Epifaunal diversity patterns within and among seagrass meadows suggest metacommunity structure, by Whippo et al

Methods

Data and package loading and organizing

Libraries

```r
library(vegan)
#library(Rcmdr)
#library(BiodiversityR)
library(plyr)
library(reshape2)
library(MuMIn)
library(lubridate)
library(knitr)
library(tidyverse)
library(metacom)
library(broom)
```

Load data

```r
data.tr <- read.csv("../data/Whippodata.csv")
data.tr <- data.tr[,-1]
sites <- read.csv("../data/site.info_201801.csv")
tempsal <- read_csv("../data/TempSalData.csv")
```

From full datasets of all sites, species and sampling dates, subset data:

1. Remove all taxa that are not epifauna:

2. Create data subsets for different sampling times

```r
# 5 sites were sampled in May, June and July
dataMAY <- data.tr[(data.tr$Time.Code2=="A"),]
dataJULY <- data.tr[(data.tr$Time.Code2=="C" & data.tr$site!="BE" & data.tr$site!="EI" & data.tr$site!=
dataAUG <- data.tr[(data.tr$Time.Code2=="E"),]

# this set has all three sampling times for the 5 sites sampled 3 times
data3times <- data.tr[(data.tr$site!="BE" & data.tr$site!="EI" & data.tr$site!="CC" & data.tr$site!="BI

# this set has the 9 sites sampled in July
dataJULY9 <- data.tr[(data.tr$Time.Code2=="C"),]
```

3. Create site-level data by collapsing across plots. Change the data used in start data to consider other temporal subsets.

4. Create the data file we will use for univariate diversity indices and ranks:

5. Process temperature and salinity data

are temps and salinities correlated?

```
##
## Call:
## lm(formula = temps[(temps$Unit == "Tem"), ]$Value ~ temps[(temps$Unit ==
##     "Sal"), ]$Value)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -6.240 -1.751 -0.688  1.622  8.724
##
## Coefficients:
##                                        Estimate Std. Error t value Pr(>|t|)
## (Intercept)                            20.58833    0.44642   46.12   <2e-16
## temps[(temps$Unit == "Sal"), ]$Value  -0.24159    0.02222  -10.87   <2e-16
##
## (Intercept)                           ***
## temps[(temps$Unit == "Sal"), ]$Value ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.57 on 346 degrees of freedom
## Multiple R-squared:  0.2546, Adjusted R-squared:  0.2525
## F-statistic: 118.2 on 1 and 346 DF,  p-value: < 2.2e-16
```

Results

Site biotic attributes: Table S2 and main text

Correlations between site-level abiotic factors

1. DFW and temperature, salinity

```
##
## Call:
## lm(formula = temp ~ dfw, data = sites)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.67243 -1.14691  0.03678  0.72317  2.46927
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  18.7998     1.1244  16.721 6.69e-07 ***
```

```
## dfw            -0.3527     0.1397  -2.524    0.0396 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.68 on 7 degrees of freedom
## Multiple R-squared:  0.4765, Adjusted R-squared:  0.4017
## F-statistic: 6.372 on 1 and 7 DF,  p-value: 0.03957

##
## Call:
## lm(formula = salinity ~ dfw, data = sites)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.3162 -1.2404 -0.1207  0.6440  2.7845
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  14.2743     1.2704   11.24 9.87e-06 ***
## dfw           0.7484     0.1579    4.74  0.00211 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 1.898 on 7 degrees of freedom
## Multiple R-squared:  0.7625, Adjusted R-squared:  0.7285
## F-statistic: 22.47 on 1 and 7 DF,  p-value: 0.002107

##
## Call:
## lm(formula = salinity ~ temp, data = sites)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -4.6441 -1.4152  0.1171  1.8204  3.9238
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  37.8855     7.7404   4.895  0.00176 **
## temp         -1.1255     0.4701  -2.394  0.04786 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.887 on 7 degrees of freedom
## Multiple R-squared:  0.4502, Adjusted R-squared:  0.3717
## F-statistic: 5.733 on 1 and 7 DF,  p-value: 0.04786
```

2. Shoot density

```
##
## Call:
## lm(formula = sites$shoot.density ~ sites$fetch.meters)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -3.195 -2.292 -1.190  1.551  5.984
```

```
## 
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        8.882e+00  1.937e+00   4.586  0.00253 **
## sites$fetch.meters -3.617e-06 2.333e-05  -0.155  0.88119
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 3.412 on 7 degrees of freedom
## Multiple R-squared:  0.003421,   Adjusted R-squared:  -0.1389
## F-statistic: 0.02403 on 1 and 7 DF,  p-value: 0.8812

## 
## Call:
## lm(formula = sites$shoot.density ~ sites$dfw)
## 
## Residuals:
##     Min     1Q  Median      3Q     Max
## -3.2525 -2.2578 -0.5105  2.3140  2.9603
## 
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)   5.5305     1.8433   3.000   0.0199 *
## sites$dfw     0.4455     0.2291   1.945   0.0929 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 2.754 on 7 degrees of freedom
## Multiple R-squared:  0.3507, Adjusted R-squared:  0.258
## F-statistic: 3.782 on 1 and 7 DF,  p-value: 0.0929
```

2. LAI

2. Epiphytes

```
## 
## Call:
## lm(formula = sites$epiphytes ~ sites$fetch.meters)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.16423 -0.10246 -0.07243  0.03475  0.41717
## 
## Coefficients:
##                     Estimate Std. Error t value Pr(>|t|)
## (Intercept)        2.328e-01  1.075e-01   2.166    0.067 .
## sites$fetch.meters 3.880e-07  1.295e-06   0.300    0.773
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.1893 on 7 degrees of freedom
## Multiple R-squared:  0.01266,   Adjusted R-squared:  -0.1284
## F-statistic: 0.08979 on 1 and 7 DF,  p-value: 0.7731
```

```
## 
## Call:
## lm(formula = sites$epiphytes ~ sites$dfw)
## 
## Residuals:
##      Min       1Q   Median       3Q      Max 
## -0.19291 -0.11295 -0.07178  0.05174  0.40531 
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.279372   0.127212   2.196   0.0641 .
## sites$dfw   -0.002935   0.015810  -0.186   0.8580
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.1901 on 7 degrees of freedom
## Multiple R-squared:  0.004901,   Adjusted R-squared:  -0.1373 
## F-statistic: 0.03448 on 1 and 7 DF,  p-value: 0.858
```

Epifauna species for in text results are below after Table 2

Table 1

1. Diversity (Gamma) Observed number of species per site for month identified in start.data:

Table 1: Observed Number of Species at each site on sample date indicated in column site.time. This information is in the 'Diversity' column in Table 1.

site.time	alpha	site
BE.C	17	BE
BI.C	20	BI
CB.C	17	CB
CC.C	11	CC
DC.C	16	DC
EI.C	19	EI
NB.C	18	NB
RP.C	24	RP
WI.C	22	WI

2. Morisita's index (aggregation)

Aggregation (I.m)	CI.lower	CI.upper	Proportion species with significant I.m	Site
0.438751899699304	0.344283533717326	0.533220265681283	0.666666666666667	DC
0.339644343303565	0.203406476118848	0.475882210488282	0.526315789473684	WI
0.440178087571884	0.29365139421322	0.586704780930547	0.615384615384615	BE
0.227153013832138	0.071589957920741	0.382716069743534	0.5	EI
0.46059728138394	0.351136763851047	0.570057798916832	0.75	RP
0.376808909910861	0.251526972272675	0.502090847549047	0.466666666666667	NB
0.351069119095654	0.213624773164587	0.488513465026721	0.4375	CB
0.253963918783698	0.0709019194109852	0.43702591815641	0.4375	BI

Aggregation (I.m)	CI.lower	CI.upper	Proportion species with significant I.m	Site
0.200895420442068	0.0180322343463955	0.383758606537741	0.4	CC

3. Rarified richness estimates for estimated species richess at the meadow scale, extrapolated to 2x the observed abundance for one sample within each meadow.

	Extrapolated Richness	CI.Lower	CI.Upper	site
RBE	18.656	14.030	23.282	BE
RRP	26.189	22.083	30.296	RP
RDC	16.432	13.683	19.182	DC
RWI	22.864	19.977	25.751	WI
RCC	11.000	9.778	12.222	CC
RCB	17.245	14.438	20.052	CB
RNB	18.633	14.765	22.501	NB
REI	19.397	16.726	22.069	EI
RBI	19.397	16.726	22.069	BI

TABLE 2. Rank abundance and aggregation of species observed in each meadow at each time.

July:

Table 4: Table 2 - July: Rank abundance and aggregation of species observed in each meadow at each time. Aggregated column indicates signficant (P < 0.05) spatial aggregation within species across plots within each meadow, based on chi-squared tests on Morisita's index I

Species	DC	WI	BE	EI	RP	NB	CB	BI	CC
Caprella.spp.	1	2	1	4	1	13	8	14	5
Aoroides.columbiae	2	19	8	6	8	12	6	11	11
Photis.brevipes	3	8	4	7	6	6	9	17	12
Idotea.resecata	4	3	5	11	10	3	5	5	4
Platynereis.bicanaliculata	5	6	3	5	4	6	15	9	12
Monocorophium.achersicum	6	13	18	20	22	10	11	8	7
Leptochelia.dubia	7	23	11	20	5	5	3	4	9
Pontogeneia.rostrata	8	15	11	11	18	8	12	10	12
Lacuna.spp.	9	5	7	13	14	14	12	7	12
Mytilus.trossulus	10	1	6	3	2	2	1	3	1
Phyllaplysia.taylori	11	10	10	2	3	14	18	21	12
Amph.E..dorsal.teeth.	12	15	2	18	25	19	18	6	3
Pugettia.richii	13	21	18	20	25	19	18	21	12
Copepod	14	13	18	13	11	17	15	21	12
Eogammarus.confervicolus	15	9	9	9	25	8	18	15	10
Cirolana.harfordi	16	17	15	20	21	19	18	21	12
Alia.carinata	17	23	18	20	25	19	18	11	12
Amphithoe.spp.	17	11	18	13	20	10	18	17	12
Balanus.spp.	17	23	18	10	15	17	18	21	12
Callianax.sp.	17	23	18	20	25	19	18	21	12
Cyprideis.beaconensis	17	4	15	13	16	14	7	15	12
Halacarid.mite	17	17	13	8	12	4	4	1	2

Species	DC	WI	BE	EI	RP	NB	CB	BI	CC
Haminoea.sp.	17	23	18	20	22	19	18	21	12
Janua.pagastecheri	17	11	13	20	7	19	18	21	12
Lirobittium.spp.	17	23	18	13	25	19	18	21	12
Lottia.pelta	17	19	18	20	25	19	17	13	12
Margarites.helicinus	17	23	18	20	25	19	18	21	12
Nebalia.sp.	17	23	18	20	25	19	18	21	12
Nematode	17	21	18	18	9	1	2	2	5
Nemertea	17	23	18	20	22	19	18	21	12
Pagurus.quaylei	17	23	18	20	25	19	18	17	12
Pandalidae	17	23	18	20	18	19	18	21	12
Pycnogonum.sp.	17	7	15	1	12	19	12	17	7
Thick.nematode.	17	23	18	20	17	19	10	21	12

May:

Table 5: Table 2 - May: Rank abundance and aggregation of species observed in each meadow at each time. Aggregated column indicates signficant ($P < 0.05$) spatial aggregation within species across plots within each meadow, based on chi-squared tests on Morisita's index I

Species	DC.rank	DC.aggregated	WI.rank	WI.aggregated	RP.rank	RP.aggregated	NB.rank
Caprella.spp.	1	Yes	13	No	1	Yes	7
Aoroides.columbiae	2	Yes	5	Yes	3	Yes	11
Idotea.resecata	3	Yes	8	No	6	Yes	1
Photis.brevipes	4	Yes	6	Yes	9	No	5
Phyllaplysia.taylori	4	No	19	NA	4	Yes	20
Monocorophium.achersicum	6	Yes	14	No	12	NA	12
Platynereis.bicanaliculata	7	Yes	2	Yes	2	Yes	7
Eogammarus.confervicolus	8	Yes	9	Yes	12	NA	15
Lacuna.spp.	9	No	10	Yes	8	No	9
Pontogeneia.rostrata	9	No	3	Yes	10	NA	10
Amphithoe.spp.	11	Yes	4	Yes	10	No	15
Leptochelia.dubia	12	No	7	Yes	7	Yes	5
Pugettia.richii	13	No	24	NA	16	NA	20
Copepod	14	NA	12	No	16	NA	2
Pagurus.quaylei	14	NA	18	No	12	NA	20
Alia.carinata	16	NA	24	NA	16	NA	20
Amph.E..dorsal.teeth.	16	NA	19	NA	12	NA	20
Balanus.spp.	16	NA	24	NA	16	NA	15
Callianax.sp.	16	NA	24	NA	16	NA	20
Cirolana.harfordi	16	NA	11	No	16	NA	13
Cyprideis.beaconensis	16	NA	16	No	16	NA	20
Halacarid.mite	16	NA	16	No	16	NA	3
Haminoea.sp.	16	NA	24	NA	16	NA	20
Janua.pagastecheri	16	NA	24	NA	4	Yes	20
Lirobittium.spp.	16	NA	24	NA	16	NA	20
Lottia.pelta	16	NA	19	NA	16	NA	20
Margarites.helicinus	16	NA	24	NA	16	NA	20
Mytilus.trossulus	16	NA	15	No	16	NA	4
Nebalia.sp.	16	NA	19	NA	16	NA	15

Species	DC.rank	DC.aggregated	WI.rank	WI.aggregated	RP.rank	RP.aggregated	NB.rank
Nematode	16	NA	1	Yes	16	NA	13
Nemertea	16	NA	24	NA	16	NA	15
Pandalidae	16	NA	24	NA	16	NA	20
Pycnogonum.sp.	16	NA	19	NA	16	NA	20
Thick.nematode.	16	NA	24	NA	16	NA	20

August:

Table 6: Ranks for August species abundances (N). Aggregated column indicates signficant (P < 0.05) spatial aggregation within species across plots within each meadow, based on chi-squared tests on Morisita's index I

Species	DC.rank	DC.aggregated	WI.rank	WI.aggregated	RP.rank	RP.aggregated	NB.rank
Caprella.spp.	1	Yes	13	No	1	Yes	7
Aoroides.columbiae	2	Yes	5	Yes	3	Yes	11
Idotea.resecata	3	Yes	8	No	6	Yes	1
Photis.brevipes	4	Yes	6	Yes	9	No	5
Phyllaplysia.taylori	4	No	19	NA	4	Yes	20
Monocorophium.achersicum	6	Yes	14	No	12	NA	12
Platynereis.bicanaliculata	7	Yes	2	Yes	2	Yes	7
Eogammarus.confervicolus	8	Yes	9	Yes	12	NA	15
Lacuna.spp.	9	No	10	Yes	8	No	9
Pontogeneia.rostrata	9	No	3	Yes	10	NA	10
Amphithoe.spp.	11	Yes	4	Yes	10	No	15
Leptochelia.dubia	12	No	7	Yes	7	Yes	5
Pugettia.richii	13	No	24	NA	16	NA	20
Copepod	14	NA	12	No	16	NA	2
Pagurus.quaylei	14	NA	18	No	12	NA	20
Alia.carinata	16	NA	24	NA	16	NA	20
Amph.E..dorsal.teeth.	16	NA	19	NA	12	NA	20
Balanus.spp.	16	NA	24	NA	16	NA	15
Callianax.sp.	16	NA	24	NA	16	NA	20
Cirolana.harfordi	16	NA	11	No	16	NA	13
Cyprideis.beaconensis	16	NA	16	No	16	NA	20
Halacarid.mite	16	NA	16	No	16	NA	3
Haminoea.sp.	16	NA	24	NA	16	NA	20
Janua.pagastecheri	16	NA	24	NA	4	Yes	20
Lirobittium.spp.	16	NA	24	NA	16	NA	20
Lottia.pelta	16	NA	19	NA	16	NA	20
Margarites.helicinus	16	NA	24	NA	16	NA	20
Mytilus.trossulus	16	NA	15	No	16	NA	4
Nebalia.sp.	16	NA	19	NA	16	NA	15
Nematode	16	NA	1	Yes	16	NA	13
Nemertea	16	NA	24	NA	16	NA	15
Pandalidae	16	NA	24	NA	16	NA	20
Pycnogonum.sp.	16	NA	19	NA	16	NA	20
Thick.nematode.	16	NA	24	NA	16	NA	20

Estimation of univariate diversity indices and rank abundance distributions

Results for main text

grazers only

```
## [1] 116.2345
```

```
## [1] 4.841379
```

```
## [1] 16854
```

```
## [1] 0.524002
```

```
## [1]   5 14
```

```
## [1] 11.33333
```

invert summaries for in text results

```
## [1] 46
```

```
## [1] 34
```

```
## [1]      0 1494
```

```
## [1] 18
```

abundance trends for in text results

```
## Analysis of Variance Table
##
## Model 1: log(div.data$N + 1) ~ 1 + div.data$site
## Model 2: log(div.data$N + 1) ~ 1
##   Res.Df    RSS Df Sum of Sq      F    Pr(>F)
## 1     136 105.40
## 2     144 210.81 -8   -105.41 17.001 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Model selection table
##      (Int) div.dat$sit df   logLik  AICc delta weight
## modN 4.485           + 10 -182.621 386.9  0.00      1
## mod0 4.780             2 -232.876 469.8 82.95      0
## Models ranked by AICc(x)
```

Statistical analysis: Spatial diversity patterns

Does plot level alpha diversity differ among meadows? [stats in text]

```
## Analysis of Variance Table
##
## Model 1: div.summary$alpha.p ~ 1 + div.summary$site
## Model 2: div.summary$alpha.p ~ 1
##   Res.Df      RSS Df Sum of Sq      F    Pr(>F)
## 1     135  713.87
## 2     143 1535.31 -8   -821.43 19.418 < 2.2e-16 ***
```

```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Model selection table
##        (Int) div.smm$sit df    logLik  AICc delta weight
## mods4 6.563           + 10 -319.592 660.8   0.0      1
## mods0 8.069             2 -374.727 753.5  92.7      0
## Models ranked by AICc(x)

##
## Call:
## lm(formula = div.summary$alpha.p ~ 1 + div.summary$site)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -8.0625 -1.3281  0.1875  1.4375  4.4375
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          6.5625     0.5749  11.415  < 2e-16 ***
## div.summary$siteBI   2.2500     0.8130   2.767  0.00644 **
## div.summary$siteCB   0.6250     0.8130   0.769  0.44339
## div.summary$siteCC  -1.3125     0.8130  -1.614  0.10878
## div.summary$siteDC   0.2500     0.8130   0.307  0.75894
## div.summary$siteEI   2.0000     0.8130   2.460  0.01516 *
## div.summary$siteNB   0.1875     0.8130   0.231  0.81796
## div.summary$siteRP   7.5000     0.8130   9.225 5.11e-16 ***
## div.summary$siteWI   2.0625     0.8130   2.537  0.01232 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 2.3 on 135 degrees of freedom
## Multiple R-squared:  0.535,  Adjusted R-squared:  0.5075
## F-statistic: 19.42 on 8 and 135 DF,  p-value: < 2.2e-16

##                        2.5 %     97.5 %
## (Intercept)         5.4255459 7.6994541
## div.summary$siteBI  0.6421041 3.8578959
## div.summary$siteCB -0.9828959 2.2328959
## div.summary$siteCC -2.9203959 0.2953959
## div.summary$siteDC -1.3578959 1.8578959
## div.summary$siteEI  0.3921041 3.6078959
## div.summary$siteNB -1.4203959 1.7953959
## div.summary$siteRP  5.8921041 9.1078959
## div.summary$siteWI  0.4546041 3.6703959

##       (Intercept) div.summary$siteBI div.summary$siteCB
##            6.5625             2.2500             0.6250
## div.summary$siteCC div.summary$siteDC div.summary$siteEI
##           -1.3125             0.2500             2.0000
## div.summary$siteNB div.summary$siteRP div.summary$siteWI
##            0.1875             7.5000             2.0625
```

Does plot level Shannon diversity differ among meadows? [results in text]

```
## Analysis of Variance Table
```

```
##
## Model 1: div.summary$H ~ div.summary$site
## Model 2: div.summary$H ~ 1
##   Res.Df    RSS Df Sum of Sq     F    Pr(>F)
## 1     135 12.970
## 2     143 33.215 -8   -20.245 26.34 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Model selection table
##        (Int) div.smm$sit df  logLik  AICc  delta weight
## mods3 0.6188           + 10 -31.011  83.7   0.00      1
## mods0 1.1160             2 -98.716 201.5 117.84      0
## Models ranked by AICc(x)

##
## Call:
## lm(formula = div.summary$H ~ div.summary$site)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -0.6072 -0.2024 -0.0299  0.1417  0.9287
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)         0.61881    0.07749   7.986 5.43e-13 ***
## div.summary$siteBI  0.82634    0.10959   7.541 6.15e-12 ***
## div.summary$siteCB  0.38601    0.10959   3.522 0.000584 ***
## div.summary$siteCC  0.31974    0.10959   2.918 0.004132 **
## div.summary$siteDC -0.14767    0.10959  -1.348 0.180075
## div.summary$siteEI  0.91236    0.10959   8.325 8.27e-14 ***
## div.summary$siteNB  0.51320    0.10959   4.683 6.80e-06 ***
## div.summary$siteRP  0.99273    0.10959   9.059 1.32e-15 ***
## div.summary$siteWI  0.67577    0.10959   6.167 7.57e-09 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.31 on 135 degrees of freedom
## Multiple R-squared:  0.6095, Adjusted R-squared:  0.5864
## F-statistic: 26.34 on 8 and 135 DF,  p-value: < 2.2e-16
```

Does plot level R' differ among meadows? [results in text]

```
## Analysis of Variance Table
##
## Model 1: div.summary$R2 ~ div.summary$site
## Model 2: div.summary$R2 ~ 1
##   Res.Df    RSS Df Sum of Sq     F    Pr(>F)
## 1     135 30.851
## 2     143 71.610 -8   -40.759 22.295 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Model selection table
##        (Int) div.smm$sit df   logLik  AICc  delta weight
```

```
## mods3 1.685            + 10  -93.400 208.5   0.00      1
## mods0 2.447             2 -154.029 312.1 103.69      0
## Models ranked by AICc(x)
##
## Call:
## lm(formula = div.summary$R2 ~ div.summary$site)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.99793 -0.31825 -0.06404  0.20284  1.32628
##
## Coefficients:
##                    Estimate Std. Error t value Pr(>|t|)
## (Intercept)          1.6850     0.1195  14.099  < 2e-16 ***
## div.summary$siteBI   1.2481     0.1690   7.385 1.42e-11 ***
## div.summary$siteCB   0.5897     0.1690   3.489 0.000655 ***
## div.summary$siteCC   0.5978     0.1690   3.537 0.000555 ***
## div.summary$siteDC  -0.1691     0.1690  -1.001 0.318743
## div.summary$siteEI   1.4325     0.1690   8.476 3.57e-14 ***
## div.summary$siteNB   0.8480     0.1690   5.018 1.62e-06 ***
## div.summary$siteRP   1.2943     0.1690   7.658 3.26e-12 ***
## div.summary$siteWI   1.0199     0.1690   6.034 1.45e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.478 on 135 degrees of freedom
## Multiple R-squared:  0.5692, Adjusted R-squared:  0.5437
## F-statistic: 22.29 on 8 and 135 DF,  p-value: < 2.2e-16
```

Model selection: Table S5

Model comparison results for Shannon Diversity in Table S6

```
## Model selection table
##        (Int) div.smm$ftc.mtr div.smm$dfw div.smm$dfw:div.smm$ftc.mtr
## mod1g 0.6188
## mod1c 1.1000      5.850e-06    -0.03980              -1.888e-07
## mod1f 1.2370     -5.434e-07
## mod1b 1.3600                   -0.03497
## mod1a 0.9296      2.780e-06
## mod1h 1.2220
## mod1d 1.1160
##      div.smm$are div.smm$are:div.smm$ftc.mtr div.smm$sit df  logLik  AICc
## mod1g                                                  + 10 -31.011  83.7
## mod1c                                                    5 -79.609 169.7
## mod1f    -0.5546              8.156e-06                   5 -81.416 173.3
## mod1b                                                    3 -92.309 190.8
## mod1a                                                    3 -92.744 191.7
## mod1h    -0.1273                                         3 -94.376 194.9
## mod1d                                                    2 -98.716 201.5
##        delta weight
## mod1g   0.00      1
## mod1c  85.98      0
```

```
## mod1f  89.59     0
## mod1b 107.11     0
## mod1a 107.98     0
## mod1h 111.25     0
## mod1d 117.84     0
## Models ranked by AICc(x)
```

Model comparison results for Abundance in Table S6

```
## Model selection table
##         (Int) div.smm$ftc.mtr div.smm$dfw div.smm$dfw:div.smm$ftc.mtr
## mod2g  102.30
## mod2c -293.50       0.007044      66.06                -0.0007946
## mod2f   60.90       0.001742
## mod2b   52.08                     24.55
## mod2h  177.50
## mod2d  223.40
## mod2a  245.20      -0.000325
##      div.smm$are div.smm$are:div.smm$ftc.mtr div.smm$sit df    logLik
## mod2g                                                  + 10  -967.009
## mod2c                                                    5  -992.054
## mod2f      341.90              -0.005165                 5  -998.939
## mod2b                                                    3 -1001.340
## mod2h       55.17                                        3 -1008.935
## mod2d                                                    2 -1011.449
## mod2a                                                    3 -1011.204
##         AICc delta weight
## mod2g 1955.7  0.00      1
## mod2c 1994.5 38.87      0
## mod2f 2008.3 52.64      0
## mod2b 2008.9 53.18      0
## mod2h 2024.0 68.37      0
## mod2d 2027.0 71.31      0
## mod2a 2028.6 72.91      0
## Models ranked by AICc(x)
```

Model comparison results for Alpha Diversity in Table S6

```
## Model selection table
##        (Int) div.smm$ftc.mtr div.smm$dfw div.smm$dfw:div.smm$ftc.mtr
## mod3g 6.563
## mod3d 8.069
## mod3a 7.532       7.993e-06
## mod3h 8.388
## mod3b 7.997                     0.01039
## mod3c 6.241       3.737e-05     0.11750              -2.86e-06
## mod3f 7.821       7.458e-06
##      div.smm$are div.smm$are:div.smm$ftc.mtr div.smm$sit df   logLik
## mod3g                                                  + 10 -319.592
## mod3d                                                    2 -374.727
## mod3a                                                    3 -373.695
## mod3h     -0.3830                                        3 -373.898
## mod3b                                                    3 -374.716
## mod3c                                                    5 -373.156
## mod3f     -0.1958              -1.956e-06                5 -373.179
##        AICc delta weight
```

```
## mod3g 660.8  0.00       1
## mod3d 753.5 92.70       0
## mod3a 753.6 92.72       0
## mod3h 754.0 93.13       0
## mod3b 755.6 94.77       0
## mod3c 756.7 95.91       0
## mod3f 756.8 95.96       0
## Models ranked by AICc(x)
```

Model comparison results for rarefied Diversity in Table S5

```
## Model selection table
##        (Int) div.smm$ftc.mtr div.smm$dfw div.smm$dfw:div.smm$ftc.mtr
## mod4g 1.685
## mod4c 2.432      8.805e-06    -0.06099                    -2.866e-07
## mod4f 2.618     -8.822e-07
## mod4b 2.824                   -0.05394
## mod4a 2.170      4.131e-06
## mod4h 2.592
## mod4d 2.447
##        div.smm$are div.smm$are:div.smm$ftc.mtr div.smm$sit df    logLik
## mod4g                                                    + 10   -93.400
## mod4c                                                       5  -133.494
## mod4f     -0.8297                   1.251e-05              5  -136.305
## mod4b                                                       3  -146.926
## mod4a                                                       3  -147.908
## mod4h     -0.1739                                          3  -150.289
## mod4d                                                       2  -154.029
##         AICc   delta weight
## mod4g 208.5   0.00      1
## mod4c 277.4  68.97      0
## mod4f 283.0  74.59      0
## mod4b 300.0  91.57      0
## mod4a 302.0  93.53      0
## mod4h 306.7  98.30      0
## mod4d 312.1 103.69      0
## Models ranked by AICc(x)
```


Variation in univariate diversity with site and time: Table 3

```
## Analysis of Variance Table
##
## Response: div.summary$alpha.p
##                                     Df  Sum Sq Mean Sq F value
## div.summary$site                     4  415.33 103.833  18.897
## div.summary$Time.Code2               2  615.71 307.857  56.028
## div.summary$site:div.summary$Time.Code2  8  543.50  67.938  12.364
## Residuals                          222 1219.82   5.495
##                                       Pr(>F)
## div.summary$site                   2.184e-13 ***
## div.summary$Time.Code2             < 2.2e-16 ***
## div.summary$site:div.summary$Time.Code2 1.288e-14 ***
## Residuals
## ---
```

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```
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Analysis of Variance Table
##
## Response: log(div.summary$N + 1)
##                                            Df  Sum Sq Mean Sq F value
## div.summary$site                            4 108.178  27.044  51.953
## div.summary$Time.Code2                      2 185.369  92.684 178.048
## div.summary$site:div.summary$Time.Code2     8  45.804   5.725  10.999
## Residuals                                 222 115.564   0.521
##                                              Pr(>F)
## div.summary$site                          < 2.2e-16 ***
## div.summary$Time.Code2                    < 2.2e-16 ***
## div.summary$site:div.summary$Time.Code2  4.737e-13 ***
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: div.summary$H
##                                            Df Sum Sq Mean Sq F value
## div.summary$site                            4 2.4019 0.60048 22.1887
## div.summary$Time.Code2                      2 0.2901 0.14505  5.3601
## div.summary$site:div.summary$Time.Code2     8 2.6962 0.33702 12.4536
## Residuals                                 222 6.0078 0.02706
##                                              Pr(>F)
## div.summary$site                          2.001e-15 ***
## div.summary$Time.Code2                     0.005329 **
## div.summary$site:div.summary$Time.Code2  1.021e-14 ***
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

## Analysis of Variance Table
##
## Response: div.summary$R2
##                                            Df  Sum Sq  Mean Sq F value
## div.summary$site                            4 0.65609 0.164023  21.306
## div.summary$Time.Code2                      2 0.19784 0.098922  12.850
## div.summary$site:div.summary$Time.Code2     8 0.79543 0.099429  12.915
## Residuals                                 222 1.70906 0.007698
##                                              Pr(>F)
## div.summary$site                          6.918e-15 ***
## div.summary$Time.Code2                    5.243e-06 ***
## div.summary$site:div.summary$Time.Code2  3.091e-15 ***
## Residuals
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Elements of Metacommunity Structure

run metacommunity analysis

```
## $Coherence
```

```
##           name        stat
## 1      embAbs 104.0000000
## 2           z   0.2349056
## 3           p   0.8142820
## 4     simMean 104.9900000
## 5 simVariance   4.2144586
## 6 method = r1          NA
```