Reisch & Hartig, Supplementary Material S2 - code and additional results

For: Species and genetic diversity patterns show diverging responses to land use intensity in central European grasslands

22/11/2020

Abstract

This document contains code and additional results from the data analysis of Reisch & Hartig: Species and genetic diversity patterns show diverging responses to land use intensity in central European grasslands. The complete analysis, code and data is available at https://github.com/florianhartig/Reisch-Hartig-2021. Note that habitats are occasionally abbreviated with German words MR (Magerrasen) = dry grassland, FW (Fettwiese) = Hay Meadow, because this is the coding used in the raw data.

Contents

Analysis of alpha diversity

In the first section of this analysis, we look at differences of local (alpha) species and genetic diversity between habitats.

Species alpha

Looking at species alpha diversity, we see a clear habitat pattern in which dry grasslands have higher local species richness (this is Fig. 2 in main paper)

```r
plot(alpha ~ as.factor(Plot) , data = sites$alpha2,
     ylab = "Species richness", xlab = "",
     col = grey.colors(2)[as.numeric(Habitat)], las = 2, notch = T)

legend("topright", c("Hay meadows", "Dry grasslands"), pch = 15, col = grey.colors(2))

library(beeswarm)
beeswarm(alpha ~ as.factor(Plot) , data = sites$alpha2,
         add = T, cex = 0.5, pch = 16)
```
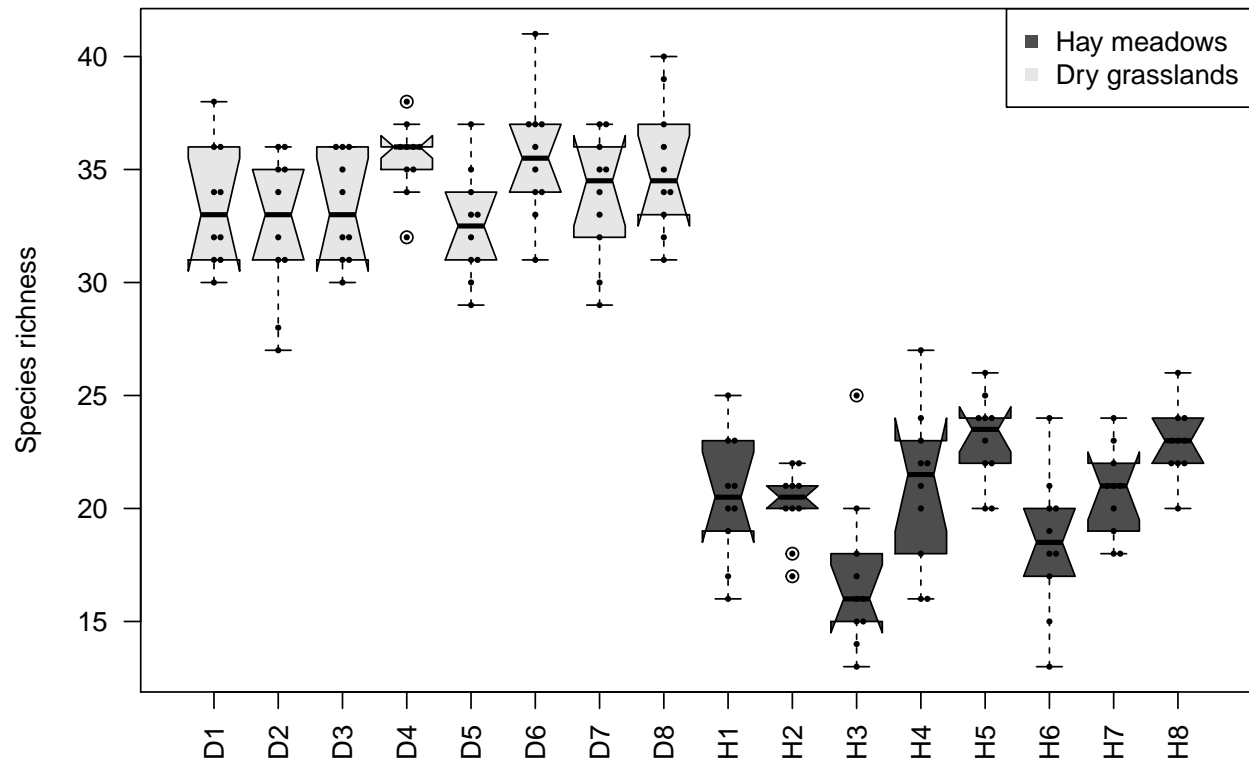
Regression to test for the dependence of alpha on all predictors confirms that these differences are significant

```
alphaT = glmer(alpha ~ Habitat + scale(Distanz) + scale(`HA (m²)`)
               + (1|Plot), data = sites$alpha2, family = poisson)
summary(alphaT)
```

```
## Generalized linear mixed model fit by maximum likelihood (Laplace
##   Approximation) [glmerMod]
##  Family: poisson  ( log )
## Formula: alpha ~ Habitat + scale(Distanz) + scale(`HA (m²)`) + (1 | Plot)
##    Data: sites$alpha2
##
##      AIC      BIC   logLik deviance df.resid
##    883.6    899.0   -436.8    873.6      155
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -1.58893 -0.39694  0.08864  0.37352  1.53683
##
## Random effects:
##  Groups Name        Variance Std.Dev.
##  Plot   (Intercept) 0        0
## Number of obs: 160, groups:  Plot, 16
##
## Fixed effects:
##                   Estimate Std. Error z value Pr(>|z|)
## (Intercept)       3.024937   0.027301 110.800   <2e-16 ***
## HabitatMagerrasen 0.492702   0.039113  12.597   <2e-16 ***
## scale(Distanz)    0.018518   0.017535   1.056    0.291
```

2

```
## scale(`HA (m²)`)  -0.003164   0.015641  -0.202     0.840
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) HbttMg scl(D)
## HabttMgrrsn -0.827
## scal(Dstnz)  0.340 -0.487
## sc(`HA(²)`)  0.319 -0.444  0.207
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

We did some further plots to explore possible nonlinear confounding with other predictors, but didn't see an issue that would question theses general result that species diversity is higher in dry grasslands.

```r
par(mfrow = c(1,2))
plot(alpha ~ Distanz , data = sites$alpha2, col = as.numeric(Habitat))
plot(alpha ~ log10(`HA (m²)`) , data = sites$alpha2, col = as.numeric(Habitat))
```
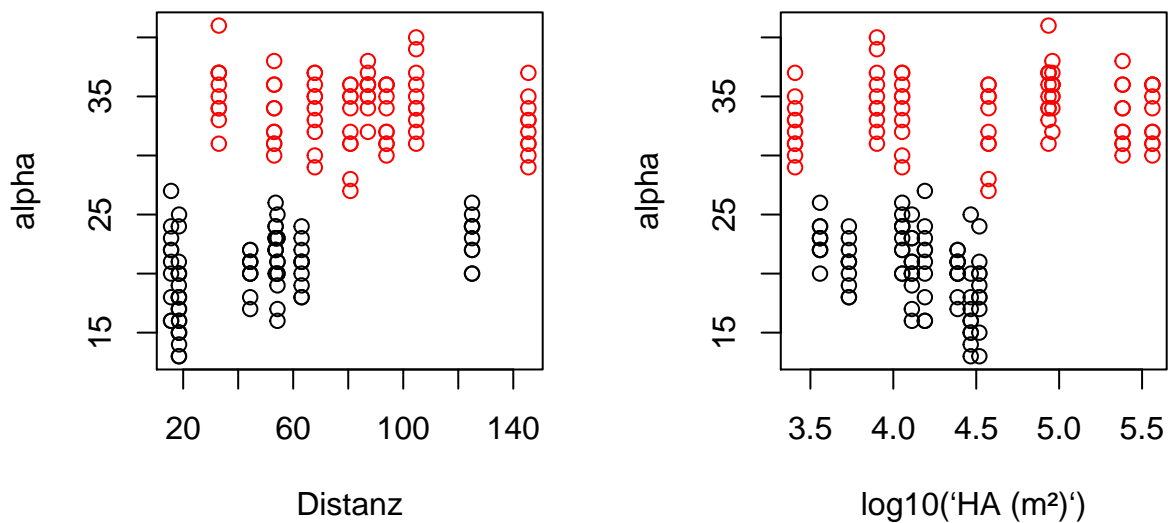

Our conclusion the main factor associated with species alpha is habitat (dry grassland has higher species alpha).

Genetic alpha

As a measure of genetic diversity, we consider AMOVA sums of squares divided by n-1 (here: SSWP/n-1). The advantage of this metric is that it is more independent of sample size than alternatives. For an analysis using an alternative metric, see below.

To analyze differences across habitats, we first plot SSWP/n-1 for the 6 species each in the dry and mesic grasslands against the frequency (FR) of subplots in which the species was found. The dashed line in each plot shows a linear regression estimate across all species in a given habitat, the solid lines show linear regression estimate per species.

```r
par(mfrow = c(1,2))
plot(`SSWP/n-1` ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Magerrasen",],
     main = "Dry grasslands", pch = as.numeric(Art), xlab = "Frequency",
     ylab = "Genetic diversity [SSWP/n-1]", ylim = c(0,70) )
```

3

```
fit <- lm(`SSWP/n-1` ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Magerrasen",])
abline(fit, lty = 2)

species = unique(sites$genAlpha$Art[sites$genAlpha$Habitat == "Magerrasen"])
for(sp in species){
  xrange = range(sites$genAlpha$FR[sites$genAlpha$Art == sp])
  fit <- lm(`SSWP/n-1` ~ FR , data = sites$genAlpha[sites$genAlpha$Art == sp,])
  y1 = predict(fit, newdata = data.frame(FR = xrange[1]))
  y2 = predict(fit, newdata = data.frame(FR = xrange[2]))
  lines(xrange, c(y1, y2))
}

legend("topleft", legend = species, pch=as.numeric(species), cex = 0.8 )

plot(`SSWP/n-1` ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Fettwiese",],
     main = "Hay Meadows", pch = as.numeric(Art), xlab = "Frequency",
     ylab = "Genetic diversity [SSWP/n-1]", ylim = c(0,70))

fit <- lm(`SSWP/n-1` ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Fettwiese",])
abline(fit, lty = 2)

species = unique(sites$genAlpha$Art[sites$genAlpha$Habitat == "Fettwiese"])
for(sp in species){
  xrange = range(sites$genAlpha$FR[sites$genAlpha$Art == sp])
  fit <- lm(`SSWP/n-1` ~ FR , data = sites$genAlpha[sites$genAlpha$Art == sp,])
  y1 = predict(fit, newdata = data.frame(FR = xrange[1]))
  y2 = predict(fit, newdata = data.frame(FR = xrange[2]))
  lines(xrange, c(y1, y2))
}

legend("topleft", legend = species, pch=as.numeric(species), cex = 0.8 )
```
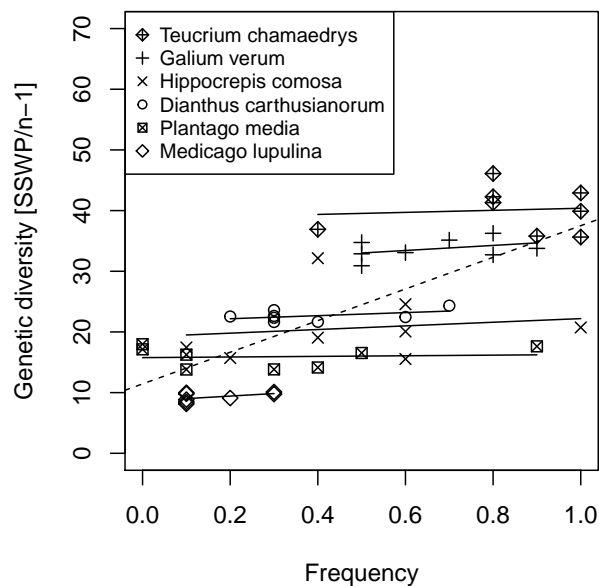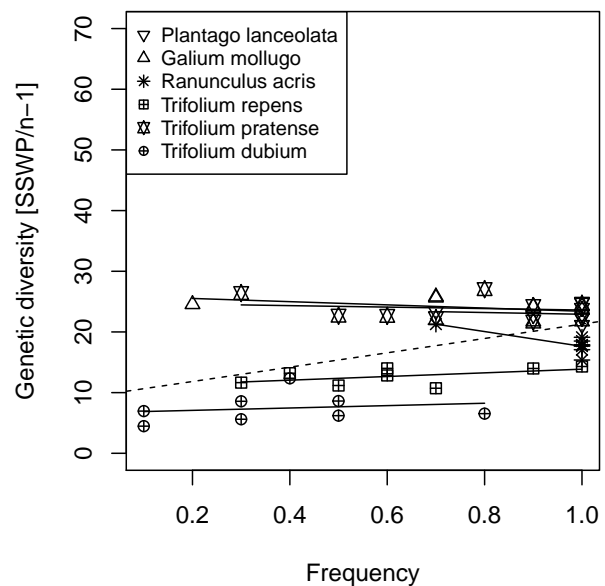
Dry grasslands **Hay Meadows**

The comparison suggests that genetic diversity differs little within species, and apparent correlations between

FR and genetic diversity occur because of a confounding of FR with species. To separate these effects, we calculated linear mixed models, with population and species as random intercepts.

```r
full <- lmer(`SSWP/n-1` ~ Habitat * scale(FR) + scale(`HA (m²)`) +
             scale(Distanz) + (1|Population) + (1|Art) , data =
             sites$genAlpha, REML = F)
summary(full)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use
##   Satterthwaite's method [lmerModLmerTest]
## Formula:
## `SSWP/n-1` ~ Habitat * scale(FR) + scale(`HA (m²)`) + scale(Distanz) +
##     (1 | Population) + (1 | Art)
##    Data: sites$genAlpha
##
##      AIC      BIC   logLik deviance df.resid
##    511.2    534.3   -246.6    493.2       87
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.3640 -0.5007 -0.0612  0.4707  4.6340
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  Population (Intercept)  0.2302   0.4798
##  Art        (Intercept) 66.9680   8.1834
##  Residual                5.4261   2.3294
## Number of obs: 96, groups:  Population, 16; Art, 12
##
## Fixed effects:
##                            Estimate Std. Error       df t value Pr(>|t|)
## (Intercept)                 18.4747     3.3823  12.0918   5.462 0.000141
## HabitatMagerrasen            5.4216     4.7906  12.1681   1.132 0.279569
## scale(FR)                   -0.1911     0.5982  85.4007  -0.319 0.750224
## scale(`HA (m²)`)             0.2236     0.3066  13.2769   0.729 0.478428
## scale(Distanz)               0.2373     0.3246  15.7950   0.731 0.475424
## HabitatMagerrasen:scale(FR)  1.1369     0.8206  83.1458   1.386 0.169593
##
## (Intercept)                 ***
## HabitatMagerrasen
## scale(FR)
## scale(`HA (m²)`)
## scale(Distanz)
## HabitatMagerrasen:scale(FR)
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr) HbttMg sc(FR) s(`HA( scl(D)
## HabttMgrrsn -0.710
## scale(FR)   -0.089  0.072
## sc(`HA(²)`)  0.054 -0.073 -0.053
## scal(Dstnz)  0.075 -0.085 -0.304  0.200
## HbttMg:(FR)  0.069 -0.027 -0.750  0.042  0.291
```

In the results, none of the considered predictors is significant. Habitat is also not significant in a single regression, as long as species identity is included as a random intercept.

```
full <- lmer(`SSWP/n-1` ~ Habitat + (1|Population) + (1|Art),
             data = sites$genAlpha, REML = F)
summary(full)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use
##   Satterthwaite's method [lmerModLmerTest]
## Formula: `SSWP/n-1` ~ Habitat + (1 | Population) + (1 | Art)
##    Data: sites$genAlpha
##
##      AIC      BIC   logLik deviance df.resid
##    506.8    519.6   -248.4    496.8       91
##
## Scaled residuals:
##     Min      1Q  Median      3Q     Max
## -2.1299 -0.5121 -0.0549  0.4621  4.7175
##
## Random effects:
##  Groups     Name        Variance Std.Dev.
##  Population (Intercept)  0.1304   0.3612
##  Art        (Intercept) 72.8985   8.5381
##  Residual                5.6877   2.3849
## Number of obs: 96, groups:  Population, 16; Art, 12
##
## Fixed effects:
##                  Estimate Std. Error     df t value Pr(>|t|)
## (Intercept)        18.186      3.505 12.030   5.189 0.000224 ***
## HabitatMagerrasen   5.530      4.957 12.030   1.116 0.286378
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##            (Intr)
## HabttMgrrsn -0.707
```

However, species (in the data called "Art") is obviously a significant predictor for genetic diversity, and taken as a single fixed effect, it is a significant predictor.

```
fit <- lmer(`SSWP/n-1` ~  Art + (1|Population)  ,  data = sites$genAlpha)
anova(fit)
```

```
## Type III Analysis of Variance Table with Satterthwaite's method
##     Sum Sq Mean Sq NumDF  DenDF F value    Pr(>F)
## Art 7709.1  700.82    11 75.813  123.25 < 2.2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The problem is that species is perfectly collinear with habitat, and closely collinear with FR, so that it's difficult to separate whether effects are really coming from the habitat (via the species that are in there), or via the current random selection of species. In fact, both habitat and frequency would be significant when not controlling for species identity, but given the previous results, and the clear collinearity between species identity and other factors, interpreting this results causally seems statistically invalid to us.

```
full <- lmer(`SSWP/n-1` ~  Habitat * scale(FR) + scale(`HA (m²)`)
             + scale(Distanz) + (1|Population)  ,
```

```
              data = sites$genAlpha, REML = F)
summary(full)
```

```
## Linear mixed model fit by maximum likelihood . t-tests use
##   Satterthwaite's method [lmerModLmerTest]
## Formula:
## `SSWP/n-1` ~ Habitat * scale(FR) + scale(`HA (m²)`) + scale(Distanz) +
##     (1 | Population)
##    Data: sites$genAlpha
##
##     AIC      BIC   logLik deviance df.resid
##   647.2    667.7   -315.6    631.2       88
##
## Scaled residuals:
##      Min       1Q   Median       3Q      Max
## -2.66122 -0.70808  0.02347  0.63996  2.32656
##
## Random effects:
##  Groups      Name        Variance Std.Dev.
##  Population (Intercept)  0.00     0.00
##  Residual               41.99     6.48
## Number of obs: 96, groups:  Population, 16
##
## Fixed effects:
##                           Estimate Std. Error       df t value
## (Intercept)              16.669891    1.212008 96.000000  13.754
## HabitatMagerrasen        10.461055    1.855476 96.000000   5.638
## scale(FR)                 3.816992    1.103762 96.000000   3.458
## scale(`HA (m²)`)          0.130509    0.761002 96.000000   0.171
## scale(Distanz)            0.004005    0.787422 96.000000   0.005
## HabitatMagerrasen:scale(FR)  4.598303  1.502450 96.000000   3.061
##                           Pr(>|t|)
## (Intercept)               < 2e-16 ***
## HabitatMagerrasen         1.73e-07 ***
## scale(FR)                 0.000812 ***
## scale(`HA (m²)`)          0.864195
## scale(Distanz)            0.995952
## HabitatMagerrasen:scale(FR) 0.002865 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Correlation of Fixed Effects:
##             (Intr) HbttMg sc(FR) s(`HA( scl(D)
## HabttMgrrsn -0.799
## scale(FR)   -0.456  0.346
## sc(`HA(²)`)  0.357 -0.456 -0.039
## scal(Dstnz)  0.441 -0.503 -0.230  0.197
## HbttMg:(FR)  0.355 -0.130 -0.746  0.031  0.220
## convergence code: 0
## boundary (singular) fit: see ?isSingular
```

Rather, as noted before, it seems that both the habitat effects and the frequency effects in the latter regression are essentially driven by species identity, in that some species simply have a higher diversity, or at least there are not enough species to separate between an effect of species identity, and true FR / Habitat effects.

To confirm that intuition, we additionally calculated a t-test between the average genetic diversity values per species for each habitat (n=6 for each group)

```
x = aggregate(`SSWP/n-1` ~ Art + Habitat, FUN = mean, data = sites$genAlpha)
t.test(`SSWP/n-1` ~ Habitat, data = x)
```

```
##
##  Welch Two Sample t-test
##
## data:  SSWP/n-1 by Habitat
## t = -1.0192, df = 8.2069, p-value = 0.3372
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -17.986717   6.927195
## sample estimates:
##  mean in group Fettwiese mean in group Magerrasen
##                 18.18584                 23.71560
```

The results show that habitat effects are n.s. when comparing only mean genetic diversity per species between habitat (i.e. n=6 per group).

Moreover, the collinearity between FR and Species is created by the fact that the species with higher FR range also seem to have higher genetic diversity, although there is no significant correlation between FR and genetic diversity within species.

To test if this relationship is significant, we correlated mean FR and mean genetic diversity per species

```
x1 = aggregate(`SSWP/n-1` ~ Art, FUN = mean, data = sites$genAlpha)
x2 = aggregate(FR ~ Art, FUN = mean, data = sites$genAlpha)
cor.test(x1$`SSWP/n-1`, x2$FR)
```

```
##
##  Pearson's product-moment correlation
##
## data:  x1$`SSWP/n-1` and x2$FR
## t = 2.1086, df = 10, p-value = 0.06119
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.02807041  0.85610208
## sample estimates:
##       cor
## 0.5547683
```

The relationship was again n.s., but given the small sample size (n=12), our results do not exclude that such an effect exists. Given the general plausibility of such a relationship, we would encourage future studies with larger sample sizes to look again for such an effect.

Alternative measure of genetic alpha diversity (gene diversity / H)

We decided to analyze genetic alpha diversity by AMOVA sums of squares divided by n-1 (here: SSWP/n-1). The advantage of this metric is that it is more independent of sample size than alternatives. A reviewer suggested to also calculated the same pattern pattern for gene diversity (H). According to this measure, differences between species and habitats are less pronounced (see below), but not in disagreement with the general conclusions of our study.

```
par(mfrow = c(1,2))
plot(GD ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Magerrasen",],
```

```r
      main = "Dry grasslands", pch = as.numeric(Art), xlab = "Frequency",
      ylab = "Genetic diversity [GD]", ylim = c(0,0.5) )

fit <- lm(GD ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Magerrasen",])
abline(fit, lty = 2)

species = unique(sites$genAlpha$Art[sites$genAlpha$Habitat == "Magerrasen"])
for(sp in species){
  xrange = range(sites$genAlpha$FR[sites$genAlpha$Art == sp])
  fit <- lm(GD ~ FR , data = sites$genAlpha[sites$genAlpha$Art == sp,])
  y1 = predict(fit, newdata = data.frame(FR = xrange[1]))
  y2 = predict(fit, newdata = data.frame(FR = xrange[2]))
  lines(xrange, c(y1, y2))
}

legend("topleft", legend = species, pch=as.numeric(species), cex = 0.8 )

plot(GD ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Fettwiese",],
      main = "Hay Meadows", pch = as.numeric(Art), xlab = "Frequency",
      ylab = "Genetic diversity [GD]", ylim = c(0,0.5))

fit <- lm(GD ~ FR , data = sites$genAlpha[sites$genAlpha$Habitat == "Fettwiese",])
abline(fit, lty = 2)

species = unique(sites$genAlpha$Art[sites$genAlpha$Habitat == "Fettwiese"])
for(sp in species){
  xrange = range(sites$genAlpha$FR[sites$genAlpha$Art == sp])
  fit <- lm(GD ~ FR , data = sites$genAlpha[sites$genAlpha$Art == sp,])
  y1 = predict(fit, newdata = data.frame(FR = xrange[1]))
  y2 = predict(fit, newdata = data.frame(FR = xrange[2]))
  lines(xrange, c(y1, y2))
}

legend("topleft", legend = species, pch=as.numeric(species), cex = 0.8 )
```

Dry grasslands

Legend:
- ⊕ Teucrium chamaedrys
- + Galium verum
- × Hippocrepis comosa
- ○ Dianthus carthusianorum
- ⊠ Plantago media
- ◇ Medicago lupulina

Hay Meadows

Legend:
- ▽ Plantago lanceolata
- △ Galium mollugo
- ✱ Ranunculus acris
- ⊞ Trifolium repens
- ⊠ Trifolium pratense
- ⊕ Trifolium dubium

Axes: Genetic diversity [GD] vs Frequency

Analysis of beta diversity

Species beta

Visualization of the log10 abundance of site / species, clustered by species. Green colors are rare / absent, yellow colors are small abundances, red colors are high abundances.

```
heatmap(log10(t(sites$community)+1), Colv = NA,scale="column", col = terrain.colors(256))
```
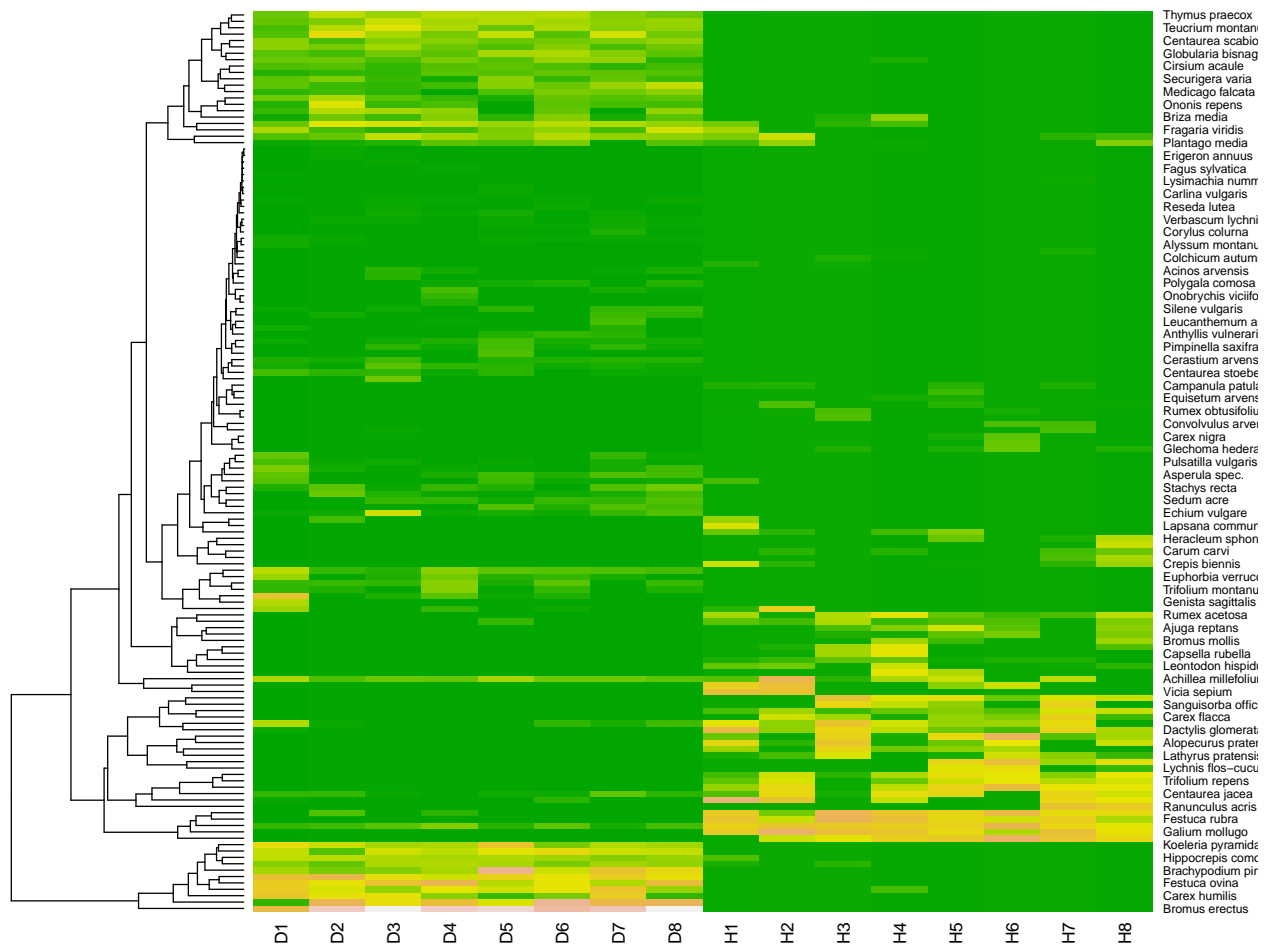
We calculate species beta via multivariate homogeneity of group dispersions (variances)

```
distSpecies = vegdist(sites$community, method="bray")
```

```
mod <- betadisper(distSpecies, sites$alpha$Habitat)
mod
```

```
##
##  Homogeneity of multivariate dispersions
##
## Call: betadisper(d = distSpecies, group = sites$alpha$Habitat)
##
## No. of Positive Eigenvalues: 15
## No. of Negative Eigenvalues: 0
##
## Average distance to median:
##  Fettwiese Magerrasen
##     0.3756     0.2435
##
## Eigenvalues for PCoA axes:
## (Showing 8 of 15 eigenvalues)
##   PCoA1   PCoA2   PCoA3   PCoA4   PCoA5   PCoA6   PCoA7   PCoA8
## 3.04065 0.40635 0.31489 0.23082 0.20848 0.14773 0.12665 0.07148
```

Plotting the results shows the clear separation of the two habitats.

```
plot(mod, ellipse = TRUE, hull = FALSE, conf = 0.90, xlim = c(-0.7, 0.7), ylim = c(-0.7, 0.7)) # 90% da
```

mod
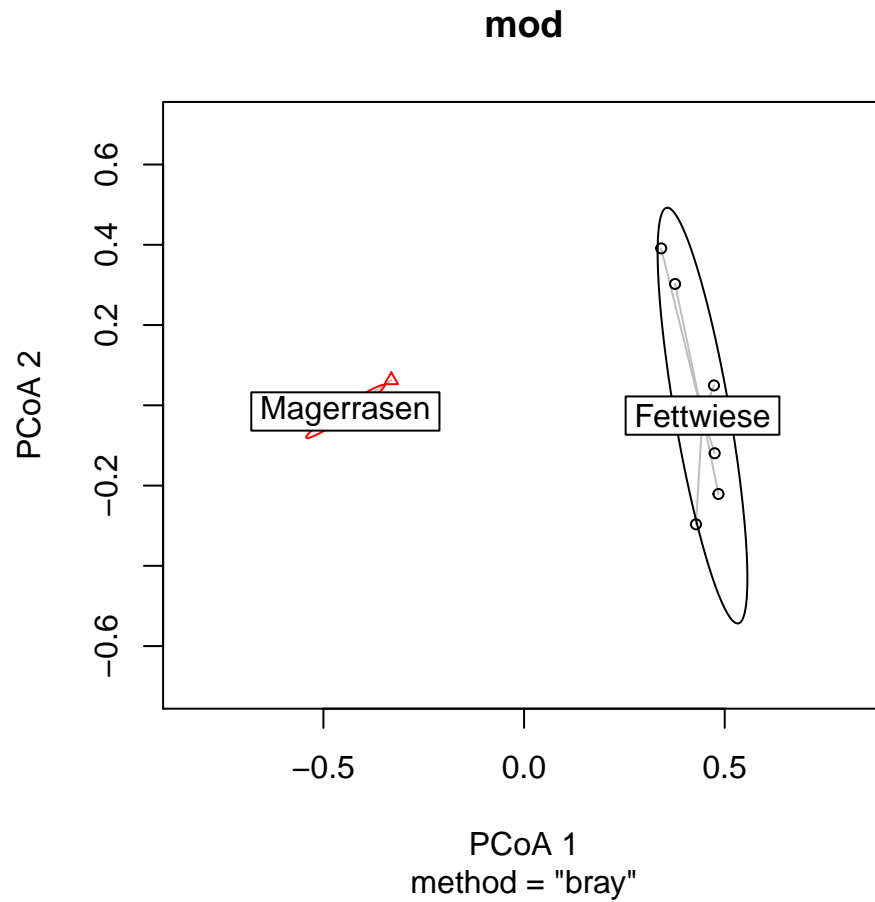
What we are mostly interest in, however, is the variation within habitat, i.e. differences of plots to the centroid.
Visually:

```
boxplot(mod)
```
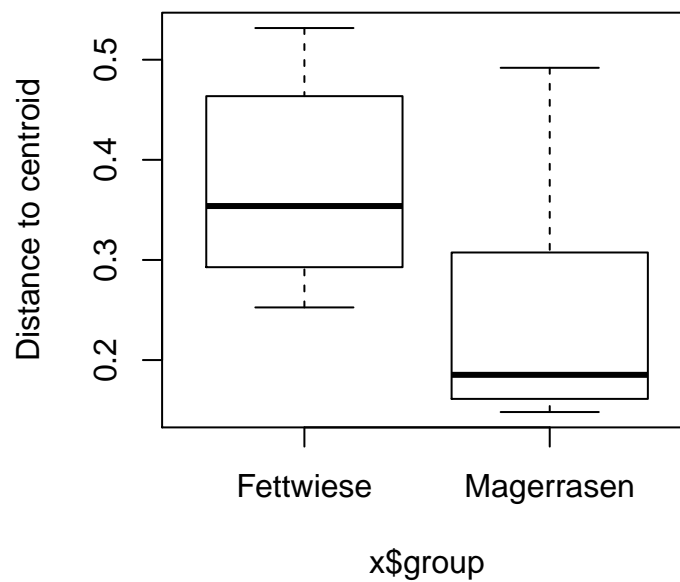
ANOVA and permutation test confirm the visual impression that the Fettwiese is more variable.

```
anova(mod)
```

```
## Analysis of Variance Table
##
## Response: Distances
##           Df    Sum Sq  Mean Sq F value  Pr(>F)
## Groups     1 0.069824 0.069824   5.515 0.03407 *
## Residuals 14 0.177250 0.012661
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
permutest(mod, pairwise = TRUE, permutations = 499)
```

```
##
## Permutation test for homogeneity of multivariate dispersions
## Permutation: free
## Number of permutations: 499
##
## Response: Distances
##           Df    Sum Sq  Mean Sq     F N.Perm Pr(>F)
## Groups     1 0.069824 0.069824 5.515    499  0.018 *
## Residuals 14 0.177250 0.012661
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Pairwise comparisons:
## (Observed p-value below diagonal, permuted p-value above diagonal)
##            Fettwiese Magerrasen
## Fettwiese               0.042
## Magerrasen  0.034066
```

Additional Mantel test for spatial structure, separate for habitats. First hay meadow (FW):

```
mantel(as.matrix(distSpecies)[1:8,1:8], sites$geoDist[1:8,1:8],
       method="pearson", permutations=999)
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = as.matrix(distSpecies)[1:8, 1:8], ydis = sites$geoDist[1:8,      1:8], method = "pears
##
## Mantel statistic r: 0.3382
##       Significance: 0.115
##
## Upper quantiles of permutations (null model):
##   90%   95% 97.5%   99%
## 0.353 0.428 0.482 0.562
## Permutation: free
## Number of permutations: 999
```

then dry grasslands (MR):

```
mantel(as.matrix(distSpecies)[9:16,9:16], sites$geoDist[9:16,9:16],
       method="pearson", permutations=999)
```

```
##
## Mantel statistic based on Pearson's product-moment correlation
##
## Call:
## mantel(xdis = as.matrix(distSpecies)[9:16, 9:16], ydis = sites$geoDist[9:16,      9:16], method = "p
##
## Mantel statistic r: 0.5542
##       Significance: 0.006
##
## Upper quantiles of permutations (null model):
##    90%   95% 97.5%   99%
## 0.263 0.349 0.423 0.498
## Permutation: free
## Number of permutations: 999
```

Result: hay meadow not significant with geographic distance, but dry grasslands are.

Genetic beta

For genetic beta, we consider PhiPT as measure of genetic turnover. Visual impressions for all species

Genetic turnover for all species

```r
par(mfrow = c(3,4))
for(i in 1:12) image(t(sites$genBeta[[i]]), col = terrain.colors(256), main = unique(sites$genAlpha$Art
```
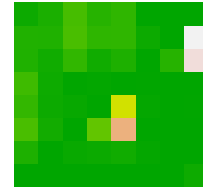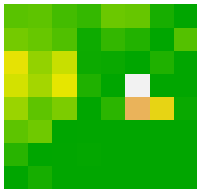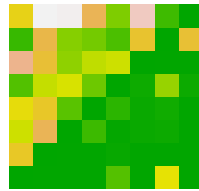
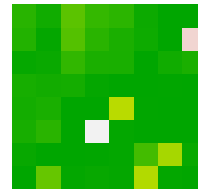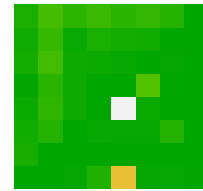| Teucrium chamaedrys | Galium verum | Hippocrepis comosa | Dianthus carthusianorum |

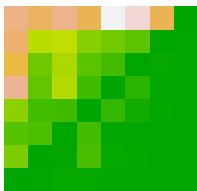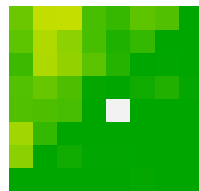| Plantago media | Medicago lupulina | Plantago lanceolata | Galium mollugo |

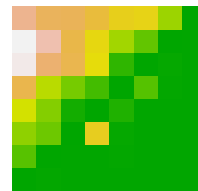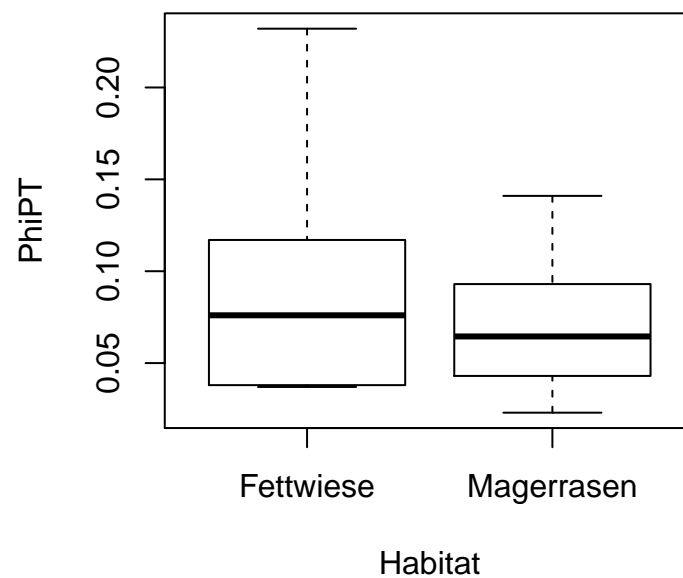| Ranunculus acris | Trifolium repens | Trifolium pratense | Trifolium dubium |

Values of PhiPT against habitat (note: we select c(1:6, 49:54) to get 1 value per species, across sites we have identical PhiPT values)

```r
boxplot(PhiPT ~ Habitat , data = sites$genAlpha[c(1:6, 49:54),])
```

t-test shows that differences are n.s.

```
t.test(sites$genAlpha$PhiPT[1:6], sites$genAlpha$PhiPT[49:54])
```

```
##
##  Welch Two Sample t-test
##
## data:  sites$genAlpha$PhiPT[1:6] and sites$genAlpha$PhiPT[49:54]
## t = -0.71424, df = 7.9428, p-value = 0.4955
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.10370052  0.05470052
## sample estimates:
## mean of x mean of y
##    0.0715    0.0960
```

Mantel tests to test for spatial signal in genetic diversity

```
# note: genetic data are ordered first the MR species, then the FW
distSpecies = vegdist(sites$community, method="bray")

outMR = rep(NA,6)
for (i in 7:12) outMR[i-6] = mantel(sites$genBeta[[i]], sites$geoDist[1:8,1:8], permutations=9999)$sign
outMR
```

```
## [1] 0.1521 0.1894 0.0250 0.0183 0.0005 0.0379
```

```
outFW = rep(NA,6)
for (i in 1:6) outFW[i] = mantel(sites$genBeta[[i]], sites$geoDist[9:16,9:16], permutations=9999)$signi
outFW
```

```
## [1] 0.0026 0.0167 0.4557 0.1061 0.0256 0.0912
```

Analysis of (species) gamma diversity

Regarding gamma diversity, we only considered species, as we did not see a sensible way to define absolute genetic gamma diversity

```
countsFW = apply(sites$community[1:8,],2, sum)
countsMR = apply(sites$community[9:16,],2, sum)
sum(countsFW > 0)
```

```
## [1] 92
```

```
sum(countsMR > 0)
```

```
## [1] 70
```

Result: FW has higher diversity

Reproducibility information

```
sessionInfo()
```

```
## R version 3.6.1 (2019-07-05)
## Platform: x86_64-apple-darwin15.6.0 (64-bit)
```

```
## Running under: macOS Catalina 10.15.7
##
## Matrix products: default
## BLAS:   /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRblas.0.dylib
## LAPACK: /Library/Frameworks/R.framework/Versions/3.6/Resources/lib/libRlapack.dylib
##
## locale:
## [1] en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] beeswarm_0.2.3 betapart_1.5.1  vegan_2.5-6      lattice_0.20-38
## [5] permute_0.9-5   lmerTest_3.1-0  lme4_1.1-21      Matrix_1.2-17
##
## loaded via a namespace (and not attached):
##  [1] Rcpp_1.0.2            compiler_3.6.1      pillar_1.4.2
##  [4] nloptr_1.2.1         magic_1.5-9         tools_3.6.1
##  [7] boot_1.3-22          digest_0.6.20       evaluate_0.14
## [10] tibble_2.1.3         gtable_0.3.0        nlme_3.1-140
## [13] mgcv_1.8-31          pkgconfig_2.0.2     rlang_0.4.7
## [16] fastmatch_1.1-0      parallel_3.6.1      yaml_2.2.0
## [19] xfun_0.9             cluster_2.1.0       stringr_1.4.0
## [22] dplyr_0.8.3          knitr_1.24          rcdd_1.2-2
## [25] grid_3.6.1           tidyselect_0.2.5    glue_1.3.1
## [28] R6_2.4.0             rmarkdown_1.15      minqa_1.2.4
## [31] purrr_0.3.3          ggplot2_3.2.1       magrittr_1.5
## [34] scales_1.0.0         htmltools_0.3.6     MASS_7.3-51.4
## [37] splines_3.6.1        abind_1.4-5         assertthat_0.2.1
## [40] picante_1.8          ape_5.3             colorspace_1.4-1
## [43] numDeriv_2016.8-1.1  geometry_0.4.4      stringi_1.4.3
## [46] lazyeval_0.2.2       munsell_0.5.0       crayon_1.3.4
```