

Survivorship

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Installing and loading required libraries.

```
if ("tidyr" %in% rownames(installed.packages()) == 'FALSE') install.packages('tidyr')
if ("tidyverse" %in% rownames(installed.packages()) == 'FALSE') install.packages('tidyverse')
if ("reshape" %in% rownames(installed.packages()) == 'FALSE') install.packages('reshape')
if ("stringr" %in% rownames(installed.packages()) == 'FALSE') install.packages('stringr')
if ("survival" %in% rownames(installed.packages()) == 'FALSE') install.packages('survival')
if ("ranger" %in% rownames(installed.packages()) == 'FALSE') install.packages('ranger')
if ("ggplot2" %in% rownames(installed.packages()) == 'FALSE') install.packages('ggplot2')
if ("dplyr" %in% rownames(installed.packages()) == 'FALSE') install.packages('dplyr')
if ("ggfortify" %in% rownames(installed.packages()) == 'FALSE') install.packages('ggfortify')
if ("gridExtra" %in% rownames(installed.packages()) == 'FALSE') install.packages('gridExtra')
if ("survminer" %in% rownames(installed.packages()) == 'FALSE') install.packages('survminer')
```

#Read in required libraries

Include Versions of libraries

```
library(tidyr)
```

```
## Warning: package 'tidyr' was built under R version 3.6.2
```

```
library(tidyverse)
```

```
## -- Attaching packages -----
```

```
## v ggplot2 3.3.1      v dplyr   1.0.0
```

```
## v tibble  3.0.1      v stringr 1.4.0
```

```
## v readr   1.3.1      v forcats 0.4.0
```

```
## v purrr   0.3.4
```

```
## Warning: package 'ggplot2' was built under R version 3.6.2
```

```
## Warning: package 'tibble' was built under R version 3.6.2
```

```
## Warning: package 'purrr' was built under R version 3.6.2
```

```
## Warning: package 'dplyr' was built under R version 3.6.2
```

```
## -- Conflicts -----
```

```
## x dplyr::filter() masks stats::filter()
```

```
## x dplyr::lag()     masks stats::lag()
```

```
library(reshape)
```

```
##
```

```
## Attaching package: 'reshape'
```

```
## The following object is masked from 'package:dplyr':
```

```
##
```

```
##      rename
## The following objects are masked from 'package:tidyr':
##
##      expand, smiths
library(stringr)
library(survival)
library(ranger)
library(ggplot2)
library(dplyr)
library(ggfortify)
```

```
## Warning: package 'ggfortify' was built under R version 3.6.2
```

```
library(gridExtra)
```

```
##
## Attaching package: 'gridExtra'
## The following object is masked from 'package:dplyr':
##
##      combine
```

```
library(survminer)
```

```
## Warning: package 'survminer' was built under R version 3.6.2
```

```
## Loading required package: ggpubr
```

```
## Loading required package: magrittr
```

```
##
## Attaching package: 'magrittr'
## The following object is masked from 'package:purrr':
##
##      set_names
```

```
## The following object is masked from 'package:tidyr':
##
##      extract
```

Loading dataframes.

```
Data <- read.csv("Physiology_variables/Survivorship/coral_survivorship_QC.csv", header=T, sep=",", na.s
Tank.Info <- read.csv("Environmental_data/Tank_to_Treatment.csv", header=T, sep=",", na.string="NA") #r
Data.Trt <- merge(Data, Tank.Info, by="Tank")
```

Replace sampled with alive.

```
Data.Trt.x <- Data.Trt %>% mutate_if(is.character, str_replace_all, pattern = 'sampled', replacement =
Data.Trt.x$lifespan <- rowSums(Data.Trt.x[,10:120] == "alive")
Data.Trt.x$status <- as.numeric(as.factor(Data.Trt.x$Day.110))
```

Survivorship analysis.

```
### Montipora capitata
Mc.Data <- subset(Data.Trt.x, Species=="Mcapitata")
Mc.Data$group <- paste0(Mc.Data$Treatment)
Mc.km <- with(Mc.Data, Surv(lifespan, status))
```

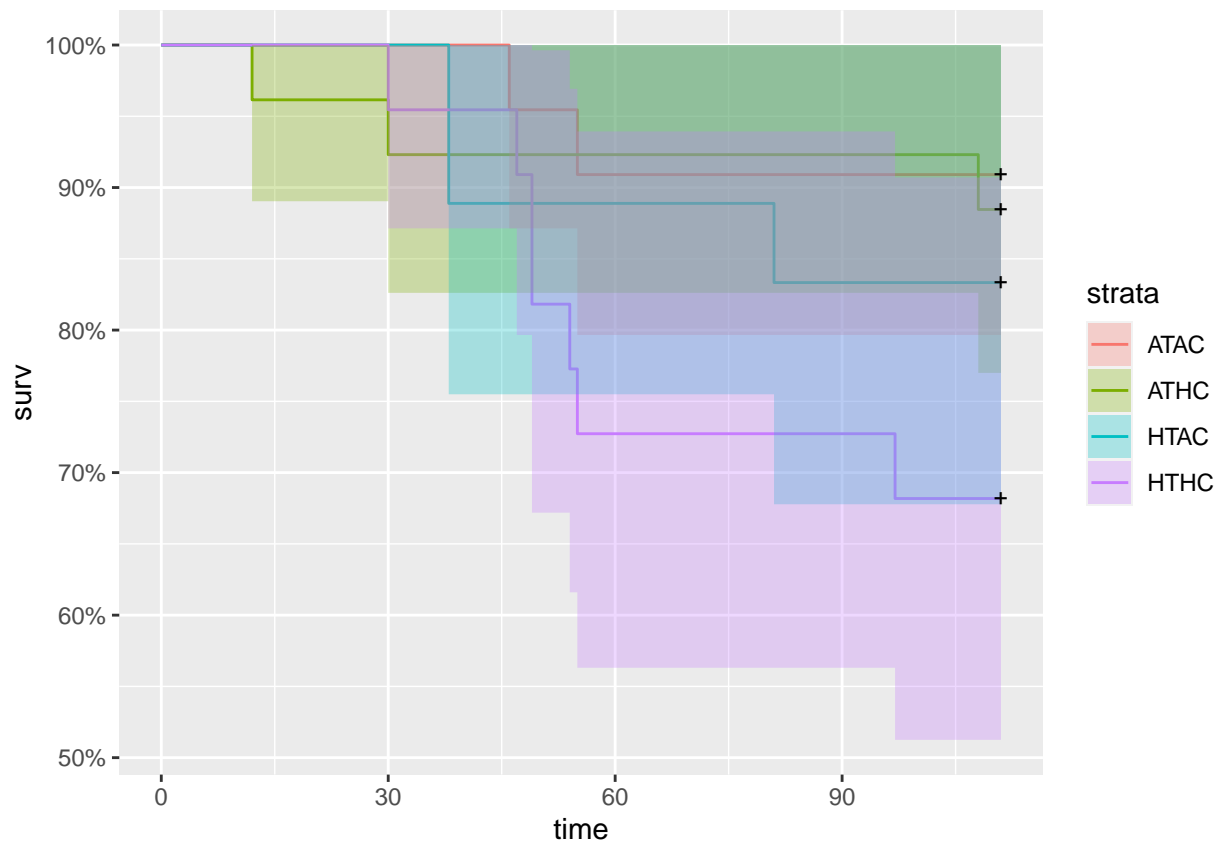
```

Mc.km_fit <- survfit(Surv(lifespan, status) ~ Treatment, data=Mc.Data)
summary(Mc.km_fit)

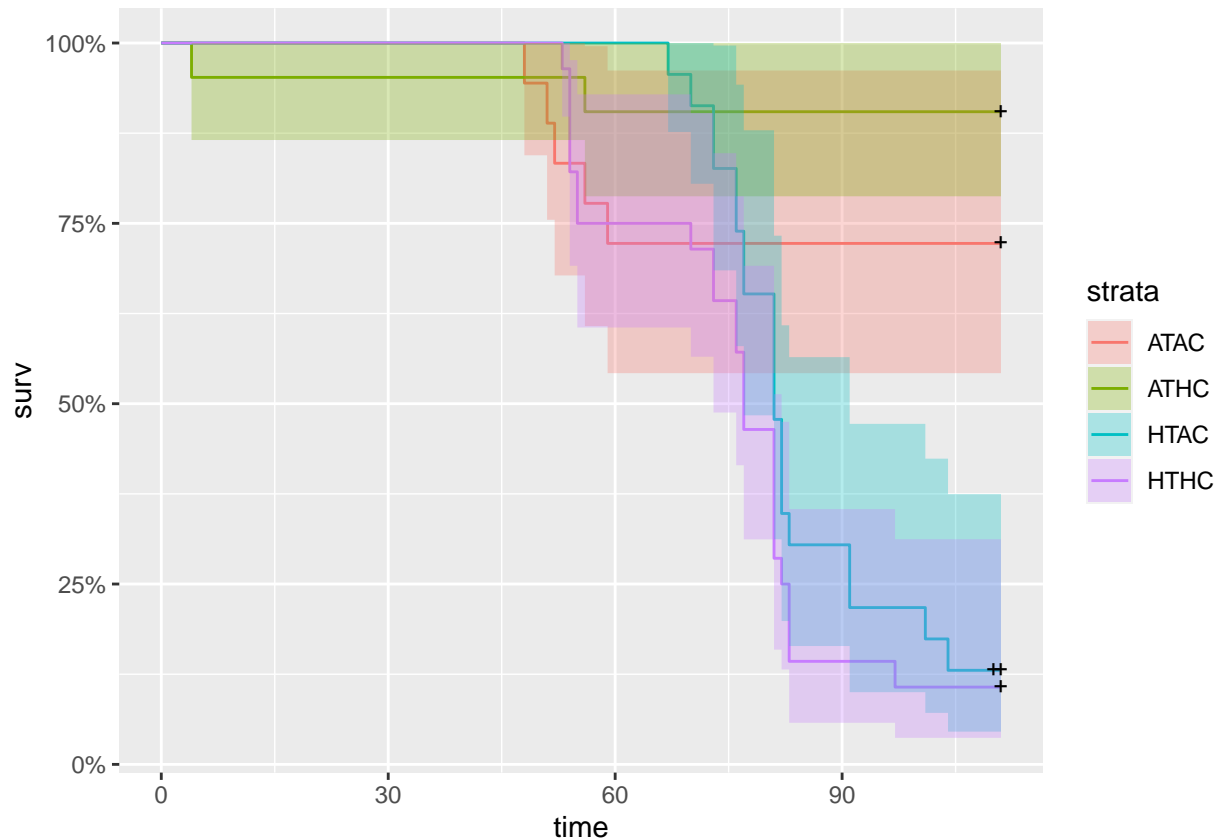
## Call: survfit(formula = Surv(lifespan, status) ~ Treatment, data = Mc.Data)
##
## 354 observations deleted due to missingness
##
##           Treatment=ATAC
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    46     22      1   0.955  0.0444    0.871      1
##    55     21      1   0.909  0.0613    0.797      1
##
##           Treatment=ATHC
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    12     26      1   0.962  0.0377    0.890      1
##    30     25      1   0.923  0.0523    0.826      1
##   108     24      1   0.885  0.0627    0.770      1
##
##           Treatment=HTAC
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    38     18      2   0.889  0.0741    0.755      1
##    81     16      1   0.833  0.0878    0.678      1
##
##           Treatment=HTHC
##   time n.risk n.event survival std.err lower 95% CI upper 95% CI
##    30     22      1   0.955  0.0444    0.871    1.000
##    47     21      1   0.909  0.0613    0.797    1.000
##    49     20      2   0.818  0.0822    0.672    0.996
##    54     18      1   0.773  0.0893    0.616    0.969
##    55     17      1   0.727  0.0950    0.563    0.939
##    97     16      1   0.682  0.0993    0.513    0.907

cols <- c("lightblue", "blue", "salmon", "red3")
MC.sur <- summary(Mc.km_fit, times = c(1:58))
Mc.km_fit <- survfit(Surv(lifespan, status) ~ Treatment, data=Mc.Data)
autoplot(Mc.km_fit)

```



```
### Pocillopora acuta
Pa.Data <- subset(Data.Trt.x, Species=="Pacuta")
Pa.km <- with(Pa.Data, Surv(lifespan, status))
Pa.km_fit <- survfit(Surv(lifespan, status) ~ Treatment, data=Pa.Data) ##Origin
Pa.sur <- summary(Pa.km_fit, times = c(1:58))
autoplot(Pa.km_fit)
```



Plotting survivorship analysis.

Montipora capitata

```
splots <- list()
```

```
splots[[1]] <- ggsurvplot(Mc.km_fit, data=Mc.Data, size = 1, # change line size
  linetype = "strata", # change line type by groups
  break.time.by = 7, # break time axis
  palette = c("blue", "lightblue", "salmon", "red3"), # custom color palette
  conf.int = TRUE, # Add confidence interval
  legend.title = "", # remove legend title
  title = "C) Montipora capitata",
  xlab = "Time in days",
  font.title = c(14, "bold.italic", "black"), #title italicized
  font.tickslab = c(8, "bold", "black"),
  legend.labs = c("ATAC", "ATHC", "HTAC", "HTHC"), pval = TRUE, # Add p-value and change legend
  legend=c(0.115, 0.5))
```

Pocillopora acuta

```
splots[[2]] <- ggsurvplot(Pa.km_fit, data=Pa.Data, size = 1, # change line size
  linetype = "strata", # change line type by groups
  break.time.by = 7, # break time axis
  palette = c("blue", "lightblue", "salmon", "red3"), # custom color palette
  conf.int = TRUE, # Add confidence interval
  legend.title = "", # remove legend title
  title = "D) Pocillopora acuta",
```

```

      xlab = "Time in days",
      font.title = c(14, "bold.italic", "black"), #title italicized
      font.tickslab = c(8, "bold", "black"),
      legend.labs = c("ATAC", "ATHC", "HTAC", "HTHC"), pval = TRUE, # Add p-value and change legend
      legend = "none")

surv <- arrange_ggsurvplots(splots, print = FALSE, ncol = 2, nrow = 1)
ggsave("Output/All_survivorship.pdf", surv, width = 10,height = 4)

ggsave("Output/All_survivorship.png", surv, width = 10,height = 4)

```