

# Survivorship

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Loading in required libraries.

```
#library(tidyr)
library(tidyverse)

## -- Attaching packages ----- tidyverse 1.3.0 --
## v ggplot2 3.3.3      v purrr   0.3.4
## v tibble  3.1.0      v dplyr  1.0.5
## v tidyr   1.1.3      v stringr 1.4.0
## v readr   1.4.0      v forcats 0.5.1

## -- Conflicts ----- tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()     masks stats::lag()

#library(reshape)
#library(stringr)
library(survival)
#library(ranger)
#library(ggplot2)
#library(dplyr)
library(ggfortify)
#library(gridExtra)
library(survminer)

## Loading required package: ggpubr

#library(graphics)
#library(grid)
library(coxme)

## Loading required package: bdsmatrix
##
## Attaching package: 'bdsmatrix'
##
## The following object is masked from 'package:base':
##
##      backsolve
#library(jstable)
```

Loading dataframes.

```

Data <- read.csv("Data/coral_survivorship_QC.csv", header=T, sep="," , na.string="NA", stringsAsFactors = F)
Sample.Info <- read.csv("Data/Master_Fragment_Sheet_Drive.csv", header=T, sep="," , na.string="NA") %>%
  select(PLUG.ID, Temperature, CO2, Timepoint)
Sample.Info$group <-paste0(Sample.Info$Temperature, " Temperature", " x ",Sample.Info$CO2, " CO2")

Data.Trt <- left_join(Sample.Info, Data, by = "PLUG.ID")
Data.Trt <- Data.Trt %>% filter(Acclimation.End== "alive")

Data.Trt$sampled <- rowSums(Data.Trt[,14:126] == "sampled", na.rm = TRUE)
Data.Trt <- Data.Trt %>% filter(sampled!= 1)

Data.Trt <- Data.Trt %>% select(PLUG.ID, group, Temperature, CO2, Timepoint, Species, Day.0:Day.112)

#Data.Trt$group <- paste0(Data.Trt$Temperature, "_",Data.Trt$CO2)
#Data.Trt$time.group <- paste0(Data.Trt$Timepoint, "_",Data.Trt$Temperature, "_",Data.Trt$CO2)

Data.Trt$time <- rowSums(Data.Trt[,7:119] == "alive", na.rm = TRUE)
#less than 113 = dead
Data.Trt$status <- as.numeric(as.factor(Data.Trt$Day.112))

```

Survivorship analysis.

```

### Montipora capitata
Mc.Data <- Data.Trt %>% filter(Species=="Mcapitata")
unique(Mc.Data$group)

## [1] "Ambient Temperature x Ambient CO2" "High Temperature x Ambient CO2"
## [3] "High Temperature x High CO2"      "Ambient Temperature x High CO2"

mc.cox <- coxph(Surv(time, status) ~ Temperature * CO2, data = Mc.Data)
mc.cox

```

```

## Call:
## coxph(formula = Surv(time, status) ~ Temperature * CO2, data = Mc.Data)
##
##              coef exp(coef) se(coef)      z      p
## TemperatureHigh    1.07538   2.93112  0.83678  1.285 0.199
## CO2High            0.26267   1.30040  0.91291  0.288 0.774
## TemperatureHigh:CO2High 0.03644   1.03711  1.08481  0.034 0.973
##
## Likelihood ratio test=5  on 3 df, p=0.1716
## n= 90, number of events= 17

```

```

Pa.Data <- Data.Trt %>% filter(Species=="Pacuta")
unique(Pa.Data$group)

## [1] "Ambient Temperature x Ambient CO2" "High Temperature x High CO2"
## [3] "Ambient Temperature x High CO2"    "High Temperature x Ambient CO2"

pa.cox <- coxph(Surv(time, status) ~ Temperature * CO2, data = Pa.Data)
pa.cox

```

```

## Call:
## coxph(formula = Surv(time, status) ~ Temperature * CO2, data = Pa.Data)
##
##              coef exp(coef) se(coef)      z      p
## TemperatureHigh    0.9266   2.5260  0.4237  2.187 0.0288

```

```
## CO2High          -1.7174    0.1795    0.7907 -2.172 0.0299
## TemperatureHigh:CO2High  2.0893    8.0795    0.8446  2.474 0.0134
##
## Likelihood ratio test=40.1 on 3 df, p=1.013e-08
## n= 95, number of events= 57
#Capture statistical results to file

Mcap.info <- as.character("Montipora capitata")
Mcap.Stats <- coxph(Surv(time, status) ~ Temperature * CO2, data = Mc.Data)
Pacuta.info <- as.character("Pocillopora acuta")
Pacuta.Stats <- coxph(Surv(time, status) ~ Temperature * CO2, data = Pa.Data)

capture.output(Mcap.info, Mcap.Stats, Pacuta.info, Pacuta.Stats, file="Output/Survivorship_Stat_Results.txt")

Plotting survivorship analysis.

## Montipora capitata
#create survivorship curve
mc <- survfit(Surv(time, status) ~ Temperature + CO2, data = Mc.Data)
mc

## Call: survfit(formula = Surv(time, status) ~ Temperature + CO2, data = Mc.Data)
##
##
##              n events median 0.95LCL 0.95UCL
## Temperature=Ambient, CO2=Ambient 22      2      NA      NA      NA
## Temperature=Ambient, CO2=High    26      3      NA      NA      NA
## Temperature=High, CO2=Ambient    20      5      NA      NA      NA
## Temperature=High, CO2=High       22      7      NA      NA      NA

splots <- list()

splots[[1]] <- ggsurvplot(mc, data=Mc.Data, size = 1, # change line size
  fun="pct", #plot survival probability in percent
  linetype = "strata", # change line type by groups
  break.time.by = 7, # break time axis
  palette = c("lightblue", "blue", "salmon", "red3"), # custom color palette
  conf.int = TRUE, # Add confidence interval
  legend.title = "", # remove legend title
  xlab = "Timepoint",
  font.title = c(14, "bold.italic", "black"), #title italicized
  font.tickslab = c(8, "black"),
  legend.labs = c("ATAC", "ATHC", "HTAC", "HTHC"), # Assign legend labels
  legend=c(0.115, 0.5))

splots[[1]]$plot <- splots[[1]]$plot +
  scale_x_continuous(breaks = sort(c(1,2,8,15,29,43,57,85,112)), labels = c("Day 1", "Day 2", "1 week",
  geom_vline(xintercept = 61, linetype = "dotted") +
  theme(axis.text.x = element_text(angle = 60, vjust = 1.2, hjust = 1.3))

## Scale for 'x' is already present. Adding another scale for 'x', which will
## replace the existing scale.

## Pocillopora acuta

pa <- survfit(Surv(time, status) ~ Temperature + CO2, data = Pa.Data)
pa
```

```
## Call: survfit(formula = Surv(time, status) ~ Temperature + CO2, data = Pa.Data)
```

```
##
```

```
##
```

	n	events	median	0.95LCL	0.95UCL
## Temperature=Ambient, CO2=Ambient	21	8	NA	58	NA
## Temperature=Ambient, CO2=High	21	2	NA	NA	NA
## Temperature=High, CO2=Ambient	23	20	81	77	91
## Temperature=High, CO2=High	30	27	77	73	81

```
## Temperature=Ambient, CO2=Ambient 21      8      NA      58      NA
```

```
## Temperature=Ambient, CO2=High 21      2      NA      NA      NA
```

```
## Temperature=High, CO2=Ambient 23     20     81     77     91
```

```
## Temperature=High, CO2=High 30     27     77     73     81
```

```
splots[[2]] <- ggsurvplot(pa, data=Pa.Data, size = 1, # change line size
  linetype = "strata", # change line type by groups
  break.time.by = 7, # break time axis
  palette = c("lightblue", "blue", "salmon", "red3"), # custom color palette
  conf.int = TRUE, # Add confidence interval
  legend.title = "", # remove legend title
  xlab = "Timepoint",
  font.title = c(14, "bold.italic", "black"), #title italicized
  font.tickslab = c(8, "black"),
  legend.labs = c("ATAC", "ATHC", "HTAC", "HTHC"), # Assign legend labels
  legend = "none")
```

```
splots[[2]]$plot <- splots[[2]]$plot +
  scale_x_continuous(breaks = sort(c(1,2,8,15,29,43,57,85,112)), labels = c("Day 1", "Day 2", "1 week",
  geom_vline(xintercept = 61, linetype = "dotted") +
  theme(axis.text.x = element_text(angle = 60, vjust = 1.2, hjust = 1.3))
```

```
## Scale for 'x' is already present. Adding another scale for 'x', which will
```

```
## replace the existing scale.
```

```
  # theme(axis.text.x = element_text(vjust = grid::unit(c(-2,0,0,0,0,0,0,0,0)), "points"))
```

```
surv <- arrange_ggsurvplots(splots, print = FALSE, ncol = 2, nrow = 1)
```

```
ggsave("Output/Survivorship.pdf", surv, width = 11, height = 6)
```

```
ggsave("Output/Survivorship.png", surv, width = 11, height = 6)
```