Selection Analyses 11.29

Valerie Martin

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### Looking at combined PCA for natural flowers and Total Seeds/Plant by Size\*Morph (directly comparing these analyses to those from the stigma analyses)

Summary of findings: No significant effects of any flower size measurements\*morph on seeds/plant (only tested for naturally pollinated plants). The PC loadings are interesting for PC2 – all negative except for a large positive loading for tube length.

### Total Seeds/Plant by Size Measurement\*Morph

fit<-lme(sqrt(Total.SeedsPerPlant)~Avg.CorollaFlare\*Morph, random=~1|Site/Habitat, data=fruit.nat, method="ML", na.action=na.omit)   
anova.lme(fit, type="marginal")

## numDF denDF F-value p-value  
## (Intercept) 1 34 2.3106076 0.1377  
## Avg.CorollaFlare 1 34 0.3950732 0.5338  
## Morph 1 34 0.0073469 0.9322  
## Avg.CorollaFlare:Morph 1 34 0.0104680 0.9191

summary(fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: fruit.nat   
## AIC BIC logLik  
## 222.325 234.6534 -104.1625  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept)  
## StdDev: 1.408012  
##   
## Formula: ~1 | Habitat %in% Site  
## (Intercept) Residual  
## StdDev: 0.5040085 2.554154  
##   
## Fixed effects: sqrt(Total.SeedsPerPlant) ~ Avg.CorollaFlare \* Morph   
## Value Std.Error DF t-value p-value  
## (Intercept) 9.101652 5.987660 34 1.5200683 0.1377  
## Avg.CorollaFlare -2.590038 4.120665 34 -0.6285485 0.5338  
## MorphSweet -0.567706 6.623248 34 -0.0857141 0.9322  
## Avg.CorollaFlare:MorphSweet 0.464076 4.535845 34 0.1023131 0.9191  
## Correlation:   
## (Intr) Avg.CF MrphSw  
## Avg.CorollaFlare -0.983   
## MorphSweet -0.868 0.872   
## Avg.CorollaFlare:MorphSweet 0.863 -0.878 -0.991  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -1.8613816 -0.6784079 -0.2445591 0.8039650 2.0472523   
##   
## Number of Observations: 43  
## Number of Groups:   
## Site Habitat %in% Site   
## 3 6

fit<-lme(sqrt(Total.SeedsPerPlant)~Avg.TubeL\*Morph, random=~1|Site/Habitat, data=fruit.nat, method="ML", na.action=na.omit)   
anova.lme(fit)

## numDF denDF F-value p-value  
## (Intercept) 1 34 42.00907 <.0001  
## Avg.TubeL 1 34 0.06453 0.8010  
## Morph 1 34 0.24602 0.6231  
## Avg.TubeL:Morph 1 34 1.24365 0.2726

summary(fit)

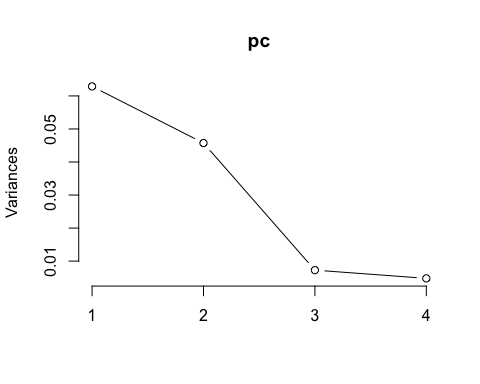
## Linear mixed-effects model fit by maximum likelihood  
## Data: fruit.nat   
## AIC BIC logLik  
## 221.9062 234.2346 -103.9531  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept)  
## StdDev: 1.18032  
##   
## Formula: ~1 | Habitat %in% Site  
## (Intercept) Residual  
## StdDev: 0.0002007795 2.592464  
##   
## Fixed effects: sqrt(Total.SeedsPerPlant) ~ Avg.TubeL \* Morph   
## Value Std.Error DF t-value p-value  
## (Intercept) 8.106821 5.398954 34 1.5015540 0.1424  
## Avg.TubeL -1.609964 3.055054 34 -0.5269839 0.6016  
## MorphSweet -7.583773 7.276165 34 -1.0422762 0.3046  
## Avg.TubeL:MorphSweet 4.791817 4.296861 34 1.1151902 0.2726  
## Correlation:   
## (Intr) Avg.TL MrphSw  
## Avg.TubeL -0.984   
## MorphSweet -0.745 0.747   
## Avg.TubeL:MorphSweet 0.712 -0.723 -0.992  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.5033062 -0.6496246 -0.2379935 0.7421583 2.0709926   
##   
## Number of Observations: 43  
## Number of Groups:   
## Site Habitat %in% Site   
## 3 6

#### Flower measurements combined via pca (all 4 traits - same as pressed) - BOTH MORPHS

measures <- c("Avg.CorollaFlare", "Avg.TubeL", "Avg.LobeL", "Avg.LobW")  
flwr.size<-as.matrix(subset(fruit.nat, select=measures))  
pc<-prcomp(flwr.size,center=TRUE)  
print(pc)

## Standard deviations (1, .., p=4):  
## [1] 0.25076852 0.21385170 0.08529390 0.06907149  
##   
## Rotation (n x k) = (4 x 4):  
## PC1 PC2 PC3 PC4  
## Avg.CorollaFlare 0.8719149 -0.15491858 0.43200595 0.17069137  
## Avg.TubeL 0.1754685 0.98308948 0.01785694 -0.04926474  
## Avg.LobeL 0.3222640 -0.01996539 -0.83421169 0.44703259  
## Avg.LobW 0.3242239 -0.09558605 -0.34226136 -0.87669796

plot(pc, type="l")



summary(pc)

## Importance of components:  
## PC1 PC2 PC3 PC4  
## Standard deviation 0.2508 0.2139 0.08529 0.06907  
## Proportion of Variance 0.5212 0.3790 0.06029 0.03954  
## Cumulative Proportion 0.5212 0.9002 0.96046 1.00000

pc.extracted <- as.data.frame(predict(pc, newdata=fruit.nat))  
##### Almost all loadings for PC2 are negative, but Avg. TubeL has a very high positive  
fruit.nat$PC1.all <- pc.extracted$PC1   
fruit.nat$PC2.all <- pc.extracted$PC2

#### Total Seeds/Plant by PC1*Morph and PC2*Morph

fit<-lme(sqrt(Total.SeedsPerPlant)~PC1.all\*Morph, random=~1|Site/Habitat, data=fruit.nat, method="ML", na.action=na.omit)   
anova.lme(fit)

## numDF denDF F-value p-value  
## (Intercept) 1 34 30.500181 <.0001  
## PC1.all 1 34 1.172983 0.2864  
## Morph 1 34 0.022052 0.8828  
## PC1.all:Morph 1 34 0.146491 0.7043

summary(fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: fruit.nat   
## AIC BIC logLik  
## 222.2617 234.5901 -104.1309  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept)  
## StdDev: 1.426372  
##   
## Formula: ~1 | Habitat %in% Site  
## (Intercept) Residual  
## StdDev: 0.3767327 2.561217  
##   
## Fixed effects: sqrt(Total.SeedsPerPlant) ~ PC1.all \* Morph   
## Value Std.Error DF t-value p-value  
## (Intercept) 5.313118 1.083925 34 4.901742 0.0000  
## PC1.all -3.057155 3.552310 34 -0.860610 0.3955  
## MorphSweet 0.132973 0.896594 34 0.148309 0.8830  
## PC1.all:MorphSweet 1.518815 3.968248 34 0.382742 0.7043  
## Correlation:   
## (Intr) PC1.ll MrphSw  
## PC1.all 0.051   
## MorphSweet -0.407 0.031   
## PC1.all:MorphSweet -0.046 -0.871 0.000  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.0115287 -0.6824185 -0.2466320 0.7988792 2.1126336   
##   
## Number of Observations: 43  
## Number of Groups:   
## Site Habitat %in% Site   
## 3 6

fit<-lme(sqrt(Total.SeedsPerPlant)~PC2.all\*Morph, random=~1|Site/Habitat, data=fruit.nat, method="ML", na.action=na.omit)   
anova.lme(fit)

## numDF denDF F-value p-value  
## (Intercept) 1 34 39.43234 <.0001  
## PC2.all 1 34 0.22096 0.6413  
## Morph 1 34 0.30656 0.5834  
## PC2.all:Morph 1 34 1.42969 0.2401

summary(fit)

## Linear mixed-effects model fit by maximum likelihood  
## Data: fruit.nat   
## AIC BIC logLik  
## 221.4972 233.8256 -103.7486  
##   
## Random effects:  
## Formula: ~1 | Site  
## (Intercept)  
## StdDev: 1.232109  
##   
## Formula: ~1 | Habitat %in% Site  
## (Intercept) Residual  
## StdDev: 0.0002724941 2.573596  
##   
## Fixed effects: sqrt(Total.SeedsPerPlant) ~ PC2.all \* Morph   
## Value Std.Error DF t-value p-value  
## (Intercept) 5.420726 1.007357 34 5.381137 0.0000  
## PC2.all -1.383117 3.120616 34 -0.443219 0.6604  
## MorphSweet 0.383607 0.935141 34 0.410213 0.6842  
## PC2.all:MorphSweet 5.204569 4.352751 34 1.195696 0.2401  
## Correlation:   
## (Intr) PC2.ll MrphSw  
## PC2.all -0.266   
## MorphSweet -0.484 0.312   
## PC2.all:MorphSweet 0.190 -0.730 -0.117  
##   
## Standardized Within-Group Residuals:  
## Min Q1 Med Q3 Max   
## -2.2892341 -0.6673516 -0.1822819 0.6603644 2.1428178   
##   
## Number of Observations: 43  
## Number of Groups:   
## Site Habitat %in% Site   
## 3 6