Advanced Ecology: Communities and Ecosystems
PCB5443-U01-1241

Exam 2 - Pulses Time Series

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March 13, 2024

**Part I: Develop a question or questions that motivate the time-series analysis of the data you chose (10 points).

A:

- Does the defaunation of medium and large herbivores affect plant abundance?

**Part II: Use a time-series model to analyze the data (pick one of the three models, or you may chose to use more than one model). Include the data, the R scripts, figures, and model output (10 points).

**A:**

- All the data and code are available *__here__*

**Part III: Interpret the results of your data (in 1-2 paragraphs) using descriptions of the model output (qualitative and quantitative) and characteristics of pulse dynamics described in Jentsch and White (2019) (40 points).

A:

- Explaing the experiment

- Interestingly, closed plots experienced an abundance boom while open plots kept almost constant. Although my predictions was that this exercise would target the peaks, it seems that the results is quite on the opposite, showing the valies insteads. Both treatments had the same peak patterns and within the same year period (with the exception of 2014, present only in closed plots while 2015 was absent). I hypothesize that maybe the data structure is not suitable enough for this method to capture the peaks precisely, as there were only 10 years of data sample comprising 2 measurements per year.

- All the patterns shown here goes in the opposite direction of my prediction that plant abundance would increase in closed plots, as shown by previous studies in the same experiment (XXX and XXX). Moreover, graph A show a clear increase in the abundance right after the beginning of the experiment, with both lines starting almost at the same intercept. Although the first years did not show a large variation, visually, peaks and valleys are present after 2014, more than was captures by the model.

- Further amaryllises should incorporate the valley *quantmod* method as well as the rate of plant mortality and recruitment. Moreover, exploring the time series at the site level might be more suitable as each location has a large variability on plant dynamic.

Open (Peaks per year: 0.4, average peak magnitude: 1290, peak standard deviation: 76.75, peak CV: 0.05) model 1: Slope: 0.14, *P-value* $= 0.15$ - Did time affected the occurance of peaks? No model 2: Slope: -0.64, *P-value* $= 0.35$ - Has the magnitude of peaks increased/decreased over time?? No

Closed (Peaks per year: 0.4, average peak magnitude: 1981.75, peak standard deviation: 95.17, peak CV: 0.04) model 1: Slope: 0.56, *P-value* $= 0.08$ - Did time affected the occurance of peaks? Almost model 2: Slope: -0.10, *P-value: 0.89* - Has the magnitude of peaks increased/decreased over time?? No
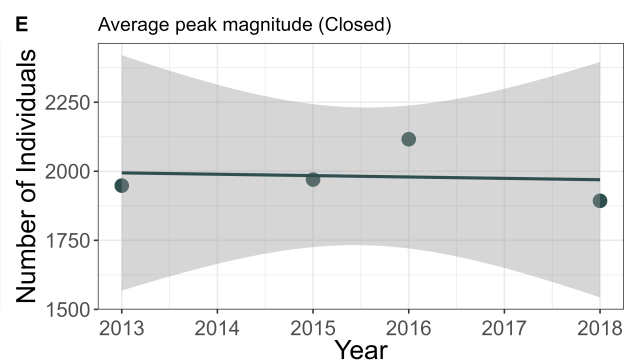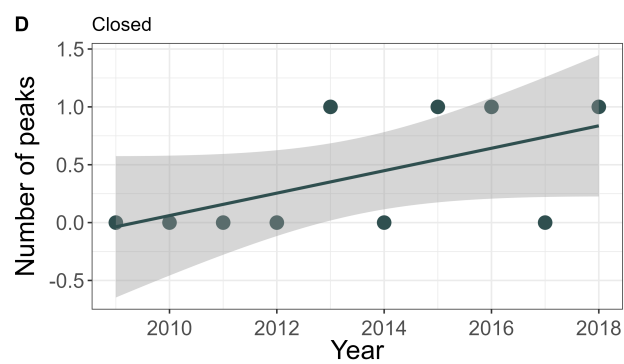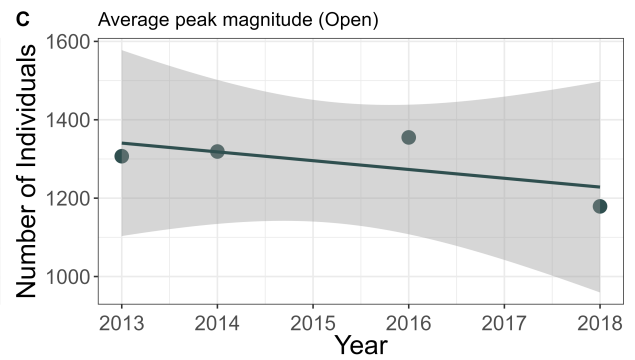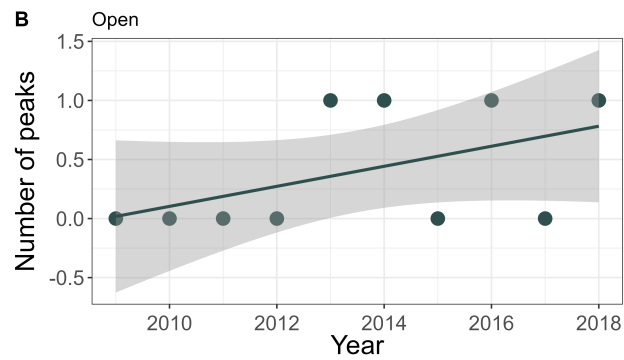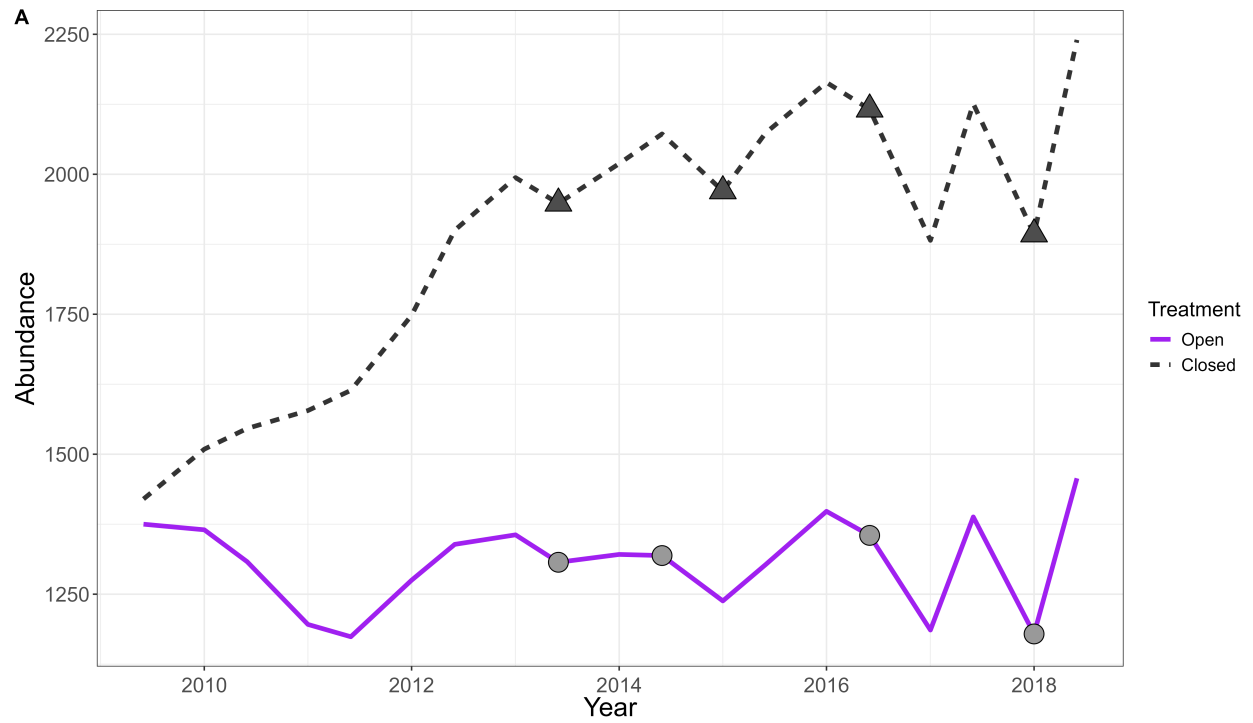
Literature

Bruce, D. G., Cornwell, J. C., Harris, L., Ihde, T. F., Lisa, M., Kellogg, S. K., ... & Vogt, B. (2021). A synopsis of research on the ecosystem services provided by Large-scale oyster restoration in the Chesapeake bay. NOAA Tech. Memo. NMFS-OHC, 8, 52.

Cottingham, K. L., Ewing, H. A., Greer, M. L., Carey, C. C., & Weathers, K. C. (2015). Cyanobacteria as biological drivers of lake nitrogen and phosphorus cycling. Ecosphere, 6(1), 1-19.

Elser, J. J., Bracken, M. E., Cleland, E. E., Gruner, D. S., Harpole, W. S., Hillebrand, H., ... & Smith, J. E. (2007). Global analysis of nitrogen and phosphorus limitation of primary producers in freshwater, marine and terrestrial ecosystems. Ecology letters, 10(12), 1135-1142.

Humphries, A. T., Ayvazian, S. G., Carey, J. C., Hancock, B. T., Grabbert, S., Cobb, D., ... & Fulweiler, R. W. (2016). Directly measured denitrification reveals oyster aquaculture and restored oyster reefs remove nitrogen at comparable high rates. Frontiers in Marine Science, 3, 74.

Keisman, J., Devereux, O. H., LaMotte, A. E., Sekellick, A., & Blomquist, J. (2018, December). Manure and fertilizer inputs to land in the Chesapeake Bay watershed, 1950-2012. In AGU Fall Meeting Abstracts (Vol. 2018, pp. H13K-1892).

Redfield, A. C. (1958). The biological control of chemical factors in the environment. American scientist, 46(3), 230A-221.

Weathers, K. C., Strayer, D. L., & Likens, G. E. (Eds.). (2021). Fundamentals of ecosystem science. Academic Press.

Script

```r
# packages -------------------------------------------------------------

rm(list=ls())

if(!require(tidyverse)) install.packages("tidyverse", dependencies = TRUE)
if(!require(quantmod)) install.packages("quantmod", dependencies = TRUE)
if(!require(xts)) install.packages("xts", dependencies = TRUE)
if(!require(emmeans)) install.packages("emmeans", dependencies = TRUE)
if(!require(ggthemes)) install.packages("ggthemes", dependencies = TRUE)
if(!require(timetk)) remotes::install_github("business-science/timetk")
if(!require(ggpubr)) install.packages("ggpubr", dependencies = TRUE)

# Abundance #  ---------------------------------------------------------


# Data -----------------------------------------------------------------

data_biota <- readr::read_csv("00_data/life_form_2020_for_abudance_recruitment_mortality.csv") |>
  dplyr::select(c(1:3,5:23)) |>
  tidyr::pivot_longer(cols = 4:22, names_to = "Date", values_to = "abnd") |>
  dplyr::mutate(Date = recode(Date,
                              "T0" = "2009-06-01", "T006" = "2010-01-01",
                              "T012" = "2010-06-01", "T018" = "2011-01-01",
                              "T024" = "2011-06-01", "T030" = "2012-01-01",
                              "T036" = "2012-06-01", "T042" = "2013-01-01",
                              "T048" = "2013-06-01", "T054" = "2014-01-01",
                              "T060" = "2014-06-01", "T066" = "2015-01-01",
                              "T072" = "2015-06-01", "T078" = "2016-01-01",
                              "T084" = "2016-06-01", "T090" = "2017-01-01",
                              "T096" = "2017-06-01", "T102" = "2018-01-01",
                              "T108" = "2018-06-01")) |>
  dplyr::group_by(Treatment, Date) |>
  dplyr::summarise(abnd = sum(abnd)) |>
  dplyr::ungroup() |>
  dplyr::mutate(Date = as.POSIXct(paste(Date, "-01", "%Y-%m-%d", tz = "UTC")))


# Open -----------------------------------------------------------------


all_open <- data_biota |>
  dplyr::filter(Treatment == "open")
all_open

all_open_ts <- all_open |>
  timetk::tk_xts()
all_open_ts

str(all_open_ts)
tzone(all_open_ts)
nmonths(all_open_ts)
```

```
nyears(all_open_ts)

chartSeries(all_open_ts,theme="white")

chartSeries(all_open_ts,up.col='blue',dn.col='red',
            subset='2010::2017-06',theme="white")

# didn't change from 1 to 10
all_open_pks.1 <- findPeaks(all_open_ts, thresh=1)
plot(all_open_ts[all_open_pks.1])

all_open_peaks1 <- as.data.frame(all_open_ts[all_open_pks.1]) |>
  rownames_to_column("Dates") |>
  dplyr::mutate(Treatment = "Open")
all_open_peaks1

#how many peaks per year?
peak_per_y_open <- length(all_open_peaks1$abnd)/nyears(all_open_ts)
peak_per_y_open

#average peak magnitude (in number of individuals per year)
all_peak_mean_open <- mean(all_open_peaks1$abnd)
all_peak_mean_open

#peak standard deviation
all_peak_sd_open <- sd(all_open_peaks1$abnd)
all_peak_sd_open

#peak CV
all_peak_CV_open <- all_peak_sd_open/all_peak_mean_open
all_peak_CV_open

all_open_summary <- cbind("Peaks per year:",peak_per_y_open,
                "average peak magnitude:", all_peak_mean_open,
                "peak standard deviation:", all_peak_sd_open,
                "peak CV:", all_peak_CV_open)
all_open_summary


all_open_peaks1$year<-as.numeric(format(as.POSIXct(all_open_peaks1$Dates),"%Y"))
all_open_peaks1

all_year_open <- min(as.numeric(
  format(as.POSIXct(all_open$Date),"%Y"))):max(as.numeric(
    format(as.POSIXct(all_open$Date),"%Y")))
all_year_open
all_years_open <- as.data.frame(all_year_open)
all_years_open

all_peak.sum_open <- all_open_peaks1 |>
  group_by(year) |>
  summarise(mean.peak=mean(abnd), count=n())
all_peak.sum_open
```

```r
all_peak.number_open <- merge(all_years_open, all_peak.sum_open,
                              by.x="all_year_open", by.y="year", all.x=TRUE)
all_peak.number_open
all_peak.number_open[is.na(all_peak.number_open)] <- 0
all_peak.number_open

all_peak.number.lm_open <- lm(scale(count)~scale(all_year_open),
                              data = all_peak.number_open)
all_lmsum.number_open <- summary(all_peak.number.lm_open)
all_lmsum.number_open
all_peak.number.slope_open <- all_peak.number.lm_open$coefficients[2]
all_peak.number.slope_open
all_peak.number.p_open <- all_lmsum.number_open$coefficients[2,4]
all_peak.number.p_open

all_peak.magnitude.lm_open <- lm(scale(abnd)~ scale(year), data = all_open_peaks1)
all_lmsum.mag_open <- summary(all_peak.magnitude.lm_open)
all_lmsum.mag_open
all_peak.magnitude.slope_open <- all_peak.magnitude.lm_open$coefficients[2]
all_peak.magnitude.slope_open
all_peak.magnitude.p_open <- all_lmsum.mag_open$coefficients[2,4]
all_peak.magnitude.p_open



# Closed ------------------------------------------------------------------


all_closed <- data_biota |>
  dplyr::filter(Treatment == "closed")
all_closed

all_closed_ts <- all_closed |>
  timetk::tk_xts()
all_closed_ts

str(all_closed_ts)
tzone(all_closed_ts)
nmonths(all_closed_ts)
nyears(all_closed_ts)

chartSeries(all_closed_ts,theme="white")

chartSeries(all_closed_ts,up.col='blue',dn.col='red',
            subset='2010::2017-06',theme="white")

# didnt change from 1 to 45
all_closed_pks.1 <- findPeaks(all_closed_ts, thresh=1)
plot(all_closed_ts[all_closed_pks.1])

all_closed_peaks1 <- as.data.frame(all_closed_ts[all_closed_pks.1]) |>
  rownames_to_column("Dates") |>
  dplyr::mutate(Treatment = "Closed")
```

```r
all_closed_peaks1

#how many peaks per year?
peak_per_y_closed <- length(all_closed_peaks1$abnd)/nyears(all_closed_ts)
peak_per_y_closed

#average peak magnitude (in number of individuals per year)
all_peak_mean_closed <- mean(all_closed_peaks1$abnd)
all_peak_mean_closed

#peak standard deviation
all_peak_sd_closed <- sd(all_closed_peaks1$abnd)
all_peak_sd_closed

#peak CV
all_peak_CV_closed <- all_peak_sd_closed/all_peak_mean_closed
all_peak_CV_closed

all_closed_summary <- cbind("Peaks per year:",peak_per_y_closed,
                            "average peak magnitude:", all_peak_mean_closed,
                            "peak standard deviation:", all_peak_sd_closed,
                            "peak CV:", all_peak_CV_closed)
all_closed_summary


all_closed_peaks1$year<-as.numeric(format(as.POSIXct(all_closed_peaks1$Dates),"%Y"))
all_closed_peaks1

all_year_closed <- min(as.numeric(
  format(as.POSIXct(all_closed$Date),"%Y"))):max(as.numeric(
    format(as.POSIXct(all_closed$Date),"%Y")))
all_year_closed
all_years_closed <- as.data.frame(all_year_closed)
all_years_closed

all_peak.sum_closed <- all_closed_peaks1 |>
  group_by(year) |>
  summarise(mean.peak=mean(abnd), count=n())
all_peak.sum_closed
all_peak.number_closed <- merge(all_years_closed, all_peak.sum_closed,
                                by.x="all_year_closed",
                                by.y="year",
                                all.x=TRUE)
all_peak.number_closed
all_peak.number_closed[is.na(all_peak.number_closed)] <- 0
all_peak.number_closed

all_peak.number.lm_closed <- lm(scale(count)~scale(all_year_closed),
                                data = all_peak.number_closed)
all_lmsum.number_closed <- summary(all_peak.number.lm_closed)
all_lmsum.number_closed
all_peak.number.slope_closed <- all_peak.number.lm_closed$coefficients[2]
all_peak.number.slope_closed
```

```r
all_peak.number.p_closed <- all_lmsum.number_closed$coefficients[2,4]
all_peak.number.p_closed

all_peak.magnitude.lm_closed <- lm(scale(abnd)~ scale(year),
                                    data = all_closed_peaks1)
all_lmsum.mag_closed <- summary(all_peak.magnitude.lm_closed)
all_lmsum.mag_closed
all_peak.magnitude.slope_closed <- all_peak.magnitude.lm_closed$coefficients[2]
all_peak.magnitude.slope_closed
all_peak.magnitude.p_closed <- all_lmsum.mag_closed$coefficients[2,4]
all_peak.magnitude.p_closed




# Graph ------------------------------------------------------------

dev.off()

all_biota <- data_biota |>
  dplyr::mutate(Treatment = stringr::str_to_title(Treatment),
                Treatment = fct_relevel(Treatment, c("Open", "Closed")))
all_biota

all_biota_graph <- ggplot(all_biota, aes(x = Date,
                          y = abnd,
                          linetype = Treatment,
                          color = Treatment,
                          fill = Treatment)) +
  geom_line(size = 1.5) +
  scale_color_manual(values=c("purple", "grey20")) +
  geom_point(data = all_open_peaks1, aes(x = as.POSIXct(Dates), y = abnd),
             colour='black', fill = "grey60", size=6, shape = 21) +
  geom_point(data = all_closed_peaks1, aes(x = as.POSIXct(Dates), y = abnd),
             colour='black', fill = "grey30", size=6, shape = 24) +
  labs(x = "Year", y = "Abundance") +
  theme_bw() +
  theme(axis.text.x= element_text(angle= 0, size = 14, vjust = 0.2),
        axis.text.y= element_text(size = 14),
        axis.title.x = element_text(size = 18),
        axis.title.y = element_text(size = 18),
        legend.title = element_text(size = 14),
        legend.text = element_text(size = 12),
        strip.text = element_text(size = 12))
all_biota_graph




# Open
all_peak.number.graph_open <- ggplot(all_peak.number_open,
                                     aes(x = all_year_open,
                                         y = count)) +
  geom_point(color='darkslategrey',size=4) +
  geom_smooth(method = "lm",  se = TRUE, color="darkslategrey") +
```

```r
  labs(x = "Year", y = "Number of peaks", title = "Open") +
  theme_bw() +
  theme(axis.text.x= element_text(angle= 0, size = 14, vjust = 0.2),
        axis.text.y= element_text(size = 14),
        axis.title.x = element_text(size = 18),
        axis.title.y = element_text(size = 18),
        legend.title = element_text(size = 14),
        legend.text = element_text(size = 12),
        strip.text = element_text(size = 12))
all_peak.number.graph_open


all_peak.mag.graph_open <- ggplot(data = all_open_peaks1,
                                  aes(x = year,
                                      y = abnd)) +
  geom_point(color = 'darkslategrey', size=4) +
  geom_smooth(method = "lm",  se = TRUE, color="darkslategrey")+
  labs(x = "Year", y = "Number of Individuals", title = "Average peak magnitude (Open)") +
  theme_bw() +
  theme(axis.text.x= element_text(angle= 0, size = 14, vjust = 0.2),
        axis.text.y= element_text(size = 14),
        axis.title.x = element_text(size = 18),
        axis.title.y = element_text(size = 18),
        legend.title = element_text(size = 18),
        legend.text = element_text(size = 16),
        strip.text = element_text(size = 12))
all_peak.mag.graph_open



# Closed

all_peak.number.graph_closed <- ggplot(all_peak.number_closed,
                                       aes(x = all_year_closed,
                                           y = count)) +
  geom_point(color='darkslategrey',size=4) +
  geom_smooth(method = "lm",  se = TRUE, color="darkslategrey") +
  labs(x = "Year", y = "Number of peaks", title = "Closed") +
  theme_bw() +
  theme(axis.text.x= element_text(angle= 0, size = 14, vjust = 0.2),
        axis.text.y= element_text(size = 14),
        axis.title.x = element_text(size = 18),
        axis.title.y = element_text(size = 18),
        legend.title = element_text(size = 14),
        legend.text = element_text(size = 12),
        strip.text = element_text(size = 12))
all_peak.number.graph_closed


all_peak.mag.graph_closed <- ggplot(data = all_closed_peaks1,
                                    aes(x = year,
                                        y = abnd)) +
  geom_point(color = 'darkslategrey', size=4) +
```

```r
  geom_smooth(method = "lm",  se = TRUE, color="darkslategrey")+
  labs(x = "Year", y = "Number of Individuals", title = "Average peak magnitude (Closed)") +
  theme_bw() +
  theme(axis.text.x= element_text(angle= 0, size = 14, vjust = 0.2),
        axis.text.y= element_text(size = 14),
        axis.title.x = element_text(size = 18),
        axis.title.y = element_text(size = 18),
        legend.title = element_text(size = 14),
        legend.text = element_text(size = 12),
        strip.text = element_text(size = 12))
all_peak.mag.graph_closed

all_graphs <- ggpubr::ggarrange(all_biota_graph,
                                ggarrange(
                                all_peak.number.graph_open,
                                all_peak.mag.graph_open,
                                all_peak.number.graph_closed,
                                all_peak.mag.graph_closed,
                                ncol = 2,
                                labels = c("B", "C", "D", "E")),
                                nrow = 3,
                                labels = "A")
all_graphs


all_biota_peaks <- ggarrange(all_peak.number.graph_open,
                        all_peak.mag.graph_open,
                        all_peak.number.graph_closed,
                        all_peak.mag.graph_closed,
                        ncol=2,
                        nrow=2,
                        labels = c("B", "C","D","E"))

ggarrange(all_biota_graph, all_biota_peaks, ncol=1, nrow=2, labels = "A")

#ggsave("02_figures/20240313_YSS_biota_abnd.png", h = 35, w = 30, units = "cm", dpi = 500)
```