check residuals
fec1r = simulateResiduals(fec1)
plot(fec1r)

```

DHARMA residual



DHARMA residual vs. predicted
Quantile deviations detected (red curves)
Combined adjusted quantile test significant



#strong deviation

`summary(fec1)`

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: FirstEgg_Centered ~ Wing_Difference_Category * Species + scale_ele +
## (1 | Year)
## Data: breedCat.fe
##
## REML criterion at convergence: 559.6
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.6420 -0.2172 -0.1135  0.2057  5.5608
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Year      (Intercept)  5.896e-31  7.678e-16
##  Residual                    9.707e+00  3.116e+00
## Number of obs: 111, groups: Year, 6
##
## Fixed effects:
##
##              Estimate Std. Error    df
## (Intercept)    0.36601    0.59013 106.00000
## Wing_Difference_CategorySlightly -0.95538    0.95822 106.00000
```

```
## SpeciesMOCH                0.29564    0.80627 106.00000
## scale_ele                  -0.04847    0.29600 106.00000
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.32913    1.22813 106.00000
##                               t value Pr(>|t|)
## (Intercept)                0.620    0.536
## Wing_Difference_CategorySlightly -0.997    0.321
## SpeciesMOCH                0.367    0.715
## scale_ele                  -0.164    0.870
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.268    0.789
##
## Correlation of Fixed Effects:
##      (Intr) Wn_D_CS SpMOCH scal_1
## Wng_Dffr_CS -0.615
## SpeciesMOCH -0.729  0.449
## scale_ele   -0.067  0.024  0.008
## W_D_CS:SMOC  0.476 -0.779 -0.656  0.034
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
catPFEB <-0.79
catPFEM <-0.76
```

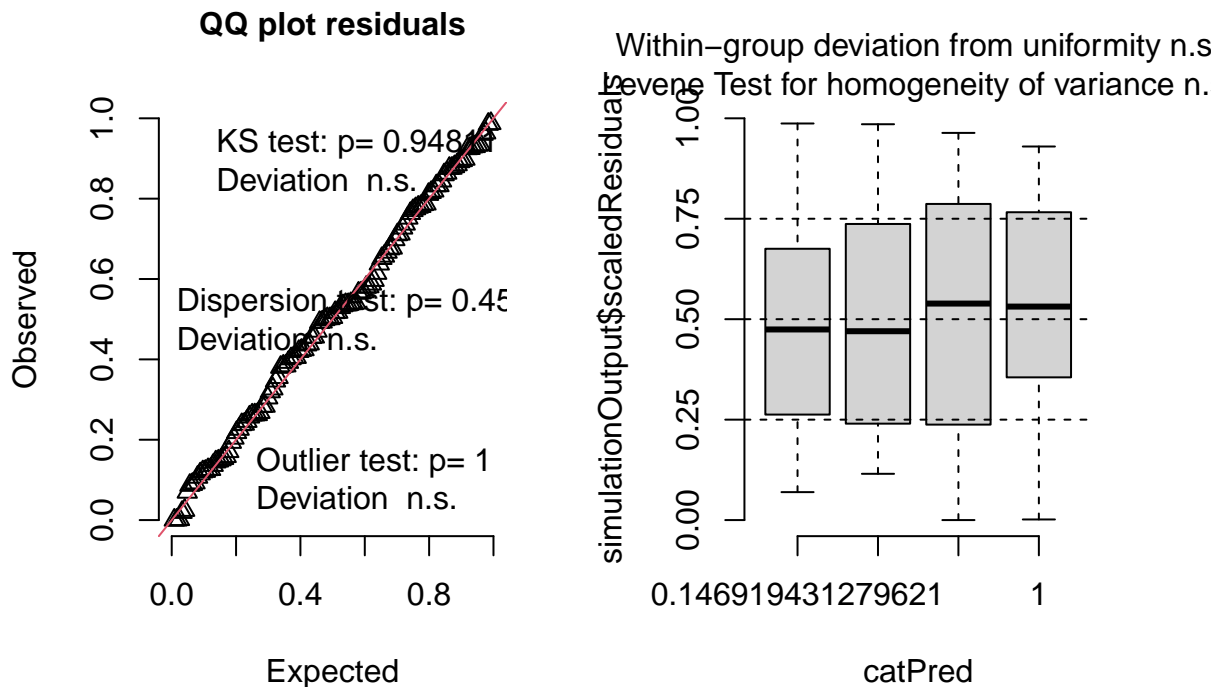
Modeling clutch size

```
cs1 <- glmmTMB(Egg_Number ~ Wing_Difference_Category*Species, data =breedCat.cs,family = "genpois")
cs2 <- glmmTMB(Egg_Number ~ Species, data=breedCat.cs, family="genpois") #got error when including (1/Y
anova(cs1,cs2) # wing difference does not improve model fit
```

```
## Data: breedCat.cs
## Models:
## cs2: Egg_Number ~ Species, zi=~0, disp=~1
## cs1: Egg_Number ~ Wing_Difference_Category * Species, zi=~0, disp=~1
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## cs2  3 411.56 420.00 -202.78  405.56
## cs1  5 413.48 427.54 -201.74  403.48 2.0835      2      0.3528
```

```
#Check residuals
cs1r = simulateResiduals(cs1)
plot(cs1r)
```


DHARMA residual



#look okay

`summary(cs1)`

```
## Family: genpois ( log )
## Formula: Egg_Number ~ Wing_Difference_Category * Species
## Data: breedCat.cs
##
##      AIC      BIC    logLik -2*log(L)  df.resid
##      413.5    427.5    -201.7    403.5      118
##
##
## Dispersion parameter for genpois family (): 0.234
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)      1.75322   0.03553  49.35
## Wing_Difference_CategorySlightly 0.06838   0.05413   1.26
## SpeciesMOCH       0.15067   0.04569   3.30
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.03902   0.06836  -0.57
##
##              Pr(>|z|)
## (Intercept)      < 2e-16 ***
## Wing_Difference_CategorySlightly 0.206523
## SpeciesMOCH       0.000976 ***
## Wing_Difference_CategorySlightly:SpeciesMOCH 0.568143
## ---
```

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

```
catPBB <- 0.206
catPBBM <- 0.568
```

Modeling brood size

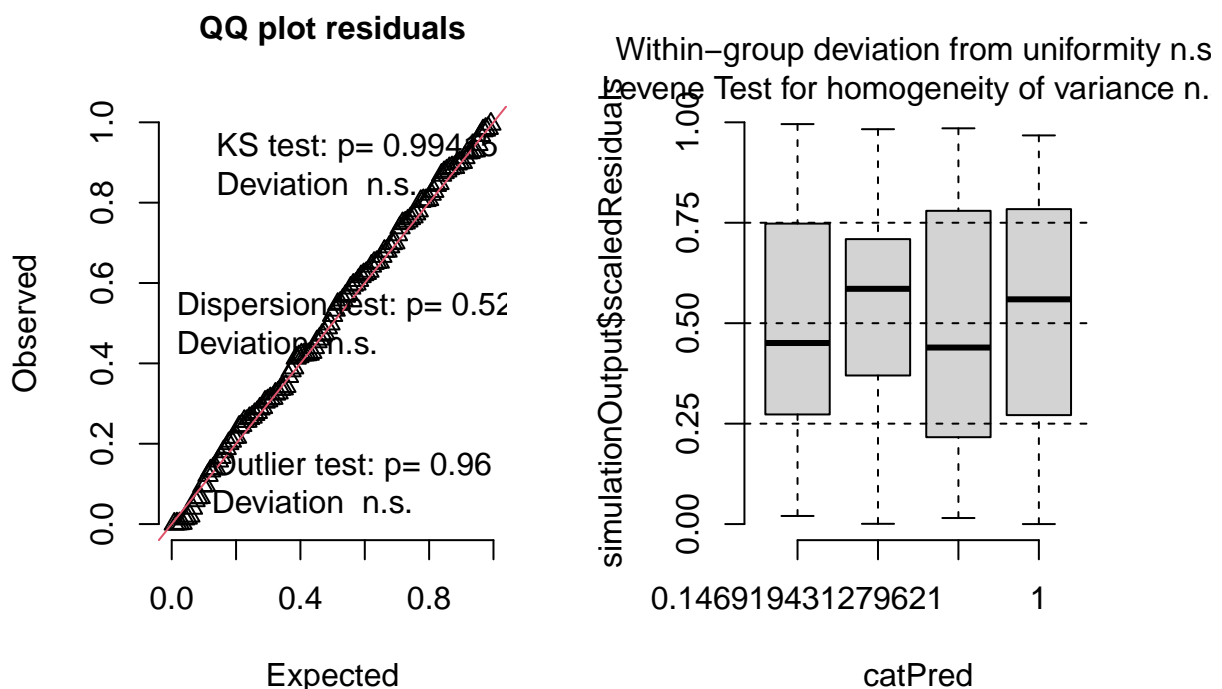
```
bs1 <- glmmTMB(Nestling_Number ~ Wing_Difference_Category*Species, data = breedCat.bs, family="genpois")
bs2 <- glmmTMB(Nestling_Number ~ Species, data = breedCat.bs, family = "genpois") #got error when inclu

anova(bs1,bs2) #wing difference doesnt improve model fit
```

```
## Data: breedCat.bs
## Models:
## bs2: Nestling_Number ~ Species, zi=~0, disp=~1
## bs1: Nestling_Number ~ Wing_Difference_Category * Species, zi=~0, disp=~1
##      Df      AIC      BIC logLik deviance Chisq Chi Df Pr(>Chisq)
## bs2  3 473.54 481.97 -233.77  467.54
## bs1  5 475.85 489.91 -232.92  465.85 1.6908      2      0.4294
```

```
#check residuals
bs1r = simulateResiduals(bs1)
plot(bs1r)
```

DHARMA residual



```
#look ok
```

```
#Results
```

```
summary(bs1)
```

```
## Family: genpois ( log )
## Formula: Nestling_Number ~ Wing_Difference_Category * Species
## Data: breedCat.bs
##
##      AIC      BIC    logLik -2*log(L)  df.resid
##    475.8    489.9   -232.9    465.8      118
##
##
## Dispersion parameter for genpois family (): 0.472
##
## Conditional model:
##
##              Estimate Std. Error z value
## (Intercept)    1.548262   0.056965  27.179
## Wing_Difference_CategorySlightly 0.009519   0.089509   0.106
## SpeciesMOCH     0.113456   0.074452   1.524
## Wing_Difference_CategorySlightly:SpeciesMOCH 0.077995   0.111941   0.697
##
##              Pr(>|z|)
## (Intercept)    <2e-16 ***
## Wing_Difference_CategorySlightly    0.915
## SpeciesMOCH     0.128
## Wing_Difference_CategorySlightly:SpeciesMOCH 0.486
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
catPNNM <- 0.486
```

```
catPNNB <- 0.915
```

Modeling average nestling mass

```
mm3 <- lmer(Avg_Nestling_Weight ~ Wing_Difference_Category*Species + (1|Year), data = breedCat.mm)
mm4 <- lmer(Avg_Nestling_Weight ~ Species + (1|Year), data = breedCat.mm)
```

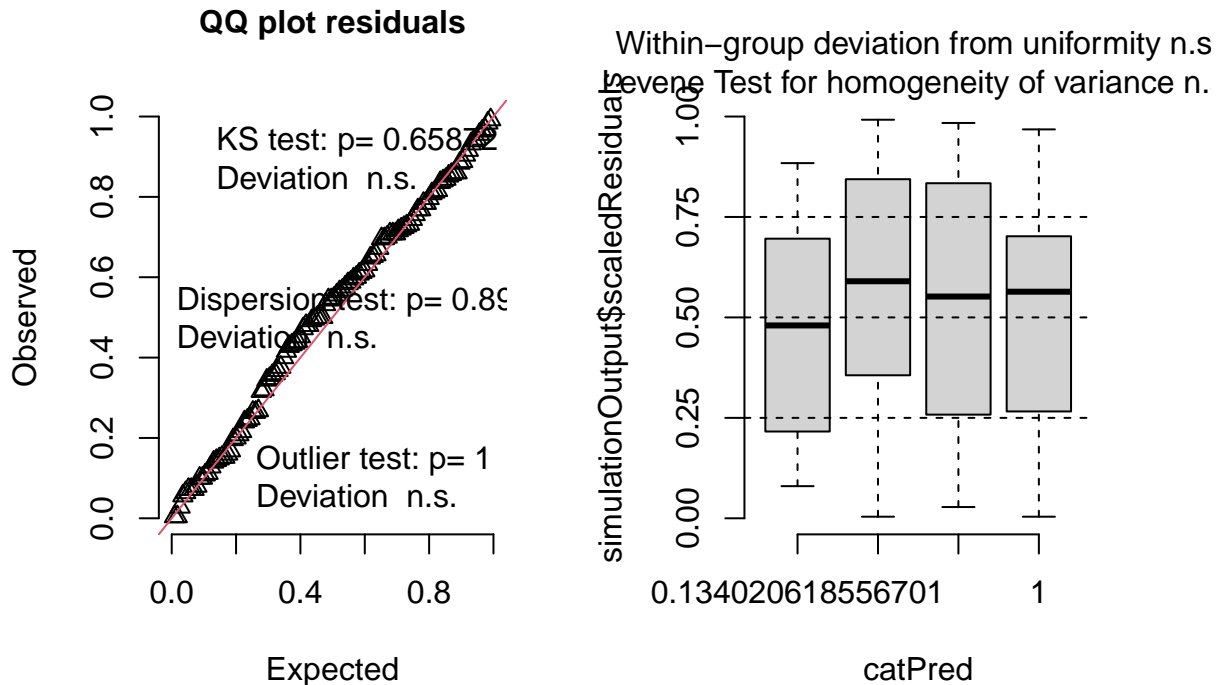
```
anova(mm3, mm4) #wing difference significantly improves model fit
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breedCat.mm
## Models:
## mm4: Avg_Nestling_Weight ~ Species + (1 | Year)
## mm3: Avg_Nestling_Weight ~ Wing_Difference_Category * Species + (1 | Year)
##      npar      AIC      BIC    logLik -2*log(L)  Chisq Df Pr(>Chisq)
## mm4     4 339.34 350.28 -165.67    331.34
## mm3     6 333.25 349.67 -160.63    321.25 10.084  2   0.006462 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#check residuals
mm3r = simulateResiduals(mm3)
plot(mm3r)
```

DHARMA residual



```
#looks good
```

```
#results
summary(mm3)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Avg_Nestling_Weight ~ Wing_Difference_Category * Species + (1 |
## Year)
## Data: breedCat.mm
##
## REML criterion at convergence: 325.3
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.09164 -0.77424  0.08091  0.67318  2.73672
##
## Random effects:
## Groups Name Variance Std.Dev.
## Year (Intercept) 0.2638 0.5137
## Residual 0.9303 0.9645
```

```
## Number of obs: 114, groups: Year, 6
##
## Fixed effects:
##
##              Estimate Std. Error      df
## (Intercept)      10.4034      0.2955    11.9423
## Wing_Difference_CategorySlightly      0.1159      0.3171    109.8133
## SpeciesMOCH        1.1673      0.2733    109.9949
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.8869      0.3926    109.1805
##
##              t value Pr(>|t|)
## (Intercept)      35.201 1.96e-13 ***
## Wing_Difference_CategorySlightly      0.366  0.7153
## SpeciesMOCH        4.272 4.14e-05 ***
## Wing_Difference_CategorySlightly:SpeciesMOCH -2.259  0.0259 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Wn_D_CS SpMOCH
## Wng_Dffr_CS -0.443
## SpeciesMOCH -0.505  0.547
## W_D_CS:SMOC  0.338 -0.794 -0.700

catPMMM <- 0.0259
catPMMB <- 0.715
```

Modeling female SMI

```
fs1 <- lmer(Female_SMI ~ Wing_Difference_Category*Species + (1|Year), data = breedCat.fs)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
fs2 <- lmer(Female_SMI ~ Species + (1|Year), data = breedCat.fs)
```

```
## boundary (singular) fit: see help('isSingular')
```

```
anova(fs1,fs2) #wing difference doesnt improve model fit
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breedCat.fs
```

```
## Models:
```

```
## fs2: Female_SMI ~ Species + (1 | Year)
```

```
## fs1: Female_SMI ~ Wing_Difference_Category * Species + (1 | Year)
```

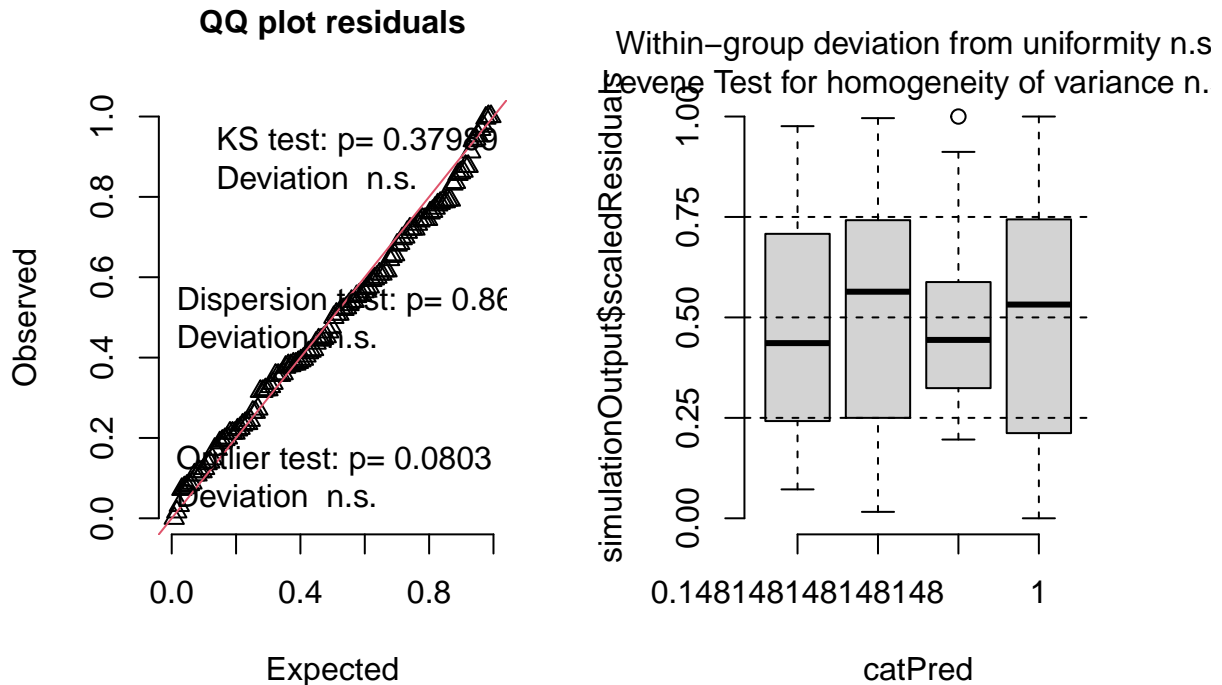
```
##      npar      AIC      BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
```

```
## fs2      4 345.34 356.68 -168.67    337.34
```

```
## fs1      6 349.05 366.07 -168.53    337.05 0.2863  2    0.8666
```

```
#check residuals
fs1r = simulateResiduals(fs1)
plot(fs1r)
```

DHARMA residual



```
#look okay
```

```
#results
summary(fs1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Female_SMI ~ Wing_Difference_Category * Species + (1 | Year)
## Data: breedCat.fs
##
## REML criterion at convergence: 344
##
## Scaled residuals:
##   Min      1Q  Median      3Q      Max
## -2.4582 -0.6162 -0.0905  0.5767  3.8977
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Year      (Intercept)  0.0000    0.0000
##   Residual                    0.8776    0.9368
## Number of obs: 126, groups: Year, 6
```

```
##
## Fixed effects:
##
##              Estimate Std. Error      df
## (Intercept)    11.28975    0.16825 122.00000
## Wing_Difference_CategorySlightly    0.09664    0.25780 122.00000
## SpeciesMOCH      0.25125    0.22809 122.00000
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.17839    0.33949 122.00000
##
##              t value Pr(>|t|)
## (Intercept)    67.101   <2e-16 ***
## Wing_Difference_CategorySlightly     0.375    0.708
## SpeciesMOCH      1.102    0.273
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.525    0.600
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##              (Intr) Wn_D_CS SpMOCH
## Wng_Dffr_CS -0.653
## SpeciesMOCH -0.738  0.481
## W_D_CS:SMOC  0.496 -0.759 -0.672
## optimizer (nloptwrap) convergence code: 0 (OK)
## boundary (singular) fit: see help('isSingular')
```

```
catPFSM <- 0.6
catPFSB <- 0.708
```

Modeling male SMI

```
ms1 <- lmer(Male_SMI ~ Wing_Difference_Category*Species + (1|Year), data = breedCat.ms)
ms2 <- lmer(Male_SMI ~ Species + (1|Year), data = breedCat.ms)
```

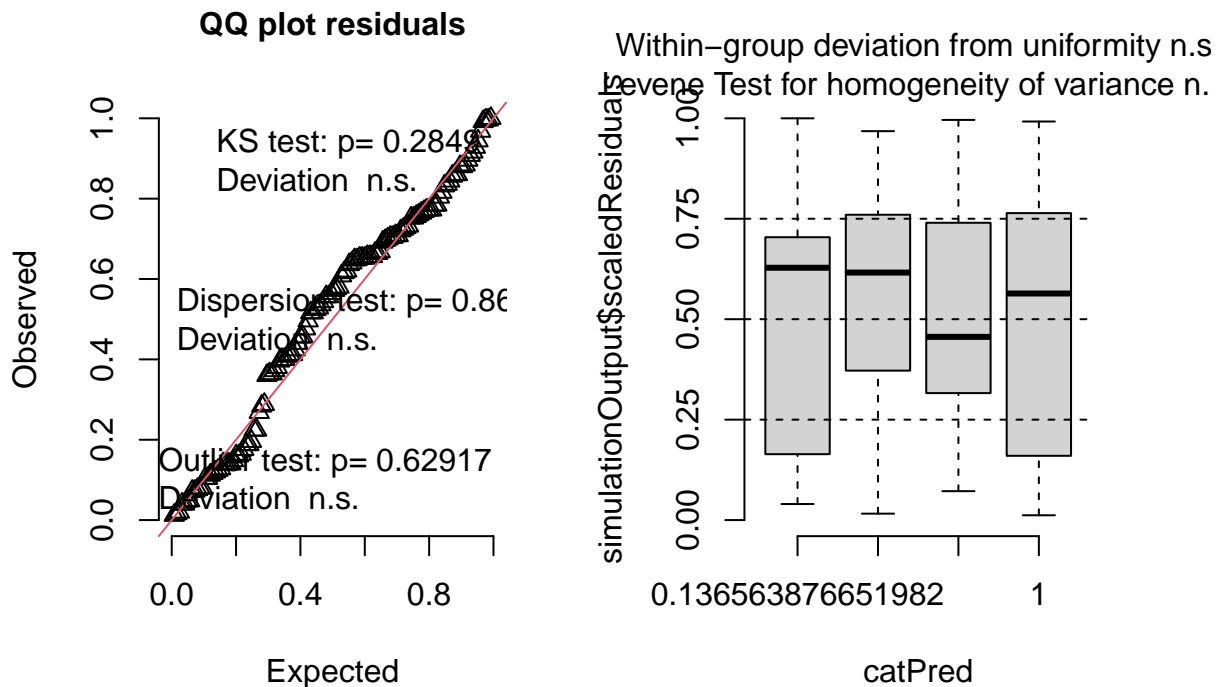
```
anova(ms1,ms2) #wing difference doesnt improve model fit
```

```
## refitting model(s) with ML (instead of REML)
```

```
## Data: breedCat.ms
## Models:
## ms2: Male_SMI ~ Species + (1 | Year)
## ms1: Male_SMI ~ Wing_Difference_Category * Species + (1 | Year)
##      npar    AIC    BIC logLik -2*log(L)  Chisq Df Pr(>Chisq)
## ms2     4 281.96 293.24 -136.98   273.96
## ms1     6 282.21 299.13 -135.10   270.21 3.7475  2    0.1535
```

```
#check residuals
ms1r = simulateResiduals(ms1)
plot(ms1r)
```

DHARMA residual



#look good

#results

summary(ms1) #wing_difference BCCH almost significant

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Male_SMI ~ Wing_Difference_Category * Species + (1 | Year)
## Data: breedCat.ms
##
## REML criterion at convergence: 278.8
##
## Scaled residuals:
##   Min       1Q   Median       3Q      Max
## -2.1800 -0.8308  0.1157  0.5899  3.0583
##
## Random effects:
##   Groups   Name                Variance Std.Dev.
##   Year      (Intercept)  0.01176  0.1084
##   Residual                    0.52614  0.7254
## Number of obs: 124, groups: Year, 6
##
## Fixed effects:
##
##              Estimate Std. Error    df
## (Intercept)    11.3815     0.1412 26.9701
## Wing_Difference_CategorySlightly    0.3715     0.2077 109.0675
```



```
## SpeciesMOCH 0.1092 0.1829 97.3425
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.2739 0.2698 117.5291
## t value Pr(>|t|)
## (Intercept) 80.617 <2e-16 ***
## Wing_Difference_CategorySlightly 1.789 0.0765 .
## SpeciesMOCH 0.597 0.5519
## Wing_Difference_CategorySlightly:SpeciesMOCH -1.015 0.3122
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Wn_D_CS SpMOCH
## Wng_Dffr_CS -0.620
## SpeciesMOCH -0.700 0.502
## W_D_CS:SMOC 0.470 -0.766 -0.678

catPMSM <- 0.3122
catPMSB <- 0.0765
```

Modeling provisioning rate

```
p1 <- lmer(Provisioning ~ Wing_Difference_Category*Species + (1|Year), data = breedCat.p)
p2 <- lmer(Provisioning ~ Species + (1|Year), data = breedCat.p)

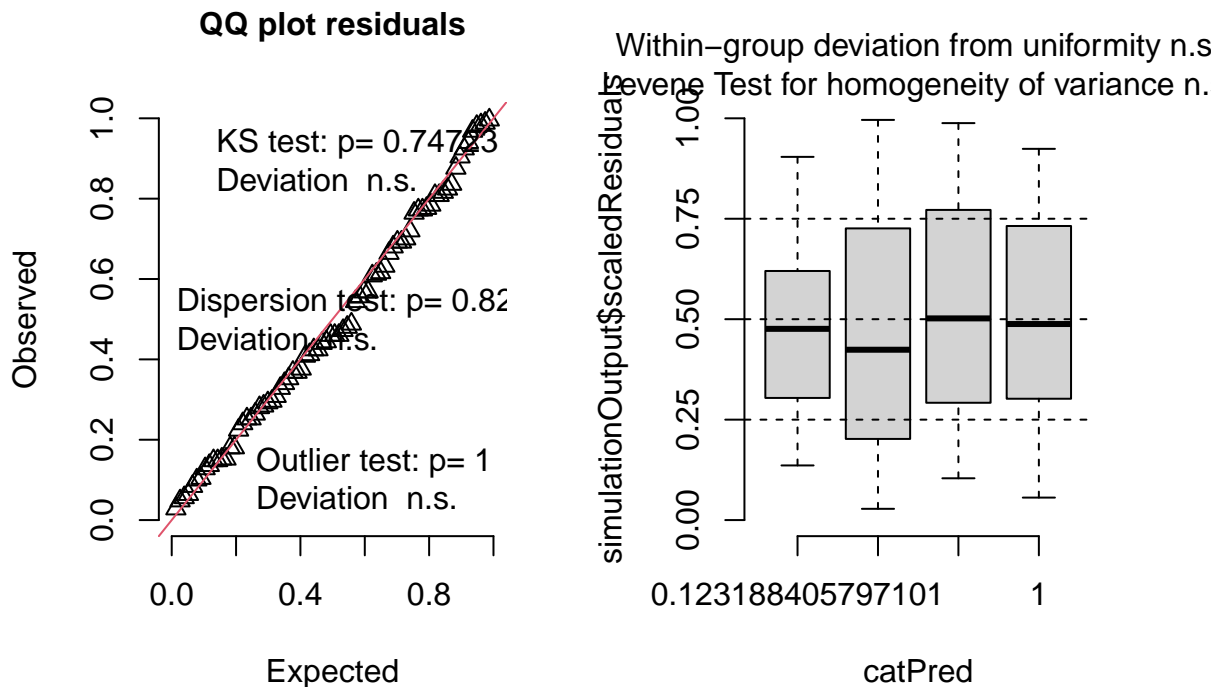
anova(p1,p2) #wing difference doesnt improve model fit

## refitting model(s) with ML (instead of REML)

## Data: breedCat.p
## Models:
## p2: Provisioning ~ Species + (1 | Year)
## p1: Provisioning ~ Wing_Difference_Category * Species + (1 | Year)
## npar AIC BIC logLik -2*log(L) Chisq Df Pr(>Chisq)
## p2 4 534.02 543.35 -263.01 526.02
## p1 6 537.22 551.20 -262.61 525.22 0.8066 2 0.6681

#check residuals
p1r = simulateResiduals(p1)
plot(p1r)
```

DHARMA residual



```
#quantile deviations
```

```
#results
```

```
summary(p1)
```

```
## Linear mixed model fit by REML. t-tests use Satterthwaite's method [
## lmerModLmerTest]
## Formula: Provisioning ~ Wing_Difference_Category * Species + (1 | Year)
## Data: breedCat.p
##
## REML criterion at convergence: 513
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.7183 -0.6090 -0.0770  0.6078  3.2634
##
## Random effects:
##  Groups   Name                Variance Std.Dev.
##  Year      (Intercept)    1.038     1.019
##  Residual                    61.288     7.829
## Number of obs: 76, groups: Year, 5
##
## Fixed effects:
##
##              Estimate Std. Error    df
## (Intercept)    18.4570     1.5806 18.2477
## Wing_Difference_CategorySlightly    1.5926     2.5626 64.0798
```

```
## SpeciesMOCH 0.4431 2.4615 41.1155
## Wing_Difference_CategorySlightly:SpeciesMOCH -2.7349 3.7549 62.4714
## t value Pr(>|t|)
## (Intercept) 11.677 6.65e-10 ***
## Wing_Difference_CategorySlightly 0.621 0.536
## SpeciesMOCH 0.180 0.858
## Wing_Difference_CategorySlightly:SpeciesMOCH -0.728 0.469
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
## (Intr) Wn_D_CS SpMOCH
## Wng_Dffr_CS -0.569
## SpeciesMOCH -0.592 0.404
## W_D_CS:SMOC 0.387 -0.692 -0.659
```

```
catPPM <- 0.469
catPPB <- 0.536
```

Adjust the p-values to account for multiple comparisons

```
p_values <- c(catPFEM, catPFEB, catPBSM, catPBSB, catPNNM, catPNNB, catPMMM, catPMMB, catPFSM, catPFBSB,
p_adjusted <- p.adjust(p_values, method = "BH")
p_adjusted
```

```
## [1] 0.8507692 0.8507692 0.8507692 0.8507692 0.8507692 0.9150000 0.3626000
## [8] 0.8507692 0.8507692 0.8507692 0.8507692 0.5355000 0.8507692 0.8507692
```

Plotting wing difference category comparisons

```
#moch first egg date ##
mochBreed.fe.plot <- subset(breed.fe, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxfe <- ggplot(data=mochBreed.fe.plot, aes(x=factor(Wing_Difference_Category, levels = c("Slightly", "Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category), outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1, height=0), alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray", "orange")) +
  xlab("") + ylab("Date of first egg") +
  theme(axis.title = element_text(size = 10)) +
  theme(axis.title.x = element_text(margin = margin(t = 8))) +
  theme(axis.title.y = element_text(margin = margin(r = 8))) +
  theme(axis.text = element_text(size=6, color = "black"))

#moch clutch size ##
mochBreed.cs.plot <- subset(breed.cs, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxcs <- ggplot(data=mochBreed.cs.plot, aes(x=factor(Wing_Difference_Category, levels = c("Slightly", "Much")),
```

```

geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
xlab("") + ylab("Clutch Size")+
theme(axis.title = element_text(size = 10))+
theme(axis.title.x = element_text(margin = margin(t = 8)))+
theme(axis.title.y = element_text(margin = margin(r = 8)))+
theme(axis.text = element_text(size=6, color = "black"))

#moch brood size ##
mochBreed.bs.plot <- subset(breed.bs, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxbs <- ggplot(data=mochBreed.bs.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","Much"))),
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Brood size")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#moch mean nestling mass ##
mochBreed.mm.plot <- subset(breed.mm, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxmm <-ggplot(data=mochBreed.mm.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","Much"))),
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Mean nestling mass")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#moch female SMI ##
mochBreed.fs.plot <- subset(breed.fs, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxfs <- ggplot(data=mochBreed.fs.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","Much"))),
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Female body condition")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

```

```

#moch male SMI ##
mochBreed.ms.plot <- subset(breed.ms, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxms <- ggplot(data=mochBreed.ms.plot, aes(x=factor(Wing_Difference_Category, levels = c("Slightly", "Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category), outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1, height=0), alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray", "orange")) +
  xlab("") + ylab("Male body condition")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#moch provisioning ##
mochBreed.p.plot <- subset(breed.p, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("MOCH"))

boxp <- ggplot(data=mochBreed.p.plot, aes(x=factor(Wing_Difference_Category, levels = c("Slightly", "Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category), outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1, height=0), alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray", "orange")) +
  xlab("") + ylab("Provisioning")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

pMOCH <- (boxfe+boxcs+boxbs+boxmm)/(boxfs+boxms+boxp)

#bcch first egg date ##
bcchBreed.fe.plot <- subset(breed.fe, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

boxfebc <- ggplot(data=bcchBreed.fe.plot, aes(x=factor(Wing_Difference_Category, levels = c("Slightly", "Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category), outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1, height=0), alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray", "orange")) +
  xlab("") + ylab("Date of first egg")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#bcch clutch size ##
bcchBreed.cs.plot <- subset(breed.cs, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

boxcsbc <- ggplot(data=bcchBreed.cs.plot, aes(x=factor(Wing_Difference_Category, levels = c("Slightly", "Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category), outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1, height=0), alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray", "orange")) +
  xlab("") + ylab("Clutch Size")+

```

```

theme(axis.title = element_text(size = 10))+
theme(axis.title.x = element_text(margin = margin(t = 8)))+
theme(axis.title.y = element_text(margin = margin(r = 8)))+
theme(axis.text = element_text(size=6, color = "black"))

#bcch brood size ##
bcchBreed.bs.plot <- subset(breed.bs, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

boxbsbc <- ggplot(data=bcchBreed.bs.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","M
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Brood size")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#bcch mean nestling mass ##
bcchBreed.mm.plot <- subset(breed.mm, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

boxmmbc <-ggplot(data=bcchBreed.mm.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","M
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Mean nestling mass")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#bcch female SMI ##
bcchBreed.fs.plot <- subset(breed.fs, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

boxfsbc <- ggplot(data=bcchBreed.fs.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","M
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Female body condition")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#bcch male SMI ##
bcchBreed.ms.plot <- subset(breed.ms, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

```

```

boxmsbc <- ggplot(data=bcchBreed.ms.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Male body condition")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

#bcch provisioning ##
bcchBreed.p.plot <- subset(breed.p, Wing_Difference_Category %in% c("Slightly", "Much")) %>%
  subset(Species %in% c("BCCH"))

boxpbc <- ggplot(data=bcchBreed.p.plot,aes(x=factor(Wing_Difference_Category, levels = c("Slightly","Much")),
  geom_boxplot(aes(fill=Wing_Difference_Category),outlier.alpha = 0) +
  geom_point(position=position_jitter(width=0.1,height=0),alpha=0.6) +
  theme_cowplot() + theme(legend.position = "") + scale_fill_manual(values=c("gray","orange")) +
  xlab("") + ylab("Provisioning")+
  theme(axis.title = element_text(size = 10))+
  theme(axis.title.x = element_text(margin = margin(t = 8)))+
  theme(axis.title.y = element_text(margin = margin(r = 8)))+
  theme(axis.text = element_text(size=6, color = "black"))

pBCCH <- (boxfbc+boxcsbc+boxbsbc+boxmmbc)/(boxfsbc+boxmsbc+boxpbc)

ggsave("boxplotMOCH.png", plot = pMOCH, width = 7, height = 5, units = "in", dpi = 300)
ggsave("boxplotBCCH.png", plot = pBCCH, width = 7, height = 5, units = "in", dpi = 300)

```