

Appendices: R code

Appendices for “Dryland rock detention structures increase herbaceous vegetation cover and stabilize shrub cover over 10 years but do not directly affect soil fertility” by Ossanna et al. (2023). Included are code and analysis used to make figures and full model output.

Contact: Lia Ossanna, lossanna@arizona.edu

Last updated: 2023-09-01

Appendices:

- Appendix A: Temporal vegetation trends, Figs 2 & S4
- Appendix B: Coefficient of variation, Figs 3 & S5
- Appendix C: Soil fertility, Figs S6-S8
- Appendix D: Structural equation modeling, models 1-4

Package versions:

- R version 4.3.1
- tidyverse 2.0.0
 - dplyr 1.1.2
 - stringr 1.5.0
 - ggplot 3.4.3
 - tidyr 3.2.1
- agricolae 1.3-6
- plotrix 3.8-2
- ggpubr 0.6.0
- rstatix 0.7.2
- scales 1.2.1
- car 3.1-2

Appendix A: Temporal vegetation trends

Setup

```
library(tidyverse)
library(agricolae)
library(plotrix)
library(ggpubr)
library(rstatix)

# Load data -----

notree.all <- read.csv("data/Herb-and-shrub-cover_2012-2021.csv")
herb.all <- read.csv("data/Herb-cover_2012-2021.csv")
shrub.all <- read.csv("data/Shrub-cover_2012-2021.csv")
invasive.all <- read.csv("data/Invasive-cover_2012-2021.csv")
plant.all <- read.csv("data/Species-cover_2012-2021.csv")
per.div <- read.csv("data/Perennial-plant-diversity_2012-2021.csv")
```

```
# Functions -----

# Convert columns to factor or date as needed
convert.cols <- function(x) {
  x$year.xaxis <- as.Date(x$year.xaxis)

  group.cols <- c("Sample", "Year", "Treatment")

  x[group.cols] <- lapply(x[group.cols], factor)

  return(x)
}
```

```
# Data wrangling -----

notree.all <- convert.cols(notree.all)
herb.all <- convert.cols(herb.all)
shrub.all <- convert.cols(shrub.all)
invasive.all <- convert.cols(invasive.all)
per.div <- convert.cols(per.div)
```

Fig 2a: Grass, forb & shrub cover

```
# Grass, forb, and shrub cover (notree) -----

# Find averages by year
notree.avg <- notree.all %>%
  group_by(Treatment, Year, year.xaxis) %>%
  summarise(mean = mean(Cover),
            SD = sd(Cover),
```

```

SE = std.error(Cover),
.groups = "keep")

# One-way ANOVA for Control
summary(aov(Cover ~ Year, data = filter(notree.all, Treatment == "Control"))) # p = 4.3e-06

```

```

##              Df Sum Sq Mean Sq F value    Pr(>F)
## Year           5    7815   1563.0      7.12 4.3e-06 ***
## Residuals     177   38854    219.5
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

notree.ctrl <- notree.all |>
  filter(Treatment == "Control")
anova.notree.ctrl <- aov(notree.ctrl$Cover ~ notree.ctrl$Year)
hsd.notree.ctrl <- HSD.test(anova.notree.ctrl, trt = "notree.ctrl$Year")
hsd.notree.ctrl$groups

```

```

##      notree.ctrl$Cover groups
## 2021         42.41935      a
## 2012         31.73194     ab
## 2014         31.58750     ab
## 2018         27.71774      b
## 2013         27.71250      b
## 2015         20.89315      b

```

```

# One-way ANOVA for Treated
summary(aov(Cover ~ Year, data = filter(notree.all, Treatment == "Treated"))) # p = 0.00304

```

```

##              Df Sum Sq Mean Sq F value    Pr(>F)
## Year           5    7804   1560.7      3.739 0.00304 **
## Residuals     178   74291    417.4
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

```

notree.trt <- notree.all |>
  filter(Treatment == "Treated")
anova.notree.trt <- aov(notree.trt$Cover ~ notree.trt$Year)
hsd.notree.trt <- HSD.test(anova.notree.trt, trt = "notree.trt$Year")
hsd.notree.trt$groups

```

```

##      notree.trt$Cover groups
## 2018         41.69960      a
## 2021         37.47581     ab
## 2014         31.40927    abc
## 2015         30.33669    abc
## 2012         26.72446     bc
## 2013         21.80029      c

```

```

# Plot with one-way ANOVA letters
notree.ctrl.letters <- hsd.notree.ctrl$groups
notree.ctrl.letters <- notree.ctrl.letters |>
  mutate(Year = rownames(notree.ctrl.letters)) |>
  arrange(Year)
notree.trt.letters <- hsd.notree.trt$groups
notree.trt.letters <- notree.trt.letters |>
  mutate(Year = rownames(notree.trt.letters)) |>
  arrange(Year)

letters.notree <- data.frame(x = rep(notree.avg$year.xaxis[1:6], 2),
  y = rep(49, 12),
  label = c(notree.ctrl.letters$groups,
    notree.trt.letters$groups),
  Treatment = c(rep("Control", 6),
    rep("Treated", 6)))
ptext.notree <- data.frame(x = rep(as.Date("2019-09-01"), 2),
  y = c(22, 22),
  label = c("ANOVA, p < 0.001", "ANOVA, p = 0.003"),
  Treatment = c("Control", "Treated"))

notree.plot <- ggplot(notree.avg, aes(x = year.xaxis, y = mean,
  group = Treatment,
  color = Treatment)) +

  geom_line() +
  geom_point() +
  geom_pointrange(aes(ymin = mean - SE, ymax = mean + SE)) +
  facet_wrap(~Treatment) +
  xlab(NULL) +
  ylab("Cover (%)") +
  ggtitle("Vegetation cover, 2012-2021") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  geom_text(data = letters.notree,
    mapping = aes(x = x, y = y, label = label),
    color = "black",
    size = 3.5) +
  geom_text(data = ptext.notree,
    aes(x = x, y = y, label = label),
    color = "gray30",
    size = 2.5) +
  theme(axis.text.x = element_text(color = "black")) +
  theme(plot.margin = margin(t = 0.1, r = 0.1, b = 0.2, l = 0.1, "in"))
notree.plot

```

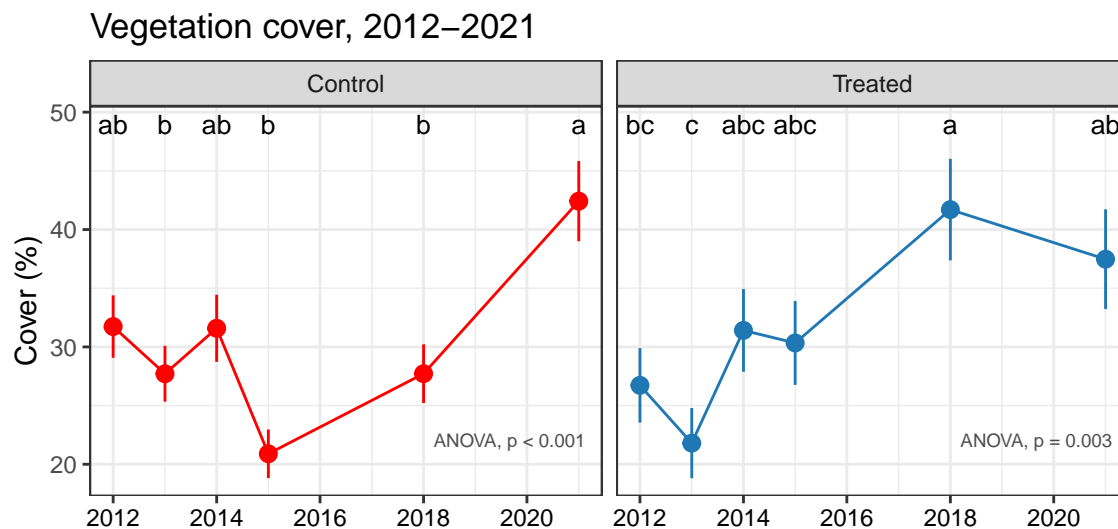


Fig 2b: Herbaceous (grass & forb) cover

```
# Herbaceous cover -----

# Find averages by year
herb.avg <- herb.all %>%
  group_by(Treatment, Year, year.xaxis) %>%
  summarise(mean = mean(Cover),
            SD = sd(Cover),
            SE = std.error(Cover),
            .groups = "keep")

# One-way ANOVA for Control
summary(aov(Cover ~ Year, data = filter(herb.all, Treatment == "Control"))) # 0.00434

##           Df Sum Sq Mean Sq F value Pr(>F)
## Year         5   2821    564.3   3.556 0.00434 **
## Residuals  177  28083    158.7
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

herb.ctrl <- herb.all |>
  filter(Treatment == "Control")
anova.herb.ctrl <- aov(herb.ctrl$Cover ~ herb.ctrl$Year)
hsd.herb.ctrl <- HSD.test(anova.herb.ctrl, trt = "herb.ctrl$Year")
hsd.herb.ctrl$groups

##      herb.ctrl$Cover groups
## 2021      26.78629      a
## 2014      22.28333     ab
## 2012      20.03472     ab
## 2018      19.89718     ab
```

```
## 2013      17.41528      b
## 2015      14.21169      b
```

```
# One-way ANOVA for Treated
```

```
summary(aov(Cover ~ Year, data = filter(herb.all, Treatment == "Treated"))) # p = 3.77e-10
```

```
##           Df Sum Sq Mean Sq F value    Pr(>F)
## Year         5    6847   1369.5    12.17 3.77e-10 ***
## Residuals   178   20035    112.6
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
herb.trt <- herb.all |>
  filter(Treatment == "Treated")
anova.herb.trt <- aov(herb.trt$Cover ~ herb.trt$Year)
hsd.herb.trt <- HSD.test(anova.herb.trt, trt = "herb.trt$Year")
hsd.herb.trt$groups
```

```
##      herb.trt$Cover groups
## 2018      24.489919      a
## 2021      22.201613     ab
## 2014      15.139113     bc
## 2015      12.368952     cd
## 2012      11.436828     cd
## 2013       6.929598      d
```

```
# Plot with one-way ANOVA letters
```

```
herb.ctrl.letters <- hsd.herb.ctrl$groups
herb.ctrl.letters <- herb.ctrl.letters |>
  mutate(Year = rownames(herb.ctrl.letters)) |>
  arrange(Year)
herb.trt.letters <- hsd.herb.trt$groups
herb.trt.letters <- herb.trt.letters |>
  mutate(Year = rownames(herb.trt.letters)) |>
  arrange(Year)

letters.herb <- data.frame(x = rep(herb.avg$year.xaxis[1:6], 2),
  y = rep(32, 12),
  label = c(herb.ctrl.letters$groups,
    herb.trt.letters$groups),
  Treatment = c(rep("Control", 6),
    rep("Treated", 6)))
ptext.herb <- data.frame(x = rep(as.Date("2019-09-01"), 2),
  y = c(8, 8),
  label = c("ANOVA, p = 0.004", "ANOVA, p < 0.001"),
  Treatment = c("Control", "Treated"))

herb.plot <- ggplot(herb.avg, aes(x = year.xaxis, y = mean,
  group = Treatment,
  color = Treatment)) +
  geom_line() +
  geom_point() +
```

```

geom_pointrange(aes(ymin = mean - SE, ymax = mean + SE)) +
facet_wrap(~Treatment) +
xlab(NULL) +
ylab("Cover (%)") +
ggtitle("Herbaceous cover") +
scale_color_manual(values = c("red", "#1F78B4")) +
theme_bw() +
theme(legend.position = "none") +
geom_text(data = letters.herb,
          mapping = aes(x = x, y = y, label = label),
          color = "black",
          size = 3.5) +
geom_text(data = ptext.herb,
          aes(x = x, y = y, label = label),
          color = "gray30",
          size = 2.5) +
theme(axis.text.x = element_text(color = "black")) +
theme(plot.margin = margin(t = 0.1, r = 0.1, b = 0.2, l = 0.1, "in"))
herb.plot

```

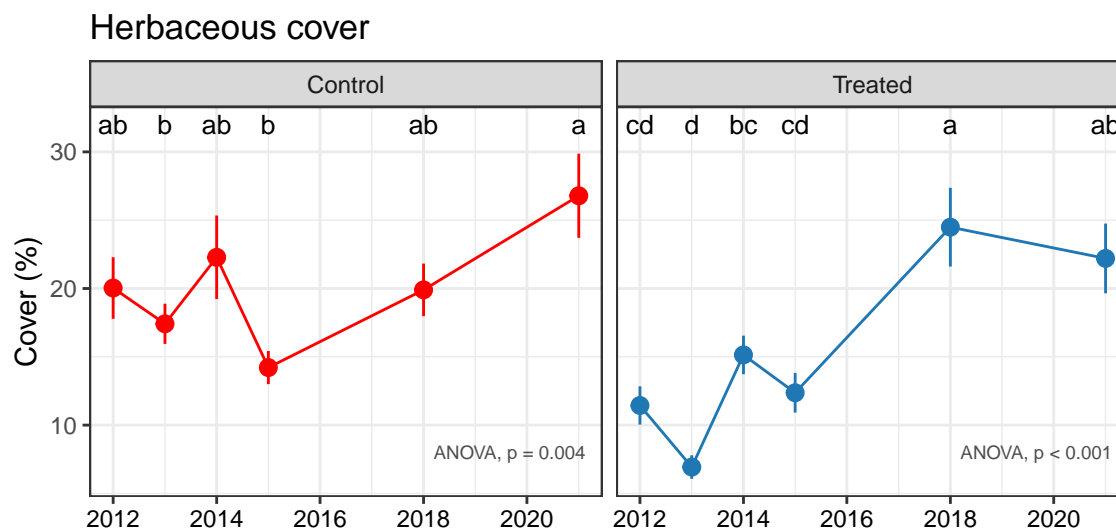


Fig 2c: Shrub cover

```

# Shrub cover -----

# Find averages by year
shrub.avg <- shrub.all %>%
  group_by(Treatment, Year, year.xaxis) %>%
  summarise(mean = mean(Cover),
            SD = sd(Cover),
            SE = std.error(Cover),
            .groups = "keep")

```

```
# One-way ANOVA for Control
summary(aov(Cover ~ Year, data = filter(shrub.all, Treatment == "Control"))) # p = 0.0112
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Year          5    1566    313.1   3.062 0.0112 *
## Residuals    177    18100    102.3
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
shrub.ctrl <- shrub.all |>
  filter(Treatment == "Control")
anova.shrub.ctrl <- aov(shrub.ctrl$Cover ~ shrub.ctrl$Year)
hsd.shrub.ctrl <- HSD.test(anova.shrub.ctrl, trt = "shrub.ctrl$Year")
hsd.shrub.ctrl$groups
```

```
##      shrub.ctrl$Cover groups
## 2021      15.633065      a
## 2012      11.697222     ab
## 2013      10.297222     ab
## 2014       9.304167     ab
## 2018       7.820565      b
## 2015       6.681452      b
```

```
# One-way ANOVA for Treated
summary(aov(Cover ~ Year, data = filter(shrub.all, Treatment == "Treated"))) # NS, p = 0.982
```

```
##              Df Sum Sq Mean Sq F value Pr(>F)
## Year          5     232     46.4   0.141 0.982
## Residuals    178   58465     328.5
```

```
# Plot with one-way ANOVA letters
shrub.ctrl.letters <- hsd.shrub.ctrl$groups
shrub.ctrl.letters <- shrub.ctrl.letters |>
  mutate(Year = rownames(shrub.ctrl.letters)) |>
  arrange(Year)

letters.shrub <- data.frame(x = shrub.avg$year.xaxis[1:6],
  y = rep(21, 6),
  label = shrub.ctrl.letters$groups,
  Treatment = rep("Control", 6))
ptext.shrub <- data.frame(x = rep(as.Date("2019-09-01"), 2),
  y = c(6.5, 6.5),
  label = c("ANOVA, p = 0.011", "ANOVA, p = 0.982"),
  Treatment = c("Control", "Treated"))

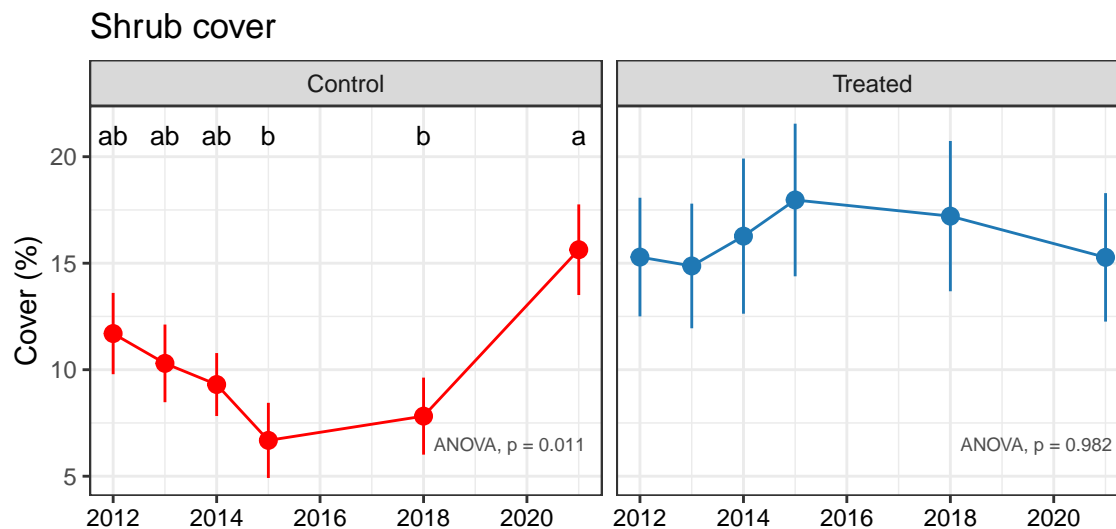
shrub.plot <- ggplot(shrub.avg, aes(x = year.xaxis, y = mean,
  group = Treatment,
  color = Treatment)) +
  geom_line() +
  geom_point() +
  geom_pointrange(aes(ymin = mean - SE, ymax = mean + SE)) +
```



```

facet_wrap(~Treatment) +
xlab(NULL) +
ylab("Cover (%)") +
ggtitle("Shrub cover") +
scale_color_manual(values = c("red", "#1F78B4")) +
theme_bw() +
theme(legend.position = "none") +
geom_text(data = letters.shrub,
          mapping = aes(x = x, y = y, label = label),
          color = "black",
          size = 3.5) +
geom_text(data = ptext.shrub,
          aes(x = x, y = y, label = label),
          color = "gray30",
          size = 2.5) +
theme(axis.text.x = element_text(color = "black")) +
theme(plot.margin = margin(t = 0.1, r = 0.1, b = 0.2, l = 0.1, "in"))
shrub.plot

```



Combine plots for Fig 2

```

# Combine notree, herb & shrub -----

tiff("figures/2023-09_publish-figures/temporal-ANOVA_notree-herb-shrub.tiff", units = "in", height = 8,
ggarrange(notree.plot, herb.plot, shrub.plot,
          ncol = 1, nrow = 3,
          labels = c("(A)", "(B)", "(C)"))

dev.off()

```

Supp Fig 4a: Perennial plant species richness

```
# Perennial plant richness -----

# Find averages by year
rich.avg <- per.div %>%
  group_by(Treatment, Year, year.xaxis) %>%
  summarise(mean = mean(rich),
            SD = sd(rich),
            SE = std.error(rich),
            .groups = "keep")

# One-way ANOVA for Control
summary(aov(rich ~ Year, data = filter(per.div, Treatment == "Control"))) # 0.00881

##              Df Sum Sq Mean Sq F value Pr(>F)
## Year          5    92.9  18.587    3.189 0.00881 **
## Residuals    177 1031.7    5.829
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

rich.ctrl <- per.div |>
  filter(Treatment == "Control")
anova.rich.ctrl <- aov(rich.ctrl$rich ~ rich.ctrl$Year)
hsd.rich.ctrl <- HSD.test(anova.rich.ctrl, trt = "rich.ctrl$Year")
hsd.rich.ctrl$groups

##      rich.ctrl$rich groups
## 2012    9.866667      a
## 2013    9.133333     ab
## 2018    8.645161     ab
## 2015    8.612903     ab
## 2014    8.200000     ab
## 2021    7.580645      b

# One-way ANOVA for Treated
summary(aov(rich ~ Year, data = filter(per.div, Treatment == "Treated"))) # p = 0.0516

##              Df Sum Sq Mean Sq F value Pr(>F)
## Year          5     76  15.207    2.247 0.0516 .
## Residuals    178   1204    6.766
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Plot with one-way ANOVA letters
rich.ctrl.letters <- hsd.rich.ctrl$groups
rich.ctrl.letters <- rich.ctrl.letters |>
  mutate(Year = rownames(rich.ctrl.letters)) |>
  arrange(Year)

letters.rich <- data.frame(x = rich.avg$year.xaxis[1:6],
```

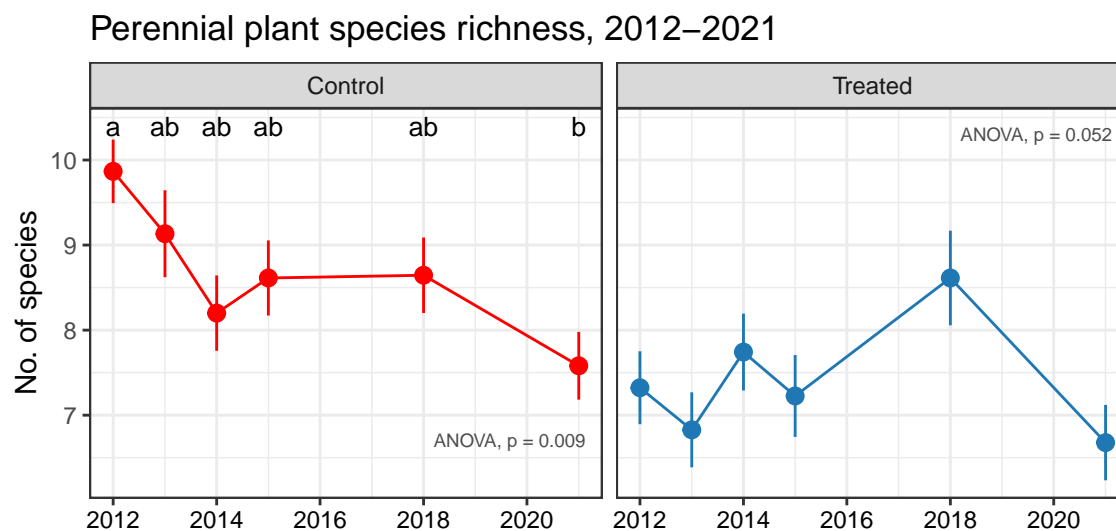
```

      y = rep(10.4, 6),
      label = rich.ctrl.letters$groups,
      Treatment = rep("Control", 6))
ptext.rich <- data.frame(x = rep(as.Date("2019-09-01"), 2),
      y = c(6.7, 10.3),
      label = c("ANOVA, p = 0.009", "ANOVA, p = 0.052"),
      Treatment = c("Control", "Treated"))

rich.plot <- ggplot(rich.avg, aes(x = year.xaxis, y = mean,
      group = Treatment,
      color = Treatment)) +

  geom_line() +
  geom_point() +
  geom_pointrange(aes(ymin = mean - SE, ymax = mean + SE)) +
  facet_wrap(~Treatment) +
  xlab(NULL) +
  ylab("No. of species") +
  ggtitle("Perennial plant species richness, 2012-2021") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  geom_text(data = letters.rich,
    mapping = aes(x = x, y = y, label = label),
    color = "black",
    size = 3.5) +
  geom_text(data = ptext.rich,
    aes(x = x, y = y, label = label),
    color = "gray30",
    size = 2.5) +
  theme(axis.text.x = element_text(color = "black")) +
  theme(plot.margin = margin(0.1, 0.1, 0.2, 0.1, "in"))
rich.plot

```



Supp Fig 4b: Perennial plant diversity

```
# Perennial plant diversity (Shannon) -----

# Find averages by year
shan.avg <- per.div %>%
  group_by(Treatment, Year, year.xaxis) %>%
  summarise(mean = mean(shan),
            SD = sd(shan),
            SE = std.error(shan),
            .groups = "keep")

# One-way ANOVA for Control
summary(aov(shan ~ Year, data = filter(per.div, Treatment == "Control"))) # p = 0.934

##              Df Sum Sq Mean Sq F value Pr(>F)
## Year          5   0.185  0.03702    0.26  0.934
## Residuals    177  25.197  0.14235

# One-way ANOVA for Treated
summary(aov(shan ~ Year, data = filter(per.div, Treatment == "Treated"))) # p = 0.725

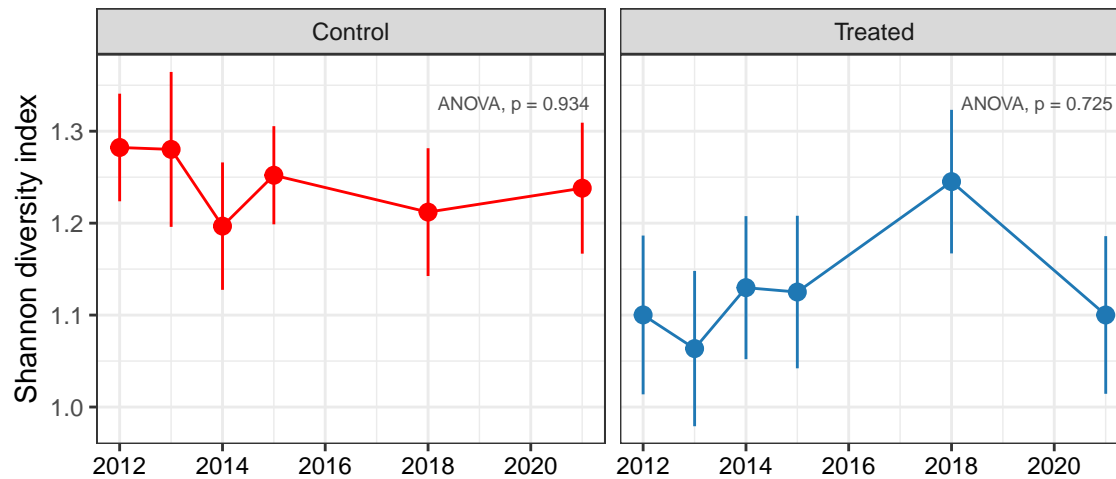
##              Df Sum Sq Mean Sq F value Pr(>F)
## Year          5    0.59  0.1189    0.568  0.725
## Residuals    178  37.27  0.2094

# Plot with one-way ANOVA
ptext.shan <- data.frame(x = rep(as.Date("2019-09-01"), 2),
                        y = c(1.33, 1.33),
                        label = c("ANOVA, p = 0.934", "ANOVA, p = 0.725"),
                        Treatment = c("Control", "Treated"))

shan.plot <- ggplot(shan.avg, aes(x = year.xaxis, y = mean,
                                group = Treatment,
                                color = Treatment)) +

  geom_line() +
  geom_point() +
  geom_pointrange(aes(ymin = mean - SE, ymax = mean + SE)) +
  facet_wrap(~Treatment) +
  xlab(NULL) +
  ylab("Shannon diversity index") +
  ggtitle("Perennial plant diversity") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "black")) +
  geom_text(data = ptext.shan,
            aes(x = x, y = y, label = label),
            color = "gray30",
            size = 2.5) +
  theme(plot.margin = margin(0.1, 0.1, 0.2, 0.1, "in"))
shan.plot
```

Perennial plant diversity



Combine plots for Supp Fig 4

```
# Combine richness & Shannon -----

tiff("figures/2023-09_publish-figures/temporal-ANOVA_richness-Shannon.tiff", units = "in", height = 5.5)
ggarrange( rich.plot, shan.plot,
            ncol = 1, nrow = 2,
            labels = c("(A)", "(B)"))

dev.off()
```

Invasive cover and most common species

```
# Average cover by year
invasive.all %>%
  select(-year.axis) |>
  group_by(Treatment, Year) %>%
  summarise(mean = mean(Cover),
            SE = std.error(Cover),
            .groups = "keep") |>
  mutate_if(is.numeric, round, digits = 2)

## 'mutate_if()' ignored the following grouping variables:
## * Columns 'Treatment', 'Year'

## # A tibble: 12 x 4
## # Groups:   Treatment, Year [12]
##   Treatment Year   mean   SE
##   <fct>      <fct> <dbl> <dbl>
## 1 Control   2012    3.34  0.6
```

```
## 2 Control 2013 2.58 0.66
## 3 Control 2014 2.46 0.98
## 4 Control 2015 2.96 0.69
## 5 Control 2018 5.1 1.17
## 6 Control 2021 7.38 1.23
## 7 Treated 2012 3.29 0.84
## 8 Treated 2013 2.18 0.51
## 9 Treated 2014 3.58 0.8
## 10 Treated 2015 5.1 1.08
## 11 Treated 2018 5.17 1.23
## 12 Treated 2021 4.79 0.85
```

```
# Most common species in Control
plant.all |>
  filter(Native == "Invasive",
         Treatment == "Control") |>
  group_by(Common) |>
  summarise(mean = mean(Cover)) |>
  arrange(desc(mean))
```

```
## # A tibble: 4 x 2
##   Common          mean
##   <chr>          <dbl>
## 1 Lehmann lovegrass 4.49
## 2 Stinkgrass       0.833
## 3 Spreading fantails 0.769
## 4 African lovegrass 0.125
```

```
# Most common species in Treated
plant.all |>
  filter(Native == "Invasive",
         Treatment == "Treated") |>
  group_by(Common) |>
  summarise(mean = mean(Cover)) |>
  arrange(desc(mean))
```

```
## # A tibble: 8 x 2
##   Common          mean
##   <chr>          <dbl>
## 1 Lehmann lovegrass 4.75
## 2 Buffelgrass      3.41
## 3 Boer lovegrass   0.625
## 4 African lovegrass 0.531
## 5 Spreading fantails 0.367
## 6 Barnyard         0.225
## 7 Rose Natal grass 0.125
## 8 Stinkgrass       0.125
```

Appendix B: Coefficient of variation

Setup

```
library(tidyverse)
library(car)
library(scales)
library(ggpubr)
```

```
# Load data -----

notree.all <- read_csv("data/Herb-and-shrub-cover_2012-2021.csv")
herb.all <- read_csv("data/Herb-cover_2012-2021.csv")
shrub.all <- read_csv("data/Shrub-cover_2012-2021.csv")
per.div <- read_csv("data/Perennial-plant-diversity_2012-2021.csv")
```

Fig 3a: CV of shrub cover

```
# Shrub cover -----

# Find CV for each sample over time
shrub.sample <- shrub.all |>
  group_by(Sample, Treatment) |>
  summarise(CV = sd(Cover) / mean(Cover),
            .groups = "keep") # NaNs produced because some have 0 cover and can't divide by 0

# Replace NaNs with 0
shrub.sample[1, 3] <- 0
shrub.sample[5, 3] <- 0
shrub.sample[8, 3] <- 0

# Compare means
wilcox.test(filter(shrub.sample, Treatment == "Treated")$CV,
             filter(shrub.sample, Treatment == "Control")$CV,
             exact = FALSE) # p = 0.01429

##
## Wilcoxon rank sum test with continuity correction
##
## data: filter(shrub.sample, Treatment == "Treated")$CV and filter(shrub.sample, Treatment == "Control")$CV
## W = 306, p-value = 0.01429
## alternative hypothesis: true location shift is not equal to 0

# Plot
letters.shrub <- data.frame(x = c(1, 2),
                           y = c(2.5, 2.5),
                           label = c("a", "b"))
```

```

shrub.plot.cv <- shrub.sample |>
  ggplot(aes(x = Treatment, y = CV)) +
  geom_boxplot(alpha = 0.3,
    outlier.shape = NA,
    aes(fill = Treatment)) +
  geom_jitter(size = 1,
    alpha = 0.8,
    aes(color = Treatment)) +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  labs(title = "Shrub cover",
    x = NULL,
    y = "Coefficient of variation") +
  theme_bw() +
  theme(legend.position = "none") +
  scale_y_continuous(labels = percent) +
  theme(axis.text.x = element_text(color = "black")) +
  geom_text(aes(x = 0.95, y = 2.75, label = "Mann-Whitney, \np = 0.014"),
    color = "gray30",
    size = 2.5) +
  geom_text(data = letters.shrub,
    aes(x = x, y = y, label = label),
    color = "black") +
  theme(plot.margin = margin(0.1, 0, 0.1, 0.1, "in")) +
  stat_summary(fun = mean, geom = "errorbar", aes(ymax = after_stat(y), ymin = after_stat(y)),
    width = 0.75, linetype = "dashed") +
  theme(plot.title = element_text(size = 12))
shrub.plot.cv

```

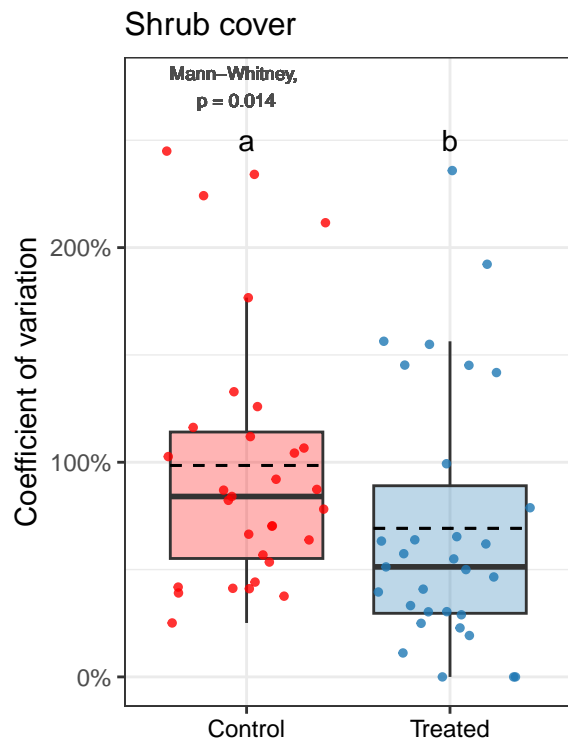


Fig 3b: CV of herbaceous cover

```
# Herb cover -----

# Find CV for each sample over time
herb.sample <- herb.all |>
  group_by(Sample, Treatment) |>
  summarise(CV = sd(Cover) / mean(Cover),
            .groups = "keep")

# Compare means
wilcox.test(filter(herb.sample, Treatment == "Treated")$CV,
            filter(herb.sample, Treatment == "Control")$CV) # NS, p = 0.148

##
## Wilcoxon rank sum exact test
##
## data: filter(herb.sample, Treatment == "Treated")$CV and filter(herb.sample, Treatment == "Control")$CV
## W = 584, p-value = 0.1479
## alternative hypothesis: true location shift is not equal to 0

# Plot
herb.plot.cv <- herb.sample |>
  ggplot(aes(x = Treatment, y = CV)) +
  geom_boxplot(alpha = 0.3,
              outlier.shape = NA,
              aes(fill = Treatment)) +
  geom_jitter(size = 1,
              alpha = 0.8,
              aes(color = Treatment)) +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  labs(title = "Herbaceous cover",
       x = NULL,
       y = NULL) +
  theme_bw() +
  theme(legend.position = "none") +
  scale_y_continuous(labels = percent) +
  theme(axis.text.x = element_text(color = "black")) +
  geom_text(aes(x = 0.95, y = 1.18, label = "Mann-Whitney, \np = 0.122"),
            color = "gray30",
            size = 2.5) +
  theme(plot.margin = margin(0.1, 0.1, 0.1, 0.2, "in")) +
  stat_summary(fun = mean, geom = "errorbar", aes(ymax = after_stat(y), ymin = after_stat(y)),
              width = 0.75, linetype = "dashed") +
  theme(plot.title = element_text(size = 12))
herb.plot.cv
```

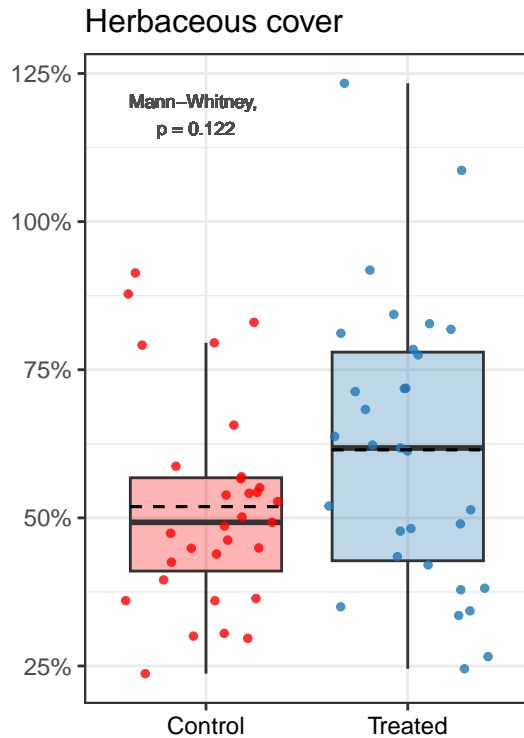


Fig 3c: CV of overall veg cover

```
# Notree cover -----

# Find CV for each sample over time
notree.sample <- notree.all |>
  group_by(Sample, Treatment) |>
  summarise(CV = sd(Cover) / mean(Cover),
    .groups = "keep")

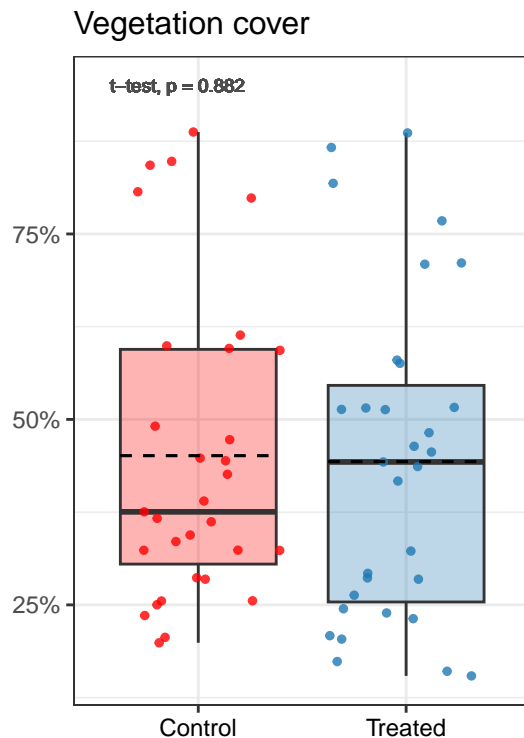
# Compare means
t.test(filter(notree.sample, Treatment == "Treated")$CV,
  filter(notree.sample, Treatment == "Control")$CV) # NS, p = 0.882
```

```
##
## Welch Two Sample t-test
##
## data: filter(notree.sample, Treatment == "Treated")$CV and filter(notree.sample, Treatment == "Control")$CV
## t = -0.14868, df = 59.846, p-value = 0.8823
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.11574119 0.09972676
## sample estimates:
## mean of x mean of y
## 0.4430859 0.4510931
```

```

# Plot
notree.plot.cv <- notree.sample |>
  ggplot(aes(x = Treatment, y = CV)) +
  geom_boxplot(alpha = 0.3,
    outlier.shape = NA,
    aes(fill = Treatment)) +
  geom_jitter(size = 1,
    alpha = 0.8,
    aes(color = Treatment)) +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  labs(title = "Vegetation cover",
    x = NULL,
    y = NULL) +
  theme_bw() +
  theme(legend.position = "none") +
  scale_y_continuous(labels = percent) +
  theme(axis.text.x = element_text(color = "black")) +
  geom_text(aes(x = 0.9, y = 0.95, label = "t-test, p = 0.882"),
    color = "gray30",
    size = 2.5) +
  theme(plot.margin = margin(0.1, 0.1, 0.1, 0.2, "in")) +
  stat_summary(fun = mean, geom = "errorbar", aes(ymax = after_stat(y), ymin = after_stat(y)),
    width = 0.75, linetype = "dashed") +
  theme(plot.title = element_text(size = 12))
notree.plot.cv

```



Combine plots for Fig 3

```
# Combine notree, herb, shrub -----

tiff("figures/2023-09_publish-figures/CV_shrub-herb-notree.tiff", units = "in", height = 4, width = 7,
ggarrange(shrub.plot.cv, herb.plot.cv, notree.plot.cv,
          ncol = 3, nrow = 1,
          labels = c("(A)", "(B)", "(C)"))

dev.off()
```

Supp Fig 5a: CV of perennial richness

```
# Richness -----

# Find CV for each sample over time
rich.sample <- per.div |>
  group_by(Sample, Treatment) |>
  summarise(CV = sd(rich) / mean(rich),
            .groups = "keep")

# Compare means
wilcox.test(filter(rich.sample, Treatment == "Treated")$CV,
             filter(rich.sample, Treatment == "Control")$CV) # NS, p = 0.093

## Warning in wilcox.test.default(filter(rich.sample, Treatment == "Treated")$CV,
## : cannot compute exact p-value with ties

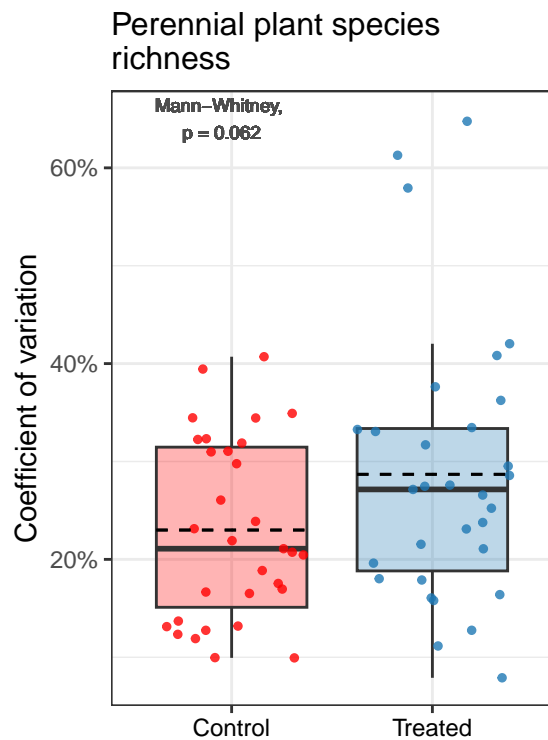
##
## Wilcoxon rank sum test with continuity correction
##
## data: filter(rich.sample, Treatment == "Treated")$CV and filter(rich.sample, Treatment == "Control")$CV
## W = 586.5, p-value = 0.1375
## alternative hypothesis: true location shift is not equal to 0

# Plot
rich.plot.cv <- rich.sample |>
  ggplot(aes(x = Treatment, y = CV)) +
  geom_boxplot(alpha = 0.3,
              outlier.shape = NA,
              aes(fill = Treatment)) +
  geom_jitter(size = 1,
              alpha = 0.8,
              aes(color = Treatment)) +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  labs(title = "Perennial plant species richness",
       x = NULL,
       y = "Coefficient of variation") +
  theme_bw() +
```

```

theme(legend.position = "none") +
scale_y_continuous(labels = percent) +
theme(axis.text.x = element_text(color = "black")) +
geom_text(aes(x = 0.95, y = 0.65, label = "Mann-Whitney, \np = 0.062"),
  color = "gray30",
  size = 2.5) +
theme(plot.margin = margin(0.1, 0.1, 0.1, 0.1, "in")) +
stat_summary(fun = mean, geom = "errorbar", aes(ymax = after_stat(y), ymin = after_stat(y)),
  width = 0.75, linetype = "dashed") +
theme(plot.title = element_text(size = 12))
rich.plot.cv

```



Supp Fig 5b: CV of perennial diversity

```

# Shannon -----

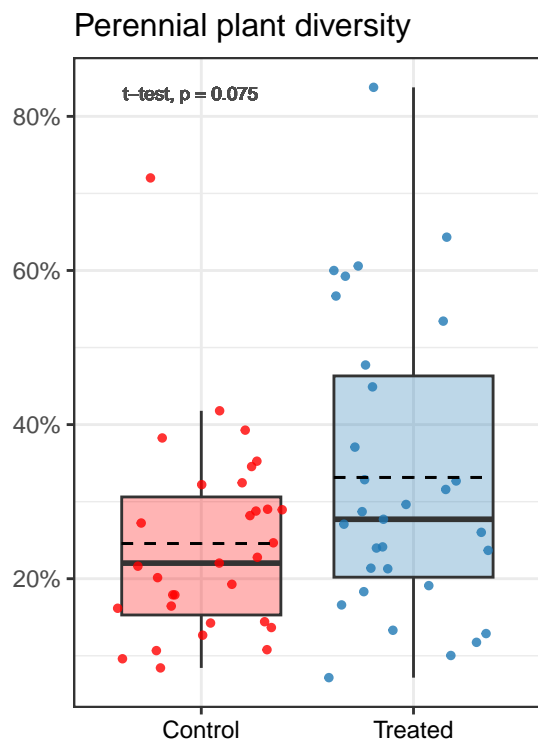
# Find CV for each sample over time
shan.sample <- per.div |>
  group_by(Sample, Treatment) |>
  summarise(CV = sd(shan) / mean(shan),
    .groups = "keep")

# Compare
t.test(filter(shan.sample, Treatment == "Treated")$CV,
  filter(shan.sample, Treatment == "Control")$CV) # NS,  $p = 0.075$ 

```

```
##
## Welch Two Sample t-test
##
## data: filter(shan.sample, Treatment == "Treated")$CV and filter(shan.sample, Treatment == "Control")
## t = 2.0794, df = 52.755, p-value = 0.04246
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## 0.00303293 0.16871186
## sample estimates:
## mean of x mean of y
## 0.3315000 0.2456276
```

```
# Plot
shan.plot.cv <- shan.sample |>
  ggplot(aes(x = Treatment, y = CV)) +
  geom_boxplot(alpha = 0.3,
               outlier.shape = NA,
               aes(fill = Treatment)) +
  geom_jitter(size = 1,
              alpha = 0.8,
              aes(color = Treatment)) +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  labs(title = "Perennial plant diversity",
       x = NULL,
       y = NULL) +
  theme_bw() +
  theme(legend.position = "none") +
  scale_y_continuous(labels = percent) +
  theme(axis.text.x = element_text(color = "black")) +
  geom_text(aes(x = 0.95, y = 0.83, label = "t-test, p = 0.075"),
            color = "gray30",
            size = 2.5) +
  theme(plot.margin = margin(0.1, 0.1, 0.1, 0.15, "in")) +
  stat_summary(fun = mean, geom = "errorbar", aes(ymax = after_stat(y), ymin = after_stat(y)),
              width = 0.75, linetype = "dashed") +
  theme(plot.title = element_text(size = 12))
shan.plot.cv
```



Combine plots for Supp Fig 5

```
# Combine richness & Shannon -----

# Supplemental figure
tiff("figures/2023-09_publish-figures/CV_rich-shan.tiff", units = "in", height = 4, width = 5.5, res = 300)
ggarrange(rich.plot.cv, shan.plot.cv,
  ncol = 2, nrow = 1,
  labels = c("(A)", "(B)"))

dev.off()
```

Appendix C: Soil fertility

Setup

Supp Fig 6a: Total soil nitrogen

Supp Fig 6b: Total soil carbon

Supp Fig 6c: Soil organic matter

Supp Fig 7a: Bacterial & archaeal richness

Supp Fig 7b: Fungal richness

Supp Fig 8a: Chemoheterotrophic bacteria & archaea

Supp Fig 8b: Nitrogen-cycling bacteria & archaea

Supp Fig 8c: Saprotrophic fungi

Appendix D: Structural equation modeling

Setup

Latent variables

Model 1

Model 2

Model 3

Model 4