

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).

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Last updated: 2023-08-31

```
sessionInfo()
```

```
## R version 4.3.1 (2023-06-16 ucrt)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 11 x64 (build 22621)
##
## Matrix products: default
##
## locale:
## [1] LC_COLLATE=English_United States.utf8
## [2] LC_CTYPE=English_United States.utf8
## [3] LC_MONETARY=English_United States.utf8
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United States.utf8
##
## time zone: America/Phoenix
## tzcode source: internal
##
## attached base packages:
## [1] stats      graphics  grDevices  utils      datasets  methods   base
##
## loaded via a namespace (and not attached):
## [1] compiler_4.3.1    fastmap_1.1.1     cli_3.6.1        tools_4.3.1
## [5] htmltools_0.5.6   rstudioapi_0.15.0 yaml_2.3.7        rmarkdown_2.24
## [9] knitr_1.43        xfun_0.40         digest_0.6.33    rlang_1.1.1
## [13] evaluate_0.21
```

Appendix A: Temporal vegetation trends

Setup

```
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
## v dplyr      1.1.2      v readr      2.1.4
## v forcats    1.0.0      v stringr    1.5.0
```

```
## v ggplot2 3.4.3 v tibble 3.2.1
## v lubridate 1.9.2 v tidyr 1.3.0
## v purrr 1.0.2
## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag() masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

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

```
##
## Attaching package: 'rstatix'
##
## The following object is masked from 'package:stats':
##
## filter
```

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

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

```
# Functions -----
```

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

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

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

  return(x)
}
```

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

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

Fig 2A: Grass, forb & shrub cover

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

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

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

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

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

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

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

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

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

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

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

letters.notree <- data.frame(x = rep(notree.avg$year.xaxis[1:6], 2),
                             y = rep(49, 12),
                             label = c(notree.ctrl.letters$groups,
                                         notree.trt.letters$groups),
                             Treatment = c(rep("Control", 6),
                                             rep("Treated", 6)))

ptext.notree <- data.frame(x = rep(as.Date("2019-09-01"), 2),
                            y = c(22, 22),
                            label = c("ANOVA, p < 0.001", "ANOVA, p = 0.003"),
                            Treatment = c("Control", "Treated"))

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

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

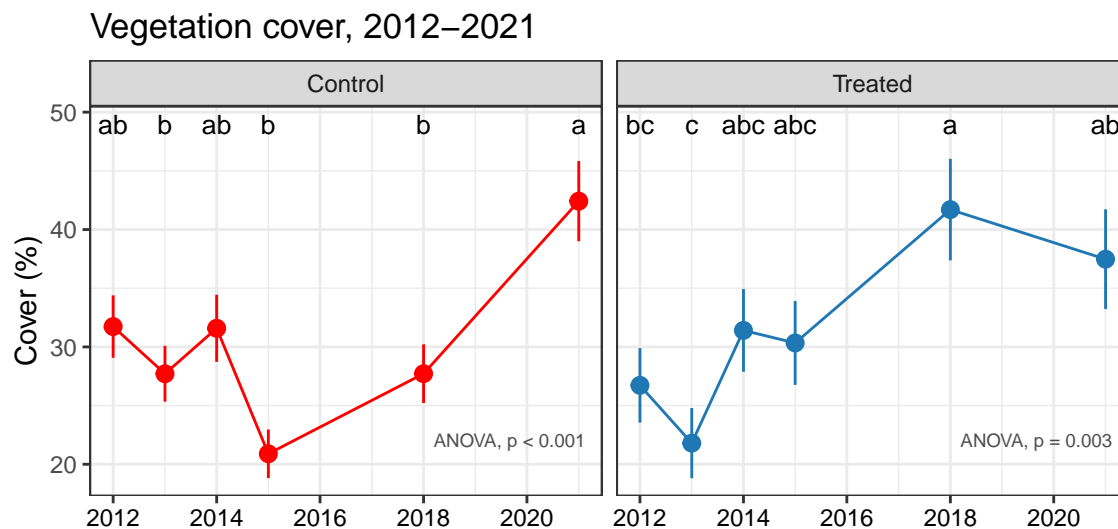


Fig 2B: Herbaceous (grass & forb) cover

```
# Herbaceous cover -----

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

```

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

```

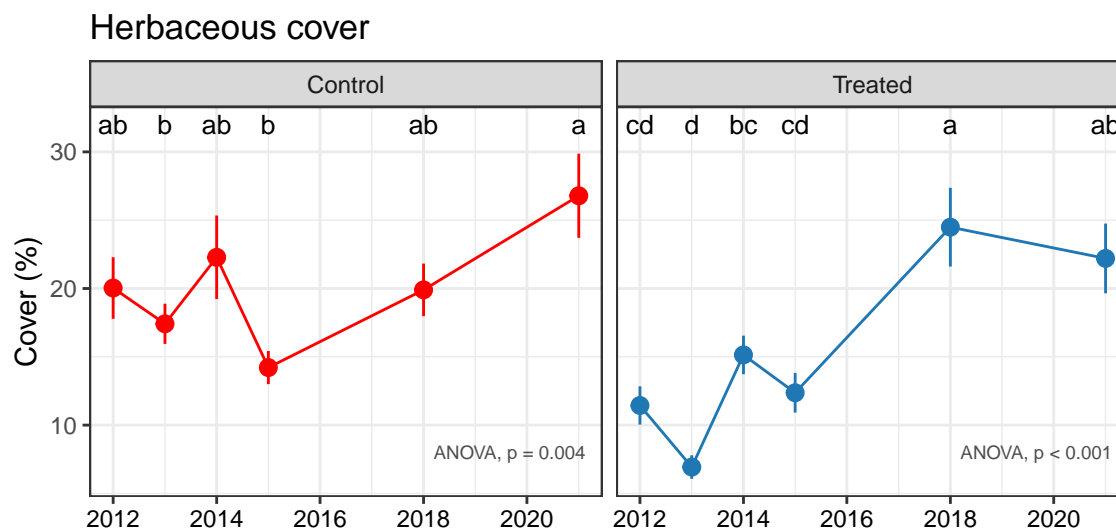


Fig 2C: Shrub cover

```

# Shrub cover -----

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

```

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

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

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

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

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

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

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

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

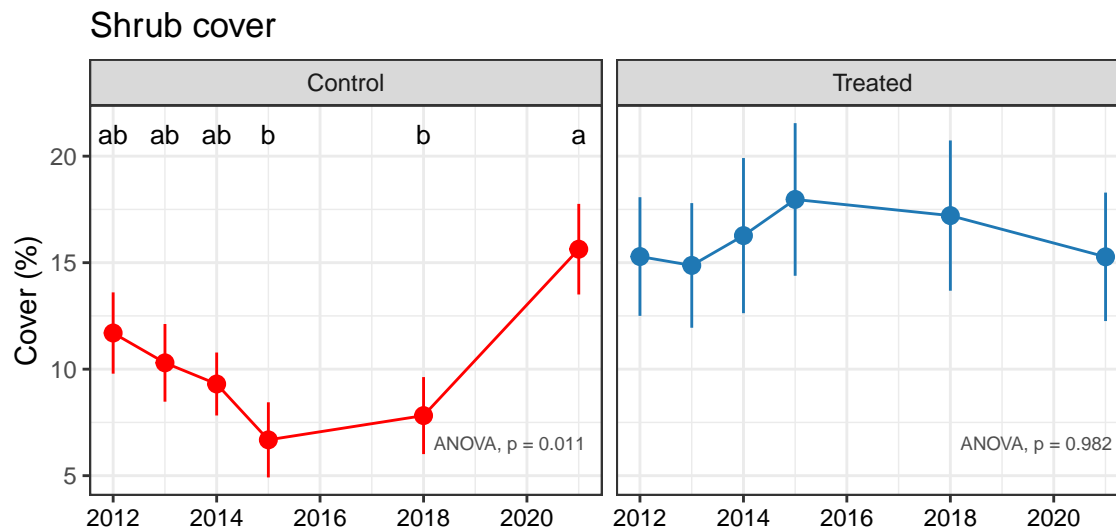
shrub.plot <- ggplot(shrub.avg, aes(x = year.xaxis, y = mean,
  group = Treatment,
  color = Treatment)) +
  geom_line() +
  geom_point() +
  geom_pointrange(aes(ymin = mean - SE, ymax = mean + SE)) +
```



```

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

```



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
```

Supp Fig 4A: Perennial plant species richness

Supp Fig 4B: Perennial plant diversity

Appendix B: Coefficient of variation

Fig 3A: CV of shrub cover

Fig 3B: CV of herbaceous cover

Fig 3C: CV of overall veg cover

Supp Fig 5A: CV of perennial richness

Supp Fig 5B: CV of perennial diversity

Appendix C: Soil fertility