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.

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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`
- `car 3.1-2`

Appendix A: Temporal vegetation trends

Setup

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

```r
# 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

```r
# 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
```
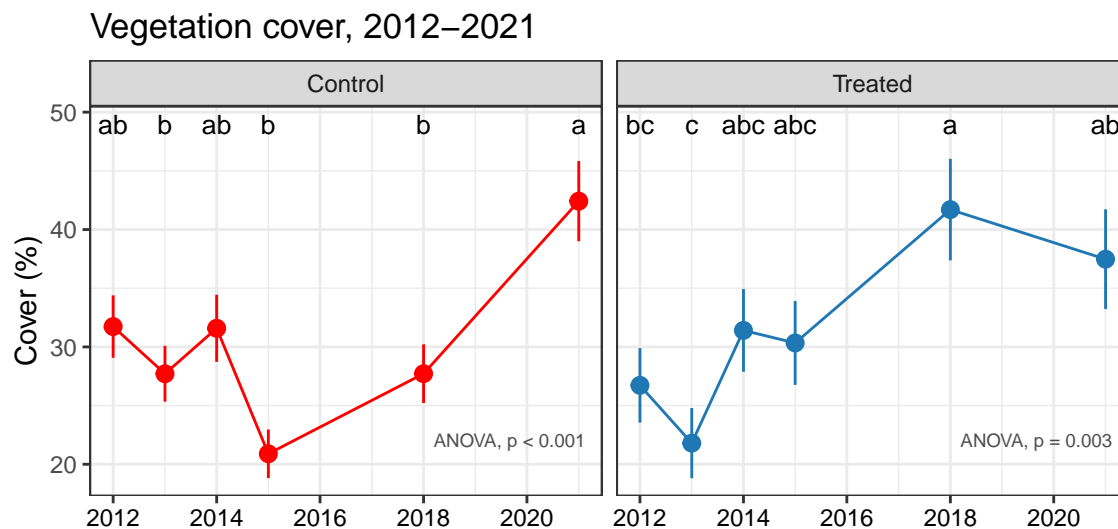
Vegetation cover, 2012–2021

Fig 2b: Herbaceous (grass & forb) cover

```r
# 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
```

```r
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
```

```r
# 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
```

```r
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
```

```r
# 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
```


Herbaceous cover
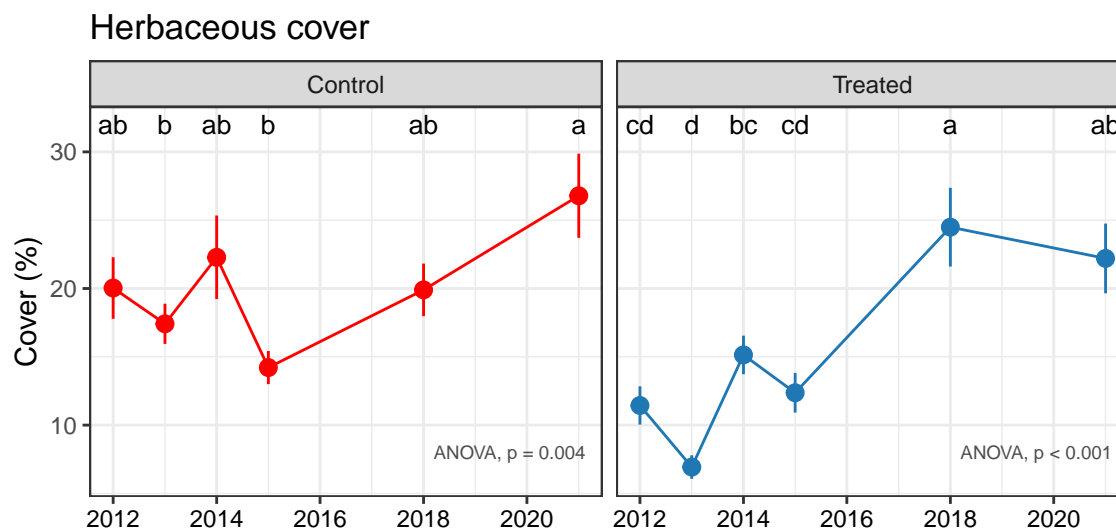
Fig 2c: Shrub cover

```
# 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")
```

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```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
```
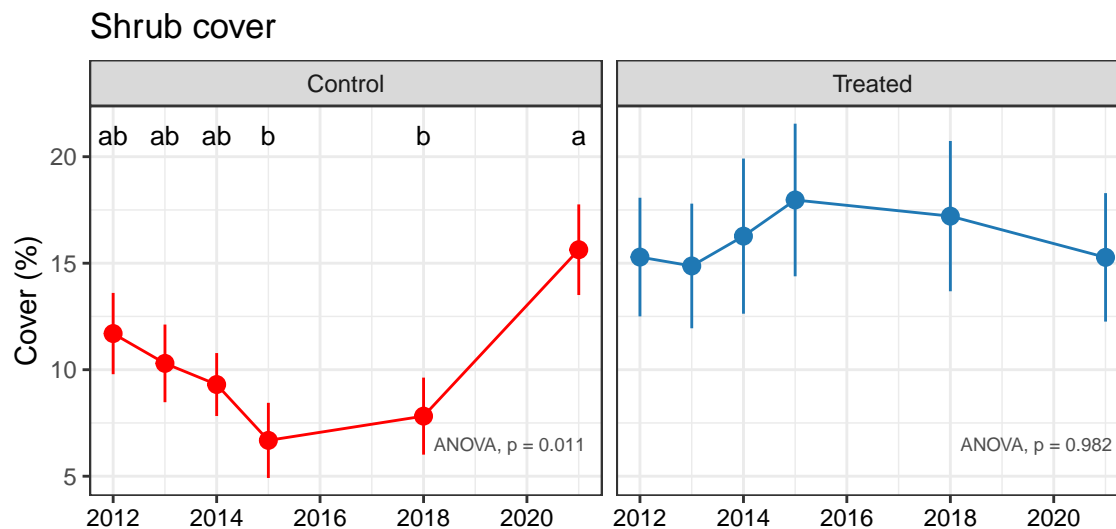

Combine plots for Fig 2

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

tiff("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
```
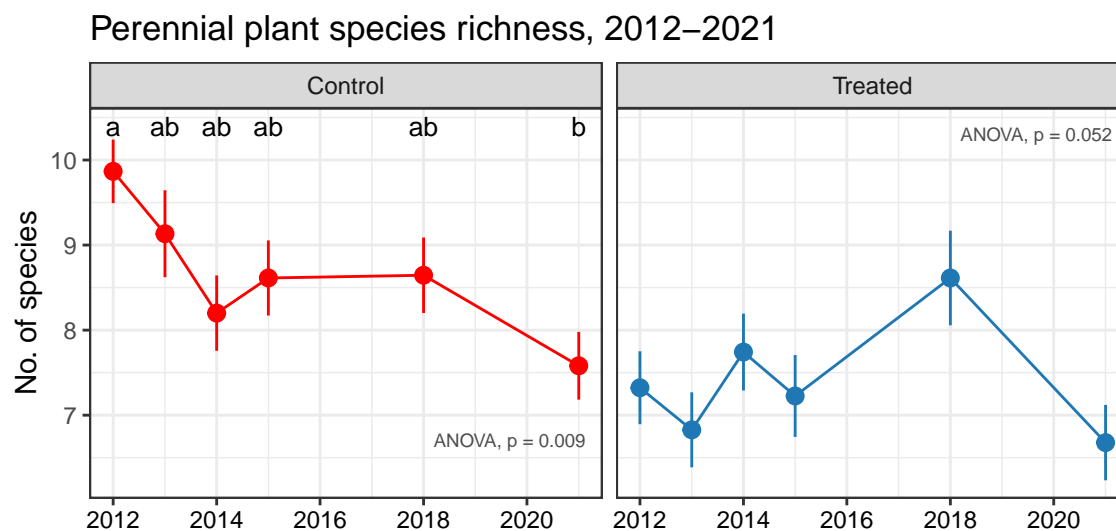

Perennial plant species richness, 2012–2021

Supp Fig 4b: Perennial plant diversity

```r
# 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
```

```r
# 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
```

```r
# 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
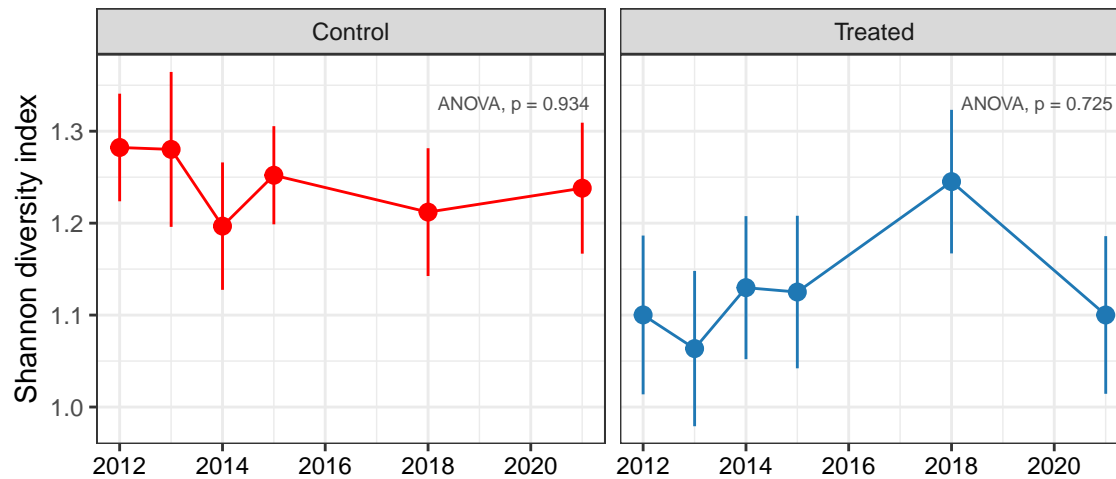
Combine plots for Supp Fig 4

```
# 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.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
```

```r
# 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
```

```r
# 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

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

```r
# 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

```r
# 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

# Explore distribution
qqPlot(filter(shrub.sample, Treatment == "Control")$CV) # not normal
```
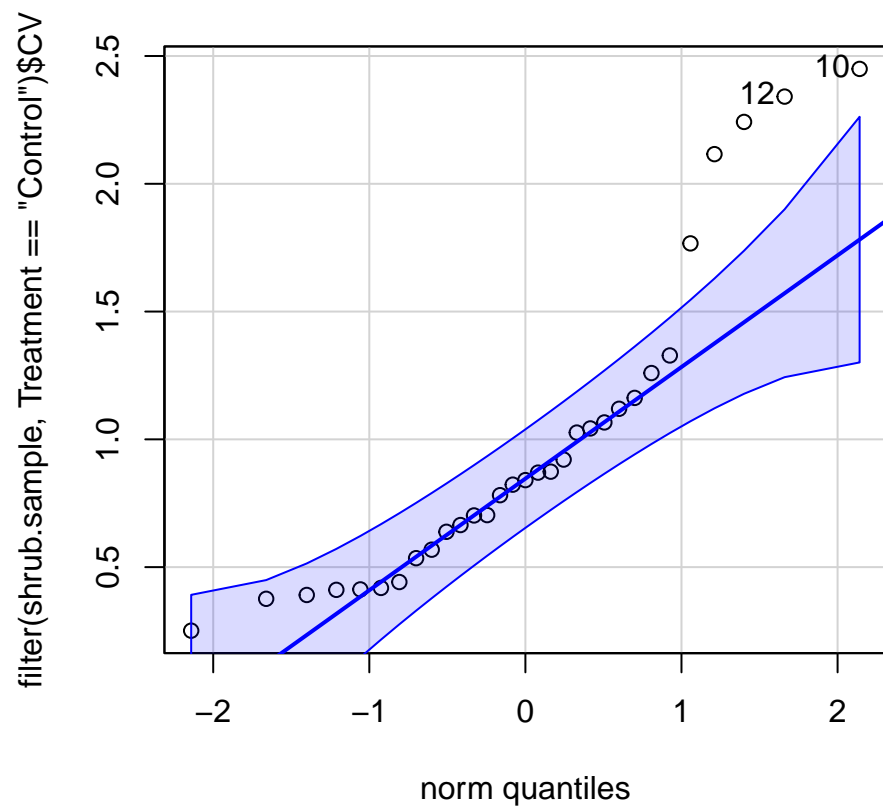
```
## [1] 10 12
```

```
qqPlot(filter(shrub.sample, Treatment == "Treated")$CV) # not normal
```
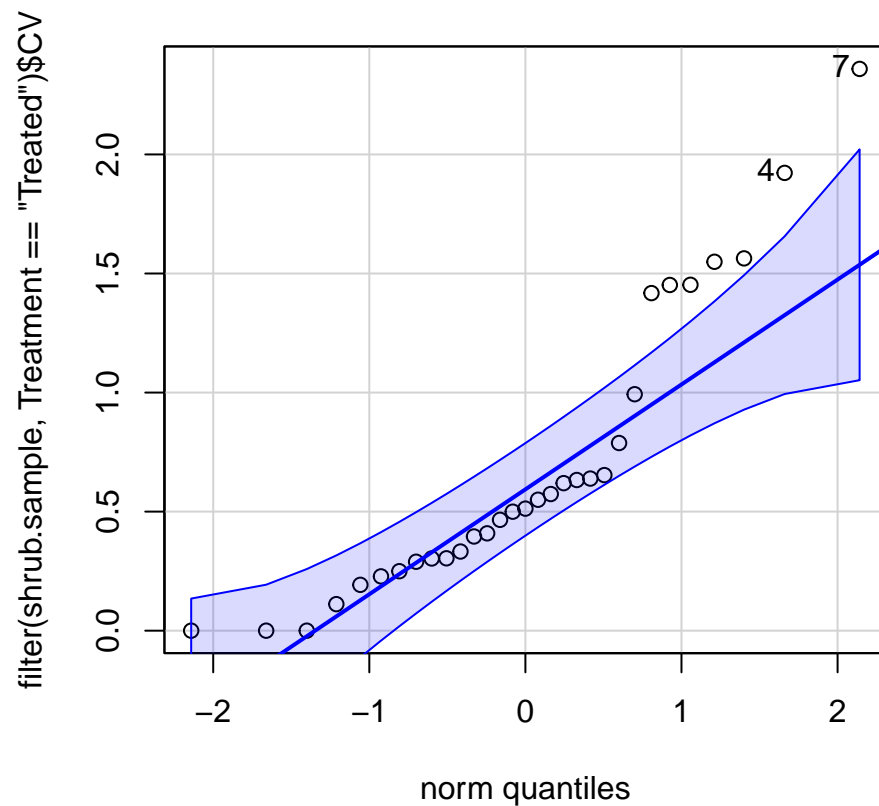
```
## [1] 7 4
```

```
# 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"))

shrub.plot.cv <- shrub.sample |>
  ggplot(aes(x = Treatment, y = CV)) +
  geom_boxplot(alpha = 0.3,
```

```r
                    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
```
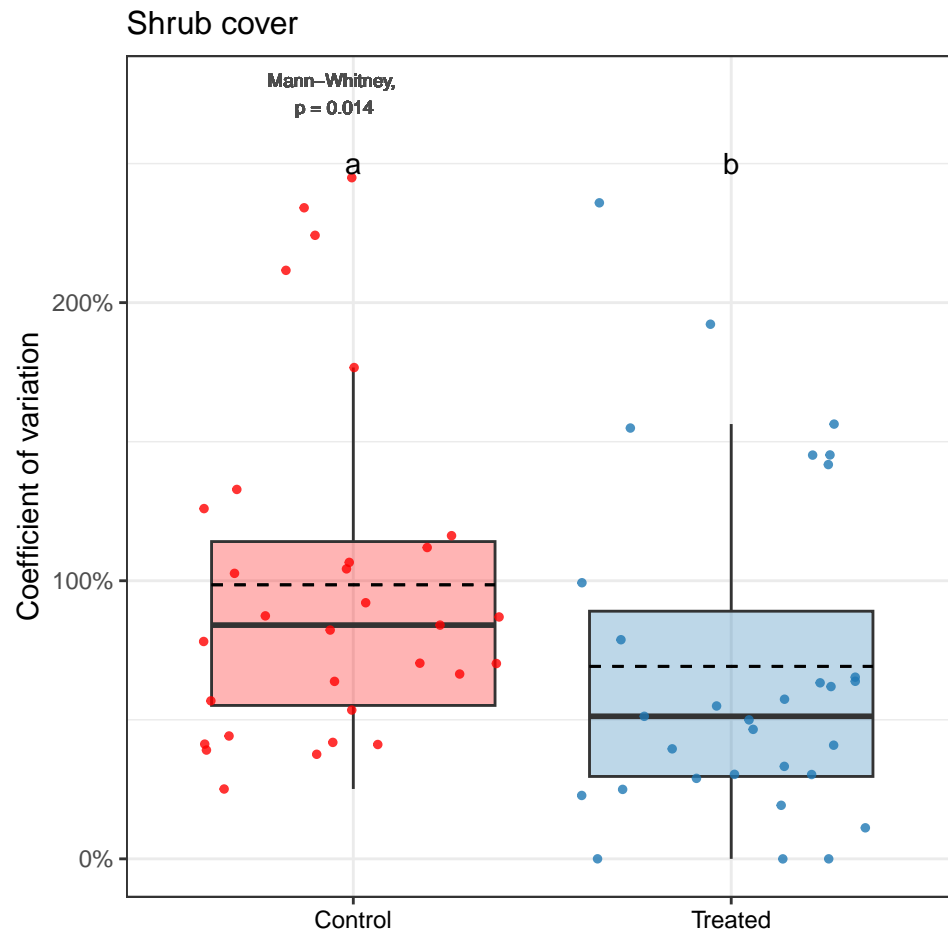
Fig 3b: CV of herbaceous cover

```
# 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")

# Explore distribution
qqPlot(filter(herb.sample, Treatment == "Treated")$CV) # normal
```
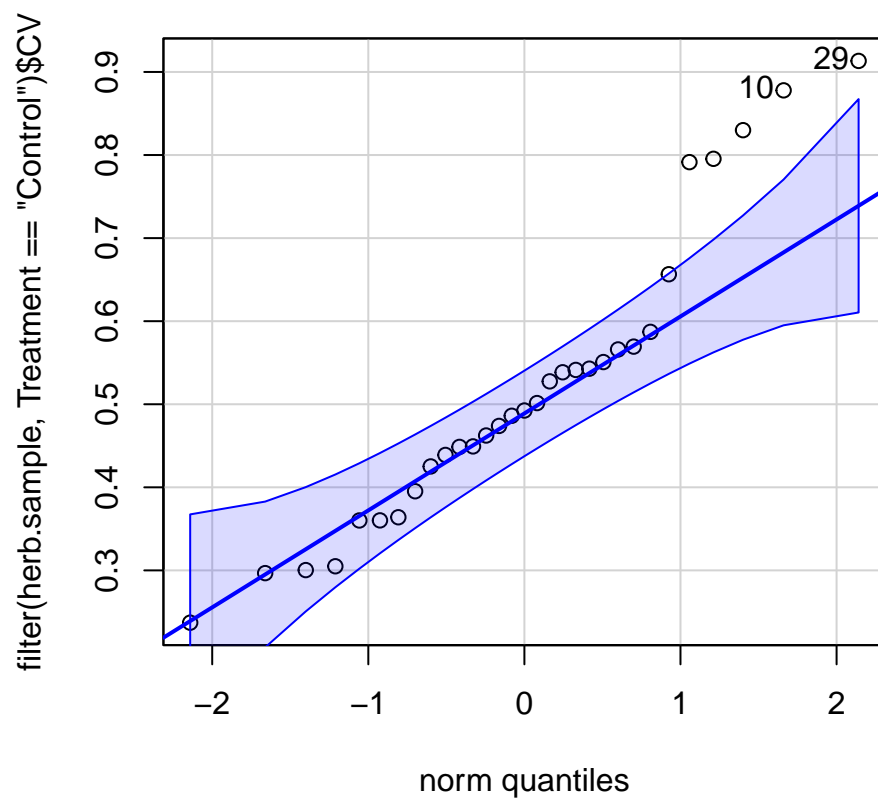
```
## [1] 17 18
```
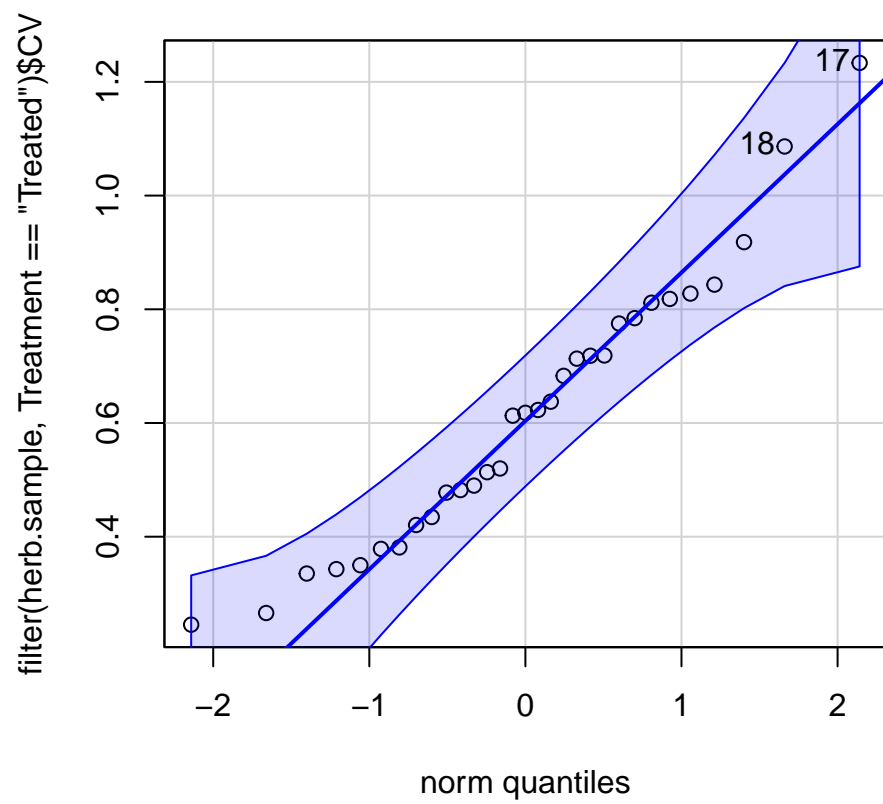
```r
qqPlot(filter(herb.sample, Treatment == "Control")$CV) # not quite normal?
```

```
## [1] 29 10
```

```r
# 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
```

```r
# 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
```
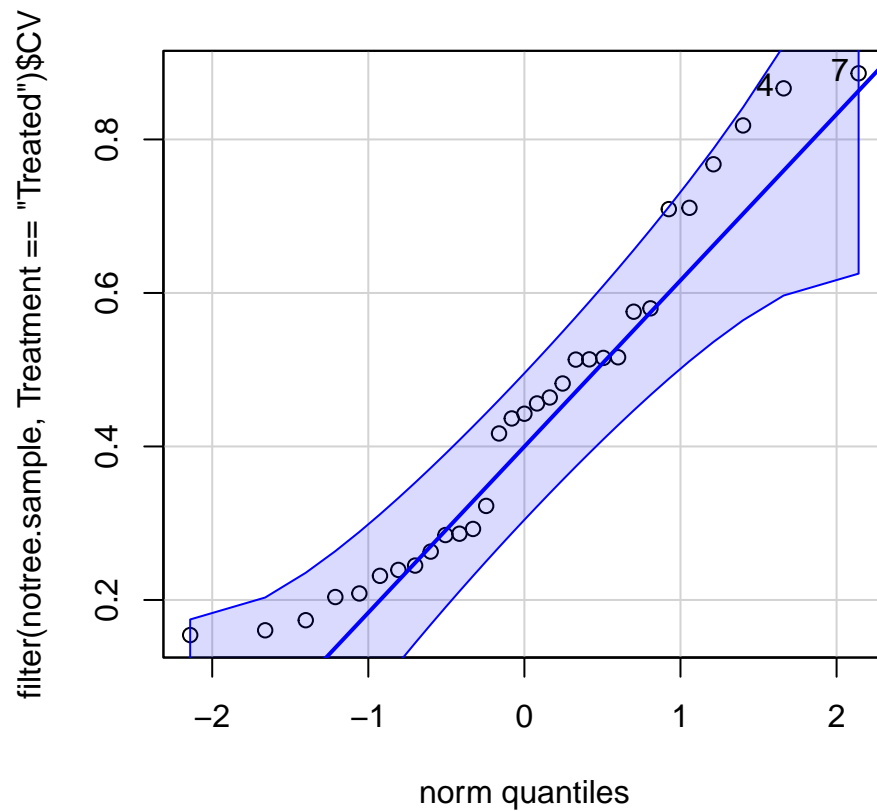

Herbaceous cover
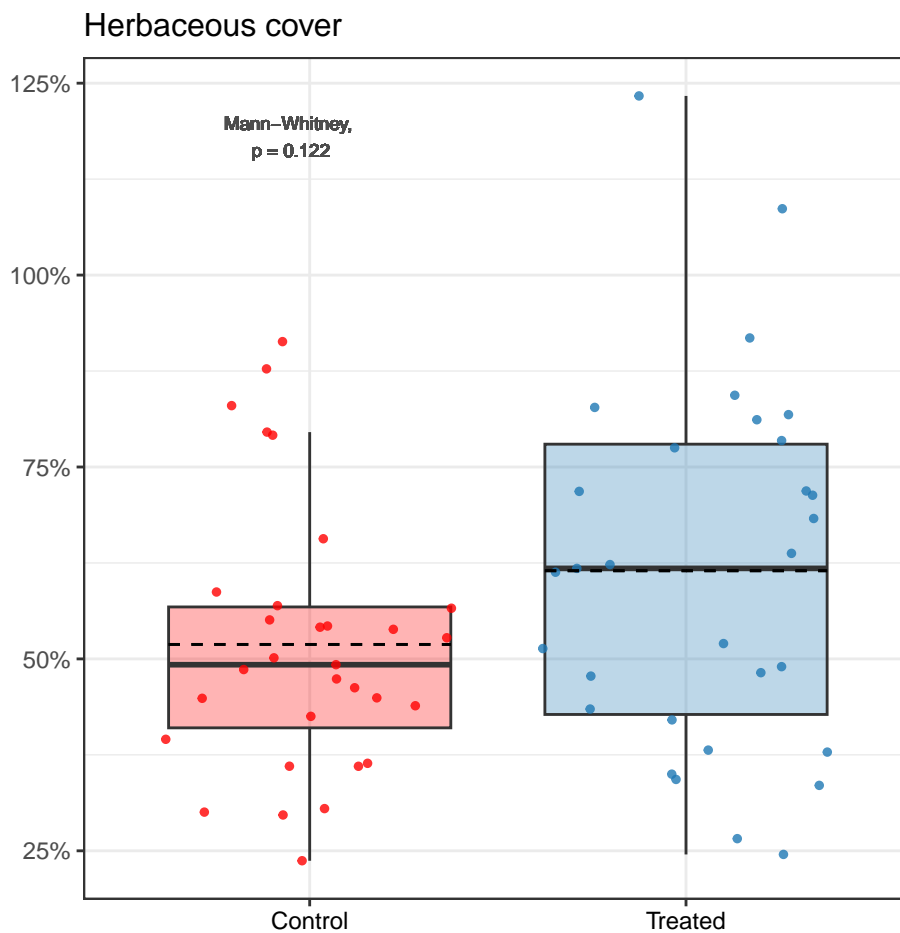
Fig 3c: CV of overall veg cover

```r
# 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")

# Explore distribution
qqPlot(filter(notree.sample, Treatment == "Treated")$CV) # normal
```
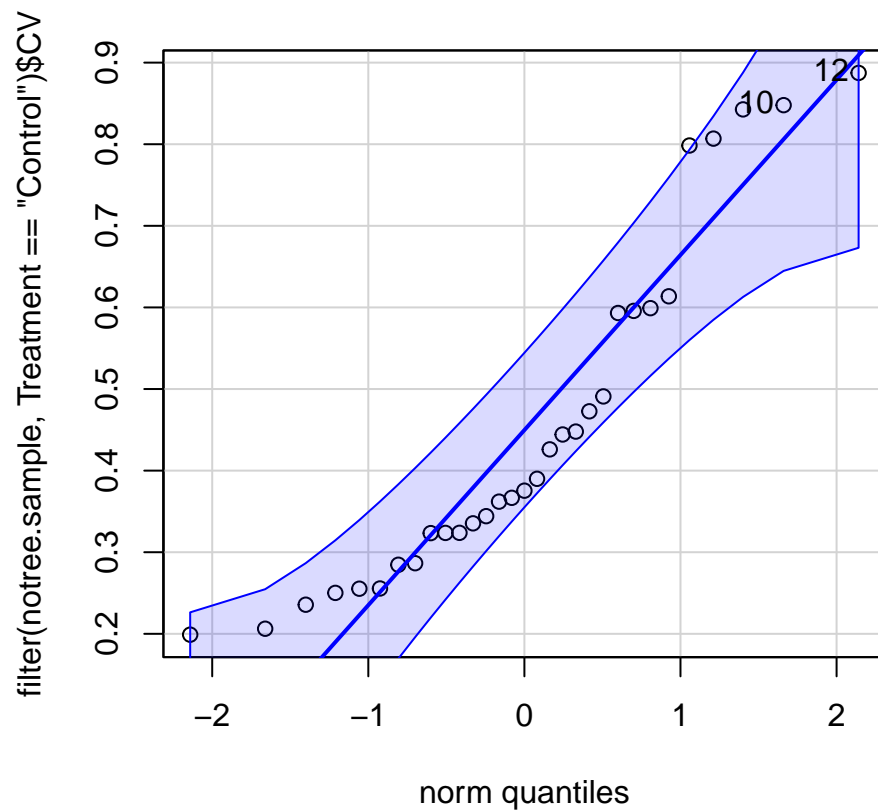


```
## [1] 7 4
```

```r
qqPlot(filter(notree.sample, Treatment == "Control")$CV) # normal
```

```
## [1] 12 10
```

```
# 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
```

```
# 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
```


Vegetation cover
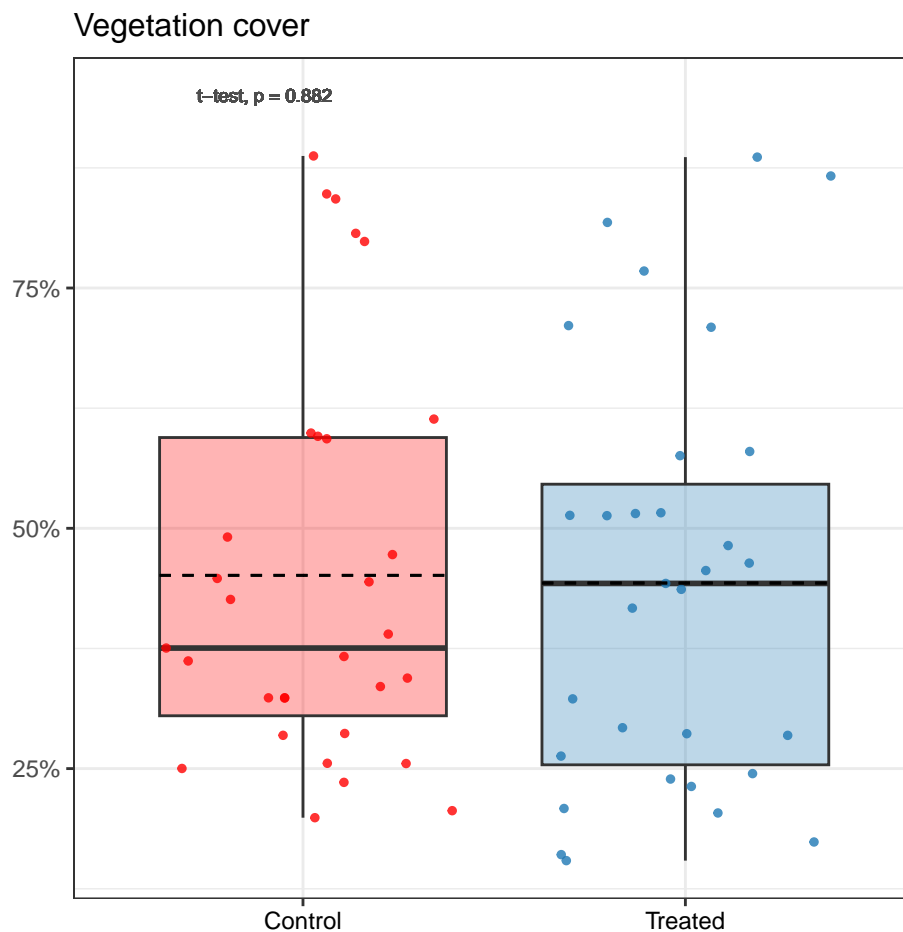
Combine plots for Fig 3

```r
# 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()
```
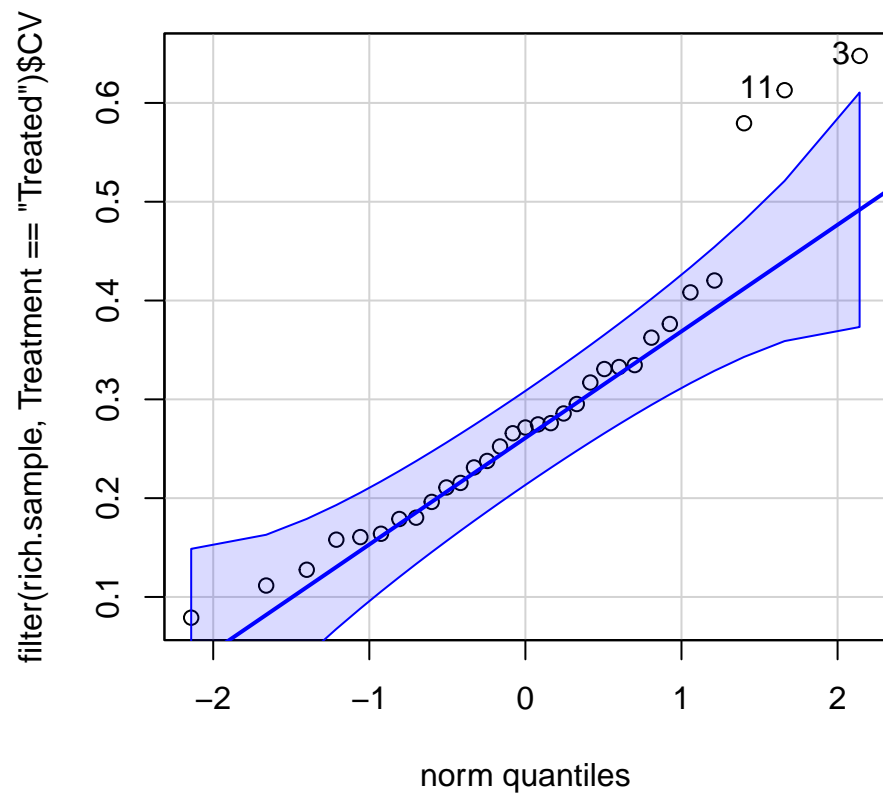
Supp Fig 5a: CV of perennial richness

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

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

# Explore distribution
qqPlot(filter(rich.sample, Treatment == "Treated")$CV) # not quite normal
```
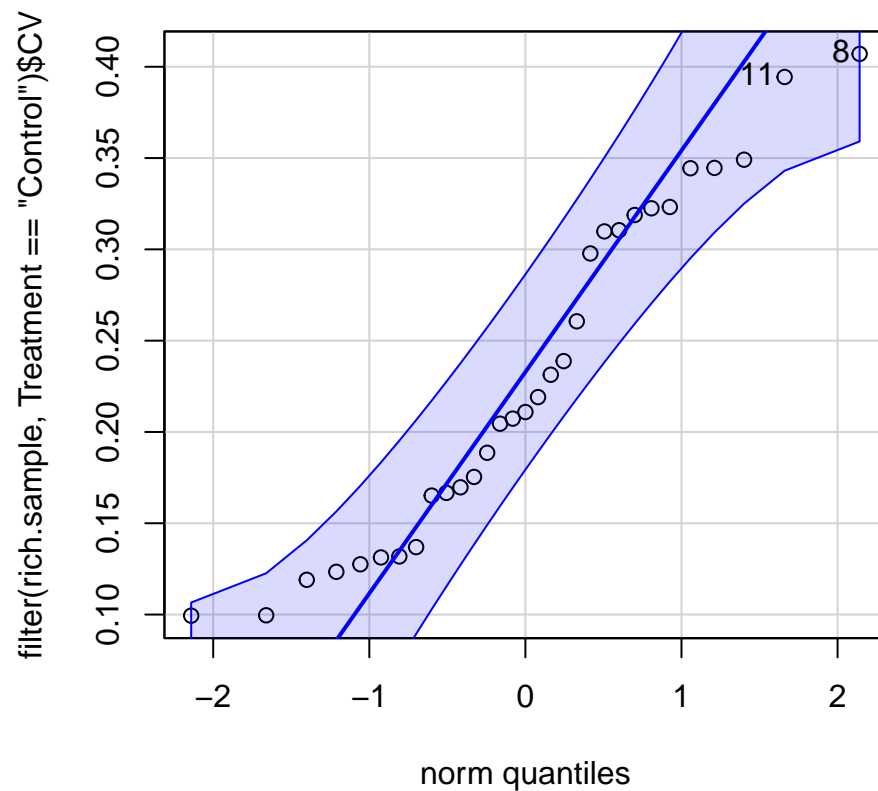
```
## [1]  3 11
```

```
qqPlot(filter(rich.sample, Treatment == "Control")$CV) # normal
```

```
## [1]   8 11
```

```r
# 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
```

```r
# 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
```
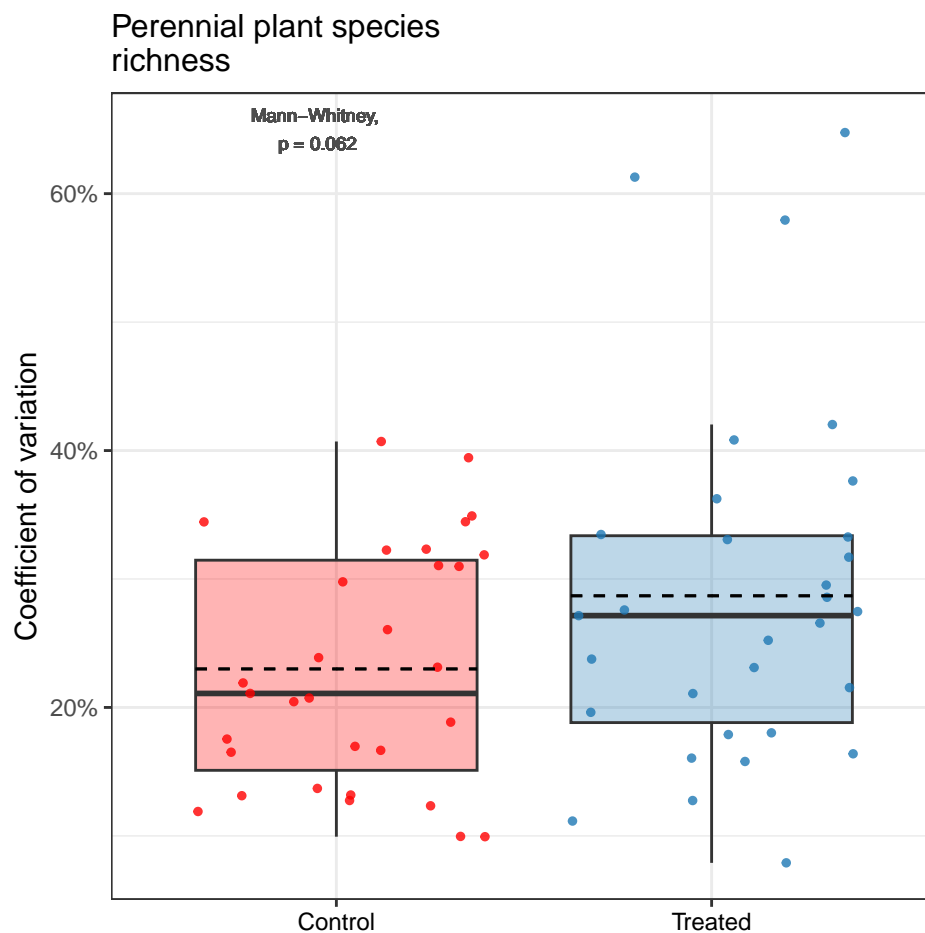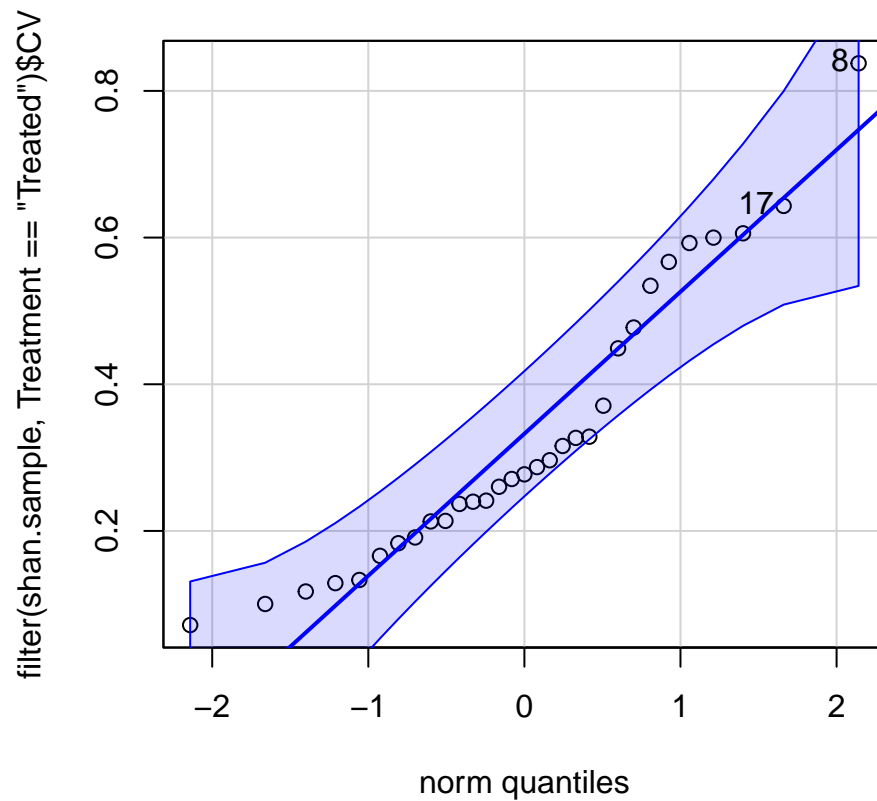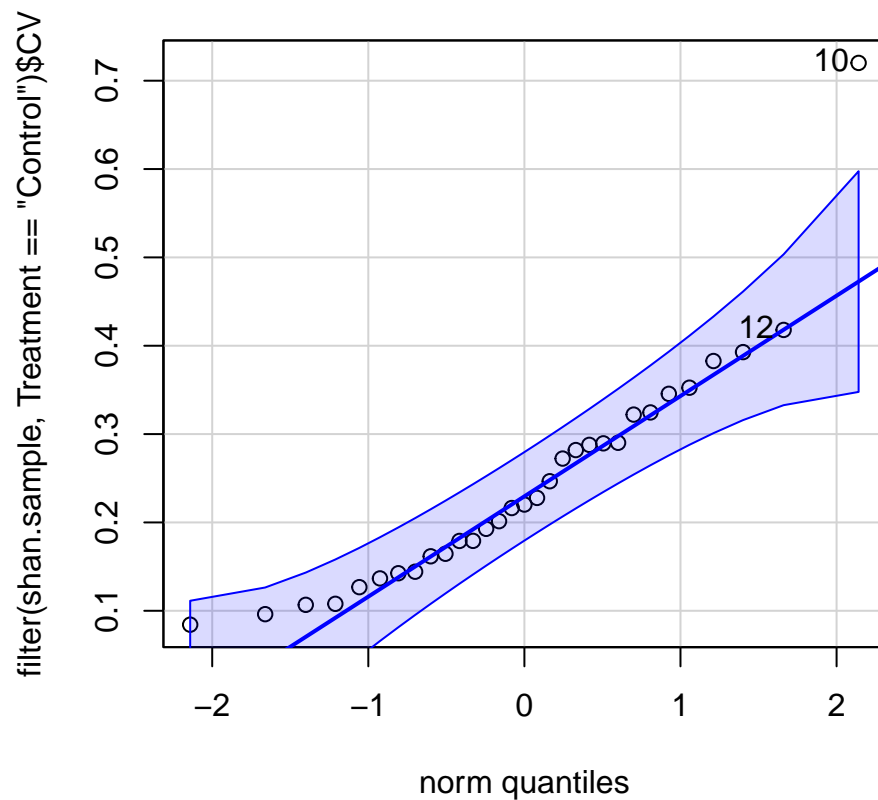
Supp Fig 5b: CV of perennial diversity

```r
# Shannon ---------------------------------------------------------------

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

# Explore distribution
qqPlot(filter(shan.sample, Treatment == "Treated")$CV) # normal
```



```
## [1]  8 17
```

```r
qqPlot(filter(shan.sample, Treatment == "Control")$CV) # almost normal
```

```
## [1] 10 12
```

```
# 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
```


Perennial plant diversity
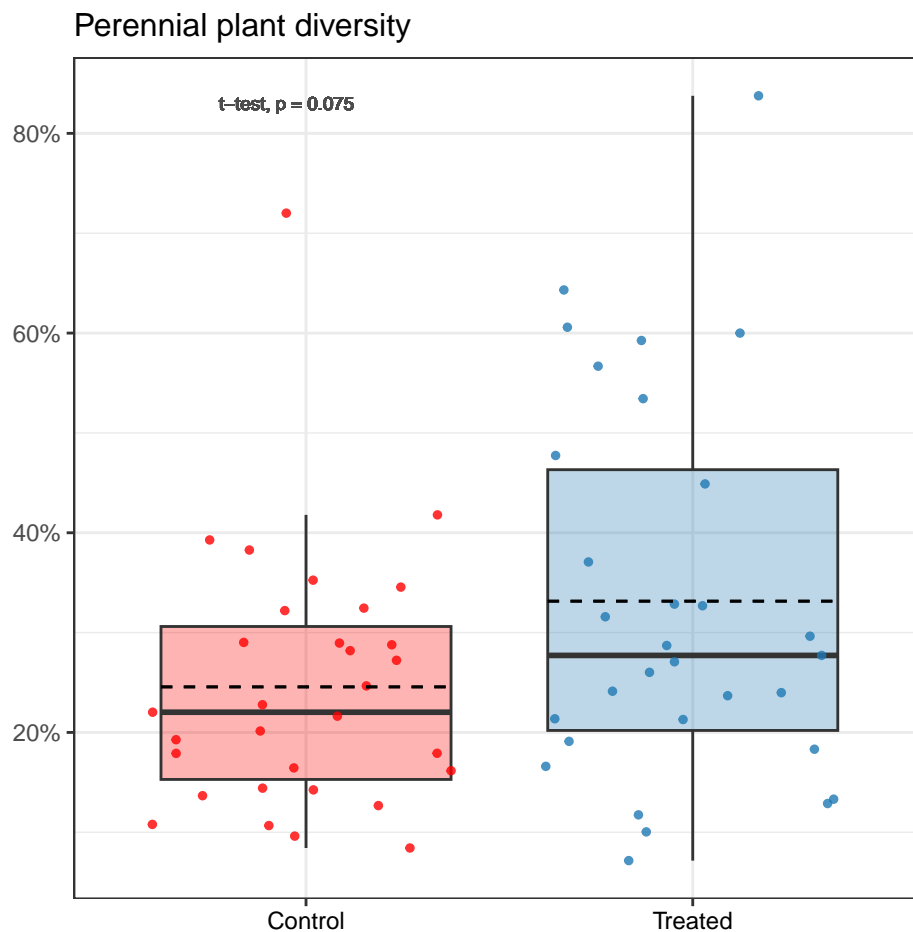
Combine plots for Supp Fig 5

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

# Supplemental figure
tiff("figures/2023-09_publish-figures/CV_rich-shan.tiff", units = "in", height = 4, width = 5.5, res = 
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