Appendices: R code

Appendices for "Dryland rock detention structures increase herbaceous vegetation cover and stabilize shrub cover over ten 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. Data can be downloaded from the Zenodo archive under the DOI 10.5281/zenodo.8310363.

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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`
- `metagenomeSeq 1.42.0`, `Biobase 2.60.0`, `BiocGenerics 0.46.0`
- `vegan 2.6-4`
- `dada2 1.28.0`, `ShortRead 1.58.0`, `Biostrings 2.68.1` used for DADA2 pipeline (code not included here)
- `lavaan 0.6-16`

Appendix A: Temporal vegetation trends

Setup

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

```
# Load data ------------------------------------------------------------------

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

```r
# 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
```

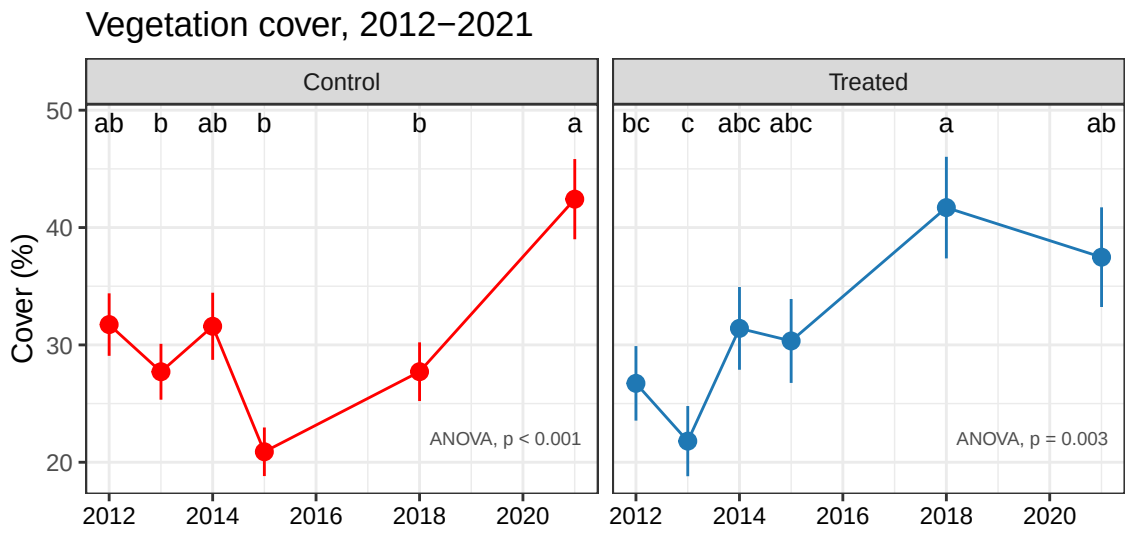


Fig 2b: Herbaceous (grass & forb) cover

```
# 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
```

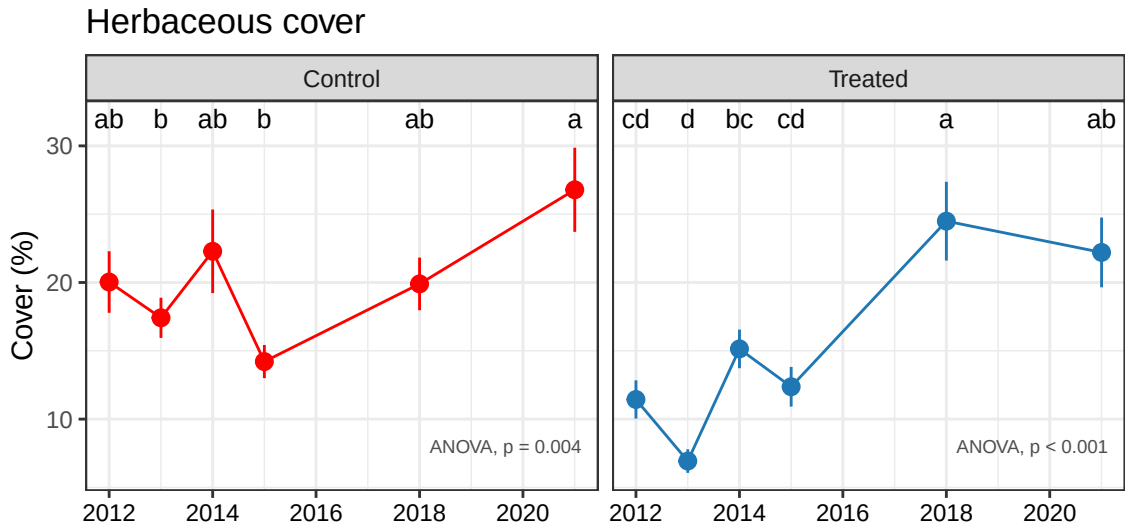


Fig 2c: Shrub cover

```
# 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")
```

```r
# 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
```

```r
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
```

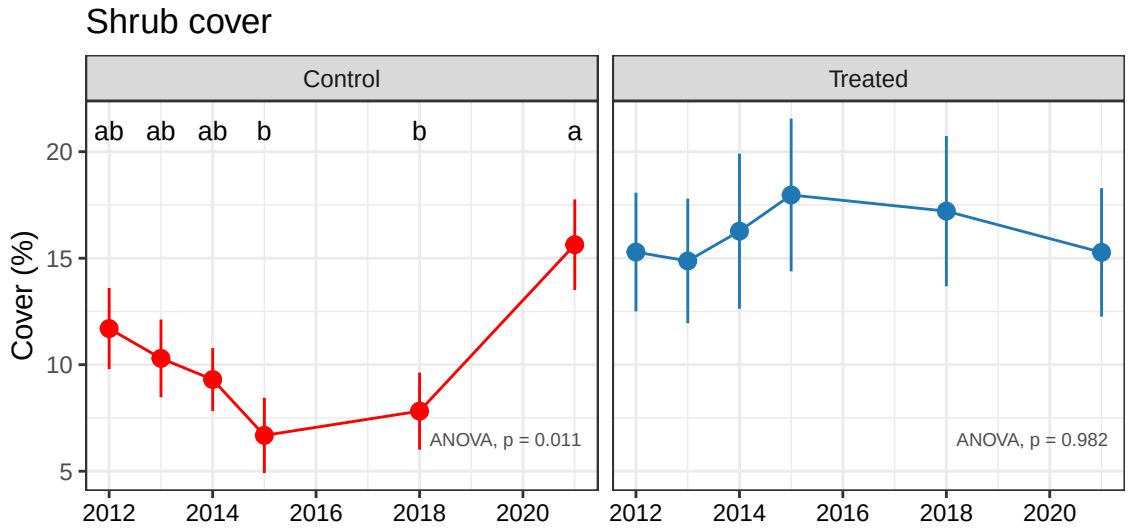
```
##      shrub.ctrl$Cover groups
## 2021        15.633065      a
## 2012        11.697222     ab
## 2013        10.297222     ab
## 2014         9.304167     ab
## 2018         7.820565      b
## 2015         6.681452      b
```

```r
# 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
```

```r
# 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("Fig2_temporal_notree-herb-shrub.tiff", units = "in", height = 8, width = 6, res = 1000)
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
```

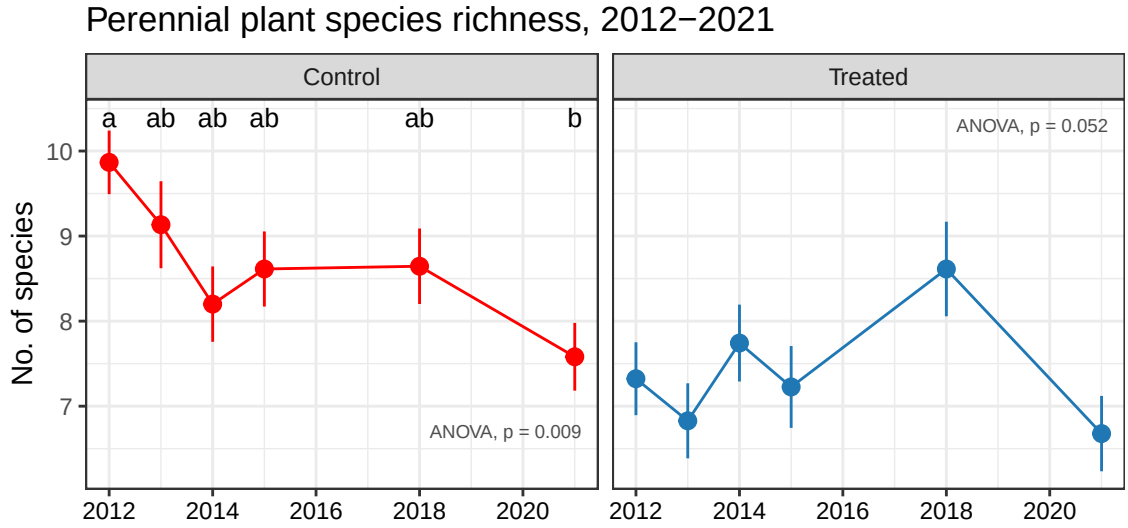
```
##      rich.ctrl$rich groups
## 2012       9.866667      a
## 2013       9.133333     ab
## 2018       8.645161     ab
## 2015       8.612903     ab
## 2014       8.200000     ab
## 2021       7.580645      b
```

```
# 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

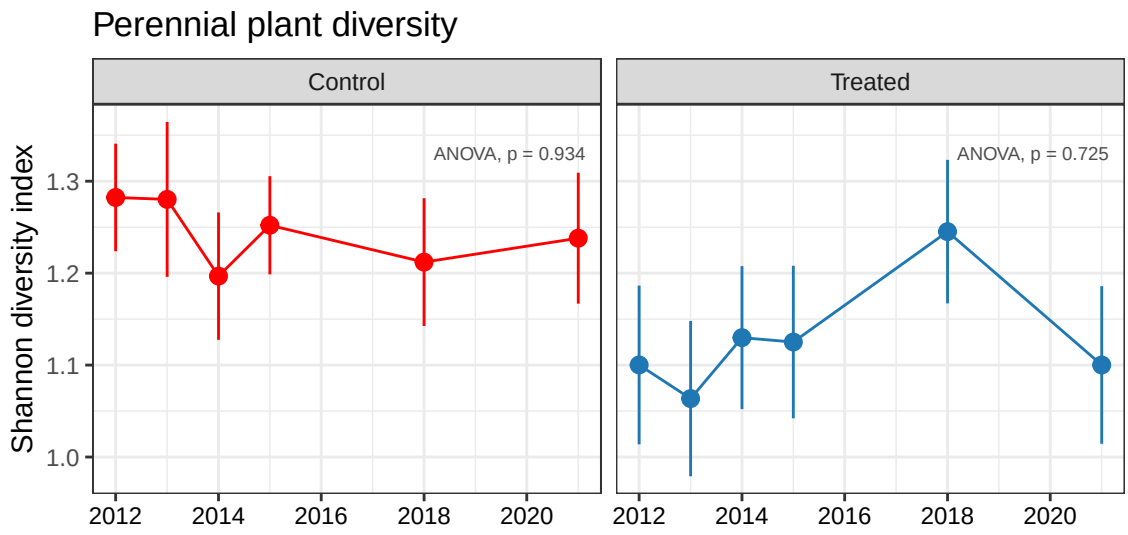
```
# Perennial plant diversity (Shannon) ------------------------------------

# 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
```



Combine plots for Supp Fig 4

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

tiff("FigS4_temporal_richness-Shannon.tiff", units = "in", height = 5.5, width = 6, res = 300)
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.xaxis) |>
  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("Herb-and-shrub-cover_2012-2021.csv")
herb.all <- read_csv("Herb-cover_2012-2021.csv")
shrub.all <- read_csv("Shrub-cover_2012-2021.csv")
per.div <- read_csv("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
## 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"))
```

```r
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
```

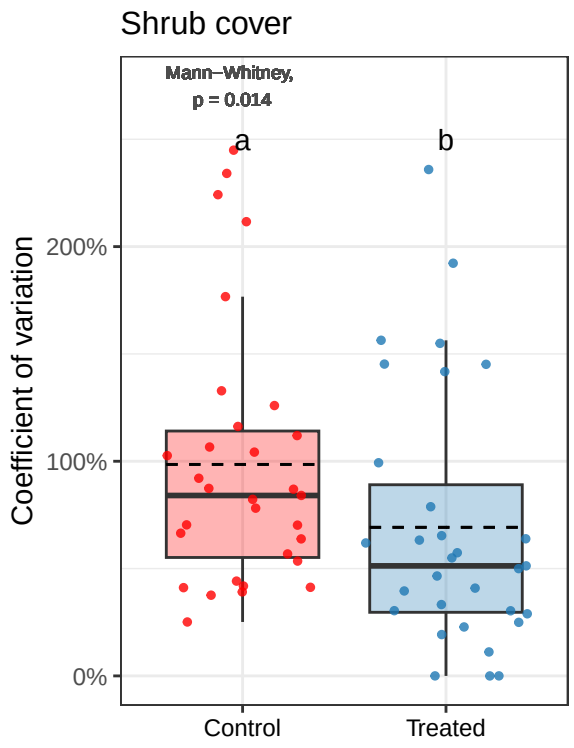


Fig 3b: CV of herbaceous cover

```
# 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")
## 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
```

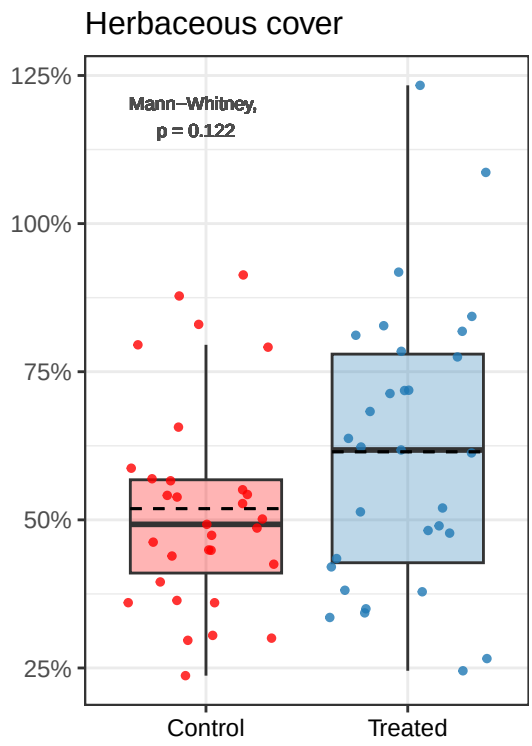
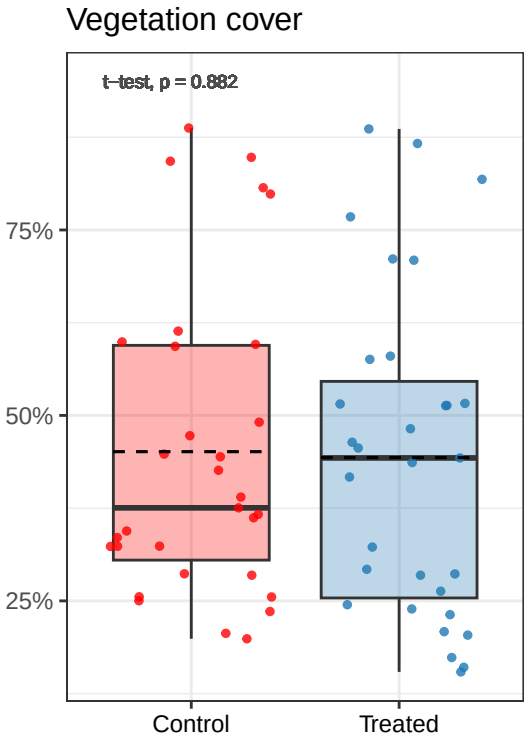


Fig 3c: CV of overall veg cover

```
# 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 == "Cont
## 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
```

```r
# 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("Fig3_CV_shrub-herb-notree.tiff", units = "in", height = 4, width = 7, res = 1000)
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

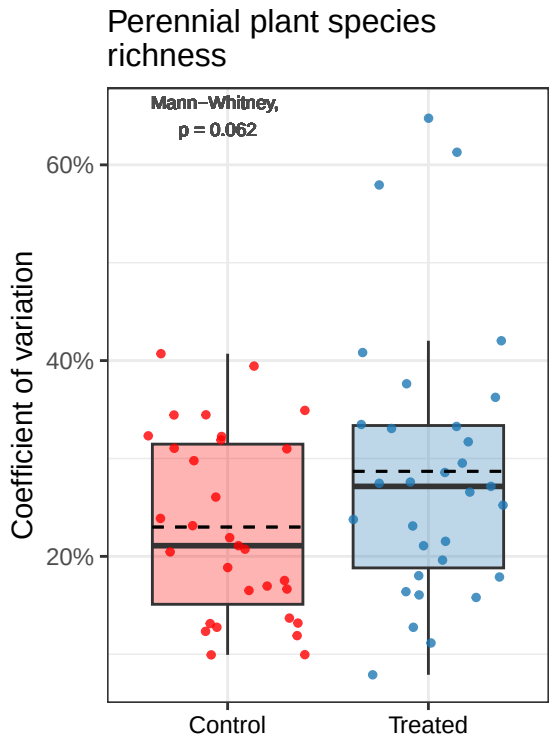
```
# Richness ---------------------------------------------------------------

# 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")
## 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 \nrichness",
       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
```

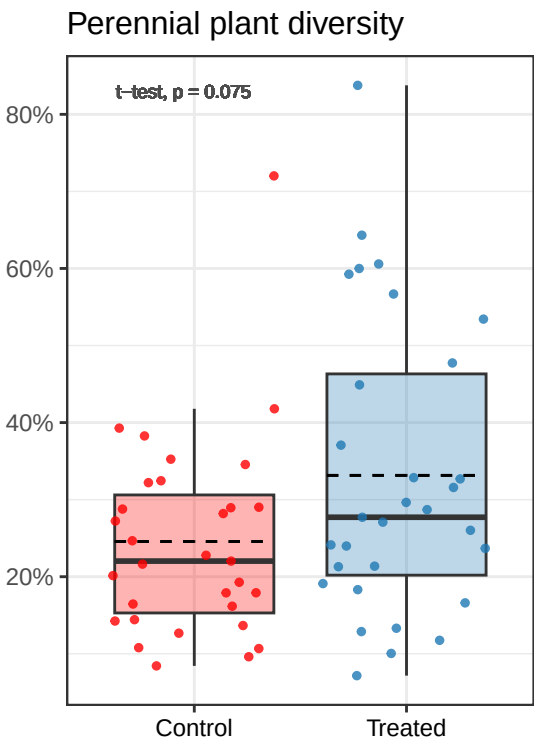


Supp Fig 5b: CV of perennial diversity

```
# 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
```

```r
# 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("FigS5_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

```
library(tidyverse)
library(ggpubr)
library(metagenomeSeq)
library(vegan)
```

```
# Load data ------------------------------------------------------------------

barc.asv <- read.table("bac-arc_clean_asv.txt", sep = "\t",
                       header = T, row.names = 1)
fungi.asv <- read.table("fungi_clean_asv.txt",
                      sep = "\t", header = T, row.names = 1)
meta <- read.csv("sequencing_metadata.csv")

dat.2021 <- read.csv("Veg-soil-elev_2021.csv")
```

```
# 16S ------------------------------------------------------------------------

# Normalization
barc.MR <- newMRexperiment(t(barc.asv))
p <- cumNormStat(barc.MR)
```

```
## Default value being used.
```

```
barc.MR <- cumNorm(barc.MR, p = p)
barc.norm <- t(MRcounts(barc.MR, norm = T, log = F))

# Richness and Shannon
meta$barc.richness <- specnumber(barc.norm)
meta$barc.shannon <- diversity(barc.norm, index = "shannon")

# Bray-Curtis distance
barc.dist <- vegdist(barc.norm, method = "bray")


# ITS ------------------------------------------------------------------------

# Normalization
fungi.MR <- newMRexperiment(t(fungi.asv))
p <- cumNormStat(fungi.MR)
```

```
## Default value being used.
```

```
fungi.MR <- cumNorm(fungi.MR, p = p)
fungi.norm <- t(MRcounts(fungi.MR, norm = T, log = F))

# Richness and Shannon
```

```
meta$fungi.richness <- specnumber(fungi.norm)
meta$fungi.shannon <- diversity(fungi.norm, index = "shannon")

# Bray-Curtis distance
fungi.dist <- vegdist(fungi.norm, method = "bray")
```

Fig 4a: Bacteria & archaea NMDS ordination

Note that PERMANOVA model results (`adonis2`) will vary slightly each time and will not exactly match values published in the paper.

```
# NMDS ordination
barc.nmds <- metaMDS(barc.dist, k = 2)
```

```
## Run 0 stress 0.1684425
## Run 1 stress 0.1702924
## Run 2 stress 0.1823107
## Run 3 stress 0.1702923
## Run 4 stress 0.1813279
## Run 5 stress 0.1851342
## Run 6 stress 0.1684426
## ... Procrustes: rmse 0.0001095144  max resid 0.0005308631
## ... Similar to previous best
## Run 7 stress 0.1829819
## Run 8 stress 0.1818475
## Run 9 stress 0.199813
## Run 10 stress 0.1691198
## Run 11 stress 0.1830973
## Run 12 stress 0.1700363
## Run 13 stress 0.1690971
## Run 14 stress 0.168046
## ... New best solution
## ... Procrustes: rmse 0.04033527  max resid 0.2923194
## Run 15 stress 0.1794557
## Run 16 stress 0.1766268
## Run 17 stress 0.182858
## Run 18 stress 0.1944114
## Run 19 stress 0.1814571
## Run 20 stress 0.2023585
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      1: no. of iterations >= maxit
##     19: stress ratio > sratmax
```

```
barc.nmds$stress
```

```
## [1] 0.168046
```

```
meta$barc.NMDS1 <- barc.nmds$points[ , 1]
meta$barc.NMDS2 <- barc.nmds$points[ , 2]

# PERMANOVA
adonis2(barc.dist ~ meta$Treatment)
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = barc.dist ~ meta$Treatment)
##                Df SumOfSqs      R2      F Pr(>F)
## meta$Treatment  1   0.2559 0.02881 1.7799  0.027 *
## Residual       60   8.6275 0.97119
## Total          61   8.8835 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Plot (using dat.2021 for same NMDS values presented in paper):
barc.nmds.plot.21 <- dat.2021 %>%
  ggplot(aes(x = barc.NMDS1, y = barc.NMDS2, color = Treatment, shape = Treatment)) +
  geom_point() +
  scale_color_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  labs(x = "Axis 1",
       y = "Axis 2",
       title = "Bacteria & archaea",
       color = "Treatment",
       shape = "Treatment") +
  theme(legend.position = "bottom") +
  theme(plot.margin = margin(0.1, 0.2, 0.1, 0.1, "in")) +
  theme(legend.title = element_blank()) +
  geom_text(aes(x = 0.2, y = -0.55, label = "PERMANOVA, p = 0.029"),
            size = 2.5, color = "gray30") +
  geom_text(aes(x = 0.25, y = -0.65, label = "Stress = 0.168"),
            size = 2.5, color = "gray30") +
  theme(plot.title = element_text(size = 12))
barc.nmds.plot.21
```

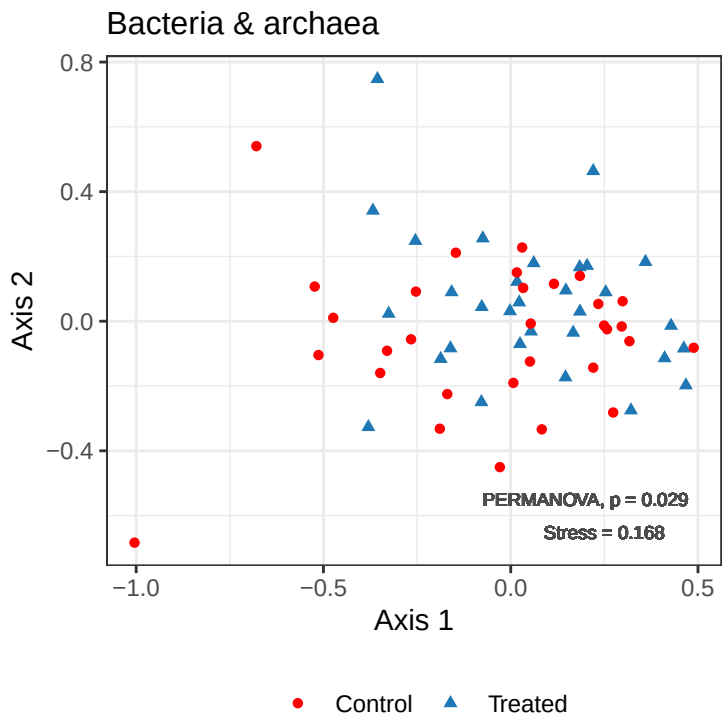


Fig 4b: Fungi NMDS ordination

Note that PERMANOVA model results (`adonis2`) will vary slightly each time and will not exactly match values published in the paper.

```
# NMDS ordination
fungi.nmds <- metaMDS(fungi.dist, k = 2)
```

```
## Run 0 stress 0.2461785
## Run 1 stress 0.2482543
## Run 2 stress 0.2482438
## Run 3 stress 0.2430824
## ... New best solution
## ... Procrustes: rmse 0.1086437  max resid 0.4501687
## Run 4 stress 0.2425487
## ... New best solution
## ... Procrustes: rmse 0.08848532  max resid 0.4675074
## Run 5 stress 0.2469196
## Run 6 stress 0.2447097
## Run 7 stress 0.2728852
## Run 8 stress 0.2456924
## Run 9 stress 0.2450755
## Run 10 stress 0.2474592
## Run 11 stress 0.2703356
## Run 12 stress 0.2465285
## Run 13 stress 0.2401766
## ... New best solution
## ... Procrustes: rmse 0.08340088  max resid 0.4962715
```

```
## Run 14 stress 0.2405417
## ... Procrustes: rmse 0.05780132  max resid 0.2100576
## Run 15 stress 0.265198
## Run 16 stress 0.250744
## Run 17 stress 0.2589465
## Run 18 stress 0.2600363
## Run 19 stress 0.268791
## Run 20 stress 0.2694536
## *** Best solution was not repeated -- monoMDS stopping criteria:
##      2: no. of iterations >= maxit
##     18: stress ratio > sratmax
```

```
fungi.nmds$stress
```

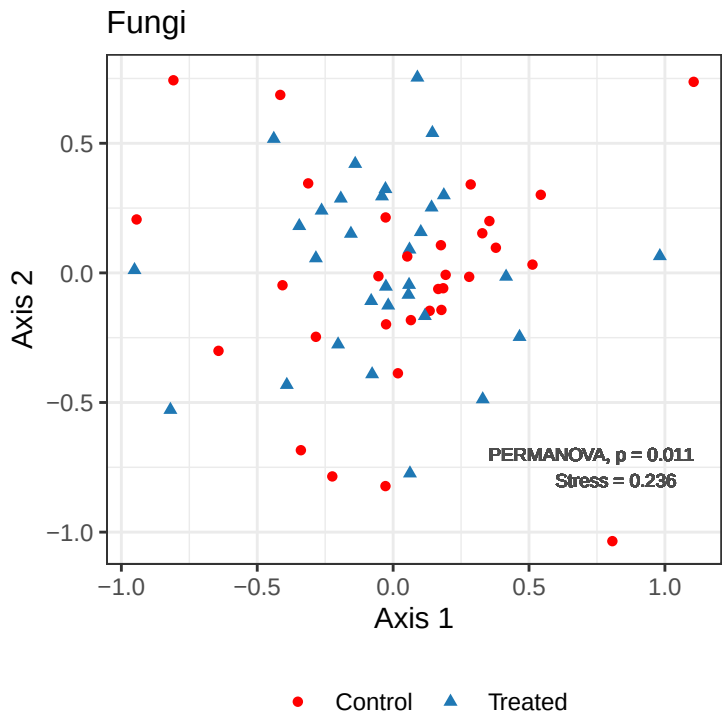
```
## [1] 0.2401766
```

```
meta$fungi.NMDS1 <- fungi.nmds$points[ , 1]
meta$fungi.NMDS2 <- fungi.nmds$points[ , 2]

# PERMANOVA
adonis2(fungi.dist ~ meta$Treatment)
```

```
## Permutation test for adonis under reduced model
## Terms added sequentially (first to last)
## Permutation: free
## Number of permutations: 999
##
## adonis2(formula = fungi.dist ~ meta$Treatment)
##                Df SumOfSqs      R2     F Pr(>F)
## meta$Treatment  1   0.4511 0.02371 1.457  0.012 *
## Residual       60  18.5783 0.97629
## Total          61  19.0294 1.00000
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Plot (using dat.2021 for same NMDS values presented in paper):
fungi.nmds.plot.21 <- dat.2021 %>%
  ggplot(aes(x = fungi.NMDS1, y = fungi.NMDS2, color = Treatment, shape = Treatment)) +
  geom_point() +
  scale_color_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  labs(x = "Axis 1",
       y = "Axis 2",
       title = "Fungi",
       color = "Treatment",
       shape = "Treatment") +
  theme(legend.position = "bottom") +
  theme(legend.title = element_blank()) +
  theme(plot.margin = margin(0.1, 0.2, 0.1, 0.1, "in")) +
  geom_text(aes(x = 0.73, y = -0.7, label = "PERMANOVA, p = 0.011"),
            size = 2.5, color = "gray30") +
  geom_text(aes(x = 0.82, y = -0.8, label = "Stress = 0.236"),
```

```
            size = 2.5, color = "gray30") +
  theme(plot.title = element_text(size = 12))
fungi.nmds.plot.21
```



Combine plots for Fig 4

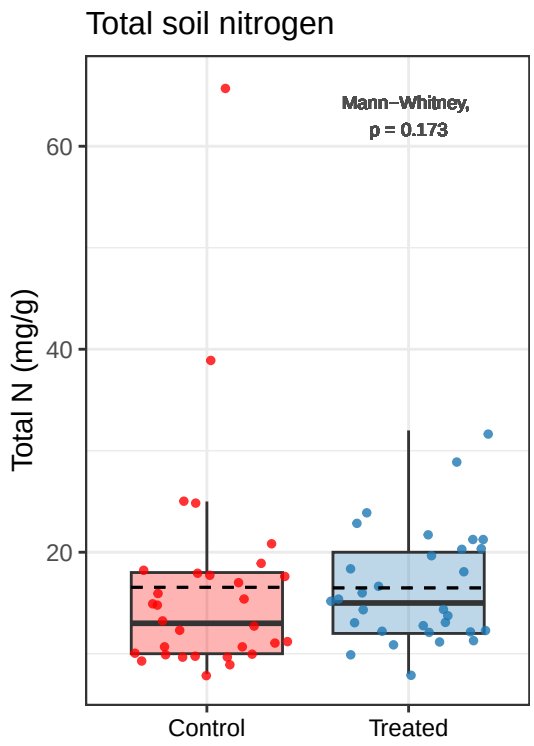
```
# Combine NMDS ------------------------------------------------------------

tiff("Fig4_Soil-NMDS.tiff", height = 4, width = 7, units = "in", res = 1000)
ggarrange(barc.nmds.plot.21, fungi.nmds.plot.21,
          nrow = 1, ncol = 2,
          labels = c("(A)", "(B)"),
          common.legend = TRUE, legend = "bottom")
dev.off()
```

Supp Fig 6a: Total soil nitrogen

```
# Total N -----------------------------------------------------------------

# Mann-Whitney
wilcox.test(filter(dat.2021, Treatment == "Control")$TN_ppt,
            filter(dat.2021, Treatment == "Treated")$TN_ppt,
            exact = FALSE) # p-value = 0.1731
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(dat.2021, Treatment == "Control")$TN_ppt and filter(dat.2021, Treatment == "Treated")$T
## W = 383.5, p-value = 0.1731
## alternative hypothesis: true location shift is not equal to 0
```

```
# Plot
tn.plot.21 <- dat.2021 |>
  ggplot(aes(x = Treatment, y = TN_ppt)) +
  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 = "Total soil nitrogen",
       x = NULL,
       y = "Total N (mg/g)") +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000"))  +
  theme(plot.margin = margin(0.1, 0.2, 0.1, 0.1, "in")) +
  geom_text(aes(x = 2, y = 63, label = "Mann-Whitney, \np = 0.173"),
            color = "gray30",
            size = 2.5) +
  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))
tn.plot.21
```



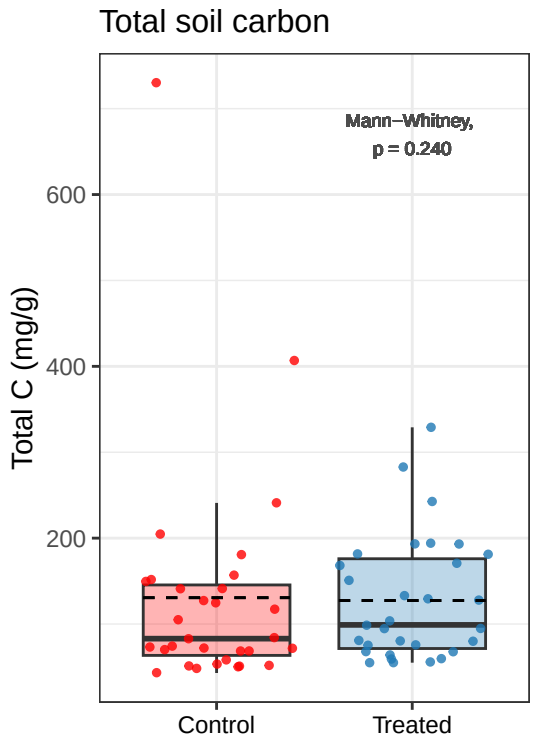
Supp Fig 6b: Total soil carbon

```
# Total C ----------------------------------------------------------------

# Mann-Whitney
wilcox.test(filter(dat.2021, Treatment == "Control")$TC_ppt,
            filter(dat.2021, Treatment == "Treated")$TC_ppt,
            exact = FALSE) # p-value = 0.2397
```

```
##
##  Wilcoxon rank sum test with continuity correction
##
## data:  filter(dat.2021, Treatment == "Control")$TC_ppt and filter(dat.2021, Treatment == "Treated")$
## W = 396.5, p-value = 0.2397
## alternative hypothesis: true location shift is not equal to 0
```

```
# Plot
tc.plot.21 <- dat.2021 |>
  ggplot(aes(x = Treatment, y = TC_ppt)) +
  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 = "Total soil carbon",
       x = NULL,
       y = "Total C (mg/g)") +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000"))  +
  theme(plot.margin = margin(0.1, 0.2, 0.1, 0.1, "in")) +
  geom_text(aes(x = 2, y = 670, label = "Mann-Whitney, \np = 0.240"),
            color = "gray30",
            size = 2.5) +
  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))
tc.plot.21
```



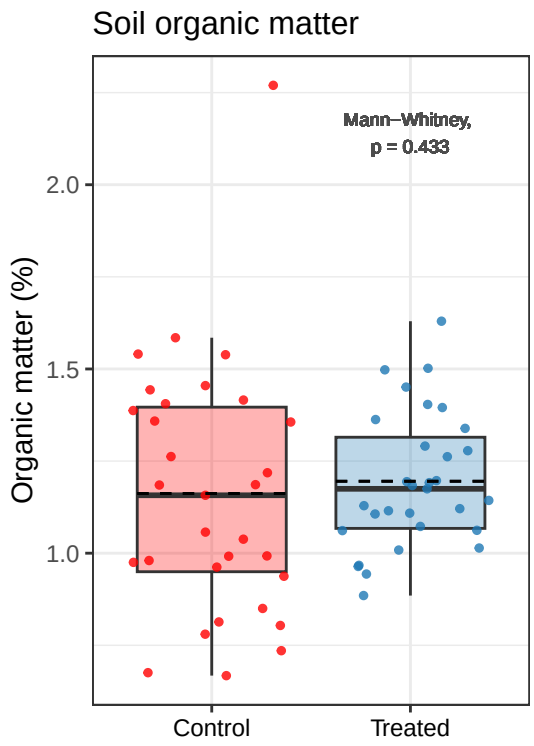
Supp Fig 6c: Soil organic matter

```
# Organic matter ---------------------------------------------------------

# Mann-Whitney
wilcox.test(filter(dat.2021, Treatment == "Control")$OM_perc,
            filter(dat.2021, Treatment == "Treated")$OM_perc) # p-value = 0.4332
```

```
##
##  Wilcoxon rank sum exact test
```

```
##
## data:  filter(dat.2021, Treatment == "Control")$OM_perc and filter(dat.2021, Treatment == "Treated")$
## W = 424, p-value = 0.4332
## alternative hypothesis: true location shift is not equal to 0
```

```r
# Plot
om.plot.21 <- dat.2021 |>
  ggplot(aes(x = Treatment, y = OM_perc)) +
  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 = "Soil organic matter",
       x = NULL,
       y = "Organic matter (%)") +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000"))  +
  theme(plot.margin = margin(0.1, 0.2, 0.1, 0.1, "in")) +
  geom_text(aes(x = 2, y = 2.14, label = "Mann-Whitney, \np = 0.433"),
            color = "gray30",
            size = 2.5) +
  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))
om.plot.21
```



Combine plots for Supp Fig 6

```
# Combine soil chem ------------------------------------------------------

# TN, TC, OM
tiff("FigS6_Soil-chem.tiff", units = "in", height = 4, width = 7, res = 300)
ggarrange(tn.plot.21, tc.plot.21, om.plot.21,
          ncol = 3, nrow = 1,
          labels = c("(A)", "(B)", "(C)"))

dev.off()
```

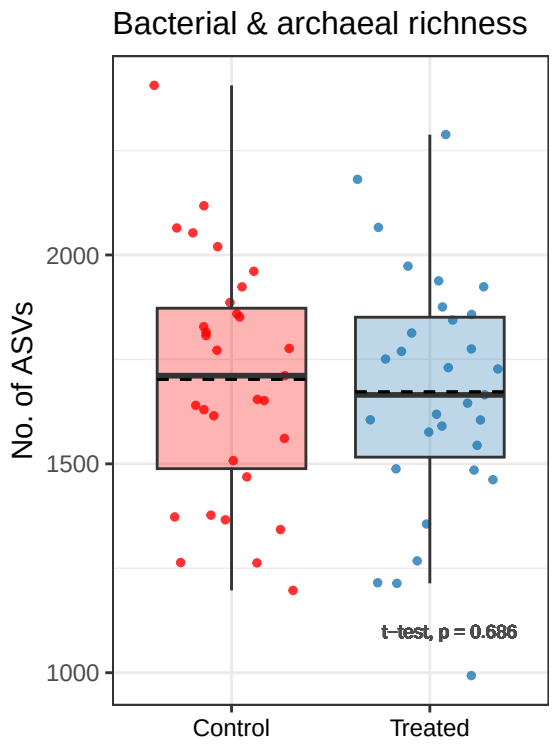
Supp Fig 7a: Bacterial & archaeal richness

```
# Barc richness ----------------------------------------------------------

# T-test
t.test(filter(dat.2021, Treatment == "Control")$barc.richness,
       filter(dat.2021, Treatment == "Treated")$barc.richness) # NS, p = 0.686
```

```
##
##  Welch Two Sample t-test
##
## data:  filter(dat.2021, Treatment == "Control")$barc.richness and filter(dat.2021, Treatment == "Trea
```

```
## t = 0.40607, df = 59.999, p-value = 0.6861
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -116.6407  176.0601
## sample estimates:
## mean of x mean of y
##  1702.065  1672.355
```

```
# Plot
barc.rich.plot.21 <- dat.2021 |>
  ggplot(aes(Treatment, barc.richness)) +
  geom_jitter(aes(color = Treatment),
              alpha = 0.8,
              size = 1) +
  geom_boxplot(aes(fill = Treatment),
               alpha = 0.3,
               outlier.shape = NA) +
  xlab(NULL) +
  ylab("No. of ASVs") +
  ggtitle("Bacterial & archaeal richness") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000")) +
  geom_text(aes(x = 2.1, y = 1100, label = "t-test, p = 0.686"),
            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 = 11.5))
barc.rich.plot.21
```



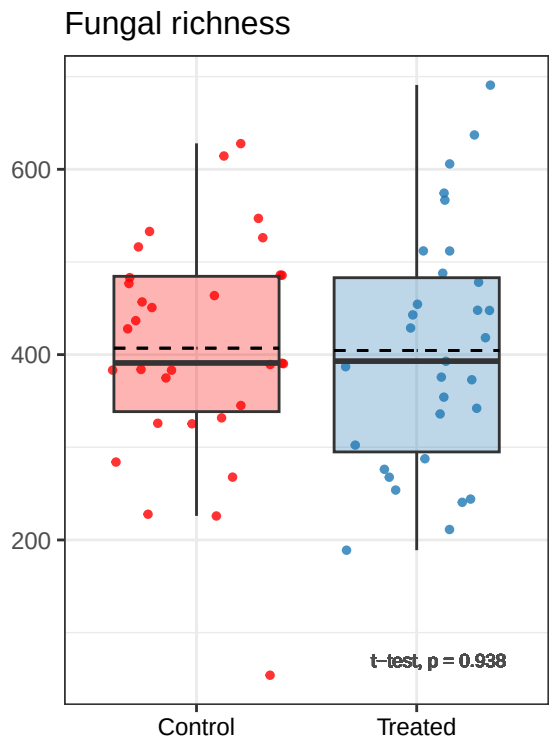
Supp Fig 7b: Fungal richness

```
# Fungi richness ------------------------------------------------------------

# T-test
t.test(filter(dat.2021, Treatment == "Control")$fungi.richness,
       filter(dat.2021, Treatment == "Treated")$fungi.richness) # NS, p = 0.938
```

```
##
##  Welch Two Sample t-test
##
## data:  filter(dat.2021, Treatment == "Control")$fungi.richness and filter(dat.2021, Treatment == "Tr
## t = 0.078, df = 59.653, p-value = 0.9381
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -61.22215  66.18989
## sample estimates:
## mean of x mean of y
##  406.9677  404.4839
```

```
# Plot
fungi.rich.plot.21 <- dat.2021 %>%
  ggplot(aes(Treatment, fungi.richness)) +
  geom_jitter(aes(color = Treatment),
              alpha = 0.8,
              size = 1) +
```

```
  geom_boxplot(aes(fill = Treatment),
               alpha = 0.3,
               outlier.shape = NA) +
  xlab(NULL) +
  ylab(NULL) +
  ggtitle("Fungal richness") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000")) +
  geom_text(aes(x = 2.1, y = 70, label = "t-test, p = 0.938"),
            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))
fungi.rich.plot.21
```



Combine plots for Supp Fig 7

```
# Combine soil richness ----------------------------------------------------

tiff("FigS7_Soil-richness.tiff", units = "in", height = 4, width = 5.5, res = 300)
ggarrange(barc.rich.plot.21, fungi.rich.plot.21,
```

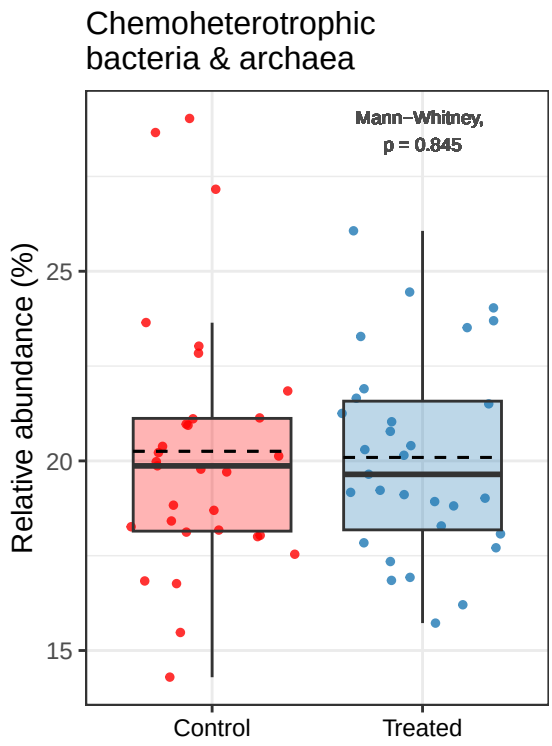
```
          ncol = 2, nrow = 1,
          labels = c("(A)", "(B)"))

dev.off()
```

Supp Fig 8a: Chemoheterotrophic bacteria & archaea

```
# Chemoheterotrophs ------------------------------------------------------

# Mann-Whitney
wilcox.test(filter(dat.2021, Treatment == "Control")$chemoheterotrophy_perc,
            filter(dat.2021, Treatment == "Treated")$chemoheterotrophy_perc) # p = 0.8449
```

```
##
##  Wilcoxon rank sum exact test
##
## data:  filter(dat.2021, Treatment == "Control")$chemoheterotrophy_perc and filter(dat.2021, Treatmen
## W = 466, p-value = 0.8449
## alternative hypothesis: true location shift is not equal to 0
```

```
# Plot
chemohet.plot.21 <- dat.2021 %>%
  ggplot(aes(Treatment, chemoheterotrophy_perc)) +
  geom_jitter(aes(color = Treatment),
              alpha = 0.8,
              size = 1) +
  geom_boxplot(aes(fill = Treatment),
               alpha = 0.3,
               outlier.shape = NA) +
  xlab(NULL) +
  ylab("Relative abundance (%)") +
  ggtitle("Chemoheterotrophic \nbacteria & archaea") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000")) +
  theme(plot.margin = margin(0.1, 0.1, 0.1, 0.1, "in")) +
  geom_text(aes(x = 2, y = 28.7, label = "Mann-Whitney, \np = 0.845"),
            color = "gray30",
            size = 2.5) +
  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))
chemohet.plot.21
```



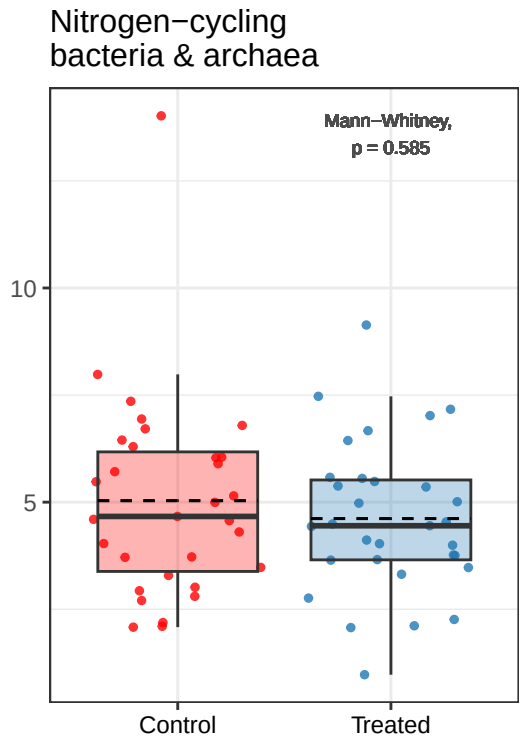
Supp Fig 8b: Nitrogen-cycling bacteria & archaea

```
# N-cyclers ------------------------------------------------------------------

# Mann-Whitney
wilcox.test(filter(dat.2021, Treatment == "Control")$n.cycler_perc,
            filter(dat.2021, Treatment == "Treated")$n.cycler_perc) # p-value = 0.5854
```

```
##
##  Wilcoxon rank sum exact test
##
## data:  filter(dat.2021, Treatment == "Control")$n.cycler_perc and filter(dat.2021, Treatment == "Trea
## W = 520, p-value = 0.5854
## alternative hypothesis: true location shift is not equal to 0
```

```
# Plot
ncycler.plot.21 <- dat.2021 %>%
  ggplot(aes(Treatment, n.cycler_perc)) +
  geom_jitter(aes(color = Treatment),
              alpha = 0.8,
              size = 1) +
  geom_boxplot(aes(fill = Treatment),
               alpha = 0.3,
               outlier.shape = NA) +
  xlab(NULL) +
  ylab(NULL) +
```

```
  ggtitle("Nitrogen-cycling \nbacteria & archaea") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000")) +
  theme(plot.margin = margin(0.1, 0.1, 0.1, 0.25, "in")) +
  geom_text(aes(x = 2, y = 13.6, label = "Mann-Whitney, \np = 0.585"),
            color = "gray30",
            size = 2.5) +
  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))
ncycler.plot.21
```



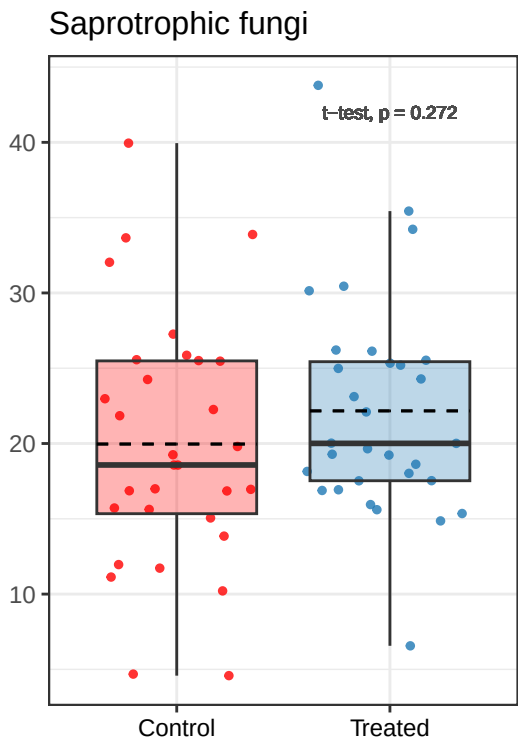
Supp Fig 8c: Saprotrophic fungi

```
# Saprotrophs ------------------------------------------------------------

# T-test
t.test(filter(dat.2021, Treatment == "Control")$saprotroph,
       filter(dat.2021, Treatment == "Treated")$saprotroph) # NS, p = 0.272
```

```
##
##  Welch Two Sample t-test
##
```

```
## data:  filter(dat.2021, Treatment == "Control")$saprotroph and filter(dat.2021, Treatment == "Treate
## t = -1.1097, df = 59.068, p-value = 0.2716
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -6.168384  1.767276
## sample estimates:
## mean of x mean of y
##  19.96490  22.16546
```

```
# Plot
sapro.plot.21 <- dat.2021 %>%
  ggplot(aes(Treatment, saprotroph)) +
  geom_jitter(aes(color = Treatment),
              alpha = 0.8,
              size = 1) +
  geom_boxplot(aes(fill = Treatment),
               alpha = 0.3,
               outlier.shape = NA) +
  xlab(NULL) +
  ylab(NULL) +
  ggtitle("Saprotrophic fungi") +
  scale_color_manual(values = c("red", "#1F78B4")) +
  scale_fill_manual(values = c("red", "#1F78B4")) +
  theme_bw() +
  theme(legend.position = "none") +
  theme(axis.text.x = element_text(color = "#000000")) +
  theme(plot.margin = margin(0.1, 0.1, 0.1, 0.25, "in")) +
  geom_text(aes(x = 2, y = 42, label = "t-test, p = 0.272"),
            color = "gray30",
            size = 2.5) +
  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))
sapro.plot.21
```



Combine plots for Supp Fig 8

```
# Combine FAPROTAX and FUNGuild ------------------------------------------

tiff("FigS8_Soil-functional.tiff", units = "in", height = 4, width = 7, res = 300)
ggarrange(chemohet.plot.21, ncycler.plot.21, sapro.plot.21,
          ncol = 3, nrow = 1,
          labels = c("(A)", "(B)", "(C)"))

dev.off()
```

```
## pdf
##   2
```

Appendix D: Structural equation modeling

Setup

```
library(lavaan)
library(tidyverse)
```

```
# Load data ------------------------------------------------------------------

dat.2021 <- read.csv("Veg-soil-elev_2021.csv")
```

```
# Data wrangling -------------------------------------------------------------

# Add Control/Treated as binary variable and select only variables needed for SEM
sem.dat.unscaled <- dat.2021 |>
  mutate(rocks = case_when(
    Treatment == "Control" ~ 0,
    Treatment == "Treated" ~ 1)) |>
  select(Sample, rocks, notree, notree.18, herb, herb.18, tree, perveg.richness, perveg.shannon,
         TN_log, TC_log, OM_log, barc.richness, fungi.richness,
         chemoheterotrophy_log, n.cycler_log, saprotroph)

# Center and scale continuous variables
sem.dat <- sem.dat.unscaled |>
  mutate(rocks = as.character(rocks),
         Sample = as.character(Sample)) |>
  mutate_if(is.numeric, scale) |>
  mutate(rocks = as.numeric(rocks))
```

Latent variables

Soil microbiome

```
lvmod.soimic <- '
  # latent variable model
  soil_microbe =~ barc.richness + fungi.richness + chemoheterotrophy_log + n.cycler_log + saprotroph
'
fit.soimic <- sem(lvmod.soimic, data = sem.dat)
summary(fit.soimic, fit.measures = TRUE, standardized = TRUE)
```

```
## lavaan 0.6.16 ended normally after 18 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of model parameters                        10
##
##   Number of observations                            62
##
## Model Test User Model:
```

```
##
##   Test statistic                                2.723
##   Degrees of freedom                                5
##   P-value (Chi-square)                          0.743
##
## Model Test Baseline Model:
##
##   Test statistic                               52.070
##   Degrees of freedom                               10
##   P-value                                       0.000
##
## User Model versus Baseline Model:
##
##   Comparative Fit Index (CFI)                   1.000
##   Tucker-Lewis Index (TLI)                      1.108
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)              -412.677
##   Loglikelihood unrestricted model (H1)      -411.315
##
##   Akaike (AIC)                                845.354
##   Bayesian (BIC)                              866.625
##   Sample-size adjusted Bayesian (SABIC)       835.162
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                         0.000
##   90 Percent confidence interval - lower        0.000
##   90 Percent confidence interval - upper        0.125
##   P-value H_0: RMSEA <= 0.050                   0.800
##   P-value H_0: RMSEA >= 0.080                   0.134
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                          0.044
##
## Parameter Estimates:
##
##   Standard errors                             Standard
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   soil_microbe =~
##     barc.richness     1.000                               0.853    0.860
##     fungi.richness    0.342    0.168    2.033    0.042    0.291    0.294
##     chmhtrtrphy_lg    0.158    0.164    0.962    0.336    0.135    0.136
##     n.cycler_log      0.892    0.241    3.699    0.000    0.761    0.767
##     saprotroph        0.461    0.172    2.675    0.007    0.393    0.397
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
```

```
##    .barc.richness     0.256    0.184    1.392    0.164    0.256    0.260
##    .fungi.richness    0.899    0.165    5.448    0.000    0.899    0.914
##    .chmhtrtrphy_lg    0.966    0.174    5.545    0.000    0.966    0.982
##    .n.cycler_log      0.405    0.160    2.538    0.011    0.405    0.412
##    .saprotroph        0.829    0.156    5.321    0.000    0.829    0.843
##     soil_microbe      0.728    0.247    2.951    0.003    1.000    1.000
```

```
modindices(fit.soimic, sort = TRUE, minimum.value = 3.5)
```

```
## [1] lhs      op       rhs      mi       epc      sepc.lv  sepc.all sepc.nox
## <0 rows> (or 0-length row.names)
```

```
# No paths to add.
```

Soil chemistry

- Soil chemistry does not do well as a latent variable because TN, TC, and OM are collinear and must be modeled separately.

```
lvmod.soichem <- '
  # latent variable model
  soil_chem =~ TN_log + OM_log
'
fit.soichem <- sem(lvmod.soichem, data = sem.dat)
```

```
## Warning in lav_model_vcov(lavmodel = lavmodel, lavsamplestats = lavsamplestats, : lavaan WARNING:
##     Could not compute standard errors! The information matrix could
##     not be inverted. This may be a symptom that the model is not
##     identified.
```

```
summary(fit.soichem)
```

```
## lavaan 0.6.16 ended normally after 13 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of model parameters                         4
##
##   Number of observations                            62
##
## Model Test User Model:
##
##   Test statistic                                    NA
##   Degrees of freedom                                -1
##   P-value (Unknown)                                 NA
##
## Parameter Estimates:
##
##   Standard errors                             Standard
##   Information                                 Expected
##   Information saturated (h1) model          Structured
```

```
##
## Latent Variables:
##                   Estimate  Std.Err  z-value  P(>|z|)
##   soil_chem =~
##     TN_log           1.000
##     OM_log           0.874       NA
##
## Variances:
##                   Estimate  Std.Err  z-value  P(>|z|)
##    .TN_log           0.139       NA
##    .OM_log           0.338       NA
##     soil_chem        0.845       NA
```

Model 1

```
mod1 <- '
  # latent variables
  soil_microbe =~ barc.richness + fungi.richness + chemoheterotrophy_log + n.cycler_log + saprotroph

  # structure
  notree ~ rocks + notree.18 + tree
  OM_log ~ rocks
  soil_microbe ~ rocks
  notree.18 ~ rocks

  # covariance
  OM_log ~~ soil_microbe
  OM_log ~~ notree
  soil_microbe ~~ notree
'
fit1 <- sem(mod1, data = sem.dat)
summary(fit1, fit.measures = TRUE, standardized = TRUE)
```

```
## lavaan 0.6.16 ended normally after 27 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of model parameters                        22
##
##   Number of observations                            62
##
## Model Test User Model:
##
##   Test statistic                                26.242
##   Degrees of freedom                                30
##   P-value (Chi-square)                           0.663
##
## Model Test Baseline Model:
##
##   Test statistic                               124.316
##   Degrees of freedom                                44
##   P-value                                        0.000
```

```
##
## User Model versus Baseline Model:
##
##   Comparative Fit Index (CFI)                    1.000
##   Tucker-Lewis Index (TLI)                       1.069
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)               -650.724
##   Loglikelihood unrestricted model (H1)       -637.603
##
##   Akaike (AIC)                                1345.448
##   Bayesian (BIC)                              1392.245
##   Sample-size adjusted Bayesian (SABIC)       1323.026
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.000
##   90 Percent confidence interval - lower         0.000
##   90 Percent confidence interval - upper         0.080
##   P-value H_0: RMSEA <= 0.050                    0.829
##   P-value H_0: RMSEA >= 0.080                    0.049
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.076
##
## Parameter Estimates:
##
##   Standard errors                             Standard
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   soil_microbe =~
##     barc.richness     1.000                               0.845    0.852
##     fungi.richness    0.361    0.165    2.194    0.028    0.305    0.308
##     chmhtrtrphy_lg    0.192    0.164    1.167    0.243    0.162    0.163
##     n.cycler_log      0.908    0.194    4.675    0.000    0.768    0.774
##     saprotroph        0.442    0.165    2.680    0.007    0.374    0.377
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   notree ~
##     rocks            -0.615    0.239   -2.567    0.010   -0.615   -0.307
##     notree.18         0.535    0.107    5.011    0.000    0.535    0.530
##     tree             -0.037    0.106   -0.347    0.728   -0.037   -0.036
##   OM_log ~
##     rocks             0.249    0.250    0.996    0.319    0.249    0.126
##   soil_microbe ~
##     rocks            -0.106    0.237   -0.446    0.656   -0.125   -0.063
##   notree.18 ~
##     rocks             0.674    0.237    2.844    0.004    0.674    0.340
```

```
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##  .soil_microbe ~~
##    .OM_log            0.370    0.129    2.861    0.004    0.439    0.446
##  .notree ~~
##    .OM_log            0.332    0.115    2.877    0.004    0.332    0.393
##  .soil_microbe ~~
##    .notree            0.213    0.107    1.991    0.046    0.252    0.294
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##    .barc.richness     0.269    0.138    1.955    0.051    0.269    0.274
##    .fungi.richness    0.891    0.164    5.442    0.000    0.891    0.905
##    .chmhtrtrphy_lg    0.958    0.173    5.535    0.000    0.958    0.973
##    .n.cycler_log      0.395    0.129    3.067    0.002    0.395    0.401
##    .saprotroph        0.844    0.157    5.367    0.000    0.844    0.858
##    .notree            0.740    0.133    5.568    0.000    0.740    0.737
##    .OM_log            0.968    0.174    5.568    0.000    0.968    0.984
##    .notree.18         0.870    0.156    5.568    0.000    0.870    0.885
##    .soil_microbe      0.712    0.213    3.349    0.001    0.996    0.996
```

```
modindices(fit1, sort = TRUE, minimum.value = 3.5)
```

```
##                      lhs op    rhs    mi    epc sepc.lv sepc.all sepc.nox
## 50            saprotroph ~~ OM_log 4.331 -0.213  -0.213   -0.235   -0.235
## 43 chemoheterotrophy_log ~~ OM_log 3.616  0.203   0.203    0.211    0.211
```

```
# OM already covaries with soil microbiome latent variable;
# does not make sense to add paths for saptrotrophs or chemoheterotrophs.
```

Model 2

```
mod2 <- '
  # latent variables
  soil_microbe =~ barc.richness + fungi.richness + chemoheterotrophy_log + n.cycler_log + saprotroph

  # structure
  notree ~ rocks + notree.18 + tree
  TN_log ~ rocks
  soil_microbe ~ rocks
  notree.18 ~ rocks

  # covariance
  TN_log ~~ soil_microbe
  TN_log ~~ notree
  soil_microbe ~~ notree
'
fit2 <- sem(mod2, data = sem.dat)
summary(fit2, fit.measures = TRUE, standardized = TRUE)
```

```
## lavaan 0.6.16 ended normally after 32 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of model parameters                        22
##
##   Number of observations                            62
##
## Model Test User Model:
##
##   Test statistic                                31.847
##   Degrees of freedom                                30
##   P-value (Chi-square)                           0.375
##
## Model Test Baseline Model:
##
##   Test statistic                               164.607
##   Degrees of freedom                                44
##   P-value                                        0.000
##
## User Model versus Baseline Model:
##
##   Comparative Fit Index (CFI)                    0.985
##   Tucker-Lewis Index (TLI)                       0.978
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)                -633.381
##   Loglikelihood unrestricted model (H1)        -617.457
##
##   Akaike (AIC)                                 1310.762
##   Bayesian (BIC)                               1357.559
##   Sample-size adjusted Bayesian (SABIC)        1288.340
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.032
##   90 Percent confidence interval - lower         0.000
##   90 Percent confidence interval - upper         0.103
##   P-value H_0: RMSEA <= 0.050                    0.595
##   P-value H_0: RMSEA >= 0.080                    0.165
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.079
##
## Parameter Estimates:
##
##   Standard errors                             Standard
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
```

```
##   soil_microbe =~
##     barc.richness     1.000                               0.808    0.815
##     fungi.richness    0.455    0.167    2.719    0.007    0.367    0.370
##     chmhtrtrphy_lg    0.284    0.169    1.679    0.093    0.229    0.231
##     n.cycler_log      0.948    0.163    5.802    0.000    0.766    0.772
##     saprotroph        0.464    0.167    2.777    0.005    0.375    0.378
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   notree ~
##     rocks            -0.651    0.237   -2.744    0.006   -0.651   -0.315
##     notree.18         0.593    0.099    6.011    0.000    0.593    0.570
##     tree             -0.033    0.098   -0.336    0.737   -0.033   -0.032
##   TN_log ~
##     rocks             0.177    0.251    0.706    0.480    0.177    0.089
##   soil_microbe ~
##     rocks            -0.102    0.230   -0.444    0.657   -0.126   -0.063
##   notree.18 ~
##     rocks             0.674    0.237    2.844    0.004    0.674    0.340
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##  .soil_microbe ~~
##    .TN_log            0.602    0.145    4.157    0.000    0.747    0.756
##  .notree ~~
##    .TN_log            0.454    0.123    3.696    0.000    0.454    0.532
##  .soil_microbe ~~
##    .notree            0.214    0.104    2.054    0.040    0.266    0.308
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##    .barc.richness     0.331    0.100    3.310    0.001    0.331    0.337
##    .fungi.richness    0.849    0.157    5.398    0.000    0.849    0.863
##    .chmhtrtrphy_lg    0.931    0.169    5.508    0.000    0.931    0.947
##    .n.cycler_log      0.397    0.103    3.867    0.000    0.397    0.404
##    .saprotroph        0.843    0.156    5.389    0.000    0.843    0.857
##    .notree            0.746    0.134    5.568    0.000    0.746    0.699
##    .TN_log            0.976    0.175    5.568    0.000    0.976    0.992
##    .notree.18         0.870    0.156    5.568    0.000    0.870    0.885
##    .soil_microbe      0.650    0.184    3.529    0.000    0.996    0.996
```

```
modindices(fit2, sort = TRUE, minimum.value = 3.5)
```

```
##                      lhs op          rhs    mi   epc sepc.lv sepc.all sepc.nox
## 43 chemoheterotrophy_log ~~       TN_log 6.485 0.207   0.207    0.217    0.217
## 29         barc.richness ~~ n.cycler_log 4.776 0.303   0.303    0.835    0.835
## 38        fungi.richness ~~       TN_log 4.552 0.170   0.170    0.187    0.187
## 39        fungi.richness ~~    notree.18 4.096 0.224   0.224    0.260    0.260
```

```
# TN already covaries with soil microbiome latent variable;
# does not make sense to add path.
# Prior veg (notree.18) is too far removed to have a plausible                co
```

Model 3

```
mod3 <- '
  # latent variables
  soil_microbe =~ barc.richness + fungi.richness + chemoheterotrophy_log +
  n.cycler_log + saprotroph

  # structure
  herb ~ rocks + herb.18 + tree
  OM_log ~ rocks
  soil_microbe ~ rocks
  herb.18 ~ rocks

  # covariance
  OM_log ~~ soil_microbe
  OM_log ~~ herb
  soil_microbe ~~ herb
'
fit3 <- sem(mod3, data = sem.dat)
summary(fit3, fit.measures = TRUE, standardized = TRUE)
```

```
## lavaan 0.6.16 ended normally after 27 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of model parameters                        22
##
##   Number of observations                            62
##
## Model Test User Model:
##
##   Test statistic                                21.703
##   Degrees of freedom                                30
##   P-value (Chi-square)                           0.865
##
## Model Test Baseline Model:
##
##   Test statistic                               113.947
##   Degrees of freedom                                44
##   P-value                                        0.000
##
## User Model versus Baseline Model:
##
##   Comparative Fit Index (CFI)                    1.000
##   Tucker-Lewis Index (TLI)                       1.174
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)               -653.639
##   Loglikelihood unrestricted model (H1)       -642.787
##
##   Akaike (AIC)                                1351.278
##   Bayesian (BIC)                              1398.075
```

```
##   Sample-size adjusted Bayesian (SABIC)       1328.856
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.000
##   90 Percent confidence interval - lower         0.000
##   90 Percent confidence interval - upper         0.052
##   P-value H_0: RMSEA <= 0.050                    0.946
##   P-value H_0: RMSEA >= 0.080                    0.011
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.069
##
## Parameter Estimates:
##
##   Standard errors                             Standard
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##
## Latent Variables:
##                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   soil_microbe =~
##     barc.richness     1.000                               0.850    0.857
##     fungi.richness    0.351    0.163    2.151    0.031    0.298    0.301
##     chmhtrtrphy_lg    0.194    0.163    1.194    0.233    0.165    0.167
##     n.cycler_log      0.899    0.189    4.762    0.000    0.764    0.770
##     saprotroph        0.442    0.163    2.703    0.007    0.375    0.378
##
## Regressions:
##                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   herb ~
##     rocks            -0.485    0.234   -2.070    0.038   -0.485   -0.250
##     herb.18           0.391    0.102    3.839    0.000    0.391    0.400
##     tree             -0.102    0.106   -0.965    0.335   -0.102   -0.104
##   OM_log ~
##     rocks             0.249    0.250    0.996    0.319    0.249    0.126
##   soil_microbe ~
##     rocks            -0.106    0.238   -0.443    0.658   -0.124   -0.062
##   herb.18 ~
##     rocks             0.334    0.248    1.347    0.178    0.334    0.169
##
## Covariances:
##                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##  .soil_microbe ~~
##    .OM_log            0.371    0.130    2.867    0.004    0.438    0.445
##  .herb ~~
##    .OM_log            0.349    0.118    2.954    0.003    0.349    0.405
##  .soil_microbe ~~
##    .herb              0.268    0.112    2.404    0.016    0.316    0.361
##
## Variances:
##                   Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##    .barc.richness     0.261    0.135    1.936    0.053    0.261    0.266
```

```
##    .fungi.richness    0.895    0.164    5.451    0.000    0.895    0.910
##    .chmhtrtrphy_lg    0.957    0.173    5.535    0.000    0.957    0.972
##    .n.cycler_log      0.400    0.126    3.172    0.002    0.400    0.407
##    .saprotroph        0.843    0.157    5.369    0.000    0.843    0.857
##    .herb              0.766    0.138    5.568    0.000    0.766    0.813
##    .OM_log            0.968    0.174    5.568    0.000    0.968    0.984
##    .herb.18           0.956    0.172    5.568    0.000    0.956    0.972
##    .soil_microbe      0.720    0.212    3.401    0.001    0.996    0.996
```

```
modindices(fit3, sort = TRUE, minimum.value = 3.5)
```

```
##           lhs op    rhs    mi   epc sepc.lv sepc.all sepc.nox
## 50 saprotroph ~~ OM_log 4.195 -0.21   -0.21   -0.232   -0.232
```

```
# OM already covaries with soil microbiome latent variable;
# does not make sense to add path for saptrotrophs.
```

Model 4

```
mod4 <- '
  # latent variables
  soil_microbe =~ barc.richness + fungi.richness + chemoheterotrophy_log +
  n.cycler_log + saprotroph

  # structure
  herb ~ rocks + herb.18 + tree
  TN_log ~ rocks
  soil_microbe ~ rocks
  herb.18 ~ rocks

  # covariance
  TN_log ~~ soil_microbe
  TN_log ~~ herb
  soil_microbe ~~ herb
'
fit4 <- sem(mod4, data = sem.dat)
summary(fit4, fit.measures = TRUE, standardized = TRUE)
```

```
## lavaan 0.6.16 ended normally after 30 iterations
##
##   Estimator                                         ML
##   Optimization method                           NLMINB
##   Number of model parameters                        22
##
##   Number of observations                            62
##
## Model Test User Model:
##
##   Test statistic                                25.702
##   Degrees of freedom                                30
##   P-value (Chi-square)                           0.690
```

```
##
## Model Test Baseline Model:
##
##   Test statistic                                148.339
##   Degrees of freedom                                44
##   P-value                                        0.000
##
## User Model versus Baseline Model:
##
##   Comparative Fit Index (CFI)                    1.000
##   Tucker-Lewis Index (TLI)                       1.060
##
## Loglikelihood and Information Criteria:
##
##   Loglikelihood user model (H0)               -638.442
##   Loglikelihood unrestricted model (H1)       -625.591
##
##   Akaike (AIC)                                1320.884
##   Bayesian (BIC)                              1367.681
##   Sample-size adjusted Bayesian (SABIC)       1298.463
##
## Root Mean Square Error of Approximation:
##
##   RMSEA                                          0.000
##   90 Percent confidence interval - lower         0.000
##   90 Percent confidence interval - upper         0.077
##   P-value H_0: RMSEA <= 0.050                    0.847
##   P-value H_0: RMSEA >= 0.080                    0.042
##
## Standardized Root Mean Square Residual:
##
##   SRMR                                           0.066
##
## Parameter Estimates:
##
##   Standard errors                             Standard
##   Information                                 Expected
##   Information saturated (h1) model          Structured
##
## Latent Variables:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   soil_microbe =~
##     barc.richness     1.000                               0.812    0.818
##     fungi.richness    0.451    0.167    2.711    0.007    0.366    0.369
##     chmhtrtrphy_lg    0.273    0.168    1.623    0.105    0.222    0.224
##     n.cycler_log      0.940    0.163    5.764    0.000    0.763    0.770
##     saprotroph        0.467    0.166    2.810    0.005    0.379    0.383
##
## Regressions:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##   herb ~
##     rocks            -0.495    0.233   -2.121    0.034   -0.495   -0.253
##     herb.18           0.413    0.098    4.236    0.000    0.413    0.418
##     tree             -0.106    0.101   -1.043    0.297   -0.106   -0.107
```

```
##   TN_log ~
##     rocks             0.177    0.251    0.706    0.480    0.177    0.089
##   soil_microbe ~
##     rocks            -0.102    0.231   -0.439    0.660   -0.125   -0.063
##   herb.18 ~
##     rocks             0.334    0.248    1.347    0.178    0.334    0.169
##
## Covariances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##  .soil_microbe ~~
##    .TN_log            0.604    0.145    4.162    0.000    0.745    0.754
##  .herb ~~
##    .TN_log            0.442    0.123    3.589    0.000    0.442    0.512
##  .soil_microbe ~~
##    .herb              0.256    0.108    2.374    0.018    0.316    0.362
##
## Variances:
##                    Estimate  Std.Err  z-value  P(>|z|)   Std.lv  Std.all
##    .barc.richness     0.325    0.101    3.225    0.001    0.325    0.330
##    .fungi.richness    0.850    0.157    5.397    0.000    0.850    0.863
##    .chmhtrtrphy_lg    0.935    0.170    5.511    0.000    0.935    0.950
##    .n.cycler_log      0.401    0.104    3.873    0.000    0.401    0.408
##    .saprotroph        0.840    0.156    5.383    0.000    0.840    0.854
##    .herb              0.765    0.137    5.568    0.000    0.765    0.798
##    .TN_log            0.976    0.175    5.568    0.000    0.976    0.992
##    .herb.18           0.956    0.172    5.568    0.000    0.956    0.972
##    .soil_microbe      0.656    0.185    3.541    0.000    0.996    0.996
```

```
modindices(fit4, sort = TRUE, minimum.value = 3.5)
```

```
##                      lhs op          rhs    mi   epc sepc.lv sepc.all sepc.nox
## 38        fungi.richness ~~       TN_log 7.073 0.220   0.220    0.241    0.241
## 29         barc.richness ~~ n.cycler_log 4.802 0.309   0.309    0.855    0.855
## 43 chemoheterotrophy_log ~~       TN_log 4.418 0.177   0.177    0.186    0.186
```

```
# TN already covaries with soil microbiome latent variable;
# does not make sense to add path for chemoheterotrophs or fungal richness.
# Effect of soil microbiome is modeled as a single latent variable,
# so bacterial/archeal richness and N-cyclers do not need to covary.
```