Code to accompany the following manuscript:

Barlow, DR, Bierlich, KC, Oestriech, WK, Chiang, G, Durban, JW, Goldbogen, JA, Johnston, DW, Leslie, MS, Moore, M, Ryan, JP, Torres, LG (2023). Shaped by their environment: variation in blue whale morphology across three productive coastal ecosystems. Integrative Organismal Biology

Analysis led by Dawn Barlow, KC Bierlich, and Will Oestreich

10 October 2023

```r
library(dplyr)
library(ggplot2)
library(tidyverse)
library(zoo)
library(lubridate)
library(ggplot2)
library(gridExtra)
library(ggpubr)
library(maps)
library(mapproj)
library(maptools)
library(ggstar)
library(outliers)
```

Upwelling seasonality comparison

```r
# upwelling data
cuti_daily <- read.csv("CUTI_daily.csv",header = TRUE)
STB_upwelling <- read.csv("STB_upwelling_2009-2019.csv")
GC_wind <- read.csv("GC_ASCATwind_2009-2019.csv")

# productivity data
Chla.df <- read.csv("VIIRS_Chla.csv")


#### California ####
###################
cuti_daily$date <- as.Date(with(cuti_daily, paste(year, month, day,sep="-")),
"%Y-%m-%d")
cuti_daily$yday <- yday(cuti_daily$date)
```

```r
## LOOP TO CALCULATE CUMULATIVE UPWELLING FOR ALL YEARS

Years <- unique(cuti_daily$year)
Years <- Years[23:32]

# apply rolling mean to whole CUTI dataset, by year - for plotting
CA_upwelling_ByYear.list <- list()

for (i in 1:length(Years)) {

  Year.i <- Years[[i]]

  ## calculate running mean of cumulative upwelling indext for the given year
  cuti_i <- filter(cuti_daily, year==Year.i)
  cuti_i <- dplyr::select(cuti_i,c("year","date","yday", "X37N"))
  cuti_i$csum <- cumsum(cuti_i$X37N) # cumulative sum

  CA_upwelling_ByYear.list[[i]] <- cuti_i

}

cuti_daily_2 <- do.call("rbind", CA_upwelling_ByYear.list)

# Quick plot
ggplot() +
  geom_line(data = cuti_daily_2, aes(x = yday, y = csum, color =
as.factor(year)))
```
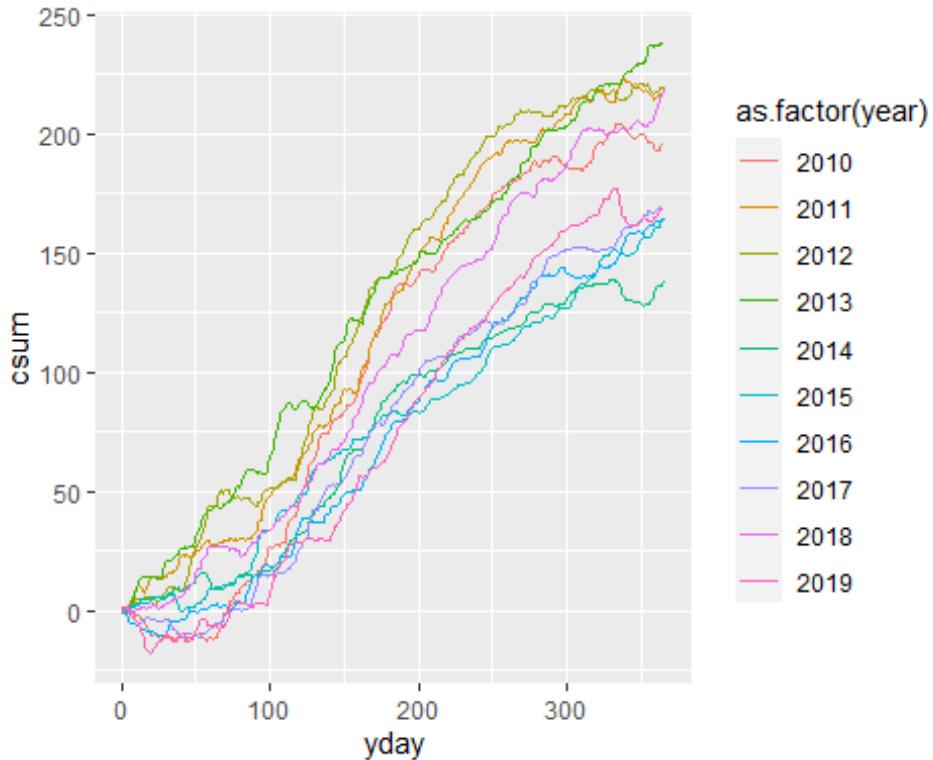
```
#### New Zealand ####
#####################
STB_upwelling$Date <- as.Date(STB_upwelling$Date)

## LOOP TO CALCULATE CUMULATIVE UPWELLING FOR ALL YEARS

Years <- unique(STB_upwelling$Year_SoHem_2)
Years <- Years[2:11] # get rid of partial (split) years at beginning and end
of time series

# apply rolling mean to whole upwelling dataset, by year (SoHem) - for
plotting
STB_upwelling_ByYear.list <- list()

for (i in 1:length(Years)) {

  Year_SoHem.i <- Years[[i]]

  ## calculate running mean of cumulative upwelling indext for the given year
  STBindex_i <- filter(STB_upwelling, Year_SoHem_2==Year_SoHem.i)
  STBindex_i$csum <- cumsum(STBindex_i$UpwellingIndex.MUR) # cumulative sum

  STB_upwelling_ByYear.list[[i]] <- STBindex_i

}
```
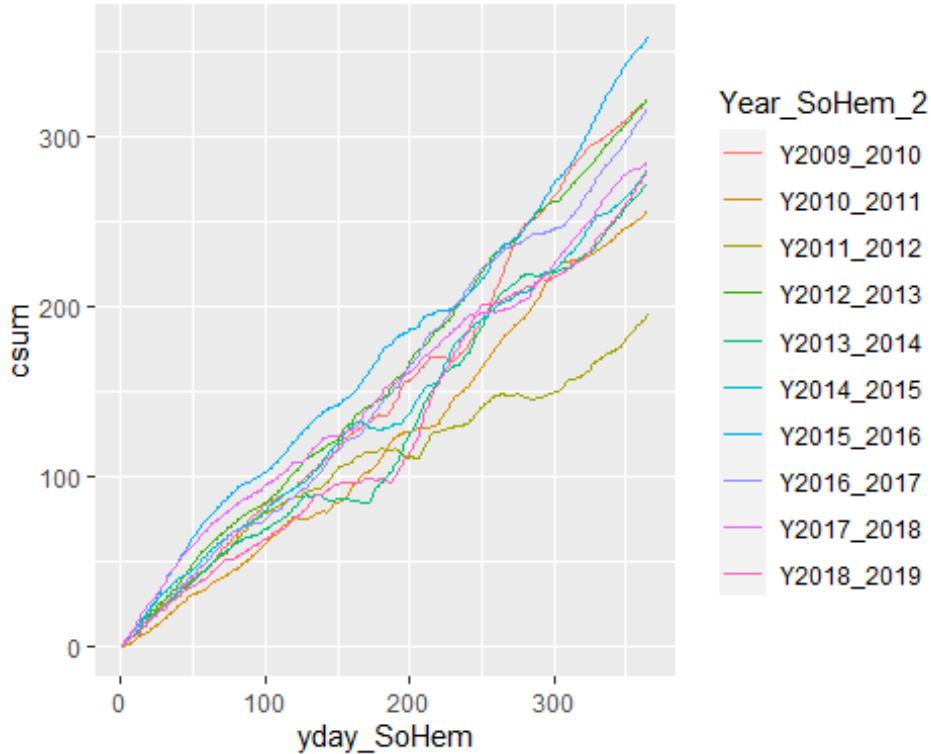
```r
STB_upwelling_2 <- do.call("rbind", STB_upwelling_ByYear.list)

# Quick plot
ggplot() +
  geom_line(data = STB_upwelling_2, aes(x = yday_SoHem, y = csum, color =
Year_SoHem_2))
```



```r
#### Chile ####
###############
GC_wind$Date <- as.Date(GC_wind$Date)

# fill NAs
GC_wind$Windstress <- na.locf(GC_wind$Windstress)
GC_wind$windstress_zonal <- na.locf(GC_wind$windstress_zonal)
GC_wind$windstress_meridional <- na.locf(GC_wind$windstress_meridional)

## LOOP TO CALCULATE CUMULATIVE WIND STRESS FOR ALL YEARS

Years <- unique(GC_wind$Year_SoHem_2)
Years <- Years[2:10] # get rid of partial (split) years at beginning and end
of time series

# apply rolling mean to whole wind dataset, by year (SoHem) - for plotting
GC_zonal_ByYear.list <- list()
```

```r
for (i in 1:length(Years)) {

  Year_SoHem.i <- Years[[i]]

  ## calculate running mean of cumulative upwelling indext for the given year
  CGzonal_i <- filter(GC_wind, Year_SoHem_2==Year_SoHem.i)
  CGzonal_i$csum <- cumsum(CGzonal_i$windstress_zonal) # cumulative sum

  GC_zonal_ByYear.list[[i]] <- CGzonal_i

}

GC_zonal_2 <- do.call("rbind", GC_zonal_ByYear.list)

# Quick plot
ggplot() +
  geom_line(data = GC_zonal_2, aes(x = yday_SoHem, y = csum, color =
Year_SoHem_2))
```
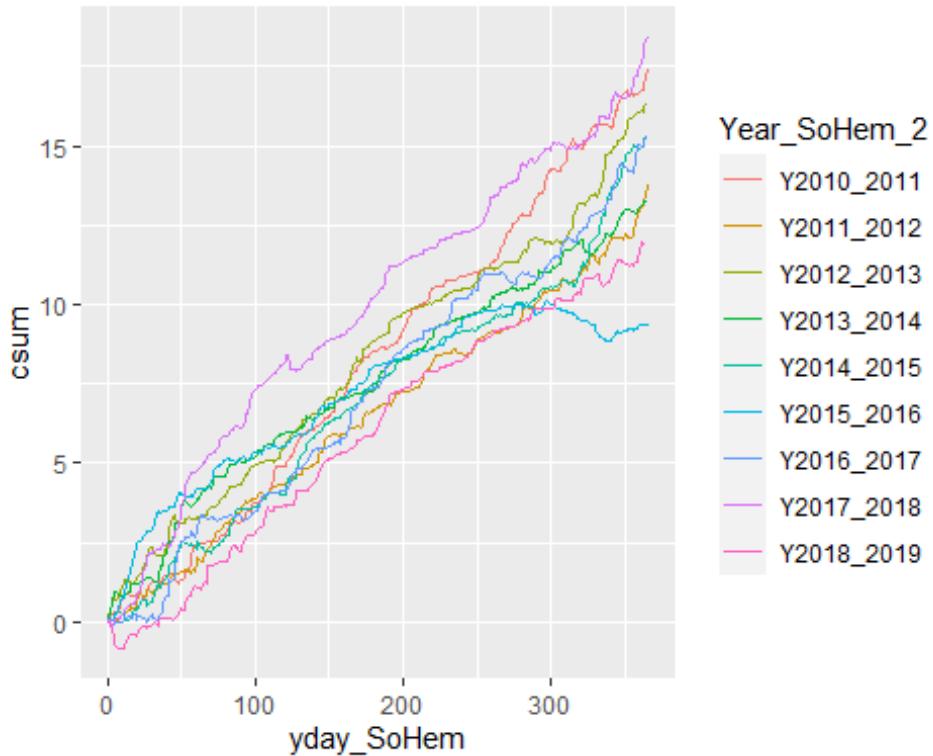


```r
#### Climatology analyses ####
##############################

## California

# calculate climatological mean cumulative upwelling curve
ca_clim <- data.frame(matrix(ncol = 2, nrow = 366))
```

```r
colnames(ca_clim) <- c("yday","csumclim")
for (i in 1:366) {
  c <- cuti_daily_2 %>% filter(yday == i)
  ca_clim$yday[i] <- i
  ca_clim$csumclim[i] <- mean(c$csum,na.rm = TRUE)
}

# calculate 50%, 25-75%, and 10-90% yeardays on the climatological upwelling
curve
ca_total <- max(ca_clim$csumclim,na.rm = TRUE)
ca_pct10 <- which.min(abs(ca_clim$csumclim-(0.1*ca_total)))
ca_pct25 <- which.min(abs(ca_clim$csumclim-(0.25*ca_total)))
ca_pct50 <- which.min(abs(ca_clim$csumclim-(0.5*ca_total)))
ca_pct75 <- which.min(abs(ca_clim$csumclim-(0.75*ca_total)))
ca_pct90 <- which.min(abs(ca_clim$csumclim-(0.9*ca_total)))

# pull dates for 50% accumulation window
ca_pct25
```

```
## [1] 120
```

```r
cuti_daily_2$date[cuti_daily_2$yday==ca_pct25]
```

```
##  [1] "2010-04-30" "2011-04-30" "2012-04-29" "2013-04-30" "2014-04-30"
##  [6] "2015-04-30" "2016-04-29" "2017-04-30" "2018-04-30" "2019-04-30"
```

```r
ca_pct75
```

```
## [1] 245
```

```r
cuti_daily_2$date[cuti_daily_2$yday==ca_pct75]
```

```
##  [1] "2010-09-02" "2011-09-02" "2012-09-01" "2013-09-02" "2014-09-02"
##  [6] "2015-09-02" "2016-09-01" "2017-09-02" "2018-09-02" "2019-09-02"
```

```r
ca_pct75 - ca_pct25
```

```
## [1] 125
```

```r
# yday 119-239; 29 April - 27 August; 120 days
```

New Zealand

```r
# calculate climatological mean cumulative upwelling curve
nz_clim <- data.frame(matrix(ncol = 2, nrow = 366))
colnames(nz_clim) <- c("yday_SoHem","csumclim")
for (i in 1:366) {
  c <- STB_upwelling_2 %>% filter(yday_SoHem == i)
  nz_clim$yday_SoHem[i] <- i
  nz_clim$csumclim[i] <- mean(c$csum,na.rm = TRUE)
}
```

```r
# calculate 50%, 25-75%, and 10-90% yeardays on the climatological upwelling
curve
nz_total <- max(nz_clim$csumclim,na.rm = TRUE)
nz_pct10 <- which.min(abs(nz_clim$csumclim-(0.1*nz_total)))
nz_pct25 <- which.min(abs(nz_clim$csumclim-(0.25*nz_total)))
nz_pct50 <- which.min(abs(nz_clim$csumclim-(0.5*nz_total)))
nz_pct75 <- which.min(abs(nz_clim$csumclim-(0.75*nz_total)))
nz_pct90 <- which.min(abs(nz_clim$csumclim-(0.9*nz_total)))

# pull dates for 50% accumulation window
nz_pct25
```

```
## [1] 88
```

```r
STB_upwelling_2$Date[STB_upwelling_2$yday_SoHem==nz_pct25]
```

```
##  [1] "2009-09-26" "2010-09-26" "2011-09-26" "2012-09-26" "2013-09-26"
##  [6] "2014-09-26" "2015-09-26" "2016-09-26" "2017-09-26" "2018-09-26"
```

```r
nz_pct75
```

```
## [1] 280
```

```r
STB_upwelling_2$Date[STB_upwelling_2$yday_SoHem==nz_pct75]
```

```
##  [1] "2010-04-06" "2011-04-06" "2012-04-05" "2013-04-06" "2014-04-06"
##  [6] "2015-04-06" "2016-04-05" "2017-04-06" "2018-04-06" "2019-04-06"
```

```r
nz_pct75 - nz_pct25
```

```
## [1] 192
```

```r
# yday_Sohem 85-275; 23 September - 1 April; 190 days

## Chile

# calculate climatological mean cumulative wind stress curve
gc_clim_zonal <- data.frame(matrix(ncol = 2, nrow = 366))
colnames(gc_clim_zonal) <- c("yday_SoHem","csumclim")
for (i in 1:366) {
  c <- GC_zonal_2 %>% filter(yday_SoHem == i)
  gc_clim_zonal$yday_SoHem[i] <- i
  gc_clim_zonal$csumclim[i] <- mean(c$csum,na.rm = TRUE)
}


# calculate 50%, 25-75%, and 10-90% yeardays on the climatological upwelling
curve
gc_zonal_total <- max(gc_clim_zonal$csumclim,na.rm = TRUE)
gc_zonal_pct10 <- which.min(abs(gc_clim_zonal$csumclim-(0.1*gc_zonal_total)))
gc_zonal_pct25 <- which.min(abs(gc_clim_zonal$csumclim-
(0.25*gc_zonal_total)))
```

```r
gc_zonal_pct50 <- which.min(abs(gc_clim_zonal$csumclim-(0.5*gc_zonal_total)))
gc_zonal_pct75 <- which.min(abs(gc_clim_zonal$csumclim-
(0.75*gc_zonal_total)))
gc_zonal_pct90 <- which.min(abs(gc_clim_zonal$csumclim-(0.9*gc_zonal_total)))

# pull dates for 50% accumulation window
gc_zonal_pct25
```

```
## [1] 81
```

```r
GC_zonal_2$Date[GC_zonal_2$yday_SoHem==gc_zonal_pct25]
```

```
## [1] "2010-09-19" "2011-09-19" "2012-09-19" "2013-09-19" "2014-09-19"
## [6] "2015-09-19" "2016-09-19" "2017-09-19" "2018-09-19"
```

```r
gc_zonal_pct75
```

```
## [1] 286
```

```r
GC_zonal_2$Date[GC_zonal_2$yday_SoHem==gc_zonal_pct75]
```

```
## [1] "2011-04-12" "2012-04-11" "2013-04-12" "2014-04-12" "2015-04-12"
## [6] "2016-04-11" "2017-04-12" "2018-04-12" "2019-04-12"
```

```r
gc_zonal_pct75 - gc_zonal_pct25
```

```
## [1] 205
```

```r
# yday_Sohem 75-266; 13 September - 23 March; 191 days

#### Climatology plots w/ percent accumulation for seasonality ####
################################################################

## only include yday 1-365 (366 is less common and therefore not robust in
the climatological curve)
ca_clim <- ca_clim[1:365,]
nz_clim <- nz_clim[1:365,]
gc_clim_zonal <- gc_clim_zonal[1:365,]

## California
annual_CUTI_CA.plot <- ggplot() +
  annotate("rect", fill = "gray", alpha = 0.4,
           xmin = ca_pct10, xmax = ca_pct90,
           ymin = -Inf, ymax = Inf) +
  annotate("rect", fill = "gray", alpha = 0.7,
           xmin = ca_pct25, xmax = ca_pct75,
           ymin = -Inf, ymax = Inf) +
  geom_line(data = cuti_daily_2, aes(x = yday, y = csum, group = year),
linetype = "dotted") +
  geom_line(data = ca_clim, aes(x = yday, y = csumclim), size = 2) +
  theme_classic() +
  theme(legend.position = "none") +
```
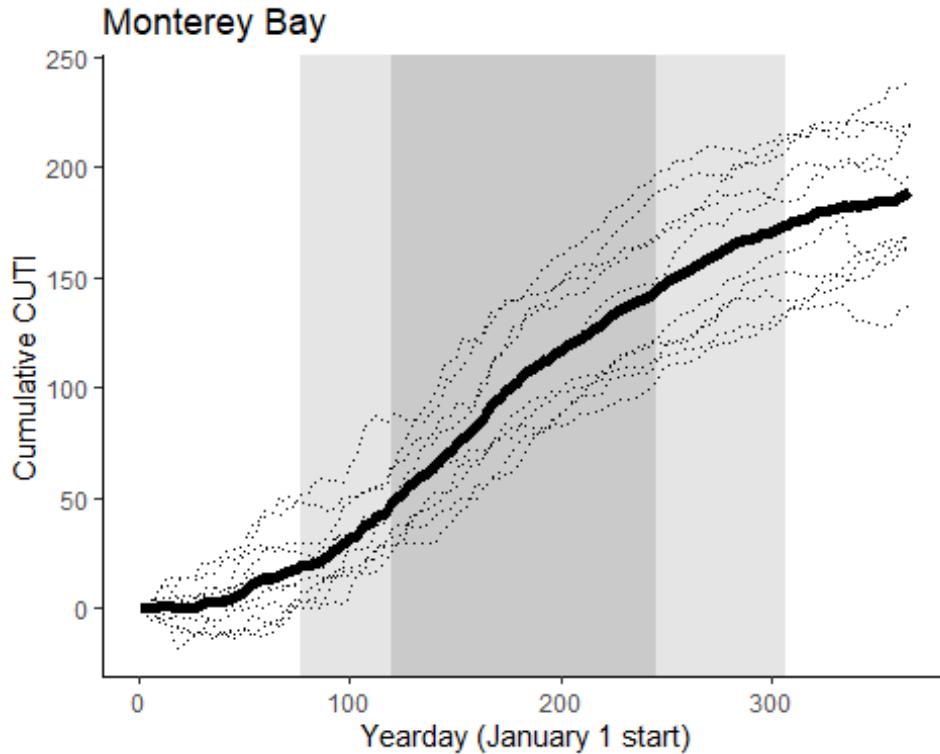
```r
  xlab("Yearday (January 1 start)") +
  ylab("Cumulative CUTI") +
  ggtitle("Monterey Bay")

annual_CUTI_CA.plot
```
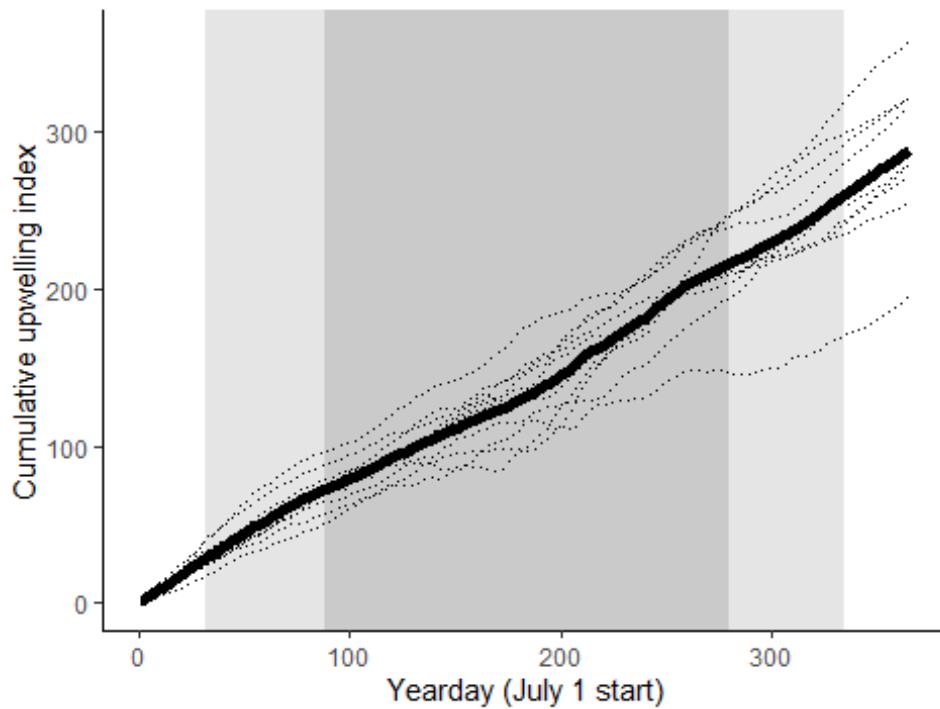

Monterey Bay

```r
## New Zealand
annual_upwelling_STB.plot <- ggplot() +
  annotate("rect", fill = "gray", alpha = 0.4,
           xmin = nz_pct10, xmax = nz_pct90,
           ymin = -Inf, ymax = Inf) +
  annotate("rect", fill = "gray", alpha = 0.7,
           xmin = nz_pct25, xmax = nz_pct75,
           ymin = -Inf, ymax = Inf) +
  geom_line(data = STB_upwelling_2, aes(x = yday_SoHem, y = csum, group =
Year_SoHem), linetype = "dotted") +
  geom_line(data = nz_clim, aes(x = yday_SoHem, y = csumclim), size = 2) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("Cumulative upwelling index") +
  ggtitle("South Taranaki Bight")

annual_upwelling_STB.plot
```
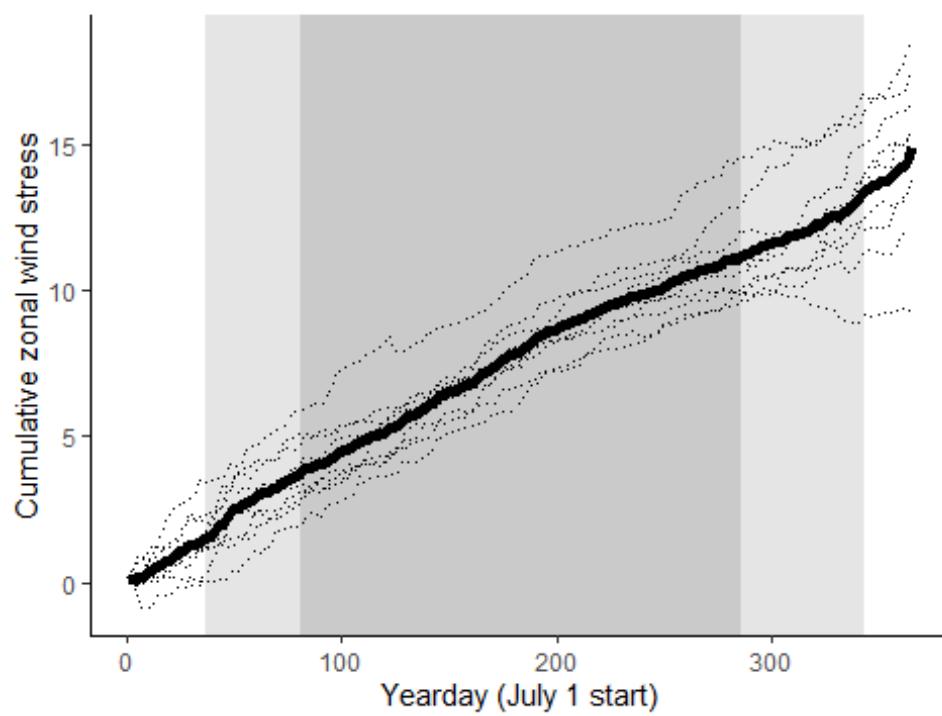
South Taranaki Bight


```
## Chile
annual_zonal_GC.plot <- ggplot() +
  annotate("rect", fill = "gray", alpha = 0.4,
           xmin = gc_zonal_pct10, xmax = gc_zonal_pct90,
           ymin = -Inf, ymax = Inf) +
  annotate("rect", fill = "gray", alpha = 0.7,
           xmin = gc_zonal_pct25, xmax = gc_zonal_pct75,
           ymin = -Inf, ymax = Inf) +
  geom_line(data = GC_zonal_2, aes(x = yday_SoHem, y = csum, group =
Year_SoHem), linetype = "dotted") +
  geom_line(data = gc_clim_zonal, aes(x = yday_SoHem, y = csumclim), size =
2) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("Cumulative zonal wind stress") +
  ggtitle("Corcovado Gulf")

annual_zonal_GC.plot
```

Productivity seasonality comparison

```r
# only include years that overlap with upwelling data
Chla.df <- Chla.df[Chla.df$Year < 2020, ]
Chla.df$Chl_STB[Chla.df$Year_SoHem=="Y2020_2021"] <- NA
Chla.df$Chl_GC[Chla.df$Year_SoHem=="Y2020_2021"] <- NA
Chla.df$logChl_STB[Chla.df$Year_SoHem=="Y2020_2021"] <- NA
Chla.df$logChl_GC[Chla.df$Year_SoHem=="Y2020_2021"] <- NA


# Separate Chl data by year
Chla.df$Year <- as.factor(Chla.df$Year)

# Aggregate monthly mean values
Chla_annual_CA <- aggregate(logChl_CA ~ Month, Chla.df, mean)
# Assign yearday to monthly mean, for plotting purposes
Chla_annual_CA$yday <- Chla.df$yday[Chla.df$Year=="2014" &
Chla.df$Month==Chla_annual_CA$Month]

# Aggregate monthly mean values
Chla_annual_STB <- aggregate(logChl_STB ~ Month, Chla.df, mean)
# Assign yearday to monthly mean, for plotting purposes
Chla_annual_STB$yday_SoHem <- Chla.df$yday_SoHem[Chla.df$Year=="2014" &
Chla.df$Month==Chla_annual_STB$Month]

# Aggregate monthly mean values
Chla_annual_GC <- aggregate(logChl_GC ~ Month, Chla.df, mean)
# Assign yearday to monthly mean, for plotting purposes
Chla_annual_GC$yday_SoHem <- Chla.df$yday_SoHem[Chla.df$Year=="2014" &
Chla.df$Month==Chla_annual_GC$Month]


Chl_CA.plot <- ggplot() +
  geom_line(data = Chla_annual_CA, aes(x=yday, y=logChl_CA), size=2) +
  geom_line(data = Chla.df,aes(x=yday, y=logChl_CA, group = Year,
color=Year)) +
  ylim(-1.1,1.5) + xlim(0,360) +
  theme_classic() +
  #theme(legend.position = "none") +
  xlab("Yearday (January 1 start)") +
  ylab("log(Chlorophyll-a)") +
  ggtitle("Monterey Bay")
Chl_CA.plot
```
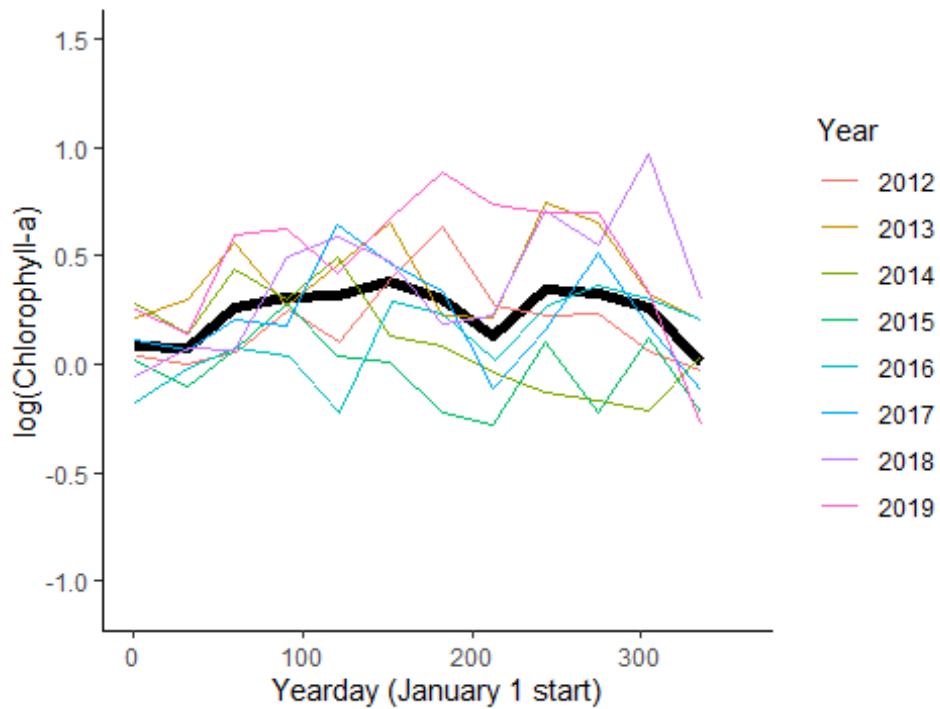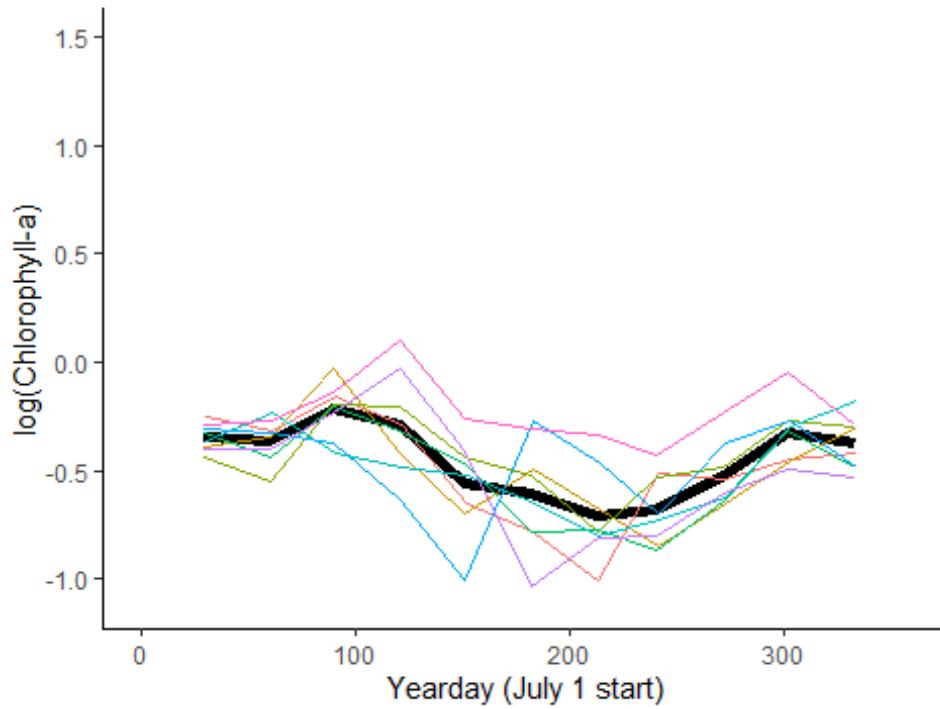
Monterey Bay
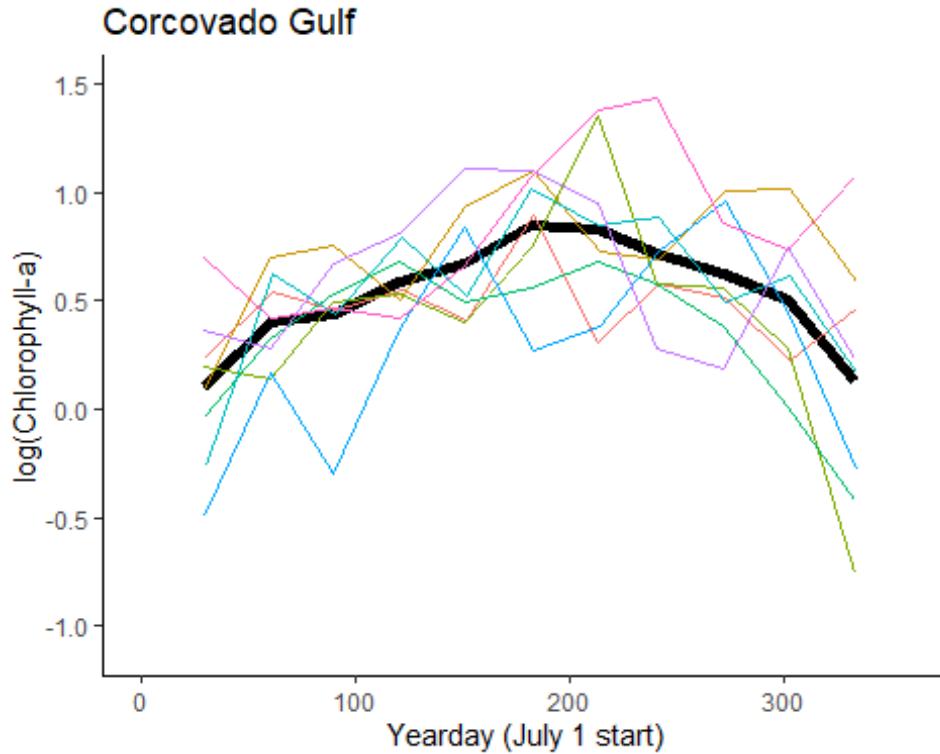
```
Chl_STB.plot <- ggplot() +
  geom_line(data = Chla_annual_STB, aes(x=yday_SoHem, y=logChl_STB), size=2)
+
  geom_line(data = Chla.df,aes(x=yday_SoHem, y=logChl_STB, group = Year,
color=Year)) +
  ylim(-1.1,1.5) + xlim(0,360) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("log(Chlorophyll-a)") +
  ggtitle("South Taranaki Bight")
Chl_STB.plot
```

South Taranaki Bight

```
Chl_GC.plot <- ggplot() +
  geom_line(data = Chla_annual_GC, aes(x=yday_SoHem, y=logChl_GC), size=2) +
  geom_line(data = Chla.df,aes(x=yday_SoHem, y=logChl_GC, group = Year,
color=Year)) +
  ylim(-1.1,1.5) + xlim(0,360) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("log(Chlorophyll-a)") +
  ggtitle("Corcovado Gulf")
Chl_GC.plot
```

Corcovado Gulf

Configure seasonality plots: highlight UAS data years, combine with total length and body condition data by year

```
# morphometric data
BAI.df <- read.csv("body_area_index.csv")
TL.df <- read.csv("total_length.csv")
UASeffort.df <- read.csv("UAS_samping_effort_corrected.csv")

# UPWELLING
## California
annual_CUTI_CA.plot <- ggplot() +
  annotate("rect", fill = "gray", alpha = 0.4,
           xmin = ca_pct10, xmax = ca_pct90,
           ymin = -Inf, ymax = Inf) +
  annotate("rect", fill = "gray", alpha = 0.7,
           xmin = ca_pct25, xmax = ca_pct75,
           ymin = -Inf, ymax = Inf) +
  geom_line(data = cuti_daily_2, aes(x = yday, y = csum, group = year),
linetype = "dotted") +
  geom_line(data = ca_clim, aes(x = yday, y = csumclim), size = 2) +
  geom_line(data = cuti_daily_2[cuti_daily_2$year=="2017",], aes(x = yday, y
= csum, group = year), color="darkgoldenrod1") +
  geom_line(data = cuti_daily_2[cuti_daily_2$year=="2018",], aes(x = yday, y
= csum, group = year), color="darkorange2") +
```

```r
  geom_line(aes(x=c(225,228), y=0), color="darkgoldenrod1", size=6) +
  geom_line(aes(x=c(237,248), y=0), color="darkorange2", size=6) +

  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (January 1 start)") +
  ylab("Cumulative CUTI") +
  annotate("text",  x= -Inf, y = Inf, label = "Monterey Bay", vjust=1,
hjust=-0.01)

## New Zealand
annual_upwelling_STB.plot <- ggplot() +
  annotate("rect", fill = "gray", alpha = 0.4,
           xmin = nz_pct10, xmax = nz_pct90,
           ymin = -Inf, ymax = Inf) +
  annotate("rect", fill = "gray", alpha = 0.7,
           xmin = nz_pct25, xmax = nz_pct75,
           ymin = -Inf, ymax = Inf) +
  geom_line(data = STB_upwelling_2, aes(x = yday_SoHem, y = csum, group =
Year_SoHem), linetype = "dotted") +
  geom_line(data = nz_clim, aes(x = yday_SoHem, y = csumclim), size = 2) +
  geom_line(data = STB_upwelling_2[STB_upwelling_2$Year_SoHem=="2016",],
aes(x = yday_SoHem, y = csum, group = Year_SoHem), color="cyan3") +
  geom_line(data = STB_upwelling_2[STB_upwelling_2$Year_SoHem=="2017",],
aes(x = yday_SoHem, y = csum, group = Year_SoHem), color="cyan4") +

  geom_line(aes(x=c(217,223), y=20), color="cyan3", size=6) +
  geom_line(aes(x=c(223,235), y=20), color="cyan4", size=6) +

  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("Cumulative upwelling index") +
  annotate("text",  x= -Inf, y = Inf, label = "South Taranaki Bight",
vjust=1, hjust=-0.01)

## Chile
annual_zonal_GC.plot <- ggplot() +
  annotate("rect", fill = "gray", alpha = 0.4,
           xmin = gc_zonal_pct10, xmax = gc_zonal_pct90,
           ymin = -Inf, ymax = Inf) +
  annotate("rect", fill = "gray", alpha = 0.7,
           xmin = gc_zonal_pct25, xmax = gc_zonal_pct75,
           ymin = -Inf, ymax = Inf) +
  geom_line(data = GC_zonal_2, aes(x = yday_SoHem, y = csum, group =
Year_SoHem), linetype = "dotted") +
  geom_line(data = gc_clim_zonal, aes(x = yday_SoHem, y = csumclim), size =
2) +
```

```r
  geom_line(data = GC_zonal_2[GC_zonal_2$Year_SoHem=="2015",], aes(x =
yday_SoHem, y = csum, group = Year_SoHem), color="red") +
  geom_line(data = GC_zonal_2[GC_zonal_2$Year_SoHem=="2017",], aes(x =
yday_SoHem, y = csum, group = Year_SoHem), color="dark red") +

  geom_line(aes(x=c(237, 252), y=0), color="red", size=6) +
  geom_line(aes(x=c(238, 241), y=0), color="dark red", size=6) +

  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("Cumulative zonal wind stress") +
  annotate("text",  x= -Inf, y = Inf, label = "Corcovado Gulf", vjust=1,
hjust=-0.01)


upwelling_season_combined.plot <- ggarrange(annual_CUTI_CA.plot,
annual_upwelling_STB.plot, annual_zonal_GC.plot, nrow = 3, align = "hv")
upwelling_season_combined.plot <-
annotate_figure(upwelling_season_combined.plot, top = text_grob("Annual
physical forcing",
              color = "Black", face = "bold", size = 12))
upwelling_season_combined.plot
```
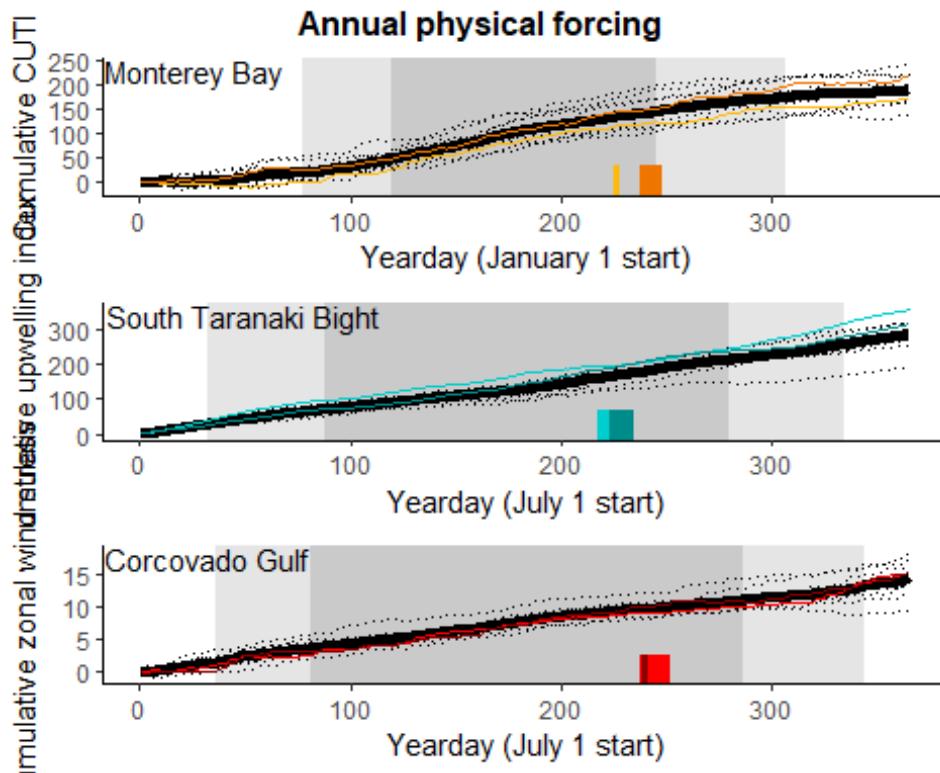
```r
# PRODUCTIVITY
Chl_CA.plot <- ggplot() +
  geom_line(data = Chla_annual_CA, aes(x=yday, y=logChl_CA), size=2) +
  geom_line(data = Chla.df,aes(x=yday, y=logChl_CA, group = Year), linetype =
"dotted") +
  geom_line(data = Chla.df[Chla.df$Year=="2017",], aes(x = yday_SoHem, y =
logChl_CA, group = Year), color="darkgoldenrod1") +
  geom_line(data = Chla.df[Chla.df$Year=="2018",], aes(x = yday_SoHem, y =
logChl_CA, group = Year), color="darkorange2") +

  geom_line(aes(x=c(225,228), y=-1), color="darkgoldenrod1", size=6) +
  geom_line(aes(x=c(237,248), y=-1), color="darkorange2", size=6) +

  ylim(-1.1,1.5) + xlim(0,360) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (January 1 start)") +
  ylab("log(Chlorophyll-a)") +
  annotate("text",  x= -Inf, y = Inf, label = "Monterey Bay", vjust=1,
hjust=-0.01)

Chl_STB.plot <- ggplot() +
  geom_line(data = Chla_annual_STB, aes(x=yday_SoHem, y=logChl_STB), size=2)
+
  geom_line(data = Chla.df,aes(x=yday_SoHem, y=logChl_STB, group =
Year_SoHem), linetype = "dotted") +
  geom_line(data = Chla.df[Chla.df$Year_SoHem=="Y2015_2016",], aes(x =
yday_SoHem, y = logChl_STB, group = Year_SoHem), color="cyan3") +
  geom_line(data = Chla.df[Chla.df$Year_SoHem=="Y2016_2017",], aes(x =
yday_SoHem, y = logChl_STB, group = Year_SoHem), color="cyan4") +

  geom_line(aes(x=c(217,223), y=-1), color="cyan3", size=6) +
  geom_line(aes(x=c(223,235), y=-1), color="cyan4", size=6) +

  ylim(-1.1,1.5) + xlim(0,360) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("log(Chlorophyll-a)") +
  annotate("text",  x= -Inf, y = Inf, label = "South Taranaki Bight",
vjust=1, hjust=-0.01)

Chl_GC.plot <- ggplot() +
  geom_line(data = Chla_annual_GC, aes(x=yday_SoHem, y=logChl_GC), size=2) +
  geom_line(data = Chla.df,aes(x=yday_SoHem, y=logChl_GC, group =
Year_SoHem), linetype = "dotted") +
  geom_line(data = Chla.df[Chla.df$Year_SoHem=="Y2014_2015",], aes(x =
yday_SoHem, y = logChl_GC, group = Year_SoHem), color="red") +
  geom_line(data = Chla.df[Chla.df$Year_SoHem=="Y2016_2017",], aes(x =
```
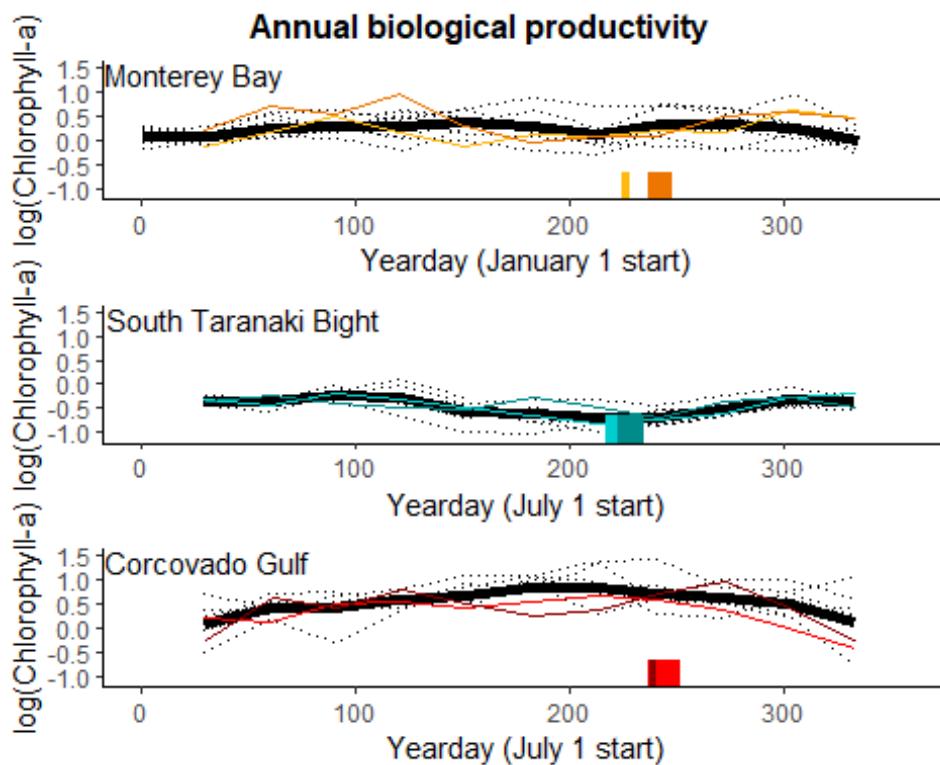
```
yday_SoHem, y = logChl_GC, group = Year_SoHem), color="dark red") +

  geom_line(aes(x=c(237, 252), y=-1), color="red", size=6) +
  geom_line(aes(x=c(238, 241), y=-1), color="dark red", size=6) +

  ylim(-1.1,1.5) + xlim(0,360) +
  theme_classic() +
  theme(legend.position = "none") +
  xlab("Yearday (July 1 start)") +
  ylab("log(Chlorophyll-a)") +
  annotate("text",  x= -Inf, y = Inf, label = "Corcovado Gulf", vjust=1,
hjust=-0.01)


Chl_annual_combined.plot <- ggarrange(Chl_CA.plot, Chl_STB.plot, Chl_GC.plot,
nrow = 3, align = "hv")
Chl_annual_combined.plot <- annotate_figure(Chl_annual_combined.plot, top =
text_grob("Annual biological productivity",
              color = "Black", face = "bold", size = 12))
Chl_annual_combined.plot
```

```r
# BODY CONDITION

BAI.df$Location <- factor(BAI.df$Location, levels = c("CA", "NZ", "Chile"))
TL.df$Location <- factor(TL.df$Location, levels = c("CA", "NZ", "Chile"))

TL.df$Location_Year <- paste0(TL.df$Location, "_", TL.df$Year)
TL_samplesizes.df <- aggregate(ID ~ Location + Year, TL.df, length)
TL_samplesizes.df$Location_Year <- paste0(TL_samplesizes.df$Location, "_",
TL_samplesizes.df$Year)
TL_samplesizes.df$Location <- factor(TL_samplesizes.df$Location, levels =
c("CA", "NZ", "Chile"))

BAI.df$Location_Year <- paste0(BAI.df$Location, "_", BAI.df$Year)
BAI_samplesizes.df <- aggregate(ID ~ Location + Year, BAI.df, length)
BAI_samplesizes.df$Location_Year <- paste0(BAI_samplesizes.df$Location, "_",
BAI_samplesizes.df$Year)
BAI_samplesizes.df$Location <- factor(BAI_samplesizes.df$Location, levels =
c("CA", "NZ", "Chile"))

fillcols_b <- c("darkgoldenrod1", "darkorange2","red", "dark red","cyan3",
"cyan4")

TL.plot <- ggplot(data = TL.df, aes(y=TL.mean, x=Location)) +
  geom_boxplot(aes(color = Location_Year, fill = Location_Year), alpha = 0.7)
+
  scale_color_manual(values = fillcols_b) + scale_fill_manual(values =
fillcols_b) +
  geom_text(aes(x = Location, y = 18, label = Year, color=Location_Year),
position=position_dodge(width=0.8), size=2.5) +
  geom_text(data = TL_samplesizes.df, aes(x = Location, y = 17.5, label =
paste("n =", ID), color=Location_Year),
          position=position_dodge(width=0.8), size=2) +
 ylab("Total length (m)") + xlab(" ") + guides(fill="none", color="none") +
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()

BAI.plot <- ggplot(data = BAI.df, aes(y=BAI.mean, x=Location)) +
  geom_boxplot(aes(color = Location_Year, fill = Location_Year), alpha = 0.7)
+
  scale_color_manual(values = fillcols_b) + scale_fill_manual(values =
fillcols_b) +
  geom_text(aes(x = Location, y = 11.5, label = Year, color=Location_Year),
position=position_dodge(width=0.8), size=2.5) +
  geom_text(data = BAI_samplesizes.df, aes(x = Location, y = 11.1, label =
paste("n =", ID), color=Location_Year),
          position=position_dodge(width=0.8), size=2) +

  geom_segment(aes(x="CA", xend="NZ", y=17.1, yend=17.1)) +
  geom_segment(aes(x="NZ", xend="Chile", y=17.35, yend=17.35)) +
```
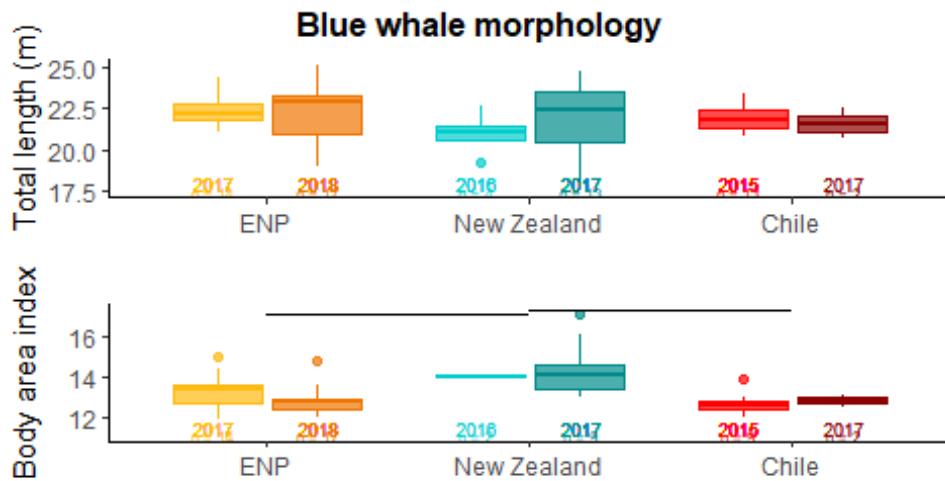
```
   geom_text(aes(x="CA", y=17.1, label="*"), vjust=-0.005, hjust=-6, size=3.5)
+
   geom_text(aes(x="NZ", y=17.35, label="*"), vjust=-0.005, hjust=-6,
size=3.5) +

   ylab("Body area index") + xlab(" ") + guides(fill="none", color="none") +
   scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
   theme_classic()

morph.plot <- ggarrange(TL.plot, BAI.plot, nrow = 3, align = "hv")
morph.plot <- annotate_figure(morph.plot, top = text_grob("Blue whale
morphology",
              color = "Black", face = "bold", size = 12))
morph.plot
```
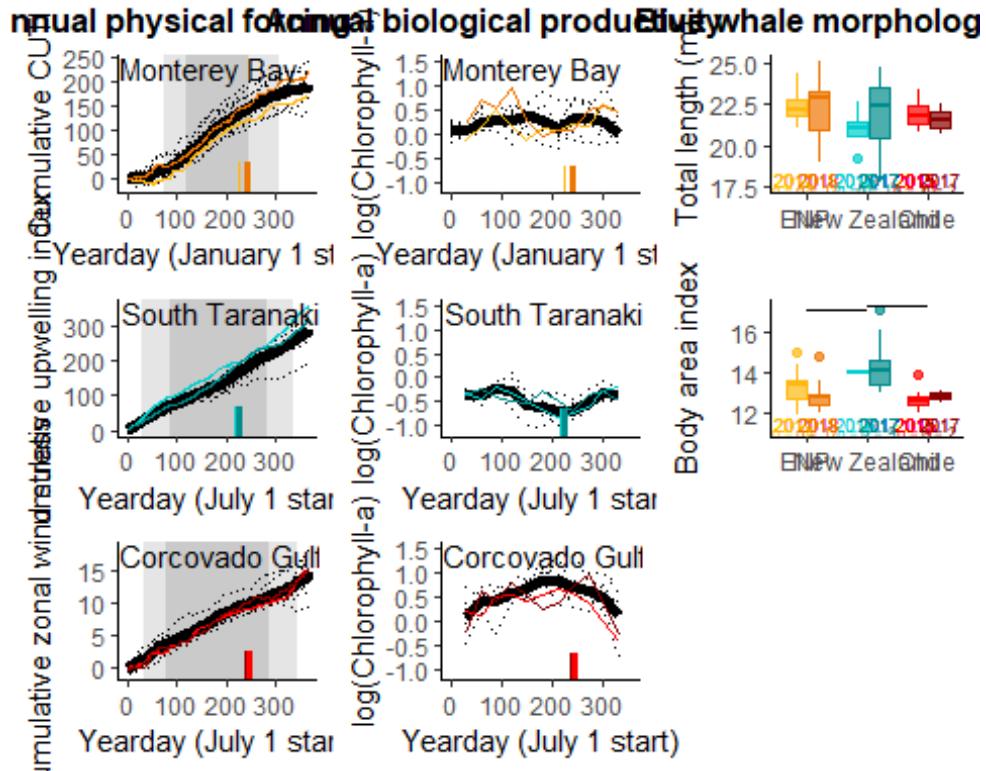


```
# ALL TOGETHER NOW

upwelling_chl_morph.plot <- ggarrange(upwelling_season_combined.plot,
Chl_annual_combined.plot, morph.plot, nrow = 1, align = "hv")

upwelling_chl_morph.plot
```

Annual physical forcing / **Annual biological productivity** / **Blue whale morphology**

Monterey Bay — Cumulative CUI — Yearday (January 1 start)
Monterey Bay — log(Chlorophyll-a) — Yearday (January 1 start)
Total length (m) — 2018 2017 2017 — Chile New Zealand

South Taranaki — Cumulative zonal wind stress / Cumulative upwelling index — Yearday (July 1 start)
South Taranaki — log(Chlorophyll-a) — Yearday (July 1 start)
Body area index — 2018 2017 2017 — Chile New Zealand

Corcovado Gulf — Yearday (July 1 start)
Corcovado Gulf — log(Chlorophyll-a) — Yearday (July 1 start)

```r
## Add map with study regions
# In the maps package, world2 is the Pacific centered map with longitude
[0,360]
world2 <- map_data("world2")

pacific.map <- ggplot() +
  geom_map(data = world2, map=world2, aes(x=long, y=lat, map_id=region),
fill="black") +
  coord_map("ortho", orientation = c(-20,235,0)) +

  geom_star(aes(x=-123, y=37), color = "darkorange", fill = "darkorange",
size=1.75) +
  geom_star(aes(x=173, y=-40), color = "cyan3", fill = "cyan3", size=1.75) +
  geom_star(aes(x=-74, y=-43), color = "red", fill = "red", size=1.75) +

  annotate(geom = "text", x=-135, y=22, label = "Monterey Bay,\nCalifornia",
color = "darkorange", size = 2.5) +
  annotate(geom = "text", x=-160.5, y=-30, label = "South Taranaki
Bight,\nNew Zealand", color = "cyan3", size = 2.5) +
  annotate(geom = "text", x=-87, y=-31, label = "Corcovado Gulf,\nChile",
color = "red", size = 2.5) +
```
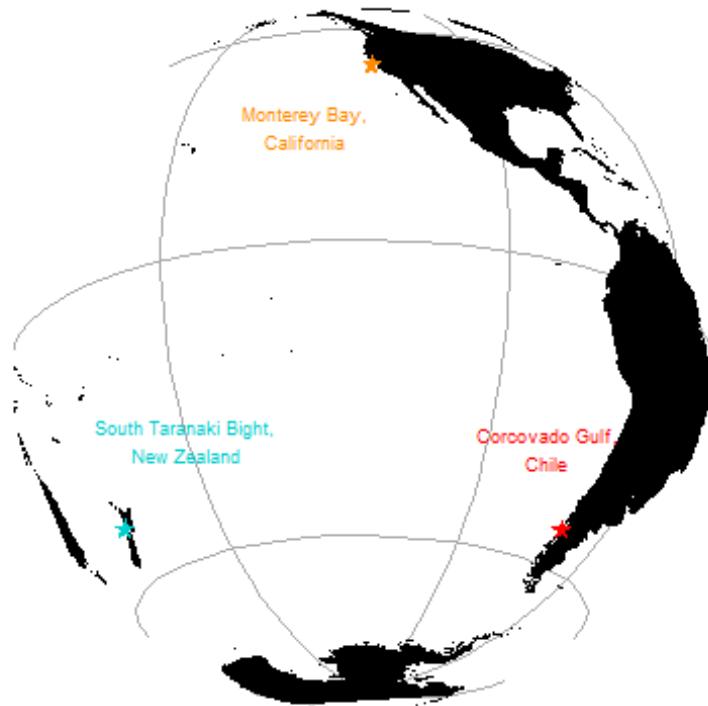
```
  xlab("") + ylab("") +
  theme(panel.grid.major = element_line(color = "dark gray"),
        panel.grid.minor = element_line(color = "dark gray"),
        axis.text = element_blank(), axis.ticks = element_blank(),
        panel.background = element_blank(),
        plot.background = element_rect(fill = "white", color = "white"))

pacific.map
```
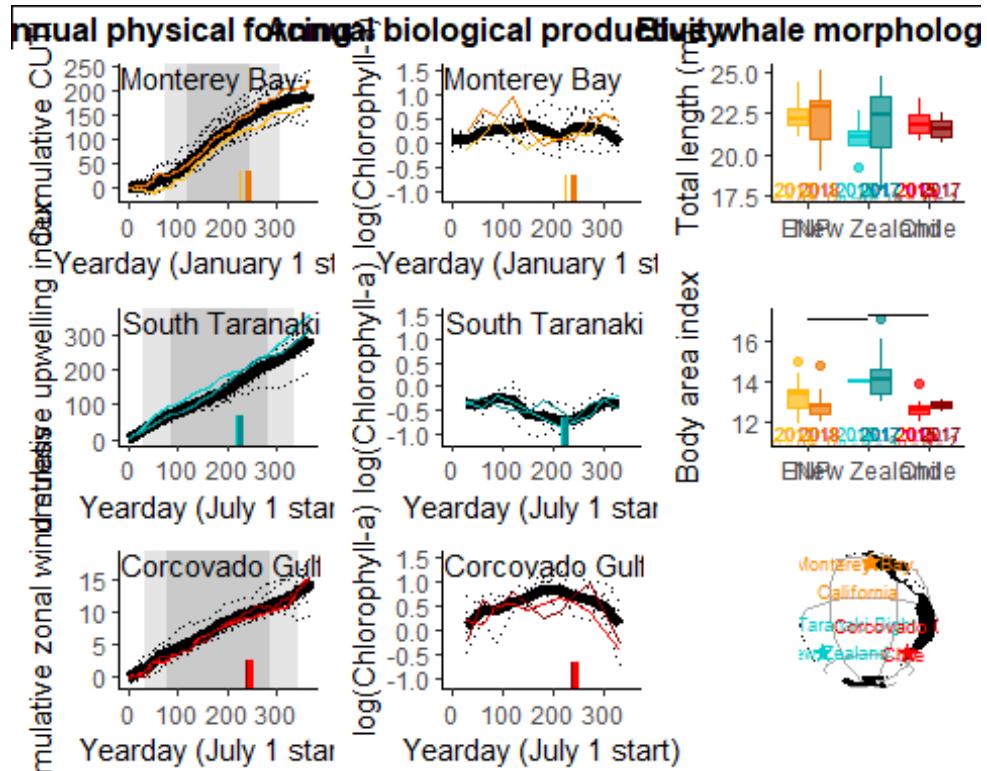


```
#######
morph.plot <- ggarrange(TL.plot, BAI.plot, pacific.map, nrow = 3, align =
"hv")
morph.plot <- annotate_figure(morph.plot, top = text_grob("Blue whale
morphology",
              color = "Black", face = "bold", size = 12))

# ALL TOGETHER NOW

upwelling_chl_morph.plot <- ggarrange(upwelling_season_combined.plot,
Chl_annual_combined.plot, morph.plot, nrow = 1, align = "hv") +
bgcolor("white")

upwelling_chl_morph.plot
```

```
ggsave(upwelling_chl_morph.plot, filename="./Figures/Barlow_Fig1.png", device
= "png", height=200, width=200, units="mm")
```

MORPHOLOGICAL COMPARISONS

Data wrangling

```r
EE_std.df <- read.csv("EE_std.csv")
Fs_std.df <- read.csv("Fs_std.csv")
Fw_std.df <- read.csv("Fw_std.csv")
JL_std.df <- read.csv("JL_std.csv")
RB_std.df <- read.csv("RB_std.csv")
Tail_std.df <- read.csv("Tail_std.csv")

morph_df.list <- list(EE_std.df, Fs_std.df, Fw_std.df, JL_std.df, RB_std.df,
Tail_std.df)

morph_sample_sizes.df <- data.frame(matrix(ncol = 4, nrow =
length(morph_df.list)))
colnames(morph_sample_sizes.df) <- c("measurement", "n_CA", "n_Chile",
"n_NZ")

for (i in 1:length(morph_df.list)) {

  morph_i <- morph_df.list[[i]]

  morph_sample_sizes.df[i,1] <- colnames(morph_i[4])

  morph_sample_sizes.df[i,2] <-
length(morph_i$Location[morph_i$Location=="CA"])
  morph_sample_sizes.df[i,3] <-
length(morph_i$Location[morph_i$Location=="Chile"])
  morph_sample_sizes.df[i,4] <-
length(morph_i$Location[morph_i$Location=="NZ"])

  morph_i$Location <- factor(morph_i$Location, levels = c("CA", "NZ",
"Chile"))


}

morph_sample_sizes.df

##       measurement n_CA n_Chile n_NZ
## 1    EE.std.lower   12      10   15
## 2    Fs.std.lower   11      13   16
## 3    Fw.std.lower   11      15   14
## 4    JL.std.lower   12      11   17
## 5    RB.std.lower   12      14   15
## 6  Tail.std.lower    6      13    6
```

```r
# Re-order factor levels
EE_std.df$Location <- factor(EE_std.df$Location, levels = c("CA", "NZ",
"Chile"))
Fs_std.df$Location <- factor(Fs_std.df$Location, levels = c("CA", "NZ",
"Chile"))
Fw_std.df$Location <- factor(Fw_std.df$Location, levels = c("CA", "NZ",
"Chile"))
JL_std.df$Location <- factor(JL_std.df$Location, levels = c("CA", "NZ",
"Chile"))
RB_std.df$Location <- factor(RB_std.df$Location, levels = c("CA", "NZ",
"Chile"))
Tail_std.df$Location <- factor(Tail_std.df$Location, levels = c("CA", "NZ",
"Chile"))
```

Configure morphology plots

```r
fillcols_a <- c("darkorange", "cyan3", "Red")

# Include ANOVA results
EE.plot <- ggplot(data = EE_std.df) +
  geom_pointrange(aes(x=Location, y=EE.std.mean, ymin=EE.std.lower,
ymax=EE.std.upper, color = Location, fill = Location),
                  position = position_jitter(), linetype='dashed', alpha =
0.2, size=0.1) +
  geom_boxplot(aes(y=EE.std.mean, x=Location, color = Location, fill =
Location), alpha = 0.7) +

  geom_segment(aes(x="CA", xend="NZ", y=0.15, yend=0.15)) +
  geom_segment(aes(x="CA", xend="Chile", y=0.152, yend=0.152)) +
  geom_text(aes(x="CA", y=0.15, label="*"), vjust=-0.005, hjust=-5, size=3.5)
+
  geom_text(aes(x="CA", y=0.152, label="*"), vjust=-0.005, hjust=-10,
size=3.5) +

  scale_color_manual(values = fillcols_a) + scale_fill_manual(values =
fillcols_a) +
  ylab("Eye-to-eye") + xlab(" ") + guides(fill="none", color="none") +
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()
# EE.plot

JL.plot <- ggplot(data = JL_std.df) +
  geom_pointrange(aes(x=Location, y=JL.std.mean, ymin=JL.std.lower,
ymax=JL.std.upper, color = Location, fill = Location),
                  position = position_jitter(), linetype='dashed', alpha =
0.2, size=0.1) +
  geom_boxplot(aes(y=JL.std.mean, x=Location, color = Location, fill =
Location), alpha = 0.7) +

  geom_segment(aes(x="CA", xend="NZ", y=0.2455, yend=0.2455)) +
  geom_segment(aes(x="CA", xend="Chile", y=0.248, yend=0.248)) +
  geom_text(aes(x="CA", y=0.2455, label="*"), vjust=-0.005, hjust=-5,
size=3.5) +
  geom_text(aes(x="CA", y=0.248, label="*"), vjust=-0.005, hjust=-10,
size=3.5) +

  scale_color_manual(values = fillcols_a) + scale_fill_manual(values =
fillcols_a) +
  ylab("Jaw length") + xlab(" ") + guides(fill="none", color="none") +
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()
# JL.plot

RB.plot <- ggplot(data = RB_std.df) +
```

```
  geom_pointrange(aes(x=Location, y=RB.std.mean, ymin=RB.std.lower,
ymax=RB.std.upper, color = Location, fill = Location),
                  position = position_jitter(), linetype='dashed', alpha =
0.2, size=0.1) +
  geom_boxplot(aes(y=RB.std.mean, x=Location, color = Location, fill =
Location), alpha = 0.7) +

  geom_segment(aes(x="CA", xend="NZ", y=0.227, yend=0.227)) +
  geom_segment(aes(x="CA", xend="Chile", y=0.23, yend=0.23)) +
  geom_text(aes(x="CA", y=0.227, label="*"), vjust=-0.005, hjust=-5,
size=3.5) +
  geom_text(aes(x="CA", y=0.23, label="*"), vjust=-0.005, hjust=-10,
size=3.5) +

  scale_color_manual(values = fillcols_a) + scale_fill_manual(values =
fillcols_a) +
  ylab("Rostrum-to-blowhole") + xlab(" ") + guides(fill="none", color="none")
+
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()
# RB.plot

Fs.plot <- ggplot(data = Fs_std.df) +
  geom_pointrange(aes(x=Location, y=Fs.std.mean, ymin=Fs.std.lower,
ymax=Fs.std.upper, color = Location, fill = Location),
                  position = position_jitter(), linetype='dashed', alpha =
0.2, size=0.1) +
  geom_boxplot(aes(y=Fs.std.mean, x=Location, color = Location, fill =
Location), alpha = 0.7) +

  geom_segment(aes(x="CA", xend="NZ", y=0.271, yend=0.271)) +
  geom_segment(aes(x="NZ", xend="Chile", y=0.275, yend=0.275)) +
  geom_text(aes(x="CA", y=0.271, label="*"), vjust=-0.005, hjust=-5,
size=3.5) +
  geom_text(aes(x="NZ", y=0.275, label="*"), vjust=-0.005, hjust=-5,
size=3.5) +

  scale_color_manual(values = fillcols_a) + scale_fill_manual(values =
fillcols_a) +
  ylab("Fluke span") + xlab(" ") + guides(fill="none", color="none") +
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()
# Fs.plot

Fw.plot <- ggplot(data = Fw_std.df) +
  geom_pointrange(aes(x=Location, y=Fw.std.mean, ymin=Fw.std.lower,
ymax=Fw.std.upper, color = Location, fill = Location),
                  position = position_jitter(), linetype='dashed', alpha =
0.2, size=0.1) +
```
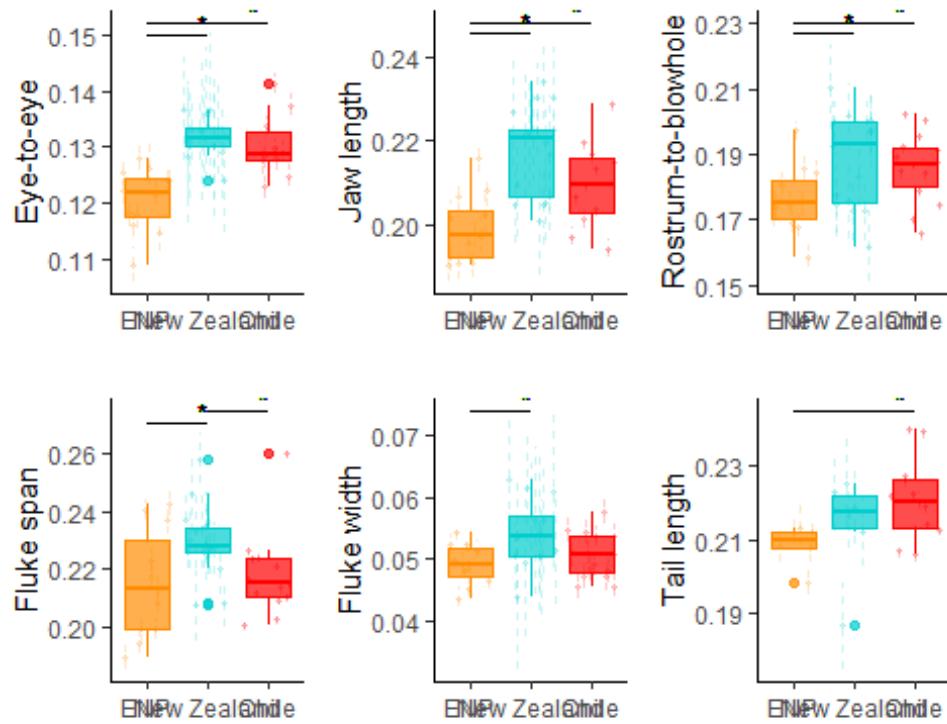
```r
  geom_boxplot(aes(y=Fw.std.mean, x=Location, color = Location, fill =
Location), alpha = 0.7) +

  geom_segment(aes(x="CA", xend="NZ", y=0.074, yend=0.074)) +
  geom_text(aes(x="CA", y=0.074, label="*"), vjust=-0.005, hjust=-5,
size=3.5) +

  scale_color_manual(values = fillcols_a) + scale_fill_manual(values =
fillcols_a) +
  ylab("Fluke width") + xlab(" ") + guides(fill="none", color="none") +
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()
# Fw.plot

Tail.plot <- ggplot(data = Tail_std.df) +
  geom_pointrange(aes(x=Location, y=Tail.std.mean, ymin=Tail.std.lower,
ymax=Tail.std.upper, color = Location, fill = Location),
                  position = position_jitter(), linetype='dashed', alpha =
0.2, size=0.1) +
  geom_boxplot(aes(y=Tail.std.mean, x=Location, color = Location, fill =
Location), alpha = 0.7) +

  geom_segment(aes(x="CA", xend="Chile", y=0.245, yend=0.245)) +
  geom_text(aes(x="CA", y=0.245, label="*"), vjust=-0.005, hjust=-10,
size=3.5) +

  scale_color_manual(values = fillcols_a) + scale_fill_manual(values =
fillcols_a) +
  ylab("Tail length") + xlab(" ") + guides(fill="none", color="none") +
  scale_x_discrete(labels=c("ENP", "New Zealand", "Chile")) +
  theme_classic()
# Tail.plot

morph.multiplot_nopecs <- grid.arrange(EE.plot, JL.plot, RB.plot, Fs.plot,
Fw.plot, Tail.plot,
                            nrow=2, ncol=3)
```

```
ggsave(morph.multiplot_nopecs, filename="./Figures/Barlow_Fig2a.png", device
= "png", height=200, width=180, units="mm")
```

Plot MCMC ANOVA results

```r
TL_anova.df <- read.csv("TL_summary_results.csv")
BAI_anova.df <- read.csv("BAI_summary_results.csv")
EE_anova.df <- read.csv("EE_summary_results.csv")
Fs_anova.df <- read.csv("Fs_summary_results.csv")
Fw_anova.df <- read.csv("Fw_summary_results.csv")
JL_anova.df <- read.csv("JL_summary_results.csv")
RB_anova.df <- read.csv("RB_summary_results.csv")
Tail_anova.df <- read.csv("Tail_summary_results.csv")


TL_anova.plot <- ggplot(data = TL_anova.df[!is.na(TL_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-1.8, 2.4) +
  xlab("") + ylab("Difference in mean\ntotal length")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

BAI_anova.plot <- ggplot(data = BAI_anova.df[!is.na(BAI_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-1.8, 2.4) +
  xlab("") + ylab("Difference in mean\nbody area index")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

EE_anova.plot <- ggplot(data = EE_anova.df[!is.na(EE_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-0.025, 0.03) +
  xlab("") + ylab("Difference in mean eye-to-eye")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

JL_anova.plot <- ggplot(data = JL_anova.df[!is.na(JL_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-0.025, 0.03) +
  xlab("") + ylab("Difference in mean jaw length")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

RB_anova.plot <- ggplot(data = RB_anova.df[!is.na(RB_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
```

```r
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-0.025, 0.03) +
  xlab("") + ylab("Difference in mean rostrum-to-blowhole")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

Fs_anova.plot <- ggplot(data = Fs_anova.df[!is.na(Fs_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-0.025, 0.03) +
  xlab("") + ylab("Difference in mean fluke span")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

Fw_anova.plot <- ggplot(data = Fw_anova.df[!is.na(Fw_anova.df$label),]) +
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-0.025, 0.03) +
  xlab("") + ylab("Difference in mean fluke width")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

Tail_anova.plot <- ggplot(data = Tail_anova.df[!is.na(Tail_anova.df$label),])
+
  geom_pointrange(aes(x = label, y = means, ymin = HPD_lwr, ymax = HPD_upr))
+
  geom_abline(intercept = 0, slope = 0, lty = 2) +
  ylim(-0.025, 0.03) +
  xlab("") + ylab("Difference in mean tail length")  +
  scale_x_discrete(labels=c("ENP-Chile", "NZ-ENP", "NZ-Chile")) +
  theme_classic()

TL_BAI_anova <- grid.arrange(TL_anova.plot, BAI_anova.plot, nrow=2, ncol=1)
```
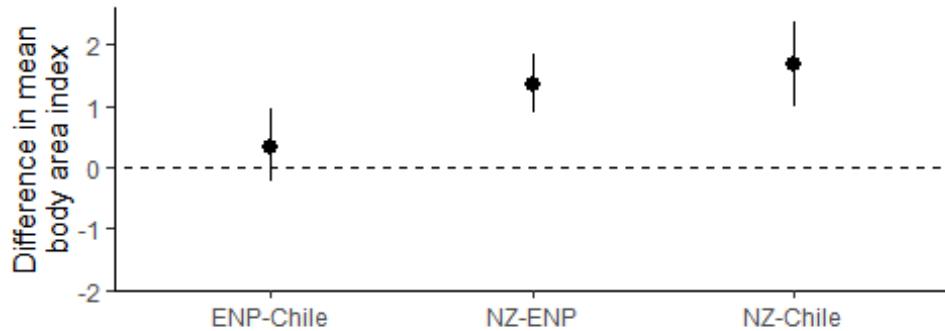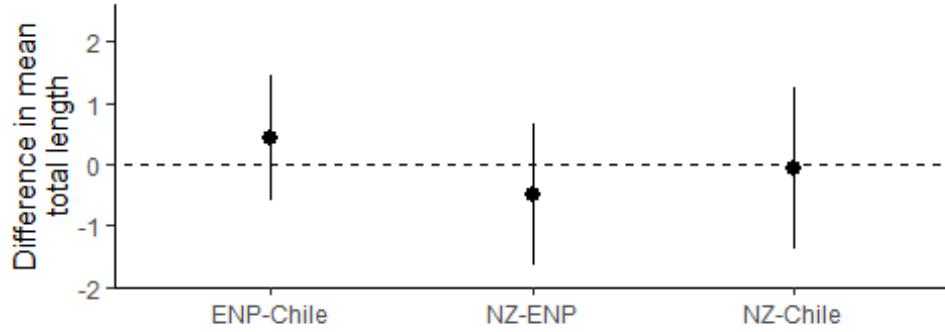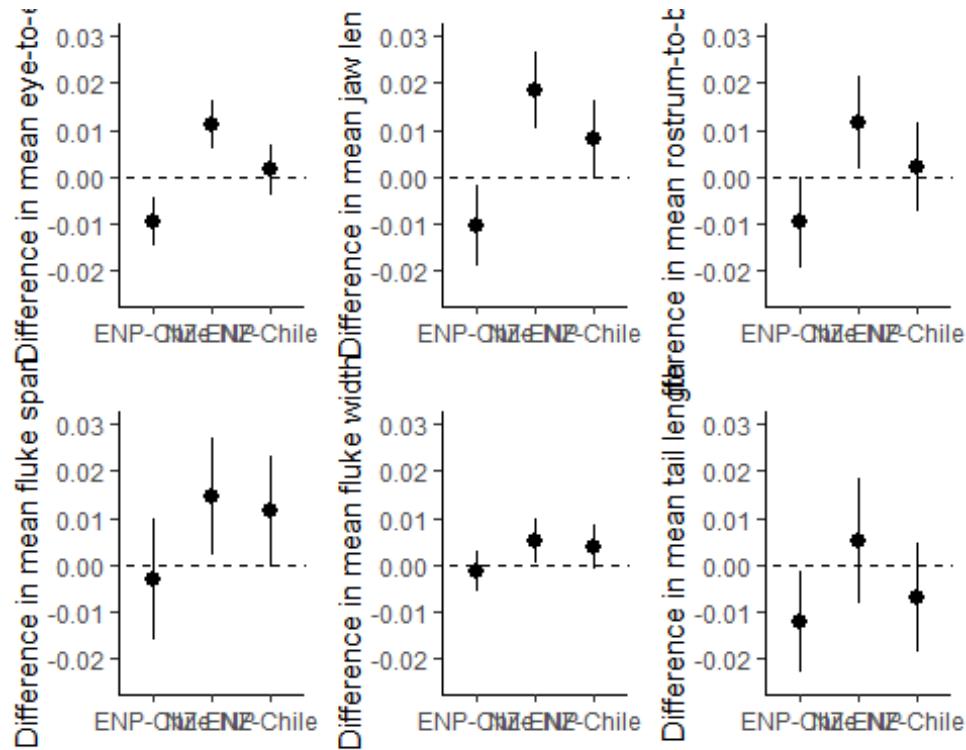
```r
ggsave(TL_BAI_anova, filename="./Figures/Barlow_FigS4.png", device = "png",
height=110, width=80, units="mm")

morph.multiplot_anova <- grid.arrange(EE_anova.plot, JL_anova.plot,
RB_anova.plot, Fs_anova.plot, Fw_anova.plot, Tail_anova.plot,
                                      nrow=2, ncol=3)
```

```r
ggsave(morph.multiplot_anova, filename="./Figures/Barlow_FigS4a.png", device
= "png", height=200, width=180, units="mm")
```

Allometry

```r
EE_abs.df <- read.csv("EE_abs.csv")
Fs_abs.df <- read.csv("Fs_abs.csv")
Fw_abs.df <- read.csv("Fw_abs.csv")
JL_abs.df <- read.csv("JL_abs.csv")
RB_abs.df <- read.csv("RB_abs.csv")
Tail_abs.df <- read.csv("Tail_abs.csv")

# Re-order factor levels
EE_abs.df$Location <- factor(EE_abs.df$Location, levels = c("CA", "NZ",
"Chile"))
Fs_abs.df$Location <- factor(Fs_abs.df$Location, levels = c("CA", "NZ",
"Chile"))
Fw_abs.df$Location <- factor(Fw_abs.df$Location, levels = c("CA", "NZ",
"Chile"))
JL_abs.df$Location <- factor(JL_abs.df$Location, levels = c("CA", "NZ",
"Chile"))
RB_abs.df$Location <- factor(RB_abs.df$Location, levels = c("CA", "NZ",
"Chile"))
Tail_abs.df$Location <- factor(Tail_abs.df$Location, levels = c("CA", "NZ",
"Chile"))


## Plot on log-log scale
log_EE_allometry.plot <- ggplot() +
  geom_abline(intercept = -2.08, color = "black", linetype = "dotted") +
  geom_point(data = EE_abs.df, aes(x = log(TL.mean), y = log(EE.mean), color
= Location)) +
  geom_smooth(data = EE_abs.df, aes(x = log(TL.mean), y = log(EE.mean), color
= Location, fill = Location), method = lm, alpha = 0.15, se=FALSE) +
  geom_pointrange(data = EE_abs.df, aes(x = log(TL.mean), y = log(EE.mean),
                                        color = Location, ymin =
log(EE.lower), ymax = log(EE.upper)), fatten = 0, alpha = 0.15) +
  geom_pointrange(data = EE_abs.df, aes(x = log(TL.mean), y = log(EE.mean),
                                        color = Location, xmin =
log(TL.lower), xmax = log(TL.upper)), fatten = 0, alpha = 0.15) +
  scale_color_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) +
  scale_fill_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) + labs(color="Population", fill="Population") +
  xlab("log(Total length)") + ylab("log(Eye-to-eye)") + xlim(2.7,3.4) +
  theme_classic()

log_Fw_allometry.plot <- ggplot() +
  geom_abline(intercept = -3, color = "black", linetype = "dotted") +
  geom_point(data = Fw_abs.df, aes(x = log(TL.mean), y = log(Fw.mean), color
= Location)) +
  geom_smooth(data = Fw_abs.df, aes(x = log(TL.mean), y = log(Fw.mean), color
= Location, fill = Location), method = lm, alpha = 0.15, se=FALSE) +
```

```r
  geom_pointrange(data = Fw_abs.df, aes(x = log(TL.mean), y = log(Fw.mean),
                                        color = Location, ymin =
log(Fw.lower), ymax = log(Fw.upper)), fatten = 0, alpha = 0.15) +
  geom_pointrange(data = Fw_abs.df, aes(x = log(TL.mean), y = log(Fw.mean),
                                        color = Location, xmin =
log(TL.lower), xmax = log(TL.upper)), fatten = 0, alpha = 0.15) +
  scale_color_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) +
  scale_fill_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) + labs(color="Population", fill="Population") +
  xlab("log(Total length)") + ylab("log(Fluke width)") + xlim(2.7,3.4) +
  theme_classic()

log_Fs_allometry.plot <- ggplot() +
  geom_abline(intercept = -1.5, color = "black", linetype = "dotted") +
  geom_point(data = Fs_abs.df, aes(x = log(TL.mean), y = log(Fs.mean), color
= Location)) +
  geom_smooth(data = Fs_abs.df, aes(x = log(TL.mean), y = log(Fs.mean), color
= Location, fill = Location), method = lm, alpha = 0.15, se=FALSE) +
  geom_pointrange(data = Fs_abs.df, aes(x = log(TL.mean), y = log(Fs.mean),
                                        color = Location, ymin =
log(Fs.lower), ymax = log(Fs.upper)), fatten = 0, alpha = 0.15) +
  geom_pointrange(data = Fs_abs.df, aes(x = log(TL.mean), y = log(Fs.mean),
                                        color = Location, xmin =
log(TL.lower), xmax = log(TL.upper)), fatten = 0, alpha = 0.15) +
  scale_color_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) +
  scale_fill_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) + labs(color="Population", fill="Population") +
  xlab("log(Total length)") + ylab("log(Fluke span)") + xlim(2.7,3.4) +
  theme_classic()

log_JL_allometry.plot <- ggplot() +
  geom_abline(intercept = -1.55, color = "black", linetype = "dotted") +
  geom_point(data = JL_abs.df, aes(x = log(TL.mean), y = log(JL.mean), color
= Location)) +
  geom_smooth(data = JL_abs.df, aes(x = log(TL.mean), y = log(JL.mean), color
= Location, fill = Location), method = lm, alpha = 0.15, se=FALSE) +
  geom_pointrange(data = JL_abs.df, aes(x = log(TL.mean), y = log(JL.mean),
                                        color = Location, ymin =
log(JL.lower), ymax = log(JL.upper)), fatten = 0, alpha = 0.15) +
  geom_pointrange(data = JL_abs.df, aes(x = log(TL.mean), y = log(JL.mean),
                                        color = Location, xmin =
log(TL.lower), xmax = log(TL.upper)), fatten = 0, alpha = 0.15) +
  scale_color_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) +
  scale_fill_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) + labs(color="Population", fill="Population") +
  xlab("log(Total length)") + ylab("log(Jaw length)") + xlim(2.7,3.4) +
  theme_classic()
```

```r
log_RB_allometry.plot <- ggplot() +
  geom_abline(intercept = -1.72, color = "black", linetype = "dotted") +
  geom_point(data = RB_abs.df, aes(x = log(TL.mean), y = log(RB.mean), color
= Location)) +
  geom_smooth(data = RB_abs.df, aes(x = log(TL.mean), y = log(RB.mean), color
= Location, fill = Location), method = lm, alpha = 0.15, se=FALSE) +
  geom_pointrange(data = RB_abs.df, aes(x = log(TL.mean), y = log(RB.mean),
                                        color = Location, ymin =
log(RB.lower), ymax = log(RB.upper)), fatten = 0, alpha = 0.15) +
  geom_pointrange(data = RB_abs.df, aes(x = log(TL.mean), y = log(RB.mean),
                                        color = Location, xmin =
log(TL.lower), xmax = log(TL.upper)), fatten = 0, alpha = 0.15) +
  scale_color_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) +
  scale_fill_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) + labs(color="Population", fill="Population") +
  xlab("log(Total length)") + ylab("log(Rostrum-to-blowhole)") +
xlim(2.7,3.4) +
  theme_classic()

log_Tail_allometry.plot <- ggplot() +
  geom_abline(intercept = -1.55, color = "black", linetype = "dotted") +
  geom_point(data = Tail_abs.df, aes(x = log(TL.mean), y = log(Tail.mean),
color = Location)) +
  geom_smooth(data = Tail_abs.df, aes(x = log(TL.mean), y = log(Tail.mean),
color = Location, fill = Location), method = lm, alpha = 0.15, se=FALSE) +
  geom_pointrange(data = Tail_abs.df, aes(x = log(TL.mean), y =
log(Tail.mean),
                                          color = Location, ymin =
log(Tail.lower), ymax = log(Tail.upper)), fatten = 0,alpha = 0.15)+
  geom_pointrange(data = Tail_abs.df, aes(x = log(TL.mean), y =
log(Tail.mean),
                                          color = Location, xmin =
log(TL.lower), xmax = log(TL.upper)), fatten = 0, alpha = 0.15) +
  scale_color_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) +
  scale_fill_manual(values = fillcols_a, labels=c("ENP", "New Zealand",
"Chile")) + labs(color="Population", fill="Population") +
  xlab("log(Total length)") + ylab("log(Tail length)") + xlim(2.7,3.4) +
  theme_classic()

allometry.multiplot<- ggarrange(log_EE_allometry.plot, log_JL_allometry.plot,
log_RB_allometry.plot, log_Fs_allometry.plot, log_Fw_allometry.plot,
log_Tail_allometry.plot, nrow=2, ncol=3, common.legend = TRUE,
legend="bottom") + bgcolor("white")

ggsave(allometry.multiplot, filename="./Figures/Barlow_Fig4.png", device =
"png", height=200, width=200, units="mm")
```

```
## Linear models on log-log scale to get slopes
## Run Dixon's Q test to detect any outliers before running each linear model

# EE
dixon.test(log(EE_abs.df$EE.mean[EE_abs.df$Location=="CA"]))

##
##   Dixon test for outliers
##
## data:  log(EE_abs.df$EE.mean[EE_abs.df$Location == "CA"])
## Q = 0.44718, p-value = 0.3092
## alternative hypothesis: lowest value 0.778846611991899 is an outlier

summary(lm(log(EE.mean) ~ log(TL.mean), data =
EE_abs.df[EE_abs.df$Location=="CA",]))

##
## Call:
## lm(formula = log(EE.mean) ~ log(TL.mean), data =
EE_abs.df[EE_abs.df$Location ==
##      "CA", ])
##
## Residuals:
##      Min      1Q  Median      3Q      Max
## -0.10018 -0.02869  0.01335  0.03251  0.05925
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.2005     0.5655  -3.891 0.003003 **
## log(TL.mean)   1.0272     0.1815   5.661 0.000209 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04901 on 10 degrees of freedom
## Multiple R-squared:  0.7622, Adjusted R-squared:  0.7384
## F-statistic: 32.05 on 1 and 10 DF,  p-value: 0.0002093

dixon.test(log(EE_abs.df$EE.mean[EE_abs.df$Location=="NZ"]))

##
##   Dixon test for outliers
##
## data:  log(EE_abs.df$EE.mean[EE_abs.df$Location == "NZ"])
## Q = 0.41717, p-value = 0.3488
## alternative hypothesis: lowest value 0.886587744362414 is an outlier

summary(lm(log(EE.mean) ~ log(TL.mean), data =
EE_abs.df[EE_abs.df$Location=="NZ",]))
```

```
##
## Call:
## lm(formula = log(EE.mean) ~ log(TL.mean), data =
EE_abs.df[EE_abs.df$Location ==
##     "NZ", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.056850 -0.013036  0.004618  0.012006  0.044951
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -1.81401    0.25085  -7.231 6.63e-06 ***
## log(TL.mean)  0.93133    0.08086  11.518 3.41e-08 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02614 on 13 degrees of freedom
## Multiple R-squared:  0.9108, Adjusted R-squared:  0.9039
## F-statistic: 132.7 on 1 and 13 DF,  p-value: 3.411e-08

dixon.test(log(EE_abs.df$EE.mean[EE_abs.df$Location=="Chile"]))

##
##   Dixon test for outliers
##
## data:  log(EE_abs.df$EE.mean[EE_abs.df$Location == "Chile"])
## Q = 0.40686, p-value = 0.204
## alternative hypothesis: highest value 1.16797023146398 is an outlier

summary(lm(log(EE.mean) ~ log(TL.mean), data =
EE_abs.df[EE_abs.df$Location=="Chile",]))

##
## Call:
## lm(formula = log(EE.mean) ~ log(TL.mean), data =
EE_abs.df[EE_abs.df$Location ==
##     "Chile", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.05772 -0.01856 -0.01133  0.01879  0.08439
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.1442     1.3173  -1.628   0.1422
## log(TL.mean)   1.0341     0.4253   2.431   0.0411 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.0455 on 8 degrees of freedom
```

```
## Multiple R-squared:  0.4249, Adjusted R-squared:  0.353
## F-statistic: 5.911 on 1 and 8 DF,  p-value: 0.04112

# JL
dixon.test(log(JL_abs.df$JL.mean[JL_abs.df$Location=="CA"]))

##
##  Dixon test for outliers
##
## data:  log(JL_abs.df$JL.mean[JL_abs.df$Location == "CA"])
## Q = 0.29069, p-value = 0.9713
## alternative hypothesis: lowest value 1.32251054418811 is an outlier

summary(lm(log(JL.mean) ~ log(TL.mean), data =
JL_abs.df[JL_abs.df$Location=="CA",]))

##
## Call:
## lm(formula = log(JL.mean) ~ log(TL.mean), data =
JL_abs.df[JL_abs.df$Location ==
##     "CA", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.047292 -0.031999  0.001039  0.026694  0.077323
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.9947     0.4656  -4.284   0.0016 **
## log(TL.mean)   1.1223     0.1494   7.512 2.04e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04035 on 10 degrees of freedom
## Multiple R-squared:  0.8495, Adjusted R-squared:  0.8344
## F-statistic: 56.43 on 1 and 10 DF,  p-value: 2.035e-05

dixon.test(log(JL_abs.df$JL.mean[JL_abs.df$Location=="NZ"]))

##
##  Dixon test for outliers
##
## data:  log(JL_abs.df$JL.mean[JL_abs.df$Location == "NZ"])
## Q = 0.35811, p-value = 0.4569
## alternative hypothesis: lowest value 1.34978025866897 is an outlier

summary(lm(log(JL.mean) ~ log(TL.mean), data =
JL_abs.df[JL_abs.df$Location=="NZ",]))

##
## Call:
## lm(formula = log(JL.mean) ~ log(TL.mean), data =
```

```
JL_abs.df[JL_abs.df$Location ==
##     "NZ", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.07820 -0.04969  0.01382  0.02363  0.07333
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.5485     0.4247  -3.646  0.00239 **
## log(TL.mean)   1.0073     0.1375   7.327  2.5e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04942 on 15 degrees of freedom
## Multiple R-squared:  0.7816, Adjusted R-squared:  0.767
## F-statistic: 53.68 on 1 and 15 DF,  p-value: 2.499e-06
```

```
dixon.test(log(JL_abs.df$JL.mean[JL_abs.df$Location=="Chile"]))
```

```
##
##   Dixon test for outliers
##
## data:  log(JL_abs.df$JL.mean[JL_abs.df$Location == "Chile"])
## Q = 0.3572, p-value = 0.7563
## alternative hypothesis: highest value 1.66719342011137 is an outlier
```

```
summary(lm(log(JL.mean) ~ log(TL.mean), data =
JL_abs.df[JL_abs.df$Location=="Chile",]))
```

```
##
## Call:
## lm(formula = log(JL.mean) ~ log(TL.mean), data =
JL_abs.df[JL_abs.df$Location ==
##     "Chile", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.064848 -0.029084 -0.007023  0.015020  0.082056
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.5648     1.1701  -3.047  0.01387 *
## log(TL.mean)   1.6474     0.3784   4.354  0.00184 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04468 on 9 degrees of freedom
## Multiple R-squared:  0.6781, Adjusted R-squared:  0.6423
## F-statistic: 18.96 on 1 and 9 DF,  p-value: 0.00184
```

```
# RB
dixon.test(log(RB_abs.df$RB.mean[RB_abs.df$Location=="CA"]))

##
##  Dixon test for outliers
##
## data:  log(RB_abs.df$RB.mean[RB_abs.df$Location == "CA"])
## Q = 0.29039, p-value = 0.9729
## alternative hypothesis: lowest value 1.20271345307593 is an outlier

summary(lm(log(RB.mean) ~ log(TL.mean), data =
RB_abs.df[RB_abs.df$Location=="CA",]))

##
## Call:
## lm(formula = log(RB.mean) ~ log(TL.mean), data =
RB_abs.df[RB_abs.df$Location ==
##      "CA", ])
##
## Residuals:
##      Min         1Q    Median         3Q        Max
## -0.105251 -0.031721 -0.006171  0.031356  0.112717
##
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -1.8501     0.6788  -2.725 0.021361 *
## log(TL.mean)    1.0359     0.2178   4.756 0.000774 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05883 on 10 degrees of freedom
## Multiple R-squared:  0.6934, Adjusted R-squared:  0.6627
## F-statistic: 22.62 on 1 and 10 DF,  p-value: 0.0007735

dixon.test(log(RB_abs.df$RB.mean[RB_abs.df$Location=="NZ"]))

##
##  Dixon test for outliers
##
## data:  log(RB_abs.df$RB.mean[RB_abs.df$Location == "NZ"])
## Q = 0.22909, p-value = 0.7741
## alternative hypothesis: lowest value 1.18432149965191 is an outlier

summary(lm(log(RB.mean) ~ log(TL.mean), data =
RB_abs.df[RB_abs.df$Location=="NZ",]))

##
## Call:
## lm(formula = log(RB.mean) ~ log(TL.mean), data =
RB_abs.df[RB_abs.df$Location ==
##      "NZ", ])
```

```
## 
## Residuals:
##      Min      1Q   Median      3Q      Max
## -0.12220 -0.06053  0.02727  0.04456  0.12395
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.9437     0.7978  -3.690 0.002723 **
## log(TL.mean)    1.4138     0.2602   5.433 0.000115 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.0742 on 13 degrees of freedom
## Multiple R-squared:  0.6942, Adjusted R-squared:  0.6707
## F-statistic: 29.52 on 1 and 13 DF,  p-value: 0.0001145
```

```r
dixon.test(log(RB_abs.df$RB.mean[RB_abs.df$Location=="Chile"]))
```

```
## 
##  Dixon test for outliers
## 
## data:  log(RB_abs.df$RB.mean[RB_abs.df$Location == "Chile"])
## Q = 0.12365, p-value = 0.2296
## alternative hypothesis: lowest value 1.27999734013336 is an outlier
```

```r
summary(lm(log(RB.mean) ~ log(TL.mean), data =
RB_abs.df[RB_abs.df$Location=="Chile",]))
```

```
## 
## Call:
## lm(formula = log(RB.mean) ~ log(TL.mean), data =
RB_abs.df[RB_abs.df$Location ==
##     "Chile", ])
## 
## Residuals:
##       Min       1Q   Median       3Q      Max
## -0.111575 -0.036991  0.009874  0.032526  0.093451
## 
## Coefficients:
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)    -2.1555     1.2530   -1.72   0.1110
## log(TL.mean)    1.1527     0.4058    2.84   0.0149 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.06053 on 12 degrees of freedom
## Multiple R-squared:  0.402,  Adjusted R-squared:  0.3522
## F-statistic: 8.068 on 1 and 12 DF,  p-value: 0.01488
```

```r
# Fw
dixon.test(log(Fw_abs.df$Fw.mean[Fw_abs.df$Location=="CA"]))
```

```
##
##   Dixon test for outliers
##
## data:  log(Fw_abs.df$Fw.mean[Fw_abs.df$Location == "CA"])
## Q = 0.17005, p-value = 0.3884
## alternative hypothesis: highest value 0.277299506415944 is an outlier
```

```r
summary(lm(log(Fw.mean) ~ log(TL.mean), data =
Fw_abs.df[Fw_abs.df$Location=="CA",]))
```

```
##
## Call:
## lm(formula = log(Fw.mean) ~ log(TL.mean), data =
Fw_abs.df[Fw_abs.df$Location ==
##     "CA", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.113352 -0.042860  0.005397  0.047801  0.098603
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.3025     0.8147  -4.054  0.00287 **
## log(TL.mean)   1.0923     0.2615   4.176  0.00239 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07046 on 9 degrees of freedom
## Multiple R-squared:  0.6596, Adjusted R-squared:  0.6218
## F-statistic: 17.44 on 1 and 9 DF,  p-value: 0.00239
```

```r
dixon.test(log(Fw_abs.df$Fw.mean[Fw_abs.df$Location=="NZ"]))
```

```
##
##   Dixon test for outliers
##
## data:  log(Fw_abs.df$Fw.mean[Fw_abs.df$Location == "NZ"])
## Q = 0.3637, p-value = 0.6287
## alternative hypothesis: lowest value -0.0325046681167922 is an outlier
```

```r
summary(lm(log(Fw.mean) ~ log(TL.mean), data =
Fw_abs.df[Fw_abs.df$Location=="NZ",]))
```

```
##
## Call:
## lm(formula = log(Fw.mean) ~ log(TL.mean), data =
Fw_abs.df[Fw_abs.df$Location ==
##     "NZ", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
```

```
## -0.20616 -0.06069 -0.01284  0.06375  0.16121
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.2358     1.2423  -1.800   0.0971 .
## log(TL.mean)   0.7788     0.4011   1.942   0.0760 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.1021 on 12 degrees of freedom
## Multiple R-squared:  0.239,  Adjusted R-squared:  0.1756
## F-statistic:  3.77 on 1 and 12 DF,  p-value: 0.07603
```

```r
dixon.test(log(Fw_abs.df$Fw.mean[Fw_abs.df$Location=="Chile"]))
```

```
##
##  Dixon test for outliers
##
## data:  log(Fw_abs.df$Fw.mean[Fw_abs.df$Location == "Chile"])
## Q = 0.27045, p-value = 0.987
## alternative hypothesis: lowest value -0.0480639931454429 is an outlier
```

```r
summary(lm(log(Fw.mean) ~ log(TL.mean), data =
Fw_abs.df[Fw_abs.df$Location=="Chile",]))
```

```
##
## Call:
## lm(formula = log(Fw.mean) ~ log(TL.mean), data =
Fw_abs.df[Fw_abs.df$Location ==
##     "Chile", ])
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.10541 -0.05508  0.01553  0.05697  0.13929
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -3.7605     1.5366  -2.447   0.0294 *
## log(TL.mean)   1.2502     0.4977   2.512   0.0260 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.07424 on 13 degrees of freedom
## Multiple R-squared:  0.3268, Adjusted R-squared:  0.275
## F-statistic:  6.31 on 1 and 13 DF,  p-value: 0.02599
```

```r
# Fs
dixon.test(log(Fs_abs.df$Fs.mean[Fs_abs.df$Location=="CA"]))
```

```
##
##  Dixon test for outliers
```

```
## 
## data:  log(Fs_abs.df$Fs.mean[Fs_abs.df$Location == "CA"])
## Q = 0.25864, p-value = 0.7699
## alternative hypothesis: lowest value 1.39999984714817 is an outlier
```

```r
summary(lm(log(Fs.mean) ~ log(TL.mean), data =
Fs_abs.df[Fs_abs.df$Location=="CA",]))
```

```
## 
## Call:
## lm(formula = log(Fs.mean) ~ log(TL.mean), data =
Fs_abs.df[Fs_abs.df$Location ==
##     "CA", ])
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.11607 -0.06030 -0.01901  0.06721  0.12543
## 
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -0.7240     1.0459  -0.692   0.5062
## log(TL.mean)   0.7374     0.3358   2.196   0.0557 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## 
## Residual standard error: 0.09045 on 9 degrees of freedom
## Multiple R-squared:  0.3489, Adjusted R-squared:  0.2766
## F-statistic: 4.823 on 1 and 9 DF,  p-value: 0.05569
```

```r
dixon.test(log(Fs_abs.df$Fs.mean[Fs_abs.df$Location=="NZ"]))
```

```
## 
##  Dixon test for outliers
## 
## data:  log(Fs_abs.df$Fs.mean[Fs_abs.df$Location == "NZ"])
## Q = 0.2756, p-value = 0.9206
## alternative hypothesis: lowest value 1.47577589162094 is an outlier
```

```r
summary(lm(log(Fs.mean) ~ log(TL.mean), data =
Fs_abs.df[Fs_abs.df$Location=="NZ",]))
```

```
## 
## Call:
## lm(formula = log(Fs.mean) ~ log(TL.mean), data =
Fs_abs.df[Fs_abs.df$Location ==
##     "NZ", ])
## 
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.11016 -0.01219  0.01087  0.02014  0.10822
## 
```

```
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -0.6485     0.4606  -1.408 0.181000
## log(TL.mean)  0.7327     0.1492   4.912 0.000229 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.05064 on 14 degrees of freedom
## Multiple R-squared:  0.6328, Adjusted R-squared:  0.6065
## F-statistic: 24.12 on 1 and 14 DF,  p-value: 0.0002293

dixon.test(log(Fs_abs.df$Fs.mean[Fs_abs.df$Location=="Chile"]))

##
##  Dixon test for outliers
##
## data:  log(Fs_abs.df$Fs.mean[Fs_abs.df$Location == "Chile"])
## Q = 0.44491, p-value = 0.2552
## alternative hypothesis: highest value 1.76990614477905 is an outlier

summary(lm(log(Fs.mean) ~ log(TL.mean), data =
Fs_abs.df[Fs_abs.df$Location=="Chile",]))

##
## Call:
## lm(formula = log(Fs.mean) ~ log(TL.mean), data =
Fs_abs.df[Fs_abs.df$Location ==
##     "Chile", ])
##
## Residuals:
##       Min       1Q    Median        3Q       Max
## -0.095616 -0.025451 -0.002776  0.012743  0.163422
##
## Coefficients:
##             Estimate Std. Error t value Pr(>|t|)
## (Intercept)  -3.0183     1.4788  -2.041   0.0660 .
## log(TL.mean)  1.4845     0.4799   3.094   0.0102 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.06545 on 11 degrees of freedom
## Multiple R-squared:  0.4652, Adjusted R-squared:  0.4166
## F-statistic:  9.57 on 1 and 11 DF,  p-value: 0.01022

# Tail
dixon.test(log(Tail_abs.df$Tail.mean[Tail_abs.df$Location=="CA"]))

##
##  Dixon test for outliers
##
## data:  log(Tail_abs.df$Tail.mean[Tail_abs.df$Location == "CA"])
```

```
## Q = 0.084293, p-value = 0.4255
## alternative hypothesis: lowest value 1.45649807330994 is an outlier

summary(lm(log(Tail.mean) ~ log(TL.mean), data =
Tail_abs.df[Tail_abs.df$Location=="CA",]))

##
## Call:
## lm(formula = log(Tail.mean) ~ log(TL.mean), data =
Tail_abs.df[Tail_abs.df$Location ==
##     "CA", ])
##
## Residuals:
##          1          2          3          4          5          6
## -0.0001675 -0.0084285  0.0262343 -0.0481266  0.0201263  0.0103620
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -1.3888     0.6378  -2.178   0.0950 .
## log(TL.mean)   0.9423     0.2051   4.593   0.0101 *
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.02995 on 4 degrees of freedom
## Multiple R-squared:  0.8406, Adjusted R-squared:  0.8008
## F-statistic:   21.1 on 1 and 4 DF,  p-value: 0.01008

dixon.test(log(Tail_abs.df$Tail.mean[Tail_abs.df$Location=="NZ"]))

##
##   Dixon test for outliers
##
## data:  log(Tail_abs.df$Tail.mean[Tail_abs.df$Location == "NZ"])
## Q = 0.28682, p-value = 0.7061
## alternative hypothesis: highest value 1.66085616244437 is an outlier

summary(lm(log(Tail.mean) ~ log(TL.mean), data =
Tail_abs.df[Tail_abs.df$Location=="NZ",]))

##
## Call:
## lm(formula = log(Tail.mean) ~ log(TL.mean), data =
Tail_abs.df[Tail_abs.df$Location ==
##     "NZ", ])
##
## Residuals:
##        20         21         22         23         24         25
##  0.035858   0.035001   0.034276   0.021668  -0.129720   0.002917
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
```

```
## (Intercept)    -0.5832      1.2881    -0.453      0.674
## log(TL.mean)    0.6875      0.4182     1.644      0.176
##
## Residual standard error: 0.07244 on 4 degrees of freedom
## Multiple R-squared:  0.4032, Adjusted R-squared:  0.254
## F-statistic: 2.703 on 1 and 4 DF,  p-value: 0.1755
```

```r
dixon.test(log(Tail_abs.df$Tail.mean[Tail_abs.df$Location=="Chile"]))
```

```
##
##   Dixon test for outliers
##
## data:  log(Tail_abs.df$Tail.mean[Tail_abs.df$Location == "Chile"])
## Q = 0.15426, p-value = 0.4102
## alternative hypothesis: lowest value 1.46827167400663 is an outlier
```

```r
summary(lm(log(Tail.mean) ~ log(TL.mean), data =
Tail_abs.df[Tail_abs.df$Location=="Chile",]))
```

```
##
## Call:
## lm(formula = log(Tail.mean) ~ log(TL.mean), data =
Tail_abs.df[Tail_abs.df$Location ==
##     "Chile", ])
##
## Residuals:
##       Min        1Q    Median        3Q       Max
## -0.065579 -0.027709 -0.008747  0.016876  0.086271
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)   -2.4553     1.0146  -2.420  0.03400 *
## log(TL.mean)   1.3059     0.3288   3.972  0.00219 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## Residual standard error: 0.04828 on 11 degrees of freedom
## Multiple R-squared:  0.5892, Adjusted R-squared:  0.5518
## F-statistic: 15.77 on 1 and 11 DF,  p-value: 0.00219
```
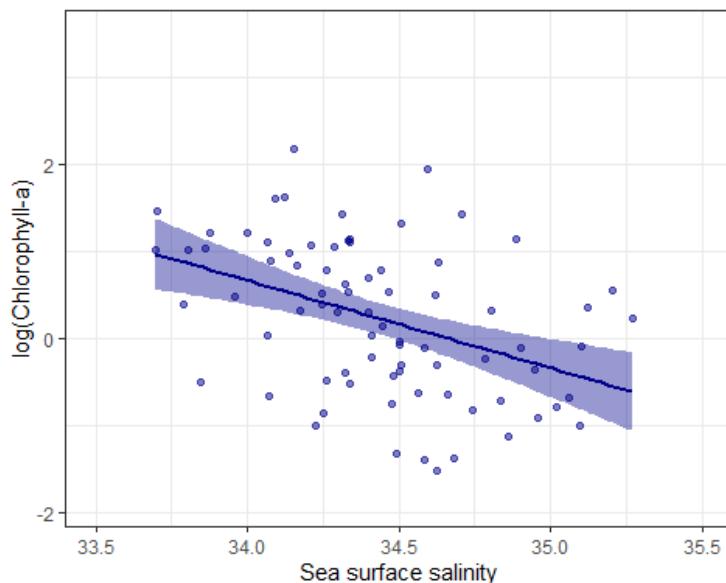
# Salinity and Chlorophyll-a in Chile

Influence of freshwater input on productivity

```
GC_oc.df <- read.csv("GC_oc.csv")

## SSS and Chl-a
SSSvChla.p <- ggplot(data = GC_oc.df, aes(y=log(Chla), x=SSS)) +
  geom_point(color = "dark blue", alpha = 0.5) + geom_smooth(method = lm,
color = "dark blue", fill = "dark blue") +
  theme_bw() + xlim(33.5, 35.5) + xlab("Sea surface salinity") +
ylab("log(Chlorophyll-a)")

SSSvChla.p
```



```
ggsave(SSSvChla.p, filename="./Figures/Barlow_FigS3.png", device = "png",
height=80, width=100, units="mm")

# Pearson's correlation
cor.test(x = GC_oc.df$SSS, y = log(GC_oc.df$Chla),  method = "pearson")

##
##  Pearson's product-moment correlation
##
## data:  GC_oc.df$SSS and log(GC_oc.df$Chla)
## t = -4.0397, df = 76, p-value = 0.0001268
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.5879630 -0.2183404
## sample estimates:
##        cor
## -0.4204429
```