

# Summary of AMF community assembly

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## 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

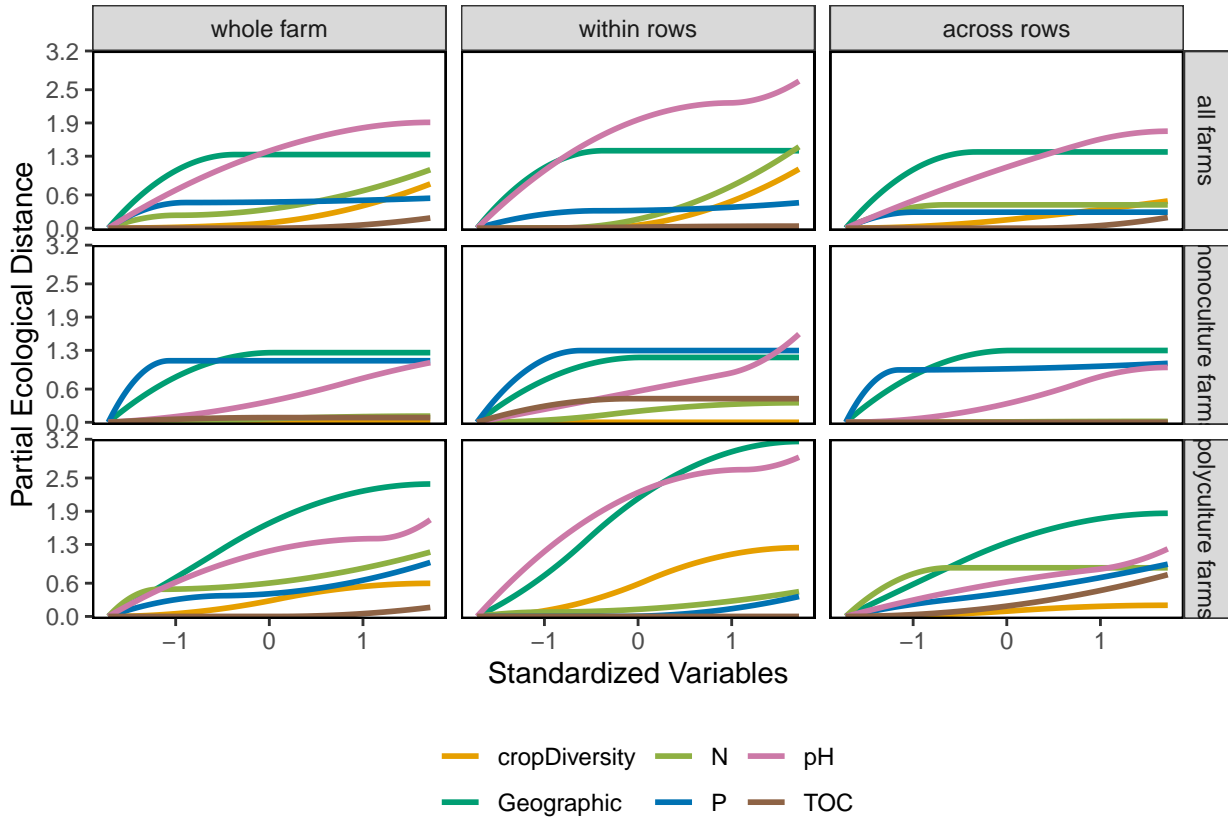
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# Drivers of AM compositional dissimilarity

## Crop diversity

### Plots

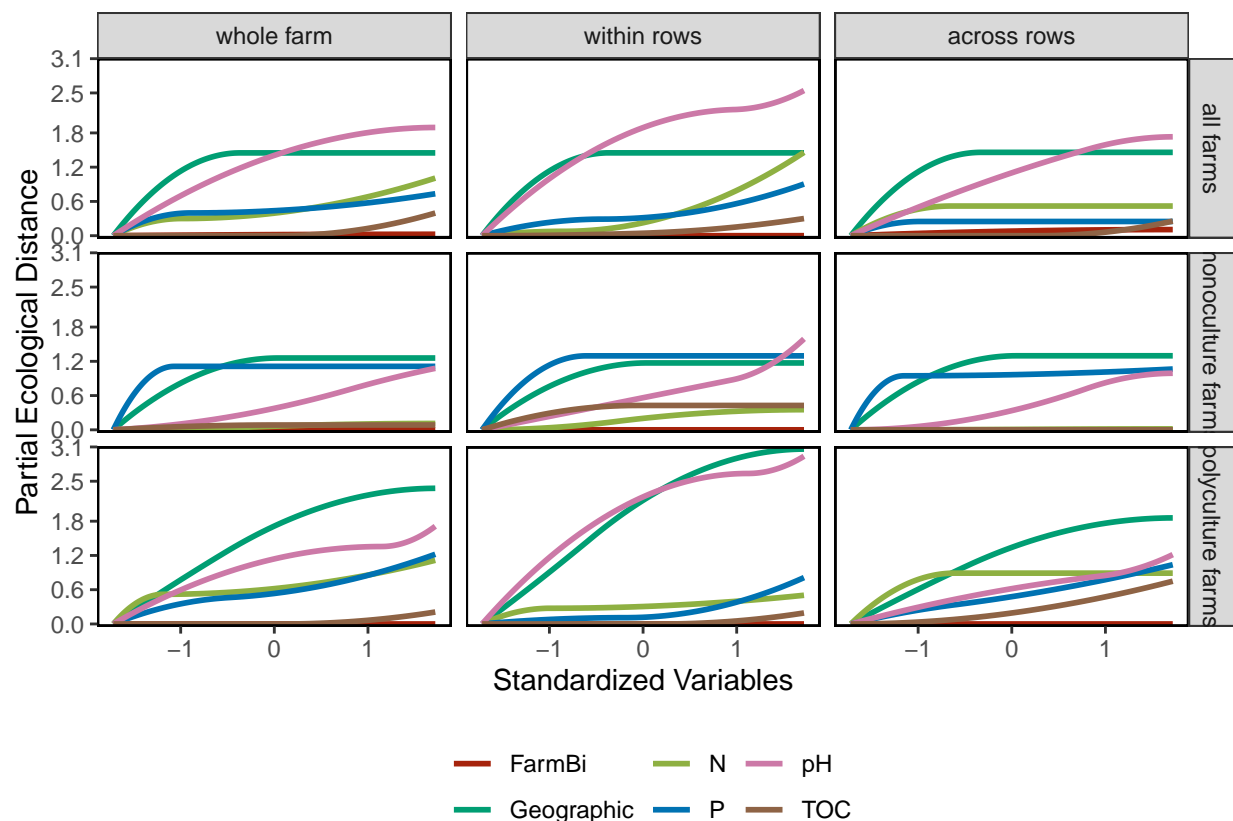


### Model output

##	dataset	location	Geographic	pH	P	TOC
## 1	all farms	whole farm	1.329 ***	1.911 ***	0.542	0.187
## 2	all farms	within rows	1.399 NA	2.674 NA	0.461 NA	0.037 NA
## 3	all farms	across rows	1.376 NA	1.751 NA	0.289 NA	0.197 NA
## 4	monoculture farms	whole farm	1.258 ***	1.083 ***	1.111 ***	0.085
## 5	monoculture farms	within rows	1.171 NA	1.62 NA	1.296 NA	0.427 NA
## 6	monoculture farms	across rows	1.297 NA	0.991 NA	1.066 NA	0 NA
## 7	polyculture farms	whole farm	2.392 ***	1.767 ***	0.985 ***	0.167
## 8	polyculture farms	within rows	3.159 NA	2.889 NA	0.366 NA	0 NA
## 9	polyculture farms	across rows	1.863 NA	1.233 NA	0.95 NA	0.761 NA
##	N cropDiversity Percent Deviance Explained					
## 1	1.066 *	0.81 ***	28.224 NA			
## 2	1.49 NA	1.083 NA	35.858 NA			
## 3	0.421 NA	0.494 NA	25.233 NA			
## 4	0.112	0	30.725 NA			
## 5	0.353 NA	0 NA	34.585 NA			
## 6	0.016 NA	0 NA	28.266 NA			
## 7	1.17 *	0.598 *	36.804 NA			
## 8	0.453 NA	1.242 NA	49.548 NA			
## 9	0.878 NA	0.202 NA	33.035 NA			

## Farm type

### Plots



### Model output

#### Coefficients

##	dataset	location	Geographic	pH	P	TOC
## 1	all farms	whole farm	1.45 ***	1.895 ***	0.739	0.405
## 2	all farms	within rows	1.451 NA	2.557 NA	0.914 NA	0.305 NA
## 3	all farms	across rows	1.459 NA	1.732 NA	0.249 NA	0.261 NA
## 4	monoculture farms	whole farm	1.258 ***	1.083 ***	1.111 ***	0.085
## 5	monoculture farms	within rows	1.171 NA	1.62 NA	1.296 NA	0.427 NA
## 6	monoculture farms	across rows	1.297 NA	0.991 NA	1.066 NA	0 NA
## 7	polyculture farms	whole farm	2.376 ***	1.733 ***	1.231 ***	0.214
## 8	polyculture farms	within rows	3.063 NA	2.955 NA	0.825 NA	0.197 NA
## 9	polyculture farms	across rows	1.858 NA	1.228 NA	1.044 NA	0.756 NA
##	N	FarmBi	Percent Deviance Explained			
## 1	1.018 *	0.025 NA	26.927 NA			
## 2	1.478 NA	0 NA	34.019 NA			
## 3	0.519 NA	0.107 NA	24.734 NA			
## 4	0.112	0 NA	30.725 NA			
## 5	0.353 NA	0 NA	34.585 NA			
## 6	0.016 NA	0 NA	28.266 NA			
## 7	1.122 *	0 NA	36.059 NA			
## 8	0.506 NA	0 NA	46.392 NA			
## 9	0.89 NA	0 NA	32.953 NA			

## MRM tests

### Crop divesrity

##	Data	pH	P	N	TOC	cropDiversity
## 1	All	0.225 ***	0.06 ***	0.053 **	0.031	0.112 ***
## 2	All across	0.215 ***	0.015	-0.024	0.038	0.109 ***
## 3	All within	0.246 ***	0.084 **	0.107 ***	0.031	0.107 ***
## 4	Mono	0.217 ***	0.04	0.017	-0.018	<NA>
## 5	Mono across	0.193 ***	0.041	-0.016	-0.055	<NA>
## 6	Mono within	0.249 ***	0.034	0.054	-0.004	<NA>
## 7	Poly	0.131 ***	0.112 ***	0.012	0.07 ***	0.062 *
## 8	Poly across	0.125 **	0.098 **	0.005	0.156 ***	0.04
## 9	Poly within	0.171 ***	0.107 **	-0.004	0.015	0.122 **
##	geography variance					
## 1	0.157 ***	0.127				
## 2	0.192 ***	0.11				
## 3	0.171 ***	0.166				
## 4	0.266 ***	0.162				
## 5	0.289 ***	0.157				
## 6	0.235 ***	0.166				
## 7	0.356 ***	0.227				
## 8	0.324 ***	0.216				
## 9	0.403 ***	0.283				

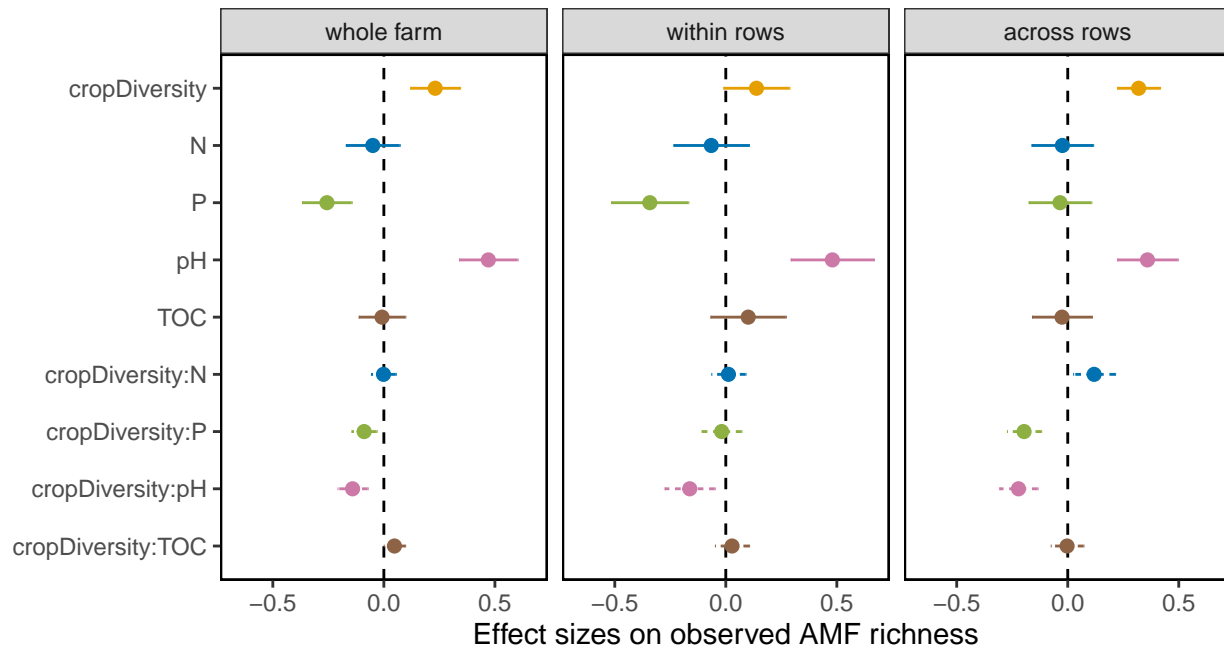
### Farm type

##	Data	variance	geography	pH	P	TOC	N
## 1	All	0.119	0.169 ***	0.22 ***	0.069 ***	0.037 *	0.054 **
## 2	All across	0.105	0.198 ***	0.209 ***	0.02	0.039	-0.023
## 3	All within	0.159	0.185 ***	0.242 ***	0.098 ***	0.043	0.107 ***
## 4	Mono	0.162	0.266 ***	0.217 ***	0.04	-0.018	0.017
## 5	Mono across	0.157	0.289 ***	0.193 ***	0.041	-0.055	-0.016
## 6	Mono within	0.166	0.235 ***	0.249 ***	0.034	-0.004	0.054
## 7	Poly	0.224	0.355 ***	0.125 ***	0.132 ***	0.079 ***	0.006
## 8	Poly across	0.214	0.321 ***	0.119 **	0.11 ***	0.162 ***	0.004
## 9	Poly within	0.271	0.402 ***	0.162 **	0.151 ***	0.033	-0.016
##	FarmBi						
## 1	0.063 ***						
## 2	0.076 ***						
## 3	0.051 **						
## 4	<NA>						
## 5	<NA>						
## 6	<NA>						
## 7	<NA>						
## 8	<NA>						
## 9	<NA>						

## 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
```

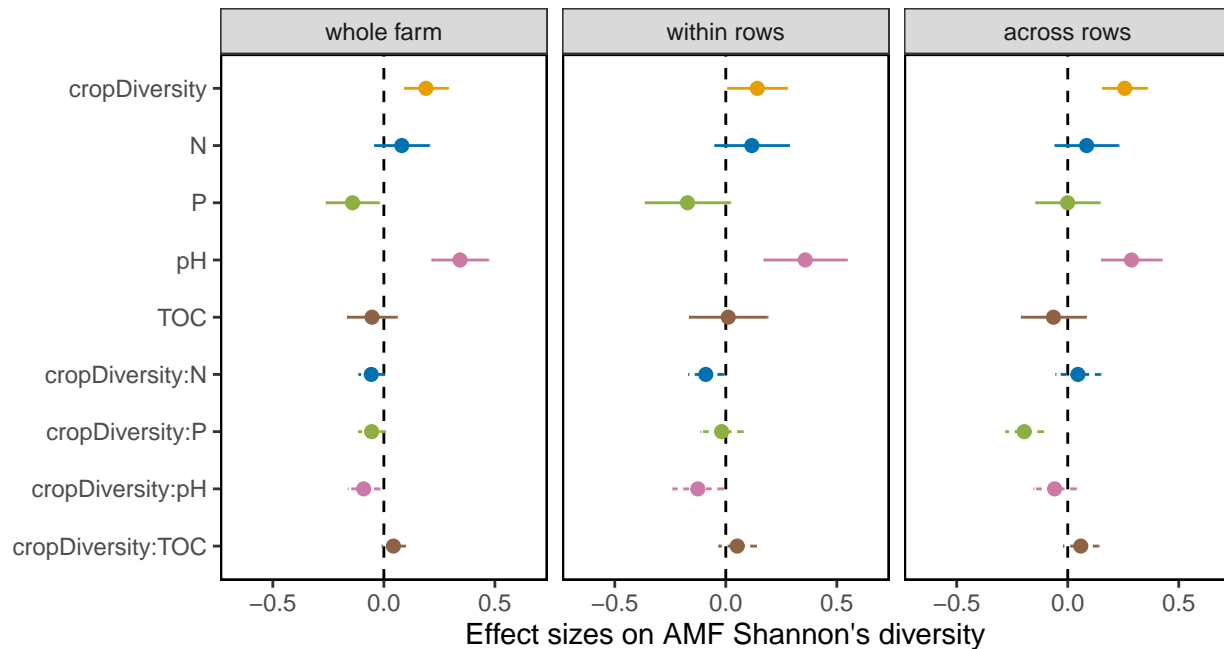
#### Across-rows

```
## $model
## glmer(formula = observed ~ cropDiversity * scale(pH) + scale(P) *
##      cropDiversity + scale(TOC) * cropDiversity + scale(N) * cropDiversity +
##      (1 | FarmKey:Year), data = all_a$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

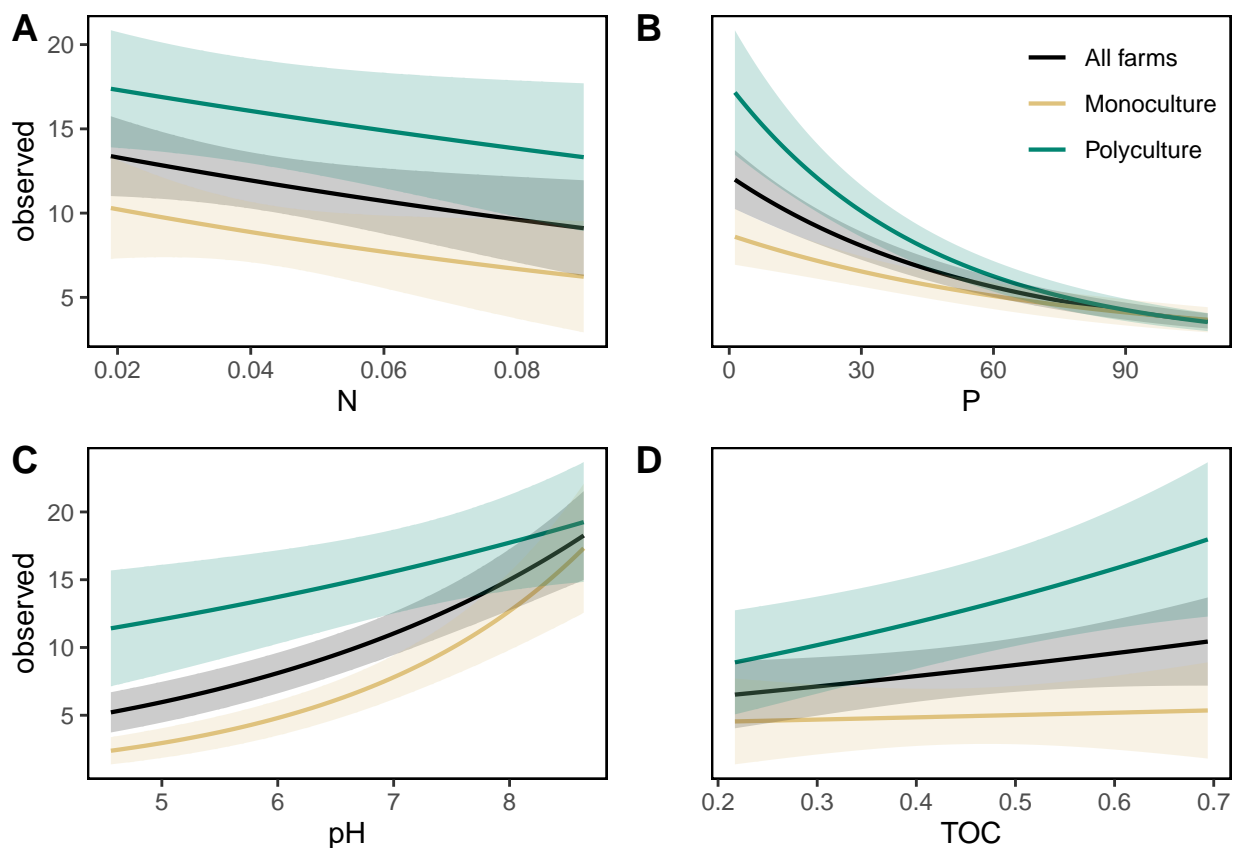
```
## $model
```

```
## 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
```

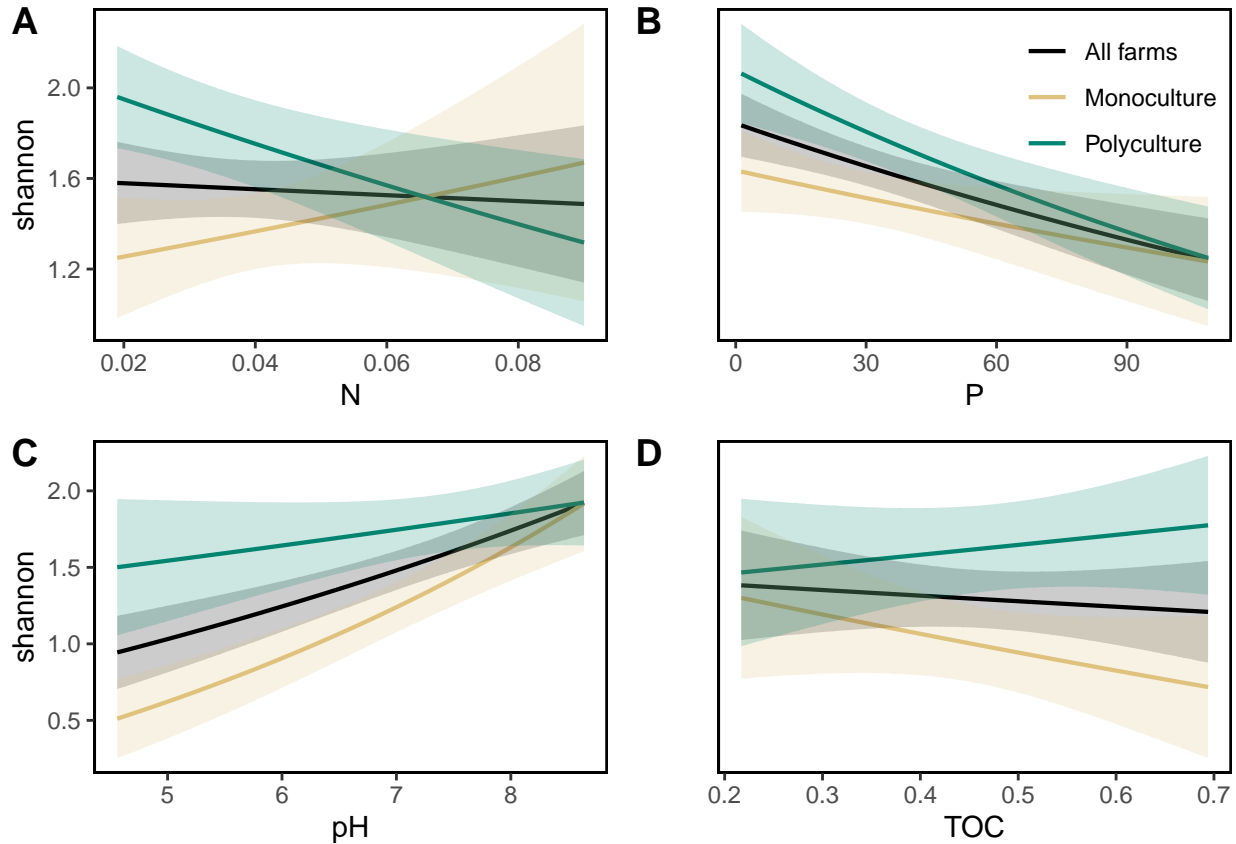
#### Across-rows

```
## $model
## glmer(formula = observed ~ FarmType * scale(pH) + scale(P) *
## FarmType + scale(TOC) * FarmType + scale(N) * FarmType +
## (1 | FarmKey:Year), data = all_a$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

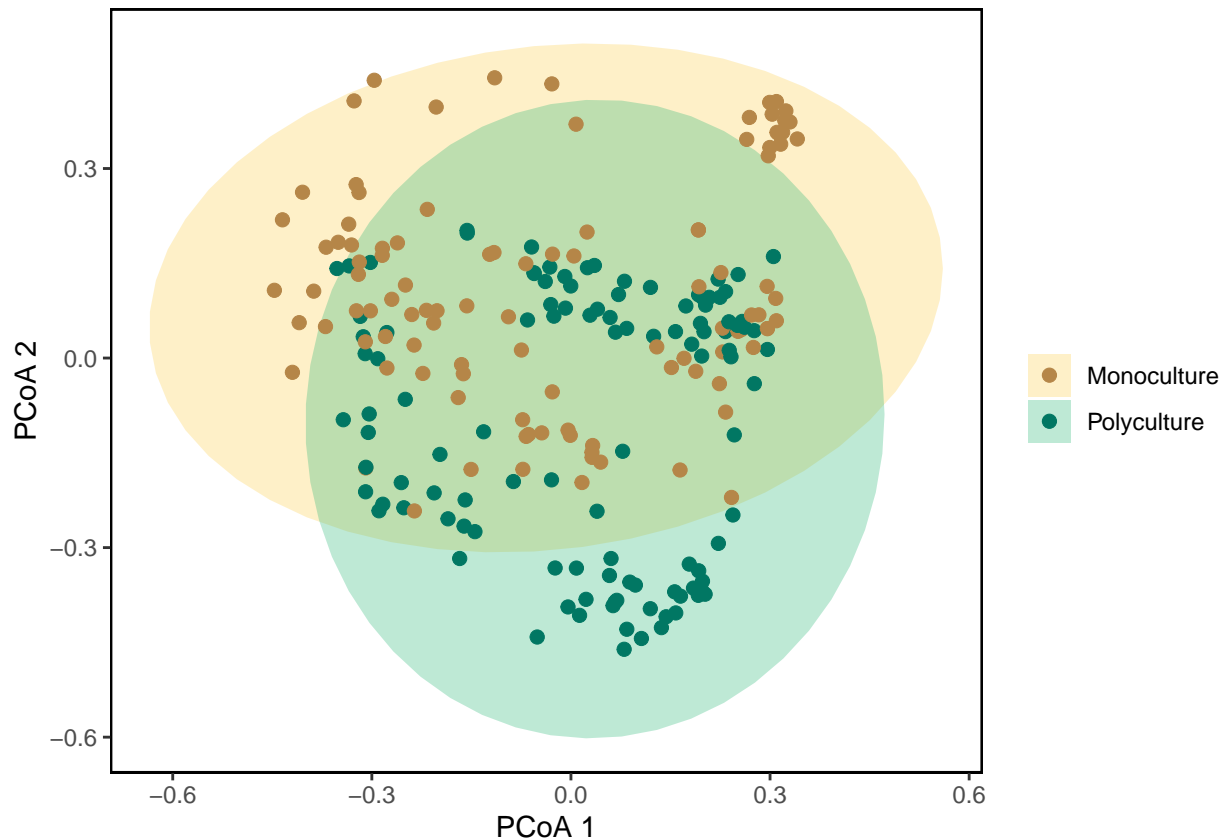
```
##
```

```
## $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



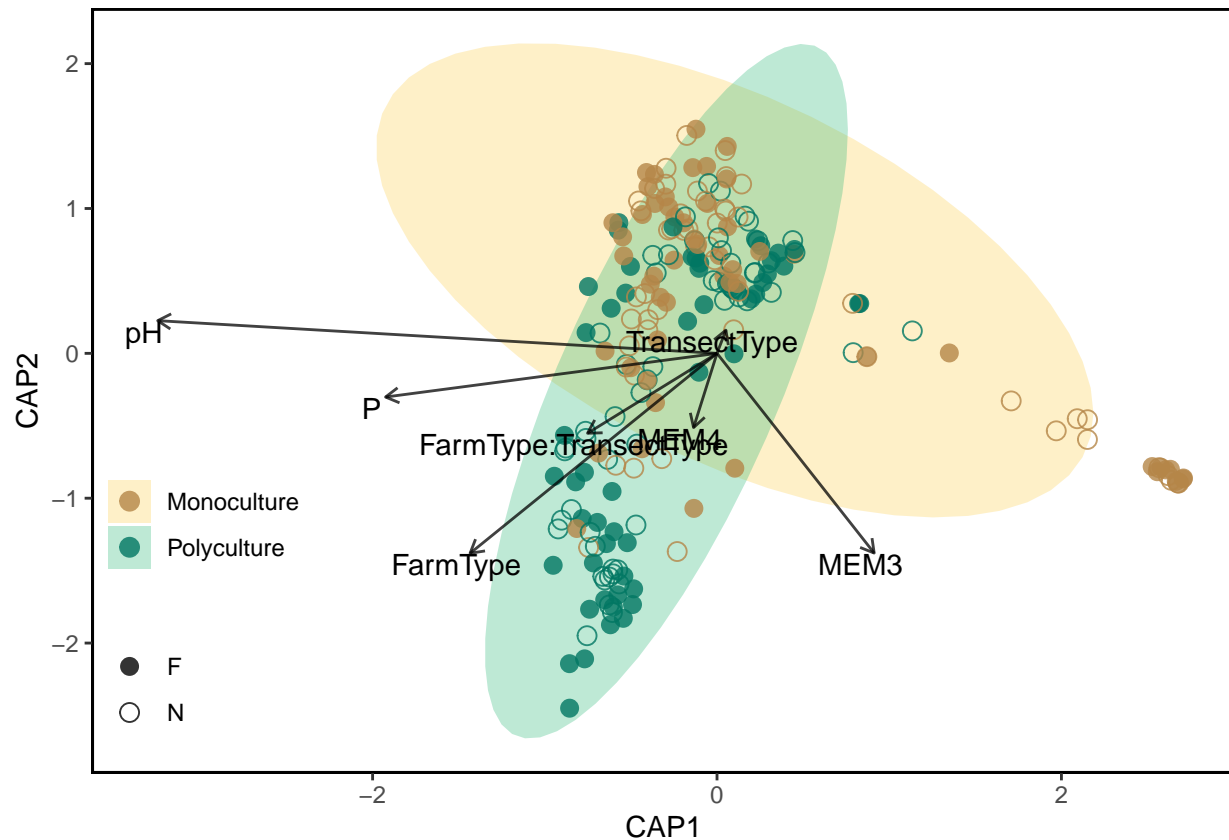
Model output

```
##
## 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)
## FarmType      1     4.950  4.9498 13.4193 0.05905 0.035 *
## Block         1     0.235  0.2353  0.6378 0.00281 0.362
## FarmType:Block 1     0.444  0.4444  1.2047 0.00530 0.007 **
## Residuals    212    78.197  0.3689          0.93284
## Total        215    83.826          1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



# dbRDA

## Plots

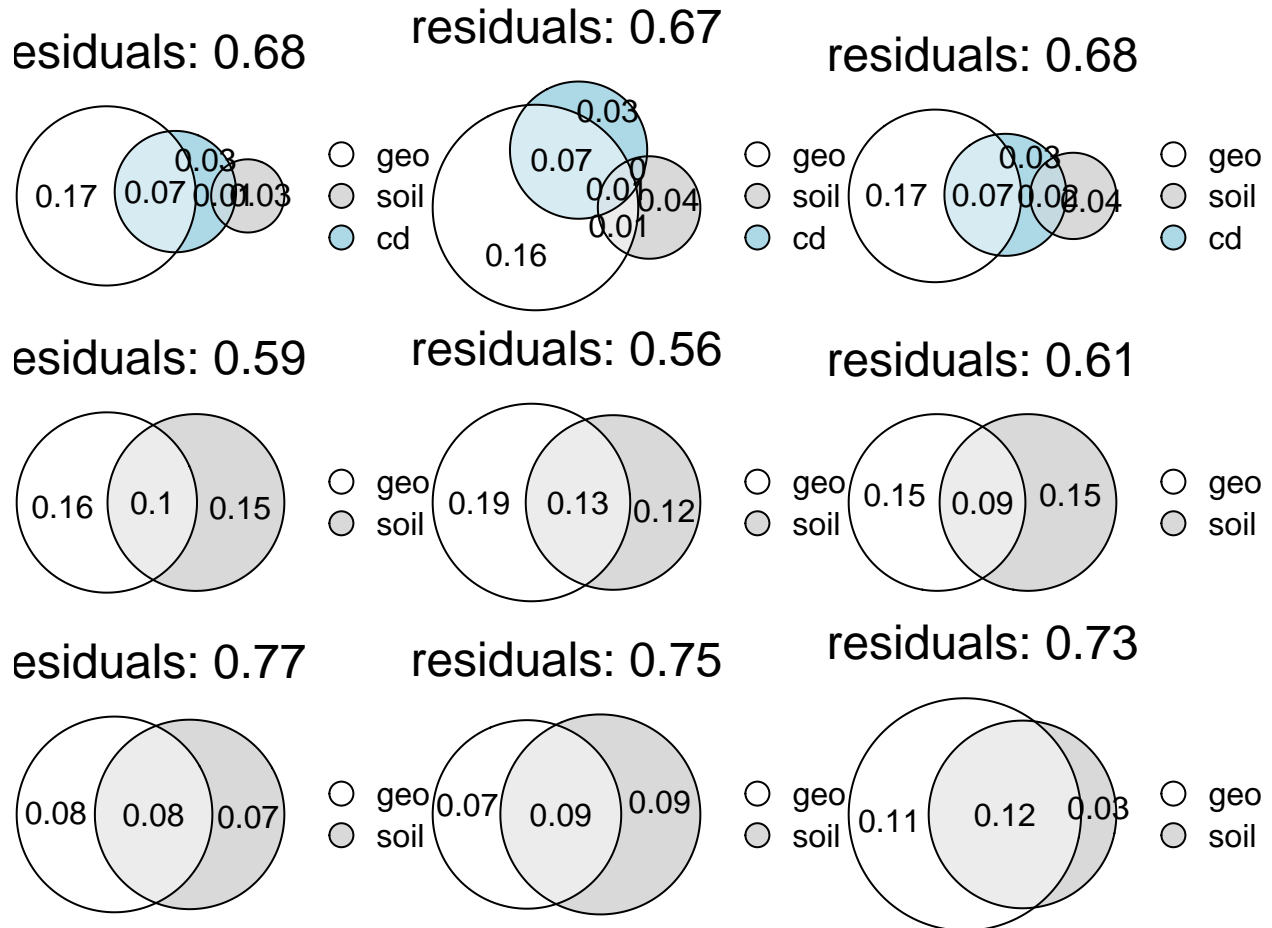


## Model output

```
## Permutation test for capscale under reduced model
## Terms added sequentially (first to last)
## Blocks: df$farmCode
## Permutation: free
## Number of permutations: 999
##
## Model: capscale(formula = decostand(amf_otu, "hellinger") ~ FarmType * Block + N + P + pH + TOC + dbmem
##
##          Df SumOfSqs      F Pr(>F)
## FarmType    1    3.222 9.0214 0.001 ***
## Block        1    0.400 1.1202 0.043 *
## N            1    1.348 3.7744 0.501
## P            1    2.057 5.7597 0.005 **
## pH           1    3.544 9.9232 0.036 *
## TOC          1    1.155 3.2352 0.321
## dbmemDF$MEM1 1    2.416 6.7656 0.721
## dbmemDF$MEM2 1    2.310 6.4687 0.697
## dbmemDF$MEM3 1    2.079 5.8211 0.054 .
## dbmemDF$MEM4 1    1.818 5.0900 0.005 **
## dbmemDF$MEM5 1    2.215 6.2019 0.294
## dbmemDF$MEM6 1    1.414 3.9579 0.406
## FarmType:Block 1    0.460 1.2893 0.017 *
## Residual    202    72.146
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

## Variation partitioning

### Plots

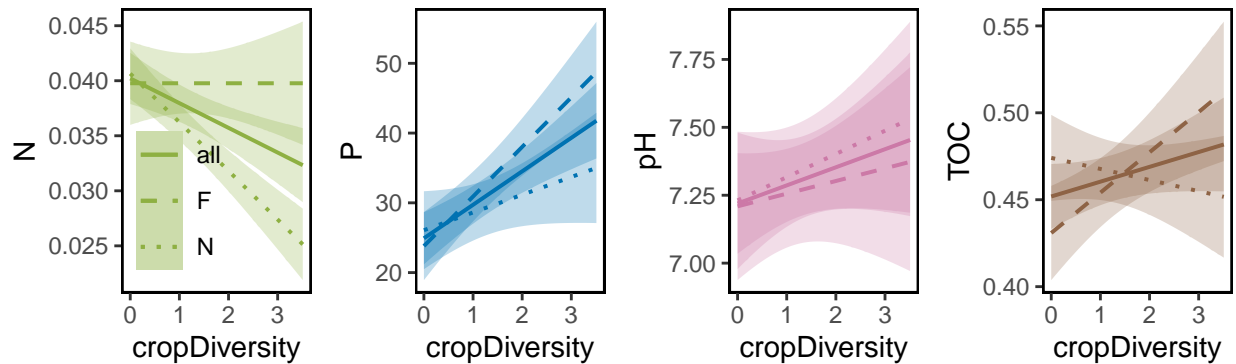


### Model output

##	dataset	location	geo	soil	cd	geo&cd	soil&cd	soil&geo
## 1	all farms	whole farm	0.17	0.03	0.03	0.07	0.01	0.00
## 2	all farms	within rows	0.16	0.04	0.03	0.07	0.00	0.01
## 3	all farms	across rows	0.17	0.04	0.03	0.07	0.02	0.00
## 4	monoculture farms	whole farm	0.16	0.15	NA	NA	NA	0.10
## 5	monoculture farms	within rows	0.19	0.12	NA	NA	NA	0.13
## 6	monoculture farms	across rows	0.15	0.15	NA	NA	NA	0.09
## 7	polyculture farms	whole farm	0.08	0.07	NA	NA	NA	0.08
## 8	polyculture farms	within rows	0.07	0.09	NA	NA	NA	0.09
## 9	polyculture farms	across rows	0.11	0.03	NA	NA	NA	0.12
##	geo&cd&soil	residuals						
## 1			0.00		0.68			
## 2			0.01		0.67			
## 3			0.00		0.68			
## 4			NA		0.59			
## 5			NA		0.56			
## 6			NA		0.61			
## 7			NA		0.77			
## 8			NA		0.75			
## 9			NA		0.73			

## Edaphic variables ~ crop diversity

### Plots

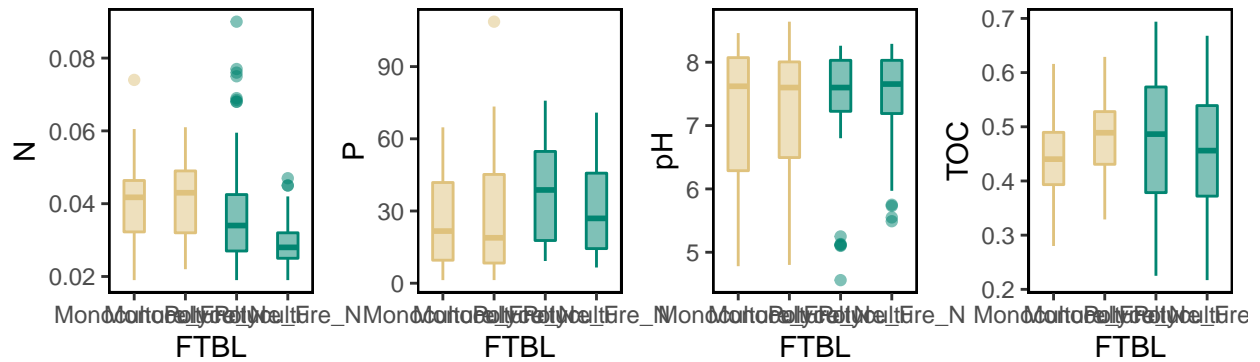


### Model output

```
## $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