Summary of AMF community assembly

Aidee Guzman

January 14, 2021

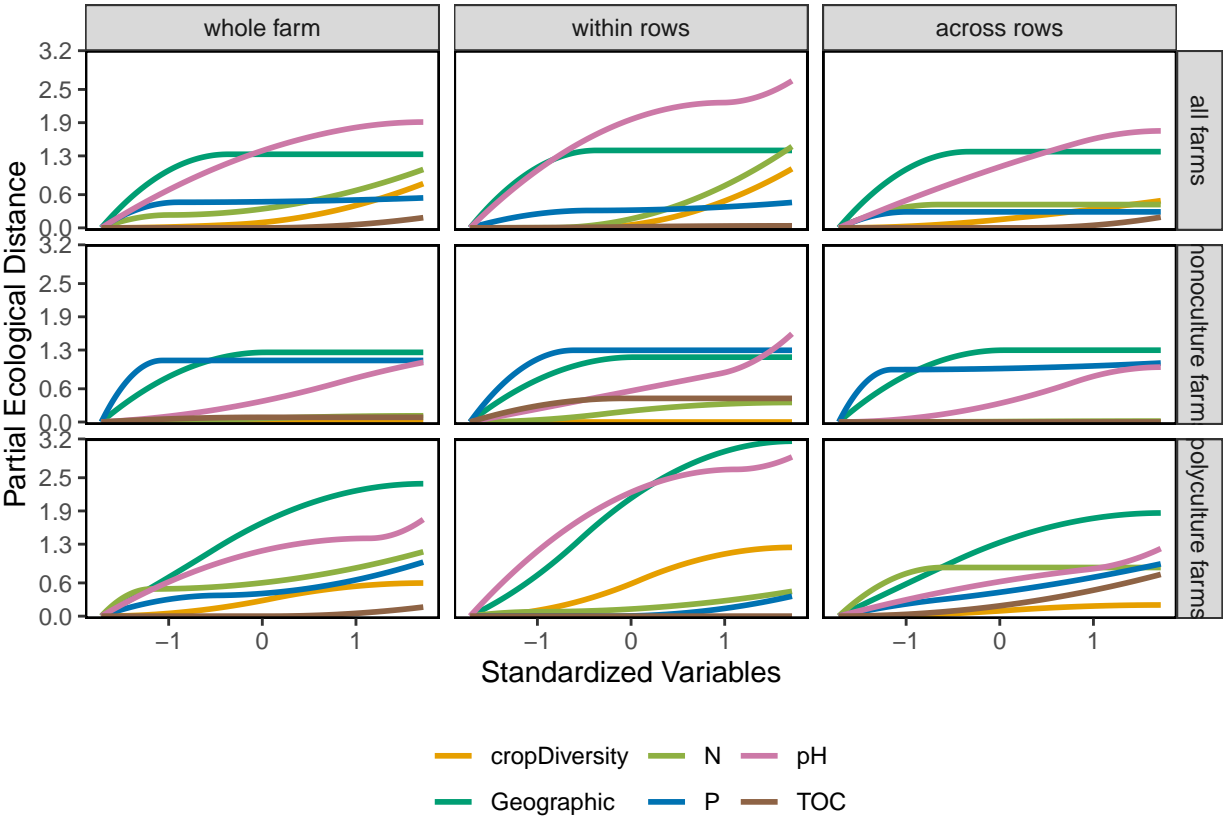## Description of study design

Study design: farm type x block

- 21 sites: 10 monoculture and 11 polyculture
- 2 transects per 2 blocks (within-rows vs across-rows) each site
- 10 = 2017 and 11 =2018

Contents

Drivers of AM compositional dissimilarity

Plots

All farms

Model output

Whole farm

```
##                   Predictors Coefficients
## 1                  Geographic        1.329
## 2                          pH        1.911
## 3                           P        0.542
## 4                         TOC        0.187
## 5                           N        1.066
## 6                cropDiversity        0.810
## 7 Percent Deviance Explained       28.224
## 8                         DIC     2109.035
```

Within-rows

```
##                   Predictors Coefficients
## 1                  Geographic        1.399
## 2                          pH        2.674
## 3                           P        0.461
## 4                         TOC        0.037
## 5                           N        1.490
## 6                cropDiversity        1.083
## 7 Percent Deviance Explained       35.858
## 8                         DIC      501.920
```

Across-rows

```
##                    Predictors Coefficients
## 1                   Geographic        1.376
## 2                           pH        1.751
## 3                            P        0.289
## 4                          TOC        0.197
## 5                            N        0.421
## 6                 cropDiversity        0.494
## 7 Percent Deviance Explained       25.233
## 8                          DIC      511.525
```

Monoculture farms

Model output

Whole farm

```
##                       Predictors Coefficients
## 1                      Geographic        1.258
## 2                              pH        1.083
## 3                               P        1.111
## 4                             TOC        0.085
## 5                               N        0.112
## 6                    cropDiversity        0.000
## 7 Percent Deviance Explained       30.725
## 8                             DIC      632.157
```

Within-rows

```
##                       Predictors Coefficients
## 1                      Geographic        1.171
## 2                              pH        1.620
## 3                               P        1.296
## 4                             TOC        0.427
## 5                               N        0.353
## 6                    cropDiversity        0.000
## 7 Percent Deviance Explained       34.585
## 8                             DIC      155.935
```

Across-rows

```
##                       Predictors Coefficients
## 1                      Geographic        1.297
## 2                              pH        0.991
## 3                               P        1.066
## 4                             TOC        0.000
## 5                               N        0.016
## 6                    cropDiversity        0.000
## 7 Percent Deviance Explained       28.266
## 8                             DIC      144.208
```

Polyculture farms

Model output

Whole farm

```
##                       Predictors Coefficients
## 1                      Geographic        2.392
## 2                              pH        1.767
## 3                               P        0.985
## 4                             TOC        0.167
## 5                               N        1.170
## 6                    cropDiversity        0.598
## 7 Percent Deviance Explained           36.804
## 8                             DIC      539.177
```
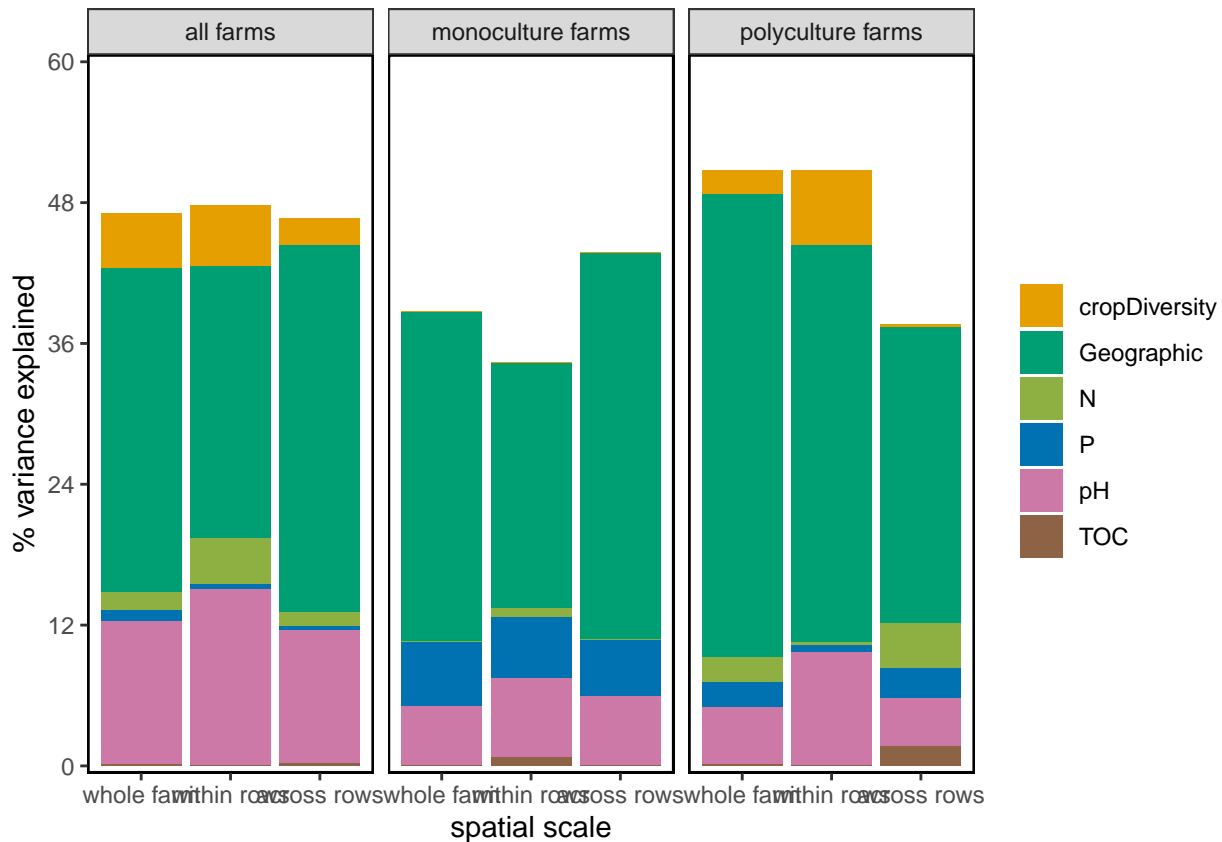
Within-rows

```
##                       Predictors Coefficients
## 1                      Geographic        3.159
## 2                              pH        2.889
## 3                               P        0.366
## 4                             TOC        0.000
## 5                               N        0.453
## 6                    cropDiversity        1.242
## 7 Percent Deviance Explained           49.548
## 8                             DIC      121.025
```

Across-rows

```
##                       Predictors Coefficients
## 1                      Geographic        1.863
## 2                              pH        1.233
## 3                               P        0.950
## 4                             TOC        0.761
## 5                               N        0.878
## 6                    cropDiversity        0.202
## 7 Percent Deviance Explained           33.035
## 8                             DIC      138.996
```

Variance importance

Plots

All farms

```
##       dataset     location      predictor variance pvalue
## 1  all farms   whole farm     Geographic   27.657    0.0
## 2  all farms   whole farm             pH   12.180    0.0
## 3  all farms   whole farm              P    0.990    0.0
## 4  all farms   whole farm            TOC    0.156    0.4
## 5  all farms   whole farm              N    1.474    0.1
## 6  all farms   whole farm  cropDiversity    4.612    0.0
## 7  all farms within rows     Geographic   23.228    0.0
## 8  all farms within rows             pH   15.097    0.0
## 9  all farms within rows              P    0.399    0.0
## 10 all farms within rows            TOC    0.008    0.8
## 11 all farms within rows              N    3.888    0.0
## 12 all farms within rows  cropDiversity    5.127    0.0
## 13 all farms across rows     Geographic   31.317    0.0
## 14 all farms across rows             pH   11.356    0.0
## 15 all farms across rows              P    0.410    0.5
## 16 all farms across rows            TOC    0.210    0.3
## 17 all farms across rows              N    1.122    0.4
## 18 all farms across rows  cropDiversity    2.279    0.0
```

Monoculture farms

```
##                  dataset     location      predictor variance pvalue
## 1  monoculture farms   whole farm     Geographic   28.082    0.0
## 2  monoculture farms   whole farm             pH    5.094    0.0
```

```
## 3  monoculture farms  whole farm           P  5.406  0.0
## 4  monoculture farms  whole farm         TOC  0.030  0.6
## 5  monoculture farms  whole farm           N  0.076  0.5
## 6  monoculture farms  whole farm cropDiversity  0.000  1.0
## 7  monoculture farms within rows    Geographic 20.919  0.0
## 8  monoculture farms within rows          pH  6.793  0.0
## 9  monoculture farms within rows           P  5.229  0.0
## 10 monoculture farms within rows         TOC  0.722  0.4
## 11 monoculture farms within rows           N  0.706  0.4
## 12 monoculture farms within rows cropDiversity  0.000  1.0
## 13 monoculture farms across rows    Geographic 33.025  0.0
## 14 monoculture farms across rows          pH  6.014  0.0
## 15 monoculture farms across rows           P  4.734  0.0
## 16 monoculture farms across rows         TOC  0.000  1.0
## 17 monoculture farms across rows           N  0.002  0.9
## 18 monoculture farms across rows cropDiversity  0.000  1.0
```

Polyculture farms

```
##             dataset    location      predictor variance pvalue
## 1  polyculture farms  whole farm    Geographic 39.497  0.0
## 2  polyculture farms  whole farm          pH  4.883  0.0
## 3  polyculture farms  whole farm           P  2.162  0.0
## 4  polyculture farms  whole farm         TOC  0.133  0.5
## 5  polyculture farms  whole farm           N  2.048  0.0
## 6  polyculture farms  whole farm cropDiversity  2.023  0.0
## 7  polyculture farms within rows    Geographic 33.828  0.0
## 8  polyculture farms within rows          pH  9.718  0.0
## 9  polyculture farms within rows           P  0.584  0.1
## 10 polyculture farms within rows         TOC  0.000  1.0
## 11 polyculture farms within rows           N  0.244  0.3
## 12 polyculture farms within rows cropDiversity  6.370  0.0
## 13 polyculture farms across rows    Geographic 25.263  0.0
## 14 polyculture farms across rows          pH  4.152  0.0
## 15 polyculture farms across rows           P  2.591  0.1
## 16 polyculture farms across rows         TOC  1.681  0.1
## 17 polyculture farms across rows           N  3.752  0.1
## 18 polyculture farms across rows cropDiversity  0.248  0.6
```

Mantel tests

Composition

```
##             Data Species v Crop Diversity Species v Geography Species v pH
## 1           All                 0.206 ***          0.218 ***    0.323 ***
## 2   All across                  0.192 ***          0.233 ***    0.279 ***
## 3   All within                   0.22 ***          0.207 ***    0.365 ***
## 4          Mono                    NA NA            0.244 ***    0.369 ***
## 5  Mono across                    NA NA             0.25 ***    0.317 ***
## 6  Mono within                    NA NA            0.209 ***    0.423 ***
## 7          Poly                    0.01            0.541 ***    0.289 ***
## 8  Poly across                   -0.013            0.464 ***     0.22 **
## 9  Poly within                    0.016              0.6 ***    0.346 ***
##    Species v P Species v N Species v TOC
## 1   0.139 ***       0.019         0.012
## 2    0.084 **      -0.013        -0.023
## 3   0.202 ***       0.028         0.076 *
## 4   0.172 ***     0.102 **          0.01
## 5    0.123 *    0.176 ***         -0.051
## 6   0.202 ***       0.049         0.137 **
## 7   0.218 ***    0.133 ***        0.096 **
## 8   0.209 ***     0.096 *          0.18 **
## 9   0.203 ***      0.087 *         0.022
```

Turnover

```
##             Data Species v Crop Diversity Species v Geography Species v pH
## 1           All                 0.205 ***          0.217 ***    0.275 ***
## 2   All across                  0.205 ***          0.223 ***    0.227 ***
## 3   All within                  0.208 ***          0.213 ***    0.324 ***
## 4          Mono                    NA NA            0.239 ***    0.276 ***
## 5  Mono across                    NA NA            0.228 ***    0.215 ***
## 6  Mono within                    NA NA            0.225 ***    0.351 ***
## 7          Poly                   0.017            0.473 ***    0.276 ***
## 8  Poly across                    0.013            0.414 ***    0.214 ***
## 9  Poly within                    0.005            0.495 ***    0.327 ***
##    Species v P Species v N Species v TOC
## 1   0.131 ***       0.019        -0.012
## 2    0.085 **      -0.013        -0.031
## 3    0.19 ***       0.028         0.025
## 4   0.161 ***     0.102 **        -0.002
## 5     0.09 *    0.176 ***         -0.044
## 6   0.223 ***       0.049         0.079
## 7   0.175 ***    0.133 ***        0.06 *
## 8   0.182 ***     0.096 *        0.158 ***
## 9   0.153 ***      0.087 *        -0.016
```

Nestedness

```
##             Data Species v Crop Diversity Species v Geography Species v pH
## 1           All                -0.151             -0.167        -0.22
## 2   All across                 -0.162             -0.182       -0.178
## 3   All within                 -0.146             -0.158       -0.255
## 4          Mono                   NA NA            -0.133       -0.184
## 5  Mono across                   NA NA            -0.162       -0.141
## 6  Mono within                   NA NA            -0.088       -0.235
## 7          Poly                  0.011             -0.372       -0.216
## 8  Poly across                   0.006              -0.32       -0.152
```
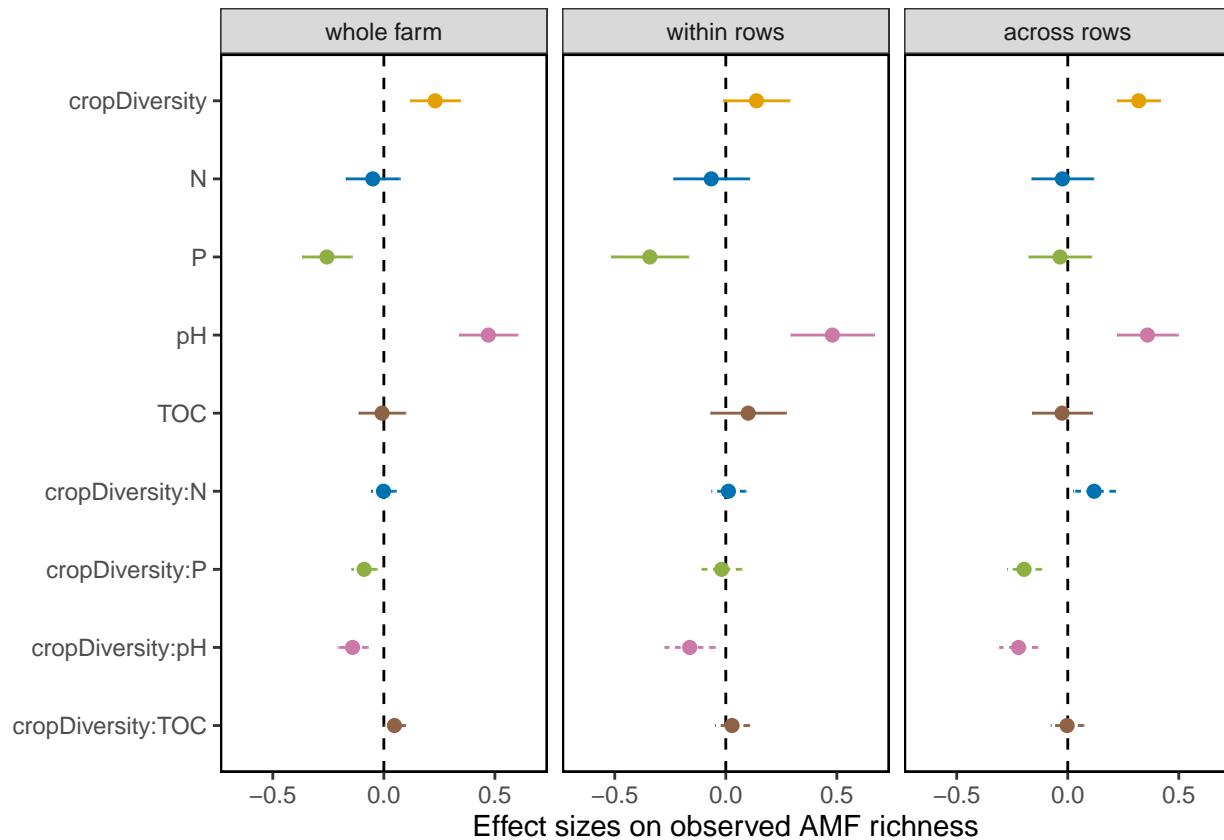
```
## 9 Poly within                      0.037              -0.38       -0.25
##    Species v P Species v N Species v TOC
## 1    -0.113       0.019        0.032
## 2    -0.072      -0.013        0.043
## 3     -0.16       0.028        0.006
## 4    -0.109      0.102 **      0.012
## 5    -0.054      0.176 **      0.031
## 6    -0.144       0.049       -0.039
## 7    -0.124      0.133 ***    -0.021
## 8    -0.106      0.096 *      -0.097
## 9    -0.104      0.087 *       0.041
```

Drivers of AMF alpha diversity

Richness ~ crop diversity

Plots

Whole farm

```
## $model
## glmer(formula = observed ~ cropDiversity * scale(pH) + scale(P) *
##     cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##     (1 | FarmKey:Year), data = all_wa$df, family = MASS::negative.binomial(theta = 8.65005438353719),
##     nAGQ = 1, na.action = na.fail)
##
## $AIC
## [1] 1415.019
##
## $summary
##   response                 covariate Estimate    SE     P sig
## 1 observed              cropDiversity    0.231 0.112 0.039   *
## 2 observed                  scale(pH)    0.470 0.132 0.000 ***
## 3 observed                   scale(P)   -0.256 0.112 0.022   *
## 4 observed                 scale(TOC)   -0.008 0.105 0.938  ns
## 5 observed                   scale(N)   -0.050 0.121 0.681  ns
## 6 observed   cropDiversity:scale(pH)   -0.141 0.068 0.038   *
## 7 observed    cropDiversity:scale(P)   -0.089 0.056 0.116  ns
## 8 observed cropDiversity:scale(TOC)    0.048 0.048 0.324  ns
## 9 observed   cropDiversity:scale(N)   -0.002 0.055 0.976  ns
##
## $Anova
```

```
##   response                    covariate  Chisq     P sig
## 1 observed                 cropDiversity  4.260 0.039   *
## 2 observed                     scale(pH) 12.713 0.000 ***
## 3 observed                      scale(P)  5.274 0.022   *
## 4 observed                    scale(TOC)  0.006 0.938  ns
## 5 observed                      scale(N)  0.169 0.681  ns
## 6 observed   cropDiversity:scale(pH)  4.288 0.038   *
## 7 observed    cropDiversity:scale(P)  2.476 0.116  ns
## 8 observed cropDiversity:scale(TOC)  0.975 0.324  ns
## 9 observed   cropDiversity:scale(N)  0.001 0.976  ns
```

Within-rows

```
## $model
## glmer(formula = observed ~ cropDiversity * scale(pH) + scale(P) *
##     cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##     (1 | FarmKey:Year), data = all_w$df, family = MASS::negative.binomial(theta = 19.7818601106867),
##     nAGQ = 1, na.action = na.fail)
##
## $AIC
## [1] 717.0261
##
## $summary
##   response                    covariate Estimate    SE     P sig
## 1 observed                 cropDiversity    0.138 0.149 0.353  ns
## 2 observed                     scale(pH)    0.480 0.187 0.010  **
## 3 observed                      scale(P)   -0.342 0.174 0.049   *
## 4 observed                    scale(TOC)    0.101 0.170 0.552  ns
## 5 observed                      scale(N)   -0.066 0.170 0.699  ns
## 6 observed   cropDiversity:scale(pH)   -0.162 0.113 0.150  ns
## 7 observed    cropDiversity:scale(P)   -0.019 0.089 0.833  ns
## 8 observed cropDiversity:scale(TOC)    0.028 0.077 0.715  ns
## 9 observed   cropDiversity:scale(N)    0.012 0.077 0.878  ns
##
## $Anova
##   response                    covariate Chisq     P sig
## 1 observed                 cropDiversity 0.864 0.353  ns
## 2 observed                     scale(pH) 6.558 0.010  **
## 3 observed                      scale(P) 3.879 0.049   *
## 4 observed                    scale(TOC) 0.354 0.552  ns
## 5 observed                      scale(N) 0.149 0.699  ns
## 6 observed   cropDiversity:scale(pH) 2.073 0.150  ns
## 7 observed    cropDiversity:scale(P) 0.044 0.833  ns
## 8 observed cropDiversity:scale(TOC) 0.133 0.715  ns
## 9 observed   cropDiversity:scale(N) 0.024 0.878  ns
```
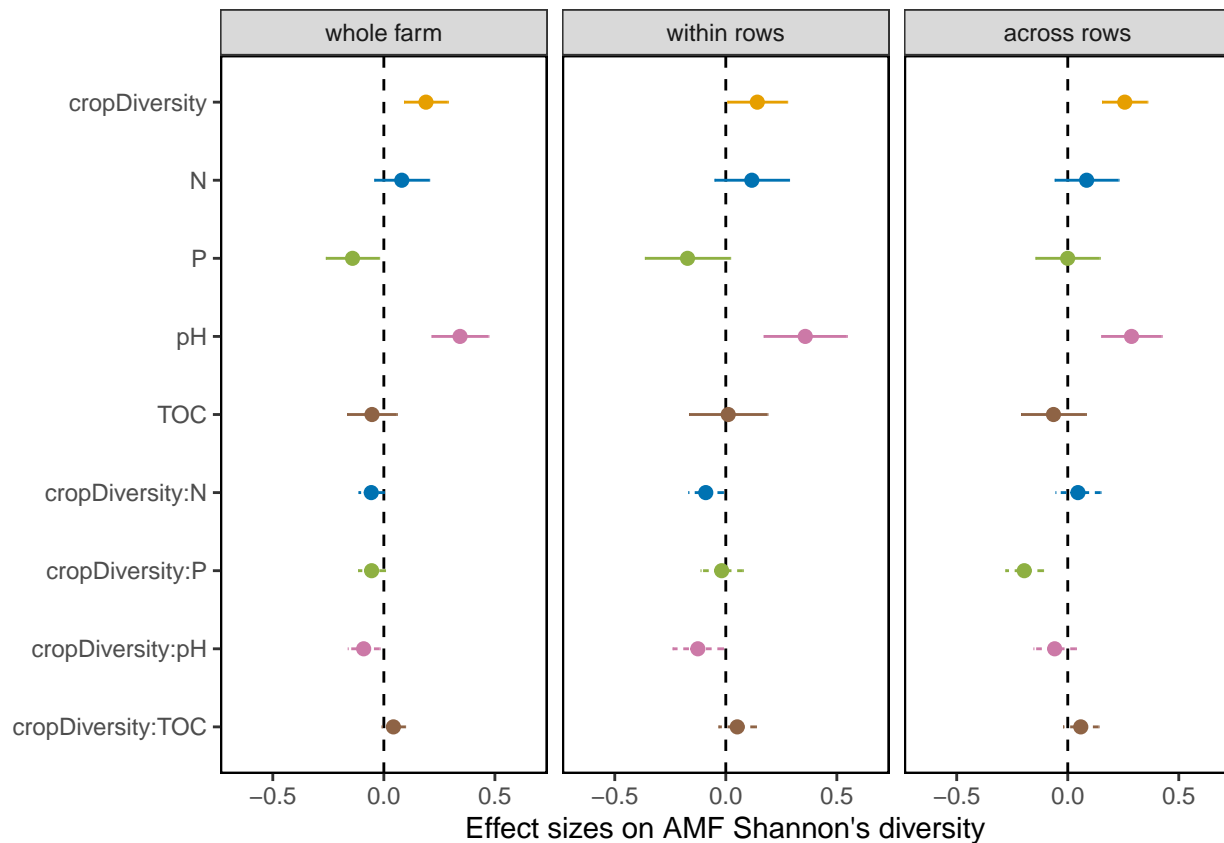
Across-rows

```
## $model
## glmer(formula = observed ~ cropDiversity * scale(pH) + scale(P) *
##     cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##     (1 | FarmKey:Year), data = all_a$df, family = MASS::negative.binomial(theta = 6.07236915915643),
##     nAGQ = 1, na.action = na.fail)
##
## $AIC
## [1] 729.5035
##
## $summary
```

```
##   response                    covariate Estimate    SE     P sig
## 1 observed                 cropDiversity    0.319 0.096 0.001 ***
## 2 observed                     scale(pH)    0.359 0.137 0.009  **
## 3 observed                      scale(P)   -0.035 0.141 0.806  ns
## 4 observed                    scale(TOC)   -0.026 0.135 0.849  ns
## 5 observed                      scale(N)   -0.024 0.139 0.863  ns
## 6 observed     cropDiversity:scale(pH)    -0.222 0.086 0.010  **
## 7 observed      cropDiversity:scale(P)    -0.197 0.077 0.011   *
## 8 observed    cropDiversity:scale(TOC)    -0.003 0.074 0.968  ns
## 9 observed      cropDiversity:scale(N)     0.119 0.094 0.208  ns
##
## $Anova
##   response                    covariate  Chisq     P sig
## 1 observed                 cropDiversity 10.968 0.001 ***
## 2 observed                     scale(pH)  6.894 0.009  **
## 3 observed                      scale(P)  0.060 0.806  ns
## 4 observed                    scale(TOC)  0.036 0.849  ns
## 5 observed                      scale(N)  0.030 0.863  ns
## 6 observed     cropDiversity:scale(pH)   6.630 0.010  **
## 7 observed      cropDiversity:scale(P)   6.522 0.011   *
## 8 observed    cropDiversity:scale(TOC)   0.002 0.968  ns
## 9 observed      cropDiversity:scale(N)   1.583 0.208  ns
```

Shannon ~ crop diversity

Plots

Whole farm

```
## $model
```

```
## lmer(formula = shannon ~ cropDiversity * scale(pH) + scale(P) *
##     cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##     (1 | FarmKey:Year), data = all_wa$df, na.action = na.exclude)
##
## $AIC
## [1] 427.6784
##
## $summary
##   response               covariate Estimate    SE     P sig
## 1  shannon            cropDiversity    0.190 0.099 0.070  ns
## 2  shannon                scale(pH)    0.343 0.128 0.009  **
## 3  shannon                 scale(P)   -0.141 0.120 0.241  ns
## 4  shannon               scale(TOC)   -0.053 0.112 0.633  ns
## 5  shannon                 scale(N)    0.081 0.123 0.514  ns
## 6  shannon  cropDiversity:scale(pH)   -0.091 0.072 0.209  ns
## 7  shannon   cropDiversity:scale(P)   -0.055 0.060 0.362  ns
## 8  shannon cropDiversity:scale(TOC)    0.043 0.053 0.416  ns
## 9  shannon   cropDiversity:scale(N)   -0.057 0.057 0.319  ns
##
## $Anova
##   response               covariate Chisq     P sig
## 1  shannon            cropDiversity 3.707 0.054  ns
## 2  shannon                scale(pH) 7.203 0.007  **
## 3  shannon                 scale(P) 1.383 0.240  ns
## 4  shannon               scale(TOC) 0.228 0.633  ns
## 5  shannon                 scale(N) 0.428 0.513  ns
## 6  shannon  cropDiversity:scale(pH) 1.598 0.206  ns
## 7  shannon   cropDiversity:scale(P) 0.834 0.361  ns
## 8  shannon cropDiversity:scale(TOC) 0.664 0.415  ns
## 9  shannon   cropDiversity:scale(N) 0.997 0.318  ns
```

Within-rows

```
## $model
## lmer(formula = shannon ~ cropDiversity * scale(pH) + scale(P) *
##     cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##     (1 | FarmKey:Year), data = all_w$df, na.action = na.exclude)
##
## $AIC
## [1] 224.9064
##
## $summary
##   response               covariate Estimate    SE     P sig
## 1  shannon            cropDiversity    0.142 0.135 0.307  ns
## 2  shannon                scale(pH)    0.358 0.187 0.061  ns
## 3  shannon                 scale(P)   -0.172 0.192 0.372  ns
## 4  shannon               scale(TOC)    0.011 0.177 0.951  ns
## 5  shannon                 scale(N)    0.117 0.168 0.486  ns
## 6  shannon  cropDiversity:scale(pH)   -0.126 0.113 0.273  ns
## 7  shannon   cropDiversity:scale(P)   -0.019 0.095 0.845  ns
## 8  shannon cropDiversity:scale(TOC)    0.051 0.084 0.543  ns
## 9  shannon   cropDiversity:scale(N)   -0.090 0.078 0.251  ns
##
## $Anova
##   response               covariate Chisq     P sig
## 1  shannon            cropDiversity 1.111 0.292  ns
## 2  shannon                scale(pH) 3.660 0.056  ns
```

```
## 3    shannon                    scale(P) 0.806 0.369  ns
## 4    shannon                  scale(TOC) 0.004 0.951  ns
## 5    shannon                    scale(N) 0.488 0.485  ns
## 6    shannon  cropDiversity:scale(pH) 1.235 0.267  ns
## 7    shannon   cropDiversity:scale(P) 0.038 0.845  ns
## 8    shannon cropDiversity:scale(TOC) 0.373 0.542  ns
## 9    shannon   cropDiversity:scale(N) 1.334 0.248  ns
```

Across-rows

```
## $model
## lmer(formula = shannon ~ cropDiversity * scale(pH) + scale(P) *
##     cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##     (1 | FarmKey:Year), data = all_a$df, na.action = na.exclude)
##
## $AIC
## [1] 249.4365
##
## $summary
##    response                  covariate Estimate    SE      P sig
## 1    shannon              cropDiversity    0.257 0.102 0.024   *
## 2    shannon                   scale(pH)    0.287 0.136 0.046   *
## 3    shannon                    scale(P)    0.000 0.145 0.998  ns
## 4    shannon                  scale(TOC)   -0.064 0.146 0.662  ns
## 5    shannon                    scale(N)    0.085 0.144 0.560  ns
## 6    shannon  cropDiversity:scale(pH)   -0.059 0.096 0.541  ns
## 7    shannon   cropDiversity:scale(P)   -0.196 0.085 0.026   *
## 8    shannon cropDiversity:scale(TOC)    0.059 0.080 0.467  ns
## 9    shannon   cropDiversity:scale(N)    0.046 0.102 0.655  ns
##
## $Anova
##    response                  covariate Chisq      P sig
## 1    shannon              cropDiversity 6.345 0.012   *
## 2    shannon                   scale(pH) 4.459 0.035   *
## 3    shannon                    scale(P) 0.000 0.998  ns
## 4    shannon                  scale(TOC) 0.193 0.660  ns
## 5    shannon                    scale(N) 0.351 0.554  ns
## 6    shannon  cropDiversity:scale(pH) 0.379 0.538  ns
## 7    shannon   cropDiversity:scale(P) 5.349 0.021   *
## 8    shannon cropDiversity:scale(TOC) 0.537 0.464  ns
## 9    shannon   cropDiversity:scale(N) 0.205 0.651  ns
```

Richness ~ farm type

Plots
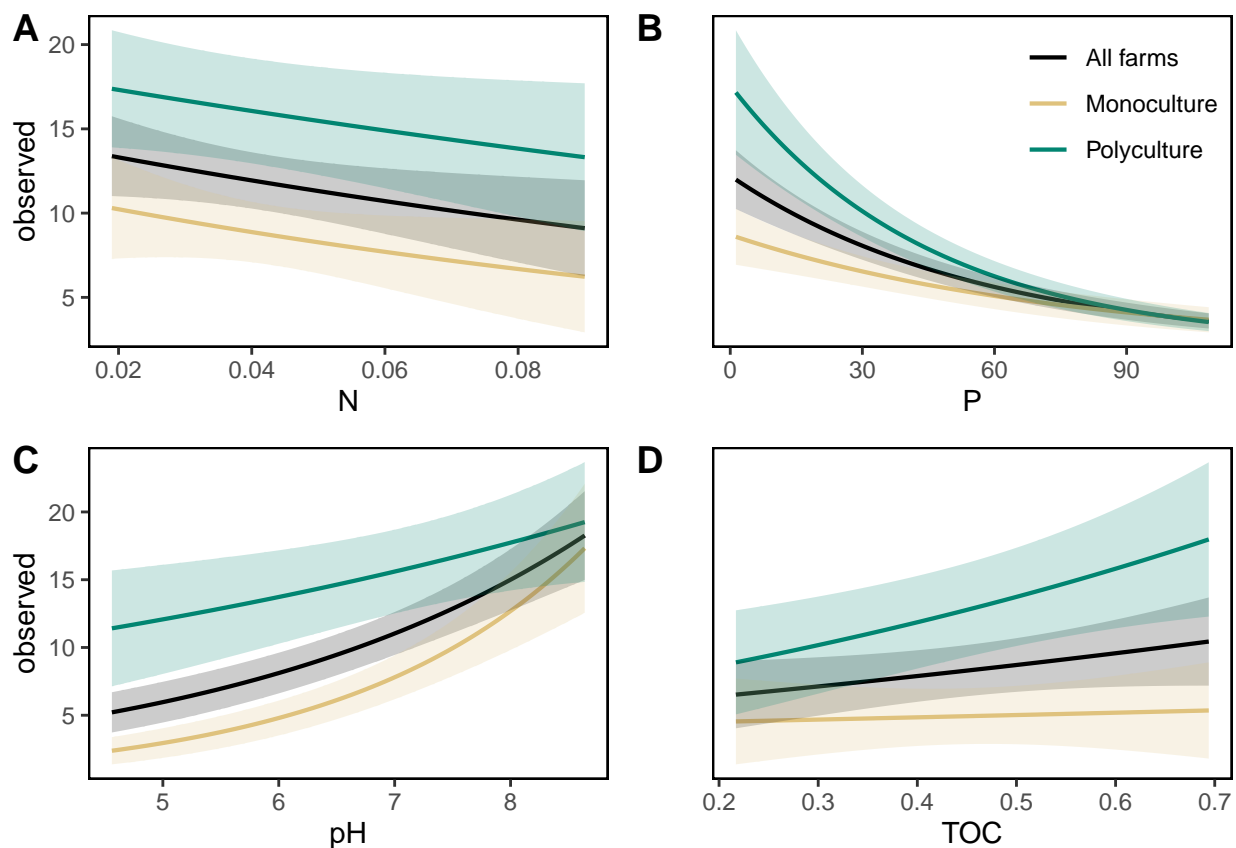
Whole farm

```
## $model
## glmer(formula = observed ~ FarmType * scale(pH) + scale(P) *
##     FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
##     (1 | FarmKey:Year), data = all_wa$df, family = MASS::negative.binomial(theta = 8.62627505625531),
##     nAGQ = 1, na.action = na.fail)
##
## $AIC
## [1] 1414.883
##
## $summary
##   response                       covariate Estimate    SE     P sig
## 1 observed           FarmTypePolyculture    0.584 0.280 0.037   *
## 2 observed                     scale(pH)    0.482 0.134 0.000 ***
## 3 observed                      scale(P)   -0.278 0.115 0.016   *
## 4 observed                    scale(TOC)    0.017 0.109 0.879  ns
## 5 observed                      scale(N)   -0.090 0.126 0.473  ns
## 6 observed  FarmTypePolyculture:scale(pH)  -0.355 0.171 0.038   *
## 7 observed   FarmTypePolyculture:scale(P)  -0.182 0.150 0.225  ns
## 8 observed FarmTypePolyculture:scale(TOC)   0.088 0.132 0.506  ns
## 9 observed   FarmTypePolyculture:scale(N)   0.043 0.139 0.759  ns
##
## $Anova
##   response      covariate  Chisq     P sig
## 1 observed       FarmType  4.364 0.037   *
## 2 observed      scale(pH) 12.867 0.000 ***
## 3 observed       scale(P)  5.842 0.016   *
## 4 observed     scale(TOC)  0.023 0.879  ns
## 5 observed       scale(N)  0.515 0.473  ns
```

```
## 6 observed    FarmType:scale(pH)   4.298 0.038    *
## 7 observed     FarmType:scale(P)   1.469 0.225   ns
## 8 observed FarmType:scale(TOC)   0.441 0.506   ns
## 9 observed     FarmType:scale(N)   0.094 0.759   ns
```

Within-rows

```
## $model
## glmer(formula = observed ~ FarmType * scale(pH) + scale(P) *
##     FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
##     (1 | FarmKey:Year), data = all_w$df, family = MASS::negative.binomial(theta = 19.901483453616),
##     nAGQ = 1, na.action = na.fail)
##
## $AIC
## [1] 716.1875
##
## $summary
##   response                           covariate Estimate    SE     P sig
## 1 observed               FarmTypePolyculture    0.465 0.362 0.199  ns
## 2 observed                         scale(pH)    0.490 0.191 0.010  **
## 3 observed                          scale(P)   -0.354 0.179 0.047   *
## 4 observed                        scale(TOC)    0.143 0.179 0.426  ns
## 5 observed                          scale(N)   -0.107 0.177 0.545  ns
## 6 observed  FarmTypePolyculture:scale(pH)     -0.452 0.289 0.118  ns
## 7 observed   FarmTypePolyculture:scale(P)     -0.022 0.234 0.924  ns
## 8 observed FarmTypePolyculture:scale(TOC)     0.010 0.201 0.961  ns
## 9 observed   FarmTypePolyculture:scale(N)      0.077 0.189 0.685  ns
##
## $Anova
##   response             covariate Chisq     P sig
## 1 observed               FarmType 1.651 0.199  ns
## 2 observed             scale(pH) 6.611 0.010  **
## 3 observed              scale(P) 3.929 0.047   *
## 4 observed            scale(TOC) 0.635 0.426  ns
## 5 observed              scale(N) 0.367 0.545  ns
## 6 observed  FarmType:scale(pH) 2.445 0.118  ns
## 7 observed   FarmType:scale(P) 0.009 0.924  ns
## 8 observed FarmType:scale(TOC) 0.002 0.961  ns
## 9 observed   FarmType:scale(N) 0.164 0.685  ns
```
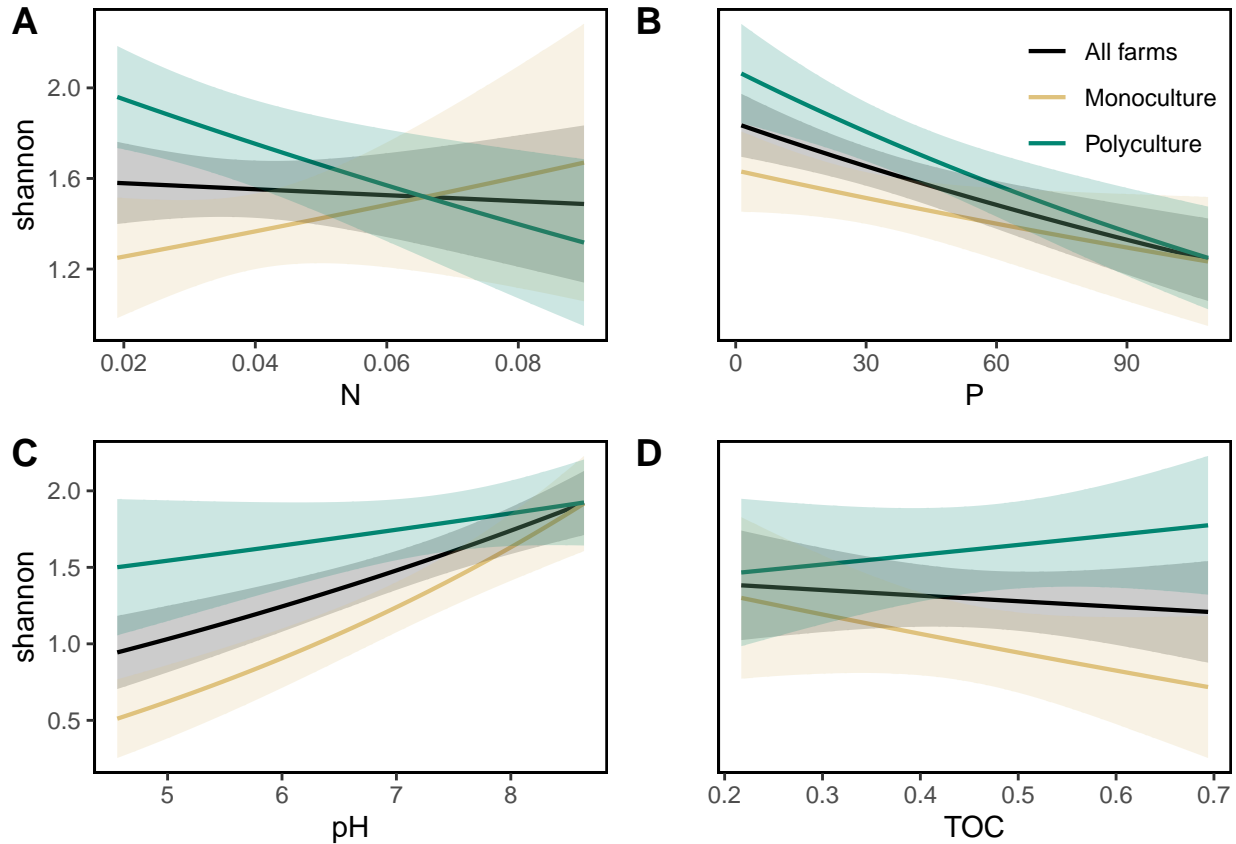
Across-rows

```
## $model
## glmer(formula = observed ~ FarmType * scale(pH) + scale(P) *
##     FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
##     (1 | FarmKey:Year), data = all_a$df, family = MASS::negative.binomial(theta = 5.93197226682143),
##     nAGQ = 1, na.action = na.fail)
##
## $AIC
## [1] 728.933
##
## $summary
##   response                           covariate Estimate    SE     P sig
## 1 observed               FarmTypePolyculture    0.739 0.225 0.001 ***
## 2 observed                         scale(pH)    0.357 0.137 0.009  **
## 3 observed                          scale(P)   -0.010 0.143 0.946  ns
## 4 observed                        scale(TOC)   -0.045 0.139 0.748  ns
## 5 observed                          scale(N)   -0.014 0.138 0.922  ns
```

```
## 6 observed   FarmTypePolyculture:scale(pH)  -0.584 0.215 0.007  **
## 7 observed    FarmTypePolyculture:scale(P)   -0.482 0.199 0.015   *
## 8 observed FarmTypePolyculture:scale(TOC)   -0.009 0.193 0.961  ns
## 9 observed    FarmTypePolyculture:scale(N)    0.289 0.243 0.234  ns
##
## $Anova
##   response              covariate  Chisq      P sig
## 1 observed                FarmType 10.779 0.001 ***
## 2 observed               scale(pH)  6.758 0.009  **
## 3 observed                scale(P)  0.005 0.946  ns
## 4 observed              scale(TOC)  0.103 0.748  ns
## 5 observed                scale(N)  0.010 0.922  ns
## 6 observed      FarmType:scale(pH)  7.357 0.007  **
## 7 observed       FarmType:scale(P)  5.867 0.015   *
## 8 observed     FarmType:scale(TOC)  0.002 0.961  ns
## 9 observed       FarmType:scale(N)  1.413 0.234  ns
```

Shannon ~ farm type

Plots

Whole farm

```
## $model
## lmer(formula = log(shannon + 1) ~ FarmType * scale(pH) + scale(P) *
##     FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
##     (1 | FarmKey:Year), data = all_wa$df, na.action = na.exclude)
##
## $AIC
## [1] 77.06143
```

```
## 
## $summary
##          response                           covariate Estimate   SE     P sig
## 1 log(shannon + 1)              FarmTypePolyculture    0.167 0.099 0.111  ns
## 2 log(shannon + 1)                        scale(pH)    0.160 0.055 0.005  **
## 3 log(shannon + 1)                         scale(P)   -0.051 0.053 0.333  ns
## 4 log(shannon + 1)                       scale(TOC)   -0.035 0.050 0.488  ns
## 5 log(shannon + 1)                         scale(N)    0.031 0.055 0.575  ns
## 6 log(shannon + 1)  FarmTypePolyculture:scale(pH)    -0.122 0.078 0.120  ns
## 7 log(shannon + 1)   FarmTypePolyculture:scale(P)    -0.042 0.069 0.548  ns
## 8 log(shannon + 1) FarmTypePolyculture:scale(TOC)    0.051 0.062 0.420  ns
## 9 log(shannon + 1)   FarmTypePolyculture:scale(N)   -0.075 0.063 0.240  ns
## 
## $Anova
##          response        covariate Chisq     P sig
## 1 log(shannon + 1)           FarmType 2.838 0.092  ns
## 2 log(shannon + 1)          scale(pH) 8.499 0.004  **
## 3 log(shannon + 1)           scale(P) 0.944 0.331  ns
## 4 log(shannon + 1)         scale(TOC) 0.482 0.488  ns
## 5 log(shannon + 1)           scale(N) 0.315 0.574  ns
## 6 log(shannon + 1)  FarmType:scale(pH) 2.467 0.116  ns
## 7 log(shannon + 1)   FarmType:scale(P) 0.364 0.547  ns
## 8 log(shannon + 1) FarmType:scale(TOC) 0.653 0.419  ns
## 9 log(shannon + 1)   FarmType:scale(N) 1.394 0.238  ns
```

Within-rows

```
## $model
## lmer(formula = log(shannon + 1) ~ FarmType * scale(pH) + scale(P) *
##     FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
##     (1 | FarmKey:Year), data = all_w$df, na.action = na.exclude)
## 
## $AIC
## [1] 59.52043
## 
## $summary
##          response                           covariate Estimate   SE     P sig
## 1 log(shannon + 1)              FarmTypePolyculture    0.172 0.136 0.226  ns
## 2 log(shannon + 1)                        scale(pH)    0.147 0.083 0.082  ns
## 3 log(shannon + 1)                         scale(P)   -0.048 0.088 0.586  ns
## 4 log(shannon + 1)                       scale(TOC)   -0.026 0.084 0.755  ns
## 5 log(shannon + 1)                         scale(N)    0.069 0.078 0.378  ns
## 6 log(shannon + 1)  FarmTypePolyculture:scale(pH)    -0.169 0.128 0.195  ns
## 7 log(shannon + 1)   FarmTypePolyculture:scale(P)    -0.046 0.112 0.683  ns
## 8 log(shannon + 1) FarmTypePolyculture:scale(TOC)    0.057 0.100 0.573  ns
## 9 log(shannon + 1)   FarmTypePolyculture:scale(N)   -0.127 0.089 0.159  ns
## 
## $Anova
##          response        covariate Chisq     P sig
## 1 log(shannon + 1)           FarmType 1.596 0.207  ns
## 2 log(shannon + 1)          scale(pH) 3.169 0.075  ns
## 3 log(shannon + 1)           scale(P) 0.299 0.584  ns
## 4 log(shannon + 1)         scale(TOC) 0.098 0.754  ns
## 5 log(shannon + 1)           scale(N) 0.786 0.375  ns
## 6 log(shannon + 1)  FarmType:scale(pH) 1.747 0.186  ns
## 7 log(shannon + 1)   FarmType:scale(P) 0.168 0.682  ns
## 8 log(shannon + 1) FarmType:scale(TOC) 0.319 0.572  ns
```

```
## 9 log(shannon + 1)    FarmType:scale(N) 2.015 0.156  ns
```

Across-rows

```
## $model
## lmer(formula = log(shannon + 1) ~ FarmType * scale(pH) + scale(P) *
##     FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
##     (1 | FarmKey:Year), data = all_a$df, na.action = na.exclude)
##
## $AIC
## [1] 70.73671
##
## $summary
##           response                      covariate Estimate    SE     P sig
## 1 log(shannon + 1)            FarmTypePolyculture    0.173 0.095 0.088  ns
## 2 log(shannon + 1)                       scale(pH)    0.142 0.054 0.017   *
## 3 log(shannon + 1)                        scale(P)    0.003 0.058 0.953  ns
## 4 log(shannon + 1)                      scale(TOC)   -0.061 0.061 0.326  ns
## 5 log(shannon + 1)                        scale(N)    0.022 0.057 0.706  ns
## 6 log(shannon + 1)  FarmTypePolyculture:scale(pH)   -0.129 0.098 0.197  ns
## 7 log(shannon + 1)   FarmTypePolyculture:scale(P)   -0.140 0.089 0.125  ns
## 8 log(shannon + 1) FarmTypePolyculture:scale(TOC)    0.081 0.086 0.352  ns
## 9 log(shannon + 1)   FarmTypePolyculture:scale(N)    0.047 0.106 0.665  ns
##
## $Anova
##           response            covariate Chisq     P sig
## 1 log(shannon + 1)             FarmType 3.356 0.067  ns
## 2 log(shannon + 1)            scale(pH) 6.836 0.009  **
## 3 log(shannon + 1)             scale(P) 0.003 0.953  ns
## 4 log(shannon + 1)           scale(TOC) 0.984 0.321  ns
## 5 log(shannon + 1)             scale(N) 0.147 0.702  ns
## 6 log(shannon + 1)  FarmType:scale(pH) 1.714 0.191  ns
## 7 log(shannon + 1)   FarmType:scale(P) 2.482 0.115  ns
## 8 log(shannon + 1) FarmType:scale(TOC) 0.887 0.346  ns
## 9 log(shannon + 1)   FarmType:scale(N) 0.192 0.661  ns
```
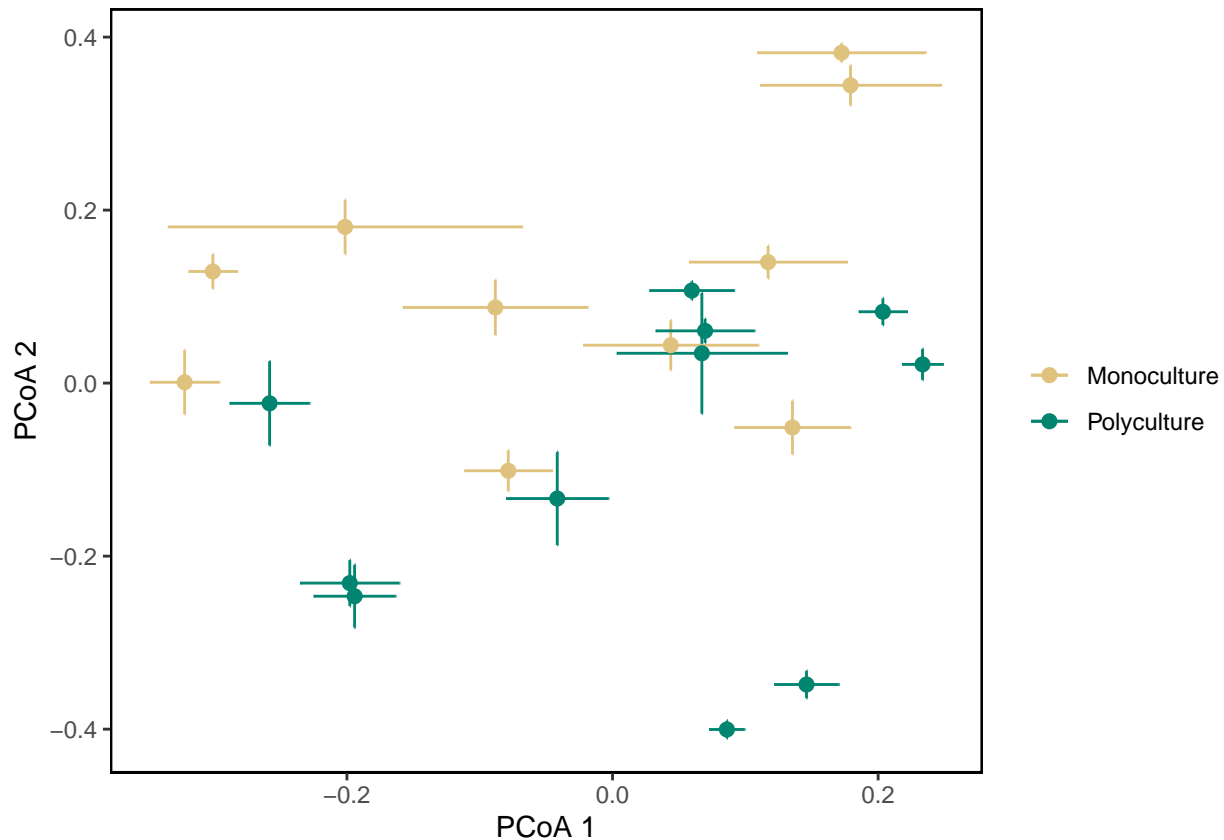
AMF compositional differences between farm type

Plots

Model output

```
## 
## Call:
## adonis(formula = finalFormula, data = permanovaDF, strata = permanovaDF$strata)
## 
## Blocks:  strata
## Permutation: free
## Number of permutations: 999
## 
## Terms added sequentially (first to last)
## 
##                Df SumsOfSqs MeanSqs F.Model      R2 Pr(>F)
## cropDiversity   1     5.268  5.2681 16.0011 0.06285  0.009 **
## P               1     2.253  2.2532  6.8437 0.02688  0.001 ***
## N               1     1.935  1.9353  5.8782 0.02309  0.651
## pH              1     4.092  4.0923 12.4297 0.04882  0.008 **
## TOC             1     1.138  1.1379  3.4564 0.01358  0.418
## Residuals     210    69.139  0.3292         0.82479
## Total         215    83.826                 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Edaphic variables ~ crop diversity

Plots
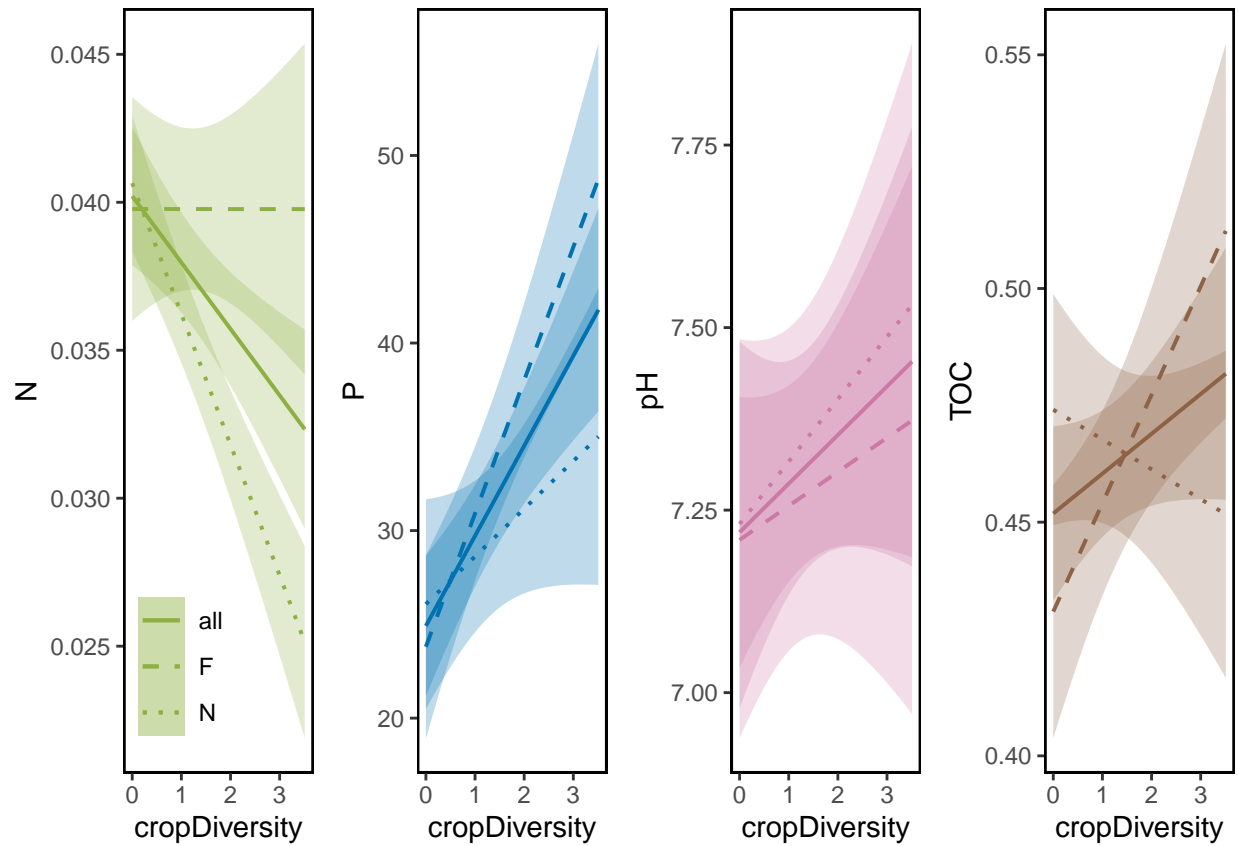
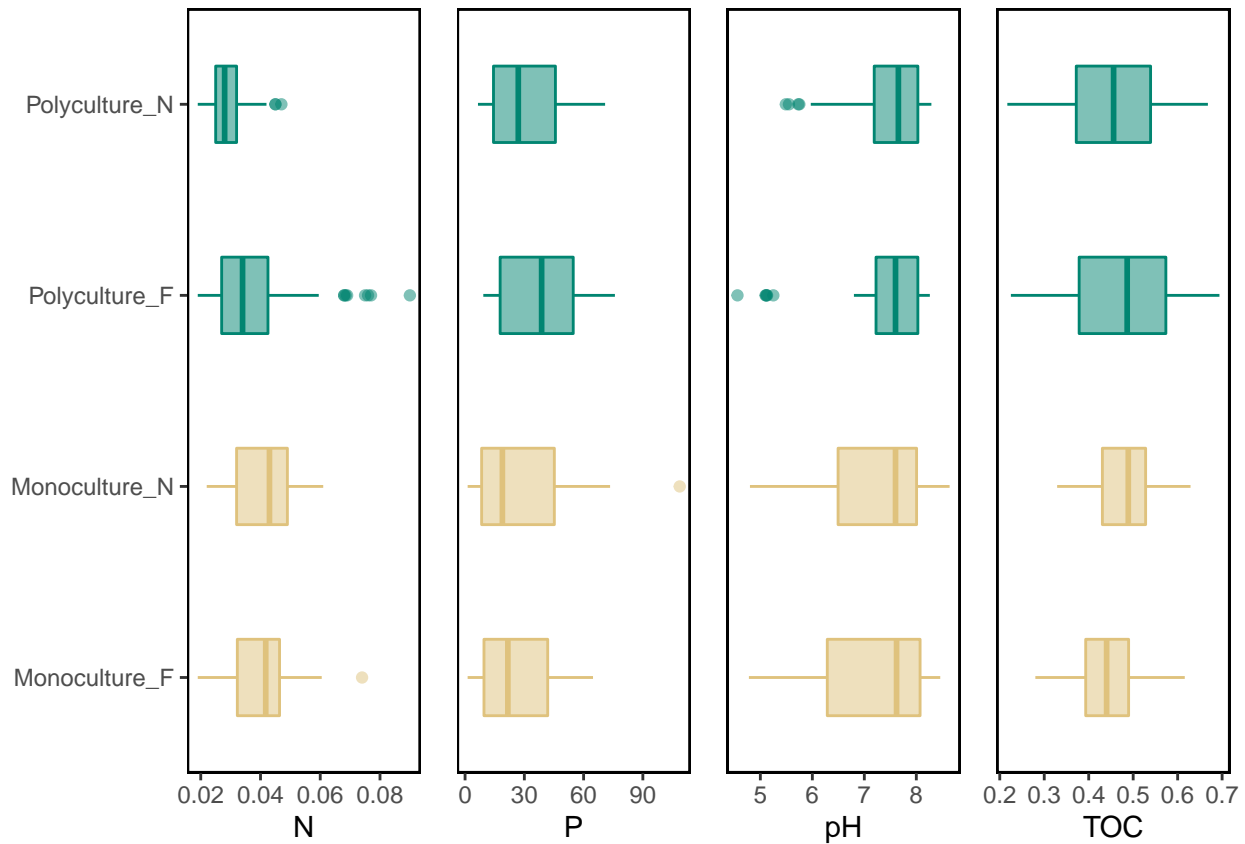**Model output**

```
## $pH
##    response            covariate Estimate    SE     P sig
## 1 scale(pH)         cropDiversity    0.057 0.162 0.729  ns
## 2 scale(pH)                BlockN    0.051 0.066 0.438  ns
## 3 scale(pH) cropDiversity:BlockN    0.014 0.037 0.709  ns
##
## $P
##    response            covariate Estimate    SE     P sig
## 1 scale(P)          cropDiversity    0.356 0.148 0.026   *
## 2 scale(P)                 BlockN    0.147 0.088 0.096  ns
## 3 scale(P) cropDiversity:BlockN    -0.252 0.049 0.000 ***
##
## $TOC
##     response            covariate Estimate    SE     P sig
## 1 scale(TOC)        cropDiversity    0.239 0.146 0.118  ns
## 2 scale(TOC)               BlockN    0.469 0.117 0.000 ***
## 3 scale(TOC) cropDiversity:BlockN   -0.322 0.065 0.000 ***
##
## $N
##    response            covariate Estimate    SE     P sig
## 1 scale(N)          cropDiversity    0.024 0.129 0.852  ns
## 2 scale(N)                 BlockN    0.078 0.131 0.550  ns
## 3 scale(N) cropDiversity:BlockN    -0.371 0.073 0.000 ***
```

Edaphic variables ~ farm type

Plots

Model output

```
## $pH
##     response              covariate Estimate    SE     P sig
## 1 scale(pH)      FarmTypePolyculture    0.233 0.408 0.575  ns
## 2 scale(pH)                   BlockN    0.084 0.068 0.214  ns
## 3 scale(pH) FarmTypePolyculture:BlockN  -0.030 0.094 0.747  ns
##
## $P
##   response                covariate Estimate    SE     P sig
## 1 scale(P)       FarmTypePolyculture    0.630 0.391 0.122  ns
## 2 scale(P)                    BlockN    0.137 0.091 0.136  ns
## 3 scale(P) FarmTypePolyculture:BlockN  -0.594 0.127 0.000 ***
##
## $TOC
##     response               covariate Estimate    SE     P sig
## 1 scale(TOC)      FarmTypePolyculture    0.354 0.373 0.353  ns
## 2 scale(TOC)                   BlockN    0.409 0.122 0.001 ***
## 3 scale(TOC) FarmTypePolyculture:BlockN  -0.668 0.171 0.000 ***
##
## $N
##   response                covariate Estimate    SE     P sig
## 1 scale(N)       FarmTypePolyculture   -0.096 0.320 0.766  ns
## 2 scale(N)                    BlockN    0.051 0.136 0.705  ns
## 3 scale(N) FarmTypePolyculture:BlockN  -0.854 0.189 0.000 ***
```

mean +/- SE

```
##       FarmType Block      variable    mean    SE    min     max
## 1  Monoculture     - cropDiversity   0.000 0.000 0.000   0.000
## 2  Polyculture     - cropDiversity   2.444 0.050 1.242   3.511
## 3  Monoculture     -             N   0.041 0.001 0.019   0.074
## 4  Polyculture     -             N   0.034 0.001 0.019   0.090
## 5  Monoculture     -      observed  10.905 0.668 1.000  27.000
## 6  Polyculture     -      observed  19.099 1.443 1.000  68.000
## 7  Monoculture     -             P  27.171 2.100 1.283 108.662
## 8  Polyculture     -             P  34.519 1.867 6.527  75.843
## 9  Monoculture     -            pH   7.175 0.110 4.780   8.640
## 10 Polyculture     -            pH   7.425 0.078 4.560   8.290
## 11 Monoculture     -       shannon   1.483 0.063 0.000   2.804
## 12 Polyculture     -       shannon   1.874 0.075 0.000   3.551
## 13 Monoculture     -           TOC   0.463 0.007 0.280   0.629
## 14 Polyculture     -           TOC   0.462 0.011 0.217   0.694
## 15                 F cropDiversity   1.226 0.122 0.000   3.511
## 16                 N cropDiversity   1.286 0.124 0.000   3.511
## 17               - F             N   0.040 0.001 0.019   0.090
## 18               - N             N   0.035 0.001 0.019   0.061
## 19               - F      observed  15.642 1.245 1.000  60.000
## 20               - N      observed  14.579 1.172 1.000  68.000
## 21               - F             P  32.516 1.986 1.283  75.843
## 22               - N             P  29.348 2.027 1.297 108.662
## 23               - F            pH   7.266 0.100 4.560   8.460
## 24               - N            pH   7.341 0.091 4.800   8.640
## 25               - F       shannon   1.714 0.075 0.000   3.377
## 26               - N       shannon   1.652 0.068 0.000   3.551
## 27               - F           TOC   0.459 0.010 0.225   0.694
## 28               - N           TOC   0.466 0.009 0.217   0.668
## 29 Monoculture     F cropDiversity   0.000 0.000 0.000   0.000
## 30 Monoculture     N cropDiversity   0.000 0.000 0.000   0.000
## 31 Polyculture     F cropDiversity   2.430 0.073 1.242   3.511
## 32 Polyculture     N cropDiversity   2.457 0.068 1.242   3.511
## 33 Monoculture     F             N   0.041 0.002 0.019   0.074
## 34 Monoculture     N             N   0.041 0.001 0.022   0.061
## 35 Polyculture     F             N   0.039 0.002 0.019   0.090
## 36 Polyculture     N             N   0.029 0.001 0.019   0.047
## 37 Monoculture     F      observed  11.778 1.027 1.000  27.000
## 38 Monoculture     N      observed   9.980 0.831 1.000  21.000
## 39 Polyculture     F      observed  19.436 2.143 1.000  60.000
## 40 Polyculture     N      observed  18.768 1.954 1.000  68.000
## 41 Monoculture     F             P  26.157 2.577 1.283  64.761
## 42 Monoculture     N             P  28.244 3.374 1.297 108.662
## 43 Polyculture     F             P  38.759 2.790 9.226  75.843
## 44 Polyculture     N             P  30.353 2.381 6.527  70.880
## 45 Monoculture     F            pH   7.151 0.157 4.780   8.460
## 46 Monoculture     N            pH   7.201 0.157 4.800   8.640
## 47 Polyculture     F            pH   7.380 0.123 4.560   8.260
## 48 Polyculture     N            pH   7.469 0.099 5.490   8.290
## 49 Monoculture     F       shannon   1.503 0.093 0.000   2.804
## 50 Monoculture     N       shannon   1.461 0.085 0.000   2.465
## 51 Polyculture     F       shannon   1.921 0.111 0.000   3.377
## 52 Polyculture     N       shannon   1.827 0.100 0.000   3.551
## 53 Monoculture     F           TOC   0.444 0.010 0.280   0.616
## 54 Monoculture     N           TOC   0.483 0.010 0.329   0.629
## 55 Polyculture     F           TOC   0.474 0.018 0.225   0.694
```

56 Polyculture   N   TOC 0.451 0.014 0.217   0.668