**Results**

* Variance Partitioning
  + >50% variance explained for 9 species out of 63 – abiotic, biotic, shared
  + Avg of 30% total, 15% env, and 13% biotic variance explained for each focal spp
  + **Figure 2** = bar plot
* GLM ran occ
  + big AIC 330605
  + Residuals – seems fairly symmetrical, so data fit relatively well by the model
  + **Figure 3** – violin plots? Nec?
  + Table 1

Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']

Family: binomial ( logit )

Formula: cbind(sp\_success, sp\_fail) ~ cs(comp\_scaled) + abs(zTemp) + abs(zElev) +

abs(zPrecip) + abs(zEVI) + forest + (1 | stateroute:Species)

Data: occumatrix1

AIC BIC logLik deviance df.resid

330604.9 330677.1 -165294.5 330588.9 61495

Scaled residuals:

Min 1Q Median 3Q Max

-3.0855 -0.6119 0.0370 0.3542 3.6478

Random effects:

Groups Name Variance Std.Dev.

stateroute:Species (Intercept) 5.21 2.283

Number of obs: 61503, groups: stateroute:Species, 4540

Fixed effects:

Estimate Std. Error z value Pr(>|z|)

(Intercept) 0.618475 0.096134 6.433 1.25e-10 \*\*\*

cs(comp\_scaled) -0.834553 0.033754 -24.725 < 2e-16 \*\*\*

abs(zTemp) -0.135884 0.055276 -2.458 0.014 \*

abs(zElev) 0.006763 0.058391 0.116 0.908

abs(zPrecip) -0.017472 0.057429 -0.304 0.761

abs(zEVI) -0.225755 0.055633 -4.058 4.95e-05 \*\*\*

forest 0.612598 0.135177 4.532 5.85e-06 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Correlation of Fixed Effects:

(Intr) cs(c\_) abs(T) abs(E) abs(P) a(EVI)

cs(cmp\_scl) 0.014

abs(zTemp) -0.369 0.011

abs(zElev) -0.231 0.016 -0.161

abs(zPrecp) -0.254 0.008 -0.165 -0.127

abs(zEVI) -0.329 0.010 0.053 -0.196 -0.189

forest -0.591 -0.065 0.043 0.008 0.007 0.036

* Traits LM
  + Residuals – not symmetrical, so data not fit well by the model
  + t-statistic values not far away from zero and are small relative to the standard error, probably no relationship exists
  + adjusted R2 adjusts for the number of variables considered – 0.334
  + Table 2, Overall, seems like a poor model

Call:

lm(formula = FocalAOU ~ Trophic.Group + migclass + EW, data = comp\_lm)

Residuals:

Min 1Q Median 3Q Max

-2411.0 -134.1 233.1 499.9 1620.8

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 4312.3 539.2 7.997 7.82e-11 \*\*\*

Trophic.Groupinsct/om 953.2 572.5 1.665 0.101483

Trophic.Groupinsectivore 1646.9 519.6 3.170 0.002472 \*\*

Trophic.Groupomnivore -965.2 752.1 -1.283 0.204652

migclassresid 1159.6 484.2 2.395 0.019987 \*

migclassshort 957.7 253.6 3.777 0.000386 \*\*\*

EW 331.8 240.4 1.380 0.173013

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 824.3 on 56 degrees of freedom

Multiple R-squared: 0.3985, Adjusted R-squared: 0.3341

F-statistic: 6.183 on 6 and 56 DF, p-value: 5.046e-05

* Occupancy and Abundance
  + provide unique information about biodiversity (1:1) line – some species occupancy was better predicted than abundance and vice versa
  + **Figure 3/4**

