

Sehner_ex2_cleancode

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This code is part of the data analyses for the manuscript titled “Timing of nanoplastic exposure during infection impacts viability of host in an aquatic host-parasite system” by Kristel F. S´anchez, Kyla Sehner, Vanderville Villegas, Amruta Rajarajan, Justyna Wolinska. This document the analyses of K. Sehners experiment 2. This experiment assessed the impact of NP exposure on Daphnia at various stages of parasite development and its effect on infection progression. This experiment was inspired by te fact that previous experiment (experiment 1) found no effect of exposing fungal parasite spores to nanoplastic on infection traits, however other studies suggest nanoplastics can impact disease by making it hosts more susceptible to parasite transmission (at some cost to the parasite tho!). This suggest that the mechanism of this is through the host since in those studies the hosts was always exposed to nanoplastics. This experiment added nanoplastics at different stages of the disease to try to get at how nanoplastics promote or disrupt disease.

```
setwd("U://K Sehner MS/code")
```

Packages needed

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:stats':  
##  
##   filter, lag
```

```
## The following objects are masked from 'package:base':  
##  
##   intersect, setdiff, setequal, union
```

```
library(kableExtra)
```

```
## Warning: package 'kableExtra' was built under R version 4.4.2
```

```
##  
## Attaching package: 'kableExtra'
```

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

```
library(tidyverse)
```

```
## — Attaching core tidyverse packages — tidyverse 2.0.0 —
## ✓ forcats 1.0.0      ✓ readr 2.1.5
## ✓ ggplot2 3.5.1      ✓ stringr 1.5.1
## ✓ lubridate 1.9.3    ✓ tibble 3.2.1
## ✓ purrr 1.0.2       ✓ tidyr 1.3.1
```

```
## — Conflicts — tidyverse_conflicts() —
## ✗ dplyr::filter() masks stats::filter()
## ✗ kableExtra::group_rows() masks dplyr::group_rows()
## ✗ dplyr::lag() masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to be
come errors
```

```
library(descr)
```

```
## Warning: package 'descr' was built under R version 4.4.2
```

```
library(MASS)
```

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

```
library(pheatmap)
library(Rmisc)
```

```
## Loading required package: lattice
## Loading required package: plyr
## -----
## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)
## -----
##
## Attaching package: 'plyr'
##
## The following object is masked from 'package:purrr':
##
##     compact
##
## The following objects are masked from 'package:dplyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize
```

```
library(survival)
library(survminer)
```

```
## Warning: package 'survminer' was built under R version 4.4.2
```

```
## Loading required package: ggpubr
##
## Attaching package: 'ggpubr'
##
## The following object is masked from 'package:plyr':
##
##     mutate
##
##
## Attaching package: 'survminer'
##
## The following object is masked from 'package:survival':
##
##     myeloma
```

```
dat2<-read.csv('Ex2_stat.csv')
```

I will create a new columns for the day of nanoplastic exposure. It will be a categorical column, specifying the treatment/time at which hosts were exposed to nanoplastics

```

dat2 <- dat2 %>% mutate(NP_treat = case_when(
  timepoint == 1 ~ "Control",
  timepoint == 2 ~ "Full-time",
  timepoint == 3 ~ "1",
  timepoint == 4 ~ "4",
  timepoint == 5 ~ "7",
  timepoint == 6 ~ "10",
))

```

We did not run an interaction term because we found high collinearity (VIF >8 for most variables. VIF>5 suggest collinearity) between size and time of NP treatment. That data exploration is in another file that K. Sanchez can share if people are curious. So the rest of the models presented here will either include just NP time as a predictor variable or both NP time and Size but without the interaction, according to whichever happens to be a better model (overdispersion parameters and AIC).

```

infexp2glm <- glm(infectivity ~ NP_treat + Size , family = binomial, data=dat2)
summary(infexp2glm)

```

```

##
## Call:
## glm(formula = infectivity ~ NP_treat + Size, family = binomial,
##      data = dat2)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.580093    0.679542  -0.854   0.3933
## NP_treat10     0.912680    0.547018   1.668   0.0952 .
## NP_treat4      0.470672    0.571124   0.824   0.4099
## NP_treat7      0.795514    0.567340   1.402   0.1609
## NP_treatControl 0.831407    0.846017   0.983   0.3257
## NP_treatFull-time 1.009542    0.610601   1.653   0.0983 .
## Size          0.003591    0.007316   0.491   0.6236
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 196.25  on 143  degrees of freedom
## Residual deviance: 191.92  on 137  degrees of freedom
## AIC: 205.92
##
## Number of Fisher Scoring iterations: 4

```

```

car::Anova(infexp2glm, type = 2)

```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: infectivity
##          LR Chisq Df Pr(>Chisq)
## NP_treat   4.1863  5    0.5229
## Size       0.2413  1    0.6233
```

```
infSE<-summarySE(dat2, measurevar= 'infectivity', groupvars = c('NP_treat', 'Size'), na.rm=TRUE)
infSE
```

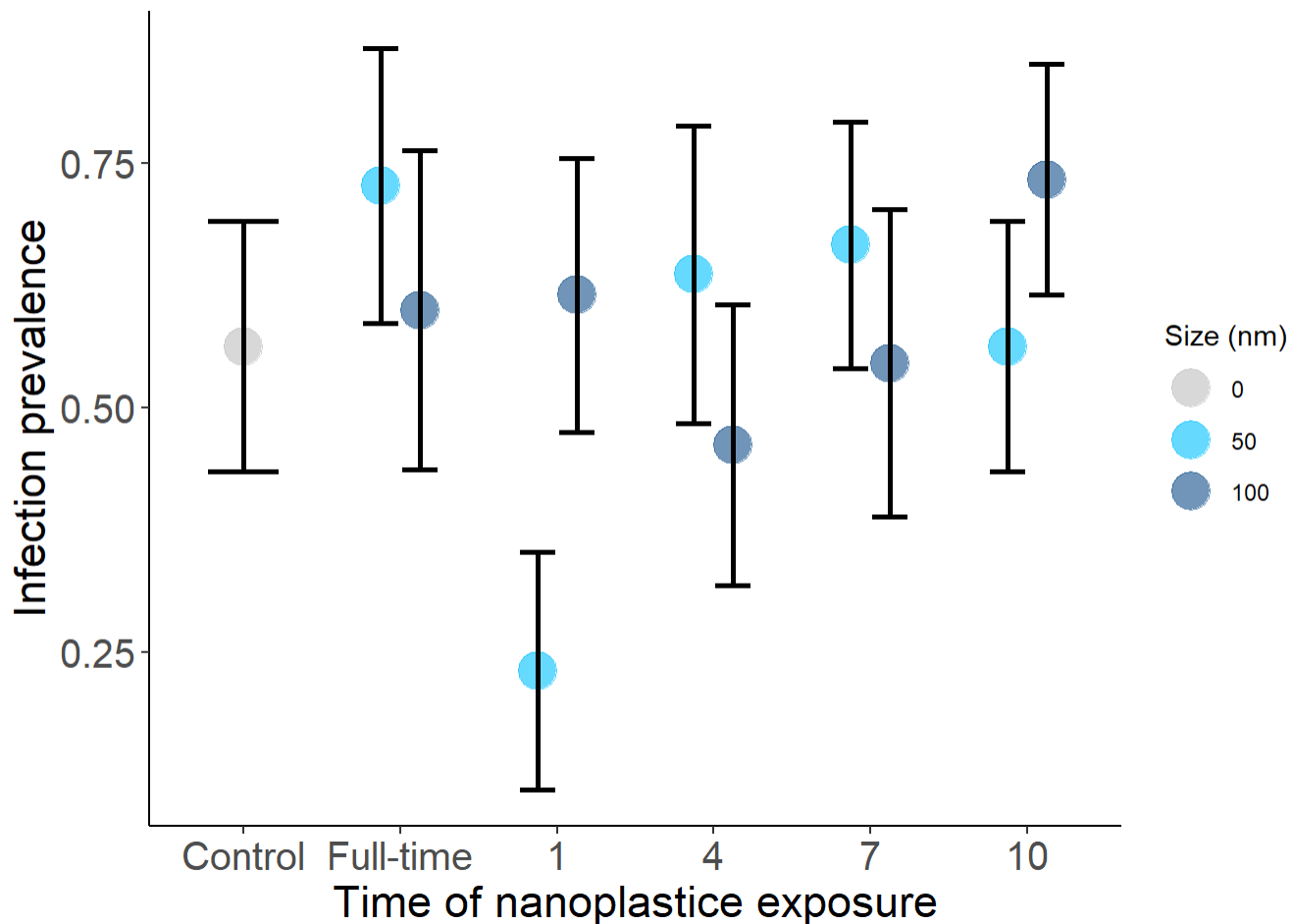
	NP_treat	Size	N	infectivity	sd	se	ci
## 1	1	50	13	0.2307692	0.4385290	0.1216261	0.2650004
## 2	1	100	13	0.6153846	0.5063697	0.1404417	0.3059961
## 3	10	50	16	0.5625000	0.5123475	0.1280869	0.2730107
## 4	10	100	15	0.7333333	0.4577377	0.1181874	0.2534867
## 5	4	50	11	0.6363636	0.5045250	0.1521200	0.3389445
## 6	4	100	13	0.4615385	0.5188745	0.1439099	0.3135527
## 7	7	50	15	0.6666667	0.4879500	0.1259882	0.2702177
## 8	7	100	11	0.5454545	0.5222330	0.1574592	0.3508409
## 9	Control	0	16	0.5625000	0.5123475	0.1280869	0.2730107
## 10	Full-time	50	11	0.7272727	0.4670994	0.1408358	0.3138016
## 11	Full-time	100	10	0.6000000	0.5163978	0.1632993	0.3694087

```
level_order <- c('Control', 'Full-time', '1', '4', '7', '10')
```

```
p1<-ggplot()+
  geom_point(data=infSE, aes(x=factor(NP_treat, level = level_order), y=infectivity, color=factor(Size)), size=7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=infSE, aes(x=factor(NP_treat, level = level_order), ymin=infectivity-se, ymax=infectivity+se), size=1, width=0.5, position= position_dodge2()) +
  scale_color_manual(values = c('grey',"deepskyblue", "dodgerblue4"),
    name = c("Size (nm)"))+
  ylab("Infection prevalence") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
    axis.text.y = element_text(size = 15),
    axis.title.x = element_text(size = 17),
    axis.title.y = element_text(size = 17))
```

```
## Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.
## i Please use `linewidth` instead.
## This warning is displayed once every 8 hours.
## Call `lifecycle::last_lifecycle_warnings()` to see where this warning was
## generated.
```

p1



```

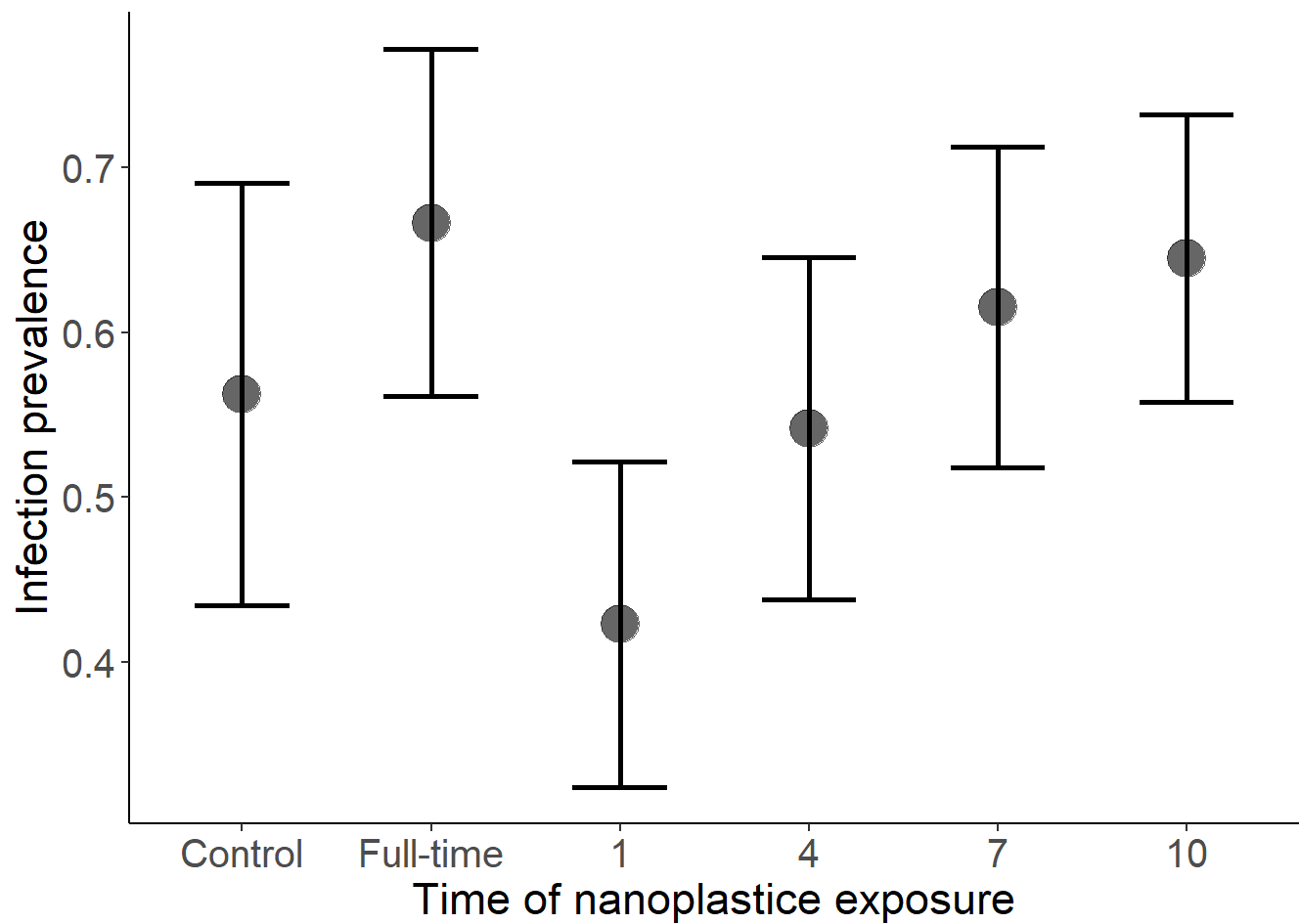
inf2SE<-summarySE(dat2, measurevar= 'infectivity', groupvars = c('NP_treat'))

level_order <- c('Control', 'Full-time', '1', '4', '7', '10')

p2<-ggplot()+
  geom_point(data=inf2SE, aes(x=factor(NP_treat, level = level_order), y=infectivity), size=
7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=inf2SE, aes(x=factor(NP_treat, level = level_order), ymin=infectivity-s
e, ymax=infectivity+se), size=1, width=0.5, position= position_dodge2()) +
  ylab("Infection prevalence") +
  xlab("Time of nanoplastics exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 17))

```

p2

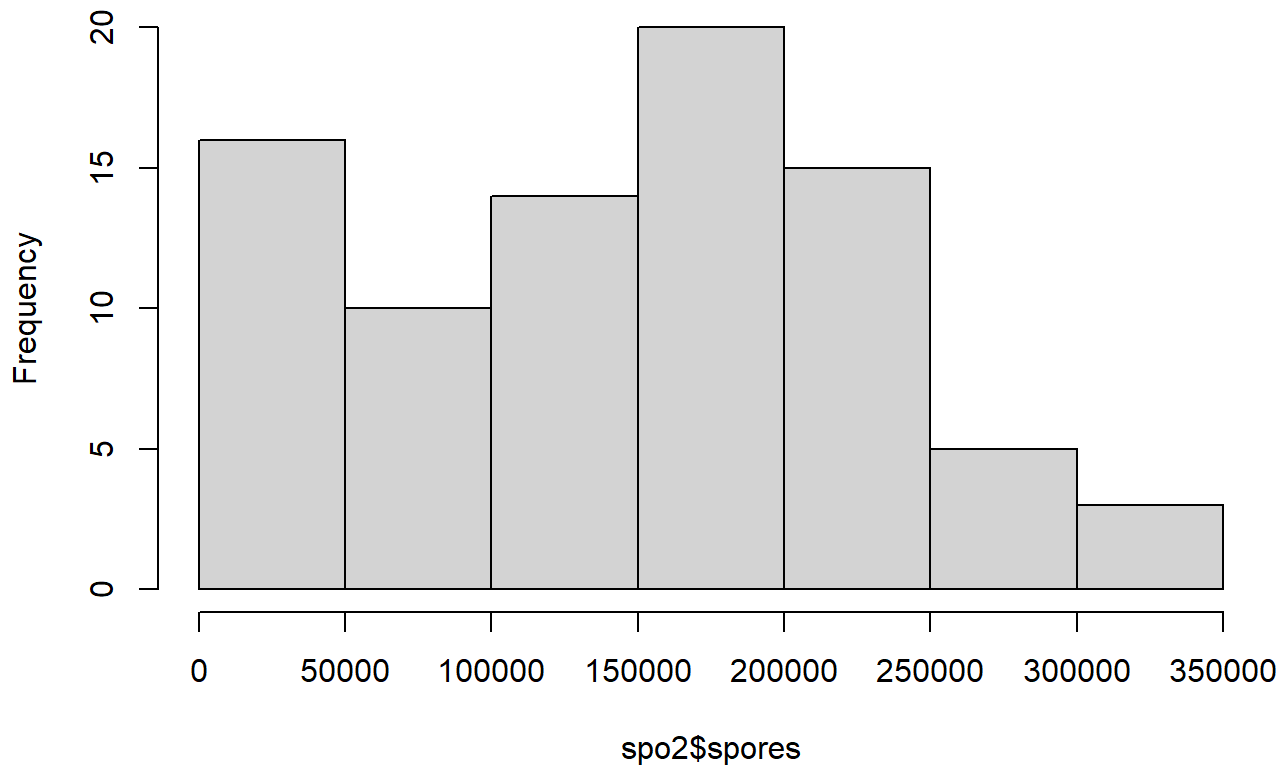


Spore production

```
spo2 <- subset(dat2, infectivity == 1)
```

```
hist(spo2$spores)
```

Histogram of spo2\$spores



```
shapiro.test(spo2$spores)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  spo2$spores  
## W = 0.96868, p-value = 0.04031
```

```
spoglm1 <- glm(spores ~ NP_treat + Size, family = Gamma, data = spo2)  
summary(spoglm1)
```

```
##
## Call:
## glm(formula = spores ~ NP_treat + Size, family = Gamma, data = spo2)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  2.638e-06  1.818e-06   1.451   0.1509
## NP_treat10    2.415e-06  1.343e-06   1.799   0.0760 .
## NP_treat4     1.917e-06  1.450e-06   1.322   0.1901
## NP_treat7     3.848e-06  1.592e-06   2.418   0.0180 *
## NP_treatControl 3.367e-06  2.184e-06   1.541   0.1274
## NP_treatFull-time 2.795e-06  1.528e-06   1.830   0.0712 .
## Size         2.920e-08  1.975e-08   1.478   0.1435
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3652924)
##
##    Null deviance: 51.252  on 82  degrees of freedom
## Residual deviance: 48.361  on 76  degrees of freedom
## AIC: 2138.1
##
## Number of Fisher Scoring iterations: 6
```

```
car::Anova(spo2, type = 2)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: spores
##           LR Chisq Df Pr(>Chisq)
## NP_treat   6.5784  5    0.2539
## Size       2.1812  1    0.1397
```

```
spoSE<-summarySE(spo2, measurevar= 'spores', groupvars = c('NP_treat', 'Size'), na.rm=TRUE)
spoSE
```

```
##      NP_treat Size  N   spores      sd      se      ci
## 1          1   50  3 220000.00 49796.46 28750.00 123701.27
## 2          1  100  8 188906.25 66202.60 23406.15  55346.76
## 3         10   50  9 146250.00 82665.55 27555.18  63542.37
## 4         10  100 11 131363.64 91238.79 27509.53  61295.05
## 5          4   50  7 170535.71 94942.02 35884.71  87806.73
## 6          4  100  6 128750.00 82078.47 33508.39  86136.07
## 7          7   50 10 130125.00 98837.78 31255.25  70704.29
## 8          7  100  6  99166.67 89650.94 36599.84  94082.90
## 9    Control    0  9 166527.78 96508.94 32169.65  74183.34
## 10 Full-time   50  8 153125.00 75781.64 26792.86  63355.04
## 11 Full-time  100  6 108958.33 62321.83 25442.78  65402.75
```

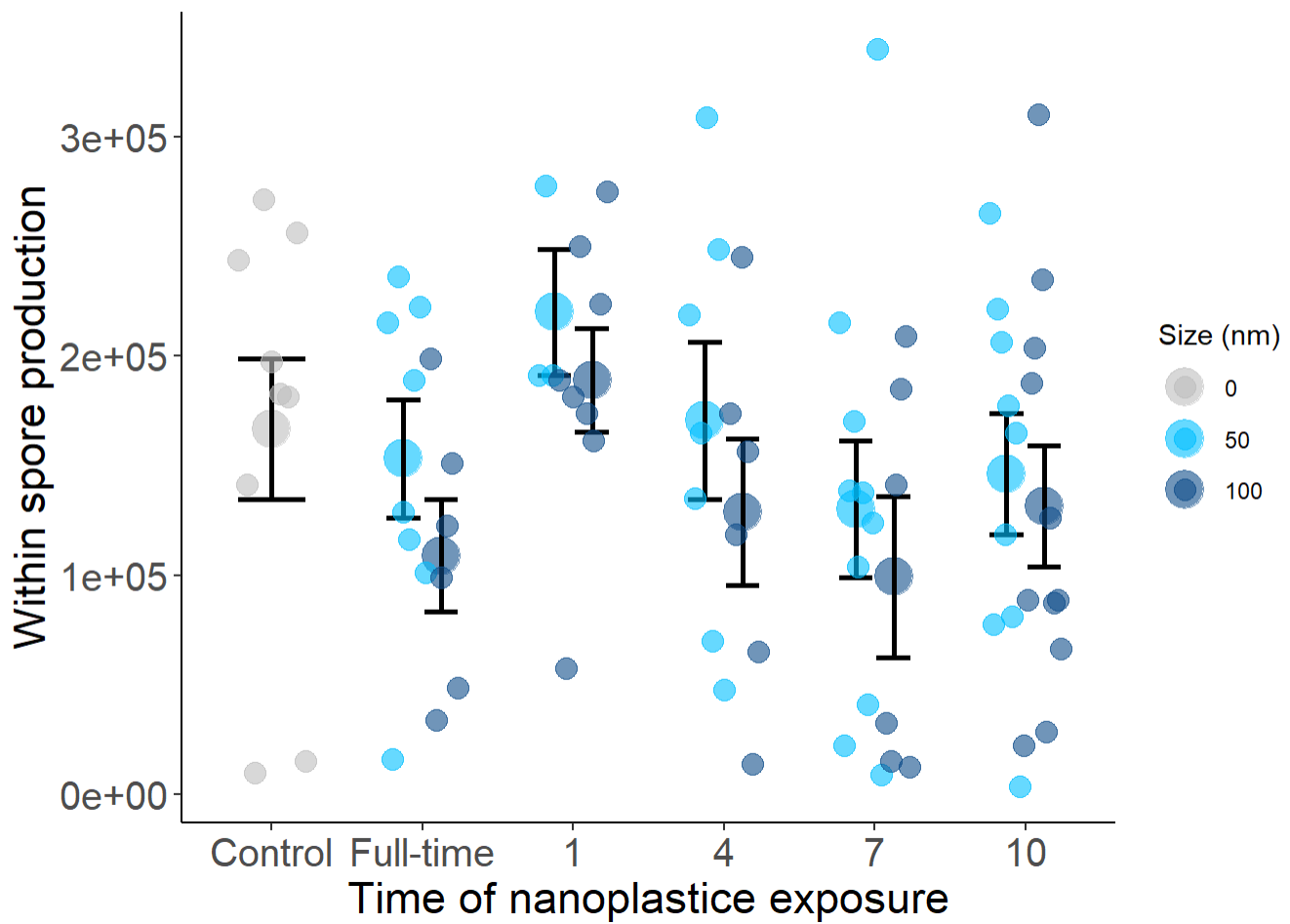
```

level_order <- c('Control', 'Full-time', '1', '4', '7', '10')

p3<-ggplot()+
  geom_point(data=spoSE, aes(x=factor(NP_treat, level = level_order), y=spores, color=factor(
Size)), size=7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=spoSE, aes(x=factor(NP_treat, level = level_order), ymin=spores-se, ymax
=spores+se), size=1, width=0.5, position= position_dodge2()) +
  geom_point(data=spo2, aes(x=factor(NP_treat, level = level_order), y=spores, color=factor(S
ize)), size=4, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  scale_color_manual(values = c('grey',"deepskyblue", "dodgerblue4"),
                      name = c("Size (nm)"))+
  ylab("Within spore production") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 17))

```

p3



```

spoSE2<-summarySE(spo2, measurevar= 'spores', groupvars = c('NP_treat'), na.rm=TRUE)
spoSE2

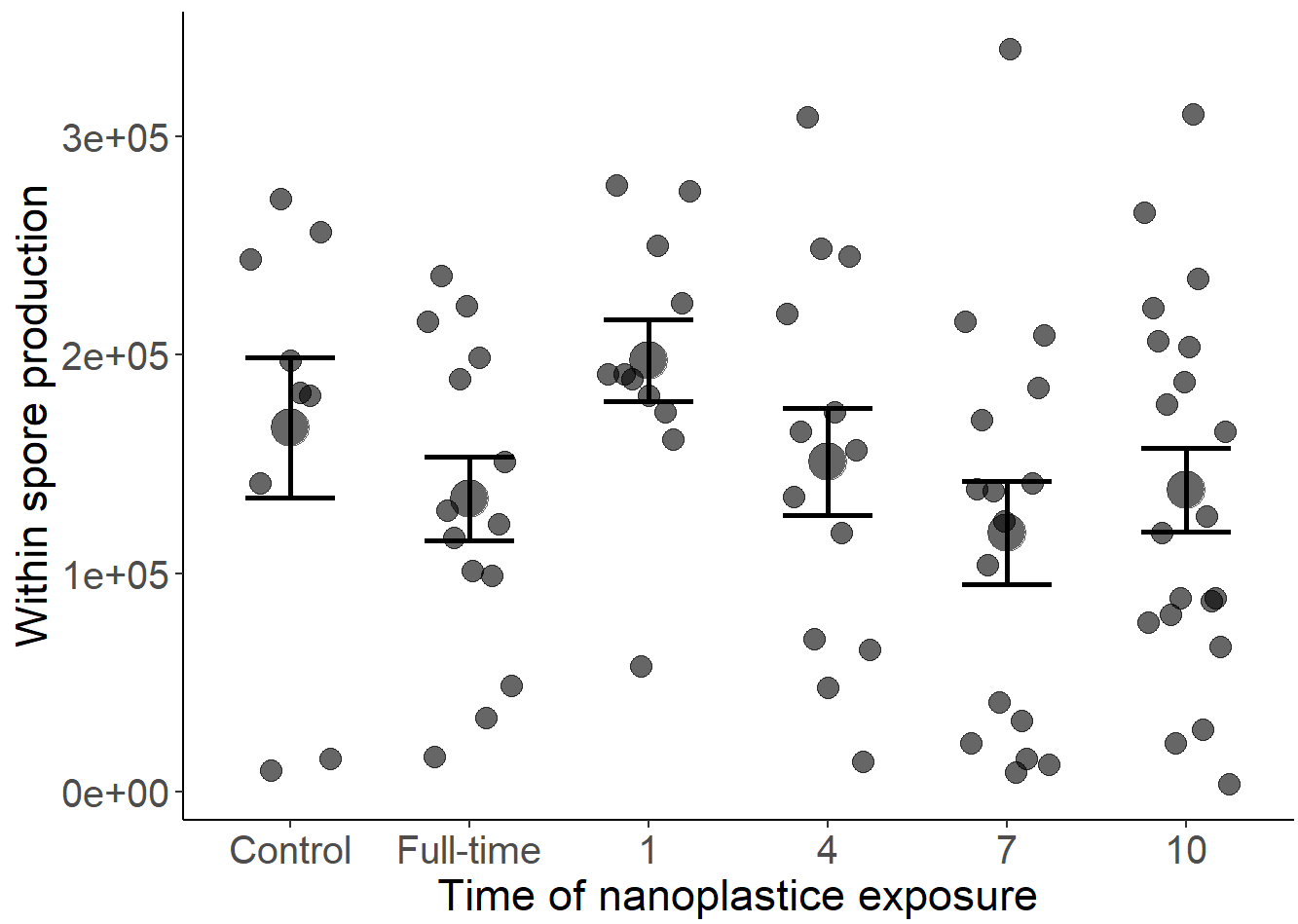
```

##	NP_treat	N	spores	sd	se	ci
## 1	1	11	197386.4	61439.64	18524.75	41275.71
## 2	10	20	138062.5	85535.73	19126.37	40031.95
## 3	4	13	151250.0	88227.63	24469.94	53315.42
## 4	7	16	118515.6	93701.90	23425.47	49930.22
## 5	Control	9	166527.8	96508.94	32169.65	74183.34
## 6	Full-time	14	134196.4	71418.67	19087.44	41235.91

```
level_order <- c('Control', 'Full-time', '1', '4', '7', '10')
```

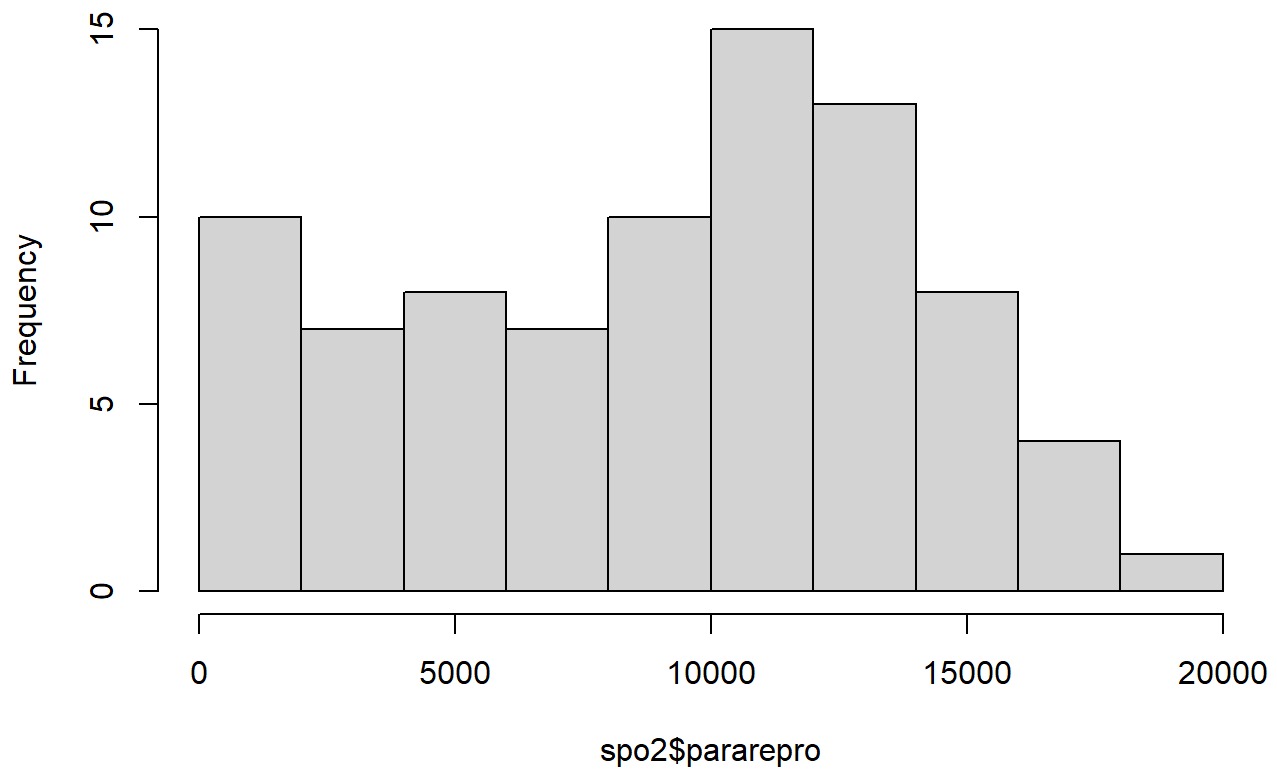
```
p3.1<-ggplot()+
  geom_point(data=spoSE2, aes(x=factor(NP_treat, level = level_order), y=spores), size=7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=spoSE2, aes(x=factor(NP_treat, level = level_order), ymin=spores-se, ymax=spores+se), size=1, width=0.5, position= position_dodge2()) +
  geom_point(data=spo2, aes(x=factor(NP_treat, level = level_order), y=spores), size=4, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  ylab("Within spore production") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 17))
```

p3.1



```
hist(spo2$pararepro)
```

Histogram of spo2\$pararepro



```
shapiro.test(spo2$pararepro)
```

```
##  
##  Shapiro-Wilk normality test  
##  
## data:  spo2$pararepro  
## W = 0.95972, p-value = 0.01075
```

```
spo2glm <- glm(pararepro ~ NP_treat + Size, family = Gamma, data = spo2 )  
summary(spo2glm)
```

```
##
## Call:
## glm(formula = pararepro ~ NP_treat + Size, family = Gamma, data = spo2)
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)    5.145e-05  2.812e-05   1.830   0.0712 .
## NP_treat10     3.872e-05  2.065e-05   1.876   0.0645 .
## NP_treat4      2.892e-05  2.216e-05   1.305   0.1958
## NP_treat7      6.119e-05  2.444e-05   2.503   0.0144 *
## NP_treatControl 4.471e-05  3.345e-05   1.337   0.1853
## NP_treatFull-time 3.964e-05  2.293e-05   1.728   0.0880 .
## Size          3.767e-07  3.000e-07   1.256   0.2131
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for Gamma family taken to be 0.3192703)
##
##    Null deviance: 44.915  on 82  degrees of freedom
## Residual deviance: 42.349  on 76  degrees of freedom
## AIC: 1670.2
##
## Number of Fisher Scoring iterations: 6
```

```
car::Anova(spo2glm, type = 2)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: pararepro
##              LR Chisq Df Pr(>Chisq)
## NP_treat    6.8605  5    0.2312
## Size        1.5722  1    0.2099
```

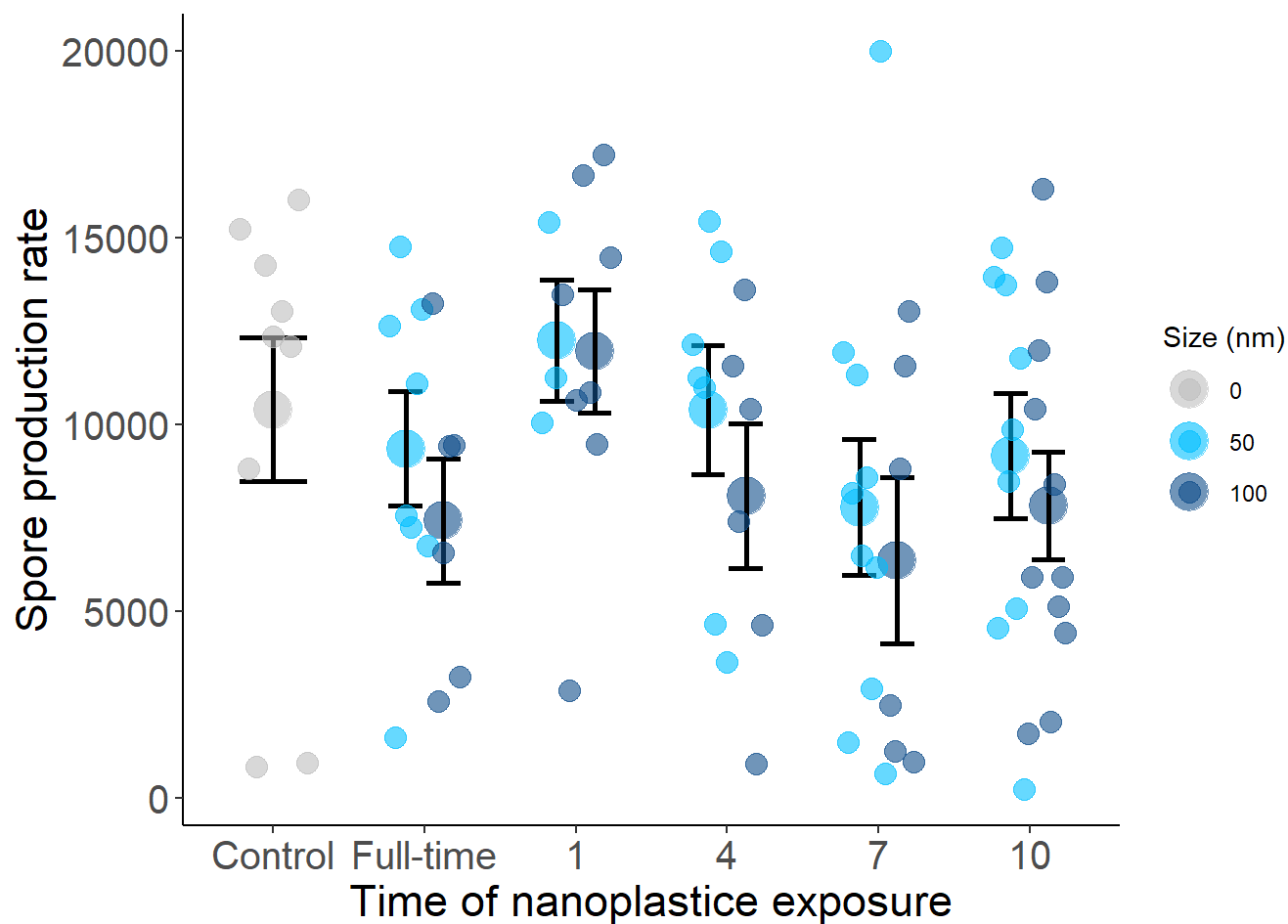
```
spo2SE<-summarySE(spo2, measurevar= 'pararepro', groupvars = c('NP_treat', 'Size'), na.rm=TRUE)
spo2SE
```

##	NP_treat	Size	N	pararepro	sd	se	ci
## 1	1	50	3	12244.153	2810.558	1622.676	6981.812
## 2	1	100	8	11964.432	4627.942	1636.225	3869.057
## 3	10	50	9	9162.587	5003.762	1667.921	3846.232
## 4	10	100	11	7830.851	4785.090	1442.759	3214.668
## 5	4	50	7	10399.021	4579.402	1730.851	4235.240
## 6	4	100	6	8098.753	4730.428	1931.189	4964.280
## 7	7	50	10	7782.467	5750.650	1818.515	4113.767
## 8	7	100	6	6358.175	5441.086	2221.314	5710.070
## 9	Control	0	9	10398.676	5777.348	1925.783	4440.862
## 10	Full-time	50	8	9352.254	4329.020	1530.540	3619.152
## 11	Full-time	100	6	7425.948	4086.394	1668.263	4288.408

```
level_order <- c('Control', 'Full-time', '1', '4', '7', '10')
```

```
p4<-ggplot()+
  geom_point(data=spo2SE, aes(x=factor(NP_treat, level = level_order), y=pararepro, color=factor(Size)), size=7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=spo2SE, aes(x=factor(NP_treat, level = level_order), ymin=pararepro-se, ymax=pararepro+se), size=1, width=0.5, position= position_dodge2()) +
  geom_point(data=spo2, aes(x=factor(NP_treat, level = level_order), y=pararepro, color=factor(Size)), size=4, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  scale_color_manual(values = c('grey',"deepskyblue", "dodgerblue4"),
    name = c("Size (nm)"))+
  ylab("Spore production rate") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
    axis.text.y = element_text(size = 15),
    axis.title.x = element_text(size = 17),
    axis.title.y = element_text(size = 17))
```

p4



```
spo2SE2 <-summarySE(spo2, measurevar= 'pararepro', groupvars = c('NP_treat'), na.rm=TRUE)
spo2SE2
```

##	NP_treat	N	pararepro	sd	se	ci
## 1	1	11	12040.720	4073.010	1228.059	2736.286
## 2	10	20	8430.132	4801.595	1073.669	2247.215
## 3	4	13	9337.359	4608.010	1278.032	2784.592
## 4	7	16	7248.358	5497.055	1374.264	2929.174
## 5	Control	9	10398.676	5777.348	1925.783	4440.862
## 6	Full-time	14	8526.694	4182.364	1117.784	2414.825

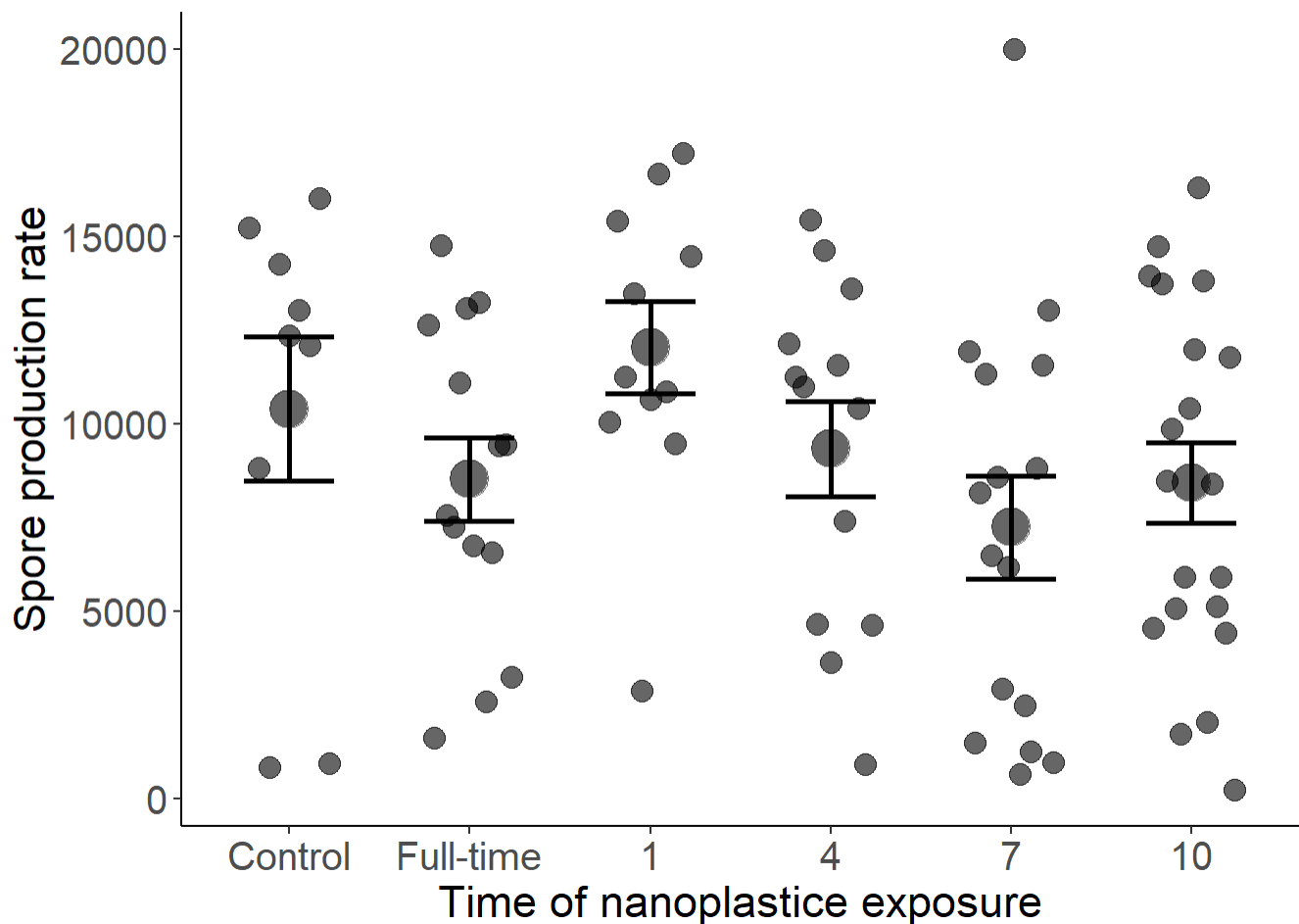
```

level_order <- c('Control', 'Full-time', '1', '4', '7', '10')

p4.1<-ggplot()+
  geom_point(data=spo2SE2, aes(x=factor(NP_treat, level = level_order), y=pararepro), size=7,
stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=spo2SE2, aes(x=factor(NP_treat, level = level_order), ymin=pararepro-se,
ymax=pararepro+se), size=1, width=0.5, position= position_dodge2()) +
  geom_point(data=spo2, aes(x=factor(NP_treat, level = level_order), y=pararepro), size=4, st
roke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  ylab("Spore production rate") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 17))

```

p4.1



Host viability

```

viaglm <- glm(viability ~ NP_treat + Size, family = binomial, data=dat2)
summary(viaglm)

```

```
##
## Call:
## glm(formula = viability ~ NP_treat + Size, family = binomial,
##      data = dat2)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)   -0.008991    0.734977  -0.012  0.99024
## NP_treat10     1.385465    0.582625   2.378  0.01741 *
## NP_treat4      0.669393    0.577190   1.160  0.24615
## NP_treat7      2.184556    0.729586   2.994  0.00275 **
## NP_treatControl 1.954901    1.054332   1.854  0.06372 .
## NP_treatFull-time 1.599578    0.681025   2.349  0.01884 *
## Size          -0.001937    0.008287  -0.234  0.81522
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##      Null deviance: 168.22  on 143  degrees of freedom
## Residual deviance: 151.81  on 137  degrees of freedom
## AIC: 165.81
##
## Number of Fisher Scoring iterations: 4
```

```
car::Anova(viaglm, type = 2)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: viability
##           LR Chisq Df Pr(>Chisq)
## NP_treat  14.7174  5    0.01164 *
## Size       0.0546  1    0.81523
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
viaSE<-summarySE(dat2, measurevar= 'viability', groupvars = c('NP_treat'), na.rm=TRUE)
viaSE
```

```
##      NP_treat  N viability      sd      se      ci
## 1           1 26 0.4615385 0.5083911 0.09970370 0.2053436
## 2          10 31 0.7741935 0.4250237 0.07633651 0.1559000
## 3           4 24 0.6250000 0.4945354 0.10094661 0.2088240
## 4           7 26 0.8846154 0.3258126 0.06389711 0.1315986
## 5    Control 16 0.8750000 0.3415650 0.08539126 0.1820072
## 6 Full-time 21 0.8095238 0.4023739 0.08780519 0.1831584
```

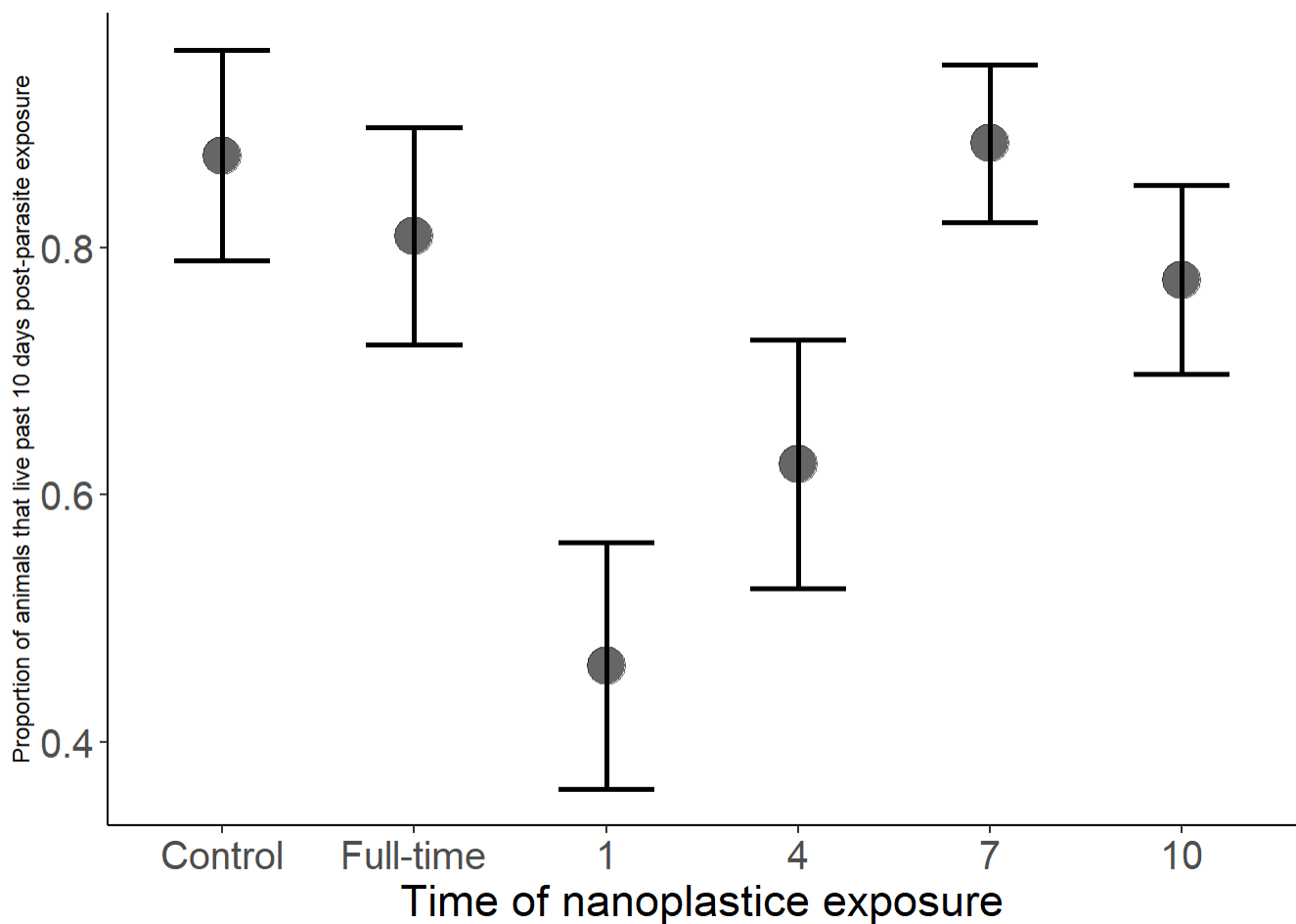
```

level_order <- c('Control', 'Full-time', '1', '4', '7', '10')

p5<-ggplot()+
  geom_point(data=viaSE, aes(x=factor(NP_treat, level = level_order), y=viability), size=7, s
stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=viaSE, aes(x=factor(NP_treat, level = level_order), ymin=viability-se, y
max=viability+se), size=1, width=0.5, position= position_dodge2()) +
  ylab("Proportion of animals that live past 10 days post-parasite exposure") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 9))

```

p5



```

survglm <- glm(post_inoc_surv ~ NP_treat + Size, family = poisson, data=dat2)
summary(survglm)

```

```
##
## Call:
## glm(formula = post_inoc_surv ~ NP_treat + Size, family = poisson,
##      data = dat2)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.5116362   0.0935381  26.851   <2e-16 ***
## NP_treat10      0.1923402   0.0753424   2.553   0.0107 *
## NP_treat4       0.0339511   0.0829519   0.409   0.6823
## NP_treat7       0.1824964   0.0784568   2.326   0.0200 *
## NP_treatControl  0.1753606   0.1140382   1.538   0.1241
## NP_treatFull-time 0.1678130   0.0828602   2.025   0.0428 *
## Size           -0.0009725   0.0009872  -0.985   0.3246
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 237.17  on 143  degrees of freedom
## Residual deviance: 221.82  on 137  degrees of freedom
## AIC: 862.74
##
## Number of Fisher Scoring iterations: 4
```

```
car::Anova(survglm, type = 2)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: post_inoc_surv
##           LR Chisq Df Pr(>Chisq)
## NP_treat  10.9916  5    0.05155 .
## Size       0.9712  1    0.32439
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
survallSE<-summarySE(dat2, measurevar= 'post_inoc_surv', groupvars = c('NP_treat'), na.rm=TRUE)
survallSE
```

```
##      NP_treat  N post_inoc_surv      sd      se      ci
## 1           1 26      11.46154 5.108665 1.0018917 2.063435
## 2          10 31      13.90323 4.213904 0.7568396 1.545673
## 3           4 24      11.83333 4.715070 0.9624596 1.990999
## 4           7 26      13.80769 3.698856 0.7254054 1.494000
## 5    Control 16      14.68750 4.437999 1.1094997 2.364843
## 6 Full-time 21      13.57143 3.668398 0.8005100 1.669835
```

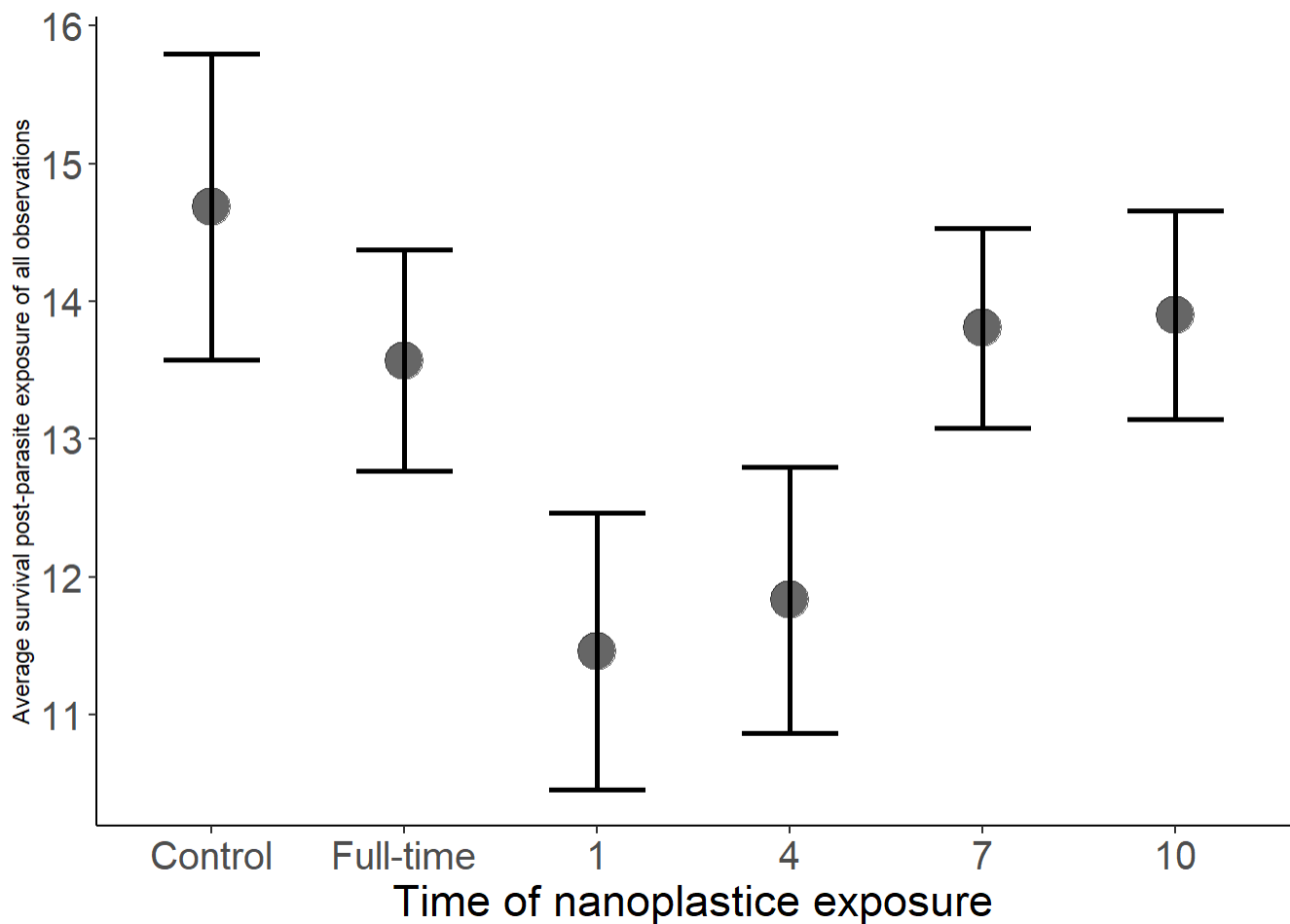
```

level_order <- c('Control', 'Full-time', '1', '4', '7', '10')

p6<-ggplot()+
  geom_point(data=survallSE, aes(x=factor(NP_treat, level = level_order), y=post_inoc_surv),
size=7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=survallSE, aes(x=factor(NP_treat, level = level_order), ymin=post_inoc_surv-se, ymax=post_inoc_surv+se), size=1, width=0.5, position= position_dodge2()) +
  ylab("Average survival post-parasite exposure of all observations") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 9))

```

p6



```

survglm2 <- glm(post_inoc_surv ~ NP_treat + Size, family = poisson, data=spo2)
summary(survglm2)

```

```
##
## Call:
## glm(formula = post_inoc_surv ~ NP_treat + Size, family = poisson,
##      data = spo2)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)    2.913817    0.126903   22.961  <2e-16 ***
## NP_treat10     -0.065614    0.093099   -0.705    0.481
## NP_treat4      -0.088370    0.102921   -0.859    0.391
## NP_treat7      -0.104397    0.099543   -1.049    0.294
## NP_treatControl -0.169399    0.152470   -1.111    0.267
## NP_treatFull-time -0.120841    0.102232   -1.182    0.237
## Size          -0.001061    0.001205   -0.880    0.379
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for poisson family taken to be 1)
##
##      Null deviance: 21.129  on 82  degrees of freedom
## Residual deviance: 19.081  on 76  degrees of freedom
## AIC: 414.51
##
## Number of Fisher Scoring iterations: 4
```

```
car::Anova(survglm2, type = 2)
```

```
## Analysis of Deviance Table (Type II tests)
##
## Response: post_inoc_surv
##           LR Chisq Df Pr(>Chisq)
## NP_treat  1.93015  5    0.8587
## Size      0.77553  1    0.3785
```

```
survinfSE<-summarySE(spo2, measurevar= 'post_inoc_surv', groupvars = c('NP_treat'), na.rm=TRUE)
survinfSE
```

```
##      NP_treat  N post_inoc_surv      sd      se      ci
## 1           1 11      16.81818 2.182576 0.6580713 1.4662743
## 2           10 20      15.90000 1.744163 0.3900067 0.8162935
## 3            4 13      15.61538 2.180920 0.6048783 1.3179165
## 4            7 16      15.43750 2.096624 0.5241561 1.1172122
## 5    Control  9      15.55556 1.878238 0.6260793 1.4437415
## 6 Full-time 14      15.14286 1.994498 0.5330520 1.1515888
```

```

level_order <- c('Control', 'Full-time', '1', '4', '7', '10')

p7<-ggplot()+
  geom_point(data=survinfSE, aes(x=factor(NP_treat, level = level_order), y=post_inoc_surv),
size=7, stroke=0, alpha=.6, position=position_dodge2(width=0.5)) +
  geom_errorbar(data=survinfSE, aes(x=factor(NP_treat, level = level_order), ymin=post_inoc_surv-se, ymax=post_inoc_surv+se), size=1, width=0.5, position= position_dodge2()) +
  ylab("Average survival post-parasite exposure of infected hosts") +
  xlab("Time of nanoplastice exposure") +
  theme_classic() +
  theme(axis.text.x = element_text(size = 15),
        axis.text.y = element_text(size = 15),
        axis.title.x = element_text(size = 17),
        axis.title.y = element_text(size = 9))

```

p7

