Statistical Supplement

Contents

13 July 2018

This is an analysis of alcid and penguin egg size and shape data for: Birkhead TR , Thompson JE, Biggins JD, Montgomerie R (2018) The evolution of egg shape in birds: selection during the incubation period. The Ibis, in press

1 R details and packages used

- File creation date: 2018-07-13
- R version 3.5.1 (2018-07-02)
- `lme4` package version: 1.1.17
- `MuMIn` package version: 1.40.4
- `lmerTest` package version: 3.0.1 #this package gives some test stats when running lmer models
- `tidyverse` package version: 1.2.1
- `arm` package version: 1.10.1
- `emmeans` package version: 1.2.2
- `sjPlot` package version: 2.4.1

- `car` package version: 3.0.0
- `multcomp` package version: 1.4.8
- `psych` package version: 1.8.4
- `ape` package version: 5.1
- `geiger` package version: 2.0.6
- `phytools` package version: 0.6.44
- `caper` package version: 1.0.1

2 Load packages

Code to load all of the packages listed above (output suppressed here)

3 Get the data

The variables in **aukpenguinDATA.csv** are

- Species = scientific name
- Order = alcid or penguin
- maxlength = egg length in mm
- maxbreadth = egg width in mm
- volcc = egg volume in cm^3 (mL)
- Pointedness = Pointedness egg shape index
- Elongation = Elongation egg shape index
- PolarAsymmetry = Polar-asymmetry egg shape index
- adult.body.mass = female body mass in g
- CS = Clutch Size, taken as the modal clutch size for each species
- Site = nest site, where CR = crevice, BU = burrow, RO = bare rock, FE = on feet, CU = cup or depression
- devel = mode of chick development where SP = semi-precocial, SA = semi-altricial, FP = fully precocial, IN = intermediate (between fully precocial and semi-precocial)
- gendev = general developmental mode (A = altricial, P - precocial)

```
dat1 <- read.csv("aukpenguinDATA.csv") #load the  data file
names(dat1)
```

```
##  [1] "Species"         "Order"           "sample.size"
##  [4] "maxlength"       "maxbreadth"      "volcc"
##  [7] "Pointedness"     "Elongation"      "PolarAsymmetry"
## [10] "adult.body.mass" "CS"              "Site"
## [13] "devel"           "gendev"
```

```
#calculate log-transformed linear measurements but NOT shape indices
dat1 <- mutate(dat1, PA = PolarAsymmetry, PT = Pointedness, EL = Elongation, LBM=log10(adult.body.mass)
dat1$FCS =as.factor(dat1$CS) #make clutch size a factor

#set option to cause analysis to fail if there is missing data
options(na.action = na.fail) #this is needed to make sure the dredge function, below, runs properly
```

4 Egg size and shape

4.1 Correlations

Looking at the relationships among egg size and shape variables and how they relate to adult female body mass in the alcids and penguins

```r
#distribution of adult female body mass and egg volume, as well as log10(bodymass) and log10(eggvolume)
qqnorm(dat1$adult.body.mass)
```

Normal Q–Q Plot
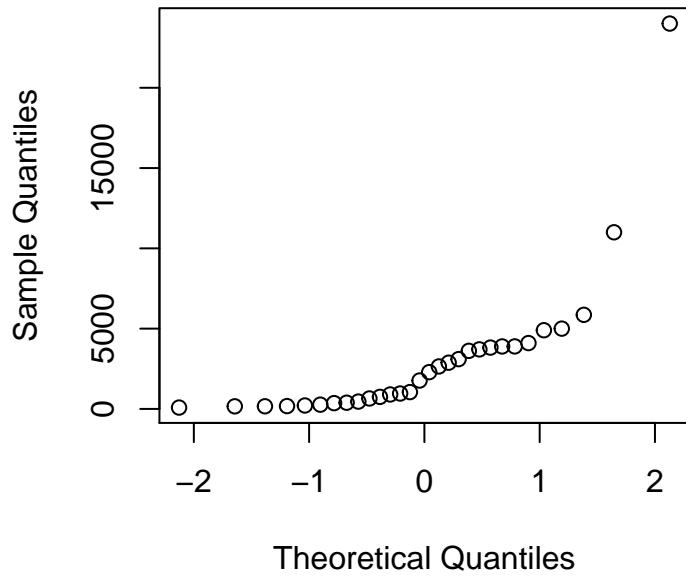

```r
qqnorm(dat1$LBM)
```

Normal Q–Q Plot

```r
qqnorm(dat1$volcc)
```

Normal Q–Q Plot


```r
qqnorm(dat1$LVOL)
```

Normal Q–Q Plot
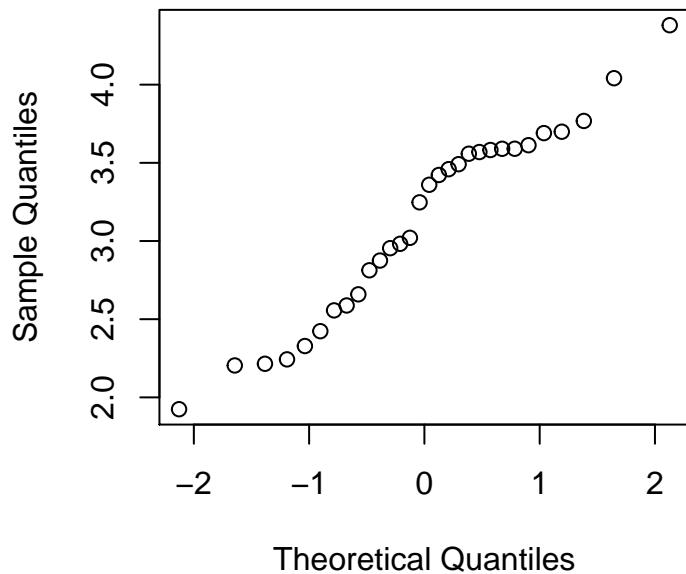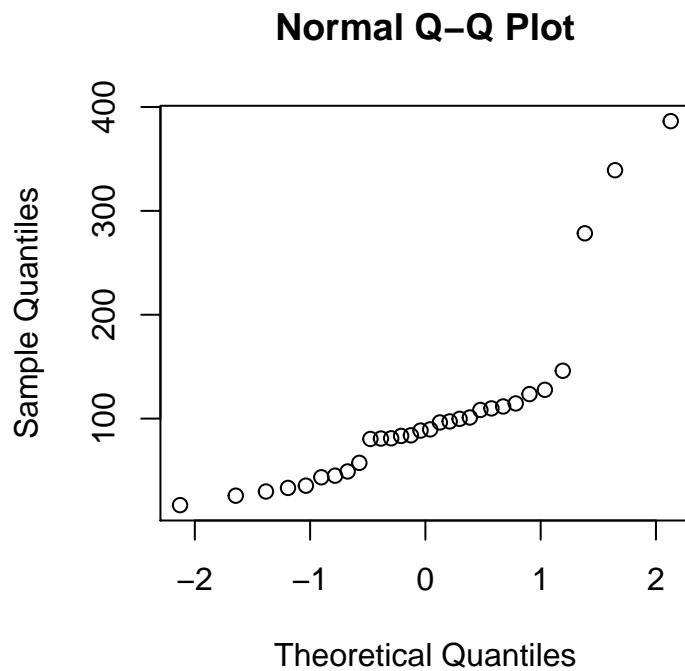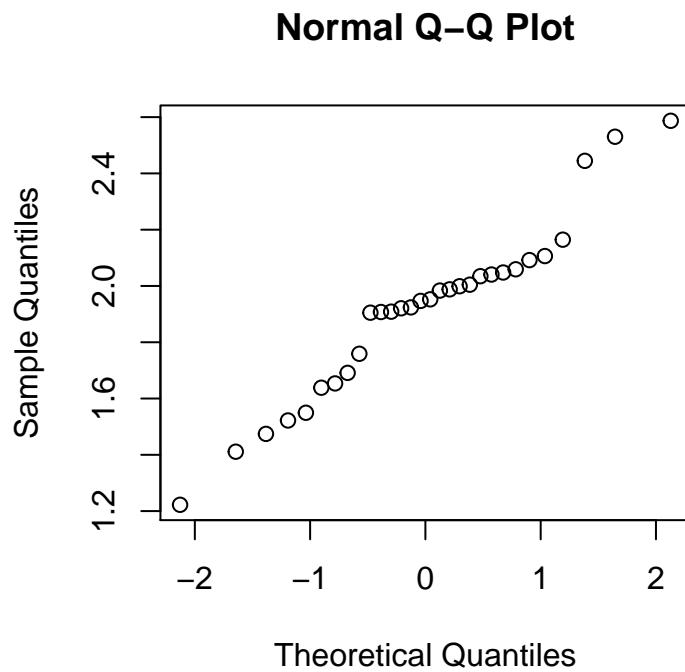

```r
#subset the data to separate alcid data from penguin data into separate datasets
dat2 <- filter(dat1, Order=="alcid")
dat3 <- filter(dat1, Order=="penguin")

#correlations among variables
#both taxa commbined
(cor1 <- corr.test(dat1[,c(11, 15:20)]))
```

```
## Call:corr.test(x = dat1[, c(11, 15:20)])
## Correlation matrix
##          CS    PA    PT    EL   LBM  LVOL  LLEN
## CS     1.00 -0.71 -0.65 -0.55  0.32  0.05 -0.10
## PA    -0.71  1.00  0.87  0.54  0.06  0.30  0.45
## PT    -0.65  0.87  1.00  0.69 -0.01  0.28  0.46
## EL    -0.55  0.54  0.69  1.00 -0.48 -0.15  0.10
## LBM    0.32  0.06 -0.01 -0.48  1.00  0.91  0.80
## LVOL   0.05  0.30  0.28 -0.15  0.91  1.00  0.97
## LLEN  -0.10  0.45  0.46  0.10  0.80  0.97  1.00
## Sample Size
## [1] 30
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##          CS   PA   PT   EL  LBM LVOL LLEN
## CS     0.00 0.00 0.00 0.02 0.79 1.00 1.00
## PA     0.00 0.00 0.00 0.03 1.00 0.88 0.13
## PT     0.00 0.00 0.00 0.00 1.00 0.99 0.12
## EL     0.00 0.00 0.00 0.00 0.08 1.00 1.00
## LBM    0.09 0.76 0.97 0.01 0.00 0.00 0.00
## LVOL   0.80 0.11 0.14 0.44 0.00 0.00 0.00
## LLEN   0.60 0.01 0.01 0.60 0.00 0.00 0.00
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```r
cor1$p
```

```
##                 CS           PA           PT           EL          LBM
## CS    0.000000e+00 2.273068e-04 1.712036e-03 0.0212959291 7.917647e-01
## PA    1.337099e-05 0.000000e+00 9.592829e-09 0.0299309391 1.000000e+00
## PT    1.141357e-04 5.048857e-10 0.000000e+00 0.0003308298 1.000000e+00
## EL    1.521138e-03 2.302380e-03 2.067686e-05 0.0000000000 8.450450e-02
## LBM   8.797386e-02 7.596705e-01 9.661498e-01 0.0070420416 0.000000e+00
## LVOL  8.021716e-01 1.104834e-01 1.408478e-01 0.4407372287 2.572024e-12
## LLEN  6.045938e-01 1.343819e-02 1.101504e-02 0.6044476447 1.205249e-07
##               LVOL         LLEN
## CS    1.000000e+00 1.000000e+00
## PA    8.838671e-01 1.343819e-01
## PT    9.859345e-01 1.211654e-01
## EL    1.000000e+00 1.000000e+00
## LBM   5.144049e-11 2.169449e-06
## LVOL  0.000000e+00 2.285337e-17
## LLEN  1.088256e-18 0.000000e+00
```

```r
cor1a <- cor(dat1[,c(11, 15:20)])
corrplot.mixed(cor1a)
```
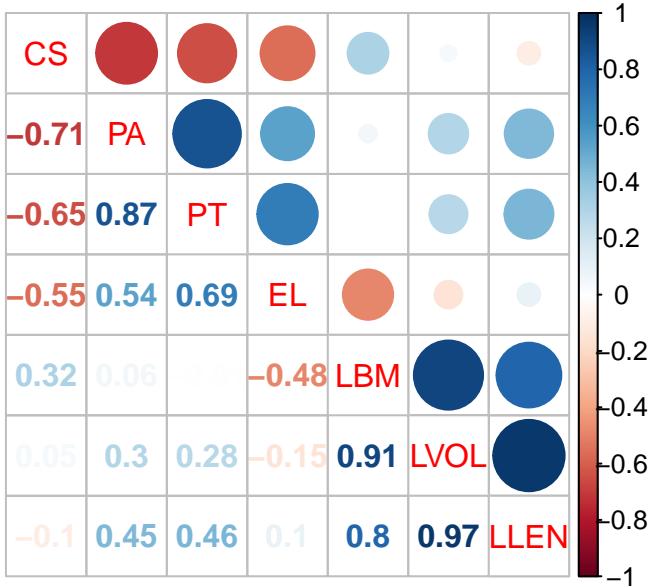
```
#alcids
(cor2 <- corr.test(dat2[,c(11, 15:20)]))
```

```
## Call:corr.test(x = dat2[, c(11, 15:20)])
## Correlation matrix
##          CS    PA    PT   EL   LBM  LVOL  LLEN
## CS     1.00 -0.68 -0.53 0.30 -0.29 -0.24 -0.19
## PA    -0.68  1.00  0.89 0.36  0.71  0.64  0.65
## PT    -0.53  0.89  1.00 0.58  0.79  0.74  0.76
## EL     0.30  0.36  0.58 1.00  0.63  0.65  0.72
## LBM   -0.29  0.71  0.79 0.63  1.00  0.98  0.98
## LVOL  -0.24  0.64  0.74 0.65  0.98  1.00  0.99
## LLEN  -0.19  0.65  0.76 0.72  0.98  0.99  1.00
## Sample Size
## [1] 14
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##         CS   PA   PT   EL  LBM LVOL LLEN
## CS    0.00 0.09 0.31 1.00 1.00 1.00 1.00
## PA    0.01 0.00 0.00 1.00 0.06 0.13 0.13
## PT    0.05 0.00 0.00 0.20 0.01 0.04 0.03
## EL    0.30 0.20 0.03 0.00 0.13 0.13 0.05
## LBM   0.32 0.00 0.00 0.02 0.00 0.00 0.00
## LVOL  0.41 0.01 0.00 0.01 0.00 0.00 0.00
## LLEN  0.52 0.01 0.00 0.00 0.00 0.00 0.00
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```
cor2$p
```

```
##                 CS           PA           PT          EL          LBM
## CS    0.000000000 8.754045e-02 0.3061038309 1.000000000 1.000000e+00
## PA    0.007295038 0.000000e+00 0.0003100100 1.000000000 6.008677e-02
## PT    0.051017305 1.722278e-05 0.0000000000 0.201956516 1.410608e-02
## EL    0.300699876 2.022510e-01 0.0288509309 0.000000000 1.304953e-01
## LBM   0.317094092 4.622060e-03 0.0008297696 0.016311910 0.000000e+00
## LVOL  0.412854672 1.282305e-02 0.0026354212 0.011663826 3.866145e-10
```

```
## LLEN 0.517871963 1.223475e-02 0.0017027100 0.003486505 1.789557e-09
##                  LVOL          LLEN
## CS    1.000000e+00 1.000000e+00
## PA    1.283021e-01 1.283021e-01
## PT    3.953132e-02 2.724336e-02
## EL    1.283021e-01 4.881108e-02
## LBM   7.732290e-09 3.400159e-08
## LVOL  0.000000e+00 5.342673e-12
## LLEN  2.544130e-13 0.000000e+00
```

```r
cor2a <- cor(dat2[,c(11, 15:20)])
corrplot.mixed(cor2a)
```
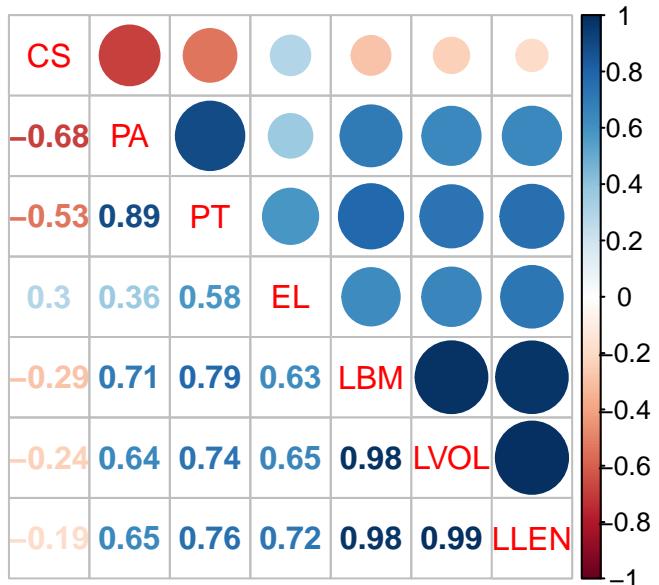


```r
#penguins
(cor3 <- corr.test(dat3[,c(11, 15:20)]))
```

```
## Call:corr.test(x = dat3[, c(11, 15:20)])
## Correlation matrix
##          CS    PA    PT    EL   LBM  LVOL  LLEN
## CS     1.00 -0.72 -0.57 -0.49 -0.79 -0.85 -0.88
## PA    -0.72  1.00  0.89  0.61  0.47  0.56  0.65
## PT    -0.57  0.89  1.00  0.81  0.26  0.42  0.55
## EL    -0.49  0.61  0.81  1.00  0.23  0.36  0.52
## LBM   -0.79  0.47  0.26  0.23  1.00  0.95  0.91
## LVOL  -0.85  0.56  0.42  0.36  0.95  1.00  0.98
## LLEN  -0.88  0.65  0.55  0.52  0.91  0.98  1.00
## Sample Size
## [1] 16
## Probability values (Entries above the diagonal are adjusted for multiple tests.)
##          CS   PA   PT   EL  LBM LVOL LLEN
## CS     0.00 0.02 0.23 0.33 0.00 0.00 0.00
## PA     0.00 0.00 0.00 0.13 0.34 0.23 0.08
## PT     0.02 0.00 0.00 0.00 0.68 0.42 0.23
## EL     0.06 0.01 0.00 0.00 0.68 0.52 0.28
## LBM    0.00 0.07 0.34 0.39 0.00 0.00 0.00
## LVOL   0.00 0.02 0.11 0.17 0.00 0.00 0.00
```

```
## LLEN 0.00 0.01 0.03 0.04 0.00 0.00 0.00
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```
cor3$p
```

```
##                    CS           PA           PT         EL          LBM
## CS    0.000000e+00 2.243170e-02 2.255415e-01 0.33267860 3.602033e-03
## PA    1.725515e-03 0.000000e+00 8.830786e-05 0.12791418 3.396024e-01
## PT    2.255415e-02 4.905992e-06 0.000000e+00 0.00212232 6.779414e-01
## EL    5.544643e-02 1.162856e-02 1.414880e-04 0.00000000 6.779414e-01
## LBM   2.572881e-04 6.792048e-02 3.389707e-01 0.38553826 0.000000e+00
## LVOL 3.089553e-05 2.408939e-02 1.059917e-01 0.17416245 1.716040e-08
## LLEN 7.544464e-06 6.952147e-03 2.782442e-02 0.03940971 7.497214e-07
##               LVOL         LLEN
## CS    4.943285e-04 1.282559e-04
## PA    2.255415e-01 8.342576e-02
## PT    4.239668e-01 2.255415e-01
## EL    5.224873e-01 2.758680e-01
## LBM   3.432081e-07 1.424471e-05
## LVOL 0.000000e+00 1.799357e-10
## LLEN 8.568365e-12 0.000000e+00
```

```
cor3a <- cor(dat3[,c(11, 15:20)])
corrplot.mixed(cor3a)
```
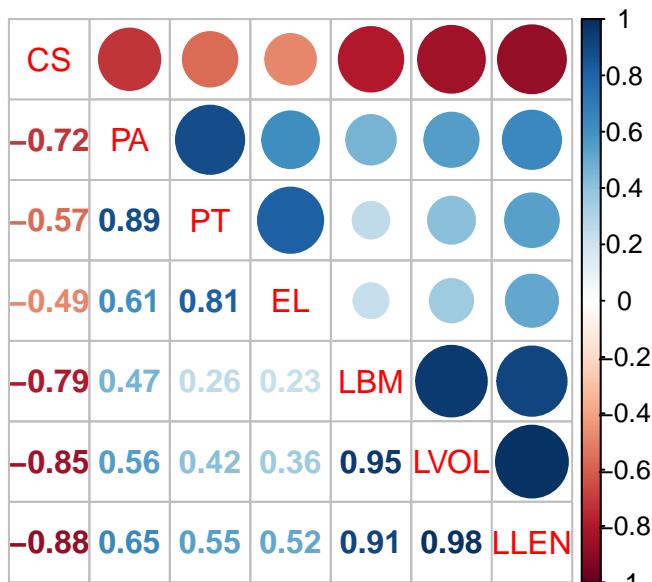


```
#scatterplot matrices
#alcids
scatterplotMatrix(~LVOL + LBM + LLEN + EL + PA + PT +LBR, data = dat2)
```
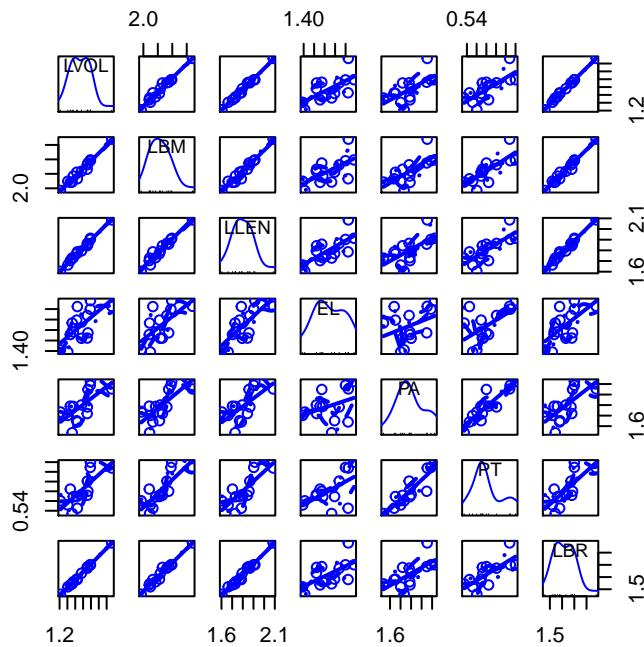
```
#penguins
scatterplotMatrix(~LVOL + LBM + LLEN + EL + PA + PT +LBR, data = dat3)
```
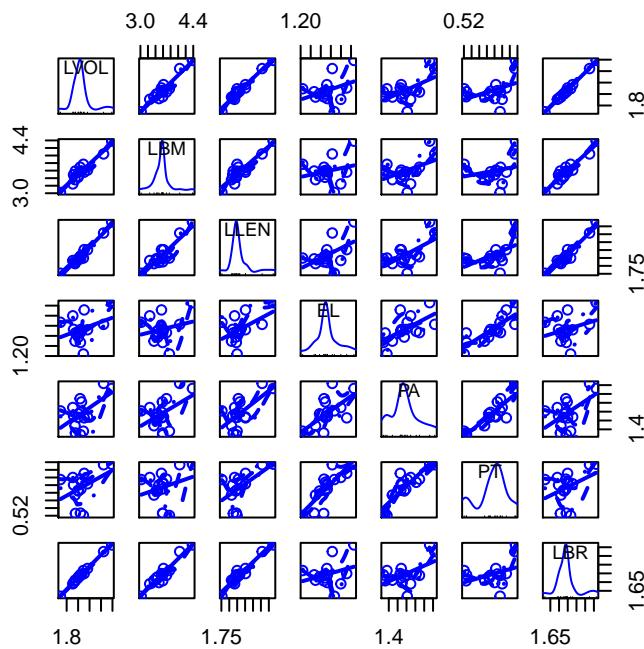

SUMMARY: The first two plots show why we needed to log10-transform body mass and egg volume to normalize their distributions. Log10-transforming the other continuous variables also makes sense though this is not needed to normalize. The correlation matrix and scatterplot matrix show that log10-transforming those other variables has very little affect on the correlations.

All of the correlations are positive within both alcids and penguins, and all 3 shape indices are intercorrelated in this sample of species. The correlation matrices show that for both alcids and penguins PA and PT are the most highly correlated pair of shape indices. PA and EL are only weakly correlated in the alcids, and EL is better correlated with PA and PT in the penguins than in the alcids.

Egg volume, egg breadth and egg length are highly correlated with female body mass in both alcids and

penguins. All of the shape indices have higher correlations with egg volume in the alcids than in the penguins.

Because some of the potential predictor variables are correlated with one another, we need to be cautious about the effects of multicollinearity in the statistical models that follow.

4.2 Egg size vs female body mass

Here we explore the correlations among log10-transformed egg measurements and adult female body mass.

```
#egg vol in relation to body size
mod1 <- lm(LVOL ~ LBM, data = dat1)
summary(mod1)
```

```
##
## Call:
## lm(formula = LVOL ~ LBM, data = dat1)
##
## Residuals:
##       Min      1Q   Median      3Q      Max
## -0.17557 -0.08156 -0.03466  0.10319  0.35611
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.49817    0.12319   4.044 0.000373 ***
## LBM          0.45311    0.03865  11.724 2.57e-12 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1294 on 28 degrees of freedom
## Multiple R-squared:  0.8308, Adjusted R-squared:  0.8247
## F-statistic: 137.5 on 1 and 28 DF,  p-value: 2.572e-12
```

```
Anova(mod1)
```

```
## Anova Table (Type II tests)
##
## Response: LVOL
##            Sum Sq Df F value    Pr(>F)
## LBM       2.30343  1  137.46 2.572e-12 ***
## Residuals 0.46919 28
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
confint(mod1)
```

```
##                  2.5 %    97.5 %
## (Intercept) 0.2458392 0.7505099
## LBM         0.3739497 0.5322797
```

```
#egg vol in relation to body size conrolling for taxon (alcids vs penguins)
mod1a <- lm(LVOL ~ LBM*Order, data = dat1)
qqnorm(residuals(mod1a))
```

Normal Q–Q Plot
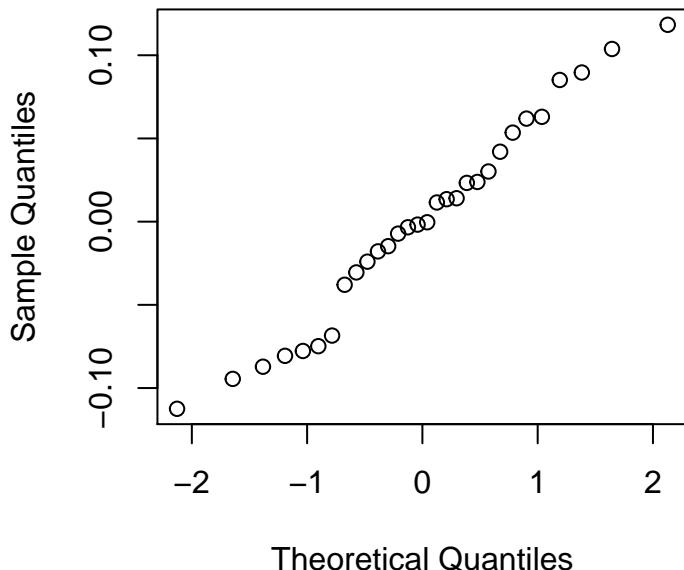

```
summary(mod1a)
```

```
##
## Call:
## lm(formula = LVOL ~ LBM * Order, data = dat1)
##
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.112468 -0.036077 -0.001078  0.039052  0.118300
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -0.11872    0.10678  -1.112    0.276
## LBM               0.71664    0.04045  17.719 4.93e-16 ***
## Orderpenguin     -0.12543    0.22395  -0.560    0.580
## LBM:Orderpenguin -0.07350    0.06803  -1.080    0.290
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06521 on 26 degrees of freedom
## Multiple R-squared:  0.9601, Adjusted R-squared:  0.9555
## F-statistic: 208.7 on 3 and 26 DF,  p-value: < 2.2e-16
```

```
anova(mod1a)
```

```
## Analysis of Variance Table
##
## Response: LVOL
##           Df  Sum Sq Mean Sq  F value     Pr(>F)
## LBM        1 2.30343 2.30343 541.6438 < 2.2e-16 ***
## Order      1 0.35366 0.35366  83.1615 1.394e-09 ***
## LBM:Order  1 0.00496 0.00496   1.1674    0.2899
## Residuals 26 0.11057 0.00425
```

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

```r
mod1b <- lm(LVOL ~ LBM + Order, data = dat1)
qqnorm(residuals(mod1b))
```

Normal Q–Q Plot
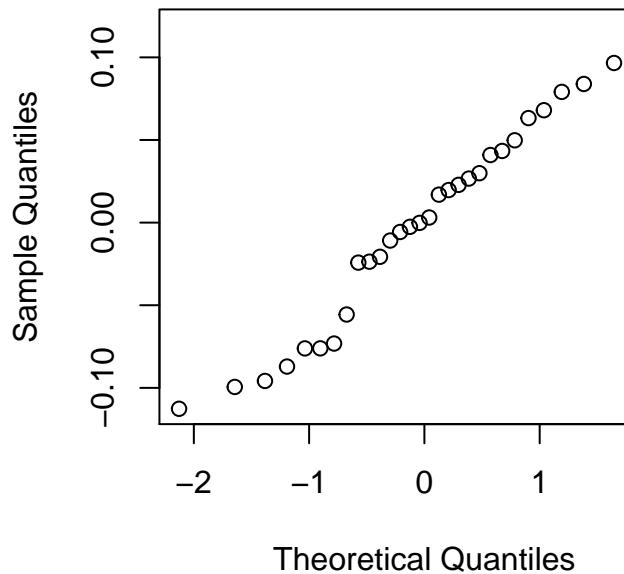

```r
summary(mod1b)
```

```
##
## Call:
## lm(formula = LVOL ~ LBM + Order, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.112651 -0.047757  0.001463  0.042749  0.119712
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.05105    0.08675  -0.589    0.561
## LBM           0.69066    0.03262  21.172  < 2e-16 ***
## Orderpenguin -0.36353    0.03999  -9.091 1.05e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06541 on 27 degrees of freedom
## Multiple R-squared:  0.9583, Adjusted R-squared:  0.9552
## F-statistic: 310.5 on 2 and 27 DF,  p-value: < 2.2e-16
```

```r
Anova(mod1b)
```

```
## Anova Table (Type II tests)
##
## Response: LVOL
##            Sum Sq Df F value    Pr(>F)
```

```
## LBM       1.91810  1 448.255 < 2.2e-16 ***
## Order     0.35366  1  82.649 1.052e-09 ***
## Residuals 0.11553 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
confint(mod1b)
```

```
##                     2.5 %      97.5 %
## (Intercept)  -0.2290408   0.1269343
## LBM           0.6237291   0.7575966
## Orderpenguin -0.4455753  -0.2814819
```

```
ggplot(dat1, aes(LBM, LVOL)) + geom_point(aes(color=Order, shape=Order)) + geom_smooth(method = lm, aes
```
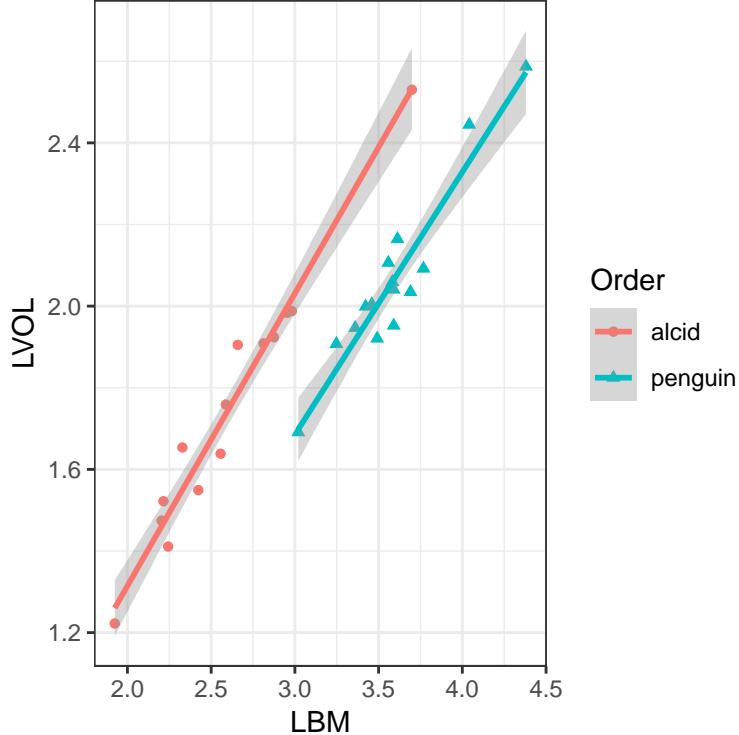


```
mod2 <- lm(LVOL ~ LLEN * Order, data = dat1) #with interaction term
summary(mod2)
```

```
##
## Call:
## lm(formula = LVOL ~ LLEN * Order, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.064492 -0.022253  0.001807  0.026377  0.081821
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -3.06898    0.15225 -20.158   <2e-16 ***
## LLEN              2.67108    0.08425  31.705   <2e-16 ***
## Orderpenguin      0.16829    0.27668   0.608    0.548
## LLEN:Orderpenguin -0.01575    0.14950  -0.105    0.917
```

13

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0369 on 26 degrees of freedom
## Multiple R-squared:  0.9872, Adjusted R-squared:  0.9858
## F-statistic: 670.1 on 3 and 26 DF,  p-value: < 2.2e-16
```
```r
anova(mod2) #interaction term P>0.20
```
```
## Analysis of Variance Table
##
## Response: LVOL
##            Df  Sum Sq Mean Sq   F value    Pr(>F)
## LLEN        1 2.60747 2.60747 1914.8931 < 2.2e-16 ***
## Order       1 0.12973 0.12973   95.2727 3.502e-10 ***
## LLEN:Order  1 0.00002 0.00002    0.0111    0.9169
## Residuals  26 0.03540 0.00136
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
```r
mod2a <- lm(LVOL ~ LLEN + Order, data = dat1) #no interaction term
qqnorm(residuals(mod2a))
```

Normal Q–Q Plot
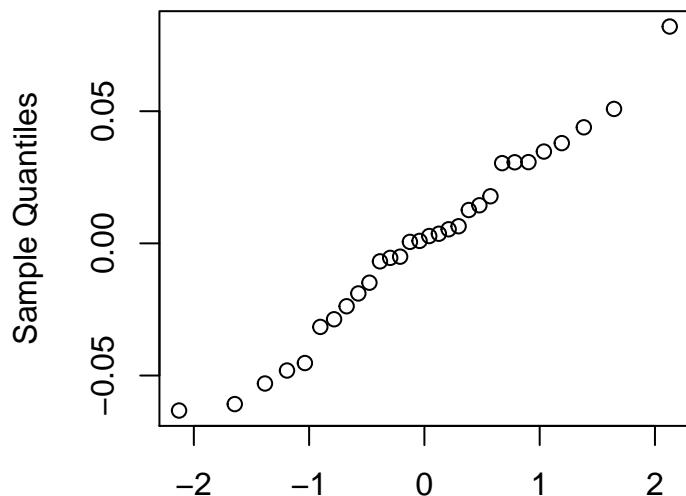

```r
summary(mod2a)
```
```
##
## Call:
## lm(formula = LVOL ~ LLEN + Order, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.06325 -0.02258  0.00185  0.02722  0.08203
##
## Coefficients:
```

```
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -3.05996    0.12357 -24.764  < 2e-16 ***
## LLEN          2.66608    0.06831  39.029  < 2e-16 ***
## Orderpenguin  0.13918    0.01400   9.945  1.6e-10 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.03622 on 27 degrees of freedom
## Multiple R-squared:  0.9872, Adjusted R-squared:  0.9863
## F-statistic:  1043 on 2 and 27 DF,  p-value: < 2.2e-16
```

```
ggplot(dat1, aes(LLEN, LVOL)) + geom_point(aes(color=Order, shape=Order)) + geom_smooth(method = lm, aes
```
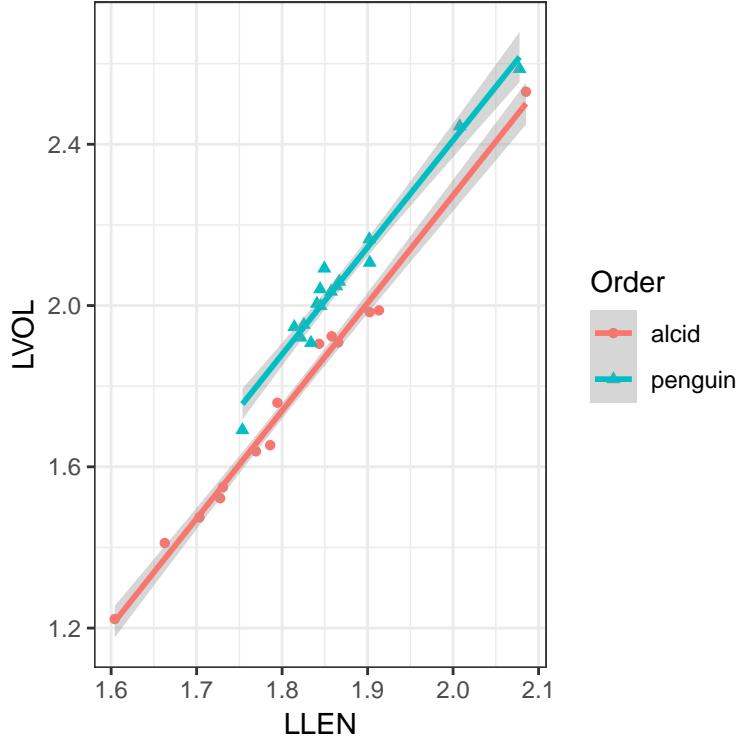


```
mod3 <- lm(LVOL ~ LBR * Order, data = dat1)
summary(mod3)
```

```
##
## Call:
## lm(formula = LVOL ~ LBR * Order, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.033500 -0.011032 -0.000984  0.008364  0.041024
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -3.23853    0.07046 -45.963   <2e-16 ***
## LBR               3.07078    0.04331  70.909   <2e-16 ***
## Orderpenguin      0.03920    0.12928   0.303    0.764
## LBR:Orderpenguin -0.05632    0.07567  -0.744    0.463
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01656 on 26 degrees of freedom
## Multiple R-squared:  0.9974, Adjusted R-squared:  0.9971
## F-statistic:  3361 on 3 and 26 DF,  p-value: < 2.2e-16
```

```r
anova(mod3)   #interaction term P>0.20
```

```
## Analysis of Variance Table
##
## Response: LVOL
##            Df  Sum Sq Mean Sq    F value    Pr(>F)
## LBR         1 2.74934 2.74934 10023.3540 < 2.2e-16 ***
## Order       1 0.01600 0.01600    58.3280 4.175e-08 ***
## LBR:Order   1 0.00015 0.00015     0.5539    0.4634
## Residuals  26 0.00713 0.00027
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
mod3a <- lm(LVOL ~ LBR + Order, data = dat1) #no interaction
qqnorm(residuals(mod3a))
```

Normal Q–Q Plot
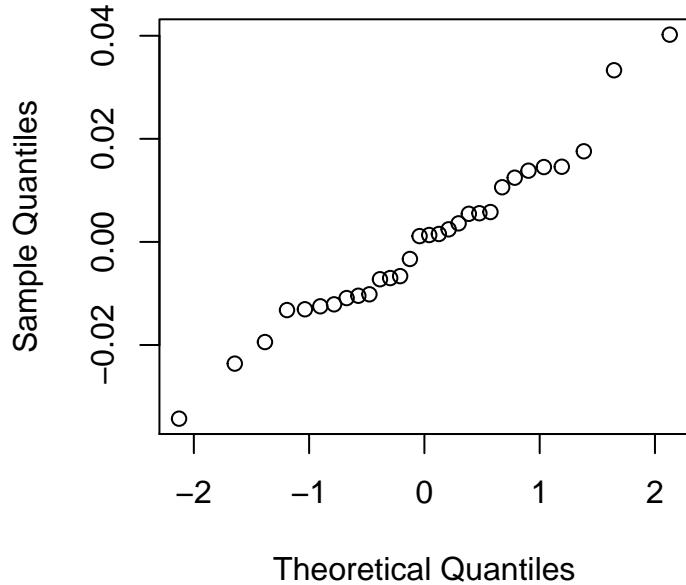

```r
summary(mod3a)
```

```
##
## Call:
## lm(formula = LVOL ~ LBR + Order, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.034292 -0.010782  0.001233  0.009404  0.040212
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)   -3.208578    0.057356 -55.942   < 2e-16 ***
## LBR             3.052337    0.035218  86.670   < 2e-16 ***
## Orderpenguin   -0.056852    0.007382  -7.701  2.78e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01642 on 27 degrees of freedom
## Multiple R-squared:  0.9974, Adjusted R-squared:  0.9972
## F-statistic:  5126 on 2 and 27 DF,  p-value: < 2.2e-16
```

```
ggplot(dat1, aes(LBR, LVOL)) + geom_point(aes(color=Order, shape=Order)) + geom_smooth(method = lm, aes
```
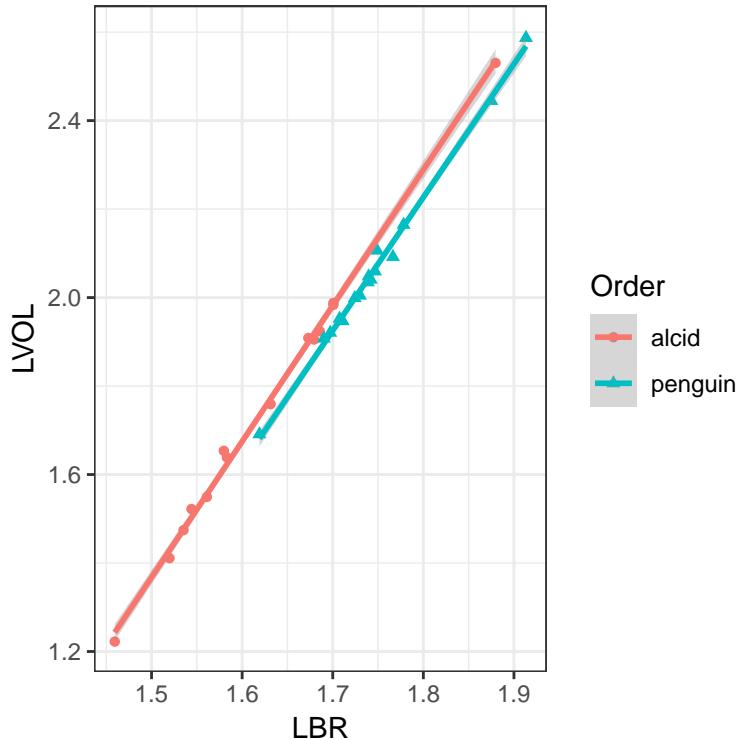


```
mod4 <- lm(LBR ~ LLEN * Order, data = dat1)
summary(mod4)
```

```
##
## Call:
## lm(formula = LBR ~ LLEN * Order, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.02910 -0.01068 -0.00007  0.01154  0.03796
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)       0.065609   0.069267   0.947    0.352
## LLEN              0.864075   0.038330  22.543   <2e-16 ***
## Orderpenguin      0.061525   0.125879   0.489    0.629
## LLEN:Orderpenguin 0.001775   0.068018   0.026    0.979
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
## 
## Residual standard error: 0.01679 on 26 degrees of freedom
## Multiple R-squared:  0.9777, Adjusted R-squared:  0.9751
## F-statistic: 379.3 on 3 and 26 DF,  p-value: < 2.2e-16
```

```r
anova(mod4)  #interaction term P>0.20
```

```
## Analysis of Variance Table
## 
## Response: LBR
##             Df   Sum Sq  Mean Sq   F value     Pr(>F)
## LLEN         1 0.292618 0.292618 1038.1743  < 2.2e-16 ***
## Order        1 0.028124 0.028124   99.7811  2.169e-10 ***
## LLEN:Order   1 0.000000 0.000000    0.0007     0.9794
## Residuals   26 0.007328 0.000282
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
mod4a <- lm(LBR ~ LLEN + Order, data = dat1) #no interaction as it was NS
qqnorm(residuals(mod4a))
```

Normal Q–Q Plot
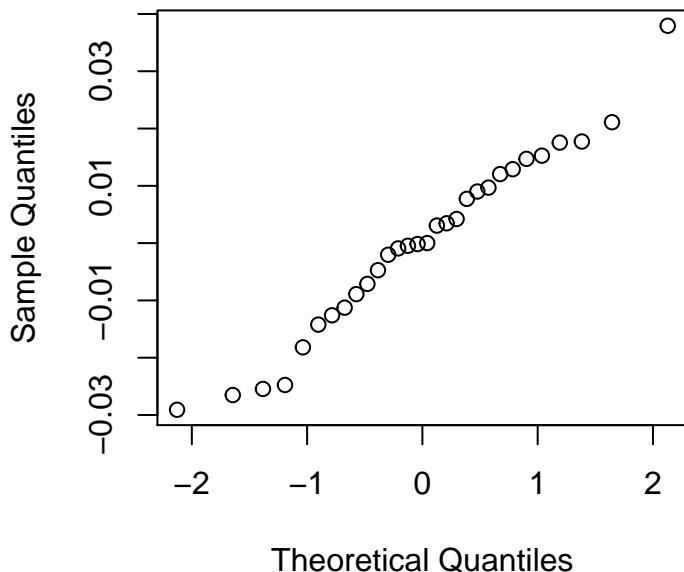

```r
summary(mod4a)
```

```
## 
## Call:
## lm(formula = LBR ~ LLEN + Order, data = dat1)
## 
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.029089 -0.010675 -0.000076  0.011463  0.037936
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.064592   0.056207   1.149    0.261
```

```
## LLEN          0.864638    0.031073   27.826   < 2e-16 ***
## Orderpenguin 0.064805    0.006366   10.179 9.69e-11 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01648 on 27 degrees of freedom
## Multiple R-squared:  0.9777, Adjusted R-squared:  0.976
## F-statistic: 590.8 on 2 and 27 DF,  p-value: < 2.2e-16
```

```
ggplot(dat1, aes(LLEN, LBR)) + geom_point(aes(color=Order, shape=Order)) + geom_smooth(method = lm, aes
```
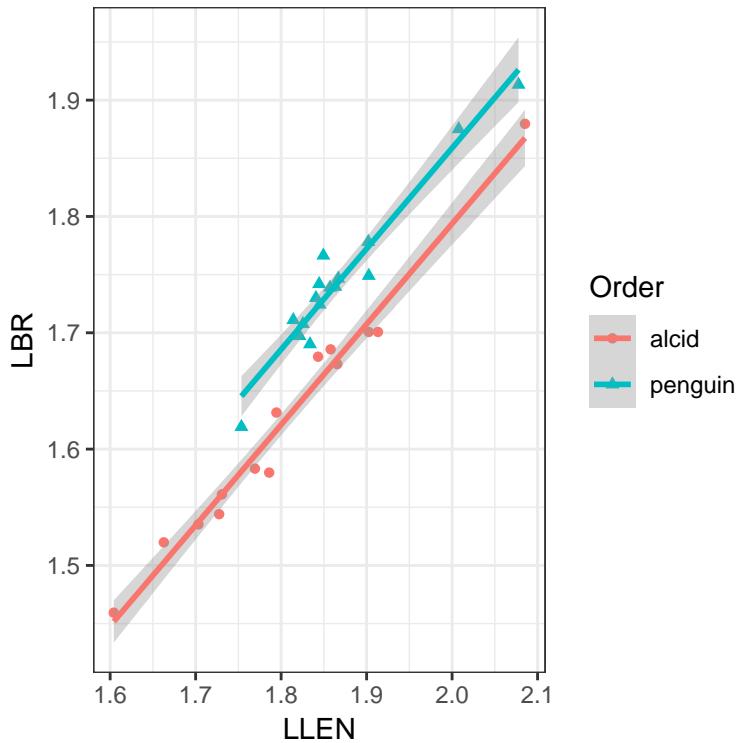

SUMMARY: There are 4 sets of linear models here. In each case we tested for an interaction between Order and the predictor of interest and none of the interactions were significant and all had P>0.20 so we removed them from the models (mod1a - 4a) Thus there is no evidence that the slopes for alcids and penguins are different in each model.

mod1a shows that female body mass explains 96% of the variation in egg volume with a common slope of 0.69

mod2a shows that egg length explains 99% of the variation in egg volume with the common slope of 2.67

mod3a shows that egg breadth explains almost 100% (99.7%) of the variation in egg volume with the common slope of 3.05

mod4a shows that egg breadth explains 98% of the variation in egg length with the common slope of 0.87

The graphs show what a good fit these models are to the data, with shaded areas indicating 95%CI. The qqnorm plots show that the residuals are close to normally distributed

4.3   Egg shape and size

Here we look at correlations between egg shape indices and (log1010-transformed) egg size measured as egg volume. Each model includes the variable *Order* to test for differences between alcids and penguins, first

including an interaction term to test for differences in slope between these two taxa

```
#Elongation
mod10 <- lm(EL ~ LVOL * Order, data = dat1)
summary(mod10)
```

```
##
## Call:
## lm(formula = EL ~ LVOL * Order, data = dat1)
##
## Residuals:
##      Min       1Q    Median       3Q       Max
## -0.126154 -0.033091 -0.006136  0.043112  0.105859
##
## Coefficients:
##                  Estimate Std. Error t value Pr(>|t|)
## (Intercept)       1.24621    0.09227  13.506 2.92e-13 ***
## LVOL              0.15724    0.05196   3.026  0.00552 **
## Orderpenguin     -0.13311    0.18207  -0.731  0.47125
## LVOL:Orderpenguin -0.05053    0.09185  -0.550  0.58696
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0611 on 26 degrees of freedom
## Multiple R-squared:  0.7586, Adjusted R-squared:  0.7308
## F-statistic: 27.24 on 3 and 26 DF,  p-value: 3.478e-08
```

```
#remove NS interaction term
mod10a <- lm(EL ~ LVOL + Order, data = dat1)
summary(mod10a)
```

```
##
## Call:
## lm(formula = EL ~ LVOL + Order, data = dat1)
##
## Residuals:
##      Min       1Q    Median       3Q       Max
## -0.127168 -0.038966 -0.003586  0.043698  0.104336
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.27447    0.07565  16.846 7.51e-16 ***
## LVOL          0.14107    0.04229   3.336  0.00248 **
## Orderpenguin -0.23223    0.02577  -9.012 1.26e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06031 on 27 degrees of freedom
## Multiple R-squared:  0.7558, Adjusted R-squared:  0.7377
## F-statistic: 41.79 on 2 and 27 DF,  p-value: 5.419e-09
```

```
confint(mod10a)
```

```
##                   2.5 %     97.5 %
## (Intercept)   1.11924168  1.4296922
## LVOL          0.05429765  0.2278388
```

```
## Orderpenguin -0.28510989 -0.1793589
```

```r
Anova(mod10a)
```

```
## Anova Table (Type II tests)
##
## Response: EL
##            Sum Sq Df F value   Pr(>F)
## LVOL      0.040470  1  11.127 0.002485 **
## Order     0.295366  1  81.213 1.26e-09 ***
## Residuals 0.098197 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
ggplot(dat1, aes(LVOL, EL)) + geom_point(aes(color=Order, shape = Order, size =2)) + geom_smooth(method
```
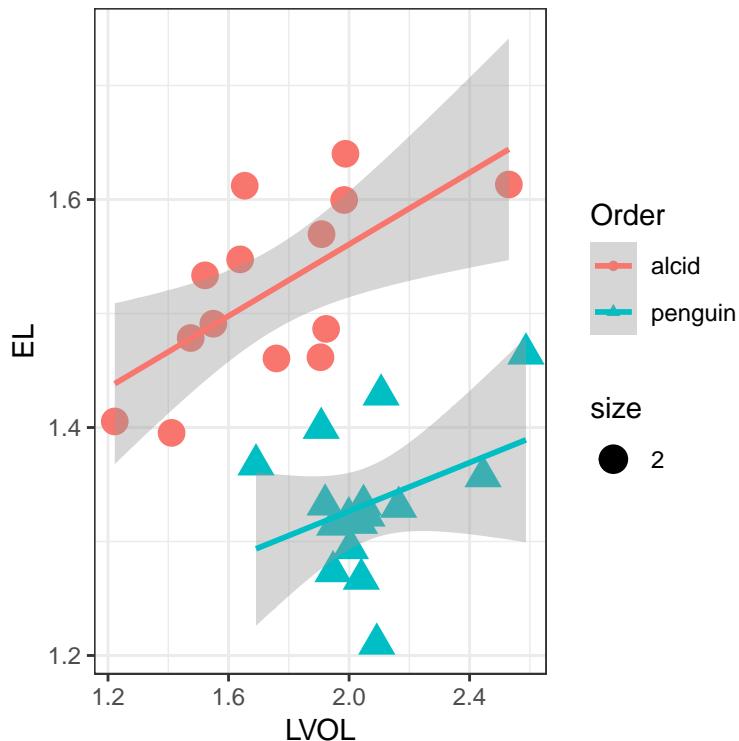


```r
#Pointedness
mod11 <- lm(PT ~ LVOL * Order, data = dat1)
summary(mod11)
```

```
##
## Call:
## lm(formula = PT ~ LVOL * Order, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.038074 -0.010099 -0.000462  0.013170  0.041141
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.45369    0.03170  14.311  7.7e-14 ***
## LVOL          0.07296    0.01785   4.087 0.000372 ***
```

```
## Orderpenguin        0.01779    0.06255    0.284 0.778345
## LVOL:Orderpenguin -0.03142    0.03156   -0.996 0.328559
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02099 on 26 degrees of freedom
## Multiple R-squared:  0.5278, Adjusted R-squared:  0.4733
## F-statistic: 9.688 on 3 and 26 DF,  p-value: 0.0001818
```

```
anova(mod11) #interaction term P>0.20
```

```
## Analysis of Variance Table
##
## Response: PT
##            Df    Sum Sq   Mean Sq F value   Pr(>F)
## LVOL        1 0.0018395 0.0018395  4.1744   0.0513 .
## Order       1 0.0105309 0.0105309 23.8979 4.51e-05 ***
## LVOL:Order  1 0.0004369 0.0004369  0.9915   0.3286
## Residuals  26 0.0114572 0.0004407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
#remove interaction term
mod11a <- lm(PT ~ LVOL + Order, data = dat1)
summary(mod11a)
```

```
##
## Call:
## lm(formula = PT ~ LVOL + Order, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.038704 -0.008697 -0.001303  0.012258  0.043556
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.471261   0.026329  17.899  < 2e-16 ***
## LVOL         0.062909   0.014718   4.274 0.000213 ***
## Orderpenguin -0.043851   0.008969  -4.889  4.1e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02099 on 27 degrees of freedom
## Multiple R-squared:  0.5098, Adjusted R-squared:  0.4735
## F-statistic: 14.04 on 2 and 27 DF,  p-value: 6.605e-05
```

```
Anova(mod11a)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##              Sum Sq Df F value     Pr(>F)
## LVOL      0.0080481  1  18.269 0.0002135 ***
## Order     0.0105309  1  23.905 4.101e-05 ***
## Residuals 0.0118941 27
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
confint(mod11a)

##                      2.5 %       97.5 %
## (Intercept)    0.41723760   0.52528388
## LVOL           0.03270994   0.09310758
## Orderpenguin  -0.06225326  -0.02544868
ggplot(dat1, aes(LVOL, PT)) + geom_point(aes(color=Order, shape = Order, size = 2)) + geom_smooth(method
```
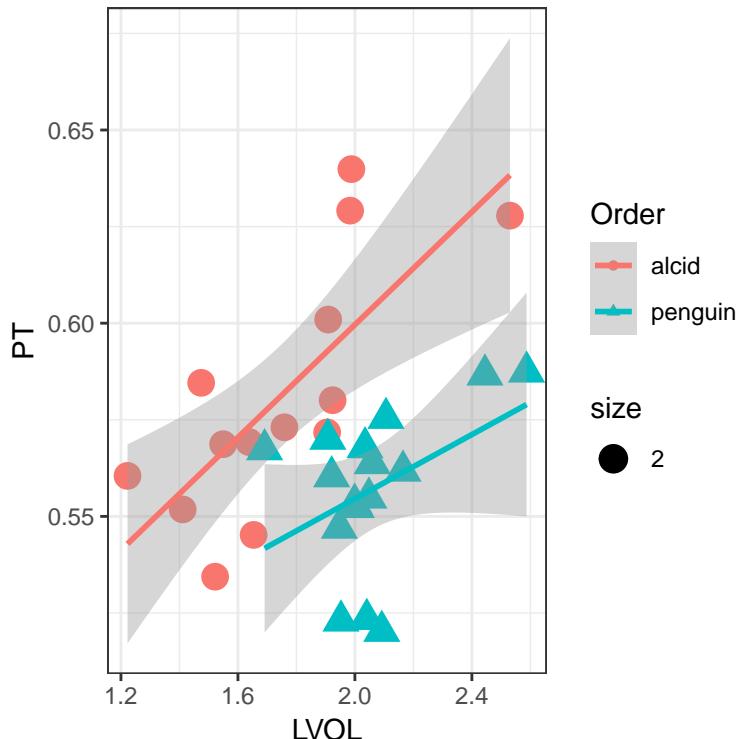


```
mod12 <- lm(PA ~ LVOL * Order, data = dat1)
summary(mod12)

##
## Call:
## lm(formula = PA ~ LVOL * Order, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.46855 -0.18076  0.02335  0.20972  0.38350
##
## Coefficients:
##                   Estimate Std. Error t value Pr(>|t|)
## (Intercept)         0.9878     0.3943   2.505   0.0188 *
## LVOL                0.5676     0.2221   2.556   0.0168 *
## Orderpenguin       -1.0703     0.7781  -1.375   0.1807
## LVOL:Orderpenguin   0.3292     0.3925   0.839   0.4093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2611 on 26 degrees of freedom
```

```
## Multiple R-squared:  0.4243, Adjusted R-squared:  0.3579
## F-statistic: 6.388 on 3 and 26 DF,  p-value: 0.002175
```

```r
anova(mod12) #interaction term P>0.20
```

```
## Analysis of Variance Table
##
## Response: PA
##             Df  Sum Sq Mean Sq F value    Pr(>F)
## LVOL         1 0.27237 0.27237  3.9945 0.0562045 .
## Order        1 0.98648 0.98648 14.4675 0.0007786 ***
## LVOL:Order   1 0.04796 0.04796  0.7034 0.4092889
## Residuals   26 1.77283 0.06819
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
#remove interaction term
mod12a <- lm(PA ~ LVOL + Order, data = dat1)
summary(mod12a)
```

```
##
## Call:
## lm(formula = PA ~ LVOL + Order, data = dat1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4734 -0.2026  0.0248  0.2241  0.4137
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     0.8036     0.3258   2.467 0.020262 *
## LVOL            0.6730     0.1821   3.696 0.000984 ***
## Orderpenguin   -0.4244     0.1110  -3.825 0.000702 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2597 on 27 degrees of freedom
## Multiple R-squared:  0.4088, Adjusted R-squared:  0.365
## F-statistic: 9.334 on 2 and 27 DF,  p-value: 0.0008294
```

```r
Anova(mod12a)
```

```
## Anova Table (Type II tests)
##
## Response: PA
##            Sum Sq Df F value     Pr(>F)
## LVOL      0.92108  1  13.658 0.0009841 ***
## Order     0.98648  1  14.628 0.0007024 ***
## Residuals 1.82079 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
confint(mod12a)
```

```
##                  2.5 %     97.5 %
## (Intercept)  0.1352202  1.4720415
## LVOL         0.2993548  1.0466351
```

Orderpenguin -0.6520994 -0.1967284

```
ggplot(dat1, aes(LVOL, PA)) + geom_point(aes(color=Order, shape = Order, size = 2)) + geom_smooth(method
```
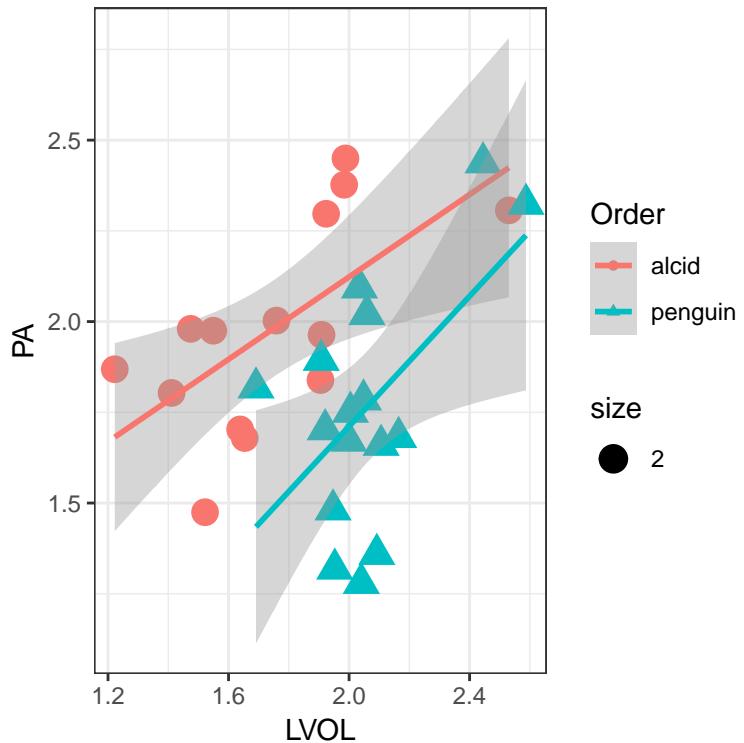


```
#egg shape relations
ggplot(dat1, aes(PT, PA)) + geom_point(aes(color=Order, shape = Order, size = 2)) + geom_smooth(method =
```

```
ggplot(dat1, aes(PT, EL)) + geom_point(aes(color=Order, shape = Order, size = 2)) + geom_smooth(method =
```
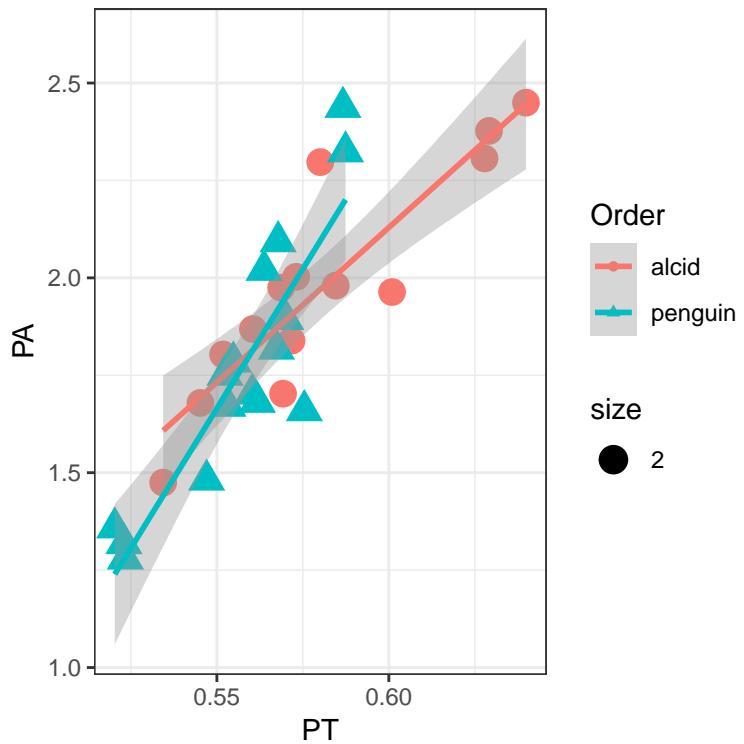

SUMMARY: All of the interaction terms have P>0.20), so we removed the interaction from the final models (mod10a, mod11a, mod12a). Egg volume is a significantly positive predictor of each egg shape index (all P 0.002), controlling for the significant difference in egg volume between alcids and penguins. Similarly, controlling for each egg shape index, alcid eggs are significantly larger than penguin eggs (all P<0.001).

5   Relation between egg size and developmental mode

Here we test whether the developmental mode of chicks influences egg size in the alcids and penguins. Other studies have reported that precocial birds have bigger eggs than altricial birds controlling for female size. In these analyses we categorize precocial species as either semi-precocial, intermediate or fully precocial. All altricial species are semi-altricial.

```
mod20a <- lm(LVOL ~ devel * LBM, data = dat1)
summary(mod20a) #interaction term NS so removed
```

```
##
## Call:
## lm(formula = LVOL ~ devel * LBM, data = dat1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.1125 -0.0315  0.0000  0.0295  0.1175
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.0461     1.8261  -0.573    0.573
## develIN        0.9067     1.8494   0.490    0.629
```

```
## develSA         0.8019      1.8364    0.437     0.667
## develSP         0.7392      1.8368    0.402     0.691
## LBM             1.1595      0.8036    1.443     0.163
## develIN:LBM    -0.4391      0.8090   -0.543     0.593
## develSA:LBM    -0.5164      0.8054   -0.641     0.528
## develSP:LBM    -0.3718      0.8077   -0.460     0.650
##
## Residual standard error: 0.06452 on 22 degrees of freedom
## Multiple R-squared:  0.967,  Adjusted R-squared:  0.9565
## F-statistic: 92.02 on 7 and 22 DF,  p-value: 8.219e-15
```

```
anova(mod20a)
```

```
## Analysis of Variance Table
##
## Response: LVOL
##           Df  Sum Sq Mean Sq  F value     Pr(>F)
## devel      3 1.44483 0.48161 115.7094 1.268e-13 ***
## LBM        1 1.22526 1.22526 294.3744 3.195e-14 ***
## devel:LBM  3 0.01096 0.00365   0.8777    0.4677
## Residuals 22 0.09157 0.00416
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod20 <- lm(LVOL ~ devel + LBM, data = dat1)
summary(mod20)
```

```
##
## Call:
## lm(formula = LVOL ~ devel + LBM, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.112668 -0.032081  0.003366  0.038979  0.138379
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.009018   0.101951   0.088    0.930
## develIN     -0.069336   0.064947  -1.068    0.296
## develSA     -0.439240   0.071429  -6.149 1.98e-06 ***
## develSP     -0.090333   0.051048  -1.770    0.089 .
## LBM          0.695024   0.040211  17.285 2.05e-15 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06404 on 25 degrees of freedom
## Multiple R-squared:  0.963,  Adjusted R-squared:  0.9571
## F-statistic: 162.8 on 4 and 25 DF,  p-value: < 2.2e-16
```

```
Anova(mod20)
```

```
## Anova Table (Type II tests)
##
## Response: LVOL
##            Sum Sq Df F value     Pr(>F)
## devel     0.36666  3  29.801 2.033e-08 ***
```

```
## LBM       1.22526  1 298.758 2.048e-15 ***
## Residuals 0.10253 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
comp1 <- glht(mod20, linfct = mcp(devel = "Tukey"))
summary(comp1)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = LVOL ~ devel + LBM, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## IN - FP == 0 -0.06934    0.06495  -1.068    0.698
## SA - FP == 0 -0.43924    0.07143  -6.149   <0.001 ***
## SP - FP == 0 -0.09033    0.05105  -1.770    0.296
## SA - IN == 0 -0.36990    0.04056  -9.119   <0.001 ***
## SP - IN == 0 -0.02100    0.04776  -0.440    0.969
## SP - SA == 0  0.34891    0.05400   6.461   <0.001 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
(g20 <- emmeans(mod20, specs = "devel"))
```

```
##   devel    emmean          SE df lower.CL upper.CL
##   FP     2.183225 0.05689557 25 2.066046 2.300404
##   IN     2.113889 0.03202681 25 2.047928 2.179849
##   SA     1.743985 0.02440860 25 1.693715 1.794256
##   SP     2.092892 0.03594099 25 2.018870 2.166913
##
## Confidence level used: 0.95
```

```r
plot(g20, xlab = "Marginal Mean log10 Egg Volume")
```
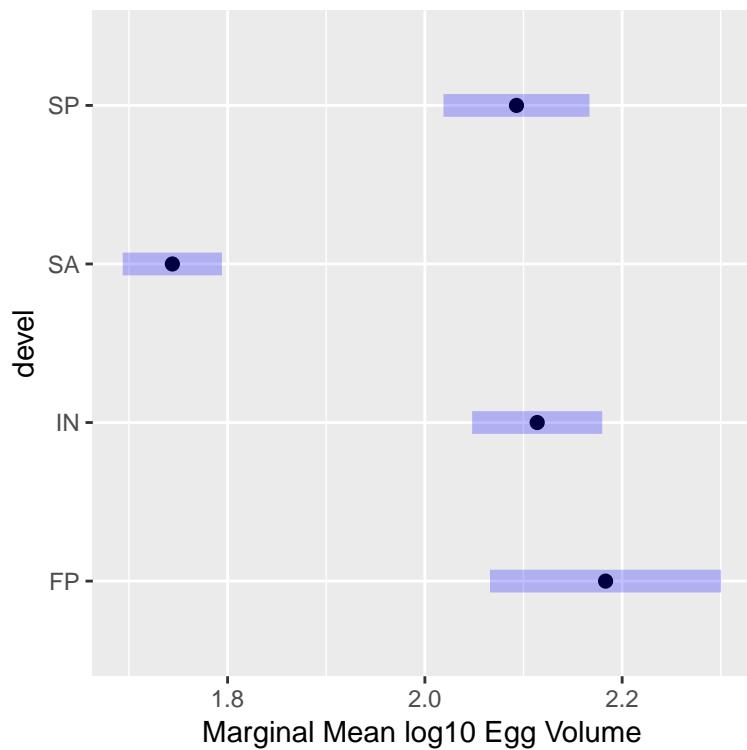
```
plot_model(mod20, type = "diag")
```

[[1]]

Variance Inflation Factors (multicollinearity)

[[2]]

29
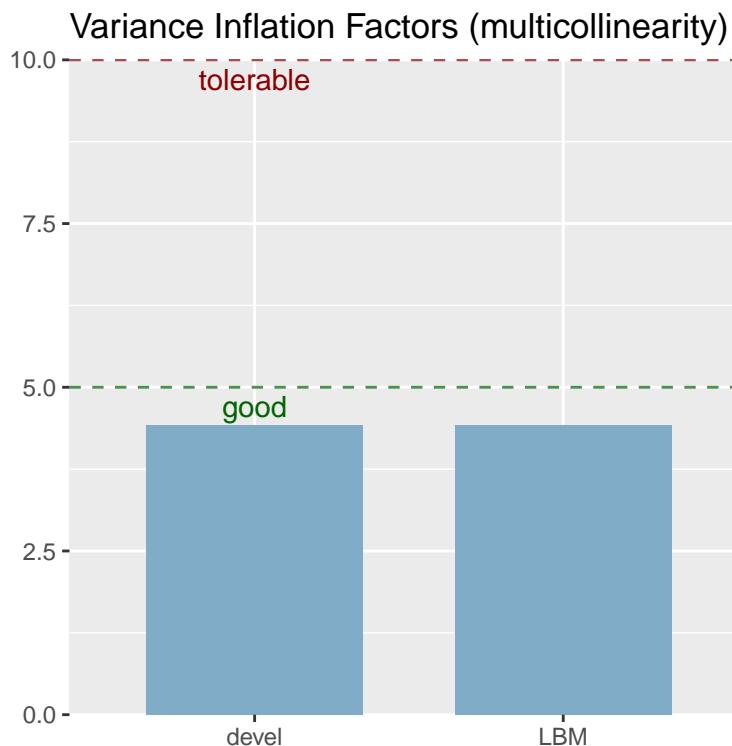
Non−normality of residuals and outliers
Dots should be plotted along the line
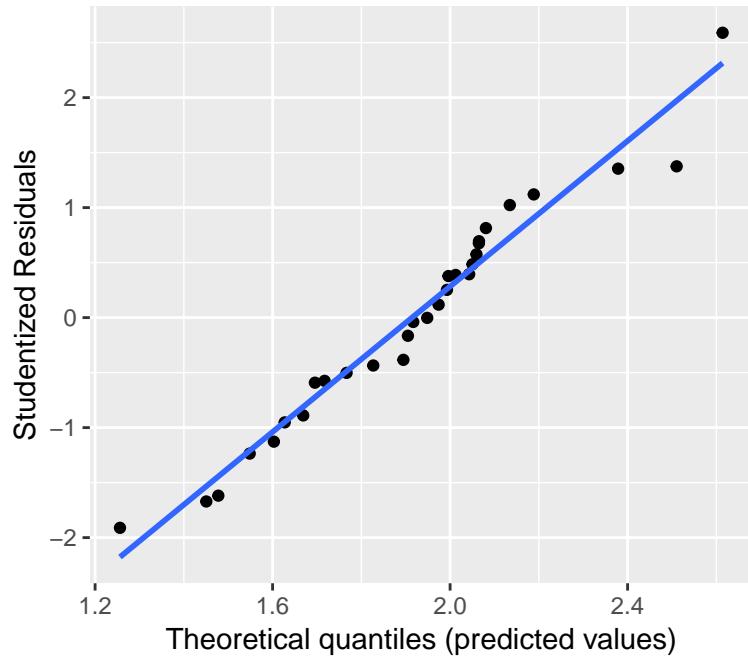
[[3]]

Non−normality of residuals
Distribution should look like normal curve
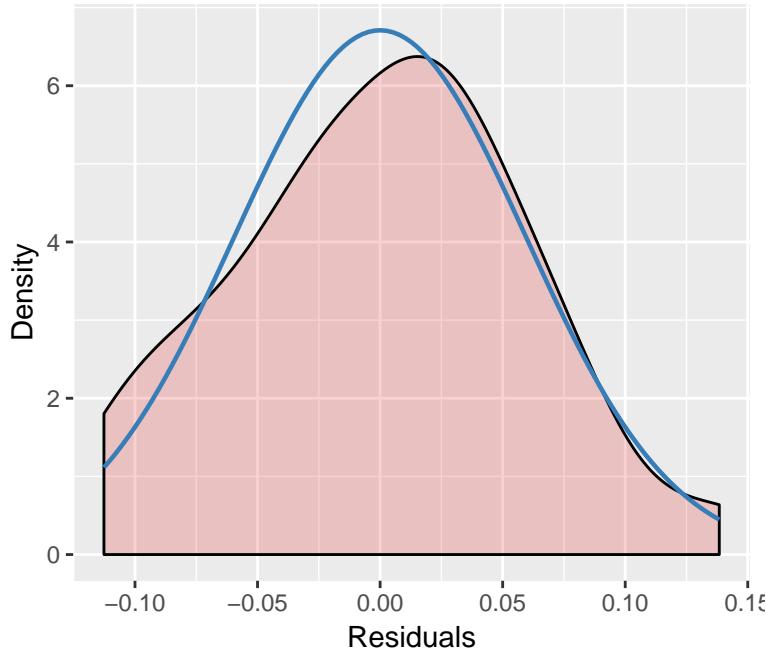
[[4]]

Homoscedasticity (constant variance of re
Amount and distance of points scattered above/be
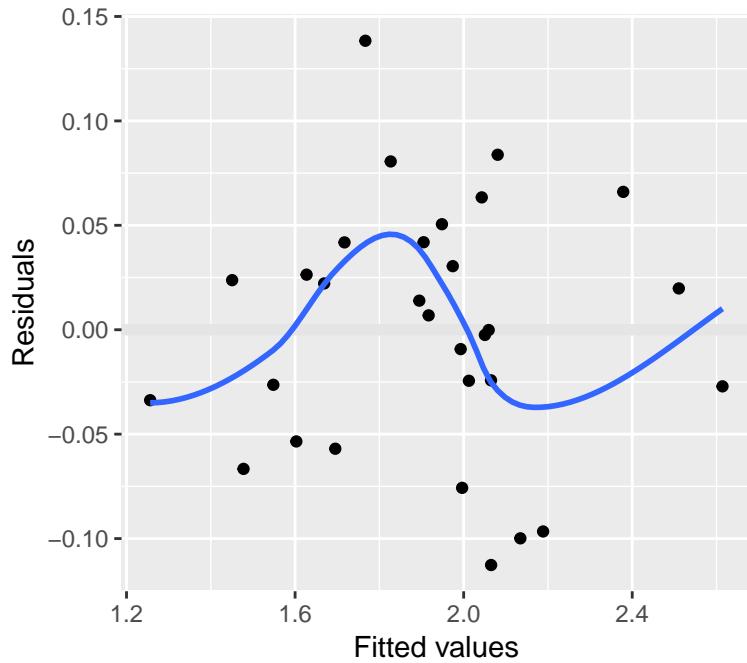
```r
ggplot(dat1, aes(LBM, LVOL)) + geom_point(aes(color=devel)) + geom_smooth(method = lm, aes(group = devel
```

```
## Warning in qt((1 - level)/2, df): NaNs produced
```
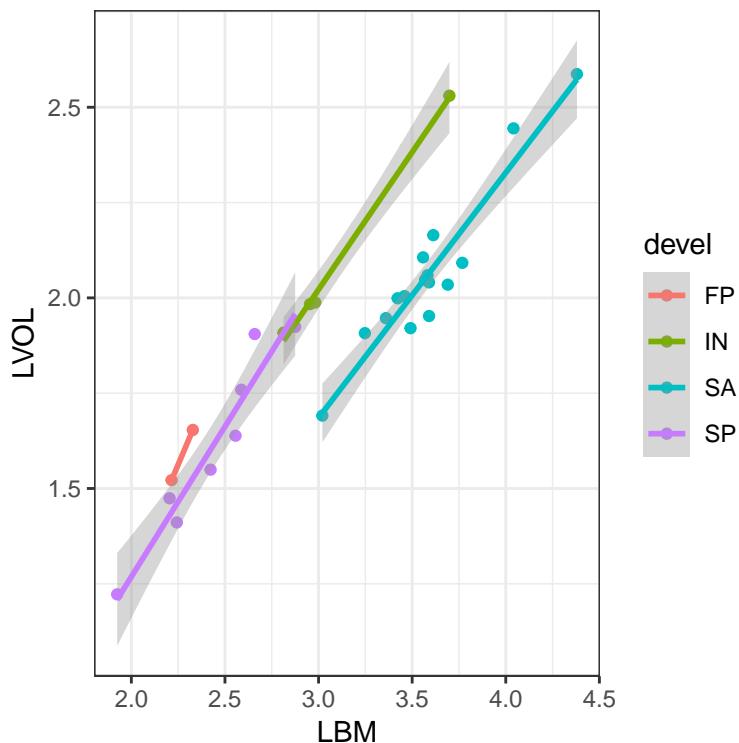

SUMMARY: Within the combined alcid and penguin dataset, egg volume varies significantly with developmental mode (mod20; P<0.0001), with the only significant differences (Tukey contrasts) between semialtricial and each of the 3 precocial modes (intermediate, semi-precocial and fully precocial). This is clearly

illustrated in the graphs.

We plotted the marginal means (also called least squares means), controlling for other variables in each model. The regression plot shows how the egg volumes within each type of development mode vary with female body mass (the warning message is due to their being only 2 species with fully precocial development so no regression could be calculated). The diagnostic plots show that the assumptions for the linear model are reasonably well satisfied.

6   Relation between egg shape indices and development mode

Here we look at the 3 shape indices across the different developmental modes. We compare each of the 4 developmental modes first (predictor = devel), but then just compare the precocial and altricial modes (predictor = gendev).

```
#Development mode (4 categories)
##PA
mod21a <- lm(PA ~ devel * LVOL, data = dat1)
summary(mod21a) #interaction NS so removed
```

```
##
## Call:
## lm(formula = PA ~ devel * LVOL, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.46855 -0.16984  0.02637  0.11446  0.38350
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.8893     4.3986  -0.202    0.842
## develIN        2.8096     4.5331   0.620    0.542
## develSA        0.8068     4.4482   0.181    0.858
## develSP        2.3167     4.4459   0.521    0.608
## LVOL           1.5531     2.7678   0.561    0.580
## develIN:LVOL  -1.3848     2.8158  -0.492    0.628
## develSA:LVOL  -0.6563     2.7862  -0.236    0.816
## develSP:LVOL  -1.2389     2.7962  -0.443    0.662
##
## Residual standard error: 0.2576 on 22 degrees of freedom
## Multiple R-squared:  0.5258, Adjusted R-squared:  0.3749
## F-statistic: 3.485 on 7 and 22 DF,  p-value: 0.0115
```

```
mod21 <- lm(PA ~ devel + LVOL, data = dat1)
summary(mod21)
```

```
##
## Call:
## lm(formula = PA ~ devel + LVOL, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.47544 -0.18472  0.01744  0.17917  0.44898
##
## Coefficients:
```

```
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.65490    0.39252   1.668   0.1077
## develIN      0.39841    0.24696   1.613   0.1192
## develSA     -0.08521    0.21685  -0.393   0.6977
## develSP      0.34355    0.20042   1.714   0.0989 .
## LVOL         0.58064    0.21993   2.640   0.0141 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2534 on 25 degrees of freedom
## Multiple R-squared:  0.4786, Adjusted R-squared:  0.3952
## F-statistic: 5.737 on 4 and 25 DF,  p-value: 0.002034
```

```
Anova(mod21)
```

```
## Anova Table (Type II tests)
##
## Response: PA
##            Sum Sq Df F value  Pr(>F)
## devel     1.20161  3  6.2363 0.00261 **
## LVOL      0.44766  1  6.9701 0.01407 *
## Residuals 1.60566 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
comp21 <- glht(mod21, linfct = mcp(devel = "Tukey"))
summary(comp21)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PA ~ devel + LVOL, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## IN - FP == 0  0.39841    0.24696   1.613   0.3752
## SA - FP == 0 -0.08521    0.21685  -0.393   0.9776
## SP - FP == 0  0.34355    0.20042   1.714   0.3241
## SA - IN == 0 -0.48363    0.14195  -3.407   0.0104 *
## SP - IN == 0 -0.05486    0.18922  -0.290   0.9907
## SP - SA == 0  0.42876    0.14807   2.896   0.0340 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
(g21 <- emmeans(mod21, specs = "devel"))
```

```
##  devel   emmean         SE df lower.CL upper.CL
##  FP    1.767199 0.19315907 25 1.369380 2.165017
##  IN    2.165613 0.13322427 25 1.891232 2.439993
##  SA    1.681985 0.07111072 25 1.535529 1.828440
##  SP    2.110748 0.11195433 25 1.880174 2.341322
##
```

```
## Confidence level used: 0.95
```

```
plot(g21, xlab = "Marginal Mean Polar Asymmetry")
```
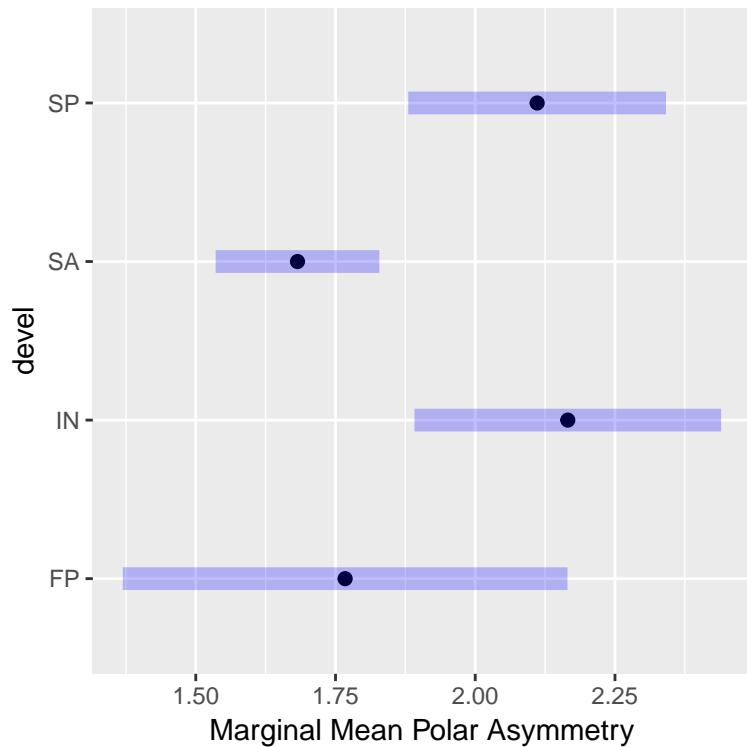


```
ggplot(dat1, aes(x = devel, y = PA)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
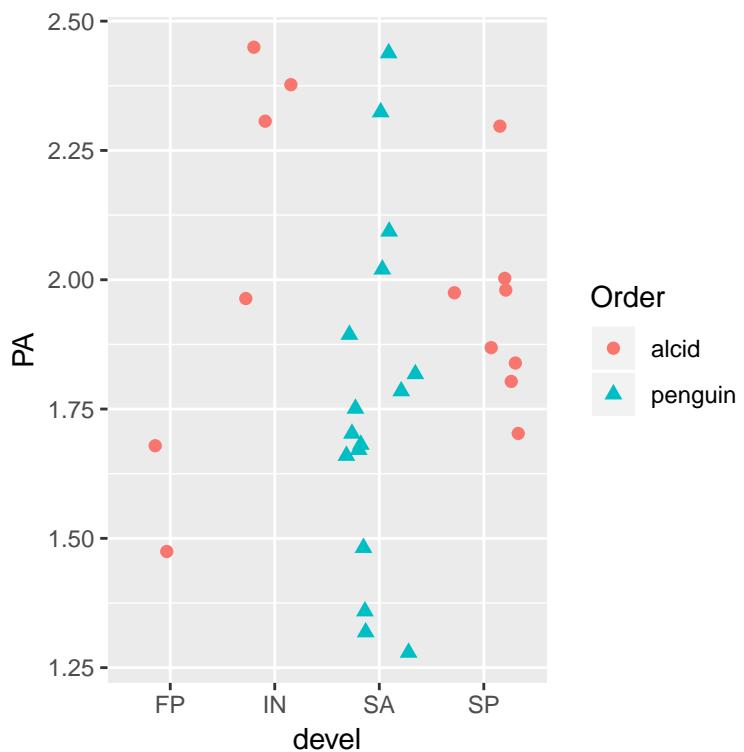
```
##PT
mod22a <- lm(PT ~ devel * LVOL, data = dat1)
summary(mod22a) #interaction NS so removed

##
## Call:
## lm(formula = PT ~ devel * LVOL, data = dat1)
##
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.038074 -0.002824  0.000000  0.008893  0.025578
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.40936    0.29503   1.387    0.179
## develIN       0.18385    0.30405   0.605    0.552
## develSA       0.06212    0.29835   0.208    0.837
## develSP       0.12414    0.29820   0.416    0.681
## LVOL          0.08215    0.18565   0.442    0.662
## develIN:LVOL -0.06729    0.18887  -0.356    0.725
## develSA:LVOL -0.04061    0.18688  -0.217    0.830
## develSP:LVOL -0.05952    0.18755  -0.317    0.754
##
## Residual standard error: 0.01728 on 22 degrees of freedom
## Multiple R-squared:  0.7292, Adjusted R-squared:  0.6431
## F-statistic: 8.464 on 7 and 22 DF,  p-value: 4.902e-05
anova(mod22a)

## Analysis of Variance Table
##
## Response: PT
##            Df    Sum Sq   Mean Sq F value    Pr(>F)
## devel       3 0.0162426 0.0054142 18.1290 3.753e-06 ***
## LVOL        1 0.0012627 0.0012627  4.2280   0.05182 .
## devel:LVOL  3 0.0001890 0.0000630  0.2109   0.88774
## Residuals  22 0.0065703 0.0002986
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
mod22 <- lm(PT ~ devel + LVOL, data = dat1)
summary(mod22)

##
## Call:
## lm(formula = PT ~ devel + LVOL, data = dat1)
##
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.037758 -0.005782  0.000532  0.010733  0.021604
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.490834   0.025467  19.273  < 2e-16 ***
## develIN     0.068770   0.016023   4.292 0.000233 ***
```

```
## develSA      0.002721    0.014069    0.193 0.848221
## develSP      0.029459    0.013003    2.265 0.032400 *
## LVOL         0.030838    0.014270    2.161 0.040469 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01644 on 25 degrees of freedom
## Multiple R-squared:  0.7214, Adjusted R-squared:  0.6769
## F-statistic: 16.19 on 4 and 25 DF,  p-value: 1.154e-06
```

```r
Anova(mod22)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##              Sum Sq Df F value    Pr(>F)
## devel     0.0156658  3 19.3139 1.077e-06 ***
## LVOL      0.0012627  1  4.6702   0.04047 *
## Residuals 0.0067593 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
comp22 <- glht(mod22, linfct = mcp(devel = "Tukey"))
summary(comp22)
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PT ~ devel + LVOL, data = dat1)
##
## Linear Hypotheses:
##                Estimate Std. Error t value Pr(>|t|)
## IN - FP == 0   0.068770   0.016023   4.292  0.00115 **
## SA - FP == 0   0.002721   0.014069   0.193  0.99718
## SP - FP == 0   0.029459   0.013003   2.265  0.12610
## SA - IN == 0  -0.066049   0.009210  -7.172  < 0.001 ***
## SP - IN == 0  -0.039311   0.012277  -3.202  0.01693 *
## SP - SA == 0   0.026738   0.009607   2.783  0.04371 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
(g22 <- emmeans(mod22, specs = "devel"))
```

```
## devel    emmean          SE df  lower.CL  upper.CL
## FP    0.5499073 0.012532515 25 0.5240961 0.5757185
## IN    0.6186774 0.008643835 25 0.6008751 0.6364797
## SA    0.5526281 0.004613794 25 0.5431258 0.5621304
## SP    0.5793663 0.007263802 25 0.5644062 0.5943263
##
## Confidence level used: 0.95
```

```r
plot(g22, xlab = "Marginal Mean Pointedness")
```
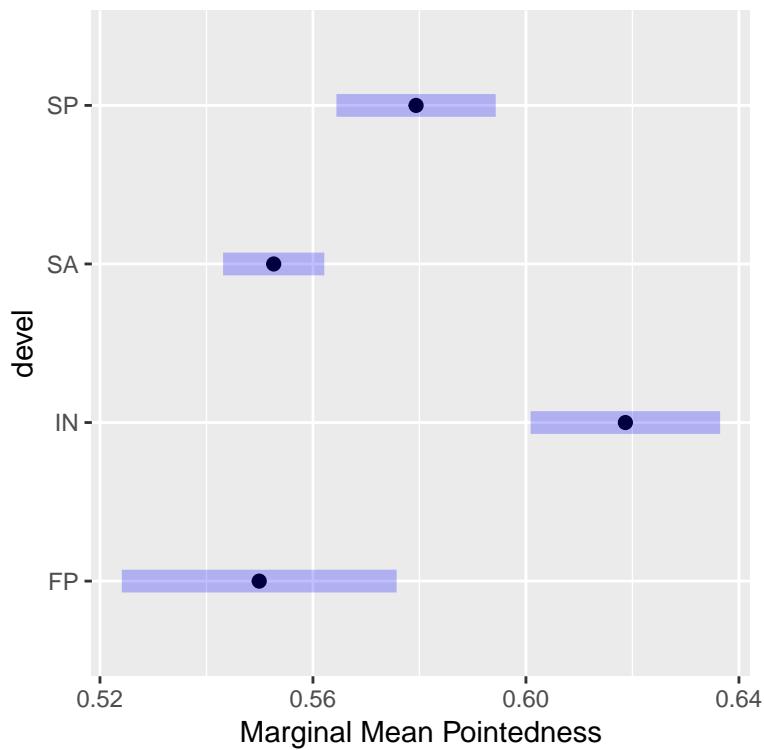
```
ggplot(dat1, aes(x = devel, y = PT)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
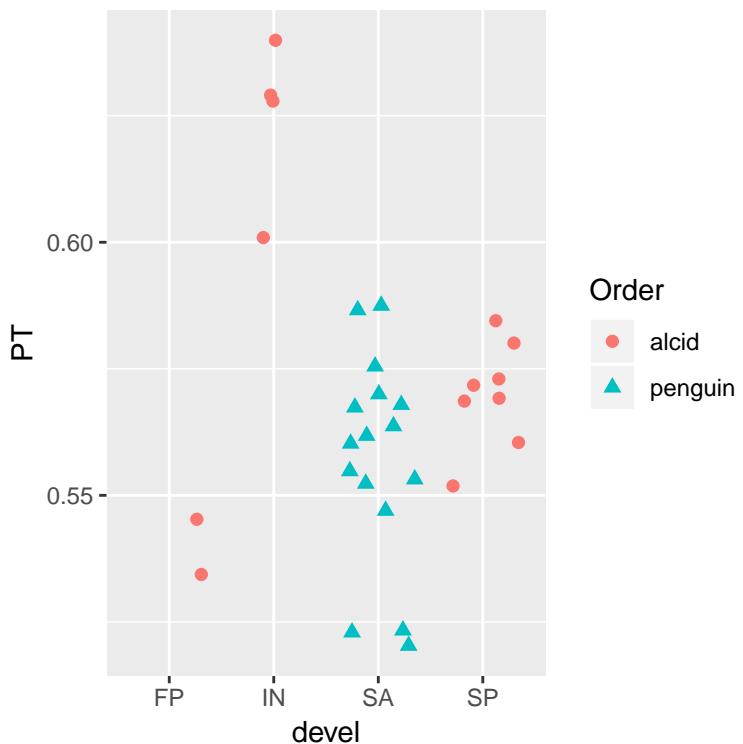


```
##EL
mod23a <- lm(EL ~ LVOL * devel, data = dat1)
summary(mod23a) #interaction NS so removed
```

```
## 
## Call:
## lm(formula = EL ~ LVOL * devel, data = dat1)
## 
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.126154 -0.021889 -0.006136  0.023036  0.090855
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     0.6247     0.9320   0.670    0.510
## LVOL            0.5971     0.5865   1.018    0.320
## develIN         0.9217     0.9605   0.960    0.348
## develSA         0.4884     0.9425   0.518    0.609
## develSP         0.6839     0.9420   0.726    0.475
## LVOL:develIN   -0.5689     0.5966  -0.954    0.351
## LVOL:develSA   -0.4904     0.5903  -0.831    0.415
## LVOL:develSP   -0.4995     0.5925  -0.843    0.408
## 
## Residual standard error: 0.05459 on 22 degrees of freedom
## Multiple R-squared:  0.837,  Adjusted R-squared:  0.7851
## F-statistic: 16.13 on 7 and 22 DF,  p-value: 2.513e-07
```

```
anova(mod23a)
```

```
## Analysis of Variance Table
## 
## Response: EL
##            Df  Sum Sq  Mean Sq F value    Pr(>F)
## LVOL        1 0.00860 0.008597  2.8847    0.1035
## devel       3 0.32462 0.108208 36.3086 1.073e-08 ***
## LVOL:devel  3 0.00337 0.001125  0.3774    0.7702
## Residuals  22 0.06557 0.002980
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod23 <- lm(EL ~ LVOL + devel, data = dat1)
summary(mod23)
```

```
## 
## Call:
## lm(formula = EL ~ LVOL + devel, data = dat1)
## 
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.125730 -0.029702 -0.009393  0.029494  0.091485
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.42613    0.08133  17.535 1.47e-15 ***
## LVOL         0.09236    0.04557   2.027   0.0535 .
## develIN     -0.01469    0.05117  -0.287   0.7764
## develSA     -0.28344    0.04493  -6.308 1.33e-06 ***
## develSP     -0.10907    0.04153  -2.627   0.0145 *
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05251 on 25 degrees of freedom
## Multiple R-squared:  0.8286, Adjusted R-squared:  0.8011
## F-statistic: 30.21 on 4 and 25 DF,  p-value: 3.028e-09
```

```r
Anova(mod23)
```

```
## Anova Table (Type II tests)
##
## Response: EL
##            Sum Sq Df F value    Pr(>F)
## LVOL      0.01133  1  4.1075   0.05349 .
## devel     0.32462  3 39.2402 1.313e-09 ***
## Residuals 0.06894 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
comp23 <- glht(mod23, linfct = mcp(devel = "Tukey"))
summary(comp23)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = EL ~ LVOL + devel, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## IN - FP == 0 -0.01469    0.05117  -0.287   0.9910
## SA - FP == 0 -0.28344    0.04493  -6.308   <1e-04 ***
## SP - FP == 0 -0.10907    0.04153  -2.627   0.0612 .
## SA - IN == 0 -0.26875    0.02941  -9.137   <1e-04 ***
## SP - IN == 0 -0.09438    0.03921  -2.407   0.0958 .
## SP - SA == 0  0.17436    0.03068   5.683   <1e-04 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
(g23 <- emmeans(mod23, specs = "devel"))
```

```
## devel   emmean         SE df lower.CL upper.CL
## FP    1.603055 0.04002418 25 1.520624 1.685486
## IN    1.588364 0.02760518 25 1.531510 1.645218
## SA    1.319618 0.01473474 25 1.289271 1.349965
## SP    1.493980 0.02319787 25 1.446203 1.541757
##
## Confidence level used: 0.95
```

```r
plot(g23, xlab ="Marginal Mean Elongation")
```
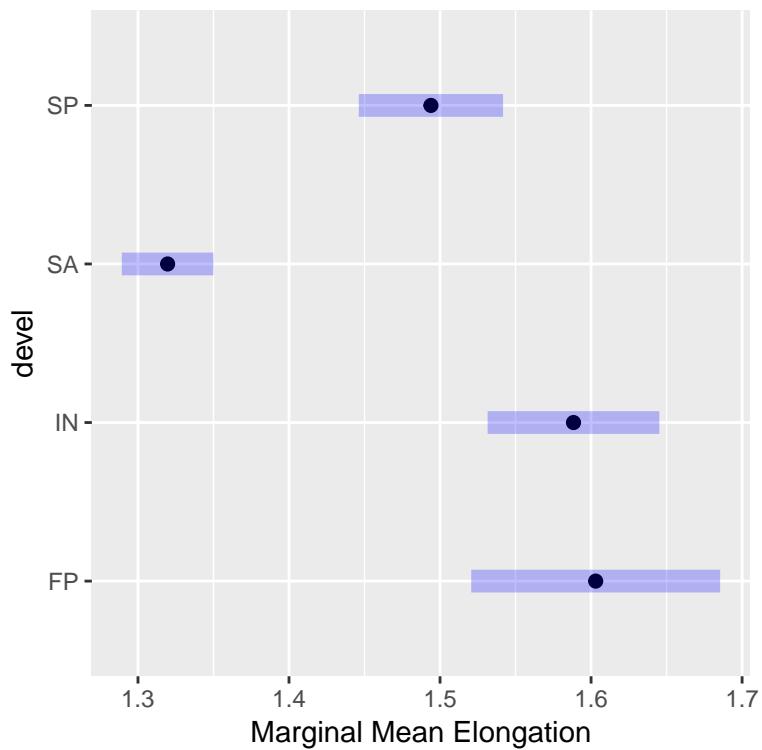
```
ggplot(dat1, aes(x = devel, y = EL)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
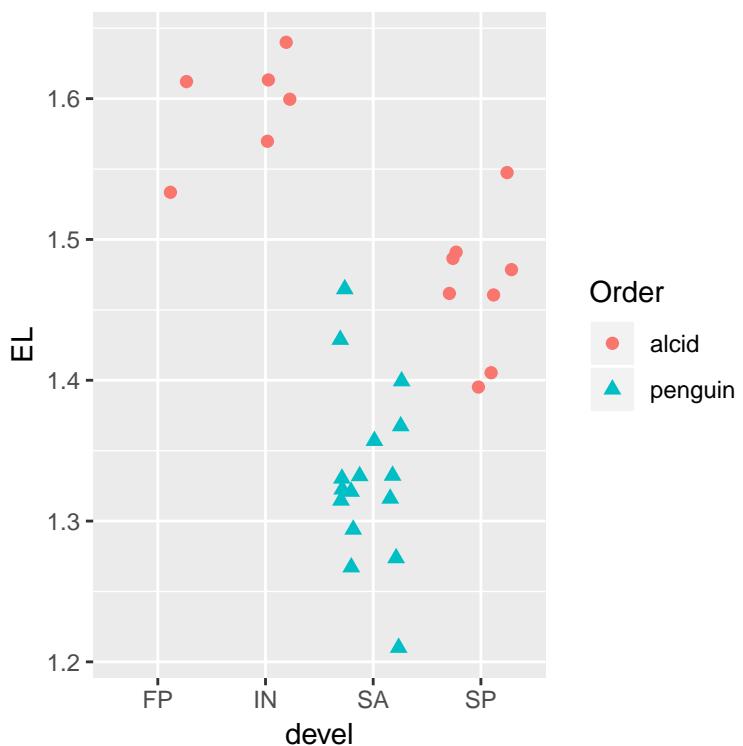


```
#General developmental mode (altricial vs precocial)
##PA
mod24a <- lm(PA ~ gendev * LVOL, data = dat1)
```

```
summary(mod24a) #interaction NS so removed
```

```
##
## Call:
## lm(formula = PA ~ gendev * LVOL, data = dat1)
##
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.46855 -0.18076  0.02335  0.20972  0.38350
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.08249    0.67078  -0.123   0.9031
## gendevP       1.07026    0.77811   1.375   0.1807
## LVOL          0.89686    0.32369   2.771   0.0102 *
## gendevP:LVOL -0.32922    0.39254  -0.839   0.4093
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2611 on 26 degrees of freedom
## Multiple R-squared:  0.4243, Adjusted R-squared:  0.3579
## F-statistic: 6.388 on 3 and 26 DF,  p-value: 0.002175
```

```
anova(mod24a)
```

```
## Analysis of Variance Table
##
## Response: PA
##            Df  Sum Sq Mean Sq F value   Pr(>F)
## gendev      1 0.33777 0.33777  4.9537 0.034917 *
## LVOL        1 0.92108 0.92108 13.5084 0.001084 **
## gendev:LVOL 1 0.04796 0.04796  0.7034 0.409289
## Residuals  26 1.77283 0.06819
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod24 <- lm(PA ~ gendev + LVOL, data = dat1)
summary(mod24)
```

```
##
## Call:
## lm(formula = PA ~ gendev + LVOL, data = dat1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.4734 -0.2026  0.0248  0.2241  0.4137
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.3792     0.3811   0.995 0.328595
## gendevP       0.4244     0.1110   3.825 0.000702 ***
## LVOL          0.6730     0.1821   3.696 0.000984 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## Residual standard error: 0.2597 on 27 degrees of freedom
## Multiple R-squared:  0.4088, Adjusted R-squared:  0.365
## F-statistic: 9.334 on 2 and 27 DF,  p-value: 0.0008294
```

```
Anova(mod24)
```

```
## Anova Table (Type II tests)
##
## Response: PA
##            Sum Sq Df F value    Pr(>F)
## gendev    0.98648  1  14.628 0.0007024 ***
## LVOL      0.92108  1  13.658 0.0009841 ***
## Residuals 1.82079 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g24 <- emmeans(mod24, specs = "gendev"))
```

```
##  gendev   emmean         SE df lower.CL upper.CL
##  A      1.668426 0.07021063 27 1.524366 1.812487
##  P      2.092840 0.07583169 27 1.937247 2.248434
##
## Confidence level used: 0.95
```

```
plot(g24, xlab ="Marginal Mean Polar Asymmetry")
```
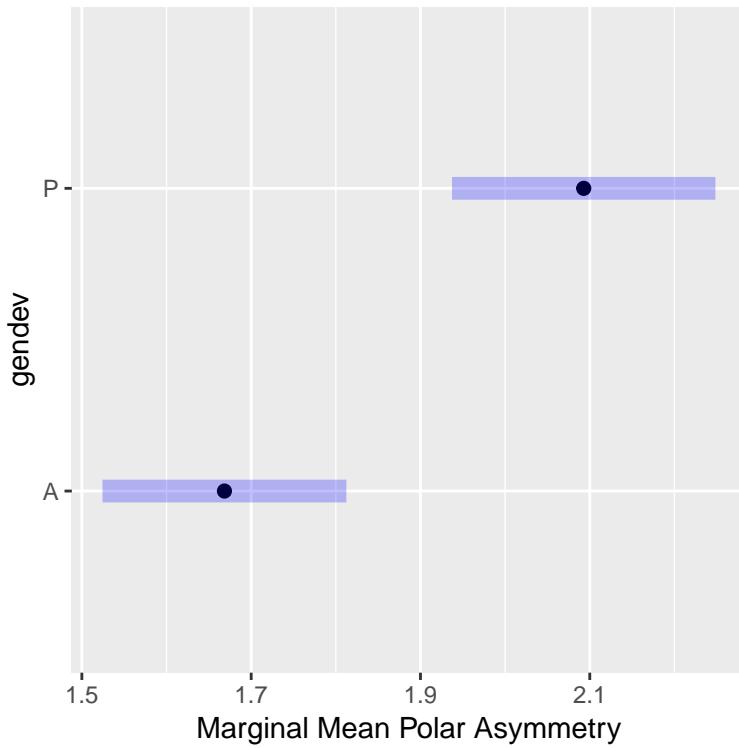


```
ggplot(dat1, aes(x = gendev, y = PA)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
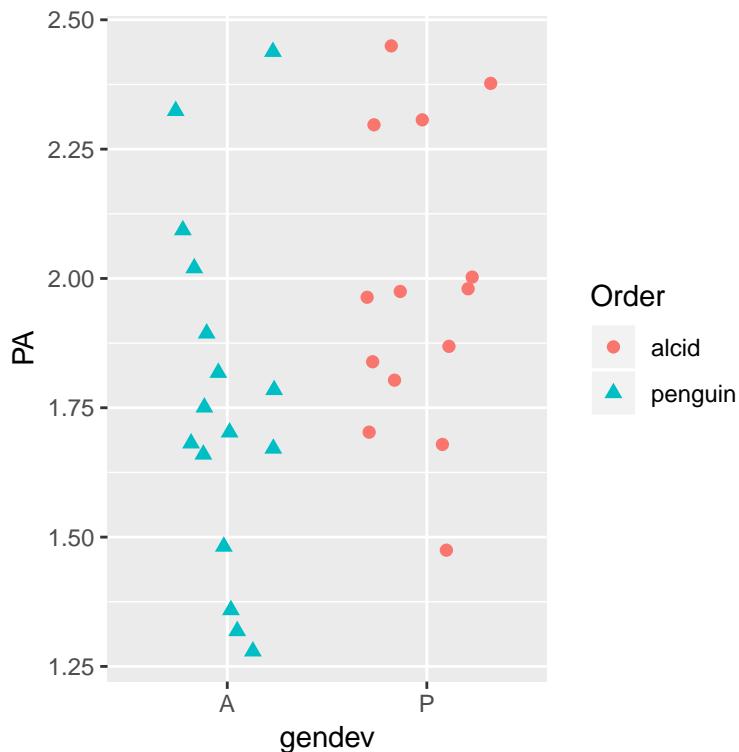
```
##PT
mod25a <- lm(PT ~ gendev * LVOL, data = dat1)
summary(mod25a) #interaction NS so removed
```

```
##
## Call:
## lm(formula = PT ~ gendev * LVOL, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.038074 -0.010099 -0.000462  0.013170  0.041141
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.47148    0.05392   8.743 3.21e-09 ***
## gendevP     -0.01779    0.06255  -0.284    0.778
## LVOL         0.04154    0.02602   1.596    0.122
## gendevP:LVOL 0.03142    0.03156   0.996    0.329
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02099 on 26 degrees of freedom
## Multiple R-squared:  0.5278, Adjusted R-squared:  0.4733
## F-statistic: 9.688 on 3 and 26 DF,  p-value: 0.0001818
```

```
anova(mod25a)
```

```
## Analysis of Variance Table
##
## Response: PT
##               Df    Sum Sq   Mean Sq F value    Pr(>F)
```

43

```
## gendev       1 0.0043223 0.0043223  9.8087 0.0042631 **
## LVOL         1 0.0080481 0.0080481 18.2637 0.0002284 ***
## gendev:LVOL  1 0.0004369 0.0004369  0.9915 0.3285589
## Residuals   26 0.0114572 0.0004407
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod25 <- lm(PT ~ gendev + LVOL, data = dat1)
summary(mod25)
```

```
##
## Call:
## lm(formula = PT ~ gendev + LVOL, data = dat1)
##
## Residuals:
##       Min       1Q    Median       3Q      Max
## -0.038704 -0.008697 -0.001303  0.012258  0.043556
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) 0.427410   0.030805  13.875 8.37e-14 ***
## gendevP     0.043851   0.008969   4.889 4.10e-05 ***
## LVOL        0.062909   0.014718   4.274 0.000213 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02099 on 27 degrees of freedom
## Multiple R-squared:  0.5098, Adjusted R-squared:  0.4735
## F-statistic: 14.04 on 2 and 27 DF,  p-value: 6.605e-05
```

```
Anova(mod25)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##              Sum Sq Df F value     Pr(>F)
## gendev    0.0105309  1  23.905 4.101e-05 ***
## LVOL      0.0080481  1  18.269 0.0002135 ***
## Residuals 0.0118941 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g25 <- emmeans(mod25, specs = "gendev"))
```

```
##  gendev    emmean          SE df  lower.CL  upper.CL
##  A      0.5479197 0.005674654 27 0.5362763 0.5595631
##  P      0.5917707 0.006128966 27 0.5791951 0.6043463
##
## Confidence level used: 0.95
```

```
plot(g25, xlab ="Marginal Mean Pointedness")
```
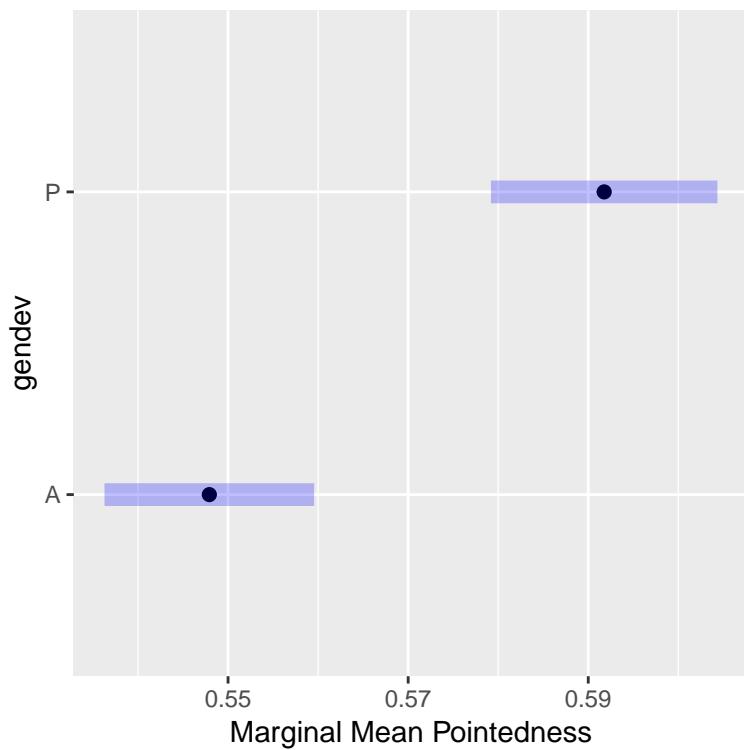
```
ggplot(dat1, aes(x = gendev, y = PT)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
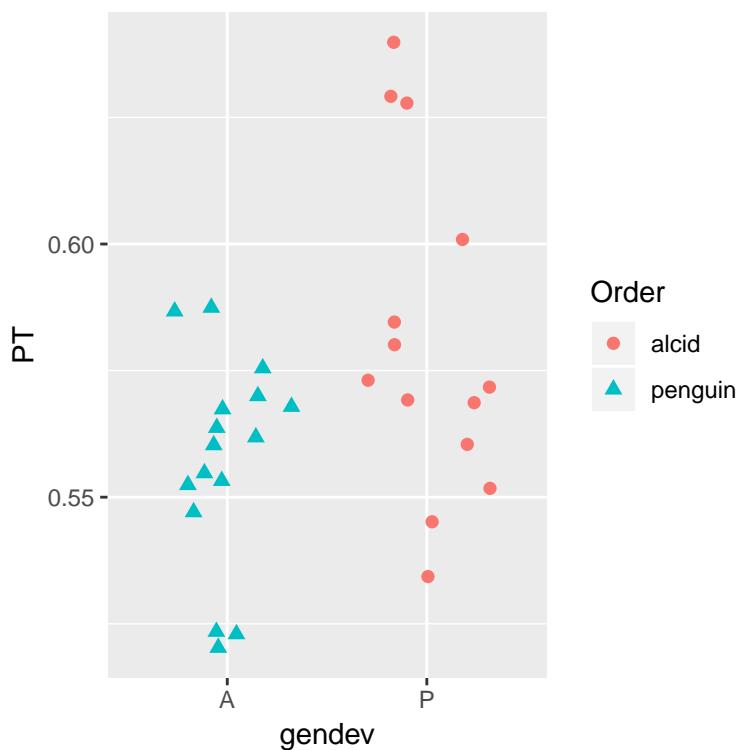


```
##EL
mod26a <- lm(EL ~ LVOL * gendev, data = dat1)
summary(mod26a) #interaction NS so removed
```

```
##
## Call:
## lm(formula = EL ~ LVOL * gendev, data = dat1)
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -0.126154 -0.033091 -0.006136  0.043112  0.105859
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.11309    0.15696   7.092 1.57e-07 ***
## LVOL          0.10671    0.07574   1.409    0.171
## gendevP       0.13311    0.18207   0.731    0.471
## LVOL:gendevP  0.05053    0.09185   0.550    0.587
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0611 on 26 degrees of freedom
## Multiple R-squared:  0.7586, Adjusted R-squared:  0.7308
## F-statistic: 27.24 on 3 and 26 DF,  p-value: 3.478e-08
```

```
anova(mod26a)
```

```
## Analysis of Variance Table
##
## Response: EL
##             Df    Sum Sq  Mean Sq F value     Pr(>F)
## LVOL         1 0.008597 0.008597  2.3028     0.1412
## gendev       1 0.295366 0.295366 79.1156 2.291e-09 ***
## LVOL:gendev  1 0.001130 0.001130  0.3026     0.5870
## Residuals   26 0.097067 0.003733
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod26 <- lm(EL ~ LVOL + gendev, data = dat1)
summary(mod26)
```

```
##
## Call:
## lm(formula = EL ~ LVOL + gendev, data = dat1)
##
## Residuals:
##        Min        1Q    Median        3Q       Max
## -0.127168 -0.038966 -0.003586  0.043698  0.104336
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.04223    0.08851  11.775 3.82e-12 ***
## LVOL         0.14107    0.04229   3.336  0.00248 **
## gendevP      0.23223    0.02577   9.012 1.26e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06031 on 27 degrees of freedom
## Multiple R-squared:  0.7558, Adjusted R-squared:  0.7377
```

```
## F-statistic: 41.79 on 2 and 27 DF,  p-value: 5.419e-09
```

```
Anova(mod26)
```

```
## Anova Table (Type II tests)
##
## Response: EL
##             Sum Sq Df F value   Pr(>F)
## LVOL      0.040470  1  11.127 0.002485 **
## gendev    0.295366  1  81.213 1.26e-09 ***
## Residuals 0.098197 27
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g26 <- emmeans(mod26, specs = "gendev"))
```

```
##  gendev   emmean         SE df lower.CL upper.CL
##  A      1.312467 0.01630504 27 1.279012 1.345922
##  P      1.544702 0.01761042 27 1.508568 1.580835
##
## Confidence level used: 0.95
```

```
plot(g26, xlab ="Marginal Mean Elongation")
```
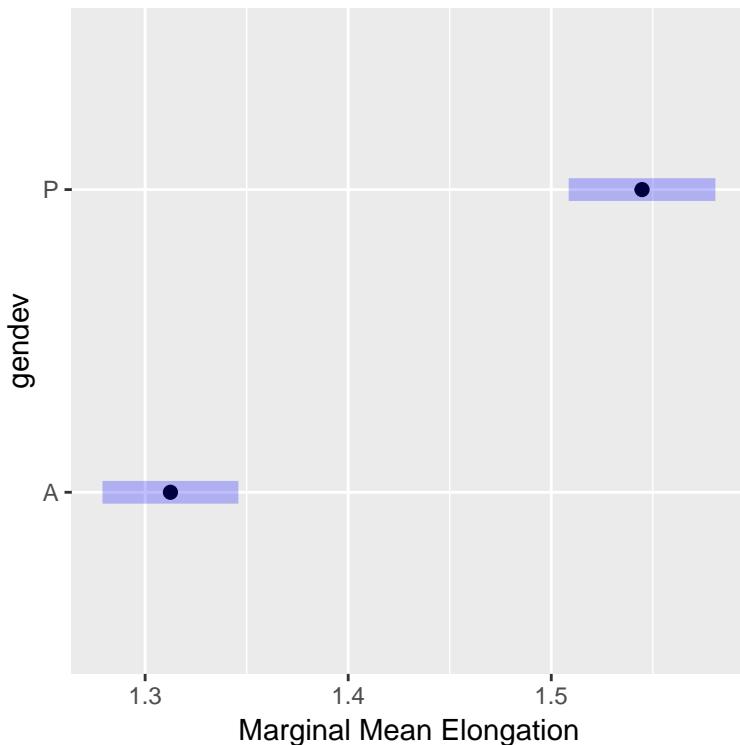


```
ggplot(dat1, aes(x = gendev, y = EL)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
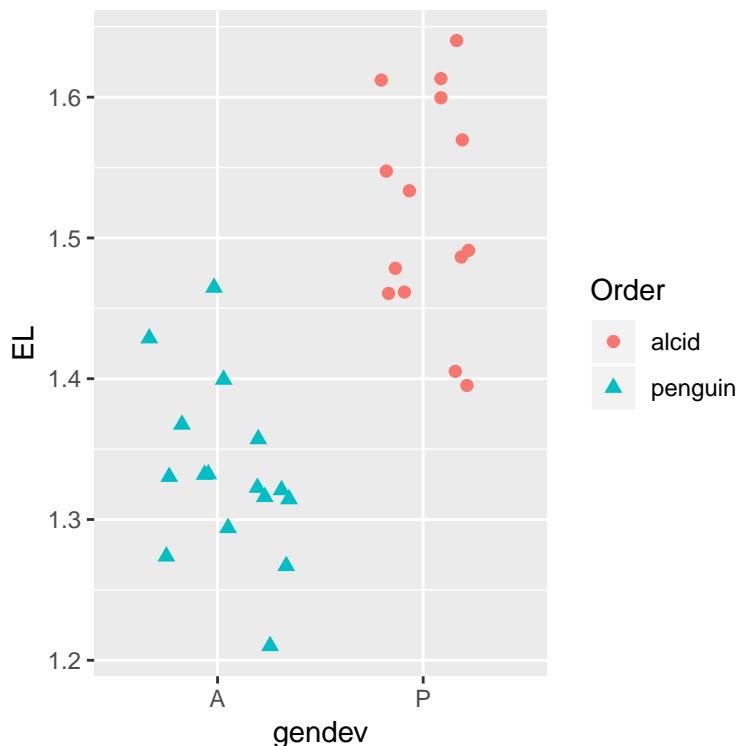
SUMMARY: Significant effects of development on all 3 egg shape indices, mainly due to semi-altricial (penguin) eggs having significantly lower values for all 3 indices for at least some of the comparisons of all 4 modes (comp21 for PA, comp22 for PT, comp23 for EL), and for all 3 indices when just comparing the semi-altricial penguins to the fully precocial alcids (comp25, 26 , 27).

For all analyses using general developmental mode (gendev) as predictor (mod24, mod25, mod26), species with precocial development (all alcids) have significantly (P<0.0001) higher egg shape indices than altricial species (all penguins), controlling for egg volume.

7 Relation between egg shape and clutch size

There are only 1- or 2-egg clutches in the alcids and penguins. We have made the clutch size variable into a factor (FCS) for analysis here so the two clutch sizes can be compared as categorical fixed effects. General developmental mode (variable = gendev) and (log10-transformed) egg volume are included in each model to control for the significant effects shown above. We used the dredge function in MuMIn to compare models using AICc in an information-theoretic approach.

```
#note that clutch size is included as a factor in these models rather than as a contiunuous variable
##PT
mod27 <-  lm(PT ~ gendev + LVOL +FCS, data = dat1)
summary(mod27)


##
## Call:
## lm(formula = PT ~ gendev + LVOL + FCS, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.035552 -0.014312  0.000907  0.011591  0.042322
##
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.47610    0.03836  12.412 1.98e-12 ***
## gendevP      0.02491    0.01287   1.936  0.06376 .
## LVOL         0.04856    0.01578   3.077  0.00488 **
## FCS2        -0.02183    0.01111  -1.966  0.06008 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01996 on 26 degrees of freedom
## Multiple R-squared:  0.5732, Adjusted R-squared:  0.524
## F-statistic: 11.64 on 3 and 26 DF,  p-value: 5.061e-05
```

```
Anova(mod27)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##             Sum Sq Df F value    Pr(>F)
## gendev    0.0014934  1  3.7497 0.063758 .
## LVOL      0.0037708  1  9.4681 0.004878 **
## FCS       0.0015391  1  3.8646 0.060080 .
## Residuals 0.0103550 26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g27 <- emmeans(mod27, specs = "FCS"))
```

```
## FCS    emmean          SE df  lower.CL  upper.CL
## 1   0.5815854 0.007001605 26 0.5671934 0.5959774
## 2   0.5597533 0.006301588 26 0.5468002 0.5727064
##
## Results are averaged over the levels of: gendev
## Confidence level used: 0.95
```

```
plot(g27, xlab ="Marginal Mean Pointedness")
```
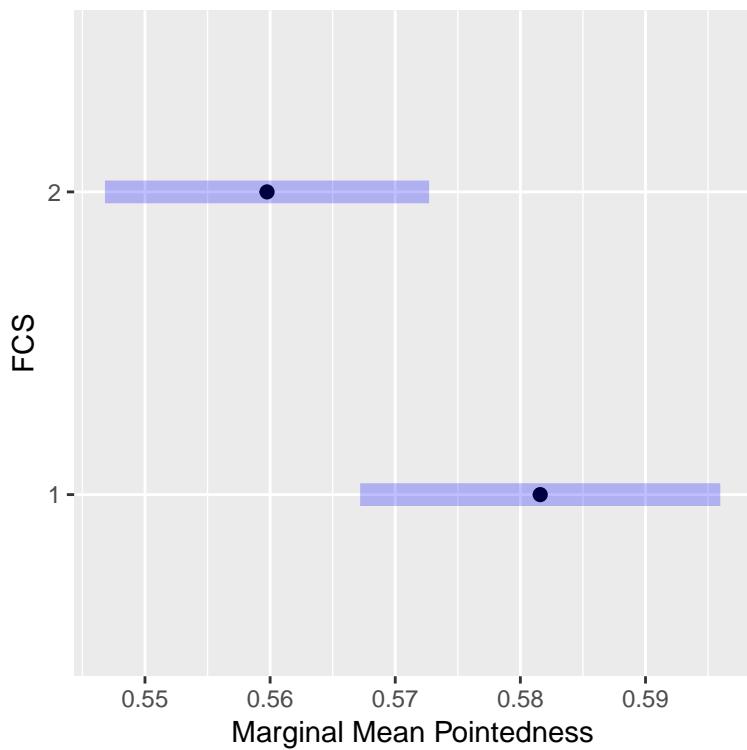
```
ggplot(dat1, aes(x = FCS, y = PT)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
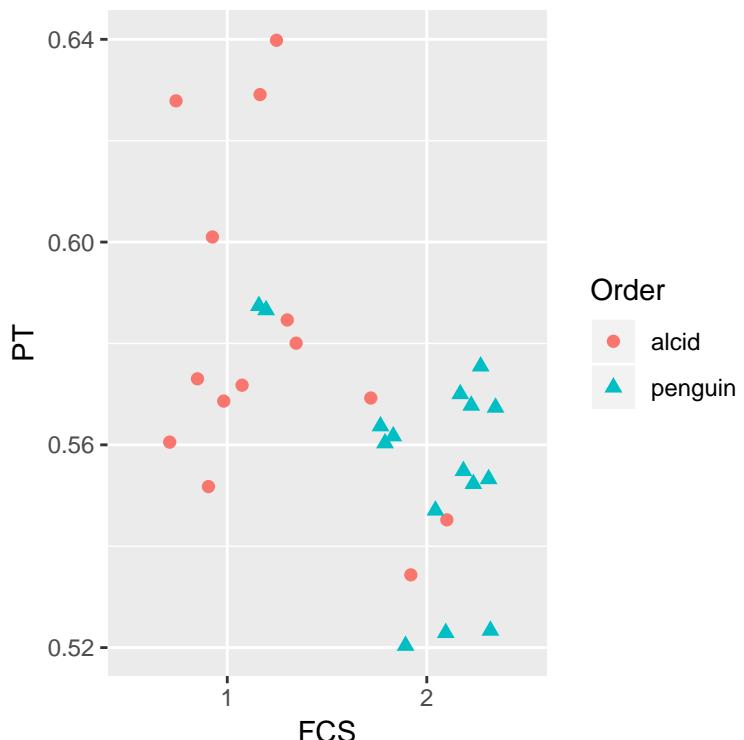


```
comp27 <- glht(mod27, linfct = mcp(FCS = "Tukey"))
summary(comp27)
```

```
##
```

```
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PT ~ gendev + LVOL + FCS, data = dat1)
##
## Linear Hypotheses:
##            Estimate Std. Error t value Pr(>|t|)
## 2 - 1 == 0 -0.02183    0.01111  -1.966   0.0601 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
dredge(mod27)
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lm(formula = PT ~ gendev + LVOL + FCS, data = dat1)
## ---
## Model selection table
##   (Intrc) FCS gendv    LVOL df logLik    AICc delta weight
## 8  0.4761   +     + 0.04856  5 77.004 -141.5  0.00  0.436
## 6  0.5349   +       0.02871  4 74.983 -140.4  1.14  0.246
## 7  0.4274         + 0.06291  4 74.925 -140.3  1.26  0.233
## 2  0.5894   +                3 72.343 -137.8  3.74  0.067
## 4  0.5901   +     +          4 72.346 -135.1  6.42  0.018
## 3  0.5572         +          3 67.174 -127.4 14.08  0.000
## 1  0.5684                    2 64.231 -124.0 17.49  0.000
## 5  0.5190           0.02576  3 65.413 -123.9 17.60  0.000
## Models ranked by AICc(x)
```

```
##PA
mod28 <-  lm(PA ~ gendev + LVOL +FCS, data = dat1)
summary(mod28)
```

```
##
## Call:
## lm(formula = PA ~ gendev + LVOL + FCS, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.42504 -0.07511 -0.00955  0.13286  0.39149
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.35412    0.41357   3.274  0.00300 **
## gendevP      0.04522    0.13871   0.326  0.74702
## LVOL         0.38576    0.17016   2.267  0.03194 *
## FCS2        -0.43714    0.11974  -3.651  0.00115 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2152 on 26 degrees of freedom
## Multiple R-squared:  0.6091, Adjusted R-squared:  0.564
## F-statistic: 13.51 on 3 and 26 DF,  p-value: 1.66e-05
```

```r
Anova(mod28)
```

```
## Anova Table (Type II tests)
##
## Response: PA
##            Sum Sq Df F value   Pr(>F)
## gendev    0.00492  1  0.1063 0.747017
## LVOL      0.23793  1  5.1393 0.031939 *
## FCS       0.61707  1 13.3285 0.001154 **
## Residuals 1.20372 26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
(g28 <- emmeans(mod28, specs = "FCS"))
```

```
##  FCS   emmean         SE df lower.CL upper.CL
##  1   2.115708 0.07548935 26 1.960537 2.270879
##  2   1.678565 0.06794196 26 1.538908 1.818222
##
## Results are averaged over the levels of: gendev
## Confidence level used: 0.95
```

```r
plot(g28, xlab ="Marginal Mean Polar Asymmetry")
```
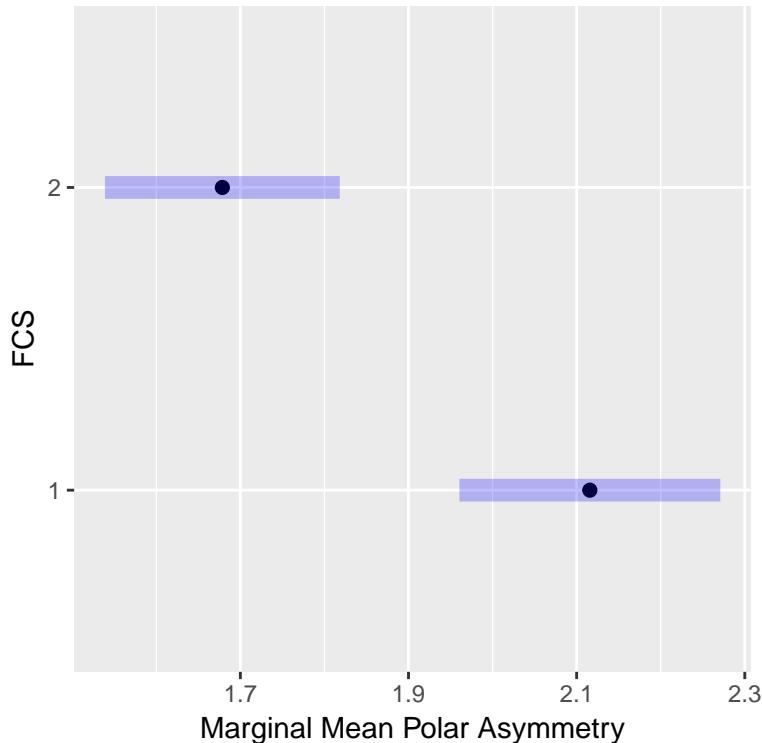


```r
ggplot(dat1, aes(x = FCS, y = PA)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
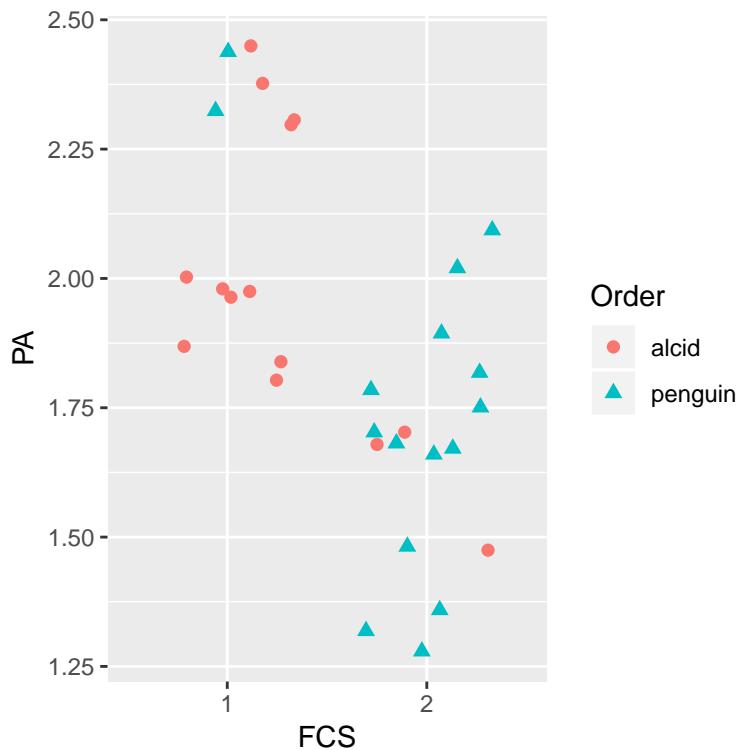
```r
comp28 <- glht(mod28, linfct = mcp(FCS = "Tukey"))
summary(comp28)
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PA ~ gendev + LVOL + FCS, data = dat1)
##
## Linear Hypotheses:
##           Estimate Std. Error t value Pr(>|t|)
## 2 - 1 == 0  -0.4371     0.1197  -3.651  0.00115 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
dredge(mod28)
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lm(formula = PA ~ gendev + LVOL + FCS, data = dat1)
## ---
## Model selection table
##    (Intrc) FCS gendv   LVOL df logLik AICc delta weight
## 6  1.4610   +        0.3497  4  5.607 -1.6  0.00  0.706
## 8  1.3540   +     +  0.3858  5  5.669  1.2  2.78  0.176
## 2  2.1250   +                3  1.905  3.1  4.73  0.066
## 4  2.2600   +     +          4  2.963  3.7  5.29  0.050
## 7  0.3792       +   0.6730  4 -0.539 10.7 12.29  0.002
```

```
## 3  1.7670          +         3 -6.680 20.3 21.90  0.000
## 5  1.2660           0.3134   3 -7.033 21.0 22.60  0.000
## 1  1.8660                    2 -8.422 21.3 22.90  0.000
## Models ranked by AICc(x)
```

```r
##EL
mod29 <-  lm(EL ~ gendev + LVOL +FCS, data = dat1)
summary(mod29)
```

```
##
## Call:
## lm(formula = EL ~ gendev + LVOL + FCS, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.13446 -0.03493 -0.00539  0.02791  0.09257
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.92958    0.11306   8.222 1.05e-08 ***
## gendevP      0.27605    0.03792   7.280 9.90e-08 ***
## LVOL         0.17426    0.04652   3.746 0.000904 ***
## FCS2         0.05051    0.03273   1.543 0.134887
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05882 on 26 degrees of freedom
## Multiple R-squared:  0.7763, Adjusted R-squared:  0.7505
## F-statistic: 30.08 on 3 and 26 DF,  p-value: 1.307e-08
```

```r
Anova(mod29)
```

```
## Anova Table (Type II tests)
##
## Response: EL
##             Sum Sq Df F value     Pr(>F)
## gendev    0.183353  1 52.9934    9.9e-08 ***
## LVOL      0.048552  1 14.0325  0.0009035 ***
## FCS       0.008239  1  2.3812  0.1348870
## Residuals 0.089958 26
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
(g29 <- emmeans(mod29, specs = "FCS"))
```

```
##  FCS  emmean          SE df lower.CL upper.CL
##  1   1.401422 0.02063682 26 1.359002 1.443841
##  2   1.451933 0.01857356 26 1.413755 1.490112
##
## Results are averaged over the levels of: gendev
## Confidence level used: 0.95
```

```r
plot(g29, xlab ="Marginal Mean Elongation")
```
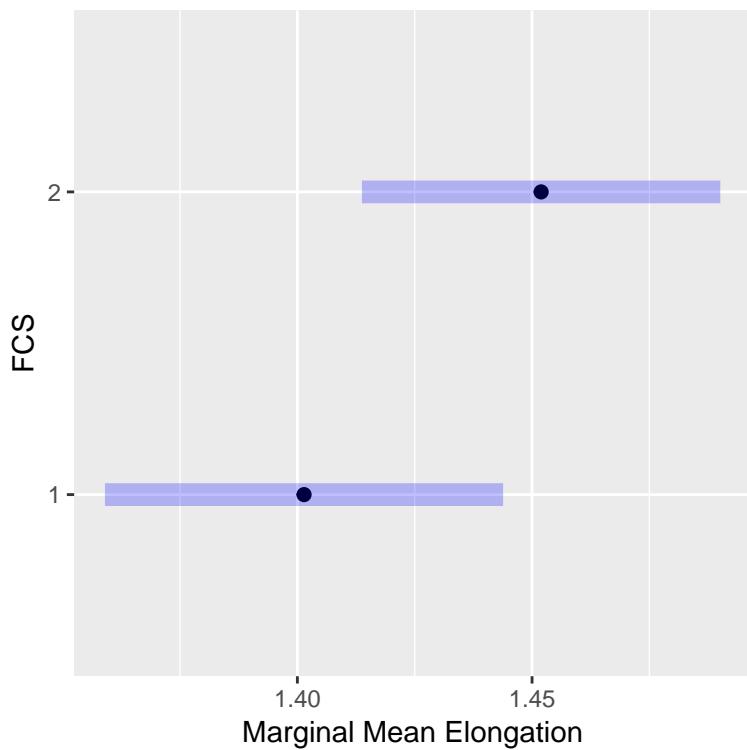
```
ggplot(dat1, aes(x = FCS, y = EL)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
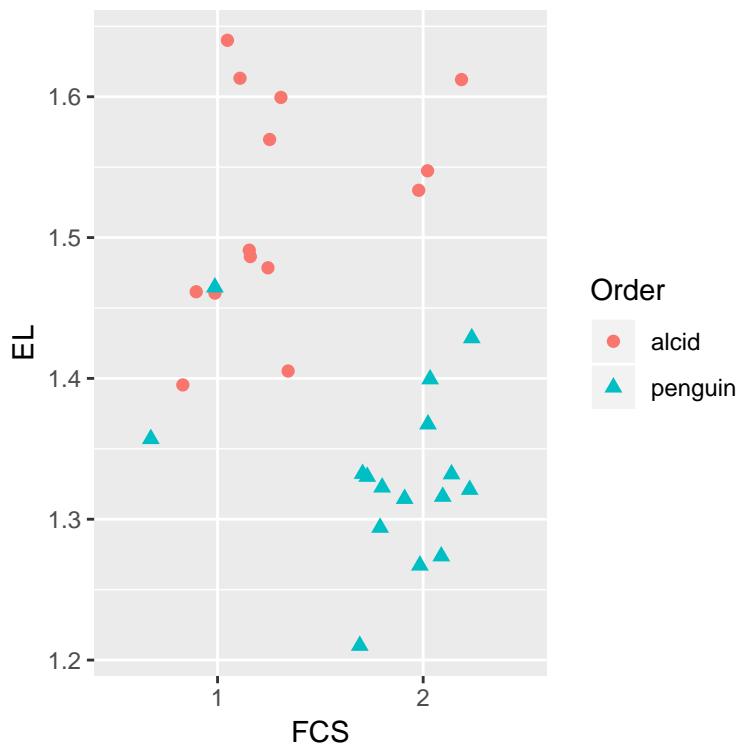


```
comp29 <- glht(mod29, linfct = mcp(FCS = "Tukey"))
summary(comp29)
```

```
##
```

```
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = EL ~ gendev + LVOL + FCS, data = dat1)
##
## Linear Hypotheses:
##           Estimate Std. Error t value Pr(>|t|)
## 2 - 1 == 0  0.05051    0.03273   1.543    0.135
## (Adjusted p values reported -- single-step method)
```

```
dredge(mod29)
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lm(formula = EL ~ gendev + LVOL + FCS, data = dat1)
## ---
## Model selection table
##    (Intrc) FCS gendv     LVOL df logLik  AICc delta weight
## 7   1.0420         +  0.14110  4 43.262 -76.9  0.00  0.526
## 8   0.9296     +   +  0.17430  5 44.576 -76.7  0.27  0.459
## 3   1.3330         +           3 38.085 -69.2  7.68  0.011
## 4   1.3390     +   +           4 38.102 -66.6 10.32  0.003
## 2   1.4940     +              3 27.593 -48.3 28.66  0.000
## 6   1.5810     +      -0.04573  4 27.907 -46.2 30.71  0.000
## 1   1.4210                     2 22.113 -39.8 37.14  0.000
## 5   1.5280          -0.05568  3 22.438 -38.0 38.97  0.000
## Models ranked by AICc(x)
```

SUMMARY: Clutch size is included in 4 of the 6 of the top models (delta AICc<2) to predict the 3 egg shape indices. One-egg clutches have higher Pointedness (P=0.06) and Polar Asymmetry (P = 0.001) than 2-egg clutches but lower Elongation (P = 0.14). We will include clutch size as a predictor in subsequent models.

8   Relation between egg shape and nest site

Here we compare egg shape indices across the 5 types of 'incubation site' (variable = Site), controlling for clutch size, egg volume and general developmental mode (variable = gendev).

```
#PT
mod30 <- lm(PT ~ gendev + LVOL +FCS + Site, data = dat1) #full model
summary(mod30)
```

```
##
## Call:
## lm(formula = PT ~ gendev + LVOL + FCS + Site, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.030129 -0.008679  0.001831  0.009232  0.024588
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.531413   0.036377  14.608 8.36e-13 ***
```

```
## gendevP     -0.010280    0.012948   -0.794   0.43573
## LVOL          0.028221    0.017293    1.632   0.11693
## FCS2         -0.025316    0.010458   -2.421   0.02420 *
## SiteCR        0.012764    0.008629    1.479   0.15328
## SiteCU       -0.014697    0.009392   -1.565   0.13188
## SiteFE       -0.015382    0.019333   -0.796   0.43475
## SiteRO        0.049982    0.013635    3.666   0.00136 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01531 on 22 degrees of freedom
## Multiple R-squared:  0.7876, Adjusted R-squared:    0.72
## F-statistic: 11.65 on 7 and 22 DF,  p-value: 4.034e-06
```

```
Anova(mod30)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##              Sum Sq Df F value    Pr(>F)
## gendev    0.0001477  1  0.6303 0.435729
## LVOL      0.0006240  1  2.6632 0.116926
## FCS       0.0013730  1  5.8595 0.024196 *
## Site      0.0052000  4  5.5480 0.003037 **
## Residuals 0.0051550 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g30 <- emmeans(mod30, specs = "Site"))
```

```
##  Site    emmean          SE df  lower.CL  upper.CL
##  BU   0.5676766 0.005803235 22 0.5556414 0.5797117
##  CR   0.5804404 0.007979930 22 0.5638911 0.5969898
##  CU   0.5529795 0.006817182 22 0.5388416 0.5671175
##  FE   0.5522949 0.016969987 22 0.5171013 0.5874885
##  RO   0.6176588 0.011918765 22 0.5929408 0.6423768
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g30, xlab ="Marginal Mean Pointedness")
```
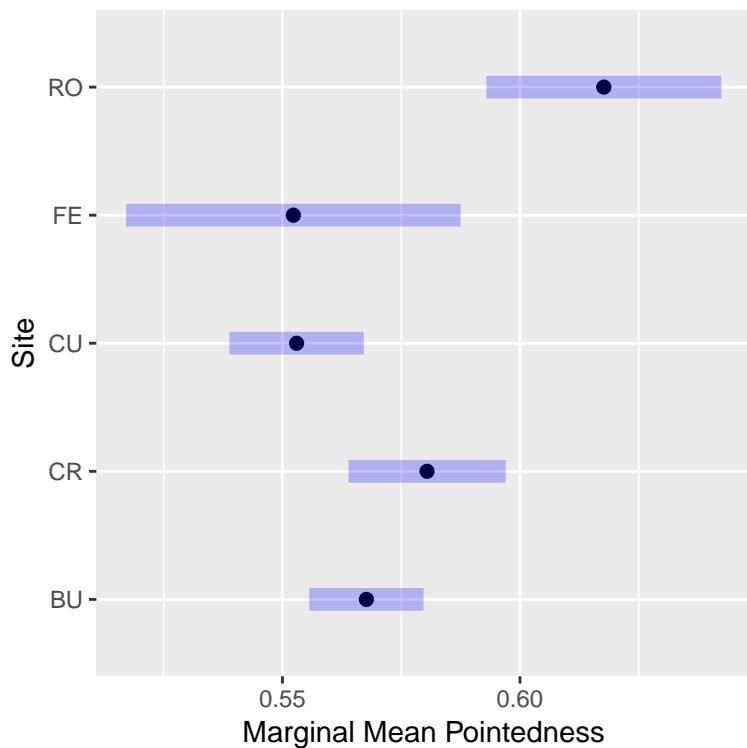
```
ggplot(dat1, aes(x = Site, y = PT)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
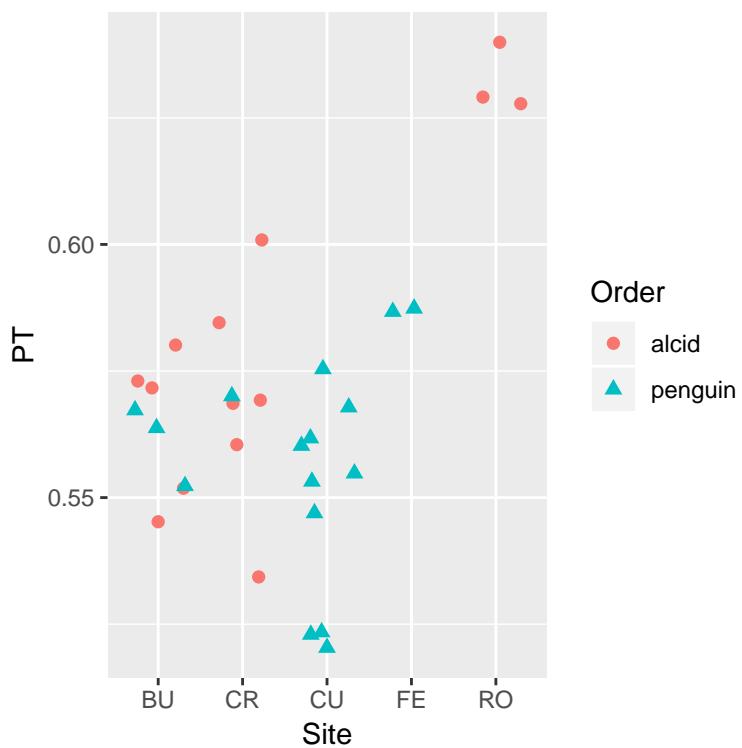


```
comp30 <- glht(mod30, linfct = mcp(Site = "Tukey"))
summary(comp30)
```

```
##
```

```
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PT ~ gendev + LVOL + FCS + Site, data = dat1)
##
## Linear Hypotheses:
##                Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0   0.0127639  0.0086293   1.479  0.55411
## CU - BU == 0  -0.0146970  0.0093916  -1.565  0.50190
## FE - BU == 0  -0.0153816  0.0193327  -0.796  0.91821
## RO - BU == 0   0.0499822  0.0136348   3.666  0.00943 **
## CU - CR == 0  -0.0274609  0.0116221  -2.363  0.14680
## FE - CR == 0  -0.0281455  0.0219737  -1.281  0.67659
## RO - CR == 0   0.0372184  0.0151589   2.455  0.12379
## FE - CU == 0  -0.0006846  0.0177687  -0.039  1.00000
## RO - CU == 0   0.0646793  0.0153408   4.216  0.00264 **
## RO - FE == 0   0.0653639  0.0186176   3.511  0.01341 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
#PA
mod31 <- lm(PA ~ gendev + LVOL +FCS + Site, data = dat1)
summary(mod31)
```

```
##
## Call:
## lm(formula = PA ~ gendev + LVOL + FCS + Site, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.32575 -0.12152  0.03054  0.07258  0.48952
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.87649    0.44776   4.191 0.000379 ***
## gendevP     -0.19361    0.15937  -1.215 0.237312
## LVOL         0.17501    0.21286   0.822 0.419779
## FCS2        -0.33890    0.12873  -2.633 0.015204 *
## SiteCR      -0.00897    0.10622  -0.084 0.933463
## SiteCU      -0.28984    0.11560  -2.507 0.020046 *
## SiteFE       0.06426    0.23796   0.270 0.789651
## SiteRO       0.31554    0.16783   1.880 0.073393 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1884 on 22 degrees of freedom
## Multiple R-squared:  0.7464, Adjusted R-squared:  0.6657
## F-statistic:  9.25 on 7 and 22 DF,  p-value: 2.51e-05
```

```r
Anova(mod31)
```

```
## Anova Table (Type II tests)
##
```

```
## Response: PA
##           Sum Sq Df F value  Pr(>F)
## gendev    0.05239  1  1.4758 0.23731
## LVOL      0.02400  1  0.6760 0.41978
## FCS       0.24604  1  6.9307 0.01520 *
## Site      0.42272  4  2.9769 0.04171 *
## Residuals 0.78100 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g31 <- emmeans(mod31, specs = "Site"))
```

```
##  Site    emmean         SE df lower.CL upper.CL
##  BU    1.945493 0.07143017 22 1.797356 2.093630
##  CR    1.936523 0.09822241 22 1.732823 2.140224
##  CU    1.655656 0.08391052 22 1.481636 1.829676
##  FE    2.009750 0.20887816 22 1.576564 2.442937
##  RO    2.261033 0.14670427 22 1.956787 2.565279
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g31, xlab ="Marginal Mean Polar Asymmetry")
```
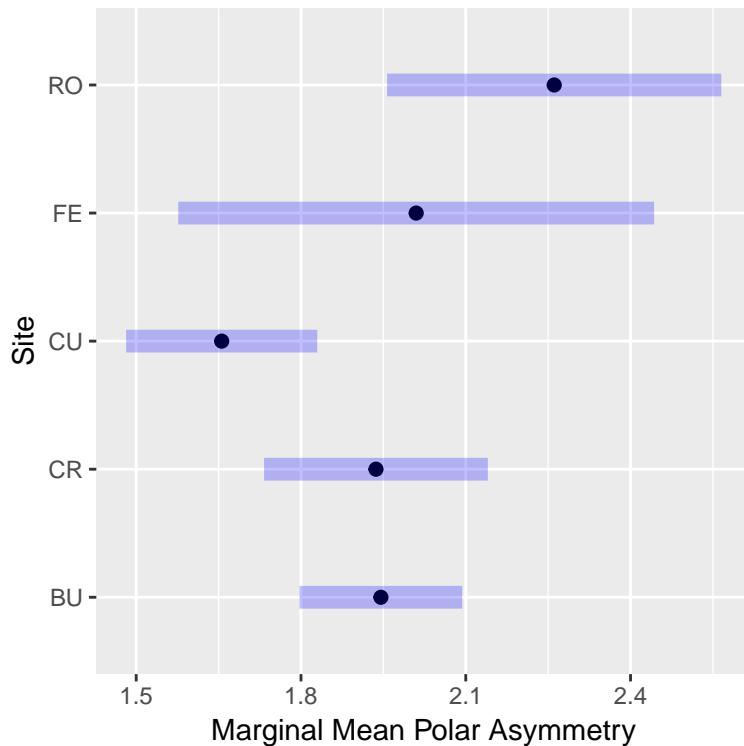


```
ggplot(dat1, aes(x = Site, y = PA)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
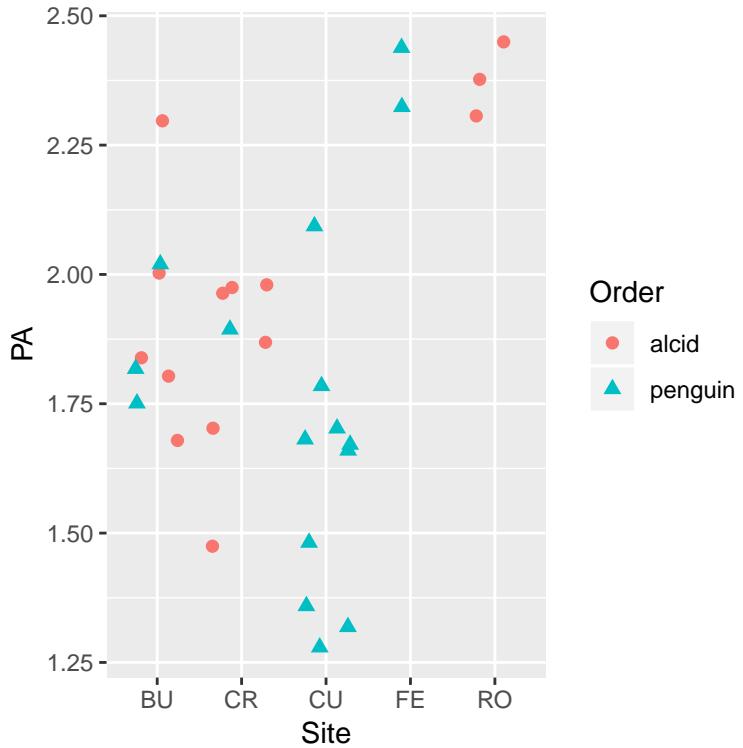
```
comp31 <- glht(mod31, linfct = mcp(Site = "Tukey"))
summary(comp31)
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PA ~ gendev + LVOL + FCS + Site, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0 -0.00897    0.10622  -0.084   1.0000
## CU - BU == 0 -0.28984    0.11560  -2.507   0.1120
## FE - BU == 0  0.06426    0.23796   0.270   0.9985
## RO - BU == 0  0.31554    0.16783   1.880   0.3285
## CU - CR == 0 -0.28087    0.14305  -1.963   0.2892
## FE - CR == 0  0.07323    0.27047   0.271   0.9985
## RO - CR == 0  0.32451    0.18659   1.739   0.4011
## FE - CU == 0  0.35409    0.21871   1.619   0.4697
## RO - CU == 0  0.60538    0.18882   3.206   0.0263 *
## RO - FE == 0  0.25128    0.22916   1.097   0.7835
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
#EL
mod32 <- lm(EL ~ gendev + LVOL +FCS  + Site, data = dat1)
summary(mod32)
```

```
## 
## Call:
## lm(formula = EL ~ gendev + LVOL + FCS + Site, data = dat1)
## 
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.108803 -0.032146  0.003422  0.024501  0.108244
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   1.04359    0.11978   8.712 1.39e-08 ***
## gendevP       0.23549    0.04264   5.523 1.50e-05 ***
## LVOL          0.10403    0.05694   1.827   0.0813 .
## FCS2          0.09375    0.03444   2.722   0.0124 *
## SiteCR        0.03688    0.02841   1.298   0.2078
## SiteCU       -0.03598    0.03092  -1.163   0.2571
## SiteFE        0.10554    0.06366   1.658   0.1115
## SiteRO        0.11310    0.04490   2.519   0.0195 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0504 on 22 degrees of freedom
## Multiple R-squared:  0.861,  Adjusted R-squared:  0.8168
## F-statistic: 19.47 on 7 and 22 DF,  p-value: 4.627e-08
```

```
Anova(mod32)
```

```
## Anova Table (Type II tests)
## 
## Response: EL
##             Sum Sq Df F value     Pr(>F)
## gendev    0.077508  1 30.5088 1.498e-05 ***
## LVOL      0.008479  1  3.3375    0.08132 .
## FCS       0.018828  1  7.4112    0.01244 *
## Site      0.034067  4  3.3523    0.02751 *
## Residuals 0.055892 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g32 <- emmeans(mod32, specs = "Site"))
```

```
##  Site  emmean         SE df lower.CL upper.CL
##  BU  1.407485 0.01910860 22 1.367856 1.447114
##  CR  1.444363 0.02627591 22 1.389870 1.498856
##  CU  1.371506 0.02244727 22 1.324953 1.418059
##  FE  1.513029 0.05587792 22 1.397145 1.628913
##  RO  1.520583 0.03924551 22 1.439193 1.601974
## 
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g32, xlab ="Marginal Mean Elongation")
```
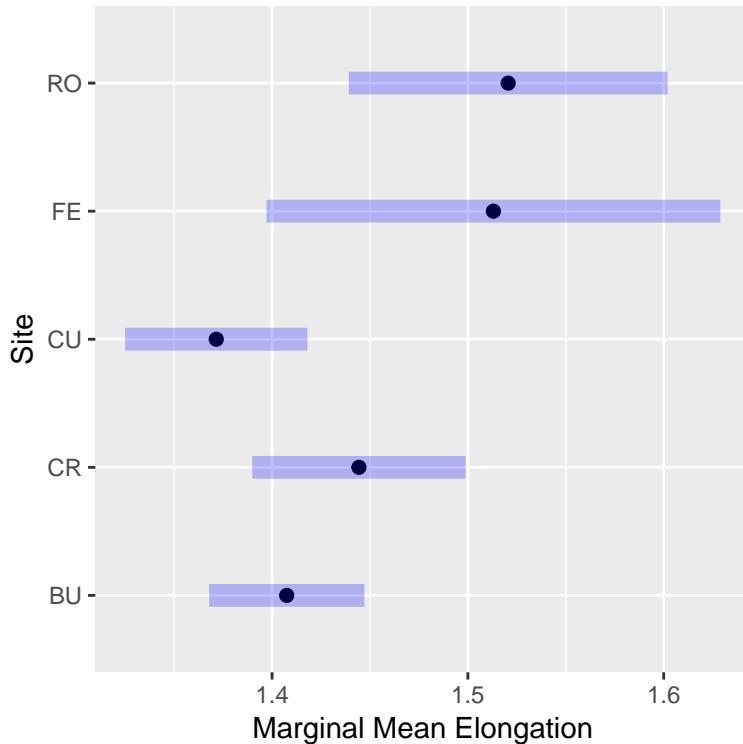
```
ggplot(dat1, aes(x = Site, y = EL)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
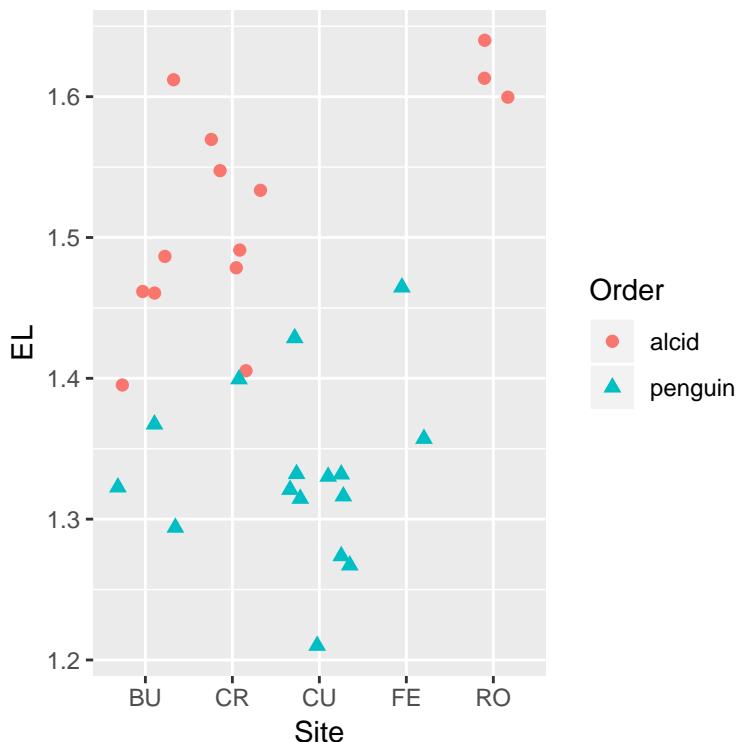


```
comp32 <- glht(mod32, linfct = mcp(Site = "Tukey"))
summary(comp32)
```

```
##
```

```
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = EL ~ gendev + LVOL + FCS + Site, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0  0.036878   0.028414   1.298   0.6662
## CU - BU == 0 -0.035979   0.030924  -1.163   0.7461
## FE - BU == 0  0.105544   0.063658   1.658   0.4473
## RO - BU == 0  0.113098   0.044896   2.519   0.1096
## CU - CR == 0 -0.072857   0.038269  -1.904   0.3169
## FE - CR == 0  0.068666   0.072354   0.949   0.8574
## RO - CR == 0  0.076221   0.049915   1.527   0.5248
## FE - CU == 0  0.141523   0.058508   2.419   0.1323
## RO - CU == 0  0.149078   0.050513   2.951   0.0457 *
## RO - FE == 0  0.007555   0.061303   0.123   0.9999
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
#using Site alone as a predictor
mod33 <- lm(EL ~  Site, data = dat1)
summary(mod33)
```

```
##
## Call:
## lm(formula = EL ~ Site, data = dat1)
##
## Residuals:
##       Min       1Q    Median       3Q      Max
## -0.131037 -0.043812  0.002775  0.036372  0.187090
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.42499    0.02604  54.716  < 2e-16 ***
## SiteCR       0.06428    0.03812   1.686 0.104217
## SiteCU      -0.11241    0.03494  -3.217 0.003563 **
## SiteFE      -0.01415    0.05824  -0.243 0.810042
## SiteRO       0.19265    0.04987   3.863 0.000704 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07366 on 25 degrees of freedom
## Multiple R-squared:  0.6627, Adjusted R-squared:  0.6087
## F-statistic: 12.28 on 4 and 25 DF,  p-value: 1.17e-05
```

```r
Anova(mod33)
```

```
## Anova Table (Type II tests)
##
## Response: EL
##           Sum Sq Df F value    Pr(>F)
## Site      0.26651  4  12.279 1.17e-05 ***
```

```
## Residuals 0.13565 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod34 <- lm(PT ~ Site, data = dat1)
summary(mod34)
```

```
##
## Call:
## lm(formula = PT ~ Site, data = dat1)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.035369 -0.008072  0.000318  0.009575  0.031178
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.563155   0.006006  93.759  < 2e-16 ***
## SiteCR       0.006606   0.008792   0.751   0.4595
## SiteCU      -0.014452   0.008058  -1.793   0.0850 .
## SiteFE       0.023876   0.013431   1.778   0.0876 .
## SiteRO       0.069125   0.011501   6.010 2.81e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.01699 on 25 degrees of freedom
## Multiple R-squared:  0.7026, Adjusted R-squared:  0.6551
## F-statistic: 14.77 on 4 and 25 DF,  p-value: 2.55e-06
```

```
Anova(mod34)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##               Sum Sq Df F value   Pr(>F)
## Site       0.0170492  4  14.768 2.55e-06 ***
## Residuals 0.0072154 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod35 <- lm(PA ~ Site, data = dat1)
summary(mod35)
```

```
##
## Call:
## lm(formula = PA ~ Site, data = dat1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.3623 -0.1155  0.0442  0.1009  0.4903
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.90122    0.07268  26.158  < 2e-16 ***
## SiteCR      -0.06431    0.10640  -0.604  0.55099
## SiteCU      -0.29810    0.09752  -3.057  0.00526 **
```

```
## SiteFE      0.47983    0.16253    2.952  0.00677 **
## SiteRO      0.47650    0.13918    3.424  0.00214 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2056 on 25 degrees of freedom
## Multiple R-squared:  0.6569, Adjusted R-squared:  0.602
## F-statistic: 11.97 on 4 and 25 DF,  p-value: 1.435e-05
```

```
Anova(mod35)
```

```
## Anova Table (Type II tests)
##
## Response: PA
##           Sum Sq Df F value    Pr(>F)
## Site      2.0231  4  11.967 1.435e-05 ***
## Residuals 1.0566 25
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

SUMMARY: Eggs laid on rock have the highest marginal mean values for each of the egg shape indices: for Pointedness (mod30) being significantly higher than eggs incubated on feet, or in cups or burrows; for Polar-asymmetry (mod31a) and Elongation (mod32a) being significantly higher than eggs incubated in cups.

9   Principal Components Analysis (egg size and shape)

These analyses reduce the egg size and shape variables into two orthogonal components that can be used as 'egg size' and 'egg shape' response variables in linear models. Here we are using *principal* in the **psych** package, varimax rotation is the default. This analysis starts by assessing (mod69) the number of factors using scree plot and cumulative proportion of variance explained, using princomp with unrotated factors.

```
#using matrix for input
mod69 <- princomp(dat1[,c(15:17, 19:21)], cor=TRUE)
mod69$loadings
```

```
##
## Loadings:
##       Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6
## PA     0.367  0.414  0.625  0.550
## PT     0.367  0.471  0.163 -0.785
## EL     0.135  0.591 -0.711  0.268 -0.151  0.181
## LVOL   0.480 -0.316 -0.109         0.502  0.637
## LLEN   0.518 -0.168 -0.254         0.281 -0.742
## LBR    0.462 -0.360                -0.804  0.104
##
##                 Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6
## SS loadings      1.000  1.000  1.000  1.000  1.000  1.000
## Proportion Var   0.167  0.167  0.167  0.167  0.167  0.167
## Cumulative Var   0.167  0.333  0.500  0.667  0.833  1.000
```

```
screeplot(mod69)
```

mod69
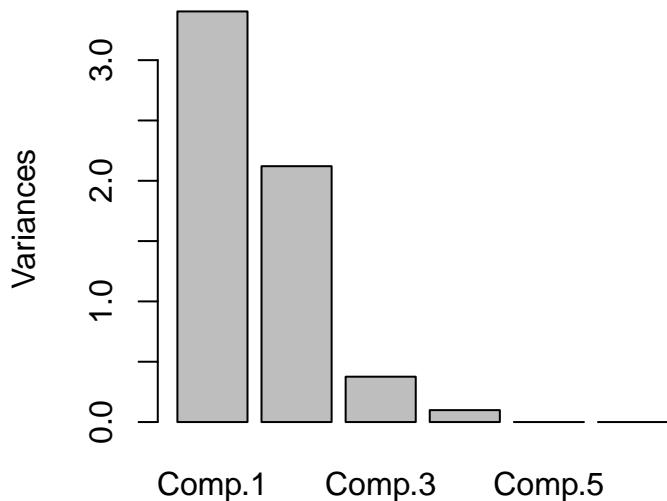

```
summary(mod69)
```

```
## Importance of components:
##                          Comp.1    Comp.2    Comp.3     Comp.4
## Standard deviation     1.8449509 1.4563752 0.6132888 0.31440830
## Proportion of Variance 0.5673073 0.3535048 0.0626872 0.01647543
## Cumulative Proportion  0.5673073 0.9208121 0.9834993 0.99997476
##                            Comp.5       Comp.6
## Standard deviation     9.833340e-03 7.398562e-03
## Proportion of Variance 1.611576e-05 9.123119e-06
## Cumulative Proportion  9.999909e-01 1.000000e+00
```

```
biplot(mod69)
```
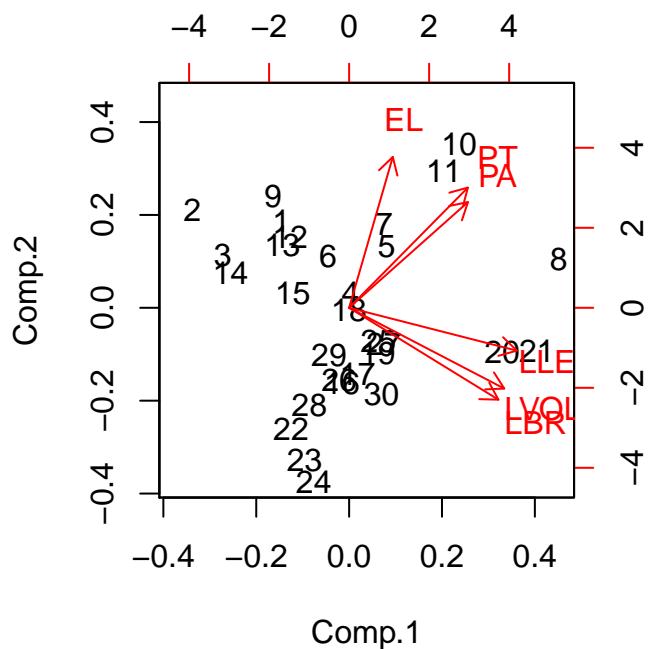
```
(eig69 <- mod69$sdev^2) #calculate eigenvalues
```

```
##        Comp.1        Comp.2        Comp.3        Comp.4        Comp.5
## 3.403844e+00 2.121029e+00 3.761232e-01 9.885258e-02 9.669458e-05
##        Comp.6
## 5.473871e-05
```

```
mod70 <- principal(dat1[,c(15:17, 19:21)], nfactors = 2)
biplot(mod70)
```


Biplot from fa
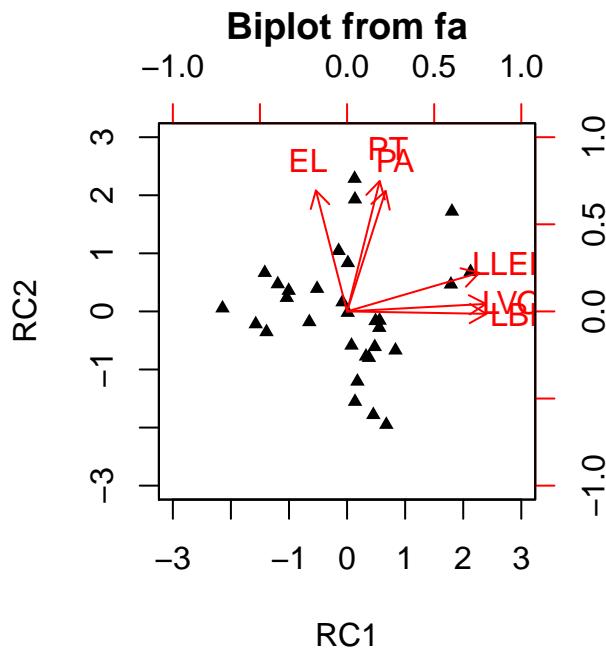
```
mod70$values
```

```
## [1] 3.403844e+00 2.121029e+00 3.761232e-01 9.885258e-02 9.669458e-05
## [6] 5.473871e-05
```

```
mod70$loadings
```

```
##
## Loadings:
##        RC1    RC2
## PA    0.276  0.864
## PT    0.234  0.935
## EL   -0.224  0.868
## LVOL  0.996
## LLEN  0.948  0.277
## LBR   1.000
##
##                  RC1    RC2
## SS loadings     3.071  2.454
## Proportion Var  0.512  0.409
## Cumulative Var  0.512  0.921
```

```
dat1$RC1 <- mod70$scores[,1] #rotated PC2 scores, mainly size
dat1$RC2 <- mod70$scores[,2] #rotated PC2 scores, mainly shape
with(dat1, corr.test(RC1, RC2))
```

```
## Call:corr.test(x = RC1, y = RC2)
## Correlation matrix
## [1] 0
## Sample Size
## [1] 30
## Probability values  adjusted for multiple tests.
## [1] 1
##
##  To see confidence intervals of the correlations, print with the short=FALSE option
```

```r
with(dat1, plot(RC1, RC2))
```
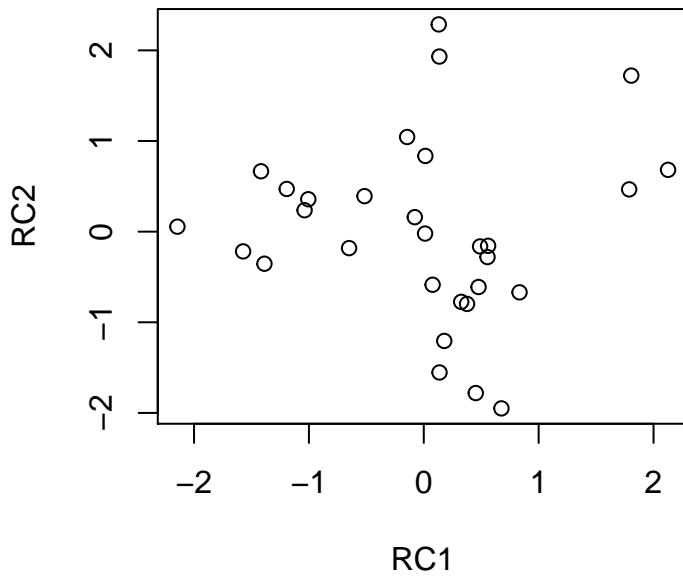

10   Models to predict general egg shape index (RC2)

```r
mod71 <- lm(RC2 ~ gendev +FCS + +LVOL +Site, data = dat1) #full model to predict shape
summary(mod71)
```

```
##
## Call:
## lm(formula = RC2 ~ gendev + FCS + +LVOL + Site, data = dat1)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.04255 -0.27617  0.06419  0.31529  0.77928
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.1937     1.1716  -1.019  0.31933
## gendevP       0.4720     0.4170   1.132  0.26987
## FCS2         -0.3689     0.3368  -1.095  0.28531
## LVOL          0.6115     0.5569   1.098  0.28413
## SiteCR        0.2838     0.2779   1.021  0.31828
## SiteCU       -0.6240     0.3025  -2.063  0.05110 .
## SiteFE        0.2294     0.6226   0.368  0.71612
```

```
## SiteRO        1.3762      0.4391    3.134   0.00482 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.493 on 22 degrees of freedom
## Multiple R-squared:  0.8156, Adjusted R-squared:  0.757
## F-statistic:  13.9 on 7 and 22 DF,  p-value: 9.176e-07
```

```
Anova(mod71)
```

```
## Anova Table (Type II tests)
##
## Response: RC2
##           Sum Sq Df F value    Pr(>F)
## gendev    0.3114  1  1.2812 0.269866
## FCS       0.2915  1  1.1993 0.285314
## LVOL      0.2929  1  1.2053 0.284133
## Site      4.2602  4  4.3822 0.009329 **
## Residuals 5.3469 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g71 <- emmeans(mod71, specs = "Site"))
```

```
##  Site      emmean        SE df    lower.CL   upper.CL
##  BU     0.02919415 0.1868982 22 -0.3584089  0.4167972
##  CR     0.31298450 0.2570005 22 -0.2200018  0.8459709
##  CU    -0.59481368 0.2195532 22 -1.0501391 -0.1394883
##  FE     0.25855247 0.5465330 22 -0.8748875  1.3919924
##  RO     1.40543644 0.3838540 22  0.6093719  2.2015009
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g71, xlab ="Marginal Mean RC2 egg shape")
```
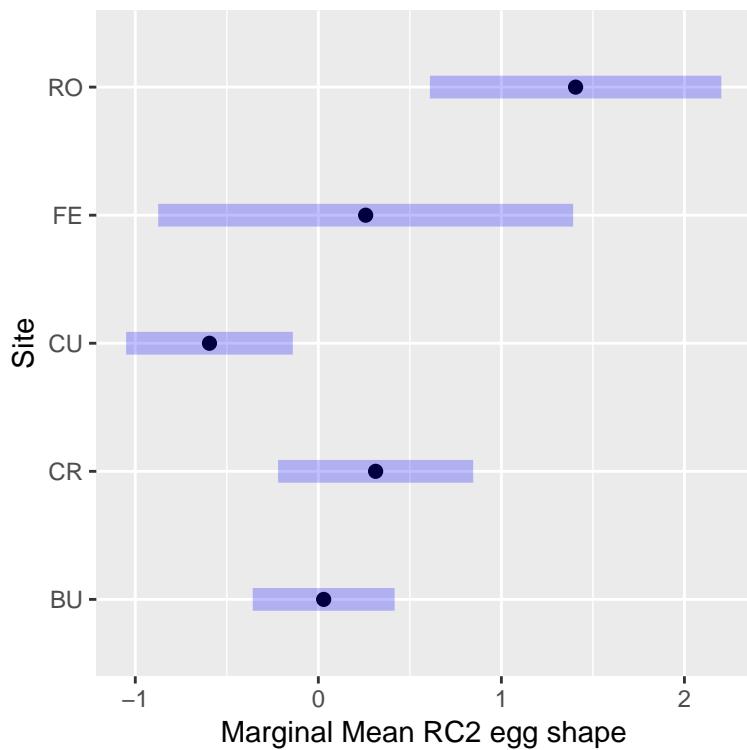
```
ggplot(dat1, aes(x = Site, y = RC2)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
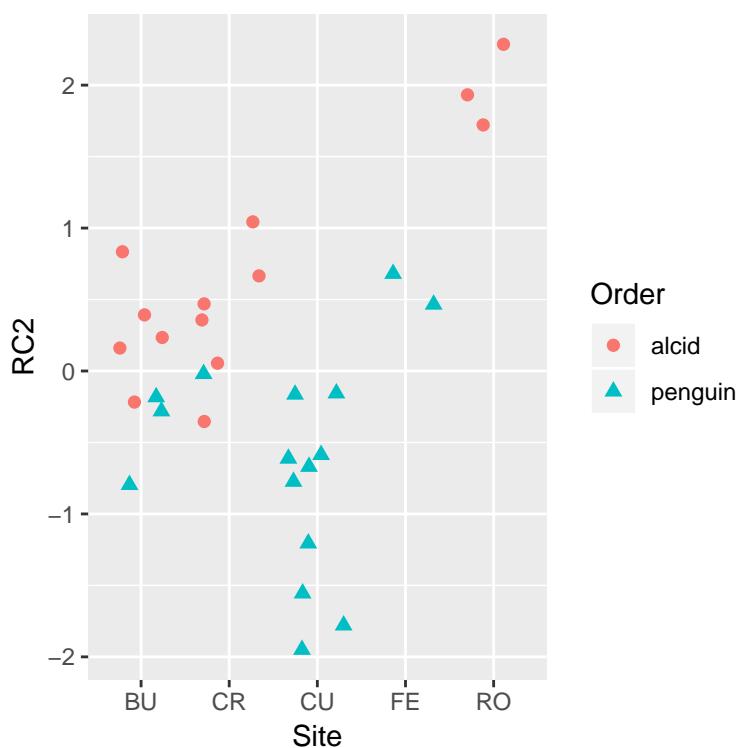


```
comp71 <- glht(mod71, linfct = mcp(Site = "Tukey"))
summary(comp71)
```

```
##
```

```
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = RC2 ~ gendev + FCS + +LVOL + Site, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0   0.28379    0.27791   1.021  0.82295
## CU - BU == 0  -0.62401    0.30247  -2.063  0.24683
## FE - BU == 0   0.22936    0.62263   0.368  0.99494
## RO - BU == 0   1.37624    0.43912   3.134  0.03105 *
## CU - CR == 0  -0.90780    0.37430  -2.425  0.13074
## FE - CR == 0  -0.05443    0.70768  -0.077  0.99999
## RO - CR == 0   1.09245    0.48821   2.238  0.18370
## FE - CU == 0   0.85337    0.57226   1.491  0.54675
## RO - CU == 0   2.00025    0.49406   4.049  0.00394 **
## RO - FE == 0   1.14688    0.59960   1.913  0.31261
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
(d71 <- dredge(mod71)) #model comparison using IT approach
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lm(formula = RC2 ~ gendev + FCS + +LVOL + Site, data = dat1)
## ---
## Model selection table
##        (Intrc) FCS gendv   LVOL Site df   logLik AICc delta weight
## 10   2.960e-01   +                 +  7 -17.915 54.9  0.00  0.345
## 11  -3.599e-01       +             +  7 -18.294 55.7  0.76  0.236
## 9    1.808e-02                     +  6 -20.624 56.9  1.98  0.128
## 15  -1.585e+00       + 0.6277      +  8 -17.494 57.8  2.92  0.080
## 12   8.921e-03   +   +             +  8 -17.498 57.9  2.93  0.080
## 14  -3.975e-01   +     0.3989      +  8 -17.547 58.0  3.03  0.076
## 13  -1.641e-01         0.1011      +  7 -20.603 60.3  5.38  0.023
## 16  -1.194e+00   +   + 0.6115      +  9 -16.698 60.4  5.47  0.022
## 8   -2.862e+00   +   + 1.3420         5 -25.488 63.5  8.55  0.005
## 7   -4.148e+00       + 1.7210         4 -27.075 63.7  8.83  0.004
## 4    2.873e-01   +   +                4 -29.420 68.4 13.52  0.000
## 2    8.071e-01   +                    3 -31.197 69.3 14.40  0.000
## 6    2.637e-01   +     0.2861         4 -30.954 71.5 16.59  0.000
## 3   -5.990e-01       +                3 -33.781 74.5 19.56  0.000
## 1   -1.216e-16                        2 -42.060 88.6 33.64  0.000
## 5   -3.345e-01         0.1746         3 -42.016 91.0 36.03  0.000
## Models ranked by AICc(x)
```

```
mod72 <- lm(RC2 ~ FCS + Site, data = dat1) #best-fitting model from IT approach
summary(mod72)
```

```
##
## Call:
## lm(formula = RC2 ~ FCS + Site, data = dat1)
##
```

```
## Residuals:
##      Min      1Q  Median      3Q     Max
## -1.00496 -0.26001  0.02874  0.32739  0.78885
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   0.2960     0.2156   1.373   0.1824
## FCS2         -0.5559     0.2551  -2.179   0.0393 *
## SiteCR        0.2591     0.2551   1.016   0.3198
## SiteCU       -0.6852     0.2658  -2.578   0.0165 *
## SiteFE        0.2780     0.4090   0.680   0.5032
## SiteRO        1.6838     0.3564   4.725 8.36e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4915 on 24 degrees of freedom
## Multiple R-squared:    0.8,  Adjusted R-squared:  0.7584
## F-statistic:  19.2 on 5 and 24 DF,  p-value: 1.091e-07
```

```
Anova(mod72)
```

```
## Anova Table (Type II tests)
##
## Response: RC2
##           Sum Sq Df F value     Pr(>F)
## FCS       1.1477  1  4.7499 0.0393432 *
## Site      8.2584  4  8.5448 0.0001955 ***
## Residuals 5.7989 24
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
comp72 <- glht(mod72, linfct = mcp(Site = "Tukey"))
summary(comp72)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = RC2 ~ FCS + Site, data = dat1)
##
## Linear Hypotheses:
##              Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0  0.25911    0.25505   1.016 0.837444
## CU - BU == 0 -0.68515    0.26576  -2.578 0.100807
## FE - BU == 0  0.27796    0.40899   0.680 0.956290
## RO - BU == 0  1.68376    0.35638   4.725 0.000659 ***
## CU - CR == 0 -0.94426    0.28270  -3.340 0.019511 *
## FE - CR == 0  0.01886    0.40899   0.046 0.999999
## RO - CR == 0  1.42465    0.35638   3.998 0.004091 **
## FE - CU == 0  0.96312    0.45828   2.102 0.240932
## RO - CU == 0  2.36892    0.41201   5.750  < 1e-04 ***
## RO - FE == 0  1.40580    0.44872   3.133 0.031207 *
## ---
```

```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
(g72 <- emmeans(mod72, specs = "Site"))
```

```
##  Site       emmean        SE df    lower.CL    upper.CL
##  BU     0.01807602 0.1737888 24 -0.3406064   0.3767584
##  CR     0.27718546 0.1866791 24 -0.1081012   0.6624722
##  CU    -0.66707662 0.2010595 24 -1.0820431  -0.2521101
##  FE     0.29604084 0.3702338 24 -0.4680841   1.0601658
##  RO     1.70183923 0.3111318 24  1.0596947   2.3439837
##
## Results are averaged over the levels of: FCS
## Confidence level used: 0.95
```

```
plot(g72, xlab ="Marginal Mean RC2 egg shape")
```
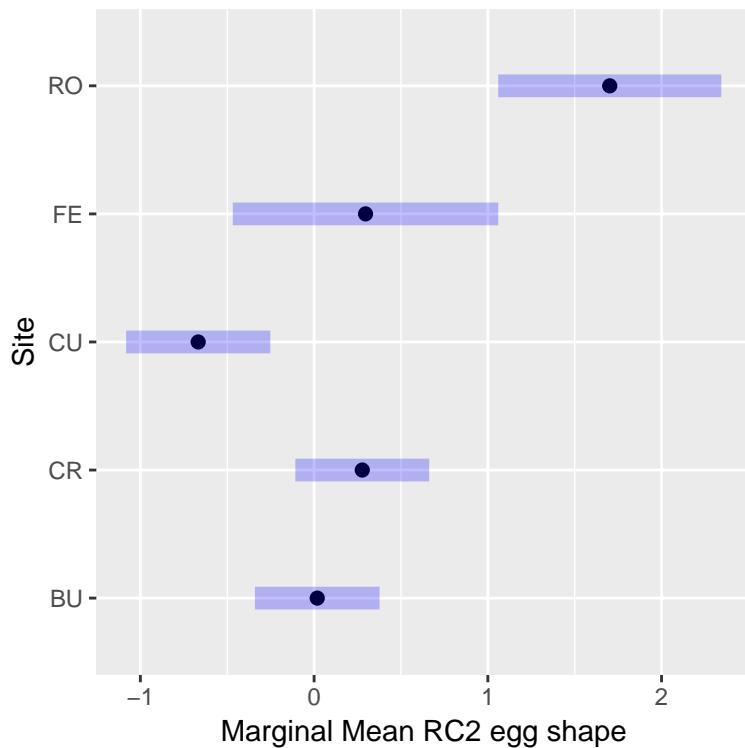


```
ggplot(dat1, aes(x = Site, y = RC2)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```
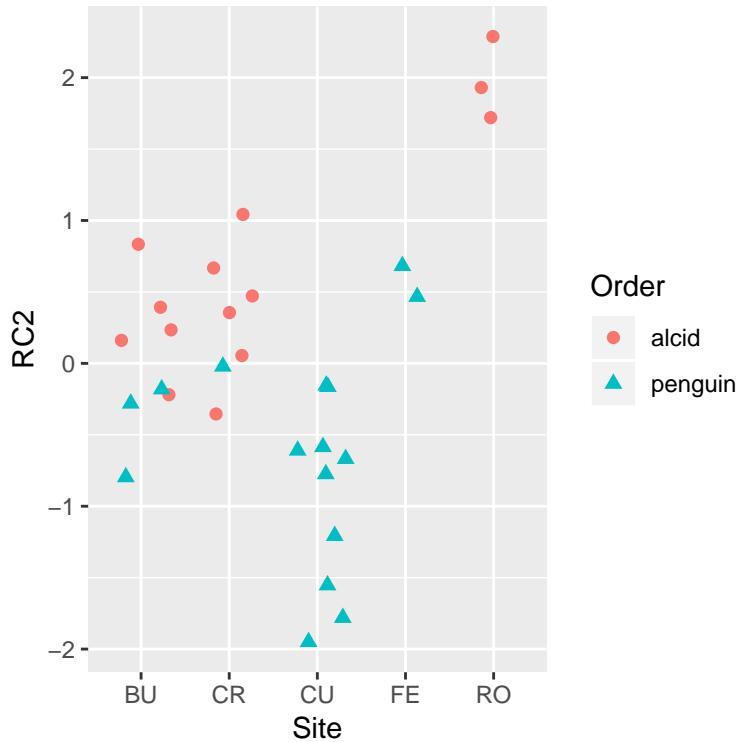
SUMMARY: The first analysis (mod69) shows that it is reasonable to extract just two factors based on all 3 of the usual criteria (scree plot elbow, eigenvectors>1, and cumulative proportion of variance explained > 0.80). In mod70, we extract only 2 factors and use the varimax rotation to include as much of the variation in egg variables on one or the other axes. It is possible that a rotation like this will result in correlated components but the plot of RC1 vs RC2 and the correlation analysis shows that this is not the case (r~0, P~1, n= 30).

Rotated component 1 (RC1) accounts for 51% of the variation in the data and RC2 for an additional 41%. RC1 loads positively on the 3 size variables (with all loadings >0.94) and RC2 loads positively on the three shape variables (with all loadings >0.86). Thus, RC1 nicely describes egg size with higher values meaning bigger eggs independent of shape, and RC2 nicely describing egg shape with bigger values meaning more pointed, more asymmetric and more elongated eggs independent of egg size. Thus higher values of RC2 describe eggs that are more pyriform in shape, irrespective of their size.

We then evaluated a full model (mod71) with RC2 as the response and the same predictors as above for the separate egg shape indices—clutch size, egg volume, general developmental mode (gendev) and incubation site. In this full model only incubation site was a significant predictor of shape (P = 0.0007), with eggs incubated on rock having significantly higher RC2 values (i.e. more pyriform) than eggs incubated in burrows, crevices, or cups. The full model (mod71) explains 81% of the variation in egg shape (RC2).

Using the IT approach to evaluate all possible models showed that the best-fitting model includes only clutch size and incubation site. There are only 3 top models (AICc<2) and these include only clutch size, breeding site and general developmental mode as predictors. The best-fitting model (mod72) explains 80% of the variation in egg shape (RC2) with eggs on rock being significantly more pyriform than those laid in crevices, cups or burrows or on feet, and eggs laid in cups are significantly less pyriform (more elliptical) than those laid in crevices and on rocks.

75

11 Controlling for phylogeny

To control for phylogeny in the key analyses described above , we constructed a phylogeny of the species studied using Figure 2 in Smith and Clarke (2014) for the Alcidae and Figure 2 in Ksepka et al (2006) for the penguins. Since there is no time scale for the penguin phylogeny we set all branch lengths at 1. In these models we predict to predict egg shape RC2, and the 3 egg shape indices, in separate models controlling for log10-transformed egg volume, general developmental mode, clutch size, and incubation site. We do not control for egg volume in the model to predict RC2 because volume was used in the PCA to generate RC2.

11.1 Get and plot the tree

```
Atree <- read.tree("aukpenguinTREE.phy")
Adata <- dat1
plot.phylo(Atree)
```

Eudyptes schlegeli

Eudyptes chrysocome

Eudyptes moseleyi

Eudyptes sclateri

Eudyptes pachyrhynchus

Megadyptes antipodes

Pygoscelis papua

Pygoscelis adeliae

Pygoscelis antarcticus

Aptenodytes forsteri

Aptenodytes patagonicus

Spheniscus humboldti

Spheniscus mendiculus

Spheniscus magellanicus

Spheniscus demersus

Eudyptula minor

Synthliboramphus wumizusume

Synthliboramphus antiquus

Cepphus grylle

Uria lomvia

Uria aalge

Alle alle

Pinguinus impennis

Alca torda

Fratercula arctica

Fratercula cirrhata

Cerorhinca monocerata

Ptychoramphus aleuticus

*Aethia pusilla*

Aethia cristatella

11.2 Analyses controlling for phylogeny

```r
#using caper for the analysis
alcidpenguin <- comparative.data(Atree, Adata, 'Species')

mod93 <- pgls(RC2 ~ LVOL + gendev +FCS +Site, data = alcidpenguin, lambda = "ML")
summary(mod93)
```

```
##
## Call:
## pgls(formula = RC2 ~ LVOL + gendev + FCS + Site, data = alcidpenguin,
##     lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.52789 -0.21468 -0.05403  0.12764  0.57017
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.902
##    lower bound : 0.000, p = 1
##    upper bound : 1.000, p = 0.64357
##    95.0% CI   : (NA, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept) -1.09078    1.32935 -0.8205  0.42071
## LVOL         0.54411    0.58567  0.9290  0.36296
## gendevP      0.47694    0.77547  0.6150  0.54484
## FCS2        -0.37799    0.41124 -0.9191  0.36799
## SiteCR       0.17980    0.26471  0.6793  0.50406
## SiteCU      -0.46082    0.37952 -1.2142  0.23754
## SiteFE       0.58650    0.76902  0.7627  0.45377
## SiteRO       0.97421    0.51481  1.8924  0.07167 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.2995 on 22 degrees of freedom
## Multiple R-squared: 0.5778,  Adjusted R-squared: 0.4435
## F-statistic: 4.302 on 7 and 22 DF,  p-value: 0.003909
```

```r
plot(mod93)
```

density.default(x = res)

Normal Q–Q Plot

N = 30   Bandwidth = 0.4516

```r
anova(mod93)
```

```
## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.90, delta = 1.00, kappa = 1.00
##
## Response: RC2
##            Df  Sum Sq Mean Sq F value   Pr(>F)
## LVOL        1 1.28478 1.28478 14.3253 0.001018 **
## gendev      1 0.32654 0.32654  3.6410 0.069510 .
## FCS         1 0.45097 0.45097  5.0284 0.035341 *
## Site        4 0.63833 0.15958  1.7794 0.168987
## Residuals  22 1.97308 0.08969
```

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

mod93b <- pgls(RC2 ~ FCS +Site, data = alcidpenguin, lambda = "ML")
summary(mod93b)

##
## Call:
## pgls(formula = RC2 ~ FCS + Site, data = alcidpenguin, lambda = "ML")
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.47741 -0.31771 -0.09982  0.07843  0.58533
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.940
##    lower bound : 0.000, p = 0.40923
##    upper bound : 1.000, p = 0.75548
##    95.0% CI    : (NA, NA)
## delta  [Fix]  : 1.000
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.22191    0.42151  0.5265 0.603399
## FCS2        -0.45898    0.39214 -1.1705 0.253302
## SiteCR       0.13736    0.24916  0.5513 0.586541
## SiteCU      -0.40574    0.34780 -1.1666 0.254830
## SiteFE       0.82561    0.63609  1.2979 0.206644
## SiteRO       1.22458    0.41686  2.9376 0.007193 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.3047 on 24 degrees of freedom
## Multiple R-squared: 0.5474,  Adjusted R-squared: 0.4531
## F-statistic: 5.806 on 5 and 24 DF,  p-value: 0.001192

plot(mod93b)
```

density.default(x = res)

Normal Q–Q Plot

N = 30   Bandwidth = 0.4558

Theoretical Quantiles

Fitted value

Observed value
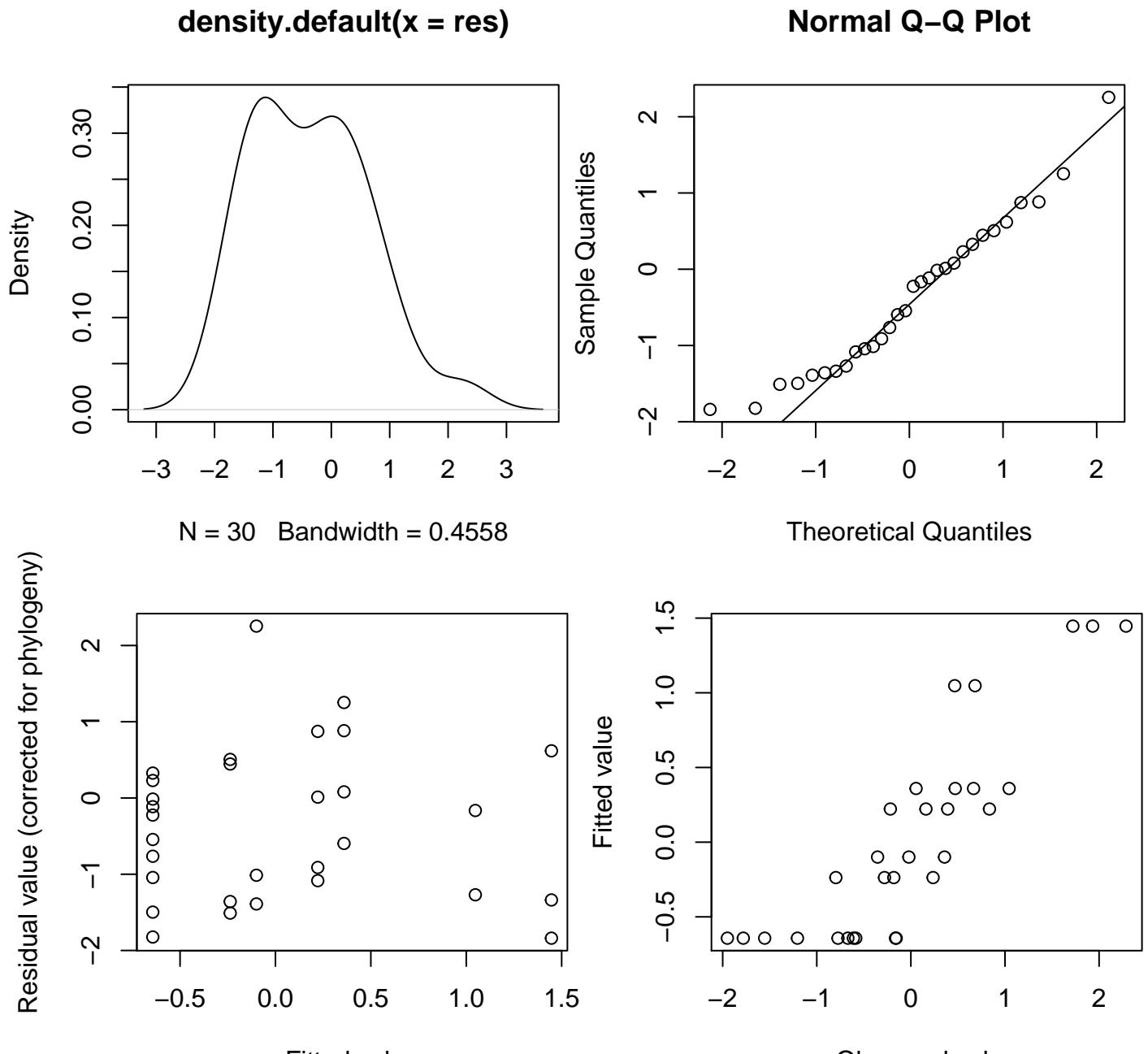
```r
anova(mod93b)
```

```
## Analysis of Variance Table
## Sequential SS for pgls: lambda = 0.94, delta = 1.00, kappa = 1.00
##
## Response: RC2
##           Df Sum Sq Mean Sq F value  Pr(>F)
## FCS        1 1.4071 1.40715 15.1565 0.00069 ***
## Site       4 1.2878 0.32196  3.4678 0.02264 *
## Residuals 24 2.2282 0.09284
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
mod94 <- pgls(EL ~ gendev + LVOL +FCS  + Site, data = alcidpenguin, lambda = "ML")
summary(mod94)
```

```
##
## Call:
## pgls(formula = EL ~ gendev + LVOL + FCS + Site, data = alcidpenguin,
##     lambda = "ML")
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.029072 -0.015502 -0.001596  0.007117  0.045724
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.000
##    lower bound : 0.000, p = 1
##    upper bound : 1.000, p = 0.00030717
##    95.0% CI   : (NA, 0.350)
## delta  [Fix]  : 1.000
##
## Coefficients:
##             Estimate Std. Error t value  Pr(>|t|)
## (Intercept)  1.037793   0.115814  8.9609 8.544e-09 ***
## gendevP      0.236925   0.040371  5.8688 6.624e-06 ***
## LVOL         0.107082   0.056062  1.9101   0.06925 .
## FCS2         0.098236   0.030547  3.2159   0.00398 **
## SiteCR       0.029337   0.027262  1.0761   0.29353
## SiteCU      -0.040094   0.032318 -1.2406   0.22782
## SiteFE       0.103651   0.063637  1.6288   0.11759
## SiteRO       0.108559   0.046526  2.3333   0.02917 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02152 on 22 degrees of freedom
## Multiple R-squared: 0.857,   Adjusted R-squared: 0.8115
## F-statistic: 18.84 on 7 and 22 DF,  p-value: 6.25e-08
```

```
mod95 <- pgls(PT ~ gendev + LVOL +FCS  + Site, data = alcidpenguin, lambda = "ML")
summary(mod94)
```

```
##
## Call:
## pgls(formula = EL ~ gendev + LVOL + FCS + Site, data = alcidpenguin,
##     lambda = "ML")
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.029072 -0.015502 -0.001596  0.007117  0.045724
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.000
```

```
##     lower bound : 0.000, p = 1
##     upper bound : 1.000, p = 0.00030717
##     95.0% CI    : (NA, 0.350)
## delta  [Fix]  : 1.000
##
## Coefficients:
##              Estimate Std. Error t value  Pr(>|t|)
## (Intercept)  1.037793   0.115814  8.9609 8.544e-09 ***
## gendevP      0.236925   0.040371  5.8688 6.624e-06 ***
## LVOL         0.107082   0.056062  1.9101   0.06925 .
## FCS2         0.098236   0.030547  3.2159   0.00398 **
## SiteCR       0.029337   0.027262  1.0761   0.29353
## SiteCU      -0.040094   0.032318 -1.2406   0.22782
## SiteFE       0.103651   0.063637  1.6288   0.11759
## SiteRO       0.108559   0.046526  2.3333   0.02917 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02152 on 22 degrees of freedom
## Multiple R-squared: 0.857,   Adjusted R-squared: 0.8115
## F-statistic: 18.84 on 7 and 22 DF,  p-value: 6.25e-08
```

```r
mod96 <- pgls(PA ~ gendev + LVOL +FCS  + Site, data = alcidpenguin, lambda = "ML")
summary(mod94)
```

```
##
## Call:
## pgls(formula = EL ~ gendev + LVOL + FCS + Site, data = alcidpenguin,
##     lambda = "ML")
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.029072 -0.015502 -0.001596  0.007117  0.045724
##
## Branch length transformations:
##
## kappa  [Fix]  : 1.000
## lambda [ ML]  : 0.000
##     lower bound : 0.000, p = 1
##     upper bound : 1.000, p = 0.00030717
##     95.0% CI    : (NA, 0.350)
## delta  [Fix]  : 1.000
##
## Coefficients:
##              Estimate Std. Error t value  Pr(>|t|)
## (Intercept)  1.037793   0.115814  8.9609 8.544e-09 ***
## gendevP      0.236925   0.040371  5.8688 6.624e-06 ***
## LVOL         0.107082   0.056062  1.9101   0.06925 .
## FCS2         0.098236   0.030547  3.2159   0.00398 **
## SiteCR       0.029337   0.027262  1.0761   0.29353
## SiteCU      -0.040094   0.032318 -1.2406   0.22782
## SiteFE       0.103651   0.063637  1.6288   0.11759
## SiteRO       0.108559   0.046526  2.3333   0.02917 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
##
## Residual standard error: 0.02152 on 22 degrees of freedom
## Multiple R-squared: 0.857,    Adjusted R-squared: 0.8115
## F-statistic: 18.84 on 7 and 22 DF,  p-value: 6.25e-08
```

SUMMARY: While there is a strong phylogenetic signal in the model to predict RC2 (mod93), it is not significantly different from either 0 or 1 , presumably due to low power resulting from the small sample of species. Controlling for phylogeny, that model explains 55% of the variation in RC2, with eggs incubated on rock significantly more pyriform than those incubated on the other sites, and the same descending order of shape with RO>FE>CR>BU>CU. Models to predict each of the egg shape parameters all have low phylogenetic signal with lamdba not significantly different from 0 but significantly <1.

12   Re-analysis without small sample species

Three of our 30 species had samples of <5 eggs (*Aethia cristatella, Alle alle, Spheniscus mendiculus*), so we re-ran the analysis of our main results, leaving out those three species. ##Create new dataset leaving out those 3 species

```
dat4 <- filter(dat1, Species != c("Aethia_cristatella","Spheniscus_mendiculus", "Alle_alle")) #remove t
#View(dat4)

#note that dat4 is compiled from the dat1 that already has the linear measurements log-transformed and
```

12.1   Analysis of egg shape in relation to incubation site

```
mod80 <- lm(PT ~ gendev + LVOL +FCS + Site, data = dat4) #full model
summary(mod80)
```

```
##
## Call:
## lm(formula = PT ~ gendev + LVOL + FCS + Site, data = dat4)
##
## Residuals:
##       Min       1Q    Median       3Q       Max
## -0.030184 -0.007854  0.001945  0.010081  0.024520
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.529603   0.038409  13.788 1.13e-11 ***
## gendevP     -0.010029   0.013572  -0.739  0.46854
## LVOL         0.029119   0.018030   1.615  0.12197
## FCS2        -0.025242   0.011645  -2.168  0.04243 *
## SiteCR       0.012831   0.009732   1.318  0.20225
## SiteCU      -0.014783   0.009773  -1.513  0.14602
## SiteFE      -0.015829   0.020063  -0.789  0.43938
## SiteRO       0.049597   0.014089   3.520  0.00215 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0158 on 20 degrees of freedom
## Multiple R-squared:  0.7919, Adjusted R-squared:  0.7191
## F-statistic: 10.87 on 7 and 20 DF,  p-value: 1.279e-05
```

```
Anova(mod80)
```

```
## Anova Table (Type II tests)
##
## Response: PT
##              Sum Sq Df F value   Pr(>F)
## gendev    0.0001363  1  0.5460 0.468543
## LVOL      0.0006511  1  2.6083 0.121970
## FCS       0.0011728  1  4.6984 0.042434 *
## Site      0.0051564  4  5.1643 0.005045 **
## Residuals 0.0049924 20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g80 <- emmeans(mod80, specs = "Site"))
```

```
##  Site    emmean          SE df  lower.CL  upper.CL
##  BU   0.5685879 0.006138805 20 0.5557825 0.5813932
##  CR   0.5814190 0.009346047 20 0.5619235 0.6009145
##  CU   0.5538046 0.007161985 20 0.5388649 0.5687442
##  FE   0.5527588 0.017403229 20 0.5164563 0.5890613
##  RO   0.6181844 0.012049060 20 0.5930505 0.6433183
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g80, xlab ="Marginal Mean Pointedness")
```
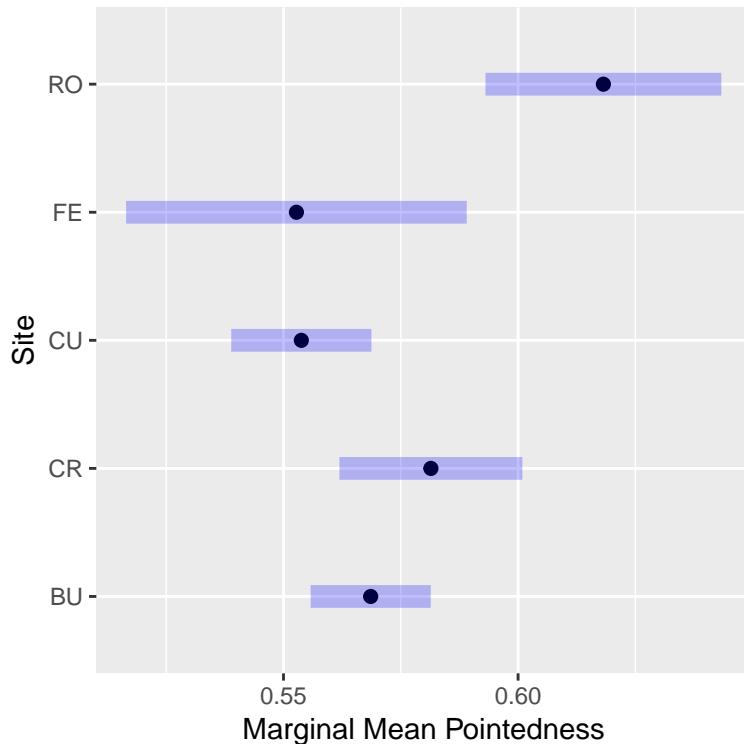


```
comp80 <- glht(mod80, linfct = mcp(Site = "Tukey"))
summary(comp80)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = PT ~ gendev + LVOL + FCS + Site, data = dat4)
##
## Linear Hypotheses:
##                Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0   0.012831   0.009732   1.318  0.65355
## CU - BU == 0  -0.014783   0.009773  -1.513  0.53439
## FE - BU == 0  -0.015829   0.020063  -0.789  0.91989
## RO - BU == 0   0.049597   0.014089   3.520  0.01441 *
## CU - CR == 0  -0.027614   0.012292  -2.246  0.18402
## FE - CR == 0  -0.028660   0.023452  -1.222  0.71156
## RO - CR == 0   0.036765   0.016259   2.261  0.17956
## FE - CU == 0  -0.001046   0.018632  -0.056  1.00000
## RO - CU == 0   0.064380   0.015930   4.041  0.00444 **
## RO - FE == 0   0.065426   0.019278   3.394  0.01891 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
mod81 <- lm(PA ~ gendev + LVOL +FCS + Site, data = dat4)
summary(mod81)
```

```
##
## Call:
## lm(formula = PA ~ gendev + LVOL + FCS + Site, data = dat4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.32587 -0.11714  0.02582  0.07709  0.48947
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.83941    0.47878   3.842  0.00102 **
## gendevP     -0.18276    0.16918  -1.080  0.29289
## LVOL         0.18634    0.22475   0.829  0.41682
## FCS2        -0.31913    0.14516  -2.198  0.03986 *
## SiteCR      -0.02657    0.12131  -0.219  0.82886
## SiteCU      -0.29554    0.12183  -2.426  0.02486 *
## SiteFE       0.07283    0.25009   0.291  0.77389
## SiteRO       0.31720    0.17562   1.806  0.08596 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1969 on 20 degrees of freedom
## Multiple R-squared:  0.7459, Adjusted R-squared:  0.657
## F-statistic: 8.389 on 7 and 20 DF,  p-value: 8.255e-05
```

```
Anova(mod81)
```

```
## Anova Table (Type II tests)
```

```
##
## Response: PA
##            Sum Sq Df F value  Pr(>F)
## gendev    0.04526  1  1.1669 0.29289
## LVOL      0.02666  1  0.6874 0.41682
## FCS       0.18746  1  4.8331 0.03986 *
## Site      0.42734  4  2.7544 0.05655 .
## Residuals 0.77573 20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g81 <- emmeans(mod81, specs = "Site"))
```

```
##  Site    emmean         SE df lower.CL upper.CL
##  BU    1.950809 0.07652162 20 1.791188 2.110431
##  CR    1.924241 0.11650064 20 1.681225 2.167257
##  CU    1.655271 0.08927580 20 1.469045 1.841497
##  FE    2.023638 0.21693527 20 1.571119 2.476157
##  RO    2.268013 0.15019432 20 1.954713 2.581313
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g81, xlab ="Marginal Mean Polar Asymmetry")
```
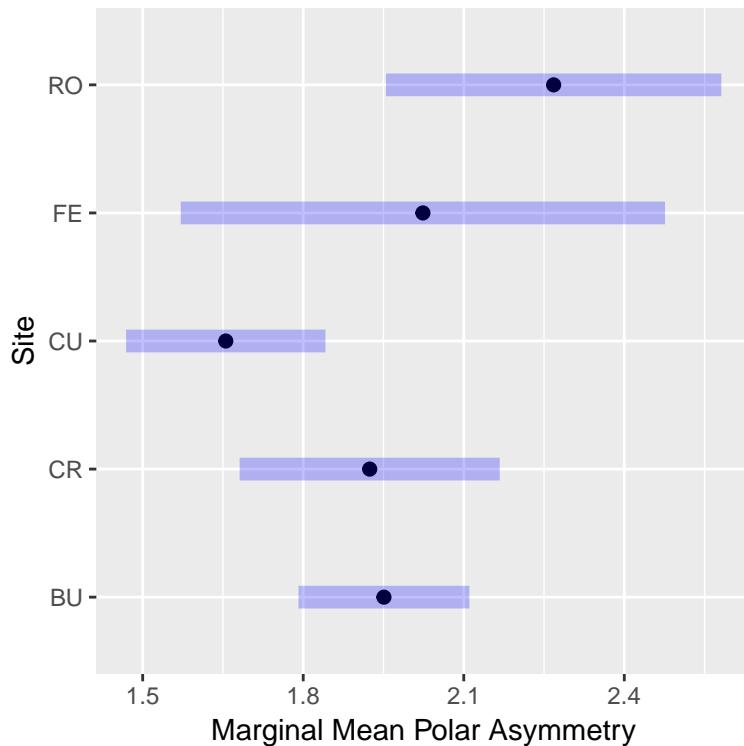


```
comp81 <- glht(mod81, linfct = mcp(Site = "Tukey"))
summary(comp81)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
```

```
##
##
## Fit: lm(formula = PA ~ gendev + LVOL + FCS + Site, data = dat4)
##
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0 -0.02657    0.12131  -0.219   0.9993
## CU - BU == 0 -0.29554    0.12183  -2.426   0.1337
## FE - BU == 0  0.07283    0.25009   0.291   0.9979
## RO - BU == 0  0.31720    0.17562   1.806   0.3679
## CU - CR == 0 -0.26897    0.15323  -1.755   0.3945
## FE - CR == 0  0.09940    0.29233   0.340   0.9962
## RO - CR == 0  0.34377    0.20267   1.696   0.4270
## FE - CU == 0  0.36837    0.23225   1.586   0.4904
## RO - CU == 0  0.61274    0.19857   3.086   0.0363 *
## RO - FE == 0  0.24438    0.24031   1.017   0.8244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```r
mod82 <- lm(EL ~ gendev + LVOL +FCS  + Site, data = dat4)
summary(mod82)
```

```
##
## Call:
## lm(formula = EL ~ gendev + LVOL + FCS + Site, data = dat4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.10898 -0.03081  0.00235  0.03095  0.10803
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  1.03356    0.12799   8.076 1.01e-07 ***
## gendevP      0.23859    0.04522   5.276 3.66e-05 ***
## LVOL         0.10689    0.06008   1.779   0.0904 .
## FCS2         0.09960    0.03880   2.567   0.0184 *
## SiteCR       0.03160    0.03243   0.974   0.3415
## SiteCU      -0.03763    0.03257  -1.155   0.2615
## SiteFE       0.10835    0.06685   1.621   0.1207
## SiteRO       0.11381    0.04695   2.424   0.0249 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05265 on 20 degrees of freedom
## Multiple R-squared:  0.8591, Adjusted R-squared:  0.8097
## F-statistic: 17.42 on 7 and 20 DF,  p-value: 3.113e-07
```

```r
Anova(mod82)
```

```
## Anova Table (Type II tests)
##
## Response: EL
##            Sum Sq Df F value    Pr(>F)
## gendev   0.077138  1 27.8313 3.66e-05 ***
```

```
## LVOL        0.008774  1  3.1657  0.09040 .
## FCS         0.018260  1  6.5881  0.01840 *
## Site        0.033839  4  3.0523  0.04082 *
## Residuals   0.055432 20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```r
(g82 <- emmeans(mod82, specs = "Site"))
```

```
##  Site    emmean          SE df lower.CL upper.CL
##  BU    1.410510 0.02045553 20 1.367841 1.453180
##  CR    1.442106 0.03114261 20 1.377143 1.507068
##  CU    1.372881 0.02386494 20 1.323100 1.422662
##  FE    1.518862 0.05799049 20 1.397896 1.639828
##  RO    1.524323 0.04014950 20 1.440573 1.608073
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```r
plot(g82, xlab ="Marginal Mean Elongation")
```
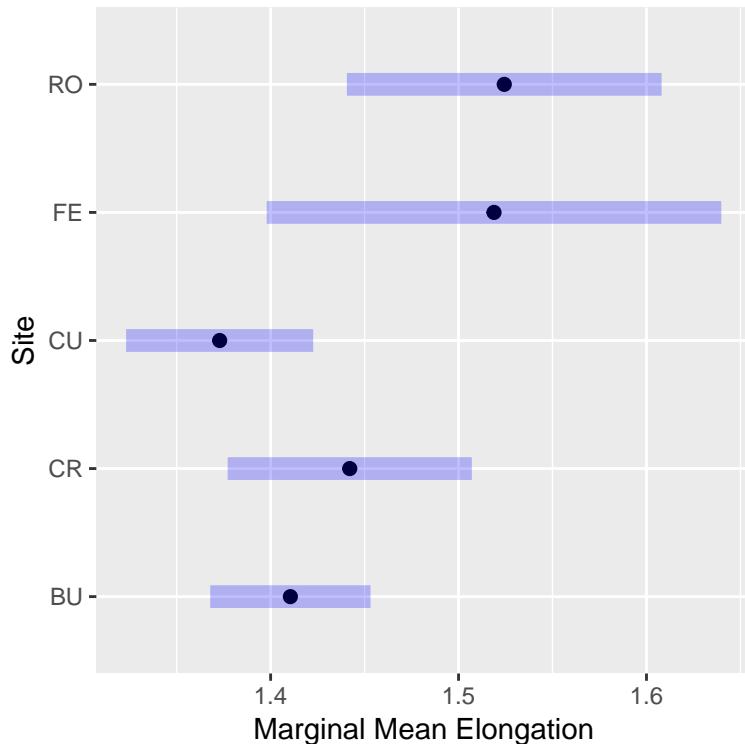


```r
comp82 <- glht(mod82, linfct = mcp(Site = "Tukey"))
summary(comp82)
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = EL ~ gendev + LVOL + FCS + Site, data = dat4)
##
```

```
## Linear Hypotheses:
##                Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0   0.031595   0.032429   0.974   0.8450
## CU - BU == 0  -0.037629   0.032567  -1.155   0.7502
## FE - BU == 0   0.108351   0.066853   1.621   0.4702
## RO - BU == 0   0.113813   0.046946   2.424   0.1345
## CU - CR == 0  -0.069225   0.040960  -1.690   0.4303
## FE - CR == 0   0.076756   0.078146   0.982   0.8413
## RO - CR == 0   0.082217   0.054177   1.518   0.5315
## FE - CU == 0   0.145981   0.062085   2.351   0.1533
## RO - CU == 0   0.151442   0.053081   2.853   0.0589 .
## RO - FE == 0   0.005461   0.064238   0.085   1.0000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

SUMMARY: With this reduced dataset, incubation site is significant or nearly so in models to predict each of the egg shape indices, controlling for general developmental mode, clutch size, and egg volume. These models explain 75-86% of the variation in those egg shape indices. In each case the 'rock' incubation site had higher index values than eggs incubated on at least one other type of site.

12.2 PCA analysis

```
#using matrix for input
mod83 <- princomp(dat4[, c(15:17, 19:21)], cor=TRUE)
mod83$loadings
```

```
##
## Loadings:
##       Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6
## PA     0.388  0.380  0.638  0.546
## PT     0.388  0.447  0.172 -0.788
## EL     0.165  0.600 -0.692  0.268 -0.151  0.195
## LVOL   0.465 -0.338 -0.118         0.531  0.611
## LLEN   0.507 -0.177 -0.263         0.249 -0.756
## LBR    0.445 -0.387               -0.796  0.134
##
##               Comp.1 Comp.2 Comp.3 Comp.4 Comp.5 Comp.6
## SS loadings    1.000  1.000  1.000  1.000  1.000  1.000
## Proportion Var 0.167  0.167  0.167  0.167  0.167  0.167
## Cumulative Var 0.167  0.333  0.500  0.667  0.833  1.000
```

```
screeplot(mod83)
```

mod83
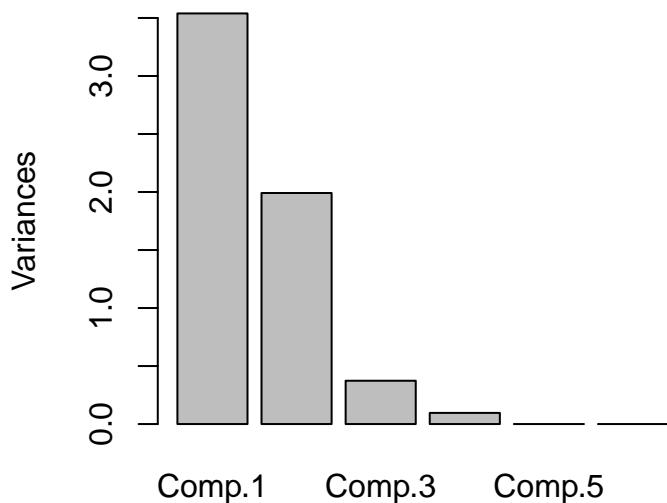

```r
summary(mod83)
```

```
## Importance of components:
##                           Comp.1    Comp.2     Comp.3     Comp.4
## Standard deviation     1.8812490 1.4111587 0.61097702 0.30996400
## Proportion of Variance 0.5898496 0.3318948 0.06221549 0.01601295
## Cumulative Proportion  0.5898496 0.9217444 0.98395991 0.99997286
##                             Comp.5      Comp.6
## Standard deviation     1.008653e-02 7.816351e-03
## Proportion of Variance 1.695633e-05 1.018256e-05
## Cumulative Proportion  9.999898e-01 1.000000e+00
```

```r
biplot(mod83)
```
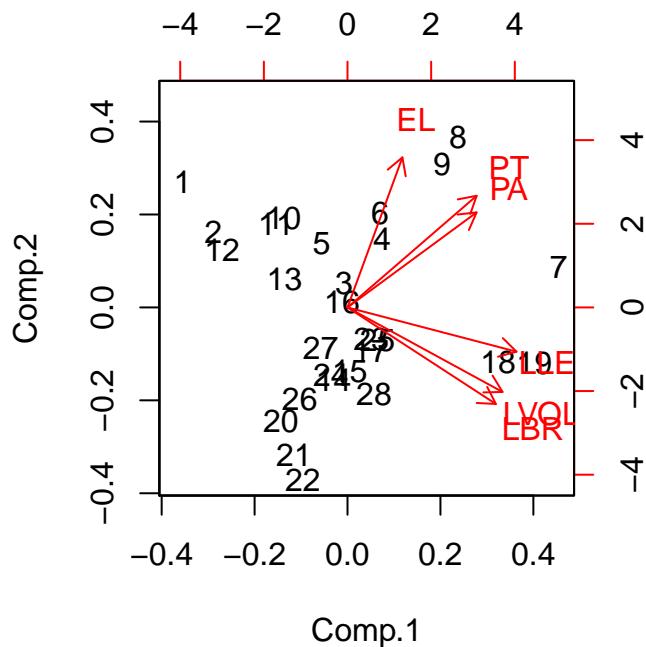
```
(eig83 <- mod83$sdev^2) #calculate eigenvalues
```

```
##        Comp.1        Comp.2        Comp.3        Comp.4        Comp.5
## 3.539098e+00 1.991369e+00 3.732929e-01 9.607768e-02 1.017380e-04
##        Comp.6
## 6.109534e-05
```

```
mod84 <- principal(dat4[, c(15:17, 19:21)], nfactors = 2)
biplot(mod84)
```


Biplot from fa
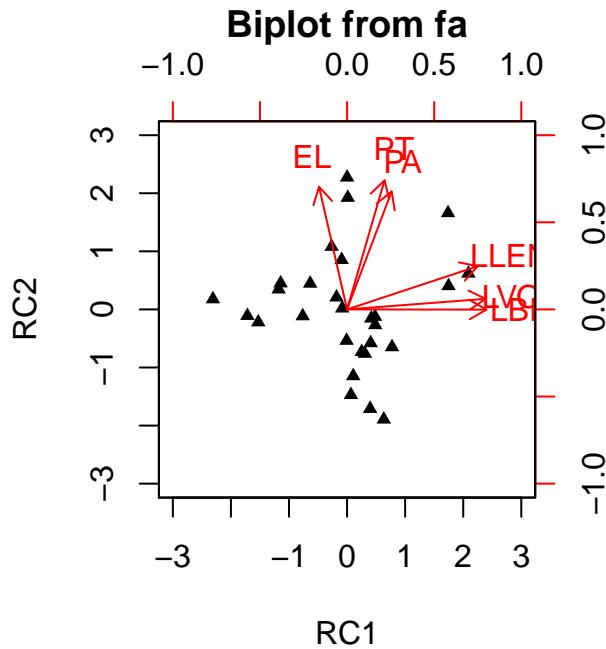
```
mod84$values
```

```
## [1] 3.539098e+00 1.991369e+00 3.732929e-01 9.607768e-02 1.017380e-04
## [6] 6.109534e-05
```

```
mod84$loadings
```

```
##
## Loadings:
##       RC1    RC2
## PA    0.320  0.847
## PT    0.269  0.926
## EL   -0.201  0.880
## LVOL  0.994
## LLEN  0.937  0.310
## LBR   1.000
##
##                  RC1   RC2
## SS loadings    3.081 2.450
## Proportion Var 0.513 0.408
## Cumulative Var 0.513 0.922
```

```
dat4$RC1new <- mod84$scores[,1] #rotated PC2 scores, mainly size
dat4$RC2new <- mod84$scores[,2] #rotated PC2 scores, mainly shape
```

SUMMARY: For this reduced dataset, the PCA generated two rotated components that loaded largely on

92

size (RC1) and shape (RC2) variables, in total explaining 92% of the variation in these variables, the same as with the full dataset. RC2 is positively correlated with Pointedness, Polar-Asymmetry and Elongation, with correlations almost identical to those with the full dataset.

12.3 Model to predict egg shape RC2

Here we re-run the full model, as above, to predict egg shape, based on RC2 calculated from the reduced dataset.

```
mod85 <- lm(RC2new ~ gendev +FCS + +LVOL +Site, data = dat4) #full model to predict shape
summary(mod85)
```

```
##
## Call:
## lm(formula = RC2new ~ gendev + FCS + +LVOL + Site, data = dat4)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.02590 -0.28045  0.06899  0.32009  0.74274
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.0496     1.2199  -0.860  0.39976
## gendevP       0.5332     0.4311   1.237  0.23041
## FCS2         -0.2885     0.3699  -0.780  0.44456
## LVOL          0.5196     0.5726   0.907  0.37499
## SiteCR        0.2458     0.3091   0.795  0.43579
## SiteCU       -0.6163     0.3104  -1.985  0.06098 .
## SiteFE        0.2540     0.6372   0.399  0.69440
## SiteRO        1.3433     0.4475   3.002  0.00704 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.5018 on 20 degrees of freedom
## Multiple R-squared:  0.8135, Adjusted R-squared:  0.7482
## F-statistic: 12.46 on 7 and 20 DF,  p-value: 4.545e-06
```

```
comp85 <- glht(mod85, linfct = mcp(Site = "Tukey"))
summary(comp85)
```

```
##
##   Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = RC2new ~ gendev + FCS + +LVOL + Site, data = dat4)
##
## Linear Hypotheses:
##                Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0   0.245812   0.309092   0.795  0.91777
## CU - BU == 0  -0.616302   0.310409  -1.985  0.28241
## FE - BU == 0   0.253995   0.637202   0.399  0.99309
## RO - BU == 0   1.343273   0.447462   3.002  0.04348 *
## CU - CR == 0  -0.862114   0.390408  -2.208  0.19655
```

```
## FE - CR == 0   0.008183    0.744842    0.011   1.00000
## RO - CR == 0   1.097462    0.516387    2.125   0.22569
## FE - CU == 0   0.870297    0.591756    1.471   0.56003
## RO - CU == 0   1.959575    0.505941    3.873   0.00657 **
## RO - FE == 0   1.089279    0.612285    1.779   0.38182
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
Anova(mod85)
```

```
## Anova Table (Type II tests)
##
## Response: RC2new
##           Sum Sq Df F value  Pr(>F)
## gendev    0.3853  1  1.5302 0.23041
## FCS       0.1532  1  0.6083 0.44456
## LVOL      0.2073  1  0.8234 0.37499
## Site      4.0400  4  4.0112 0.01508 *
## Residuals 5.0359 20
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(dat4, aes(x = Site, y = RC2new)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35))
```



```
(g85 <- emmeans(mod85, specs = "Site"))
```
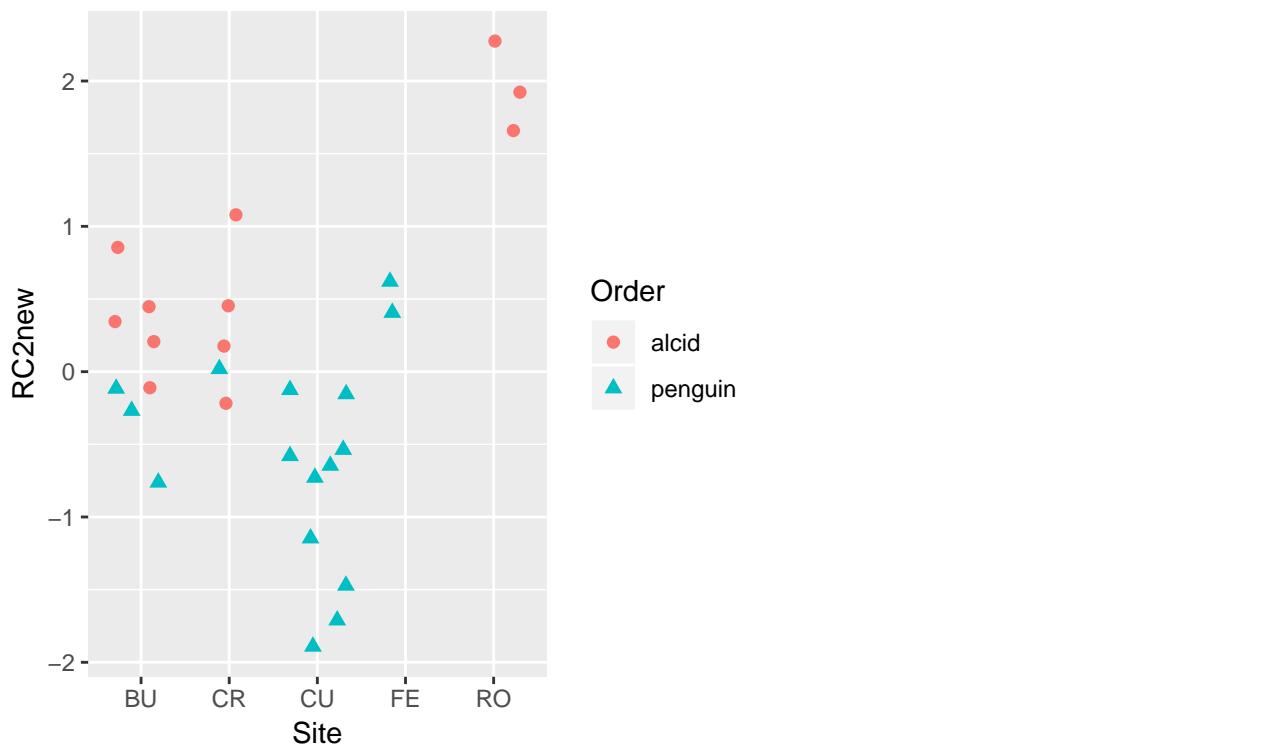
```
##  Site     emmean        SE df   lower.CL    upper.CL
##  BU    0.08314243 0.1949708 20 -0.3235595  0.48984437
##  CR    0.32895411 0.2968340 20 -0.2902308  0.94813905
##  CU   -0.53315970 0.2274674 20 -1.0076483 -0.05867106
```

```
##  FE     0.33713710 0.5527332 20 -0.8158441  1.49011833
##  RO     1.42641573 0.3826828 20  0.6281535  2.22467797
##
## Results are averaged over the levels of: gendev, FCS
## Confidence level used: 0.95
```

```
plot(g85, xlab ="Marginal Mean RC2 egg shape")
```
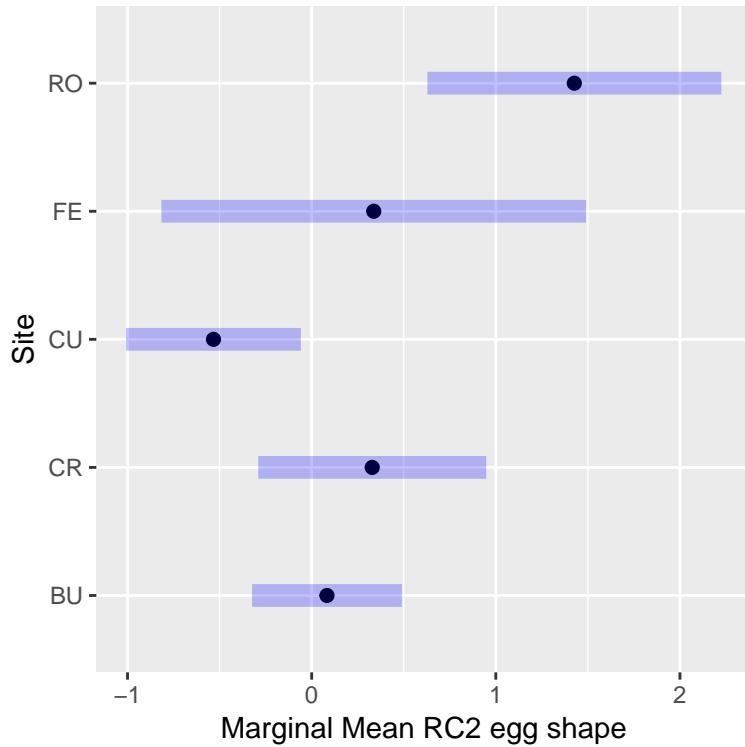


```
(d85 <- dredge(mod85))
```

```
## Fixed term is "(Intercept)"
```

```
## Global model call: lm(formula = RC2new ~ gendev + FCS + +LVOL + Site, data = dat4)
## ---
## Model selection table
##        (Intrc) FCS gendv    LVOL Site df  logLik AICc delta weight
## 11 -3.108e-01        +            +  7 -16.752 53.1  0.00  0.312
## 10  3.491e-01   +               +  7 -16.908 53.4  0.31  0.267
## 9   7.522e-02                   +  6 -19.166 54.3  1.23  0.169
## 15 -1.385e+00        + 0.55210   +  8 -16.131 55.8  2.74  0.079
## 12 -1.554e-02   +    +           +  8 -16.277 56.1  3.03  0.069
## 14 -1.227e-01   +      0.27020   +  8 -16.744 57.1  3.96  0.043
## 13 -9.963e-03        0.04730   +  7 -19.161 57.9  4.82  0.028
## 16 -1.050e+00   +    + 0.51960   +  9 -15.712 59.4  6.32  0.013
## 7  -3.951e+00        + 1.64000      4 -25.068 59.9  6.77  0.011
## 8  -2.702e+00   +    + 1.25100      5 -23.958 60.6  7.54  0.007
## 4   2.749e-01   +    +             4 -26.929 63.6 10.49  0.002
## 2   8.672e-01   +                  3 -29.386 65.8 12.67  0.001
## 6   6.857e-01   +      0.09215      4 -29.365 68.5 15.36  0.000
## 3  -5.684e-01        +             3 -30.934 68.9 15.76  0.000
## 1  -8.917e-16                      2 -39.221 82.9 29.82  0.000
```

95

```
## 5   -4.933e-01              0.25370          3 -39.140 85.3 32.18   0.000
## Models ranked by AICc(x)
```

```r
mod85a <- lm(RC2new ~ FCS + Site, data = dat4) #best-fitting model from IT approach
summary(mod85a)
```

```
##
## Call:
## lm(formula = RC2new ~ FCS + Site, data = dat4)
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.99396 -0.29493   0.02801   0.33124   0.77511
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    0.3491     0.2250    1.551 0.135149
## FCS2          -0.5477     0.2791   -1.962 0.062526 .
## SiteCR         0.2813     0.2860    0.983 0.336071
## SiteCU        -0.7007     0.2749   -2.549 0.018304 *
## SiteFE         0.1626     0.4187    0.388 0.701519
## SiteRO         1.6040     0.3657    4.386 0.000235 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.4993 on 22 degrees of freedom
## Multiple R-squared:  0.7968, Adjusted R-squared:  0.7507
## F-statistic: 17.26 on 5 and 22 DF,  p-value: 5.758e-07
```

```r
comp85a <- glht(mod85a, linfct = mcp(Site = "Tukey"))
summary(comp85a)
```

```
##
##    Simultaneous Tests for General Linear Hypotheses
##
## Multiple Comparisons of Means: Tukey Contrasts
##
##
## Fit: lm(formula = RC2new ~ FCS + Site, data = dat4)
##
## Linear Hypotheses:
##               Estimate Std. Error t value Pr(>|t|)
## CR - BU == 0    0.2813     0.2860    0.983  0.85232
## CU - BU == 0   -0.7007     0.2749   -2.549  0.10973
## FE - BU == 0    0.1626     0.4187    0.388  0.99444
## RO - BU == 0    1.6040     0.3657    4.386  0.00183 **
## CU - CR == 0   -0.9820     0.2954   -3.324  0.02160 *
## FE - CR == 0   -0.1187     0.4501   -0.264  0.99876
## RO - CR == 0    1.3227     0.4013    3.296  0.02320 *
## FE - CU == 0    0.8633     0.4770    1.810  0.37990
## RO - CU == 0    2.3047     0.4312    5.344  < 0.001 ***
## RO - FE == 0    1.4414     0.4558    3.162  0.03116 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## (Adjusted p values reported -- single-step method)
```

```
Anova(mod85a)
```

```
## Anova Table (Type II tests)
##
## Response: RC2new
##           Sum Sq Df F value    Pr(>F)
## FCS       0.9599  1  3.8497 0.0625264 .
## Site      7.8889  4  7.9101 0.0004136 ***
## Residuals 5.4852 22
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
(g85a <- emmeans(mod85a, specs = "Site"))
```

```
##  Site      emmean        SE df    lower.CL   upper.CL
##  BU     0.07522265 0.1765393 22 -0.2908974  0.4413427
##  CR     0.35651991 0.2250443 22 -0.1101934  0.8232332
##  CU    -0.62546204 0.2107409 22 -1.0625118 -0.1884122
##  FE     0.23780759 0.3796621 22 -0.5495633  1.0251785
##  RO     1.67922210 0.3202943 22  1.0149723  2.3434719
##
## Results are averaged over the levels of: FCS
## Confidence level used: 0.95
```

```
plot(g85a, xlab ="Marginal Mean RC2 egg shape")
```
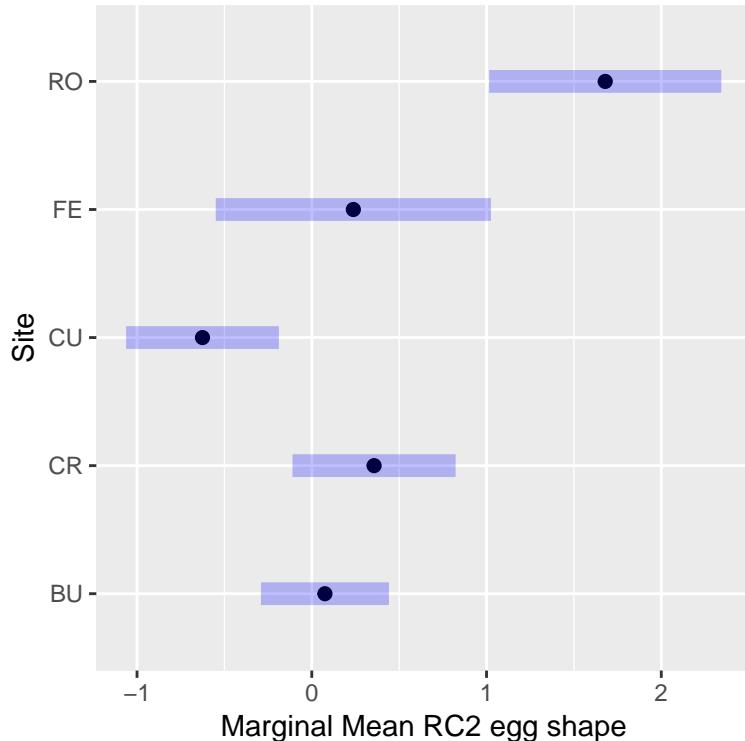


```
ggplot(dat4, aes(Order, y = RC2new)) +
  geom_point(aes(shape=Order, color=Order), size =2, position=position_jitter(width = .35)) +theme_bw()
```
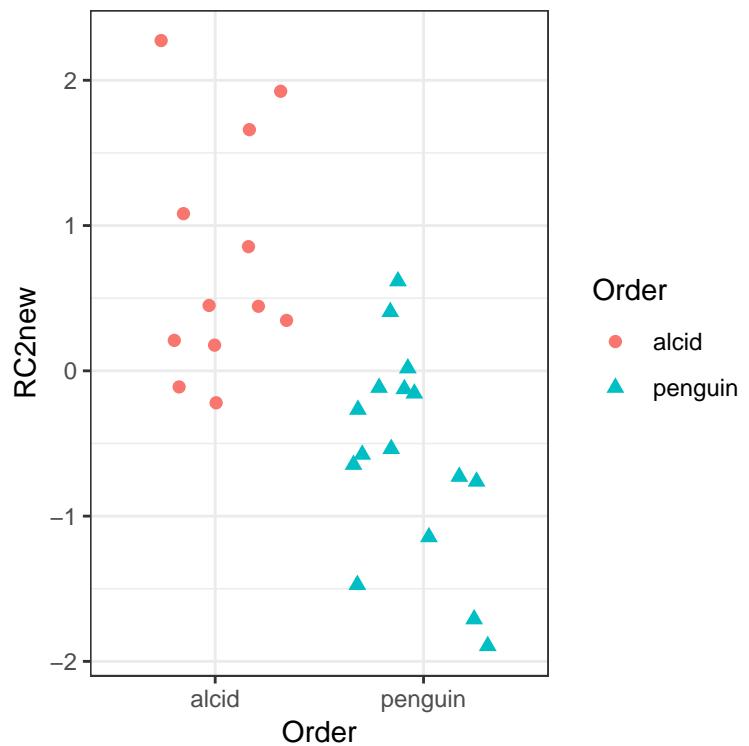
SUMMARY: Incubation site is still a significant predictor of egg shape RC2, with RC2 being highest for eggs incubated on rock, significantly higher than for eggs laid on crevice, cup and burrow sites, and in decreasing order such that rock>crevice>feet>burrow>cup, very similar to the pattern for model based on the full dataset. We conclude that the 3 species with a small sample of eggs measured had no appreciable affect on the analyses above