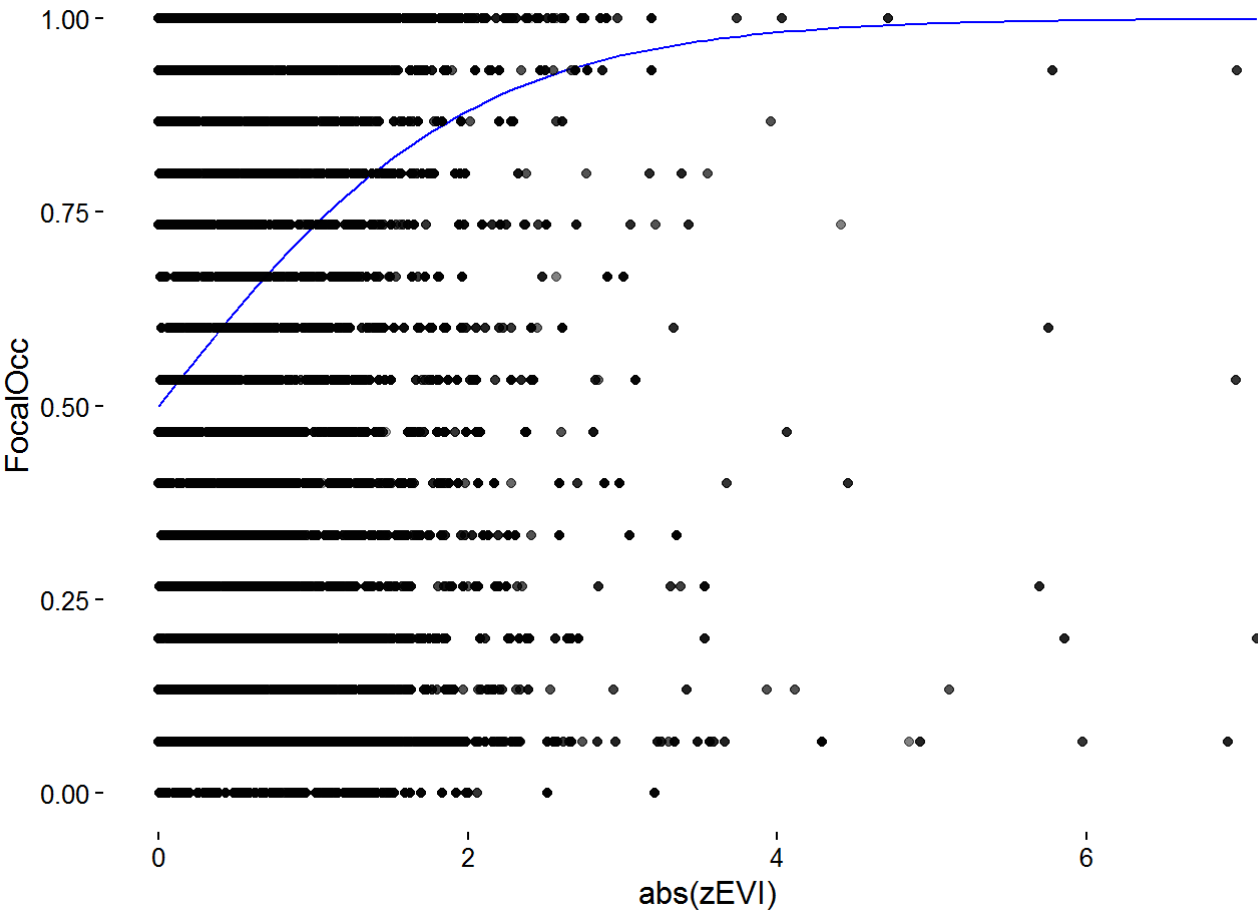
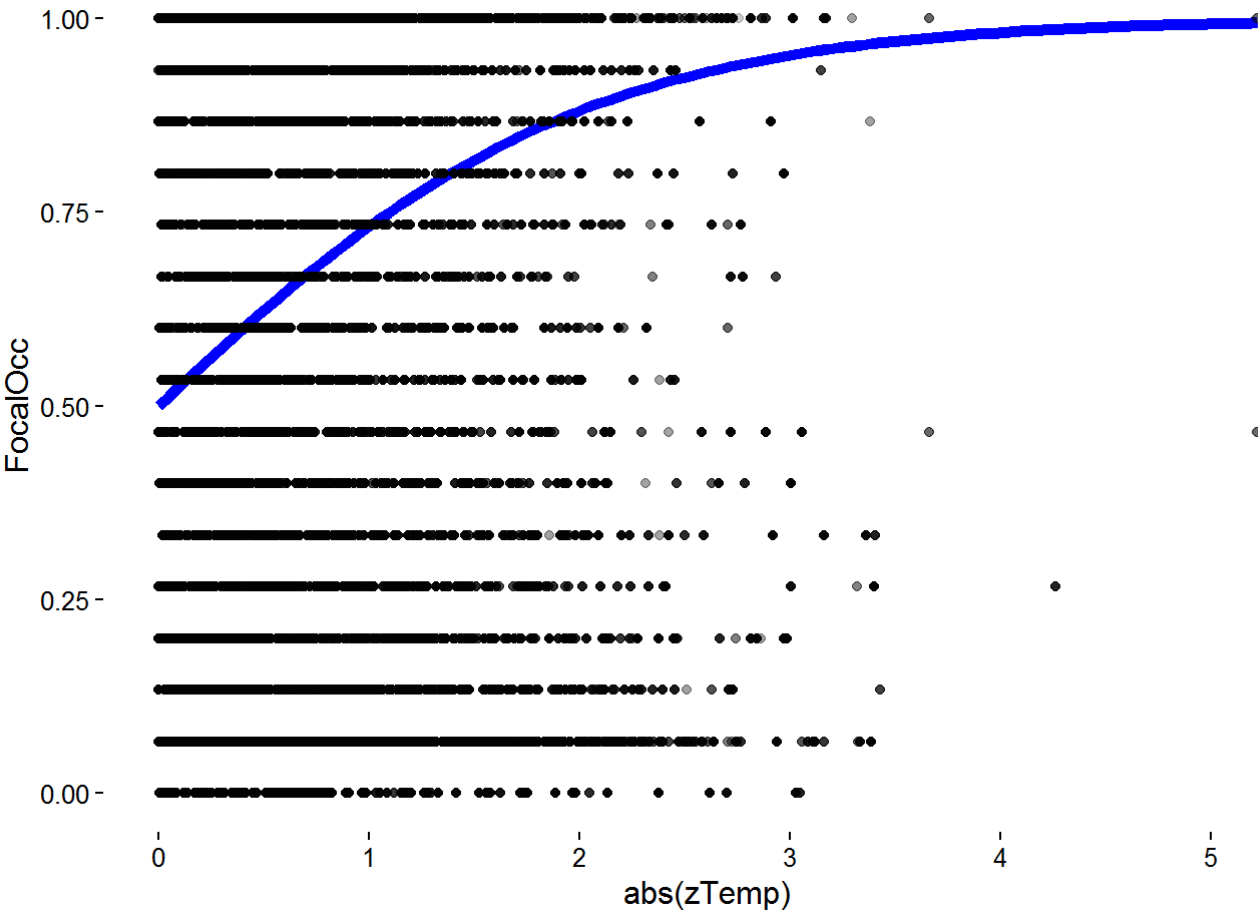
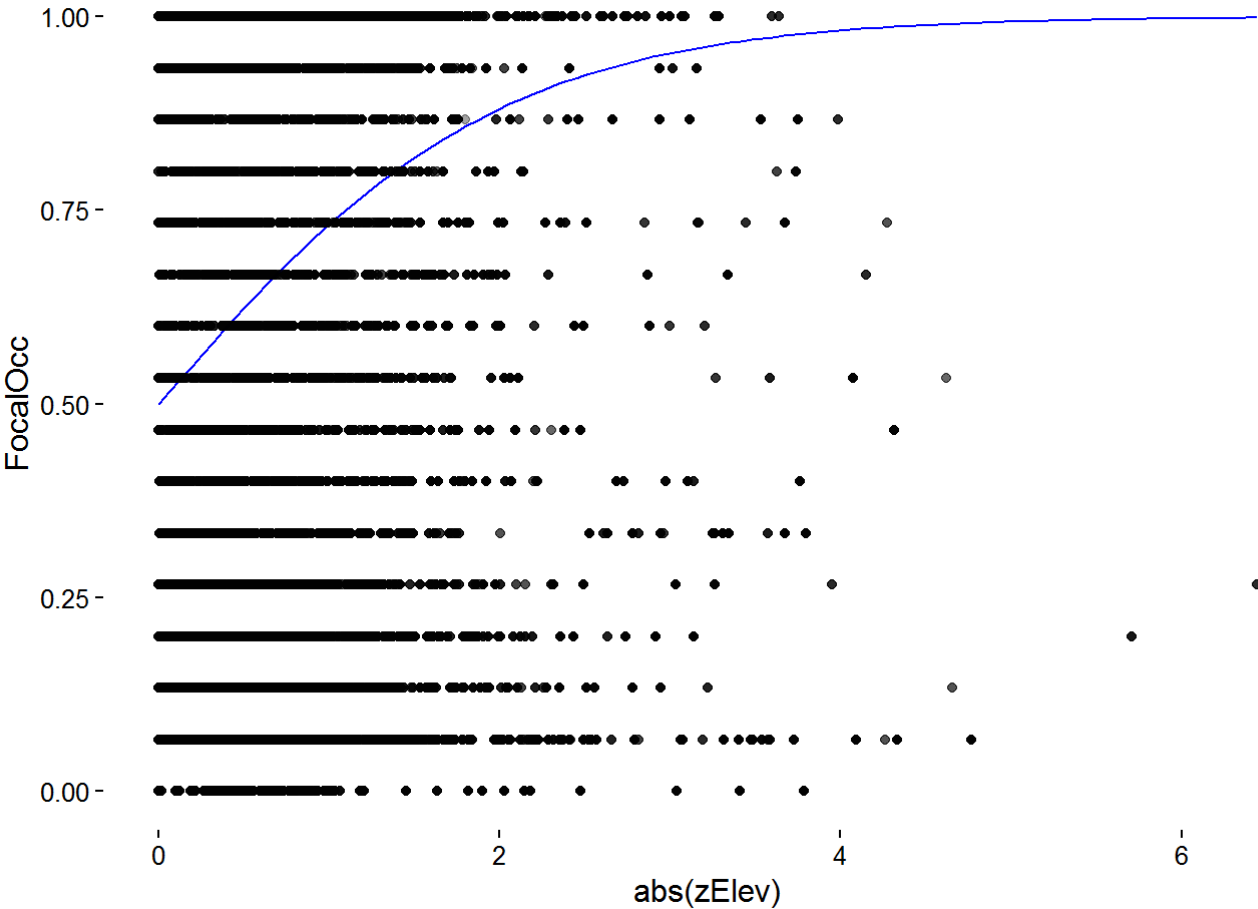
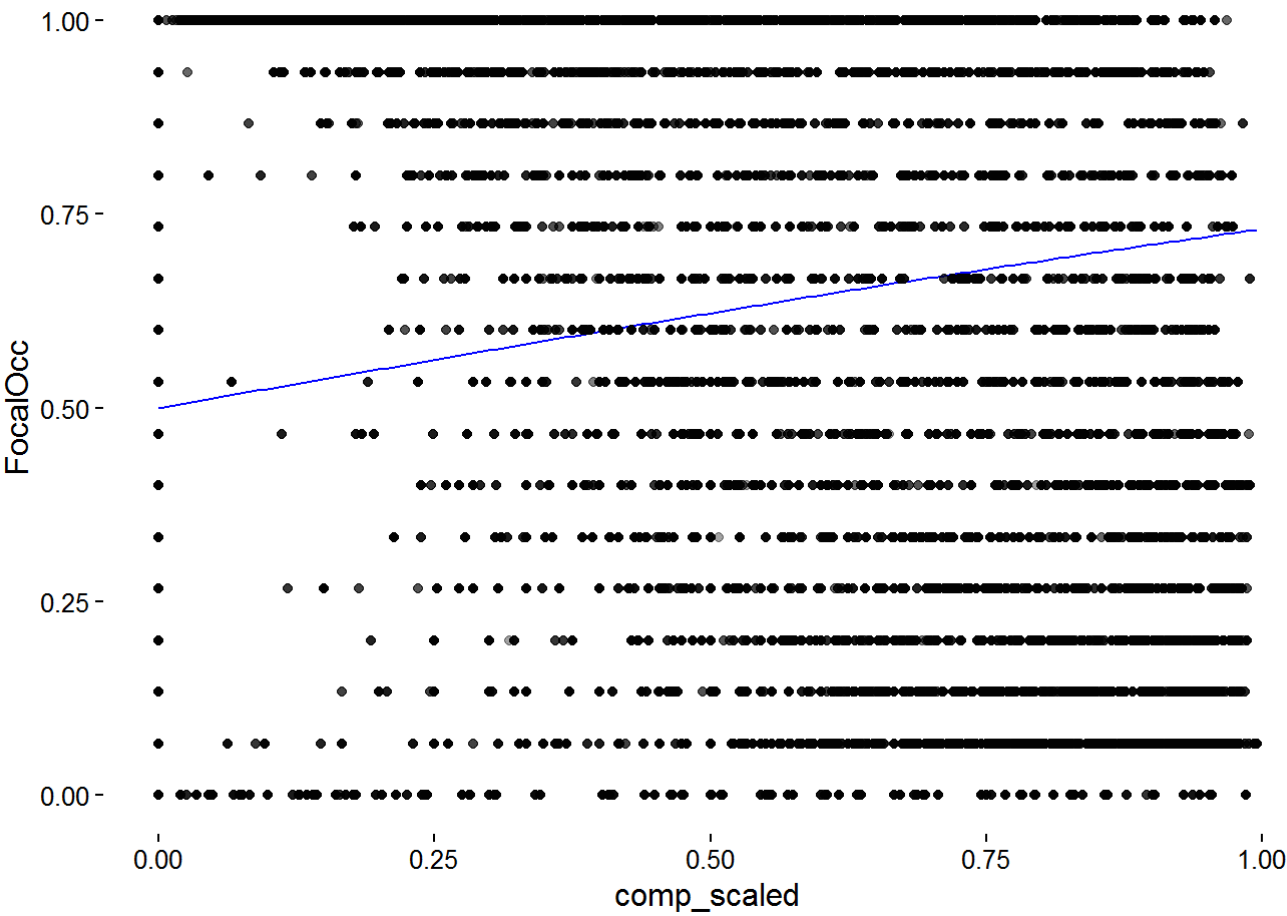
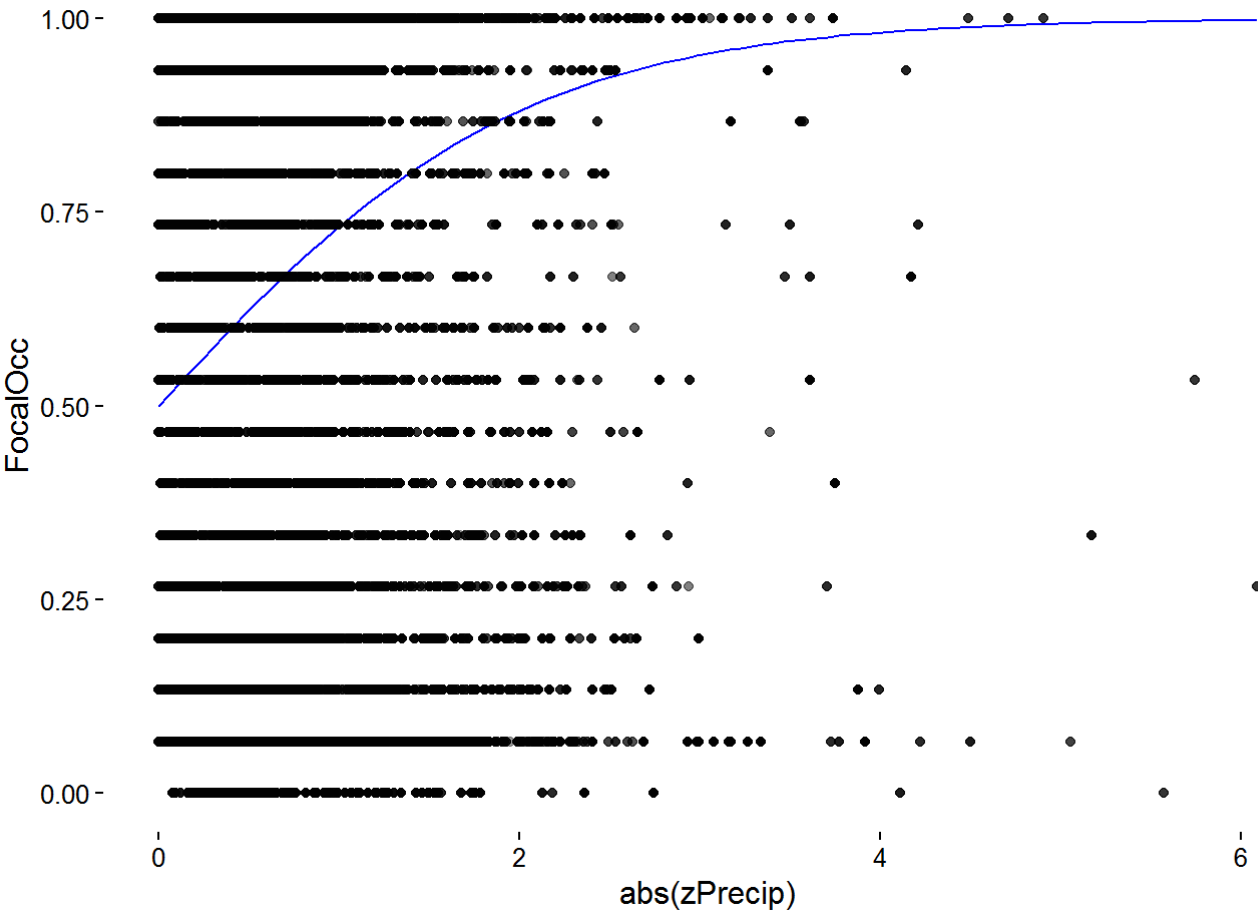


o Table 1

```
## 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) + (1 | stateroute:Species)
## Data: occumatrix
##
##          AIC          BIC      logLik deviance df.resid
## 430324.7 430389.7 -215155.3 430310.7      80105
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -3.0836 -0.6292  0.0326  0.3643  3.6480
##
## Random effects:
## Groups              Name              Variance Std.Dev.
## stateroute:Species (Intercept) 5.327      2.308
## Number of obs: 80112, groups: stateroute:Species, 5530
##
## Fixed effects:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    0.7903637  0.0709383  11.142 < 2e-16 ***
## cs(comp_scaled) -0.7494032  0.0308046 -24.328 < 2e-16 ***
## abs(zTemp)      -0.1250657  0.0507595  -2.464 0.013744 *
## abs(zElev)      -0.0001065  0.0531607  -0.002 0.998401
## abs(zPrecip)    -0.0380579  0.0519444  -0.733 0.463762
## abs(zEVI)       -0.1789163  0.0501221  -3.570 0.000358 ***
## ---
## 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)
## cs(cmp_scl) -0.015
## abs(zTemp)  -0.418  0.011
## abs(zElev)  -0.294  0.000 -0.145
## abs(zPrecp) -0.317  0.000 -0.182 -0.126
## abs(zEVI)   -0.367  0.010  0.031 -0.211 -0.160
```





Traits LM

o Residuals - not symmetrical, so data not fit well by the model

o t-statistic values not far away from zero and are small relative to the standard error, probably no relationship exists

o adjusted R2 adjusts for the number of variables considered - 0.148 env only highest

o Table 2

```
envflip=read.csv("envflip.csv", header = TRUE)
env_lm = subset(envflip, Type == 'ENV')

env_traits = lm(value ~ Trophic.Group + migclass + EW, data = env_lm)
summary(env_traits)
```

```
##
## Call:
## lm(formula = value ~ Trophic.Group + migclass + EW, data = env_lm)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.16898 -0.07031 -0.03246  0.05336  0.24962
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.31415    0.06816   4.609 2.39e-05 ***
## Trophic.Groupinsct/om -0.07272    0.07236  -1.005  0.31924
## Trophic.Groupinsectivore -0.12711    0.06568  -1.935  0.05800 .
## Trophic.Groupomnivore -0.13524    0.09507  -1.423  0.16042
## migclassresid      -0.03977    0.06120  -0.650  0.51851
## migclassshort      -0.03269    0.03205  -1.020  0.31216
## EW                 -0.09319    0.03039  -3.067  0.00333 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1042 on 56 degrees of freedom
## Multiple R-squared:  0.2301, Adjusted R-squared:  0.1476
## F-statistic:  2.79 on 6 and 56 DF,  p-value: 0.01911
```

```
comp_lm = subset(envflip, Type == 'COMP')

comp_traits = lm(value ~ Trophic.Group + migclass + EW, data = comp_lm)
summary(comp_traits)
```

```
##
## Call:
## lm(formula = value ~ Trophic.Group + migclass + EW, data = comp_lm)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.19238 -0.09934 -0.04444  0.05245  0.50394
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.17843    0.09883   1.805  0.0764 .
## Trophic.Groupinsct/om  0.07829    0.10492   0.746  0.4587
## Trophic.Groupinsectivore -0.06594    0.09523  -0.692  0.4915
## Trophic.Groupomnivore  0.02740    0.13785   0.199  0.8431
## migclassresid      -0.08292    0.08874  -0.934  0.3541
## migclassshort      -0.03851    0.04648  -0.829  0.4108
## EW                 0.03418    0.04406   0.776  0.4412
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1511 on 56 degrees of freedom
## Multiple R-squared:  0.1387, Adjusted R-squared:  0.04639
## F-statistic: 1.503 on 6 and 56 DF,  p-value: 0.1942
```

```
env_sum = subset(envflip, Type != 'NONE')
total = env_sum %>%
  group_by(FocalAOU) %>%
  summarise(sum(value))

total_traits = lm(value ~ Trophic.Group + migclass + EW, data = env_sum)
summary(total_traits)
```



```
##
## Call:
## lm(formula = value ~ Trophic.Group + migclass + EW, data = env_sum)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.28964 -0.08054 -0.04458  0.05279  0.51042
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.18890    0.04825   3.915 0.000128 ***
## Trophic.Groupinsct/om -0.02317    0.05123  -0.452 0.651598
## Trophic.Groupinsectivore -0.08289    0.04649  -1.783 0.076271 .
## Trophic.Groupomnivore -0.05718    0.06730  -0.850 0.396677
## migclassresid      -0.04574    0.04333  -1.056 0.292495
## migclassshort      -0.02404    0.02269  -1.059 0.290812
## EW                 -0.01635    0.02151  -0.760 0.448244
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1278 on 182 degrees of freedom
## Multiple R-squared:  0.04428,    Adjusted R-squared:  0.01277
## F-statistic: 1.405 on 6 and 182 DF,  p-value: 0.2147
```

Occupancy and Abundance

o provide unique information about biodiversity (1:1) line - some species occupancy was better predicted than abundance and vice versa

o Figure 3/4

