Reproducing Powell et Al. 2017

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#Reproducing code from #[@Powell:2017dd]

#@article{RN14, #author = {Powell, Scott and Donaldson-Matasci, Matina and Woodrow-Tomizuka, Augustus and Dornhaus, Anna}, #title = {Context-dependent defences in turtle ants: Resource defensibility and threat #level induce dynamic shifts in soldier deployment}, #journal = {Functional Ecology}, #volume = {31}, #number = {12}, #pages = {2287-2298}, #ISSN = {0269-8463}, #DOI = {10.1111/1365-2435.12926}, #url = {https://besjournals.onlinelibrary.wiley.com/doi/abs/10.1111/1365-2435.12926}, #year = {2017}, #type = {Journal Article} }

#STUCK: I cannot figure out how to put this paper into the necessary citation format from endnote into a bibliography file

#COMPLETED: loaded in data and packages

```
rm(list=ls())

library(survival)
```

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

```
library(tidyverse)
```

```
## -- Attaching packages ---------------------------------------------- tidyverse 1.3.0 --
```

```
## v ggplot2 3.3.2     v purrr   0.3.3
## v tibble  3.0.3     v dplyr   0.8.3
## v tidyr   1.0.0     v stringr 1.4.0
## v readr   1.3.1     v forcats 0.5.0
```

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

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

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

```
knitr::opts_chunk$set(echo = TRUE)
```

#package 'survival' was built under R version 3.6.2 and was downloaded in the binary format, not the source version

```
Collection_data <- read_csv("~/Google Drive/AA Graduate /Data and Software Tools EBIO6660/data/Cephalot
```

```
## Parsed with column specification:
## cols(
##   colony = col_character(),
##   nest_no = col_double(),
##   workers = col_double(),
##   soldiers = col_double(),
##   ent_area_mm = col_double()
## )
```

```
Field_expt <- read_csv("~/Google Drive/AA Graduate /Data and Software Tools EBIO6660/data/Cephalotes_ro
```

```
## Parsed with column specification:
## cols(
##   tree = col_character(),
##   entrance_size = col_character(),
##   nest_pop = col_character(),
##   week_death = col_character()
## )
```

```
Lab_expt <- read_csv("~/Google Drive/AA Graduate /Data and Software Tools EBIO6660/data/Cephalotes_rohw
```

```
## Parsed with column specification:
## cols(
##   colony = col_character(),
##   treatment = col_character(),
##   position = col_double(),
##   entrance = col_character(),
##   treatment_phase = col_character(),
##   workers = col_character(),
##   soldiers = col_double(),
##   eggs = col_character(),
##   larvae = col_character(),
##   pupae = col_character()
## )
```

#data was readily available by the author in csv format. So far no metadata or code has been located for this paper.

#STILL WORKING ON IT: Next I will work with the data to generate summarizing graphics and work on the first boxplot which I seek to reproduce. Next I will familiarize myself with the survival package in order to generate the survivorship curve.

PROGRESS REPORT OCT 25

##STUCK: need to understand difference between col character and col double: running the above data into R gets this in response (below), likely because Powell used solely R (not R Studio) to peform his analysis. Code has not yet been receieved, but contact was made. #Parsed with column specification: cols(colony = col_character(), nest_no = col_double(), workers = col_double(), soldiers = col_double(),

ent_area_mm = col_double()) Parsed with column specification: cols(tree = col_character(), entrance_size = col_character(), nest_pop = col_character(), week_death = col_character()) Parsed with column specification: cols(colony = col_character(), treatment = col_character(), position = col_double(), entrance = col_character(), treatment_phase = col_character(), workers = col_character(), soldiers = col_double(), eggs = col_character(), larvae = col_character(), pupae = col_character())