

Effects of Soil Warming Plus Nitrogen Addition on Plant Richness and Diversity at Harvard Forest

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PROJECT OVERVIEW

The overall objective of this project is to investigate whether soil warming and N fertilization alter plant biodiversity through time (2006-2009). The data for this project came from the Harvard Forest LTER site. [link](#)

Research Question: What are the short-term effects of soil warming plus N additions on plant richness and diversity at Harvard Forest from 2006-2009?

Hypothesis 1: Richness and diversity will decrease over time in warming treatments

Hypothesis 2: Richness and diversity will increase over time with the addition of nitrogen

BACKGROUND

Write about study design/ methods/ Time period

1) SETUP

A. Retrieve and Set your Working Directory

B. Install Packages

This analysis will require several packages. The `require()` function in R returns TRUE if the package was successfully loaded or FALSE if the package failed to load. This for loop loads each package and installs the package when `require()` returns FALSE.

```
package.list = c('vegan', 'tidyr', 'dplyr', 'codyn', 'ggplot2',  
'cowplot', 'MullerPlot', 'RColorBrewer', 'lubridate', 'reshape2', 'lubridate', 'wesanderson',  
'TTR', 'xtable', 'multcomp', 'pander', 'png', 'grid', 'tseries', 'nlme', 'forecast', 'lsmeans')  
  
for (package in package.list) {  
  if (!require(package, character.only = TRUE, quietly = TRUE)) {  
    install.packages(package, repos='http://cran.us.r-project.org')  
    library(package, character.only = TRUE) }  
}
```

2) LOADING DATA

A. Description of Data Set

[Explain what is contained in the different data sheets...] 1. 'plant' 2. 'nmin' 3. 'resp'

```
setwd("/Users/bhbeidler/GitHub/QB2017_DivPro/Data")
plant = read.csv("./HF_plants_treat.csv")
nmin = read.csv("./HF_nmin.csv", stringsAsFactors = FALSE)
resp = read.csv("./HF_soilresp.csv", stringsAsFactors = FALSE)
```

B. Data Wrangling

Subsetting the data by year and producing site by species matrices.

```
# Making the Site by Species Matrix for the plant data set
plant_sbys = plant[,6:43]

# Subsetting the data into the different years
plant_06 = (filter(plant, year == 2006))
plant_07 = (filter(plant, year == 2007))
plant_08 = (filter(plant, year == 2008))
plant_09 = (filter(plant, year == 2009))

# Separating out the treatments from the site by species matrices
plant_06_sbys = plant_06[,6:43]
plant_07_sbys = plant_07[,6:43]
plant_08_sbys = plant_08[,6:43]
plant_09_sbys = plant_09[,6:43]
```

3) DATA VISUALIZATION & EDA

[plots that show richness for each site/ abundance for a particular species] Visualizing Beta Diversity

```
# Visualizing the Plant data set
str(plant, max.level = 1)
```

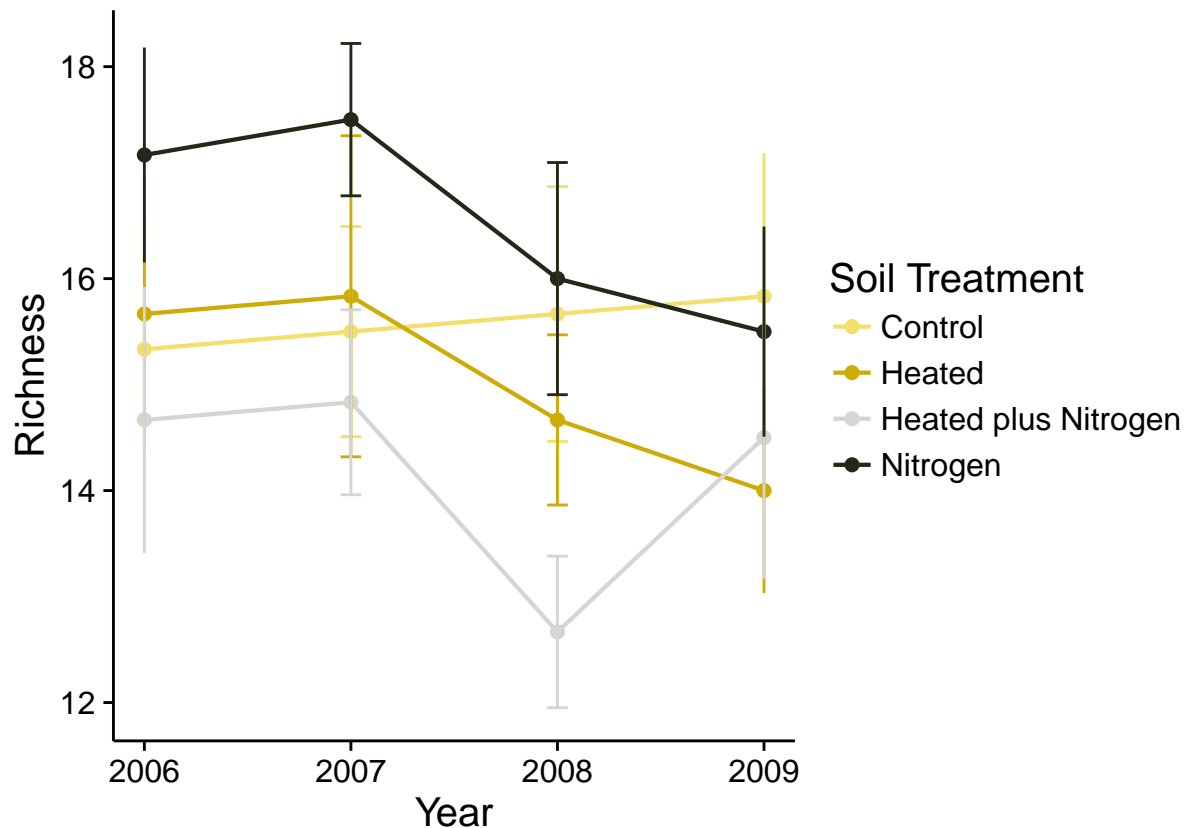
```
## 'data.frame':   96 obs. of  45 variables:
## $ year      : int  2006 2006 2006 2006 2006 2006 2007 2007 2007 2007 ...
## $ plot      : int   1 12 14 19 20 24 1 12 14 19 ...
## $ treatment : int   1 1 1 1 1 1 1 1 1 1 ...
## $ N_treat   : Factor w/ 2 levels "control","N fertilized": 1 1 1 1 1 1 1 1 1 1 ...
## $ heat_treat: Factor w/ 2 levels "control","heated": 1 1 1 1 1 1 1 1 1 1 ...
## $ acersp    : int   0 1 0 0 0 0 0 0 0 0 ...
## $ acepen    : int   2 4 13 17 8 18 3 5 13 12 ...
## $ acerub    : int   3 2 6 0 1 1 5 5 7 2 ...
## $ aranud    : int  14 0 16 19 9 7 11 0 15 28 ...
## $ aritri    : int   0 0 0 0 0 0 0 0 0 0 ...
## $ betale    : int   0 0 1 0 0 0 1 0 2 0 ...
## $ betlen    : int   1 0 0 0 0 0 0 0 0 0 ...
## $ betspp    : int   0 0 0 0 0 0 1 0 0 0 ...
## $ carpen    : int   2 0 2 139 1 0 32 0 1 65 ...
## $ casden    : int   0 0 0 0 0 0 0 0 0 0 ...
## $ clibor    : int   0 8 0 0 0 0 0 13 0 0 ...
## $ coptri    : int   0 0 0 0 0 0 0 0 0 0 ...
## $ craspp    : int   0 0 0 0 0 0 0 0 0 0 ...
## $ denobs    : int   0 7 50 28 127 7 0 8 0 31 ...
```

```
## $ denpun      : int  0 814 9 324 2 0 3 667 11 275 ...
## $ dipcom      : int  0 0 0 0 16 0 0 0 26 0 ...
## $ dryspp      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ faggra      : int  1 0 0 2 0 3 1 0 0 2 ...
## $ gaupro      : int 117 43 124 275 95 15 87 50 80 269 ...
## $ goopub      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ hupluc      : int  0 21 0 0 152 0 0 5 0 0 ...
## $ lyolig      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ maican      : int 170 334 3 233 27 70 117 236 0 147 ...
## $ medvir      : int  3 0 1 3 1 0 0 0 5 22 ...
## $ mitrep      : int  50 467 142 0 0 0 44 570 185 0 ...
## $ monuni      : int  0 0 4 0 0 0 0 0 1 0 ...
## $ pinstr      : int  0 2 1 0 0 0 0 3 1 0 ...
## $ pruser      : int  0 0 3 1 2 0 2 0 6 2 ...
## $ quealb      : int  0 0 0 0 0 1 0 0 0 0 ...
## $ querub      : int  1 5 0 0 1 0 1 1 0 1 ...
## $ smirac      : int  0 0 0 0 0 0 0 0 2 1 ...
## $ snag        : int  0 0 0 0 0 0 0 0 0 0 ...
## $ tribor      : int 14 1 11 30 36 27 5 1 9 22 ...
## $ tsucan      : int  0 0 0 0 0 0 0 0 0 0 ...
## $ unksp      : int  0 0 0 0 1 0 0 1 0 0 ...
## $ uvuses      : int 27 19 35 24 24 9 31 38 35 32 ...
## $ vaccsp      : int 56 0 48 14 145 31 47 0 46 13 ...
## $ vibace      : int  0 0 0 4 3 18 0 0 0 4 ...
## $ vibden      : int  0 0 5 0 0 0 0 0 3 0 ...
## $ viblen      : int  0 0 57 0 5 0 0 0 55 0 ...
```

```
# Calculate observed richness from time-by-species matrix
p_richness = as.data.frame(rowSums(plant[,-c(1:5)] > 0))
# Create data frame with experimental design and richness data
p_rich.all = data.frame(plant[,1:5,], p_richness)
# Rename column
names(p_rich.all)[6] = "richness"

# avg. richness per group
# stand. dev. per group
# num. obs. per group
# calc. std. err. mean.
p_rich.treat.plot = group_by(p_rich.all, treatment, year) %>%
  summarise(mean = mean(richness), sd = sd(richness), n = n(), sem = sd/sqrt(n))

p_rich.plot = ggplot(p_rich.treat.plot, aes(x = year, y = mean, color = as.factor(treatment))) +
  geom_point(size = 2, show.legend = T) +
  geom_line(size = 0.75) +
  geom_errorbar(aes(ymin = mean - sem, ymax = mean + sem), width = .1) +
  scale_color_manual(values = wes_palette("Moonrise1", 4, type = "discrete"), name="Soil Treatment") +
  xlim(2006, 2009) + xlab("Year") + ylab("Richness") +
  theme_classic(base_size=15) +
  theme(axis.line.x = element_line(color = "black"), axis.line.y = element_line(color = "black"))
plot(p_rich.plot)
```

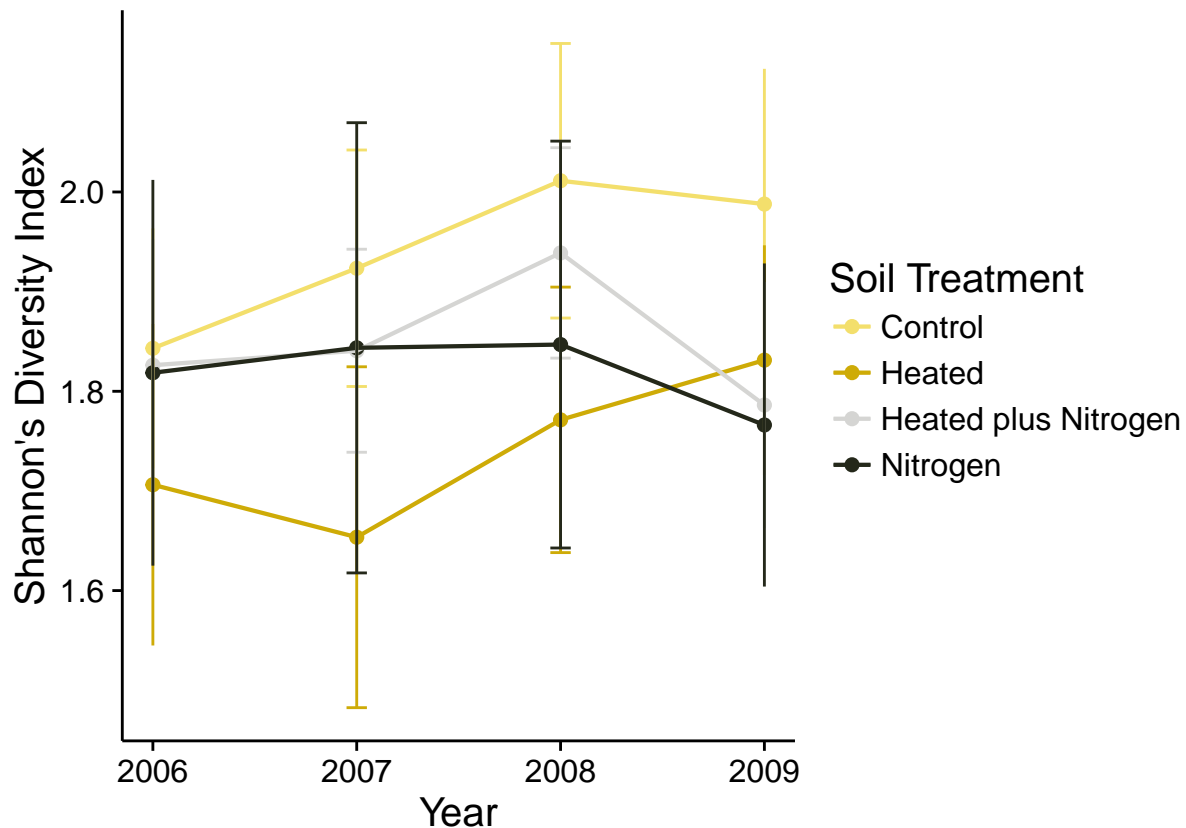


```
# Calculate diversity from time-by-species matrix
p_diversity = diversity(plant[, -c(1:5)], "shannon")

# Create data frame with experimental design and diversity data
p_div.all = data.frame(plant[, 1:5, ], p_diversity)
# Rename column
names(p_div.all)[6] = "diversity"

p_div.treat.plot = group_by(p_div.all, treatment, year) %>%
  summarise(mean = mean(diversity), sd = sd(diversity), n = n(), sem = sd/sqrt(n))

p_div.plot = ggplot(p_div.treat.plot, aes(x = year, y = mean, color = as.factor(treatment))) +
  geom_point(size = 2, show.legend = T) +
  geom_line(size = 0.75) +
  geom_errorbar(aes(ymin = mean - sem, ymax = mean + sem), width = .1) +
  scale_color_manual(values = wes_palette("Moonrise1", 4, type = "discrete"), name = "Soil Treatment") +
  xlim(2006, 2009) + xlab("Year") + ylab("Shannon's Diversity Index") +
  theme_classic(base_size = 15) +
  theme(axis.line.x = element_line(color = "black"), axis.line.y = element_line(color = "black"))
plot(p_div.plot)
```



4)

Hypothesis Testing

```
p_rich.rm = lme(richness ~ year + heat_treat + N_treat * heat_treat * N_treat * year, random = ~ 1 | plot, data = p_rich.all)
summary(p_rich.rm) # Obtain F-test
```

```
## Linear mixed-effects model fit by REML
## Data: p_rich.all
##      AIC      BIC    logLik
##  418.1614 445.4121 -198.0807
##
## Random effects:
## Formula: ~1 | plot
##      (Intercept) Residual
## StdDev:    2.253468 1.497991
##
## Correlation Structure: AR(1)
## Formula: ~1 | plot
## Parameter estimate(s):
##      Phi
## -0.09584397
## Fixed effects: richness ~ year + heat_treat + N_treat * heat_treat * N_treat * year
##
##              Value Std.Error DF
## (Intercept)   -319.0000   533.6371 68
## year              0.1667    0.2658 68
## heat_treatheated  1589.7925   754.6768 20
## N_treatN fertilized 1667.9090   754.6768 20
## heat_treatheated:N_treatN fertilized -2327.7884 1067.2742 20
## year:N_treatN fertilized    -0.8304    0.3759 68
```

```

## year:heat_treatheated          -0.7922    0.3759 68
## year:heat_treatheated:N_treatN fertilized    1.1586    0.5316 68
##                                t-value p-value
## (Intercept)          -0.5977845    0.5520
## year                  0.6269876    0.5328
## heat_treatheated      2.1065871    0.0480
## N_treatN fertilized    2.2100970    0.0389
## heat_treatheated:N_treatN fertilized    -2.1810593    0.0413
## year:N_treatN fertilized    -2.2088181    0.0306
## year:heat_treatheated    -2.1072957    0.0388
## year:heat_treatheated:N_treatN fertilized    2.1793094    0.0328
## Correlation:
##                                (Intr) year    ht_trt N_trNf
## year                      -1.000
## heat_treatheated          -0.707    0.707
## N_treatN fertilized        -0.707    0.707    0.500
## heat_treatheated:N_treatN fertilized    0.500 -0.500 -0.707 -0.707
## year:N_treatN fertilized    0.707 -0.707 -0.500 -1.000
## year:heat_treatheated      0.707 -0.707 -1.000 -0.500
## year:heat_treatheated:N_treatN fertilized -0.500    0.500    0.707    0.707
##                                h_:N_f y:N_Nf yr:ht_
## year
## heat_treatheated
## N_treatN fertilized
## heat_treatheated:N_treatN fertilized
## year:N_treatN fertilized    0.707
## year:heat_treatheated      0.707    0.500
## year:heat_treatheated:N_treatN fertilized -1.000 -0.707 -0.707
##
## Standardized Within-Group Residuals:
##          Min          Q1          Med          Q3          Max
## -2.5089111 -0.5625465  0.1048975  0.6703417  1.6948990
##
## Number of Observations: 96
## Number of Groups: 24

```

```
anova(p_rich.rm)
```

```

##                                numDF denDF    F-value p-value
## (Intercept)                   1      68 1014.4761 <.0001
## year                           1      68   7.1322  0.0095
## heat_treat                     1     20   2.3242  0.1430
## N_treat                        1     20   0.0011  0.9737
## heat_treat:N_treat             1     20   0.9445  0.3427
## year:N_treat                   1     68   0.8920  0.3483
## year:heat_treat                1     68   0.6414  0.4260
## year:heat_treat:N_treat        1     68   4.7494  0.0328

```

```

# Make cleaner ANOVA table
set.caption("RMANOVA for Plant Richness Data")
pander(anova(p_rich.rm))

```

Table 1: RMANOVA for Plant Richness Data

	numDF	denDF	F-value	p-value
(Intercept)	1	68	1014	0
year	1	68	7.132	0.009464
heat_treat	1	20	2.324	0.143
N_treat	1	20	0.001114	0.9737
heat_treat:N_treat	1	20	0.9445	0.3427
year:N_treat	1	68	0.892	0.3483
year:heat_treat	1	68	0.6414	0.426
year:heat_treat:N_treat	1	68	4.749	0.03278

```
# Perform an RM-ANOVA and construct a F-test using the AR(1)
```

```
p_div.rm = lme(diversity ~ year + heat_treat + N_treat * heat_treat * N_treat * year, random = ~ 1 | plot, data = p_div.all)
summary(p_div.rm) # Obtain F-test
```

```
## Linear mixed-effects model fit by REML
```

```
## Data: p_div.all
```

```
##      AIC      BIC    logLik
```

```
## 45.91417 73.16488 -11.95709
```

```
##
```

```
## Random effects:
```

```
## Formula: ~1 | plot
```

```
##      (Intercept)  Residual
```

```
## StdDev: 0.2416783 0.2710299
```

```
##
```

```
## Correlation Structure: AR(1)
```

```
## Formula: ~1 | plot
```

```
## Parameter estimate(s):
```

```
##      Phi
```

```
## 0.6311864
```

```
## Fixed effects: diversity ~ year + heat_treat + N_treat * heat_treat * N_treat * year
```

```
##
```

```
##      Value Std.Error DF
```

```
## (Intercept) -96.42080 90.53669 68
```

```
## year 0.04899 0.04510 68
```

```
## heat_treatheated 11.63861 128.03821 20
```

```
## N_treatN fertilized 132.51317 128.03821 20
```

```
## heat_treatheated:N_treatN fertilized -23.36506 181.07338 20
```

```
## year:N_treatN fertilized -0.06607 0.06378 68
```

```
## year:heat_treatheated -0.00589 0.06378 68
```

```
## year:heat_treatheated:N_treatN fertilized 0.01174 0.09020 68
```

```
##
```

```
##      t-value p-value
```

```
## (Intercept) -1.0649915 0.2906
```

```
## year 1.0863041 0.2812
```

```
## heat_treatheated 0.0908995 0.9285
```

```
## N_treatN fertilized 1.0349501 0.3130
```

```
## heat_treatheated:N_treatN fertilized -0.1290364 0.8986
```

```
## year:N_treatN fertilized -1.0359107 0.3039
```

```
## year:heat_treatheated -0.0922735 0.9268
```

```
## year:heat_treatheated:N_treatN fertilized 0.1301299 0.8968
```

```
## Correlation:
```

```
##      (Intr) year ht_trt N_trNf
```

```
## year -1.000
```

```
## heat_treatheated -0.707 0.707
## N_treatN fertilized -0.707 0.707 0.500
## heat_treatheated:N_treatN fertilized 0.500 -0.500 -0.707 -0.707
## year:N_treatN fertilized 0.707 -0.707 -0.500 -1.000
## year:heat_treatheated 0.707 -0.707 -1.000 -0.500
## year:heat_treatheated:N_treatN fertilized -0.500 0.500 0.707 0.707
## h_:N_f y:N_Nf yr:ht_
## year
## heat_treatheated
## N_treatN fertilized
## heat_treatheated:N_treatN fertilized
## year:N_treatN fertilized 0.707
## year:heat_treatheated 0.707 0.500
## year:heat_treatheated:N_treatN fertilized -1.000 -0.707 -0.707
##
## Standardized Within-Group Residuals:
## Min Q1 Med Q3 Max
## -2.0663335 -0.2975686 0.1382110 0.5149486 1.6528550
##
## Number of Observations: 96
## Number of Groups: 24
```

```
anova(p_div.rm)
```

```
## numDF denDF F-value p-value
## (Intercept) 1 68 786.2574 <.0001
## year 1 68 0.5002 0.4818
## heat_treat 1 20 0.3474 0.5622
## N_treat 1 20 0.0334 0.8568
## heat_treat:N_treat 1 20 0.5754 0.4569
## year:N_treat 1 68 1.7819 0.1864
## year:heat_treat 1 68 0.0000 0.9997
## year:heat_treat:N_treat 1 68 0.0169 0.8968
```

```
set.caption("RMANOVA for Plant Diversity Data")
pander(anova(p_div.rm))
```

Table 2: RMANOVA for Plant Diversity Data ## 4) Hypothesis Testing

	numDF	denDF	F-value	p-value
(Intercept)	1	68	786.3	0
year	1	68	0.5002	0.4818
heat_treat	1	20	0.3474	0.5622
N_treat	1	20	0.03342	0.8568
heat_treat:N_treat	1	20	0.5754	0.4569
year:N_treat	1	68	1.782	0.1864
year:heat_treat	1	68	1.329e-07	0.9997
year:heat_treat:N_treat	1	68	0.01693	0.8968