

Timestep Data Analyses

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```
library(here)
library(reshape2)
library(FSA)
library(fGarch)
library(LambertW)
library(patchwork)
library(DHARMA)
library(mgcv)
library(fitdistrplus)
library(goft)
library(gamlss)
library(rstatix)
library(performance)
library(scales)
library(viridis)
library(ggpubr)
library(tidyverse)
```

Load required libraries

Manipulate Raw Tube Growth Data for Plotting and Stats

Load raw data

```
tube_growth = read_csv(here("./data/tube-growth.csv"))
knitr::kable(tube_growth, caption = "Tube growth rates of all marked worms in various treatments.")
```

Table 1: Tube growth rates of all marked worms in various treatments.

tank	zone	worm	trial	worm_and_trial	length_0	length_1	length_2	length_3	length_4	length_5	growth_1	growth_2	growth_3	growth_4	total	mortality			
A	1	A_1low_salinity	1	A_1low_sal_1	16.95	2.260	3.55	5.77	9.10	9.20	9.90	9.90	1.290	2.22	3.33	0.70	0.00	7.640	0
A	1	A_1low_salinity	2	A_1low_sal_2	15.04	5.690	6.00	6.60	7.00	7.00	7.00	7.00	0.310	0.60	0.40	0.00	0.00	1.310	0
A	1	A_1low_salinity	3	A_1low_sal_3	14.95	5.390	7.50	7.70	7.70	8.35	8.45	8.45	2.110	0.20	0.00	0.10	0.00	3.060	0
A	1	A_1low_salinity	4	A_1low_sal_4	15.58	4.220	6.70	6.70	6.70	6.70	7.00	8.80	2.480	0.00	0.00	0.30	1.80	4.580	0

tankzonewormtrialneworm and low string length length length length length length growth growth growth growth growth growth total growth																				
A	1	A_1	low	sad	black	15.23	7.460	7.90	7.90	8.00	8.00	8.00	8.00	0.440	0.00	0.10	0.00	0.00	0.540	0
A	1	A_1	low	sad	pink	14.76	5.910	7.00	8.95	9.00	9.20	9.40	9.70	1.090	1.95	0.05	0.20	0.30	3.790	0
A	1	A_1	low	sad	red	14.46	5.950	8.05	9.40	9.40	9.40	9.40	10.00	2.100	1.35	0.00	0.00	0.60	4.050	0
A	1	A_1	low	sad	blue	14.75	5.180	6.10	6.10	6.40	6.50	8.55	8.55	0.920	0.00	0.30	2.05	0.00	3.370	0
A	1	A_1	low	sad	white	15.20	3.920	7.10	7.20	8.40	8.70	10.00	10.00	3.180	0.10	1.20	1.30	0.00	6.080	0
A	1	A_1	low	sad	yellow	13.49	2.810	6.25	6.35	6.35	6.40	6.40	6.75	3.440	0.10	0.00	0.00	0.35	3.940	0
A	2	A_2	low	sad	black	14.90	5.830	9.40	12.20	12.50	12.70	13.40	14.40	3.570	2.80	0.30	0.70	1.00	8.570	0
A	2	A_2	low	sad	pink	14.79	4.570	5.80	6.10	7.10	8.05	8.05	8.50	1.230	0.30	1.00	0.00	0.45	3.930	0
A	2	A_2	low	sad	red	14.82	7.460	7.50	8.55	10.40	10.40	11.00	11.20	0.040	1.05	1.85	0.60	0.20	3.740	0
A	2	A_2	low	sad	blue	15.03	6.090	7.00	7.45	7.50	8.80	8.80	8.80	0.910	0.45	0.05	0.00	0.00	2.710	0
A	2	A_2	low	sad	white	15.16	6.590	8.10	9.55	9.55	9.55	9.55	9.55	1.510	1.45	0.00	0.00	0.00	2.960	0
A	2	A_2	low	sad	yellow	16.45	7.880	10.00	11.10	12.20	13.05	13.05	14.00	2.120	1.10	1.10	0.00	0.95	6.120	0
A	2	A_2	low	sad	black	15.22	8.880	10.00	10.25	10.25	10.50	10.50	11.00	1.120	0.25	0.00	0.00	0.50	2.120	0
A	2	A_2	low	sad	pink	15.79	6.160	7.50	8.30	8.30	9.80	9.80	9.80	1.340	0.80	0.00	0.00	0.00	3.640	0
A	2	A_2	low	sad	red	15.59	4.930	4.93	6.70	10.80	12.20	12.20	12.20	0.000	1.77	4.10	0.00	0.00	7.270	0
A	2	A_2	low	sad	blue	16.52	5.370	9.00	9.00	9.40	10.25	10.25	10.25	3.630	0.00	0.40	0.00	0.00	4.880	0
A	3	A_3	low	sad	black	14.42	5.560	8.00	8.30	10.00	10.00	10.40	10.50	2.440	0.30	1.70	0.40	0.10	4.940	0
A	3	A_3	low	sad	pink	15.36	5.500	6.40	6.50	10.10	12.00	12.60	13.50	0.900	0.10	3.60	0.60	0.90	8.000	0
A	3	A_3	low	sad	red	15.02	6.290	7.65	8.90	9.90	11.10	12.20	13.20	1.360	1.25	1.00	1.10	1.00	6.910	0
A	3	A_3	low	sad	blue	15.40	5.200	6.00	6.80	6.80	7.40	8.20	8.30	0.800	0.80	0.00	0.80	0.10	3.100	0
A	3	A_3	low	sad	white	14.19	3.640	5.50	5.70	7.00	7.10	8.30	8.30	1.860	0.20	1.30	1.20	0.00	4.660	0
A	3	A_3	low	sad	yellow	16.15	4.310	6.40	7.00	9.00	9.40	10.00	10.40	2.090	0.60	2.00	0.60	0.40	6.090	0
A	3	A_3	low	sad	black	14.31	6.660	7.70	8.50	11.10	11.40	11.70	12.20	1.040	0.80	2.60	0.30	0.50	5.540	0
A	3	A_3	low	sad	pink	14.82	5.920	9.90	9.90	9.90	10.00	10.10	11.00	3.980	0.00	0.00	0.10	0.90	5.080	0
A	3	A_3	low	sad	red	14.71	6.120	7.35	8.70	8.70	9.00	9.00	9.00	1.230	1.35	0.00	0.00	0.00	2.880	0
A	3	A_3	low	sad	blue	14.24	5.010	7.00	7.70	9.70	10.50	10.50	10.50	1.990	0.70	2.00	0.00	0.00	5.490	0
B	1	B_1	high	teal	pw	15.98	6.350	7.20	7.20	7.55	9.15	9.15	9.15	0.850	0.00	0.35	0.00	0.00	2.800	0
B	1	B_1	high	teal	blue	16.02	2.640	8.10	10.50	11.10	13.05	14.15	15.00	5.460	2.40	0.60	1.10	0.85	12.360	0
B	1	B_1	high	teal	orange	3.62	6.870	9.00	10.00	10.00	11.10	12.70	12.70	2.130	1.00	0.00	1.60	0.00	5.830	0
B	1	B_1	high	teal	green	7.55	7.550	9.00	12.45	12.45	15.00	17.05	17.05	1.450	3.45	0.00	2.05	0.00	9.500	0
B	1	B_1	high	teal	black	16.15	5.820	7.10	10.25	13.60	15.50	15.50	15.95	1.280	3.15	3.35	0.00	0.45	10.130	0
B	1	B_1	high	teal	pink	15.41	3.260	10.00	10.00	10.00	10.00	11.10	12.50	6.740	0.00	0.00	1.10	1.40	9.240	0
B	1	B_1	high	teal	red	16.42	3.400	5.10	5.10	5.80	6.35	7.00	7.00	1.700	0.00	0.70	0.65	0.00	3.600	0
B	1	B_1	high	teal	blue	16.00	6.000	11.10	12.45	14.20	16.10	18.45	18.45	5.100	1.35	1.75	2.35	0.00	12.450	0
B	1	B_1	high	teal	white	12.27	5.400	6.25	8.05	10.50	10.50	11.35	11.35	0.850	1.80	2.45	0.85	0.00	5.950	0
B	1	B_1	high	teal	orange	14.00	6.000	9.15	10.50	13.00	14.40	15.50	15.50	3.150	1.35	2.50	1.10	0.00	9.500	0
B	2	B_2	high	teal	pw	16.17	3.890	5.20	5.60	6.60	6.60	7.45	8.00	1.310	0.40	1.00	0.85	0.55	4.110	0
B	2	B_2	high	teal	blue	15.85	9.980	10.30	10.30	10.65	11.10	12.20	12.20	0.320	0.00	0.35	1.10	0.00	2.220	0
B	2	B_2	high	teal	orange	5.30	9.310	13.00	14.60	18.10	19.40	23.55	24.15	3.690	1.60	3.50	4.15	0.60	14.840	0
B	2	B_2	high	teal	green	4.04	1.550	3.20	4.70	4.70	4.70	4.70	5.00	1.650	1.50	0.00	0.00	0.30	3.450	0
B	2	B_2	high	teal	black	15.55	5.810	7.10	9.00	9.20	9.40	10.50	10.50	1.290	1.90	0.20	1.10	0.00	4.690	0
B	2	B_2	high	teal	pink	19.46	6.270	9.20	13.60	15.40	12.00	19.90	22.45	2.930	4.40	1.80	7.90	2.55	16.180	0
B	2	B_2	high	teal	red	15.36	7.370	9.40	9.70	10.50	10.60	12.35	12.45	2.030	0.30	0.80	1.75	0.10	5.080	0
B	2	B_2	high	teal	blue	15.04	3.270	3.27	8.50	9.10	10.30	13.05	14.15	0.000	5.23	0.60	2.75	1.10	10.880	0
B	2	B_2	high	teal	white	16.64	5.250	7.60	8.50	8.50	8.50	10.00	10.50	2.350	0.90	0.00	1.50	0.50	5.250	0
B	2	B_2	high	teal	orange	16.76	6.700	7.60	7.60	8.00	8.20	11.10	11.10	0.900	0.00	0.40	2.90	0.00	4.400	0
B	3	B_3	high	teal	pw	17.67	7.660	8.30	8.30	8.45	9.80	9.80	10.70	0.640	0.00	0.15	0.00	0.90	3.040	0
B	3	B_3	high	teal	blue	16.45	6.230	7.85	10.00	10.60	11.10	11.30	12.20	1.620	2.15	0.60	0.20	0.90	5.970	0
B	3	B_3	high	teal	orange	5.08	13.110	13.30	16.60	18.35	18.35	18.35	18.50	0.190	3.30	1.75	0.00	0.15	5.390	0
B	3	B_3	high	teal	green	7.210	7.210	10.20	11.10	11.60	12.20	12.20	12.50	2.990	0.90	0.50	0.00	0.30	5.290	0
B	3	B_3	high	teal	black	17.62	8.910	10.00	11.35	11.35	12.20	12.20	12.20	1.090	1.35	0.00	0.00	0.00	3.290	0
B	3	B_3	high	teal	pink	15.35	3.700	4.15	5.75	6.00	7.10	7.10	8.50	0.450	1.60	0.25	0.00	1.40	4.800	0

tank	zone	worm	trial	mean	and	color	string	length	length	length	length	length	length	length	growth	growth	growth	growth	growth	total	5	mortality
B	3	B_3	high	trap	16.69	4.090	6.10	8.30	9.10	9.15	9.15	9.15	2.010	2.20	0.80	0.00	0.00	5.060	0			
B	3	B_3	high	daily	14.94	6.680	9.25	9.25	9.60	9.90	9.90	10.80	2.570	0.00	0.35	0.00	0.90	4.120	0			
B	3	B_3	high	twince	15.90	5.950	8.30	10.75	12.50	13.30	13.60	15.30	2.350	2.45	1.75	0.30	1.70	9.350	0			
B	3	B_3	high	trap	13.92	6.110	7.20	9.05	9.05	9.15	9.15	9.15	1.090	1.85	0.00	0.00	0.00	3.040	0			
C	1	C_1	control	yellow	17.61	6.830	7.50	7.60	8.30	8.30	9.15	10.25	0.670	0.10	0.70	0.85	1.10	3.420	0			
C	1	C_1	control	dark	10.78	4.920	6.50	6.90	7.70	7.70	8.70	10.25	1.580	0.40	0.80	1.00	1.55	5.330	0			
C	1	C_1	control	orange	18.67	10.640	14.20	14.50	15.30	17.50	20.25	21.10	3.560	0.30	0.80	2.75	0.85	10.460	0			
C	1	C_1	control	lime	14.72	5.790	8.00	8.20	8.20	8.35	9.55	11.10	2.210	0.20	0.00	1.20	1.55	5.310	0			
C	1	C_1	control	black	17.58	8.390	9.30	10.90	12.20	12.30	14.15	15.50	0.910	1.60	1.30	1.85	1.35	7.110	0			
C	1	C_1	control	pink	15.99	6.640	8.55	10.60	11.45	11.45	14.15	17.00	1.910	2.05	0.85	2.70	2.85	10.360	0			
C	1	C_1	control	red	17.40	8.480	10.75	11.40	12.10	12.10	12.20	13.45	2.270	0.65	0.70	0.10	1.25	4.970	0			
C	1	C_1	control	baby	12.57	8.250	9.30	10.10	10.30	10.50	11.35	11.60	1.050	0.80	0.20	0.85	0.25	3.350	0			
C	1	C_1	control	white	13.67	7.070	8.00	8.50	9.70	10.10	10.25	13.45	0.930	0.50	1.20	0.15	3.20	6.380	0			
C	1	C_1	control	jade	13.73	6.960	7.40	7.80	8.00	8.00	9.15	11.50	0.440	0.40	0.20	1.15	2.35	4.540	0			
C	2	C_2	control	yellow	18.35	6.000	14.90	16.10	16.10	17.00	17.00	17.00	8.900	1.20	0.00	0.00	0.00	11.000	0			
C	2	C_2	control	dark	15.04	12.720	16.10	16.10	16.10	16.35	16.35	16.35	3.380	0.00	0.00	0.00	0.00	3.630	0			
C	2	C_2	control	orange	14.89	8.080	9.10	10.00	10.10	11.10	11.10	11.10	1.020	0.90	0.10	0.00	0.00	3.020	1			
C	2	C_2	control	lime	14.89	9.370	10.20	10.50	10.50	10.50	10.50	11.60	0.830	0.30	0.00	0.00	1.10	2.230	0			
C	2	C_2	control	black	13.83	8.150	13.30	15.25	15.60	17.00	17.00	17.00	5.150	1.95	0.35	0.00	0.00	8.850	0			
C	2	C_2	control	pink	12.33	6.150	7.20	8.55	9.60	11.00	11.00	11.00	1.050	1.35	1.05	0.00	0.00	4.850	0			
C	2	C_2	control	red	14.09	6.340	10.50	12.45	13.40	14.65	14.65	17.15	4.160	1.95	0.95	0.00	2.50	10.810	0			
C	2	C_2	control	baby	11.47	5.390	7.70	8.00	8.45	9.40	9.40	9.60	2.310	0.30	0.45	0.00	0.20	4.210	0			
C	2	C_2	control	white	17.22	2.900	10.00	10.00	10.10	11.00	11.50	13.80	7.100	0.00	0.10	0.50	2.30	10.900	0			
C	2	C_2	control	jade	13.25	8.100	10.50	10.50	10.70	10.70	10.70	11.00	2.400	0.00	0.20	0.00	0.30	2.900	0			
C	3	C_3	control	yellow	12.33	8.340	11.10	14.10	16.00	16.15	17.60	18.00	2.760	3.00	1.90	1.45	0.40	9.660	0			
C	3	C_3	control	dark	15.04	7.010	8.10	9.80	9.80	10.20	11.60	11.60	1.090	1.70	0.00	1.40	0.00	4.590	0			
C	3	C_3	control	orange	14.23	5.225	6.70	6.80	6.80	6.80	7.70	9.15	1.475	0.10	0.00	0.90	1.45	3.925	0			
C	3	C_3	control	lime	12.04	8.900	9.70	10.20	11.65	12.10	12.90	13.30	0.800	0.50	1.45	0.80	0.40	4.400	0			
C	3	C_3	control	black	16.41	3.100	4.50	5.15	6.50	8.00	8.00	8.00	1.400	0.65	1.35	0.00	0.00	4.900	1			
C	3	C_3	control	pink	14.95	7.440	10.00	11.10	13.60	14.00	16.10	16.35	2.560	1.10	2.50	2.10	0.25	8.910	0			
C	3	C_3	control	red	13.33	7.750	8.30	9.20	9.20	9.30	10.25	10.25	0.550	0.90	0.00	0.95	0.00	2.500	0			
C	3	C_3	control	baby	13.45	5.020	6.60	6.80	7.70	8.00	8.30	9.90	1.580	0.20	0.90	0.30	1.60	4.880	0			
C	3	C_3	control	white	13.70	4.050	7.30	12.30	16.10	17.50	19.15	19.40	3.250	5.00	3.80	1.65	0.25	15.350	0			
C	3	C_3	control	jade	16.42	4.950	8.00	8.80	9.90	10.50	12.20	12.60	3.050	0.80	1.10	1.70	0.40	7.650	0			

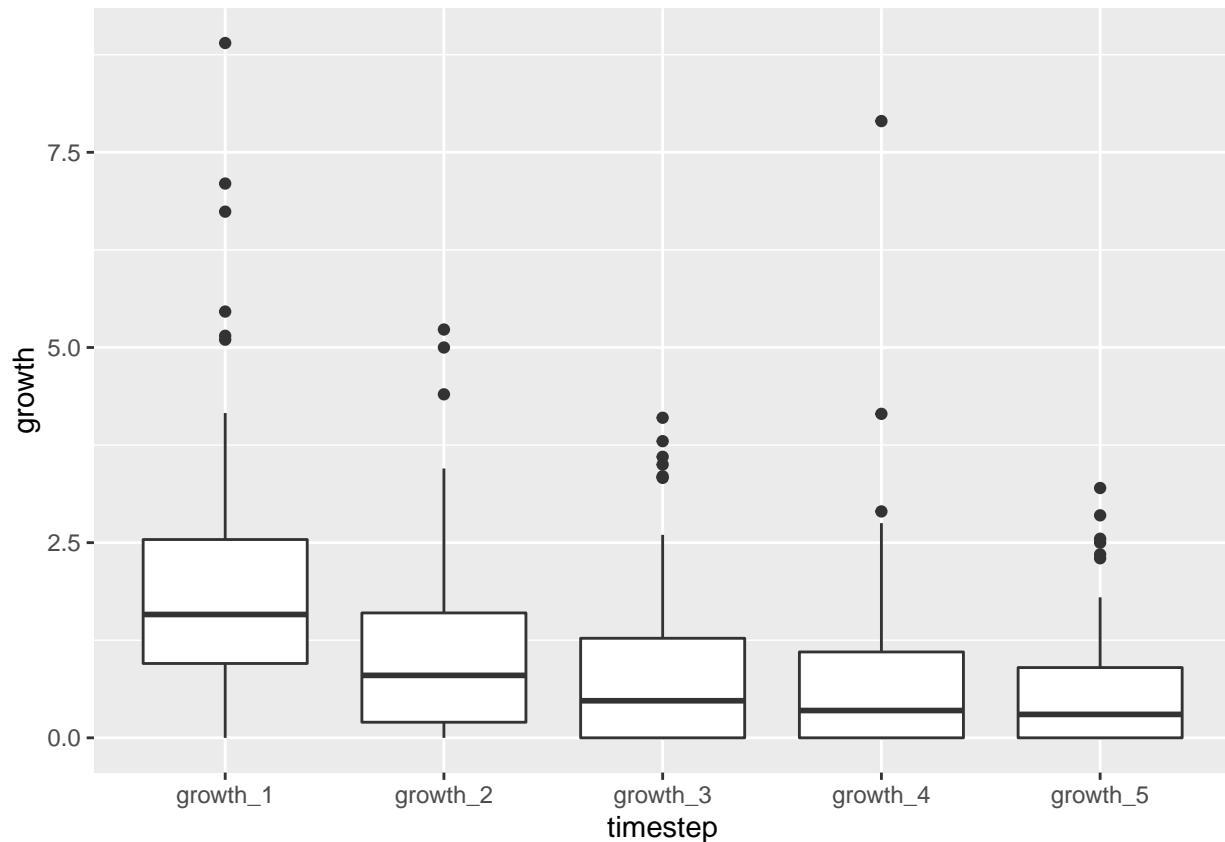
Wraggle data

```
# Clean tube_growth data for plotting and statistical tests
clean_tube_growth <- tube_growth %>%
  mutate(zone = as.factor(zone)) %>%
  unite("replicate", tank:zone, remove = TRUE) %>%
  dplyr::select(replicate, worm_id, amt_cut_mm, treatment, growth_1, growth_2, growth_3, growth_4, growth_5) %>%
  pivot_longer(!c(replicate, worm_id, amt_cut_mm, treatment),
               names_to = "timestep",
               values_to = "growth") %>%
  mutate(treatment = as.factor(treatment),
         worm_id = as.factor(worm_id),
         timestep = as.factor(timestep),
         growth = as.double(growth))
```

Statistical Analyses

Checking Assumptions of a One-way Repeated Measures ANOVA

```
# visualize data
ggplot(clean_tube_growth, aes(x= timestep, y = growth)) +
  geom_boxplot()
```



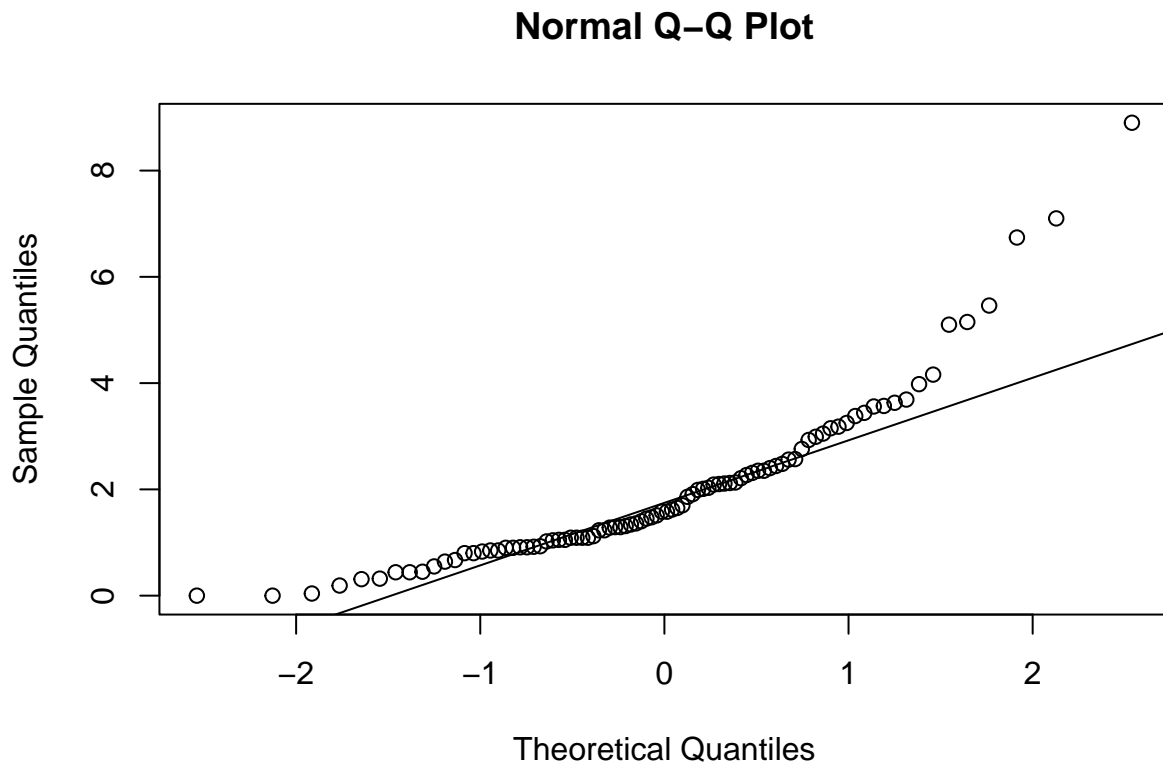
```
# check for normality of the growth at each timestep using Shapiro Wilks test
clean_tube_growth %>%
  group_by(timestep) %>%
  shapiro_test(growth)
```

```
## # A tibble: 5 x 4
##   timestep variable statistic      p
##   <fct>      <chr>      <dbl>  <dbl>
## 1 growth_1 growth      0.848 3.67e- 8
## 2 growth_2 growth      0.847 3.21e- 8
## 3 growth_3 growth      0.811 2.22e- 9
## 4 growth_4 growth      0.678 9.56e-13
## 5 growth_5 growth      0.782 3.17e-10
```

```
# investigate distribution of the growth at each timestep using qqplots since shapiro-wilk test found g

# timestep 1
growth_1 <- clean_tube_growth %>%
  dplyr::filter(timestep == "growth_1")

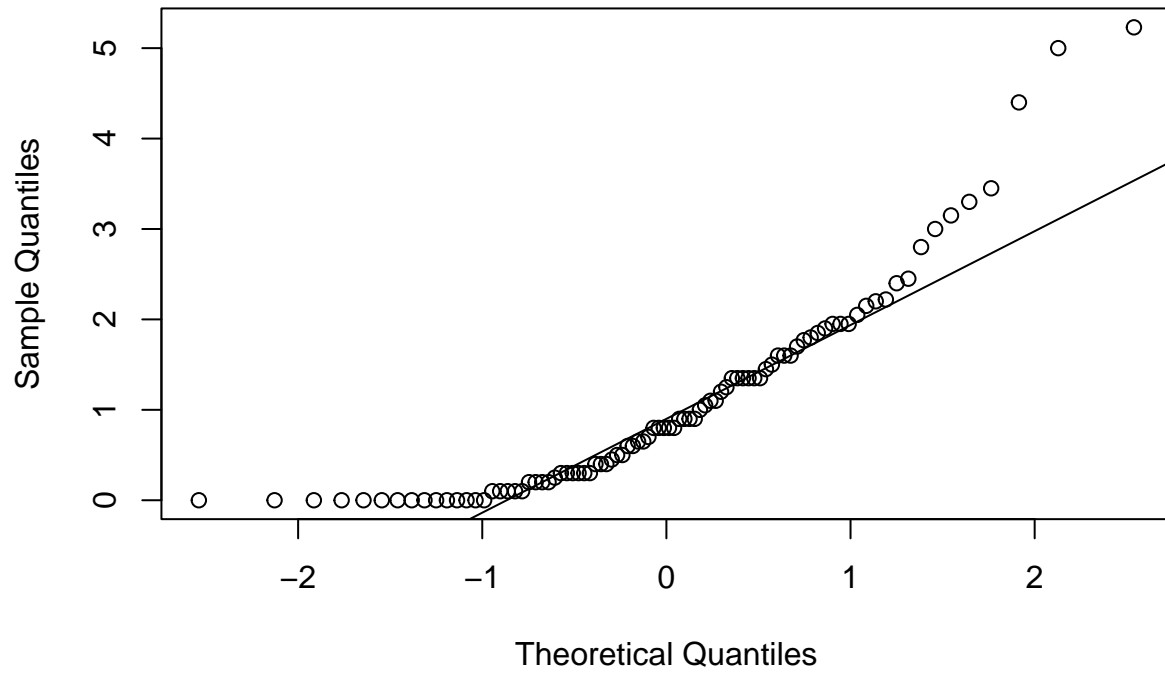
qqnorm(growth_1$growth)
qqline(growth_1$growth)
```



```
# timestep 2
growth_2 <- clean_tube_growth %>%
  dplyr::filter(timestep == "growth_2")

qqnorm(growth_2$growth)
qqline(growth_2$growth)
```

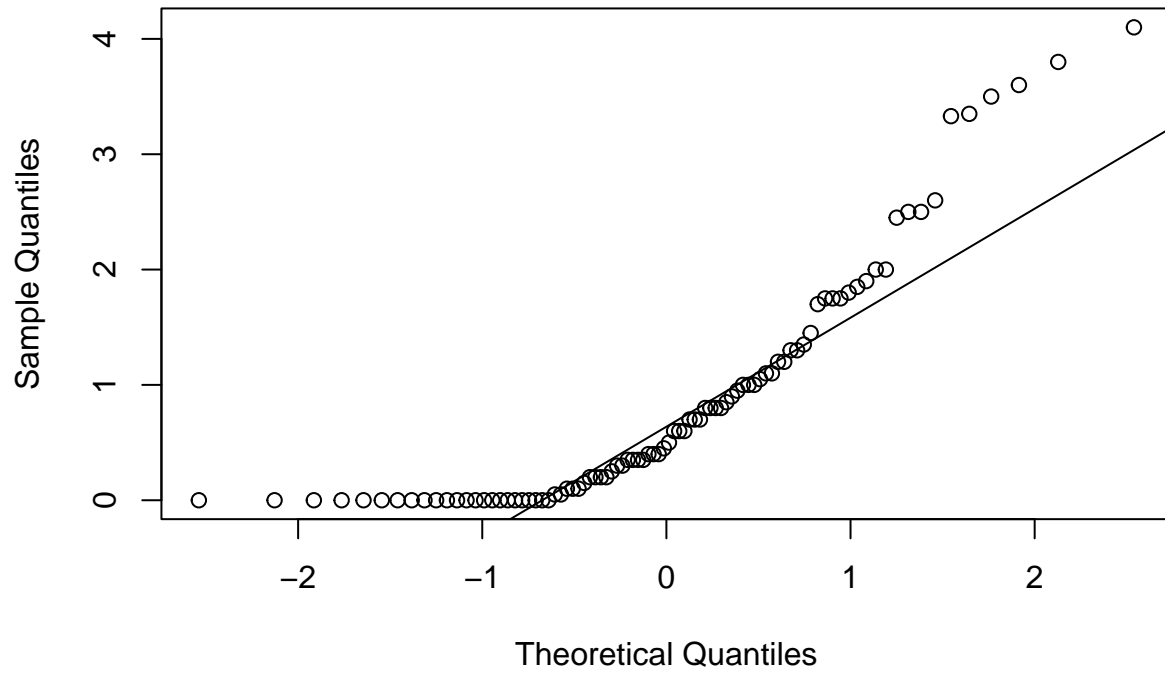
Normal Q-Q Plot



```
# timestep 3
growth_3 <- clean_tube_growth %>%
  dplyr::filter(timestep == "growth_3")

qqnorm(growth_3$growth)
qqline(growth_3$growth)
```

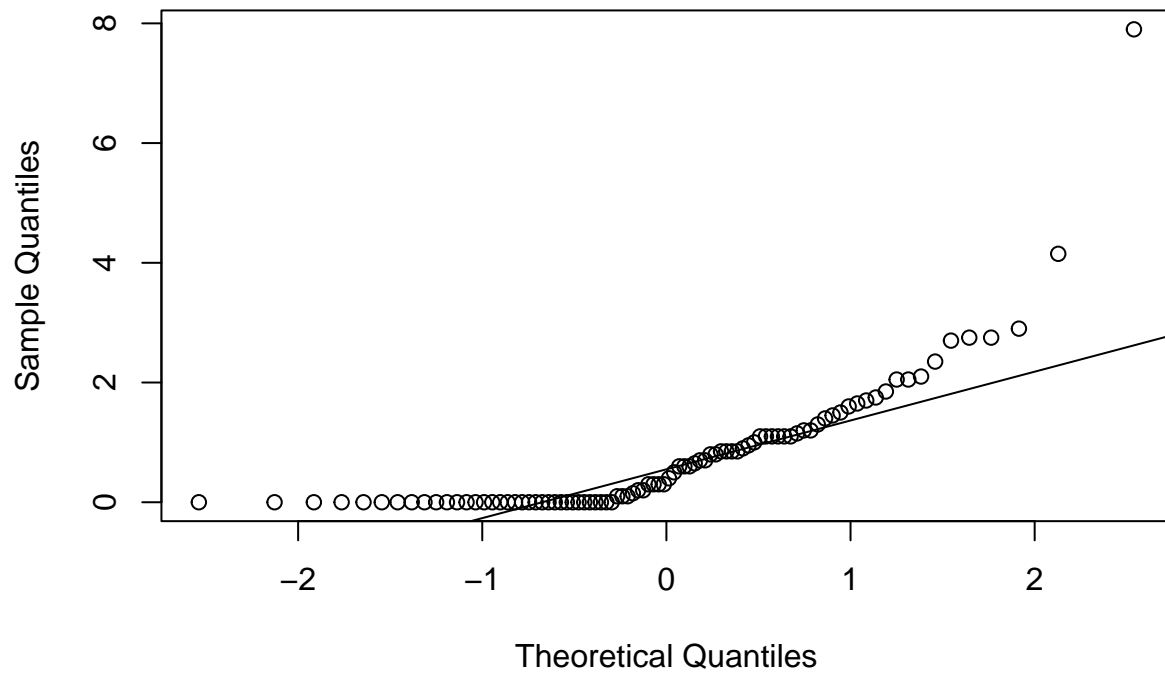
Normal Q-Q Plot



```
# timestep 4
growth_4 <- clean_tube_growth %>%
  dplyr::filter(timestep == "growth_4")

qqnorm(growth_4$growth)
qqline(growth_4$growth)
```

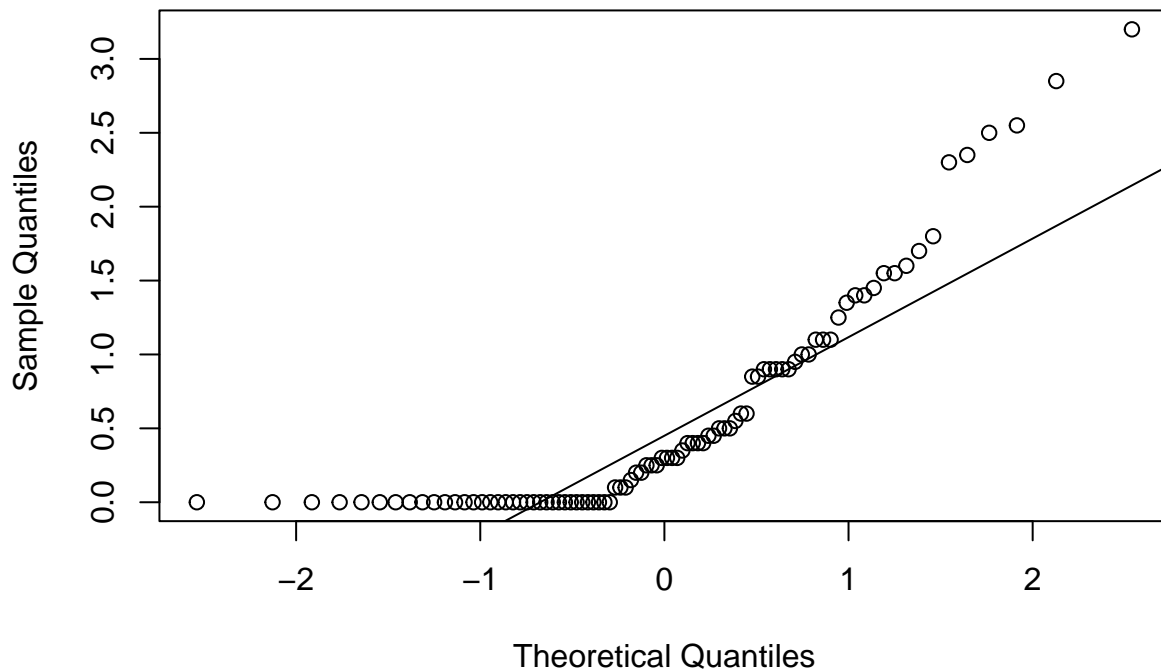
Normal Q-Q Plot



```
# timestep 5
growth_5 <- clean_tube_growth %>%
  dplyr::filter(timestep == "growth_5")

qqnorm(growth_5$growth)
qqline(growth_5$growth)
```


Normal Q-Q Plot



Since sample size is N=90 overall and n= 30 for each treatment, sample size is large enough to ignore

Checking for extreme outliers

```
clean_tube_growth %>%
  group_by(timestep) %>%
  identify_outliers(growth)
```

```
## # A tibble: 24 x 8
##   timestep replicate worm_id amt_cut_mm treatment growth is.outlier is.extreme
##   <fct>      <chr>    <fct>      <dbl> <fct>      <dbl> <lgl>    <lgl>
## 1 growth_1 B_1      B_1_2      16.1 high_temp  5.46 TRUE     FALSE
## 2 growth_1 B_1      B_1_6      15.4 high_temp  6.74 TRUE     FALSE
## 3 growth_1 B_1      B_1_8      14   high_temp  5.1  TRUE     FALSE
## 4 growth_1 C_2      C_2_1      18.4 control   8.9  TRUE     TRUE
## 5 growth_1 C_2      C_2_5      13.8 control   5.15 TRUE     FALSE
## 6 growth_1 C_2      C_2_9      17.2 control   7.1  TRUE     FALSE
## 7 growth_2 B_2      B_2_6      19.5 high_temp  4.4  TRUE     FALSE
## 8 growth_2 B_2      B_2_8      15.0 high_temp  5.23 TRUE     FALSE
## 9 growth_2 C_3      C_3_9      13.7 control   5    TRUE     FALSE
## 10 growth_3 A_1      A_1_1      17.0 low_salin~ 3.33 TRUE     FALSE
## # ... with 14 more rows
```

Since two extreme outliers were found (B_2_6, C_2_1) remove extreme outliers so that results of ANOVA

```
no_exouts <- clean_tube_growth %>%
  dplyr::filter(growth < 7.90)
```

```
#check that extreme outliers were successfully removed
```

```
no_exouts %>%
  group_by(timestep) %>%
  identify_outliers(growth)
```

```
## # A tibble: 22 x 8
##   timestep replicate worm_id amt_cut_mm treatment growth is.outlier is.extreme
##   <fct>    <chr>    <fct>      <dbl> <fct>      <dbl> <lgl>    <lgl>
## 1 growth_1 B_1      B_1_2      16.1 high_temp  5.46 TRUE     FALSE
## 2 growth_1 B_1      B_1_6      15.4 high_temp  6.74 TRUE     FALSE
## 3 growth_1 B_1      B_1_8      14   high_temp  5.1  TRUE     FALSE
## 4 growth_1 C_2      C_2_5      13.8 control   5.15 TRUE     FALSE
## 5 growth_1 C_2      C_2_9      17.2 control   7.1  TRUE     FALSE
## 6 growth_2 B_2      B_2_6      19.5 high_temp  4.4  TRUE     FALSE
## 7 growth_2 B_2      B_2_8      15.0 high_temp  5.23 TRUE     FALSE
## 8 growth_2 C_3      C_3_9      13.7 control   5    TRUE     FALSE
## 9 growth_3 A_1      A_1_1      17.0 low_salin~ 3.33 TRUE     FALSE
## 10 growth_3 A_2      A_2_9      15.6 low_salin~ 4.1  TRUE     FALSE
## # ... with 12 more rows
```

```
#assumption of sphericity automatically checked by ANOVA test
```

One-way Repeated Measures Analysis of Variance (ANOVA)

```
# run one-way repeated measures ANOVA and obtain ANOVA table
```

```
tube.aov <- anova_test(data = clean_tube_growth, dv = growth,
                      wid = worm_id,
                      within = timestep)
get_anova_table(tube.aov)
```

```
## ANOVA Table (type III tests)
```

```
##
##      Effect  DFn  DFd      F      p p<.05  ges
## 1 timestep 3.01 268.12 23.846 9.41e-14 * 0.159
```

```
# run one-way repeated measures ANOVA for data with extreme outliers removed
```

```
noexouts.aov <- anova_test(data = no_exouts, dv = growth,
                          wid = worm_id,
                          within = timestep)
get_anova_table(noexouts.aov)
```

```
## ANOVA Table (type III tests)
```

```
##
##      Effect  DFn  DFd      F      p p<.05  ges
## 1 timestep 3.13 272.12 25.107 8.18e-15 * 0.174
```

```
# results of ANOVA do not change significantly (both are statistically significant) when extreme outliers
```

Pairwise Comparison

```
# performing pairwise comparison between timesteps
pwc <- clean_tube_growth %>%
  pairwise_t_test(growth ~ timestep, paired = TRUE,
    p.adjust.method = "bonferroni")

pwc <- pwc %>% add_xy_position(x = "timestep")

pwc
```

```
## # A tibble: 10 x 14
##   .y.    group1    group2      n1      n2 statistic    df          p    p.adj
##   <chr> <chr>    <chr>    <int> <int>    <dbl> <dbl>    <dbl>    <dbl>
## 1 growth growth_1 growth_2     90     90     4.50    89 2.08e- 5 2.08e- 4
## 2 growth growth_1 growth_3     90     90     5.63    89 2.09e- 7 2.09e- 6
## 3 growth growth_1 growth_4     90     90     6.27    89 1.26e- 8 1.26e- 7
## 4 growth growth_1 growth_5     90     90     8.22    89 1.54e-12 1.54e-11
## 5 growth growth_2 growth_3     90     90     1.72    89 8.8 e- 2 8.83e- 1
## 6 growth growth_2 growth_4     90     90     2.22    89 2.9 e- 2 2.88e- 1
## 7 growth growth_2 growth_5     90     90     3.67    89 4.18e- 4 4 e- 3
## 8 growth growth_3 growth_4     90     90     0.555    89 5.8 e- 1 1 e+ 0
## 9 growth growth_3 growth_5     90     90     2.10    89 3.8 e- 2 3.83e- 1
## 10 growth growth_4 growth_5     90     90     1.62    89 1.1 e- 1 1 e+ 0
## # ... with 5 more variables: p.adj.signif <chr>, y.position <dbl>,
## #   groups <named list>, xmin <dbl>, xmax <dbl>
```

Finding the Mean and Standard Error of Tube Growth in each Timestep

```
# finding the mean and standard error of tube growth in timestep 1
summary(tube_growth$growth_1)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.9525  1.5800  2.0116  2.5400  8.9000
```

```
se(tube_growth$growth_1)
```

```
## [1] 0.1663338
```

```
# finding the mean and standard error of tube growth in timestep 2
summary(tube_growth$growth_2)
```

```
##   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.000  0.200   0.800   1.089   1.600   5.230
```

```
se(tube_growth$growth_2)
```

```
## [1] 0.1190655
```

```
# finding the mean and standard error of tube growth in timestep 3
```

```
summary(tube_growth$growth_3)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.0000  0.4750  0.8648  1.2750  4.1000
```

```
se(tube_growth$growth_3)
```

```
## [1] 0.1078754
```

```
# finding the mean and standard error of tube growth in timestep 4
```

```
summary(tube_growth$growth_4)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.0000  0.3500  0.7856  1.1000  7.9000
```

```
se(tube_growth$growth_4)
```

```
## [1] 0.1211917
```

```
# finding the mean and standard error of tube growth in timestep 5
```

```
summary(tube_growth$growth_5)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.0000  0.3000  0.5794  0.9000  3.2000
```

```
se(tube_growth$growth_5)
```

```
## [1] 0.07921231
```

Finding the Mean and Standard Error of Tube Growth for Each Treatment Within all Timesteps

```
# Making a dataset containing only control growth values
```

```
control <- tube_growth %>%  
  dplyr::filter(treatment == "control")
```

```
# making a dataset containing only low salinity treatment growth values
```

```
salinity <- tube_growth %>%  
  dplyr::filter(treatment == "low_salinity")
```

```
# making a dataset containing only high temperature treatment growth values

temperature <- tube_growth %>%
  dplyr::filter(treatment == "high_temp")

# finding the mean and standard error of tube growth of all treatments for timestep 1

summary(control$growth_1)
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##    0.440   1.028   1.745   2.345   2.978   8.900
```

```
se(control$growth_1)
```

```
## [1] 0.3538703
```

```
summary(salinity$growth_1)
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##    0.000   0.950   1.350   1.684   2.118   3.980
```

```
se(salinity$growth_1)
```

```
## [1] 0.196041
```

```
summary(temperature$growth_1)
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##    0.0000   0.9475   1.6350   2.0060   2.5150   6.7400
```

```
se(temperature$growth_1)
```

```
## [1] 0.2890319
```

```
# finding the mean and standard error of tube growth of all treatments for timestep 2

summary(control$growth_2)
```

```
##      Min. 1st Qu.  Median      Mean 3rd Qu.      Max.
##    0.0000   0.3000   0.6500   0.9633   1.3125   5.0000
```

```
se(control$growth_2)
```

```
## [1] 0.1942408
```

```
summary(salinity$growth_2)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.000   0.125   0.600   0.753   1.212   2.800
```

```
se(salinity$growth_2)
```

```
## [1] 0.1356171
```

```
summary(temperature$growth_2)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.000   0.325   1.425   1.551   2.188   5.230
```

```
se(temperature$growth_2)
```

```
## [1] 0.2502065
```

```
# finding the mean and standard error of tube growth of all treatments for timestep 3
```

```
summary(control$growth_3)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.000   0.100   0.700   0.765   1.087   3.800
```

```
se(control$growth_3)
```

```
## [1] 0.1563622
```

```
summary(salinity$growth_3)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.000   0.000   0.350   0.946   1.600   4.100
```

```
se(salinity$growth_3)
```

```
## [1] 0.2195579
```

```
summary(temperature$growth_3)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##    0.0000   0.1625   0.5500   0.8833   1.5625   3.5000
```

```
se(temperature$growth_3)
```

```
## [1] 0.184131
```

```
# finding the mean and standard error of tube growth of all treatments for timestep 4
```

```
summary(control$growth_4)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0000  0.0000  0.8250  0.8117  1.3500  2.7500
```

```
se(control$growth_4)
```

```
## [1] 0.1536095
```

```
summary(salinity$growth_4)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##  0.0000  0.0000  0.1000  0.3683  0.6000  2.0500
```

```
se(salinity$growth_4)
```

```
## [1] 0.09329484
```

```
summary(temperature$growth_4)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   0.000   0.850   1.177   1.575   7.900
```

```
se(temperature$growth_4)
```

```
## [1] 0.3026961
```

```
# finding the mean and standard error of tube growth of all treatments for timestep 5
```

```
summary(control$growth_5)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   0.050   0.400   0.915   1.525   3.200
```

```
se(control$growth_5)
```

```
## [1] 0.1764944
```

```
summary(salinity$growth_5)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   0.000   0.000   0.100   0.335   0.500   1.800
```

```
se(salinity$growth_5)
```

```
## [1] 0.08228595
```

```
summary(temperature$growth_5)
```

```
##      Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
## 0.0000  0.0000  0.2250  0.4883  0.8875  2.5500
```

```
se(temperature$growth_5)
```

```
## [1] 0.1166999
```

Plotting the Timestep Data

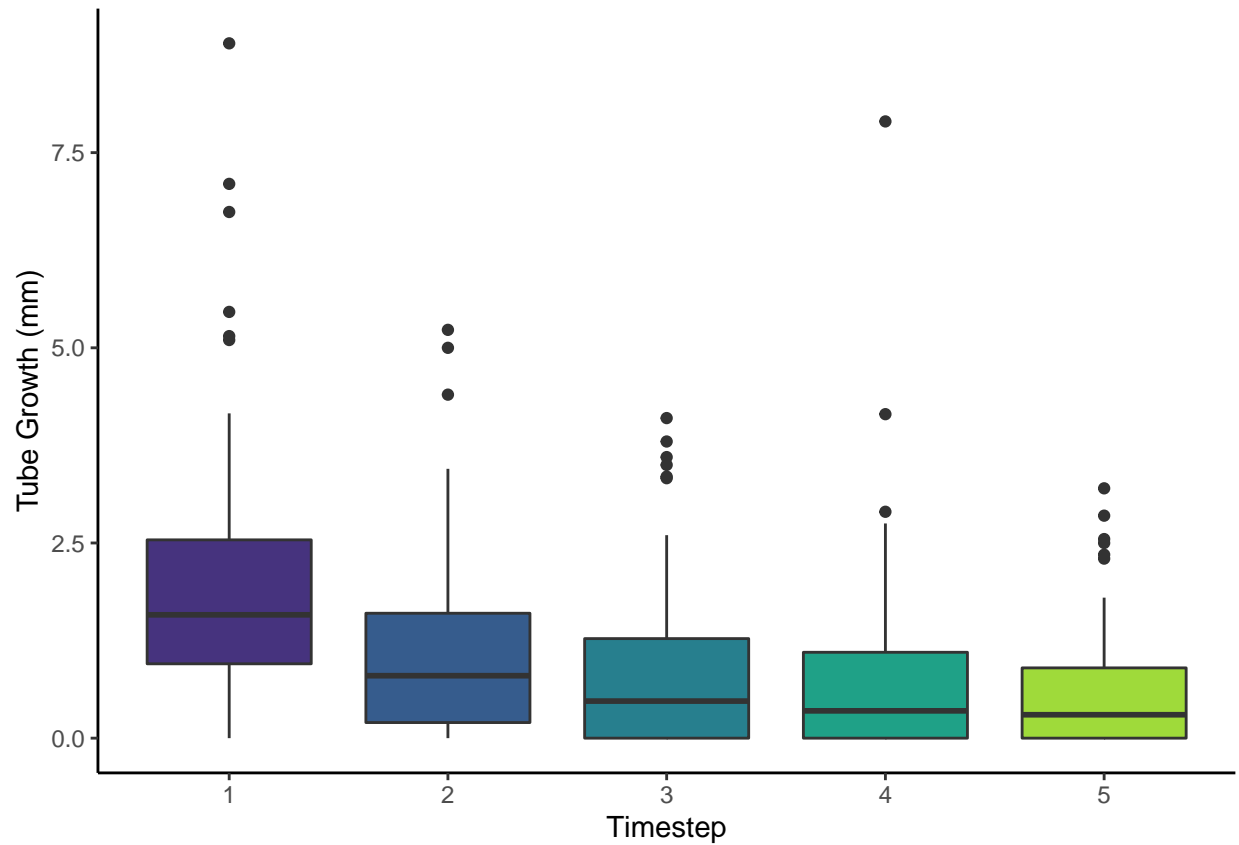
```
# choosing colours for one.way plot
```

```
one.way.cols = c("growth_1" = "#46337EFF", "growth_2" = "#365C8DFF", "growth_3" = "#277F8EFF", "growth_4" = "#1E6E9EFF", "growth_5" = "#0D5E8EFF")
```

```
# Making a plot of the mean growth of all treatments over all timesteps
```

```
one.way =  
  ggplot(clean_tube_growth, aes(x = timestep, y = growth)) +  
  geom_boxplot(aes(fill = timestep)) +  
  theme_classic() +  
  theme(legend.position = "none") +  
  xlab("Timestep") +  
  ylab("Tube Growth (mm)") +  
  scale_x_discrete(labels=c("growth_1" = "1", "growth_2" = "2", "growth_3" = "3", "growth_4" = "4", "growth_5" = "5")) +  
  scale_color_manual(values = one.way.cols) +  
  scale_fill_manual(values = one.way.cols)
```

```
one.way
```

```
# saving one.way plot
```

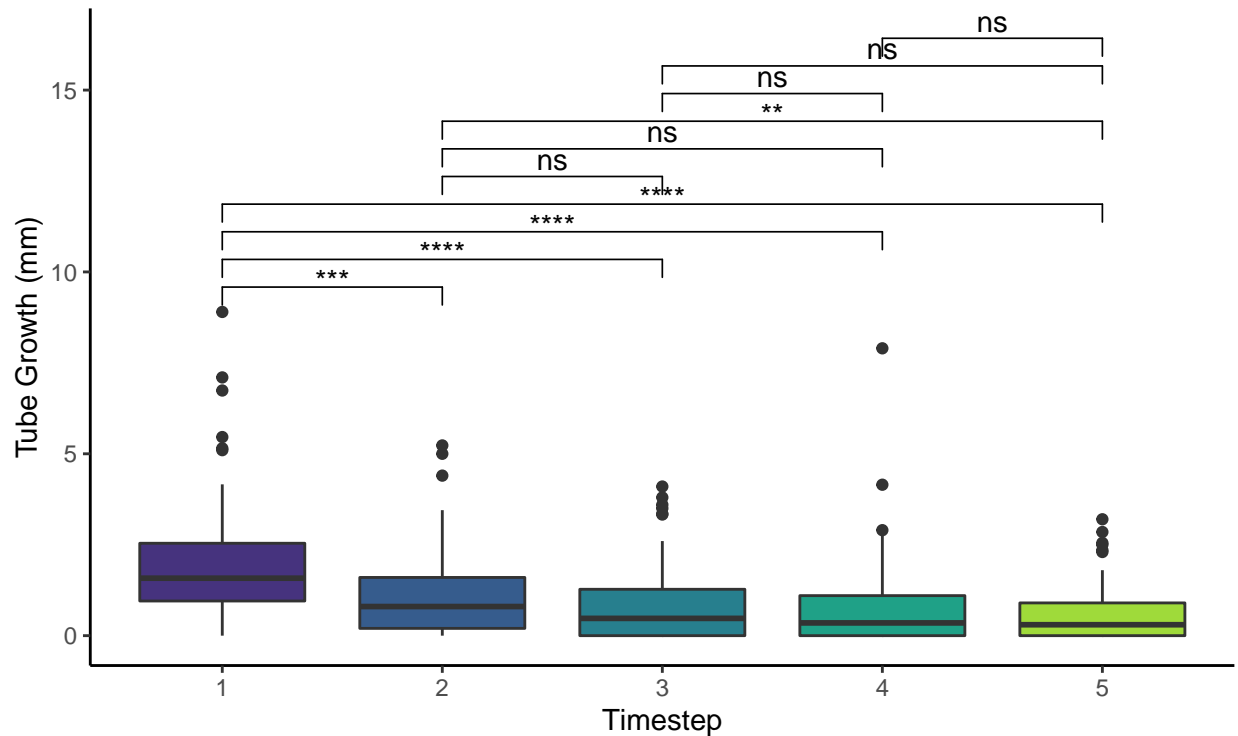
```
ggsave(plot = one.way, filename = "timestep-growth.jpg")
```

```
#adding significance bars from pairwise comparisons to one.way plot (significant bars labelled ns were )
```

```
p.one.way <- one.way +  
  stat_pvalue_manual(pwc) +  
  labs(subtitle = get_test_label(tube.aov, detailed = TRUE),  
       caption = get_pwc_label(pwc))
```

```
p.one.way
```

Anova, $F(3.01, 268.12) = 23.85$, $p = < 0.0001$, $\eta_g^2 = 0.16$



pwc: T test; p.adjust: Bonferroni

```
# saving p.one.way plot
```

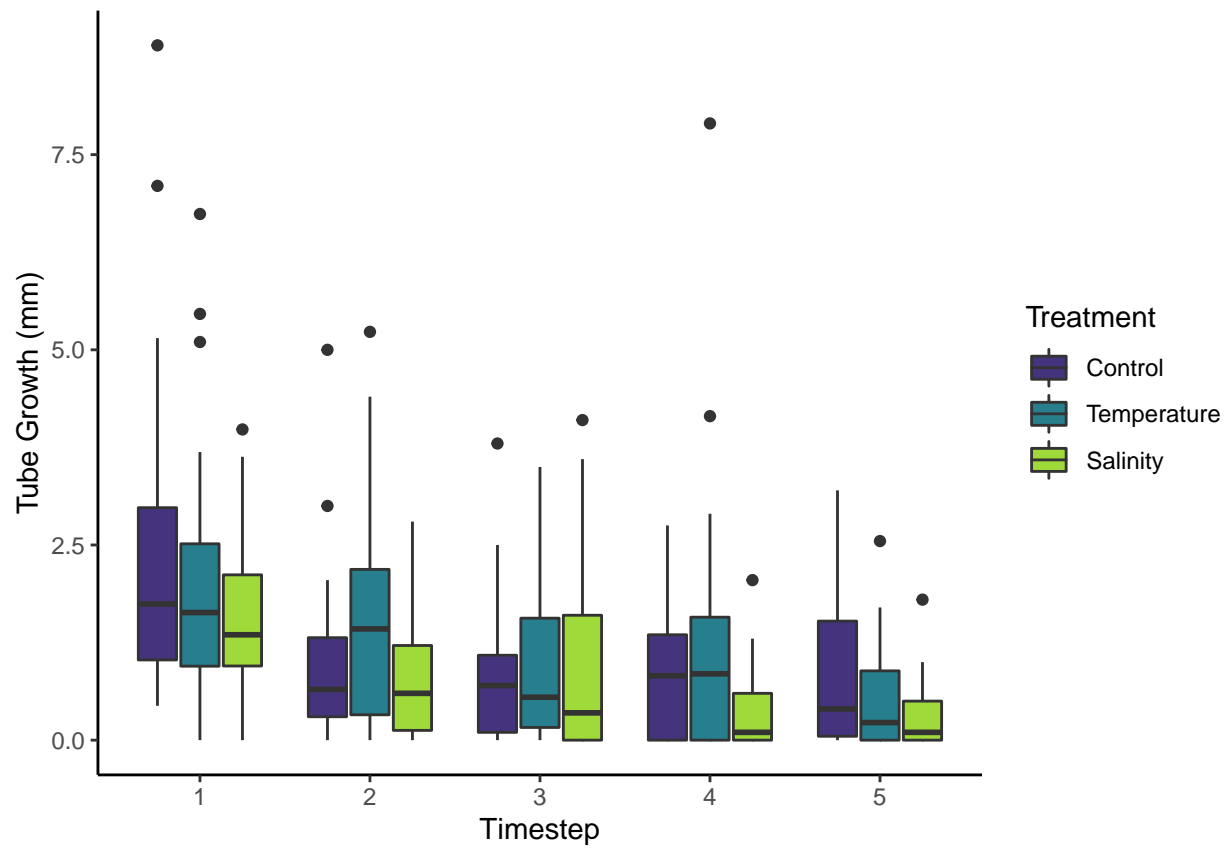
```
ggsave(plot = p.one.way, filename = "p-value-timestep-growth.jpg", width = 6, height = 7, dpi = 200, un
```

```
# Making a plot of the mean tube growth per treatment over all timesteps
```

```
treat.growth =
```

```
  ggplot(clean_tube_growth, aes(x = timestep, y = growth, fill = treatment)) +
    geom_boxplot() +
    scale_fill_manual(name = "Treatment", labels = c("Control", "Temperature", "Salinity"), values = c(
    theme_classic() +
    xlab("Timestep") +
    ylab("Tube Growth (mm)") +
    scale_x_discrete(labels=c("growth_1" = "1", "growth_2" = "2", "growth_3" = "3", "growth_4" = "4", "g
```

```
treat.growth
```



```
# saving treat.growth plot
```

```
ggsave(plot = treat.growth, filename = "treatment-timestep-growth.jpg")
```