

Results-analysis.r

sofyarabinovich

2021-03-18

```
#Download librarians
```

```
library(ggplot2)
```

```
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(viridis)
```

```
## Loading required package: viridisLite
```

```
library(tidyverse)
```

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

```
## v tibble 3.0.3      v purrr 0.3.4
```

```
## v tidyr 1.1.0      v stringr 1.4.0
```

```
## v readr 1.3.1      v forcats 0.5.0
```

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

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

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

```
library(ggpubr)
```

```
library(ggrepel)
```

```
library(ggsci)
```

```
library(ggsignif)
```

```
library(ggthemes)
```

```
#DISK DIFFUSION TESTS ANALYSIS
```

```
# make a variable that contains all bacterial names and print it out.
```

```

Titles <- c("Bacillus subtilis", "Mycobacterium smegmatis", "Proteus mirabilis")
#Order the titels
Titles_test <- c(rep("Bacillus subtilis", 3), rep("Mycobacterium smegmatis", 3), rep("Proteus mirabilis", 3))
#Treatment names
Treatment_names <- c("Compound combination", "penicillin only", "Tebipenem only")
#Create variables that contain ZOIs measurements according to the bacteria and the treatment
Bacillus_subtilis_Combination <- c(36.9, 34.44, 35.67)
Bacillus_subtilis_Tebipenem <- c(34.44, 29.52, 35.67)
Bacillus_subtilis_Penicillin <- c(0, 0, 0)
Mycobacterium_smeqmatis_Combination <- c(39.36, 36.9, 44.28)
Mycobacterium_smeqmatis_Tebipenem <- c(39.36, 34.44, 41.82)
Mycobacterium_smeqmatis_Penicillin <- c(0, 0, 0)
Proteus_mirabilis_Combination <- c(30.75, 31.98, 33.21)
Proteus_mirabilis_Tebipenem <- c(33.21, 31.98, 34.44)
Proteus_mirabilis_Penicillin <- c(27.06, 29.52, 31.98)
#Create a data frame of pLates results(this will make a table of the results) and print it out
results <- data.frame(Bacteria=Titles_test,
                      Compound_combination= c(Bacillus_subtilis_Combination,
                                                Mycobacterium_smeqmatis_Combination,
                                                Proteus_mirabilis_Combination),
                      Tebipenem_only= c(Bacillus_subtilis_Tebipenem,
                                          Mycobacterium_smeqmatis_Tebipenem,
                                          Proteus_mirabilis_Tebipenem),
                      Penicillin_only= c(Bacillus_subtilis_Penicillin,
                                          Mycobacterium_smeqmatis_Penicillin,
                                          Proteus_mirabilis_Penicillin))

print(results)

```

##	Bacteria	Compound_combination	Tebipenem_only	Penicillin_only
## 1	Bacillus subtilis	36.90	34.44	0.00
## 2	Bacillus subtilis	34.44	29.52	0.00
## 3	Bacillus subtilis	35.67	35.67	0.00
## 4	Mycobacterium smegmatis	39.36	39.36	0.00
## 5	Mycobacterium smegmatis	36.90	34.44	0.00
## 6	Mycobacterium smegmatis	44.28	41.82	0.00
## 7	Proteus mirabilis	30.75	33.21	27.06
## 8	Proteus mirabilis	31.98	31.98	29.52
## 9	Proteus mirabilis	33.21	34.44	31.98

```

#make up the variable that constructs the boxplot for Compound combination effect on three bacteria
my_comparisons <- list(c("Bacillus subtilis", "Mycobacterium smegmatis"),
                      c("Bacillus subtilis", "Proteus mirabilis"),
                      c("Mycobacterium smegmatis", "Proteus mirabilis"))
combin<-ggboxplot(results, x="Bacteria", y="Compound_combination", fill = "Bacteria")+
  theme(
    legend.position="none",
    plot.title = element_text(size=11)
  ) +
  ggtitle("c)Compound combination") +
  xlab("Bacteria")+
  ylab("ZOI in mm")+
  stat_boxplot(geom = "errorbar")+
  stat_compare_means(comparisons = my_comparisons,

```

```

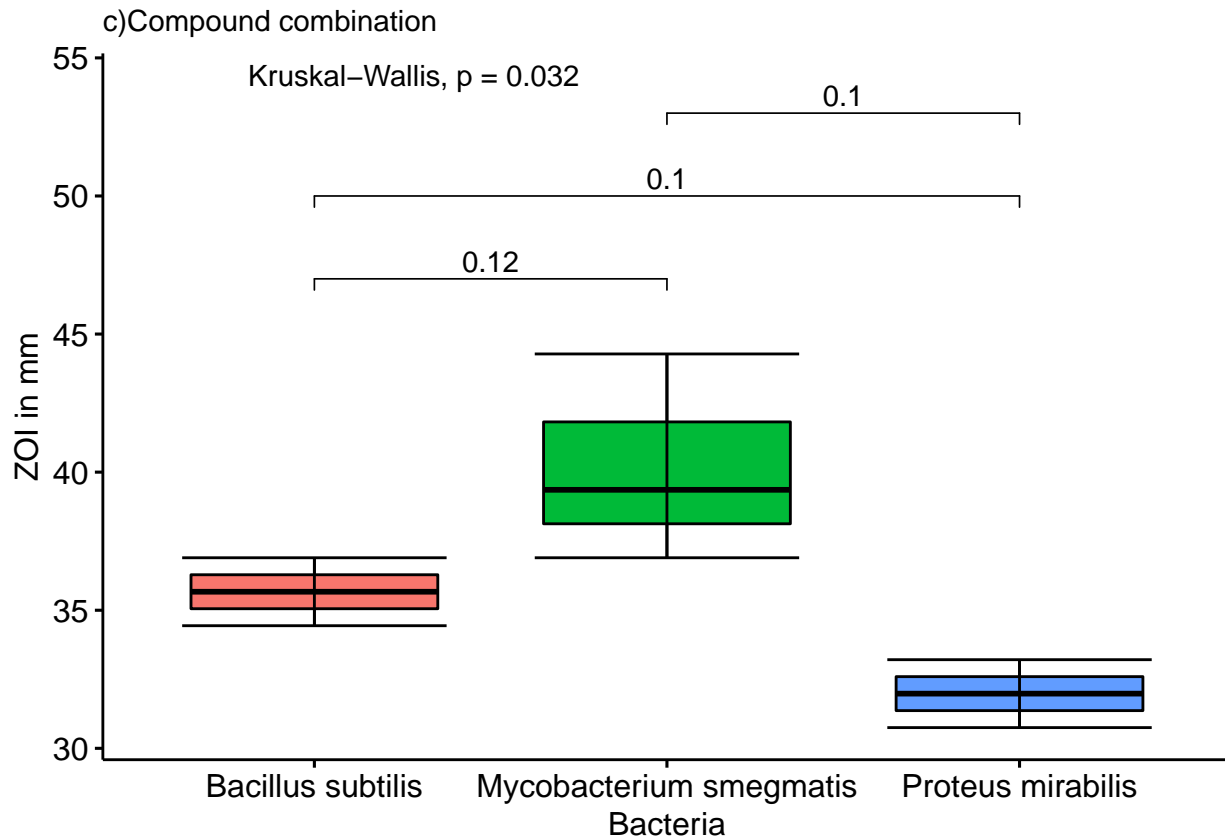
      label.y = c(47, 50, 53))+
  stat_compare_means(label.y = 54)
print(combin)

```

```

## Warning in wilcox.test.default(c(36.9, 34.44, 35.67), c(39.36, 36.9, 44.28):
## cannot compute exact p-value with ties

```



```

#Make up the boxplot for Tebipenem only on three bacteria
tebip <- ggboxplot(results,x="Bacteria",y="Tebipenem_only",fill = "Bacteria")+
  theme(
    legend.position="none",
    plot.title = element_text(size=11)
  ) +
  ggtitle("b)Tebipenem only") +
  xlab("Bacteria")+
  ylab("ZOI in mm")+
  stat_boxplot(geom = "errorbar")+
  stat_compare_means(comparisons = my_comparisons,
    label.y = c(44, 46, 48))+
  stat_compare_means(label.y = 50)
print(tebip)

```

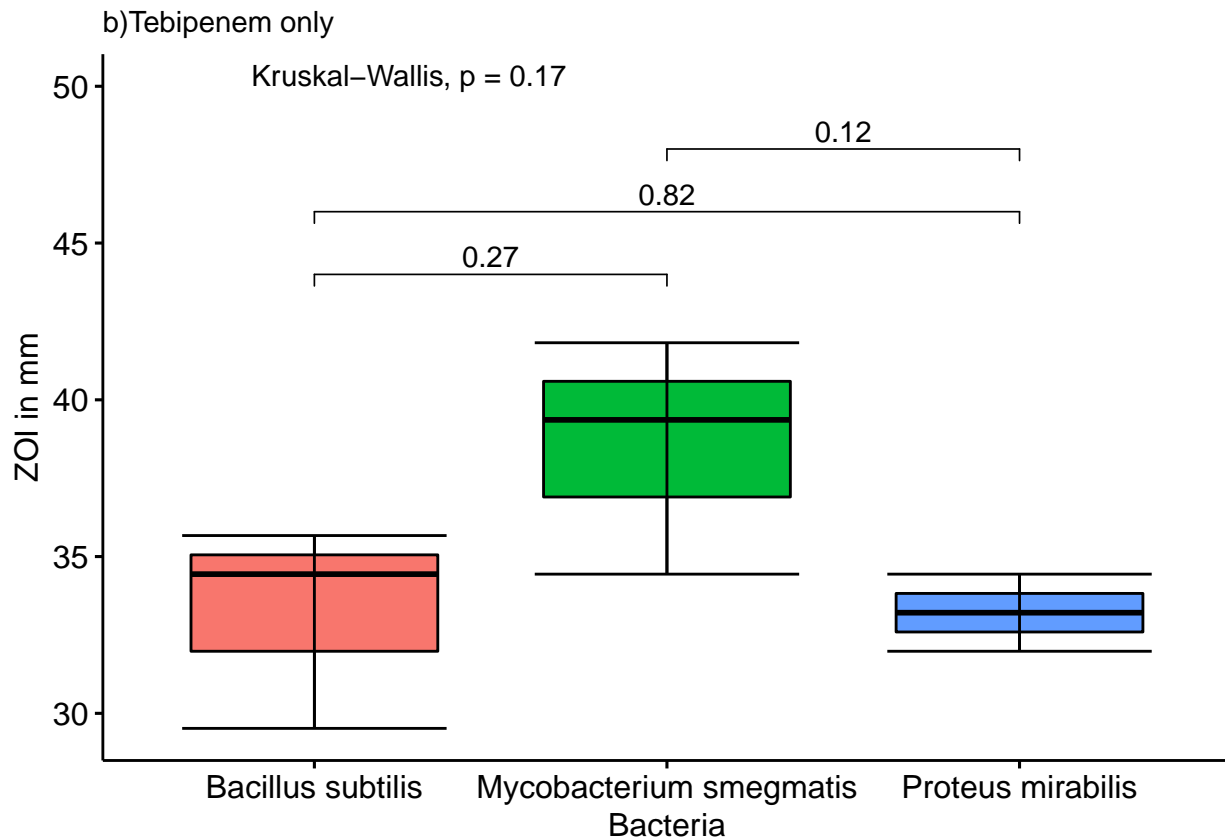
```

## Warning in wilcox.test.default(c(34.44, 29.52, 35.67), c(39.36, 34.44, 41.82):
## cannot compute exact p-value with ties

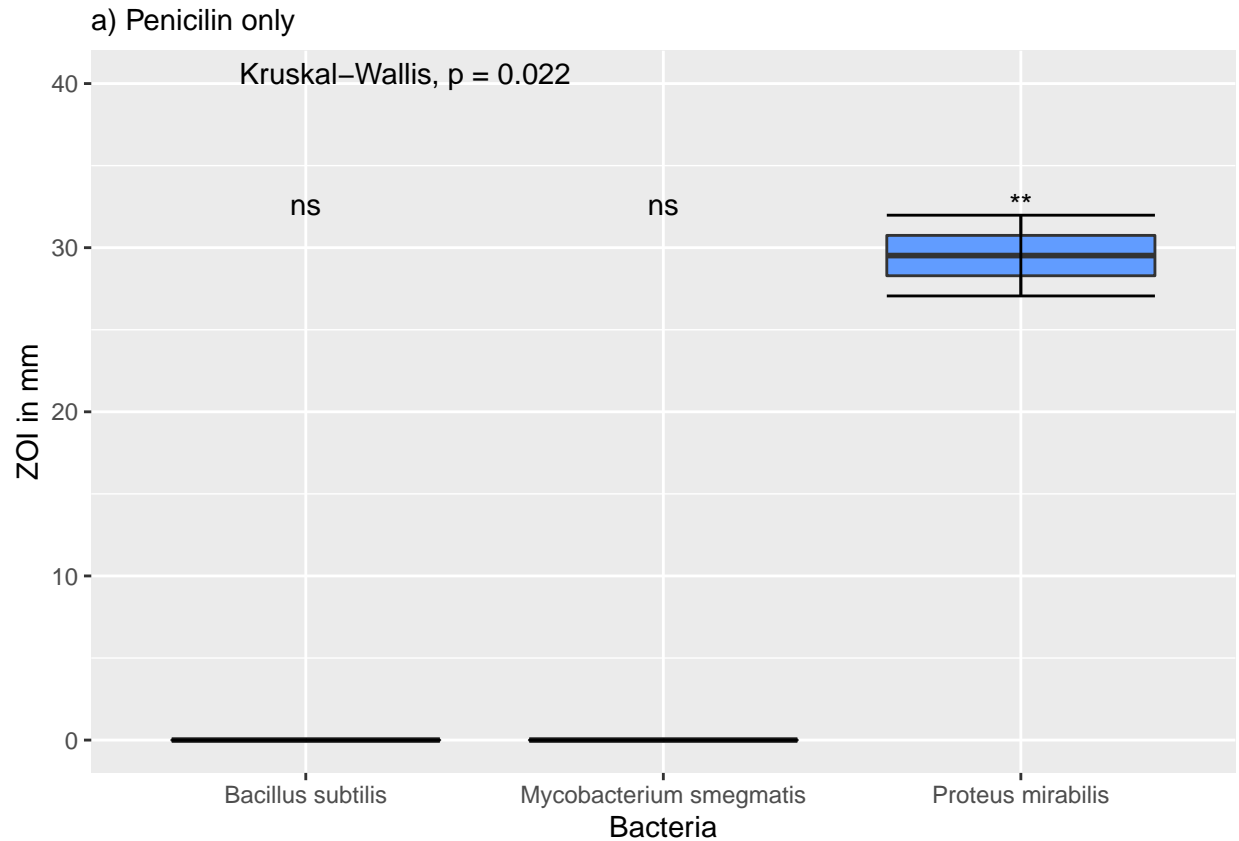
```

```
## Warning in wilcox.test.default(c(34.44, 29.52, 35.67), c(33.21, 31.98, 34.44):
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(39.36, 34.44, 41.82), c(33.21, 31.98, 34.44):
## cannot compute exact p-value with ties
```



```
#Make up boxplot for Penicillin only on three bacteria
p<-results %>%
  ggplot(aes(x=Bacteria,y=Penicillin_only,fill=Bacteria))+
  geom_boxplot() +
  theme(
    legend.position="none",
    plot.title = element_text(size=11)
  ) +
  ggtitle("a) Penicilin only") +
  xlab("Bacteria")+
  ylab("ZOI in mm")+
  stat_boxplot(geom = "errorbar")+
#Cannot compare pairwise because of the zero's
  stat_compare_means(method = "kruskal.test", label.y = 40)+
  stat_compare_means(label = "p.signif", method = "t.test",
    ref.group = ".all.")
print(p)
```



```
#Compare drug effect on the Bacillus subtilis with a new dataframe + boxplot
my_comparisons_2 <- list(c("Compound combination", "Tebipenem only"),
                        c("Compound combination", "Penicillin only"),
                        c("Penicillin only", "Tebipenem only"))
Bacillus_subtilis_data_frame <- data.frame(Treatments_names= c(rep("Compound combination", 3),
                                                                rep("Tebipenem only", 3),
                                                                rep("Penicillin only", 3)),
                                           Treatment=c(Bacillus_subtilis_Combination,
                                                         Bacillus_subtilis_Tebipenem,
                                                         Bacillus_subtilis_Penicilin))
print(Bacillus_subtilis_data_frame)
```

```
##      Treatments_names Treatment
## 1 Compound combination    36.90
## 2 Compound combination    34.44
## 3 Compound combination    35.67
## 4      Tebipenem only    34.44
## 5      Tebipenem only    29.52
## 6      Tebipenem only    35.67
## 7      Penicillin only     0.00
## 8      Penicillin only     0.00
## 9      Penicillin only     0.00
```

```
#Making a boxplot
Bacillus_subtilis_boxplot <-
```

```

ggboxplot(Bacillus_subtilis_data_frame,x="Treatments_names",y="Treatment",
          fill = "Treatment")+
theme(
  legend.position="none",
  plot.title = element_text(size=11)
) +
ggtitle("c) Effect of drugs n Bacillus subtilis") +
xlab("Antibiotic")+
ylab("ZOI in mm")+
stat_boxplot(geom = "errorbar")+
stat_compare_means(comparisons = my_comparisons_2,
                  label.y = c(39, 41, 43))+
stat_compare_means(label.y = 44)
print(Bacillus_subtilis_boxplot)

```

```

## Warning in wilcox.test.default(c(36.9, 34.44, 35.67), c(34.44, 29.52, 35.67):
## cannot compute exact p-value with ties

```

```

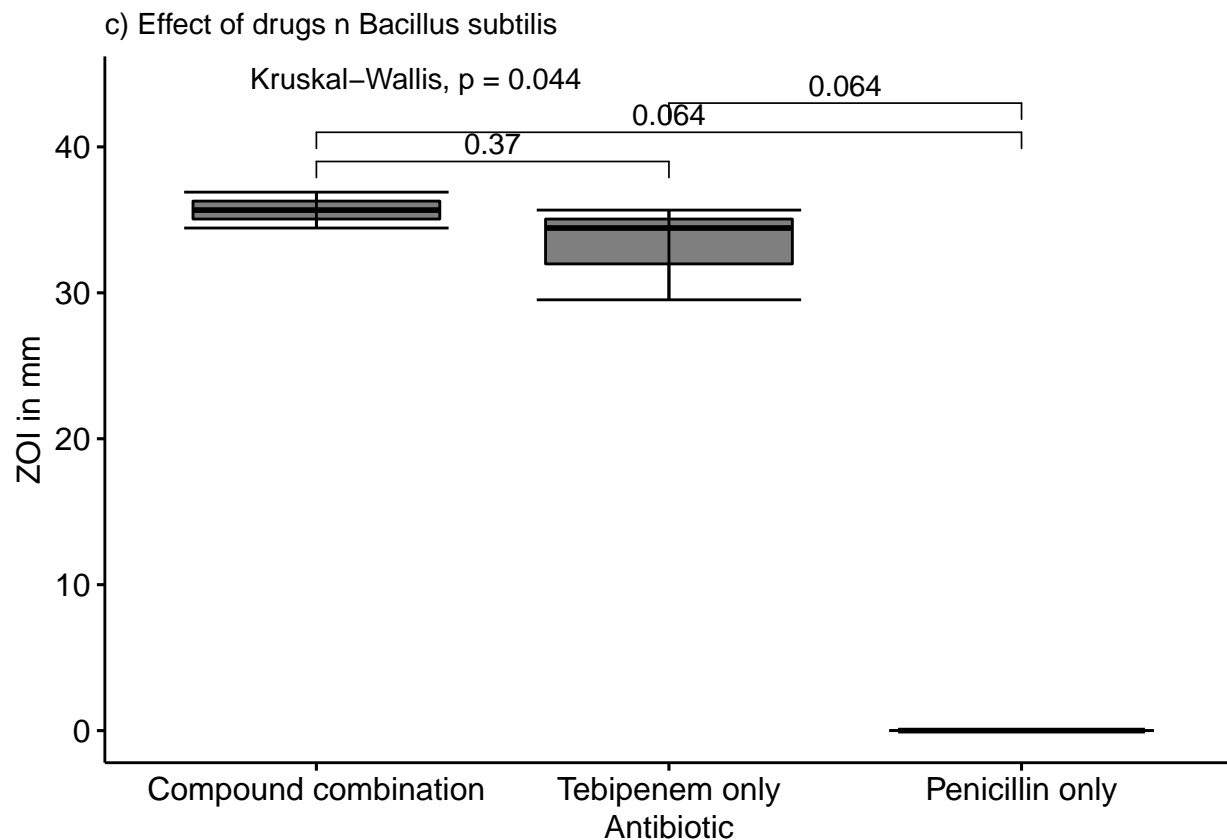
## Warning in wilcox.test.default(c(36.9, 34.44, 35.67), c(0, 0, 0), paired =
## FALSE): cannot compute exact p-value with ties

```

```

## Warning in wilcox.test.default(c(0, 0, 0), c(34.44, 29.52, 35.67), paired =
## FALSE): cannot compute exact p-value with ties

```



```

#Compare drugs effects on Mycobacterium smegmatis (do the same as the previous part)
Mycobacterium_smegmatis_data_frame <- data.frame(Treatments_names_2=
c(rep("Compound combination",3),
  rep("Tebipenem only",3),
  rep("Penicillin only",3)),
  Treatment_2=c(Mycobacterium_smegmatis_Combination,
    Mycobacterium_smegmatis_Tebipenem,
    Mycobacterium_smegmatis_Penicillin))

print(Mycobacterium_smegmatis_data_frame)

```

```

##      Treatments_names_2 Treatment_2
## 1 Compound combination      39.36
## 2 Compound combination      36.90
## 3 Compound combination      44.28
## 4      Tebipenem only      39.36
## 5      Tebipenem only      34.44
## 6      Tebipenem only      41.82
## 7      Penicillin only       0.00
## 8      Penicillin only       0.00
## 9      Penicillin only       0.00

```

```

Mycobacterium_smegmatis_boxplot <-
  ggboxplot(Mycobacterium_smegmatis_data_frame,x="Treatments_names_2",
    y="Treatment_2",fill="Treatment_2")+
  theme(
    legend.position="none",
    plot.title = element_text(size=11)
  ) +
  ggtitle("a) Effect of drugs on Mycobacterium smegmatis") +
  xlab("Antibiotic")+
  ylab("ZOI in mm")+
  stat_boxplot(geom = "errorbar")+
  stat_compare_means(comparisons = my_comparisons_2,
    label.y = c(45, 47 , 50))+
  stat_compare_means(label.y = 50)
print(Mycobacterium_smegmatis_boxplot)

```

```

## Warning in wilcox.test.default(c(39.36, 36.9, 44.28), c(39.36, 34.44, 41.82):
## cannot compute exact p-value with ties

```

```

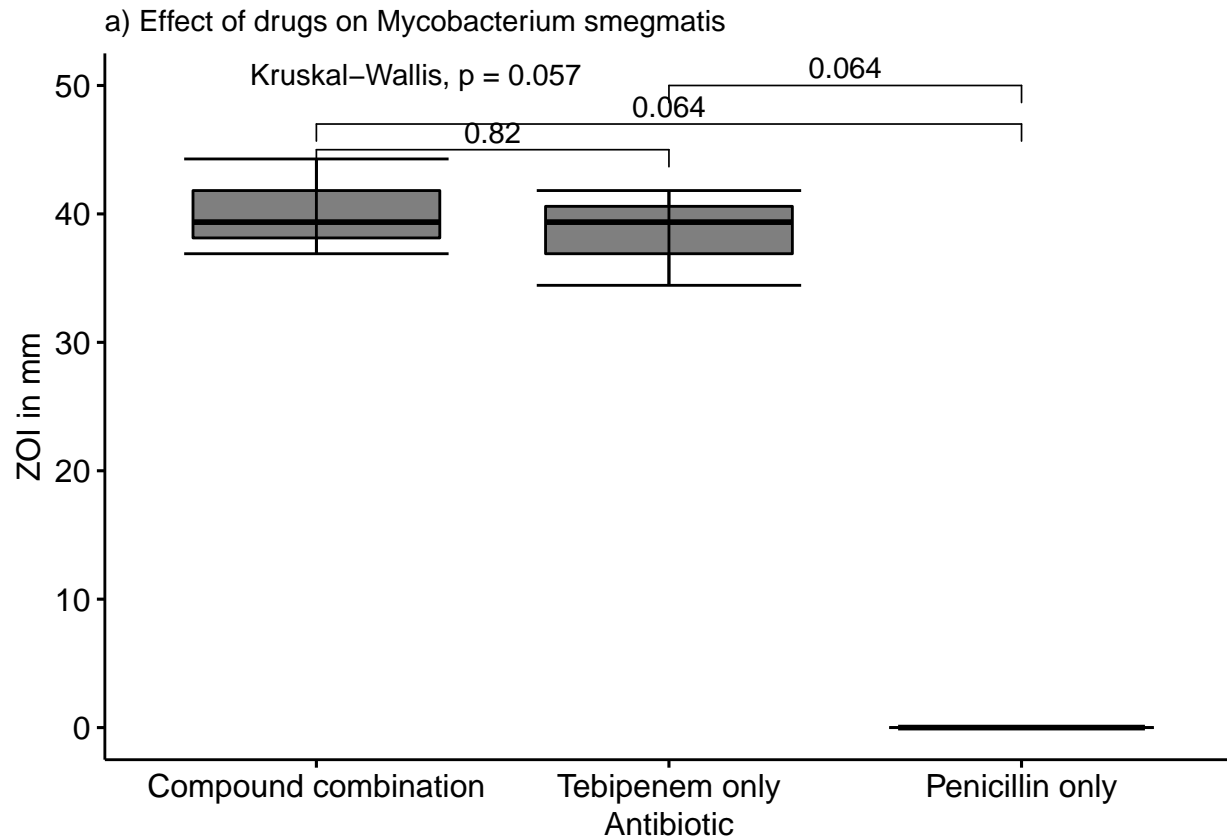
## Warning in wilcox.test.default(c(39.36, 36.9, 44.28), c(0, 0, 0), paired =
## FALSE): cannot compute exact p-value with ties

```

```

## Warning in wilcox.test.default(c(0, 0, 0), c(39.36, 34.44, 41.82), paired =
## FALSE): cannot compute exact p-value with ties

```



```
# Compare drugs effects on Proteus mirabilis (do the same as the previous part)
Proteus_mirabilis_dataframe <- data.frame(Treatments_names_3 =
  c(rep("Compound combination", 3),
    rep("Tebipenem only", 3),
    rep("Penicillin only", 3)),
  Treatment_3 = c(Proteus_mirabilis_Combination,
    Proteus_mirabilis_Tebipenem,
    Proteus_mirabilis_Penicillin))

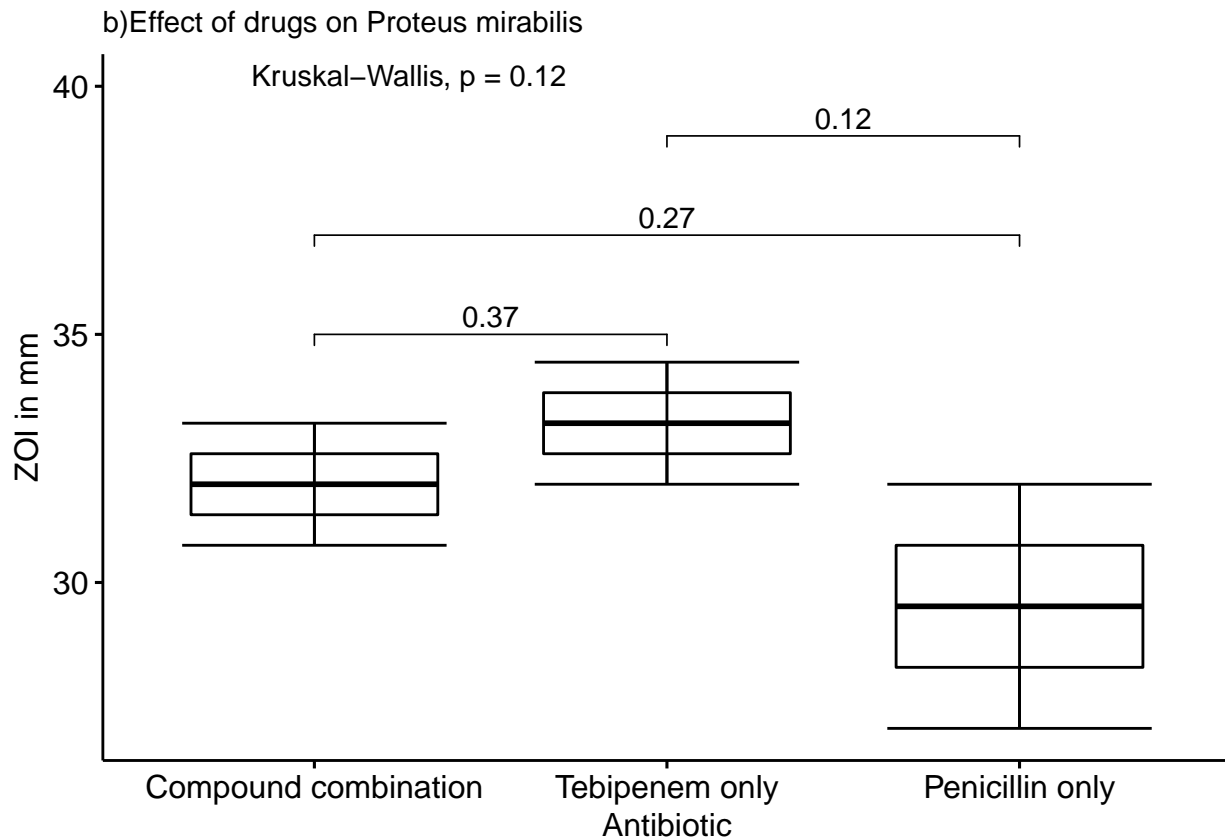
Proteus_mirabilis_boxplot <-
  ggboxplot(Proteus_mirabilis_dataframe, x = "Treatments_names_3",
    y = "Treatment_3", fill = "Treatment_3") +
  theme(
    legend.position = "none",
    plot.title = element_text(size = 11)
  ) +
  ggtitle("b) Effect of drugs on Proteus mirabilis") +
  xlab("Antibiotic") +
  ylab("ZOI in mm") +
  stat_boxplot(geom = "errorbar") +
  stat_compare_means(comparisons = my_comparisons_2,
    label.y = c(35, 37, 39)) +
  stat_compare_means(label.y = 40)
print(Proteus_mirabilis_boxplot)
```

```
## Warning in wilcox.test.default(c(30.75, 31.98, 33.21), c(33.21, 31.98, 34.44):
## cannot compute exact p-value with ties
```



```
## Warning in wilcox.test.default(c(30.75, 31.98, 33.21), c(27.06, 29.52, 31.98):
## cannot compute exact p-value with ties
```

```
## Warning in wilcox.test.default(c(27.06, 29.52, 31.98), c(33.21, 31.98, 34.44):
## cannot compute exact p-value with ties
```



```
# CHECHERBOARD ASSAY TESTS ANALYSIS
#BACILLUS SUBTILIS RESULTS AND PLOTS
#Penicillin 100 ug/mL
```

```
Bacillus_Penicillin_100ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
Optical_density_mean_values=c((mean(0.053 , 0.052 , 0.051)-
(mean(0.054 , 0.052 , 0.052)-
(mean(0.054 , 0.052 , 0.052)-
(mean(0.053,0.054,0.053)-0.3
(mean(0.054,0.044,0.053)-0.3
(mean(0.052,0.054,0.054)-0.3
(mean(0.054,0.054,0.053)-0.3
(mean(0.054,0.055,0.054)-0.3
(mean(0.038 , 0.038,0.038)-me
(mean(0.038,0.038,0.362)-mea
(mean(0.038,0.038,0.038)-mea
(mean(0.041,0.04,0.041)-mean
(mean(0.041,0.372,0.039)-mea
(mean(0.055,0.041,0.146)-mea
```

```

((mean(0.181,0.176,0.187)-mea
((mean(0.374,0.367,0.364)-mea
((mean(0.038,0.038,0.039)-mea
((mean(0.038,0.038,0.289)-mea
((mean(0.038,0.038,0.039)-mea
((mean(0.041,0.039,0.041)-mea
((mean(0.04,0.397,0.041)-mea
((mean(0.118,0.039,0.213)-mea
((mean(0.212,0.227,0.252)-mea
((mean(0.352,0.389,0.409)-mea
((mean(0.038,0.037,0.038)-0.
((mean(0.038,0.038,0.518)-0.
((mean(0.038,0.038,0.038)-0.
((mean(0.04,0.04,0.038)-0.03
((mean(0.193,0.449,0.039)-0.
((mean(0.4,0.122,0.568)-0.03
((mean(0.426,0.36,0.521)-0.03
((mean(0.478,0.444,0.57)-0.03
((mean(0.038,0.042,0.037)-0.
((mean(0.038,0.037,0.479)-0.
((mean(0.038,0.038,0.039)-0.
((mean(0.039,0.039,0.06)-0.03
((mean(0.244,0.503,0.048)-0.
((mean(0.473,0.205,0.575)-0.
((mean(0.454,0.371,0.478)-0.
((mean(0.517,0.452,0.566)-0.

print(Bacillus_Penicillin_100ug_data)

```

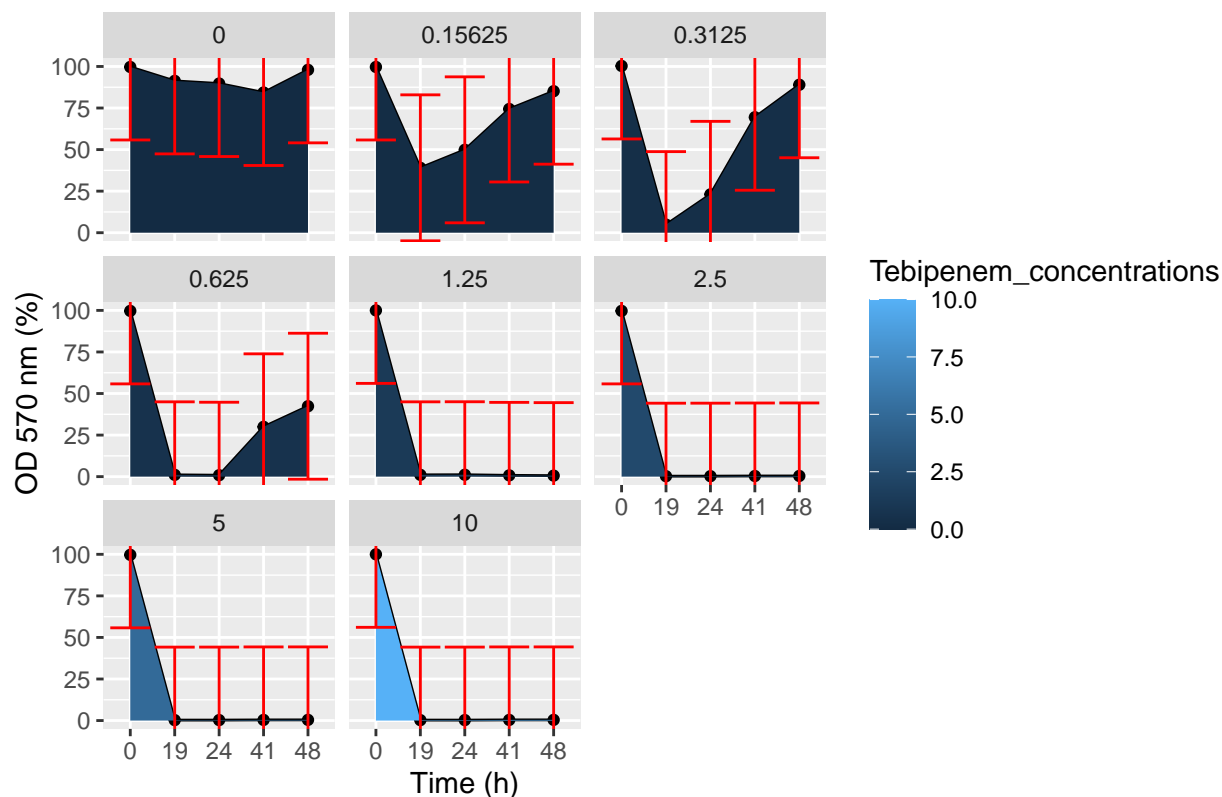
##	Time	Tebipenem_concentrations	Optical_density_mean_values
## 1	0	10.00000	100.0000000
## 2	0	5.00000	99.6941896
## 3	0	2.50000	99.6941896
## 4	0	1.25000	100.0000000
## 5	0	0.62500	99.6941896
## 6	0	0.31250	100.3058104
## 7	0	0.15625	99.6941896
## 8	0	0.00000	99.6941896
## 9	19	10.00000	0.2710027
## 10	19	5.00000	0.2710027
## 11	19	2.50000	0.2710027
## 12	19	1.25000	1.0840108
## 13	19	0.62500	1.0840108
## 14	19	0.31250	4.8780488
## 15	19	0.15625	39.0243902
## 16	19	0.00000	91.3279133
## 17	24	10.00000	0.2849003
## 18	24	5.00000	0.2849003
## 19	24	2.50000	0.2849003
## 20	24	1.25000	1.1396011
## 21	24	0.62500	0.8547009
## 22	24	0.31250	23.0769231
## 23	24	0.15625	49.8575499
## 24	24	0.00000	89.7435897

## 25	41	10.00000	0.3816794
## 26	41	5.00000	0.3816794
## 27	41	2.50000	0.3816794
## 28	41	1.25000	0.7633588
## 29	41	0.62500	29.9618321
## 30	41	0.31250	69.4656489
## 31	41	0.15625	74.4274809
## 32	41	0.00000	84.3511450
## 33	48	10.00000	0.4073320
## 34	48	5.00000	0.4073320
## 35	48	2.50000	0.4073320
## 36	48	1.25000	0.6109980
## 37	48	0.62500	42.3625255
## 38	48	0.31250	89.0020367
## 39	48	0.15625	85.1323829
## 40	48	0.00000	97.9633401

#Make a line graphs for changing in OD with time according to Tebipenem concentrations

```
bp1<- Bacillus_Penicillin_100ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 100 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_Penicillin_100ug_data$Optical_density_mean_values-sd(Bacillus_Penicillin_
  ymax=Bacillus_Penicillin_100ug_data$Optical_density_mean_values+sd(Bacillus_Penicillin_
print(bp1)
```

Penicillin 100 ug/mL



#Penicillin 50 ug/mL

```
Bacillus_subtilis_50ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values=c((mean(0.054,0.051,0.05)-0.036),
((mean(0.053,0.078,0.052)-0.036),
((mean(0.052,0.06,0.052)-0.036),
((mean(0.052,0.056,0.053)-0.036),
((mean(0.052,0.046,0.054)-0.036),
((mean(0.052,0.056,0.054)-0.036),
((mean(0.053,0.054,0.055)-0.036),
((mean(0.053,0.054,0.054)-0.036),
((mean(0.037,0.036,0.036)-mean(0.036)),
((mean(0.04,0.037,0.049)-mean(0.036)),
((mean(0.037,0.037,0.04)-mean(0.036)),
((mean(0.04,0.04,0.041)-mean(0.036)),
((mean(0.041,0.0404,0.041)-mean(0.036)),
((mean(0.096,0.041,0.105)-mean(0.036)),
((mean(0.194,0.173,0.219)-mean(0.036)),
((mean(0.406,0.414,0.414)-mean(0.036)),
((mean(0.038,0.039,0.039)-mean(0.036)),
((mean(0.038,0.039,0.049)-mean(0.036)),
((mean(0.039,0.038,0.042)-mean(0.036)),
((mean(0.043,0.042,0.044)-mean(0.036)),
((mean(0.065,0.431,0.043)-mean(0.036)),
((mean(0.143,0.045,0.158)-mean(0.036)),
((mean(0.222,0.216,0.262)-mean(0.036))
```

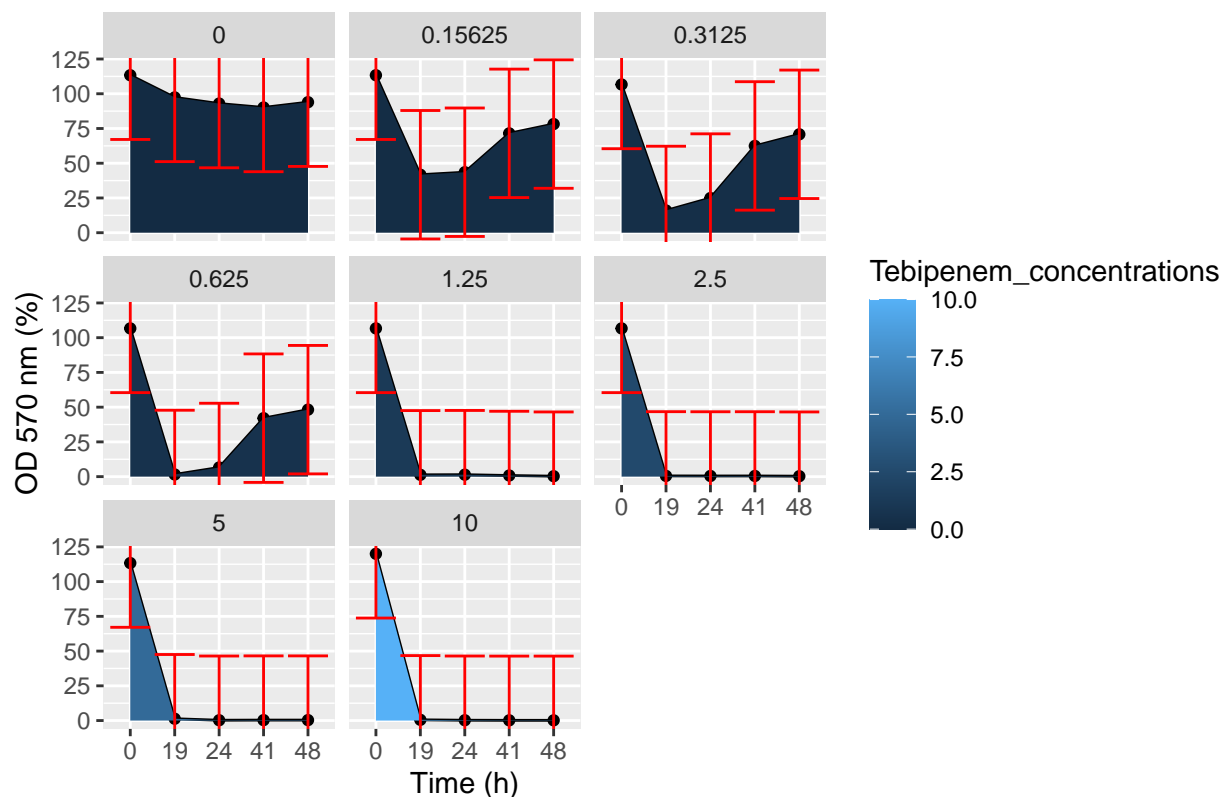
```

((mean(0.432,0.467,0.442)-mean(
((mean(0.038,0.039,0.038)-mean(
((mean(0.039,0.039,0.047)-mean(
((mean(0.04,0.039,0.041)-mean(0
((mean(0.042,0.041,0.041)-mean(
((mean(0.297,0.575,0.044)-mean(
((mean(0.423,0.078,0.467)-mean(
((mean(0.479,0.379,0.51)-mean(0
((mean(0.594,0.517,0.632)-mean(
((mean(0.038,0.042,0.059)-mean(
((mean(0.039,0.04,0.048)-mean(0
((mean(0.039,0.039,0.041)-mean(
((mean(0.039,0.041,0.041)-mean(
((mean(0.331,0.595,0.06)-mean(0
((mean(0.469,0.153,0.506)-mean(
((mean(0.514,0.448,0.54)-mean(0
((mean(0.61,0.573,0.643)-mean(0

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
bp2 <-Bacillus_subtilis_50ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 50 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_50ug_data$Optical_density_mean_values-sd(Bacillus_subtilis_50ug_c
    ymax=Bacillus_subtilis_50ug_data$Optical_density_mean_values+sd(Bacillus_subtilis_50ug_c
print(bp2)

```

Penicillin 50 ug/mL



#Penicillin 25 ug/mL

```
Bacillus_subtilis_25ug_data <-data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
Optical_density_mean_values =c(((mean(0.051,0.05,0.049)-0.035),
((mean(0.059,0.05,0.052)-0.035),
((mean(0.05,0.051,0.05)-0.035)/
((mean(0.051,0.053,0.053)-0.035),
((mean(0.052,0.051,0.053)-0.035),
((mean(0.051,0.053,0.051)-0.035),
((mean(0.052,0.054,0.053)-0.035),
((mean(0.052,0.053,0.054)-0.035),
((mean(0.038,0.039,0.04)-mean(0.035)),
((mean(0.038,0.039,0.041)-mean(0.035)),
((mean(0.038,0.039,0.039)-mean(0.035)),
((mean(0.042,0.043,0.043)-mean(0.035)),
((mean(0.043,0.385,0.043)-mean(0.035)),
((mean(0.29,0.044,0.088)-mean(0.035)),
((mean(0.179,0.173,0.201)-mean(0.035)),
((mean(0.384,0.402,0.401)-mean(0.035)),
((mean(0.036,0.068,0.039)-mean(0.035)),
((mean(0.036,0.037,0.038)-mean(0.035)),
((mean(0.036,0.037,0.037)-mean(0.035)),
((mean(0.041,0.042,0.041)-mean(0.035)),
((mean(0.061,0.384,0.041)-mean(0.035)),
((mean(0.25,0.041,0.142)-mean(0.035)),
((mean(0.208,0.212,0.233)-mean(0.035)))))
```

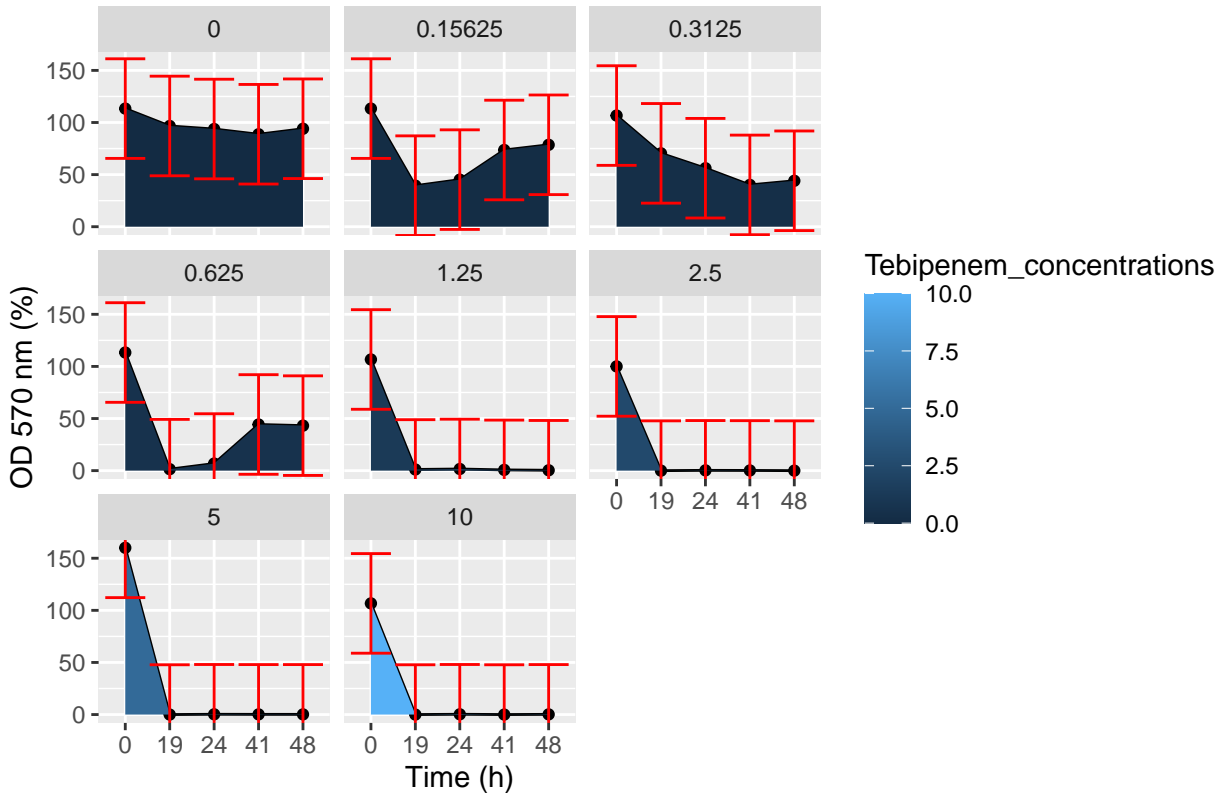
```

((mean(0.394,0.405,0.402)-mean(
((mean(0.034,0.049,0.036)-mean(
((mean(0.035,0.036,0.044)-mean(
((mean(0.035,0.036,0.039)-mean(
((mean(0.038,0.04,0.039)-mean(0
((mean(0.289,0.543,0.15)-mean(0
((mean(0.265,0.079,0.438)-mean(
((mean(0.458,0.338,0.488)-mean(
((mean(0.545,0.409,0.602)-mean(
((mean(0.035,0.055,0.036)-mean(
((mean(0.035,0.037,0.042)-mean(
((mean(0.034,0.068,0.036)-mean(
((mean(0.036,0.038,0.037)-mean(
((mean(0.278,0.557,0.226)-mean(
((mean(0.283,0.145,0.477)-mean(
((mean(0.478,0.417,0.511)-mean(
((mean(0.565,0.5,0.628)-mean(0.

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
bp3 <- Bacillus_subtilis_25ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 25 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_25ug_data$Optical_density_mean_values-sd(Bacillus_subtilis_25ug_c
                ymax=Bacillus_subtilis_25ug_data$Optical_density_mean_values+sd(Bacillus_subtilis_25ug_c
print(bp3)

```

Penicillin 25 ug/mL



#Penicillin 12.5 ug/mL

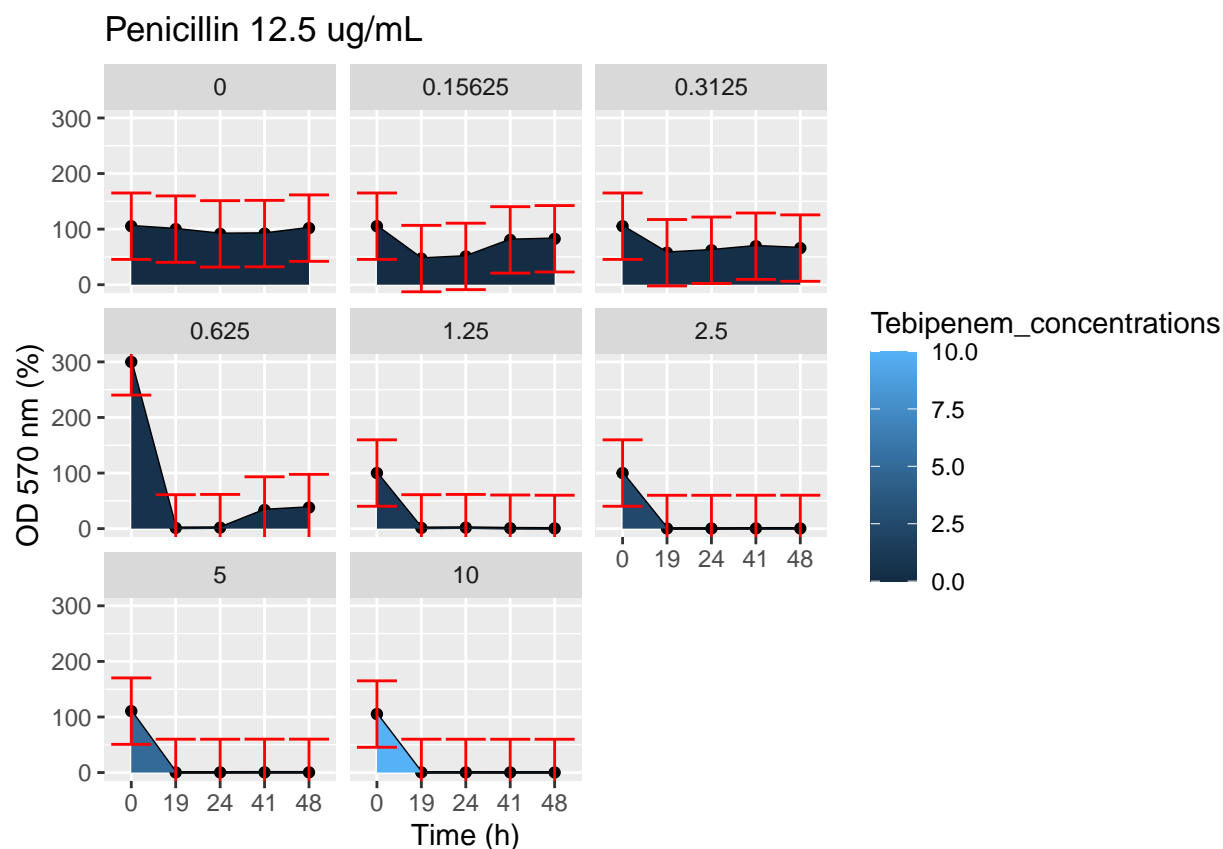
[illegible]


```

((mean(0.391,0.395,0.396)-mean
((mean(0.038,0.054,0.039)-mean
((mean(0.039,0.041,0.045)-mean
((mean(0.039,0.039,0.04)-mean
((mean(0.041,0.042,0.042)-mean
((mean(0.217,0.505,0.358)-mean
((mean(0.409,0.142,0.54)-mean
((mean(0.47,0.339,0.494)-mean
((mean(0.531,0.393,0.58)-mean
((mean(0.038,0.059,0.04)-mean
((mean(0.039,0.04,0.041)-mean
((mean(0.039,0.086,0.04)-mean
((mean(0.039,0.04,0.041)-mean
((mean(0.245,0.533,0.351)-mean
((mean(0.398,0.241,0.532)-mean
((mean(0.49,0.408,0.507)-mean
((mean(0.558,0.483,0.624)-mean

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
bp4 <- Bacillus_subtilis_12.5ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point() +
  geom_area()+
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 12.5 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_12.5ug_data$Optical_density_mean_values-sd(Bacillus_subtilis_12.5
                ymax=Bacillus_subtilis_12.5ug_data$Optical_density_mean_values+sd(Bacillus_subtilis_12.5
print(bp4)

```



#Penicillin 6.25 ug/mL

```
Bacillus_subtilis_6.25ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep(
  Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
  Optical_density_mean_values =c(((mean(0.055,0.055,0.052)-mean(0.057,0.053,0.054))-mean(0.057,0.056,0.054))-mean(0.057,0.061,0.056))-mean(0.055,0.054,0.056))-mean(0.055,0.055,0.054))-mean(0.055,0.058,0.057))-mean(0.059,0.055,0.057))-mean(0.036,0.036,0.038))-mean(0.036,0.037,0.037))-mean(0.036,0.037,0.037))-mean(0.04,0.04,0.041))-mean(0.04,0.403,0.042))-mean(0.107,0.042,0.111))-mean(0.188,0.183,0.233))-mean(0.393,0.411,0.408))-mean(0.036,0.037,0.039))-mean(0.036,0.037,0.037))-mean(0.036,0.037,0.036))-mean(0.041,0.041,0.041))-mean(0.041,0.391,0.067))-mean(0.175,0.041,0.174))-mean(0.239,0.224,0.271))-mean(0.239,0.224,0.271))
```

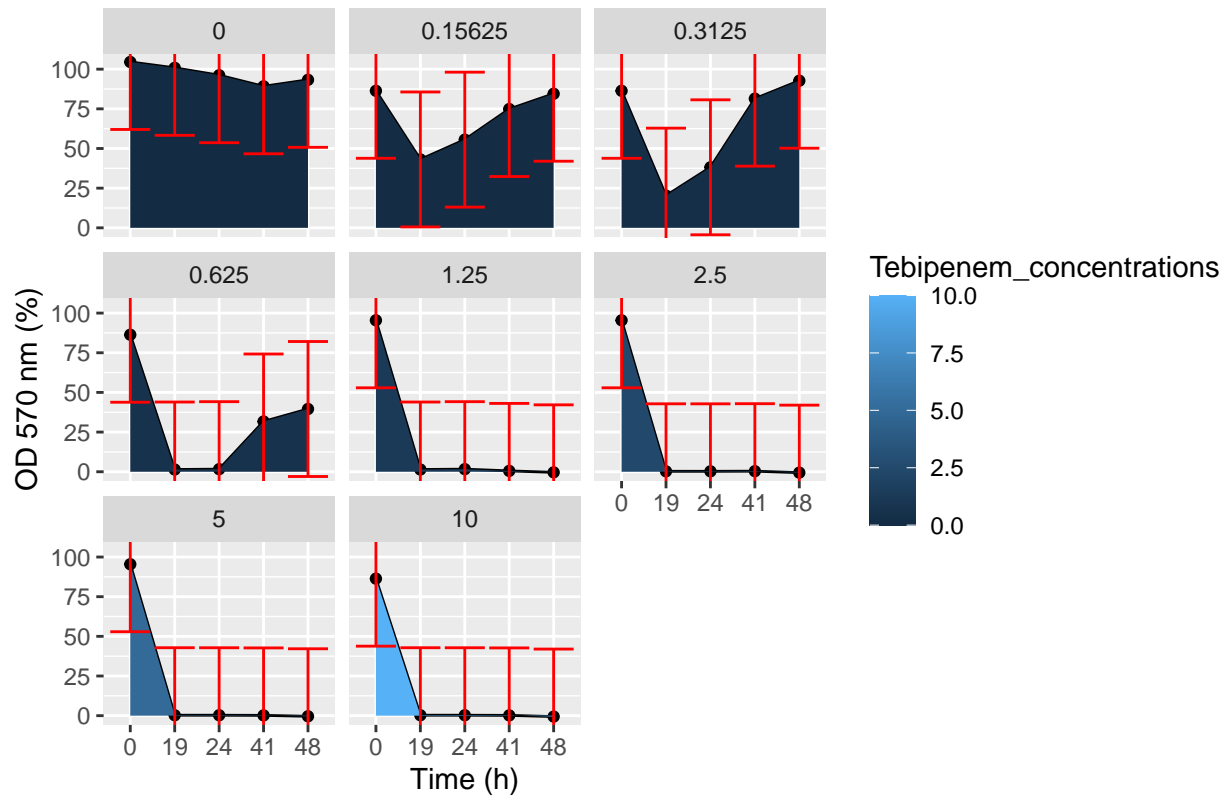
```

((mean(0.388,0.394,0.392)-mea
((mean(0.036,0.097,0.041)-mea
((mean(0.036,0.037,0.044)-mea
((mean(0.037,0.038,0.037)-mea
((mean(0.038,0.212,0.04)-mea
((mean(0.214,0.516,0.358)-mea
((mean(0.495,0.14,0.488)-mea
((mean(0.458,0.33,0.5)-mean(
((mean(0.539,0.374,0.579)-mea
((mean(0.036,0.104,0.04)-mea
((mean(0.037,0.038,0.038)-mea
((mean(0.036,0.038,0.037)-mea
((mean(0.037,0.216,0.038)-mea
((mean(0.251,0.517,0.374)-mea
((mean(0.536,0.257,0.504)-mea
((mean(0.492,0.392,0.51)-mea
((mean(0.539,0.464,0.62)-mea

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
bp5<- Bacillus_subtilis_6.25ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 6.25 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_6.25ug_data$Optical_density_mean_values-sd(Bacillus_subtilis_6.2
    ymax=Bacillus_subtilis_6.25ug_data$Optical_density_mean_values+sd(Bacillus_subtilis_6.2
print(bp5)

```

Penicillin 6.25 ug/mL



#Penicillin 3.125 ug/mL

```
Bacillus_subtilis_3.125ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values =c((mean(0.053,0.054,0.053)-mean(0.054,0.054,0.053))-mean(0.054,0.055,0.053)-mean(0.055,0.056,0.054)-mean(0.052,0.055,0.055)-mean(0.054,0.055,0.054)-mean(0.053,0.057,0.056)-mean(0.057,0.055,0.055)-mean(0.037,0.037,0.041)-mean(0.037,0.038,0.04)-mean(0.038,0.038,0.04)-mean(0.042,0.041,0.043)-mean(0.041,0.399,0.046)-mean(0.123,0.042,0.135)-mean(0.191,0.209,0.229)-mean(0.392,0.43,0.41)-mean(0.037,0.038,0.041)-mean(0.038,0.038,0.04)-mean(0.039,0.038,0.039)-mean(0.042,0.042,0.043)-mean(0.041,0.385,0.077)-mean(0.169,0.042,0.193)-mean(0.224,0.247,0.264))-mean(0.054,0.054,0.053))-mean(0.054,0.055,0.053))-mean(0.055,0.056,0.054))-mean(0.052,0.055,0.055))-mean(0.054,0.055,0.054))-mean(0.053,0.057,0.056))-mean(0.057,0.055,0.055))-mean(0.037,0.037,0.041))-mean(0.037,0.038,0.04))-mean(0.038,0.038,0.04))-mean(0.042,0.041,0.043))-mean(0.041,0.399,0.046))-mean(0.123,0.042,0.135))-mean(0.191,0.209,0.229))-mean(0.392,0.43,0.41))-mean(0.037,0.038,0.041))-mean(0.038,0.038,0.04))-mean(0.039,0.038,0.039))-mean(0.042,0.042,0.043))-mean(0.041,0.385,0.077))-mean(0.169,0.042,0.193))-mean(0.224,0.247,0.264))
```

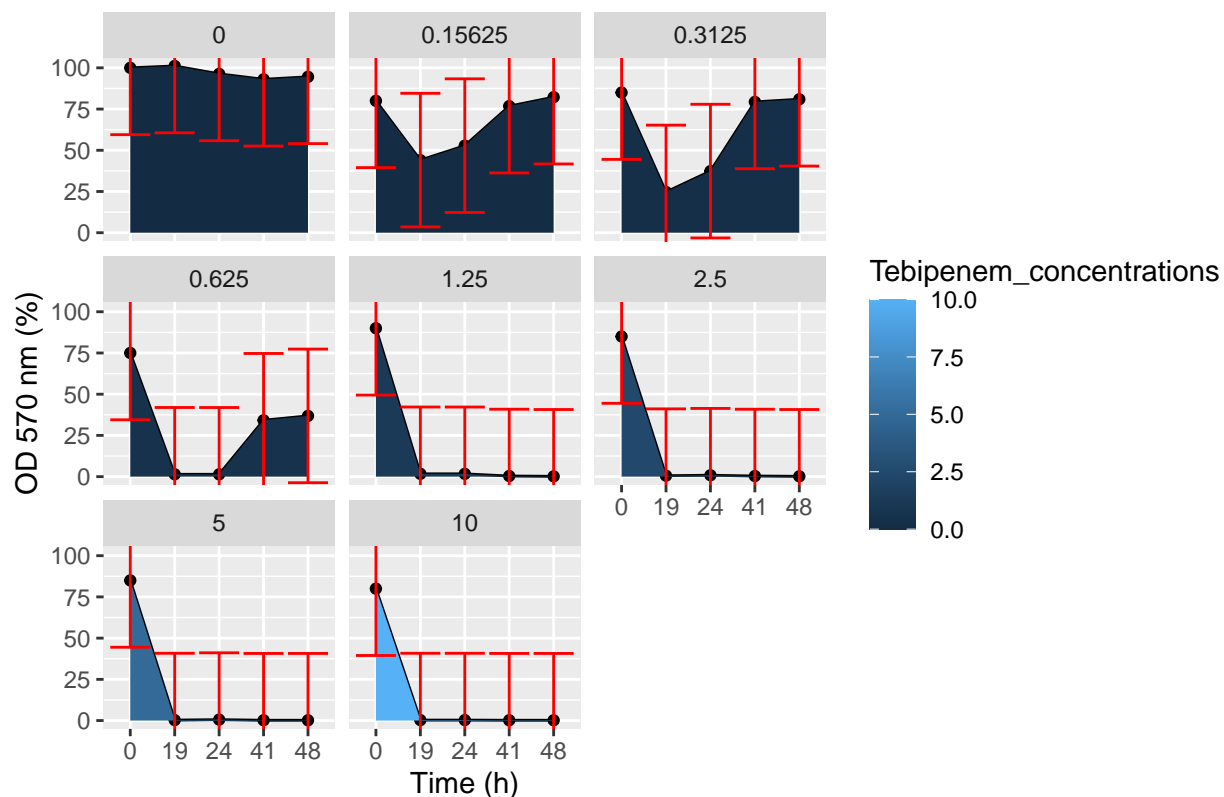
```

((mean(0.379,0.416,0.399))-me
((mean(0.037,0.037,0.043))-me
((mean(0.037,0.039,0.045))-me
((mean(0.038,0.038,0.039))-me
((mean(0.038,0.041,0.04))-mea
((mean(0.223,0.498,0.291))-mea
((mean(0.47,0.109,0.54))-mea
((mean(0.456,0.335,0.497))-me
((mean(0.545,0.436,0.585))-me
((mean(0.037,0.038,0.04))-mea
((mean(0.037,0.038,0.039))-me
((mean(0.037,0.075,0.038))-me
((mean(0.037,0.039,0.039))-me
((mean(0.239,0.513,0.275))-me
((mean(0.482,0.234,0.527))-me
((mean(0.489,0.403,0.535))-me
((mean(0.557,0.507,0.673))-me

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
bp6 <- Bacillus_subtilis_3.125ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 3.125 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_3.125ug_data$Optical_density_mean_values-sd(Bacillus_subtilis_3.
    ymax=Bacillus_subtilis_3.125ug_data$Optical_density_mean_values+sd(Bacillus_subtilis_3.
print(bp6)

```

Penicillin 3.125 ug/mL



```
# Penicillin 1.5625
```

```
Bacillus_subtilis_1.5625ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values =c(((mean(0.052,0.053,0.053)-0.052),
((mean(0.053,0.053,0.052)-0.052),
((mean(0.054,0.054,0.052)-0.052),
((mean(0.052,0.054,0.054)-0.052),
((mean(0.053,0.054,0.054)-0.052),
((mean(0.053,0.053,0.054)-0.052),
((mean(0.053,0.056,0.054)-0.052),
((mean(0.054,0.054,0.054)-0.052),
((mean(0.037,0.037,0.039)-0.037),
((mean(0.037,0.375,0.038)-0.037),
((mean(0.037,0.037,0.039)-0.037),
((mean(0.041,0.041,0.042)-0.041),
((mean(0.041,0.393,0.043)-0.041),
((mean(0.115,0.044,0.116)-0.044),
((mean(0.202,0.199,0.229)-0.199),
((mean(0.387,0.421,0.398)-0.421),
((mean(0.037,0.038,0.039)-0.037),
((mean(0.038,0.364,0.038)-0.038),
((mean(0.038,0.039,0.038)-0.038),
((mean(0.042,0.042,0.041)-0.042),
((mean(0.042,0.374,0.041)-0.042),
((mean(0.165,0.043,0.171)-0.043),
((mean(0.233,0.243,0.259)-0.243))
```

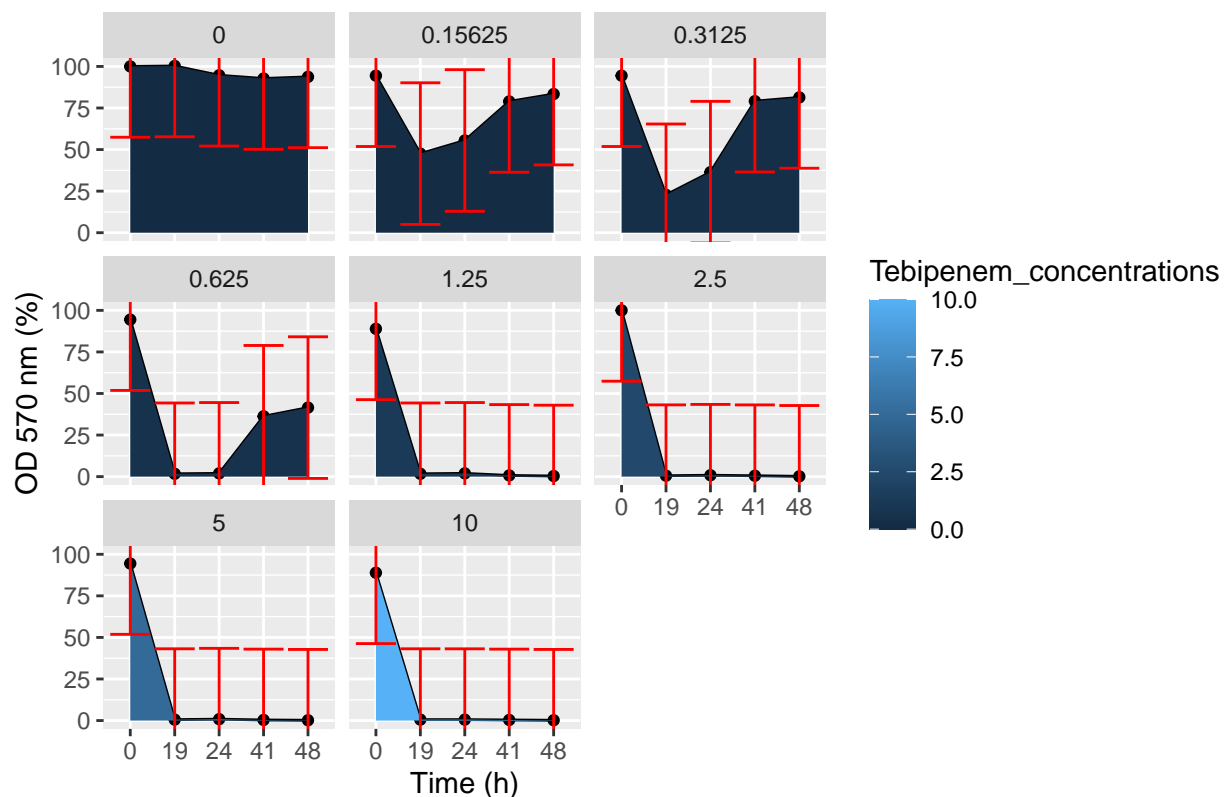
```

((mean(0.373,0.421,0.388))-r
((mean(0.037,0.037,0.04))-m
((mean(0.037,0.45,0.038))-m
((mean(0.038,0.038,0.038))-r
((mean(0.039,0.041,0.039))-r
((mean(0.235,0.476,0.266))-r
((mean(0.471,0.122,0.548))-r
((mean(0.47,0.321,0.503))-m
((mean(0.546,0.474,0.583))-r
((mean(0.037,0.038,0.038))-r
((mean(0.037,0.463,0.038))-r
((mean(0.037,0.038,0.037))-r
((mean(0.038,0.039,0.039))-r
((mean(0.261,0.495,0.341))-r
((mean(0.477,0.243,0.556))-r
((mean(0.488,0.393,0.532))-r
((mean(0.544,0.511,0.63))-m

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
bp7 <- Bacillus_subtilis_1.5625ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 1.5625 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_1.5625ug_data$Optical_density_mean_values-sd(Bacillus_subtilis_1
    ymax=Bacillus_subtilis_1.5625ug_data$Optical_density_mean_values+sd(Bacillus_subtilis_1
print(bp7)

```

Penicillin 1.5625 ug/mL



#Penicillin 0 ug/mL

```
Bacillus_subtilis_Oug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values =c(((mean(0.059,0.054,0.054)-0.036),
((mean(0.064,0.054,0.055)-0.036),
((mean(0.054,0.054,0.053)-0.036),
((mean(0.054,0.054,0.054)-0.036),
((mean(0.053,0.055,0.055)-0.036),
((mean(0.054,0.062,0.054)-0.036),
((mean(0.054,0.054,0.054)-0.036),
((mean(0.055,0.056,0.055)-0.036),
((mean(0.042,0.038,0.038)-mean(0.036)),
((mean(0.048,0.038,0.039)-mean(0.036)),
((mean(0.039,0.038,0.039)-mean(0.036)),
((mean(0.043,0.041,0.045)-mean(0.036)),
((mean(0.043,0.406,0.044)-mean(0.036)),
((mean(0.128,0.041,0.127)-mean(0.036)),
((mean(0.21,0.184,0.229)-mean(0.036)),
((mean(0.401,0.418,0.42)-mean(0.036)),
((mean(0.041,0.038,0.038)-mean(0.036)),
((mean(0.044,0.039,0.039)-mean(0.036)),
((mean(0.039,0.039,0.039)-mean(0.036)),
((mean(0.041,0.042,0.042)-mean(0.036)),
((mean(0.042,0.413,0.042)-mean(0.036)),
((mean(0.16,0.044,0.189)-mean(0.036)),
((mean(0.226,0.233,0.266)-mean(0.036)))))
```



```

((mean(0.407,0.455,0.414)-mean(
((mean(0.04,0.038,0.038)-mean(0
((mean(0.043,0.038,0.04)-mean(0
((mean(0.038,0.039,0.038)-mean(
((mean(0.04,0.042,0.04)-mean(0.
((mean(0.186,0.52,0.277)-mean(0
((mean(0.529,0.093,0.567)-mean(
((mean(0.476,0.373,0.534)-mean(
((mean(0.582,0.531,0.606)-mean(
((mean(0.04,0.038,0.073)-mean(0
((mean(0.042,0.038,0.066)-mean(
((mean(0.038,0.039,0.092)-mean(
((mean(0.039,0.04,0.041)-mean(0
((mean(0.244,0.551,0.27)-mean(0
((mean(0.479,0.199,0.562)-mean(
((mean(0.511,0.432,0.592)-mean(
((mean(0.598,0.568,0.704)-mean(

print(Bacillus_subtilis_Oug_data)

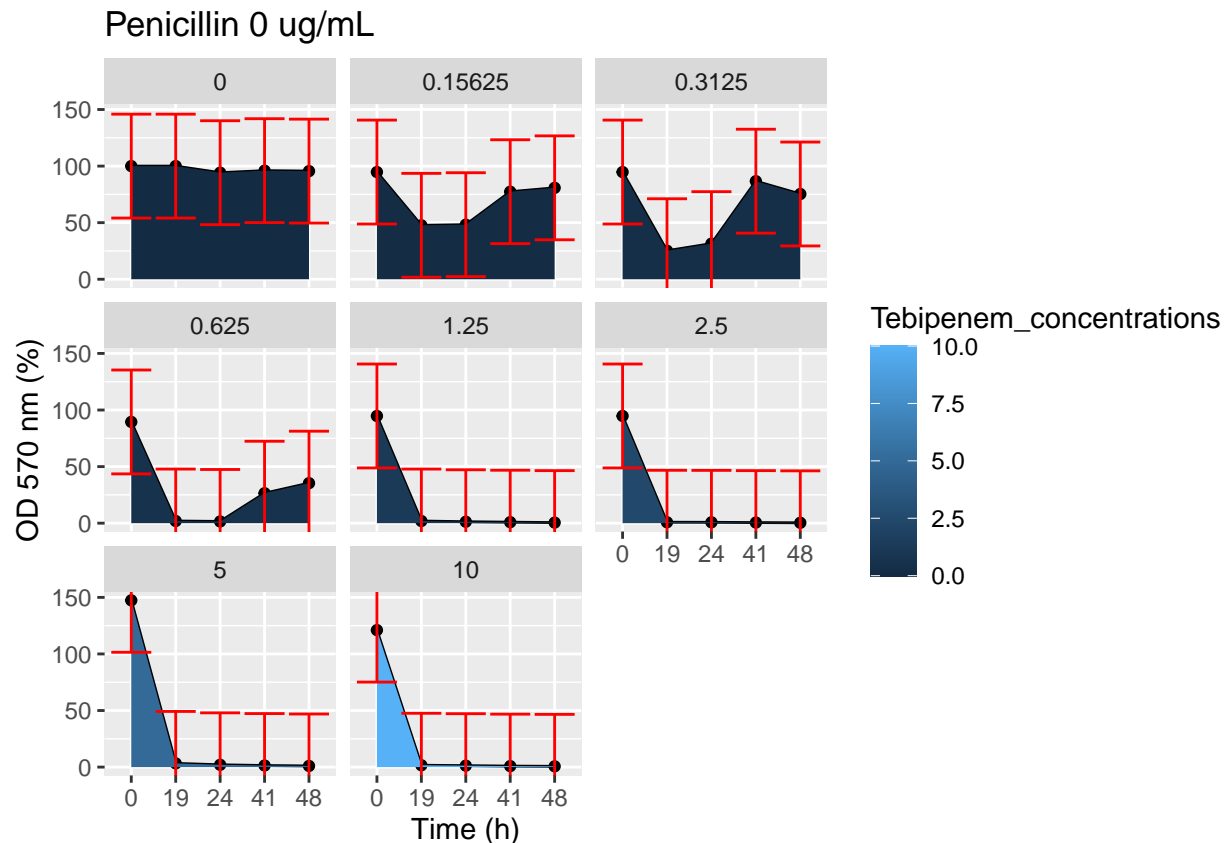
```

##	Time	Tebipenem_concentrations	Optical_density_mean_values
## 1	0	10.00000	121.0526316
## 2	0	5.00000	147.3684211
## 3	0	2.50000	94.7368421
## 4	0	1.25000	94.7368421
## 5	0	0.62500	89.4736842
## 6	0	0.31250	94.7368421
## 7	0	0.15625	94.7368421
## 8	0	0.00000	100.0000000
## 9	19	10.00000	1.6438356
## 10	19	5.00000	3.2876712
## 11	19	2.50000	0.8219178
## 12	19	1.25000	1.9178082
## 13	19	0.62500	1.9178082
## 14	19	0.31250	25.2054795
## 15	19	0.15625	47.6712329
## 16	19	0.00000	100.0000000
## 17	24	10.00000	1.2690355
## 18	24	5.00000	2.0304569
## 19	24	2.50000	0.7614213
## 20	24	1.25000	1.2690355
## 21	24	0.62500	1.5228426
## 22	24	0.31250	31.4720812
## 23	24	0.15625	48.2233503
## 24	24	0.00000	94.1624365
## 25	41	10.00000	0.8771930
## 26	41	5.00000	1.4035088
## 27	41	2.50000	0.5263158
## 28	41	1.25000	0.8771930
## 29	41	0.62500	26.4912281
## 30	41	0.31250	86.6666667
## 31	41	0.15625	77.3684211
## 32	41	0.00000	95.9649123
## 33	48	10.00000	0.6802721

## 34	48	5.00000	1.0204082
## 35	48	2.50000	0.3401361
## 36	48	1.25000	0.5102041
## 37	48	0.62500	35.3741497
## 38	48	0.31250	75.3401361
## 39	48	0.15625	80.7823129
## 40	48	0.00000	95.5782313

#Make a line graphs for changing in OD with time according to Tebipenem concentrations

```
bp8 <-Bacillus_subtilis_Oug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 0 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Bacillus_subtilis_Oug_data$Optical_density_mean_values-sd(Bacillus_subtilis_Oug_da
  ymax=Bacillus_subtilis_Oug_data$Optical_density_mean_values+sd(Bacillus_subtilis_Oug_da
print(bp8)
```



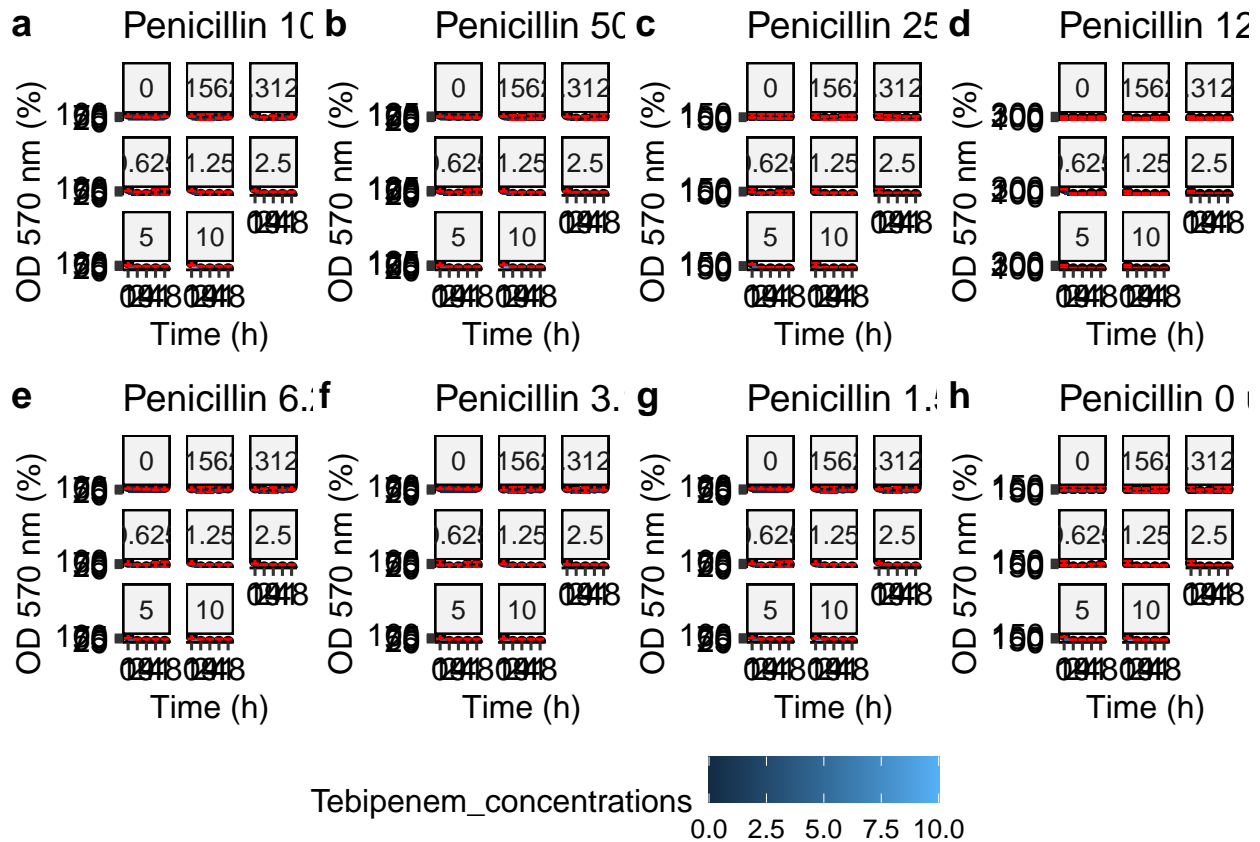
#Align all graphs together

```
library(ggplot2)
library(ggpubr)
```

```

theme_set(theme_pubr())
figure <-
  ggarrange(bp1,bp2,bp3,bp4, bp5, bp6, bp7, bp8,
    labels=c("a","b","c","d","e","f","g","h"),
    ncol=4,nrow=2,
    common.legend = TRUE,legend = "bottom")
print(figure)

```



```

#Final Plot and Data frame that contain only values that inhibited the growth of the bacteria
Final_Bacillus_data <- data.frame(Time_f1=c("0","19","24","41","48"),
  Penicillin_concentrations= c(rep("PenV+Tebipenem (100 ug/mL+1.25 ug/mL)",3),
    rep("PenV+Tebipenem (25 ug/mL+1.25 ug/mL)",3),
    rep("PenV+Tebipenem (6.25 ug/mL+1.25 ug/mL)",3),
    rep("PenV+Tebipenem (1.5625 ug/mL+1.25 ug/mL)",3)),
  Optical_density_values= c((mean(0.053,0.054,0.053)-0.38)/(mean(0.053,0.054,0.053)-0.38),
    (mean(0.041,0.04,0.041)-mean(0.037,0.038,0.037))/(mean(0.041,0.04,0.041)-mean(0.037,0.038,0.037)),
    (mean(0.041,0.039,0.041)-mean(0.037,0.037,0.037))/(mean(0.041,0.039,0.041)-mean(0.037,0.037,0.037)),
    (mean(0.04,0.04,0.038)-mean(0.036,0.036,0.036))/(mean(0.04,0.04,0.038)-mean(0.036,0.036,0.036)),
    (mean(0.039,0.039,0.06)-0.036)/(mean(0.039,0.039,0.06)-0.036),
    (mean(0.052,0.056,0.053)-mean(0.036,0.036,0.036))/(mean(0.052,0.056,0.053)-mean(0.036,0.036,0.036)),
    (mean(0.04,0.04,0.041)-mean(0.035,0.282,0.035))/(mean(0.04,0.04,0.041)-mean(0.035,0.282,0.035)),
    (mean(0.043,0.042,0.044)-mean(0.037,0.402,0.037))/(mean(0.043,0.042,0.044)-mean(0.037,0.402,0.037)),
    (mean(0.042,0.041,0.041)-mean(0.037,0.548,0.037))/(mean(0.042,0.041,0.041)-mean(0.037,0.548,0.037)),
    (mean(0.039,0.041,0.041)-mean(0.037,0.632,0.037))/(mean(0.039,0.041,0.041)-mean(0.037,0.632,0.037)),
    (mean(0.051,0.053,0.053)-mean(0.035,0.035,0.035))/(mean(0.051,0.053,0.053)-mean(0.035,0.035,0.035)))

```

```

((mean(0.042,0.043,0.043)-mean(0.038,0.038,0.038))/((mean(0.055,0.056,0.054)-mean(0.037,0.037,0.037)))/((mean(0.043,0.041,0.045)-mean(0.036,0.036,0.036)))/((mean(0.041,0.042,0.042)-mean(0.036,0.037,0.037)))/((mean(0.04,0.042,0.04)-mean(0.035,0.037,0.037)))/((mean(0.039,0.04,0.041)-mean(0.036,0.038,0.038)))/((mean(0.038,0.04,0.039)-mean(0.034,0.035,0.035)))/((mean(0.036,0.038,0.037)-mean(0.034,0.036,0.036)))/((mean(0.057,0.058,0.058)-mean(0.038,0.039,0.039)))/((mean(0.042,0.043,0.043)-mean(0.037,0.038,0.038)))/((mean(0.044,0.044,0.044)-mean(0.037,0.038,0.038)))/((mean(0.041,0.042,0.042)-mean(0.037,0.039,0.039)))/((mean(0.039,0.04,0.041)-mean(0.037,0.038,0.038)))/((mean(0.057,0.061,0.056)-mean(0.036,0.036,0.036)))/((mean(0.04,0.04,0.041)-mean(0.035,0.036,0.036)))/((mean(0.041,0.041,0.041)-mean(0.035,0.039,0.039)))/((mean(0.038,0.041,0.04)-mean(0.035,0.037,0.037)))/((mean(0.037,0.041,0.038)-mean(0.039,0.037,0.037)))/((mean(0.055,0.056,0.054)-mean(0.037,0.037,0.037)))/((mean(0.042,0.041,0.043)-mean(0.036,0.038,0.038)))/((mean(0.042,0.042,0.043)-mean(0.036,0.038,0.038)))/((mean(0.038,0.041,0.04)-mean(0.036,0.042,0.042)))/((mean(0.037,0.039,0.039)-mean(0.036,0.034,0.034)))/((mean(0.052,0.054,0.054)-mean(0.036,0.036,0.036)))/((mean(0.041,0.041,0.042)-mean(0.035,0.035,0.035)))/((mean(0.042,0.042,0.041)-mean(0.035,0.043,0.043)))/((mean(0.039,0.041,0.039)-mean(0.035,0.054,0.054)))/((mean(0.038,0.039,0.039)-mean(0.036,0.067,0.067)))/((mean(0.054,0.054,0.054)-0.036)/(0.055-0.036)))/((mean(0.043,0.041,0.045)-mean(0.036,0.036,0.036)))/((mean(0.041,0.042,0.042)-mean(0.036,0.037,0.037)))/((mean(0.04,0.042,0.04)-mean(0.035,0.037,0.037)))/((mean(0.039,0.04,0.041)-mean(0.036,0.038,0.038)))/
print(Final_Bacillus_data)

```

##	Time_f1	Penicillin_concentrations	Optical_density_values
## 1	0	PenV+Tebipenem (100 ug/mL+1.25 ug/mL)	100.0000000
## 2	19	PenV+Tebipenem (100 ug/mL+1.25 ug/mL)	1.0840108
## 3	24	PenV+Tebipenem (100 ug/mL+1.25 ug/mL)	1.1396011
## 4	41	PenV+Tebipenem (100 ug/mL+1.25 ug/mL)	0.7633588
## 5	48	PenV+Tebipenem (100 ug/mL+1.25 ug/mL)	0.6109980
## 6	0	PenV+Tebipenem (50 ug/mL+1.25 ug/mL)	106.6666667
## 7	19	PenV+Tebipenem (50 ug/mL+1.25 ug/mL)	1.3123360
## 8	24	PenV+Tebipenem (50 ug/mL+1.25 ug/mL)	1.4117647
## 9	41	PenV+Tebipenem (50 ug/mL+1.25 ug/mL)	0.8090615
## 10	48	PenV+Tebipenem (50 ug/mL+1.25 ug/mL)	0.3278689
## 11	0	PenV+Tebipenem (25 ug/mL+1.25 ug/mL)	106.6666667
## 12	19	PenV+Tebipenem (25 ug/mL+1.25 ug/mL)	1.1173184
## 13	24	PenV+Tebipenem (25 ug/mL+1.25 ug/mL)	1.5665796
## 14	41	PenV+Tebipenem (25 ug/mL+1.25 ug/mL)	0.6944444
## 15	48	PenV+Tebipenem (25 ug/mL+1.25 ug/mL)	0.3539823
## 16	0	PenV+Tebipenem (12.5 ug/mL+1.25 ug/mL)	100.0000000
## 17	19	PenV+Tebipenem (12.5 ug/mL+1.25 ug/mL)	1.3440860
## 18	24	PenV+Tebipenem (12.5 ug/mL+1.25 ug/mL)	1.8087855
## 19	41	PenV+Tebipenem (12.5 ug/mL+1.25 ug/mL)	0.7448790
## 20	48	PenV+Tebipenem (12.5 ug/mL+1.25 ug/mL)	0.3649635
## 21	0	PenV+Tebipenem (6.25 ug/mL+1.25 ug/mL)	95.4545455

```
## 22      19   PenV+Tebipenem (6.25 ug/mL+1.25 ug/mL)          1.4084507
## 23      24   PenV+Tebipenem (6.25 ug/mL+1.25 ug/mL)          1.6348774
## 24      41   PenV+Tebipenem (6.25 ug/mL+1.25 ug/mL)          0.5309735
## 25      48   PenV+Tebipenem (6.25 ug/mL+1.25 ug/mL)         -0.3731343
## 26         0   PenV+Tebipenem (3.125 ug/mL+1.25 ug/mL)        90.0000000
## 27      19   PenV+Tebipenem (3.125 ug/mL+1.25 ug/mL)          1.7045455
## 28      24   PenV+Tebipenem (3.125 ug/mL+1.25 ug/mL)          1.6853933
## 29      41   PenV+Tebipenem (3.125 ug/mL+1.25 ug/mL)          0.3656307
## 30      48   PenV+Tebipenem (3.125 ug/mL+1.25 ug/mL)          0.1814882
## 31         0   PenV+Tebipenem (1.5625 ug/mL+1.25 ug/mL)        88.8888889
## 32      19   PenV+Tebipenem (1.5625 ug/mL+1.25 ug/mL)          1.7094017
## 33      24   PenV+Tebipenem (1.5625 ug/mL+1.25 ug/mL)          1.9607843
## 34      41   PenV+Tebipenem (1.5625 ug/mL+1.25 ug/mL)          0.7259528
## 35      48   PenV+Tebipenem (1.5625 ug/mL+1.25 ug/mL)          0.3690037
## 36         0   PenV+Tebiepenem (0 ug/mL+1.25 ug/mL)           94.7368421
## 37      19   PenV+Tebiepenem (0 ug/mL+1.25 ug/mL)            1.9178082
## 38      24   PenV+Tebiepenem (0 ug/mL+1.25 ug/mL)            1.2690355
## 39      41   PenV+Tebiepenem (0 ug/mL+1.25 ug/mL)            0.8771930
## 40      48   PenV+Tebiepenem (0 ug/mL+1.25 ug/mL)            0.5102041
```

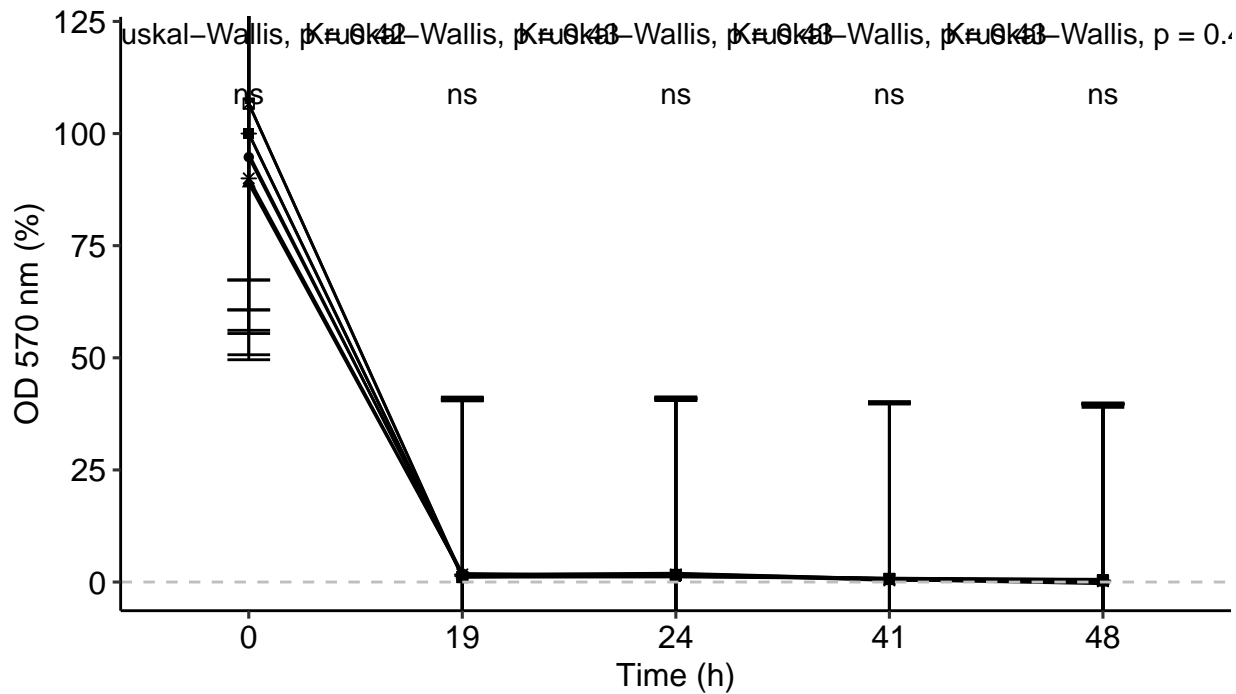
#Line graph

```
Final_Bac <- Final_Bacillus_data %>%
  ggplot(aes(x=Time_f1, y=Optical_density_values, group=Penicillin_concentrations, shape=Penicillin_concentrations)) +
  geom_line() +
  geom_point() +
  xlab("Time (h)") +
  ylab("OD 570 nm (%)") +
  stat_compare_means(method = "kruskal.test", label.y = 120) +
  stat_compare_means(label = "p.signif") +
  geom_errorbar(ymin=Final_Bacillus_data$Optical_density_values-sd(Final_Bacillus_data$Optical_density_values),
                ymax=Final_Bacillus_data$Optical_density_values+sd(Final_Bacillus_data$Optical_density_values),
                width=.2) +
  geom_hline(yintercept = 0, linetype="dashed", col="grey")
print(Final_Bac)
```

```
## Warning: The shape palette can deal with a maximum of 6 discrete values because
## more than 6 becomes difficult to discriminate; you have 8. Consider
## specifying shapes manually if you must have them.
```

```
## Warning: Removed 10 rows containing missing values (geom_point).
```

g/mL+1.25 ug/mL) ■ PenV+Tebipenem (100 ug/mL+1.25 ug/mL ▣ PenV+Tebipenem (25 ug/n
25 ug/mL+1.25 ug/mL) + PenV+Tebipenem (12.5 ug/mL+1.25 ug/mL) * PenV+Tebipenem (3.125 u



#PROTEUS MIRABILIS RESULTS AND PLOTS

#Penicillin 100 ug/mL

```
Proteus_mirabilis_100ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
      Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
      Optical_density_mean_values =c((mean(0.04, 0.06, 0.0806)-0.03),
      (mean(0.06,0.061, 0.061)-0.03),
      (mean(0.06,0.061,0.061)-0.03),
      (mean(0.062,0.061,0.061)-0.03),
      (mean(0.062,0.061,0.066)-0.03),
      (mean(0.062,0.061,0.064)-0.03),
      (mean(0.062,0.061,0.061)-0.03),
      (mean(0.063,0.062,0.062)-0.03),
      (mean(0.04,0.049,0.051)-mean(0.04,0.049,0.051)),
      (mean(0.05,0.06,0.054)-mean(0.05,0.06,0.054)),
      (mean(0.089,0.1,0.093)-mean(0.089,0.1,0.093)),
      (mean(0.122,0.127,0.121)-mean(0.122,0.127,0.121)),
      (mean(0.137,0.152,0.141)-mean(0.137,0.152,0.141)),
      (mean(0.144,0.159,0.146)-mean(0.144,0.159,0.146)),
      (mean(0.145,0.161,0.14)-mean(0.145,0.161,0.14)),
      (mean(0.313,0.319,0.321)-mean(0.313,0.319,0.321)),
      (mean(0.04,0.048,0.043)-mean(0.04,0.048,0.043)),
      (mean(0.051,0.052,0.051)-mean(0.051,0.052,0.051)),
      (mean(0.097,0.1,0.098)-mean(0.097,0.1,0.098)),
      (mean(0.123,0.125,0.12)-mean(0.123,0.125,0.12)),
      (mean(0.143,0.149,0.139)-mean(0.143,0.149,0.139)),
      (mean(0.149,0.159,0.149)-mean(0.149,0.159,0.149))
```

```

((mean(0.154,0.167,0.15)-mean
((mean(0.346,0.344,0.337)-mean
((mean(0.041,0.049,0.039)-mean
((mean(0.053,0.053,0.051)-mean
((mean(0.074,0.081,0.081)-mean
((mean(0.11,0.114,0.11)-mean(
((mean(0.133,0.152,0.14)-mean
((mean(0.155,0.182,0.157)-mean
((mean(0.167,0.201,0.165)-mean
((mean(0.49,0.494,0.416)-mean
((mean(0.041,0.048,0.036)-mean
((mean(0.051,0.051,0.052)-mean
((mean(0.068,0.075,0.085)-mean
((mean(0.105,0.109,0.111)-mean
((mean(0.131,0.144,0.141)-mean
((mean(0.154,0.176,0.161)-mean
((mean(0.174,0.206,0.186)-mean
((mean(0.513,0.501,0.49)-mean

print(Proteus_mirabilis_100ug_data)

```

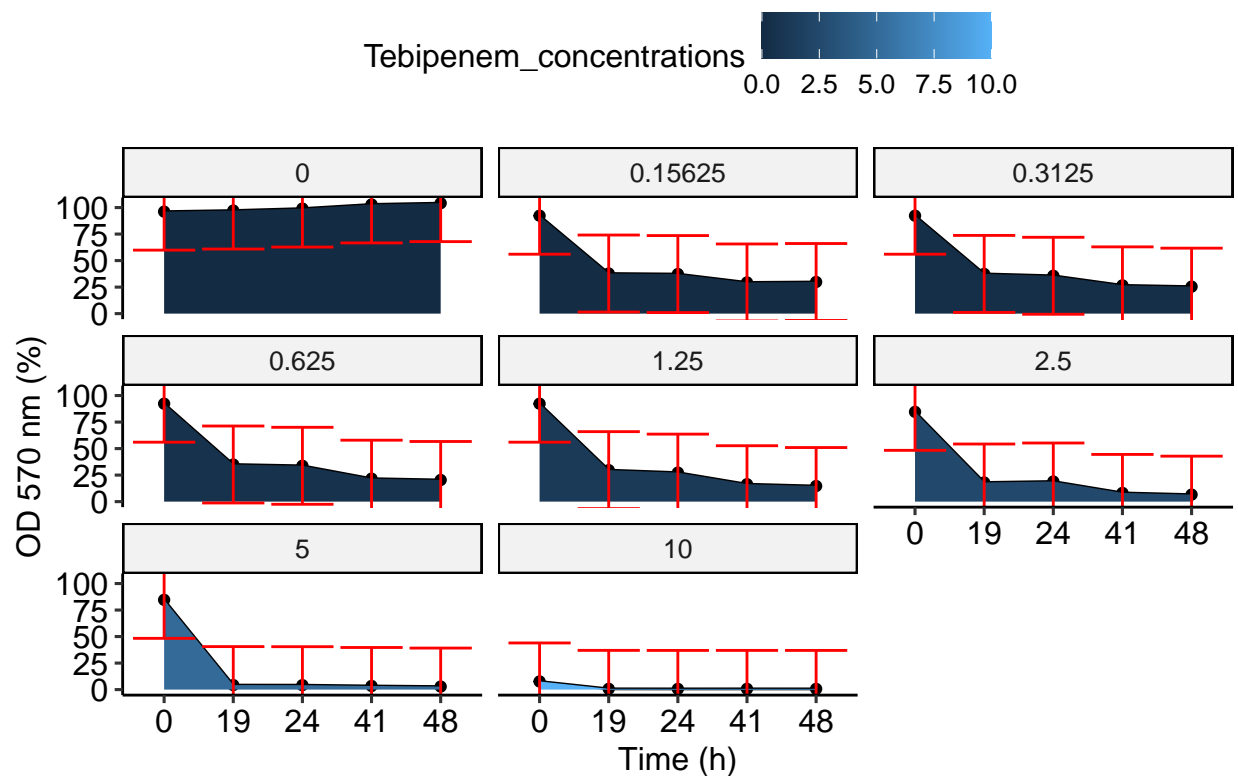
##	Time	Tebipenem_concentrations	Optical_density_mean_values
## 1	0	10.00000	7.6923077
## 2	0	5.00000	84.6153846
## 3	0	2.50000	84.6153846
## 4	0	1.25000	92.3076923
## 5	0	0.62500	92.3076923
## 6	0	0.31250	92.3076923
## 7	0	0.15625	92.3076923
## 8	0	0.00000	96.1538462
## 9	19	10.00000	0.7067138
## 10	19	5.00000	4.2402827
## 11	19	2.50000	18.0212014
## 12	19	1.25000	29.6819788
## 13	19	0.62500	34.9823322
## 14	19	0.31250	37.4558304
## 15	19	0.15625	37.8091873
## 16	19	0.00000	97.1731449
## 17	24	10.00000	0.6430868
## 18	24	5.00000	4.1800643
## 19	24	2.50000	18.9710611
## 20	24	1.25000	27.3311897
## 21	24	0.62500	33.7620579
## 22	24	0.31250	35.6913183
## 23	24	0.15625	37.2990354
## 24	24	0.00000	99.0353698
## 25	41	10.00000	0.6833713
## 26	41	5.00000	3.4168565
## 27	41	2.50000	8.2004556
## 28	41	1.25000	16.4009112
## 29	41	0.62500	21.6400911
## 30	41	0.31250	26.6514806
## 31	41	0.15625	29.3849658
## 32	41	0.00000	102.9612756

## 33	48	10.00000	0.6578947
## 34	48	5.00000	2.8508772
## 35	48	2.50000	6.5789474
## 36	48	1.25000	14.6929825
## 37	48	0.62500	20.3947368
## 38	48	0.31250	25.4385965
## 39	48	0.15625	29.8245614
## 40	48	0.00000	104.1666667

#Make a line graphs for changing in OD with time according to Tebipenem concentrations

```
Pp1 <- Proteus_mirabilis_100ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations)) +
  geom_line() +
  geom_point() +
  geom_area() +
  facet_wrap(~Tebipenem_concentrations) +
  ggtitle("Penicillin 100 ug/mL") +
  xlab("Time (h)") +
  ylab("OD 570 nm (%)") +
  geom_errorbar(ymin=Proteus_mirabilis_100ug_data$Optical_density_mean_values-sd(Proteus_mirabilis_100ug_data$Optical_density_mean_values),
               ymax=Proteus_mirabilis_100ug_data$Optical_density_mean_values+sd(Proteus_mirabilis_100ug_data$Optical_density_mean_values))
print(Pp1)
```

Penicillin 100 ug/mL



#Penicillin 50 ug/mL

```
Proteus_mirabilis_50ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)))
```



```

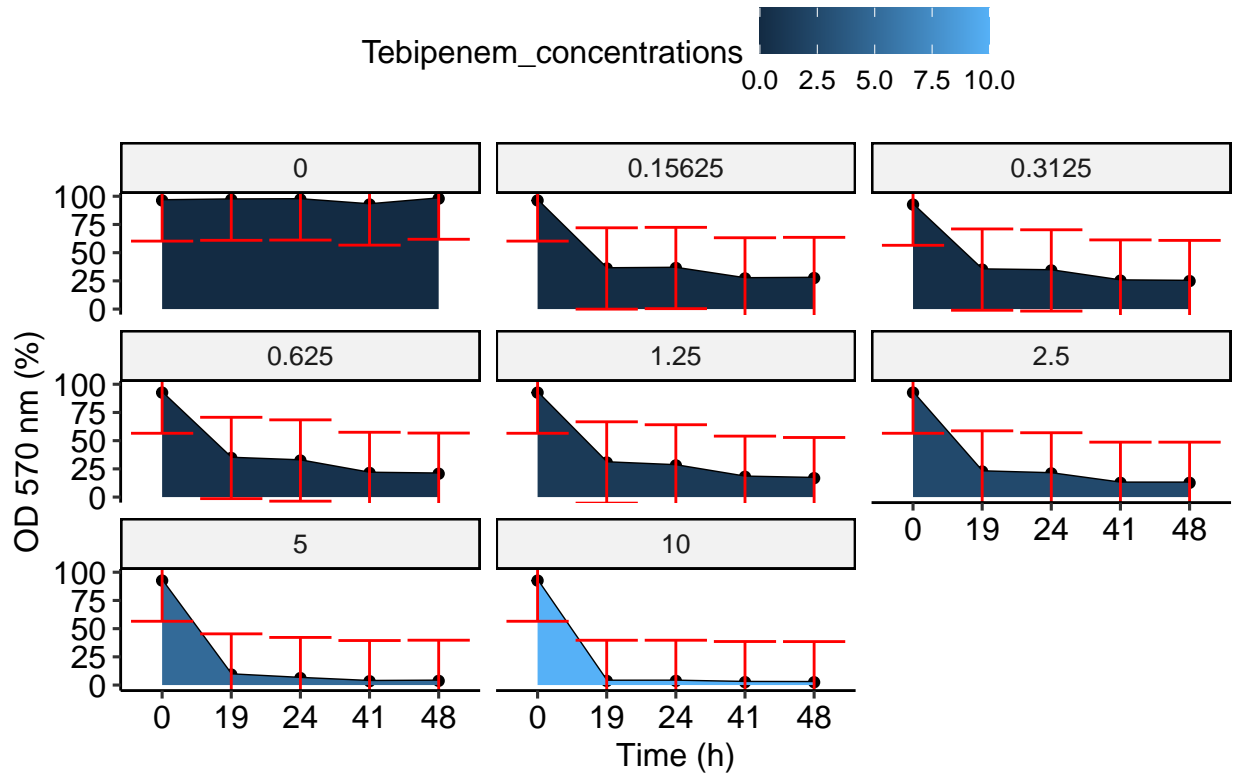
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625)
Optical_density_mean_values =c((mean(0.06,0.06,0.04)-mean(0.04,0.04,0.04))-(
    (mean(0.06,0.06,0.06)-mean(0.04,0.04,0.04))-(
    (mean(0.06,0.061,0.06)-mean(0.04,0.04,0.04))-(
    (mean(0.06,0.06,0.061)-mean(0.04,0.04,0.04))-(
    (mean(0.06,0.06,0.06)-mean(0.04,0.04,0.04))-(
    (mean(0.06,0.06,0.061)-mean(0.04,0.04,0.04))-(
    (mean(0.061,0.06,0.059)-mean(0.04,0.04,0.04))-(
    (mean(0.061,0.06,0.06)-mean(0.04,0.04,0.04))-(
    (mean(0.046,0.048,0.194)-mean(0.04,0.04,0.04))-(
    (mean(0.063,0.097,0.069)-mean(0.04,0.04,0.04))-(
    (mean(0.103,0.108,0.106)-mean(0.04,0.04,0.04))-(
    (mean(0.127,0.129,0.124)-mean(0.04,0.04,0.04))-(
    (mean(0.139,0.143,0.137)-mean(0.04,0.04,0.04))-(
    (mean(0.14,0.15,0.138)-mean(0.04,0.04,0.04))-(
    (mean(0.143,0.154,0.143)-mean(0.04,0.04,0.04))-(
    (mean(0.326,0.341,0.327)-mean(0.04,0.04,0.04))-(
    (mean(0.049,0.051,0.239)-mean(0.04,0.04,0.04))-(
    (mean(0.057,0.1,0.067)-mean(0.04,0.04,0.04))-(
    (mean(0.105,0.11,0.11)-mean(0.04,0.04,0.04))-(
    (mean(0.128,0.129,0.127)-mean(0.04,0.04,0.04))-(
    (mean(0.142,0.145,0.144)-mean(0.04,0.04,0.04))-(
    (mean(0.148,0.156,0.147)-mean(0.04,0.04,0.04))-(
    (mean(0.155,0.166,0.154)-mean(0.04,0.04,0.04))-(
    (mean(0.352,0.346,0.337)-mean(0.04,0.04,0.04))-(
    (mean(0.05,0.052,0.239)-0.038)-(
    (mean(0.054,0.082,0.056)-0.038)-(
    (mean(0.097,0.104,0.104)-0.038)-(
    (mean(0.122,0.125,0.12)-0.038)-(
    (mean(0.138,0.149,0.145)-0.038)-(
    (mean(0.156,0.176,0.159)-0.038)-(
    (mean(0.165,0.19,0.162)-0.038)-(
    (mean(0.471,0.504,0.413)-0.038)-(
    (mean(0.05,0.051,0.168)-0.038)-(
    (mean(0.056,0.083,0.061)-0.038)-(
    (mean(0.099,0.107,0.109)-0.038)-(
    (mean(0.119,0.121,0.12)-0.038)-(
    (mean(0.138,0.148,0.147)-0.038)-(
    (mean(0.158,0.177,0.162)-0.038)-(
    (mean(0.171,0.2,0.171)-0.038)-(
    (mean(0.511,0.525,0.474)-0.038)

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Pp2 <- Proteus_mirabilis_50ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations)) +
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 50 ug/mL")+
  xlab("Time (h)") +
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Proteus_mirabilis_50ug_data$Optical_density_mean_values-sd(Proteus_mirabilis_50ug_data$Optical_density_mean_values),
               ymax=Proteus_mirabilis_50ug_data$Optical_density_mean_values+sd(Proteus_mirabilis_50ug_data$Optical_density_mean_values))

```

```
print(Pp2)
```

Penicillin 50 ug/mL



```
#Penicillin 25 ug/mL
```

```
Proteus_mirabilis_25ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125,0.0390625,0.01953125),
Optical_density_mean_values =c((mean(0.058,0.057,0.056)-0.035),
((mean(0.06,0.057,0.06)-0.035),
((mean(0.058,0.056,0.058)-0.035),
((mean(0.058,0.057,0.059)-0.035),
((mean(0.058,0.058,0.058)-0.035),
((mean(0.059,0.062,0.057)-0.035),
((mean(0.059,0.057,0.057)-0.035),
((mean(0.059,0.058,0.057)-0.035),
((mean(0.05,0.05,0.05)-mean(0.058,0.057,0.056)-0.035),
((mean(0.095,0.09,0.094)-mean(0.058,0.057,0.056)-0.035),
((mean(0.108,0.106,0.109)-mean(0.058,0.057,0.056)-0.035),
((mean(0.124,0.127,0.12)-mean(0.058,0.057,0.056)-0.035),
((mean(0.132,0.137,0.133)-mean(0.058,0.057,0.056)-0.035),
((mean(0.136,0.144,0.132)-mean(0.058,0.057,0.056)-0.035),
((mean(0.135,0.144,0.136)-mean(0.058,0.057,0.056)-0.035),
((mean(0.311,0.333,0.32)-mean(0.058,0.057,0.056)-0.035),
((mean(0.048,0.048,0.046)-mean(0.058,0.057,0.056)-0.035),
((mean(0.096,0.089,0.098)-mean(0.058,0.057,0.056)-0.035),
((mean(0.106,0.103,0.109)-mean(0.058,0.057,0.056)-0.035),
((mean(0.121,0.124,0.122)-mean(0.058,0.057,0.056)-0.035))
```

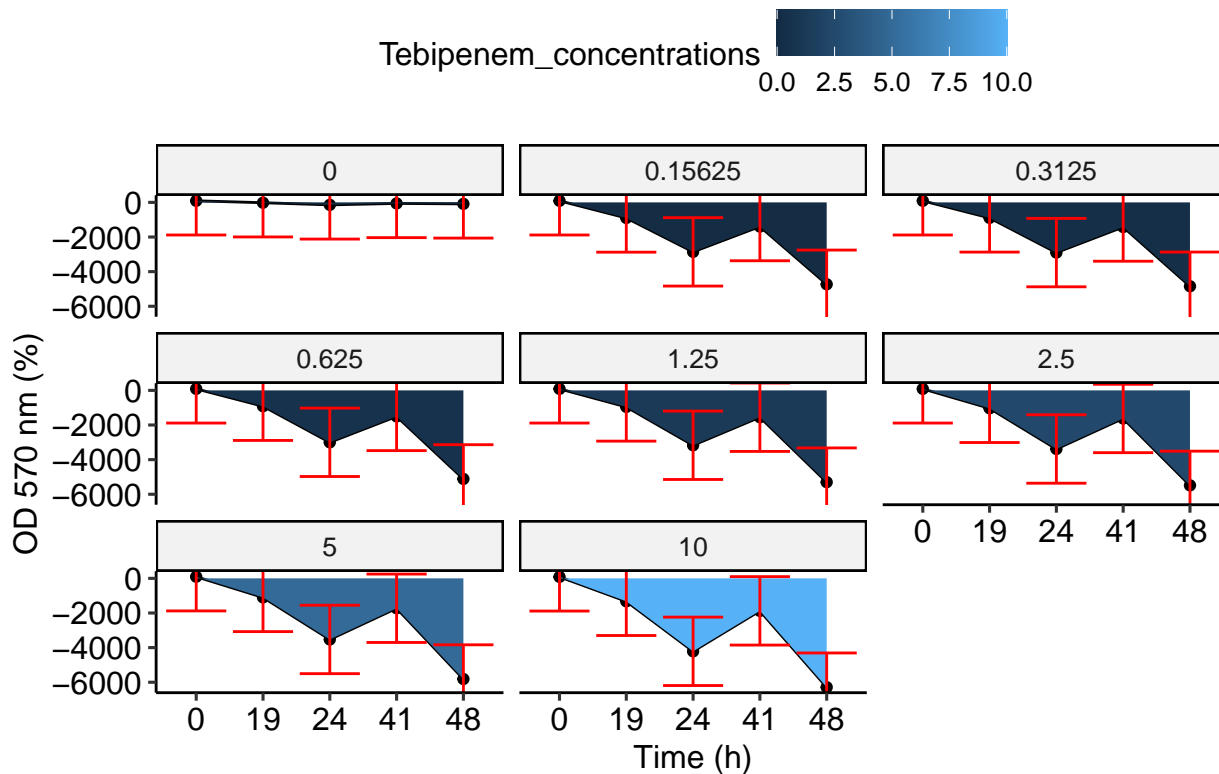
```

((mean(0.133,0.136,0.136)-mean(
((mean(0.14,0.146,0.135)-mean(
((mean(0.143,0.152,0.144)-mean(
((mean(0.333,0.335,0.324)-mean(
((mean(0.047,0.048,0.046)-mean(
((mean(0.08,0.055,0.088)-mean(
((mean(0.103,0.102,0.104)-mean(
((mean(0.119,0.12,0.117)-mean(
((mean(0.129,0.137,0.135)-mean(
((mean(0.147,0.162,0.147)-mean(
((mean(0.153,0.175,0.152)-mean(
((mean(0.447,0.489,0.399)-mean(
((mean(0.048,0.048,0.046)-mean(
((mean(0.081,0.057,0.09)-mean(
((mean(0.104,0.104,0.108)-mean(
((mean(0.117,0.117,0.117)-mean(
((mean(0.13,0.137,0.137)-mean(
((mean(0.149,0.163,0.149)-mean(
((mean(0.157,0.179,0.157)-mean(
((mean(0.482,0.495,0.45)-mean(

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Pp3 <- Proteus_mirabilis_25ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 25 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Proteus_mirabilis_25ug_data$Optical_density_mean_values-sd(Proteus_mirabilis_25ug_
    ymax=Proteus_mirabilis_25ug_data$Optical_density_mean_values+sd(Proteus_mirabilis_25ug_
print(Pp3)

```

Penicillin 25 ug/mL



#Penicillin 12.5 ug/mL

[illegible]

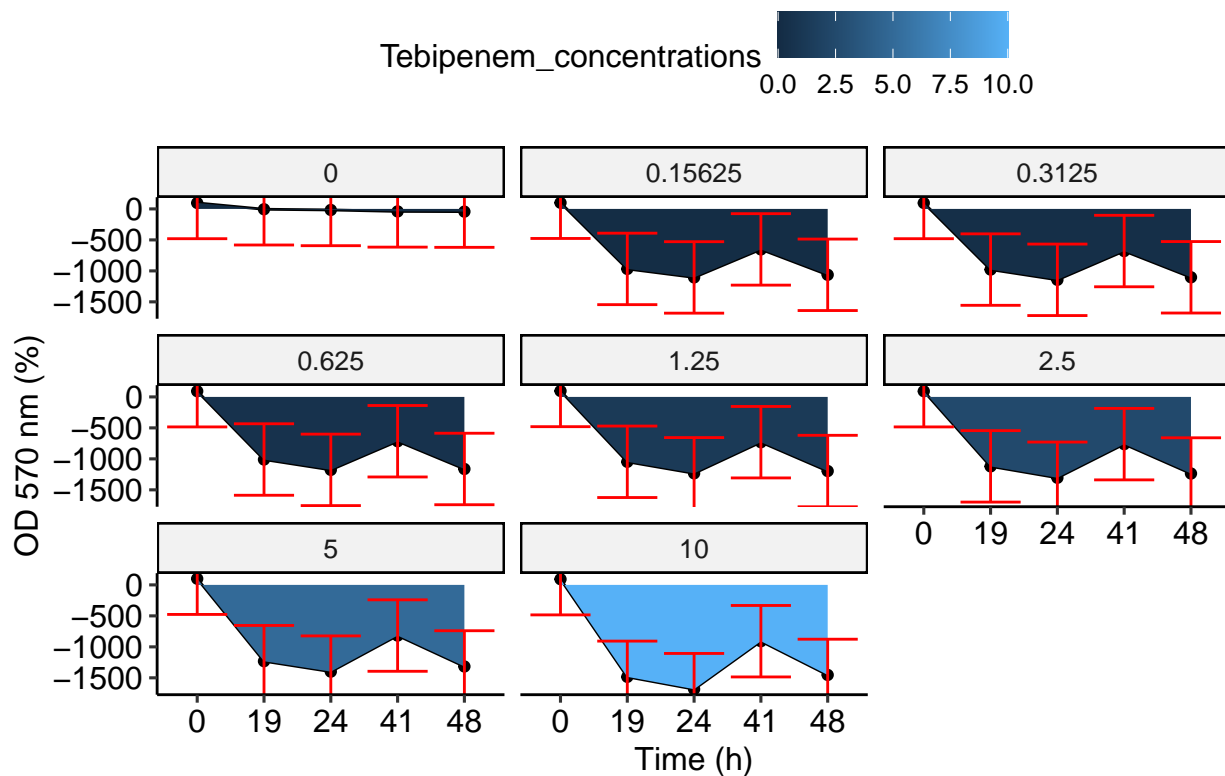
```

((mean(0.352,0.351,0.334)-mean
((mean(0.053,0.054,0.053)-mean
((mean(0.094,0.091,0.104)-mean
((mean(0.119,0.115,0.111)-mean
((mean(0.133,0.132,0.129)-mean
((mean(0.14,0.148,0.149)-mean(
((mean(0.156,0.169,0.16)-mean(
((mean(0.168,0.185,0.166)-mean
((mean(0.444,0.492,0.405)-mean
((mean(0.054,0.054,0.055)-mean
((mean(0.095,0.093,0.103)-mean
((mean(0.119,0.117,0.115)-mean
((mean(0.131,0.13,0.128)-mean(
((mean(0.141,0.149,0.15)-mean(
((mean(0.159,0.171,0.162)-mean
((mean(0.171,0.187,0.171)-mean
((mean(0.477,0.501,0.447)-mean

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Pp4 <- Proteus_mirabilis_12.5ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 12.5 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Proteus_mirabilis_12.5ug_data $Optical_density_mean_values-sd(Proteus_mirabilis_12
                ymax=Proteus_mirabilis_12.5ug_data $Optical_density_mean_values+sd(Proteus_mirabilis_12
print(Pp4)

```

Penicillin 12.5 ug/mL



#Penicillin 6.25 ug/mL

```
Proteus_mirabilis_6.25ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0625),
Optical_density_mean_values =c((mean(0.062,0.063,0.061)-0.062),
(mean(0.062,0.065,0.062)-0.062),
(mean(0.061,0.062,0.062)-0.062),
(mean(0.062,0.063,0.063)-0.062),
(mean(0.063,0.062,0.063)-0.062),
(mean(0.061,0.062,0.062)-0.062),
(mean(0.062,0.062,0.061)-0.062),
(mean(0.062,0.062,0.063)-0.062),
(mean(0.057,0.057,0.05)-0.057),
(mean(0.105,0.106,0.107)-0.106),
(mean(0.122,0.121,0.117)-0.121),
(mean(0.133,0.143,0.135)-0.135),
(mean(0.149,0.155,0.149)-0.149),
(mean(0.151,0.156,0.153)-0.153),
(mean(0.152,0.165,0.157)-0.157),
(mean(0.339,0.351,0.349)-0.349),
(mean(0.05,0.051,0.05)-0.05),
(mean(0.108,0.106,0.109)-0.108),
(mean(0.121,0.122,0.119)-0.121),
(mean(0.132,0.141,0.138)-0.138),
(mean(0.148,0.154,0.153)-0.153),
(mean(0.154,0.16,0.156)-0.156),
(mean(0.158,0.173,0.164)-0.164))
```

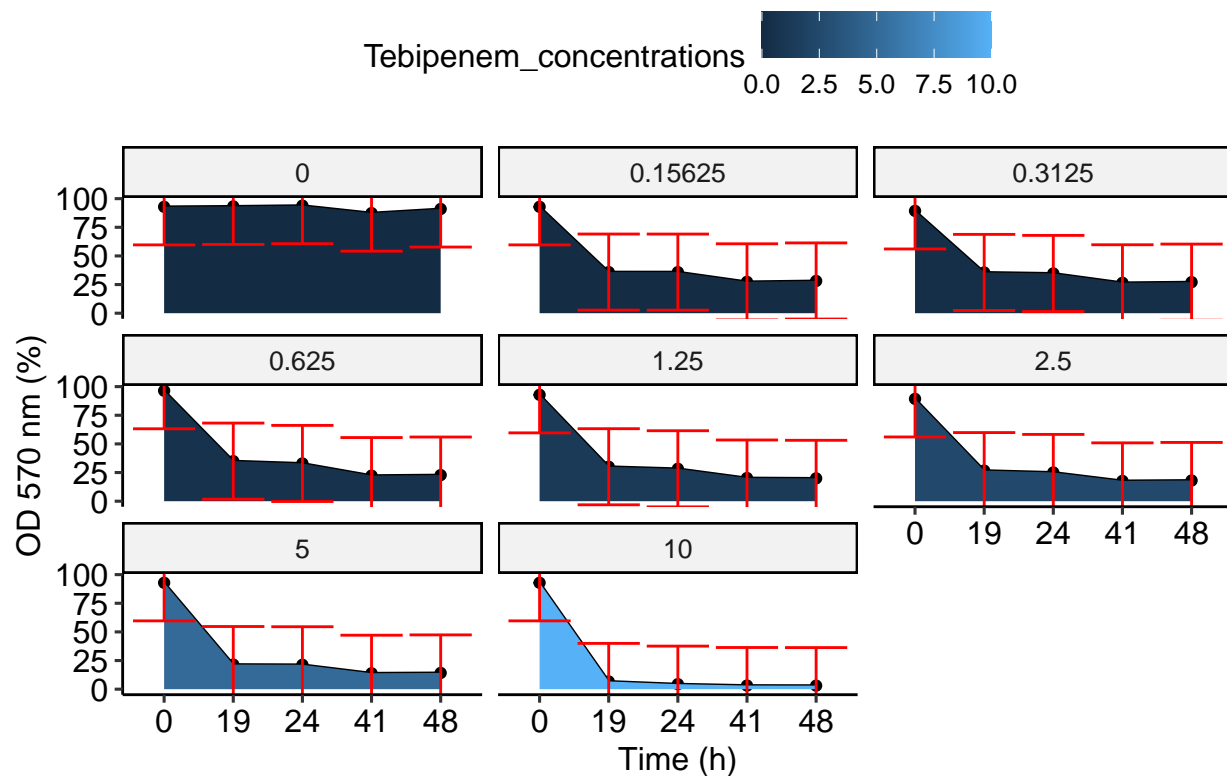
```

((mean(0.357,0.353,0.342))-mea
((mean(0.051,0.052,0.052))-mea
((mean(0.102,0.097,0.111))-mea
((mean(0.12,0.121,0.115))-mea
((mean(0.132,0.135,0.131))-mea
((mean(0.142,0.151,0.152))-mea
((mean(0.162,0.172,0.164))-mea
((mean(0.166,0.189,0.169))-mea
((mean(0.451,0.475,0.407))-mea
((mean(0.051,0.052,0.055))-mea
((mean(0.105,0.101,0.113))-mea
((mean(0.124,0.125,0.121))-mea
((mean(0.133,0.135,0.134))-mea
((mean(0.147,0.154,0.157))-mea
((mean(0.168,0.178,0.171))-mea
((mean(0.173,0.194,0.177))-mea
((mean(0.479,0.493,0.453))-mea

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Pp5 <- Proteus_mirabilis_6.25ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 6.25 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Proteus_mirabilis_6.25ug_data$Optical_density_mean_values-sd(Proteus_mirabilis_6.2
    ymax=Proteus_mirabilis_6.25ug_data$Optical_density_mean_values+sd(Proteus_mirabilis_6.2
print(Pp5)

```

Penicillin 6.25 ug/mL



#Penicillin 3.125 ug/mL

```
Proteus_mirabilis_3.125ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
Optical_density_mean_values =c((mean(0.061,0.063,0.06)-mean(0.061,0.061,0.061)),
(mean(0.062,0.062,0.062)-mean(0.061,0.061,0.061)),
(mean(0.062,0.061,0.062)-mean(0.061,0.062,0.062)),
(mean(0.061,0.062,0.062)-mean(0.061,0.062,0.063)),
(mean(0.061,0.061,0.063)-mean(0.062,0.061,0.061)),
(mean(0.062,0.061,0.061)-mean(0.062,0.06,0.063)),
(mean(0.057,0.054,0.052)-mean(0.104,0.106,0.105)),
(mean(0.115,0.118,0.114)-mean(0.131,0.137,0.131)),
(mean(0.141,0.151,0.141)-mean(0.147,0.151,0.143)),
(mean(0.151,0.159,0.151)-mean(0.34,0.352,0.339)),
(mean(0.05,0.052,0.052)-mean(0.107,0.107,0.108)),
(mean(0.115,0.12,0.118)-mean(0.131,0.136,0.134)),
(mean(0.142,0.151,0.146)-mean(0.151,0.158,0.15)-mean(0.157,0.169,0.159))
```



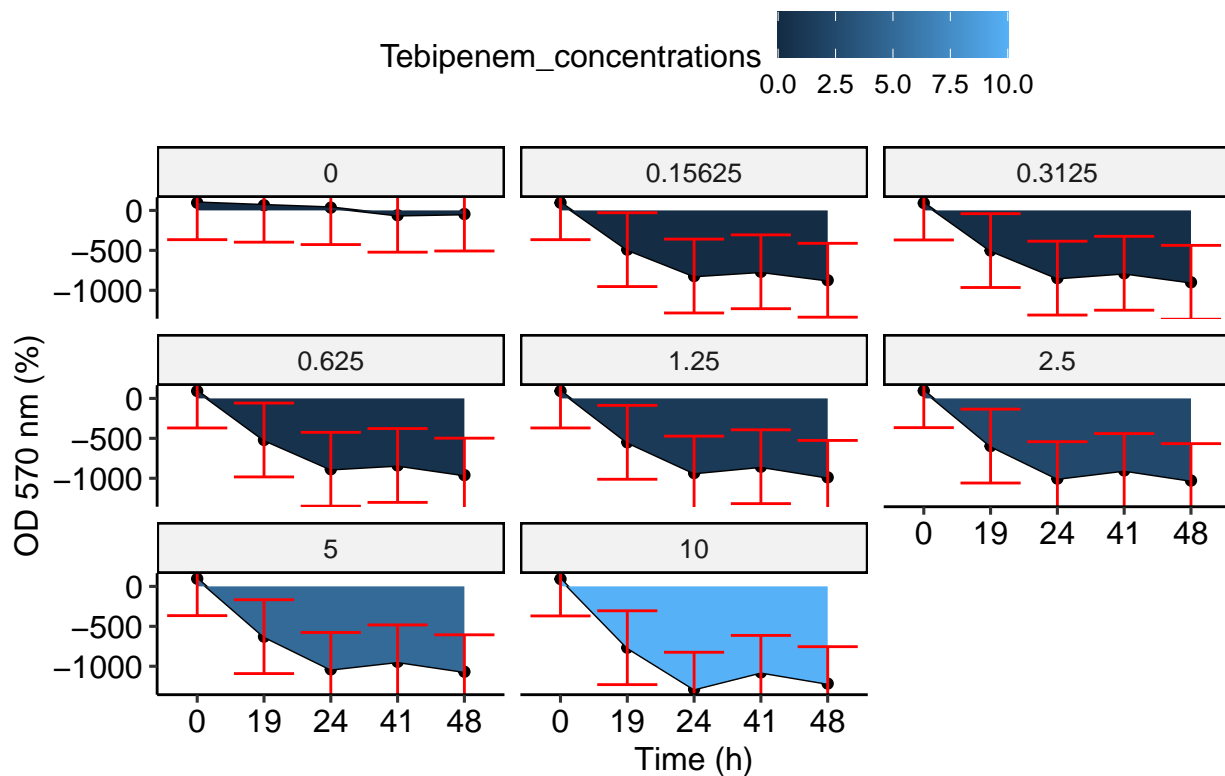
```

((mean(0.354,0.347,0.332))-mea
((mean(0.051,0.053,0.052))-mea
((mean(0.101,0.099,0.111))-mea
((mean(0.117,0.122,0.116))-mea
((mean(0.135,0.135,0.131))-mea
((mean(0.141,0.153,0.149))-mea
((mean(0.161,0.171,0.162))-mea
((mean(0.168,0.185,0.168))-mea
((mean(0.437,0.475,0.402))-mea
((mean(0.052,0.053,0.053))-mea
((mean(0.104,0.103,0.112))-mea
((mean(0.118,0.122,0.12))-mea
((mean(0.132,0.132,0.13))-mea
((mean(0.142,0.154,0.151))-mea
((mean(0.163,0.176,0.164))-mea
((mean(0.172,0.185,0.171))-mea
((mean(0.462,0.482,0.437))-mea

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Pp6 <- Proteus_mirabilis_3.125ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 3.125 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Proteus_mirabilis_3.125ug_data$Optical_density_mean_values-sd(Proteus_mirabilis_3.
    ymax=Proteus_mirabilis_3.125ug_data$Optical_density_mean_values+sd(Proteus_mirabilis_3.
print(Pp6)

```

Penicillin 3.125 ug/mL



#Penicillin 1.5625 ug/mL

```
Proteus_mirabilis_1.5625ug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values =c(((mean(0.06,0.063,0.059)-0.03)-0.03),
((mean(0.059,0.062,0.06)-0.03)-0.03),
((mean(0.06,0.06,0.06)-0.03)-0.03),
((mean(0.06,0.06,0.061)-0.03)-0.03),
((mean(0.06,0.06,0.061)-0.03)-0.03),
((mean(0.06,0.06,0.061)-0.03)-0.03),
((mean(0.06,0.06,0.06)-0.03)-0.03),
((mean(0.061,0.06,0.061)-0.03)-0.03),
((mean(0.051,0.054,0.051)-0.03)-0.03),
((mean(0.1,0.106,0.102)-0.03)-0.03),
((mean(0.111,0.115,0.112)-0.03)-0.03),
((mean(0.127,0.133,0.127)-0.03)-0.03),
((mean(0.137,0.139,0.345)-0.03)-0.03),
((mean(0.144,0.152,0.138)-0.03)-0.03),
((mean(0.15,0.157,0.142)-0.03)-0.03),
((mean(0.343,0.349,0.341)-0.03)-0.03),
((mean(0.049,0.051,0.053)-0.03)-0.03),
((mean(0.104,0.108,0.112)-0.03)-0.03),
((mean(0.112,0.117,0.116)-0.03)-0.03),
((mean(0.127,0.133,0.13)-0.03)-0.03),
((mean(0.137,0.14,0.337)-0.03)-0.03),
((mean(0.149,0.158,0.147)-0.03)-0.03),
((mean(0.157,0.167,0.154)-0.03)-0.03))
```

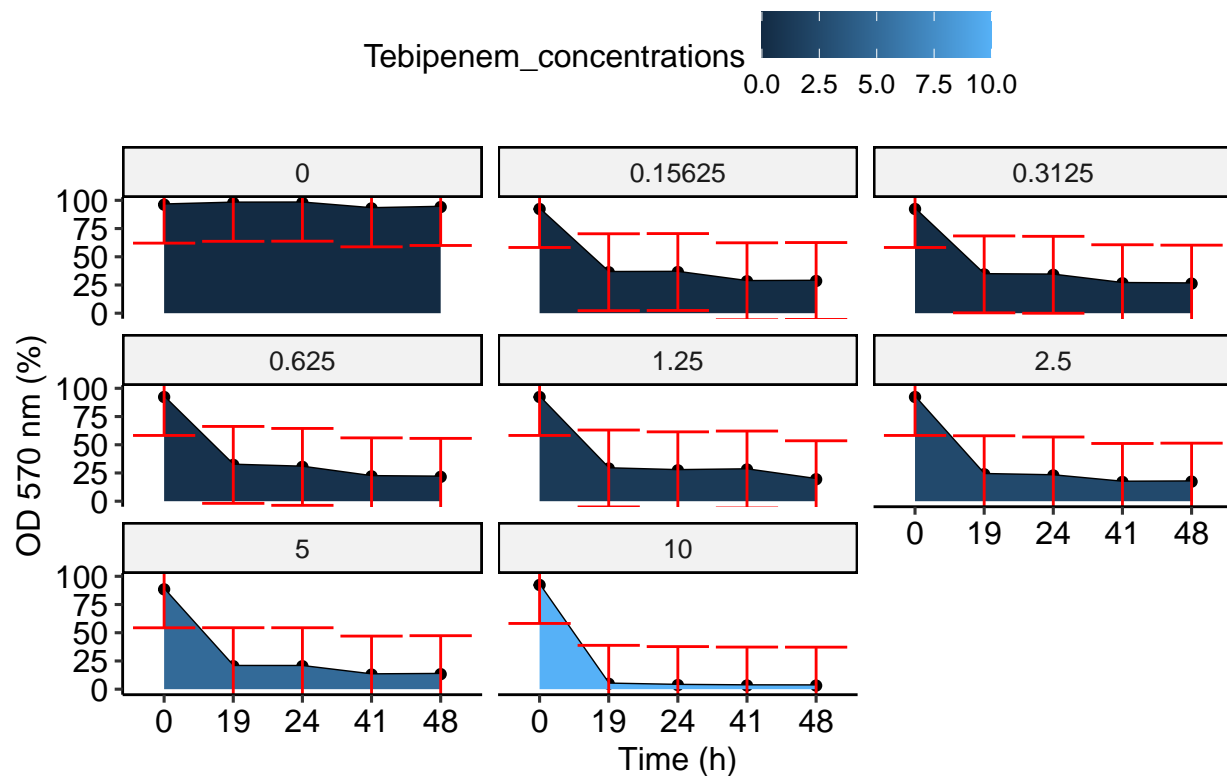
```

((mean(0.359,0.347,0.335)-me
((mean(0.052,0.053,0.053)-me
((mean(0.097,0.102,0.111)-me
((mean(0.116,0.119,0.116)-me
((mean(0.13,0.132,0.129)-mea
((mean(0.139,0.138,0.406)-me
((mean(0.16,0.173,0.158)-mea
((mean(0.168,0.183,0.163)-me
((mean(0.467,0.502,0.408)-me
((mean(0.052,0.052,0.052)-me
((mean(0.1,0.105,0.109)-mea
((mean(0.119,0.123,0.119)-me
((mean(0.129,0.13,0.13)-mea
((mean(0.139,0.136,0.427)-me
((mean(0.161,0.174,0.16)-mea
((mean(0.172,0.187,0.166)-me
((mean(0.482,0.478,0.44)-mea

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Pp7 <- Proteus_mirabilis_1.5625ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 1.5625 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Proteus_mirabilis_1.5625ug_data$Optical_density_mean_values-sd(Proteus_mirabilis_1
    ymax=Proteus_mirabilis_1.5625ug_data$Optical_density_mean_values+sd(Proteus_mirabilis_1
print(Pp7)

```

Penicillin 1.5625 ug/mL



#Penicillin 0 ug/mL

```
Proteus_mirabilis_Oug_data <- data.frame(Time= c(rep("0",8),rep("19",8),rep("24",8),rep("41",8),rep("48",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values =c(((mean(0.062,0.066,0.062)-rnorm(3,0.062,0.005))),
((mean(0.062,0.064,0.062)-rnorm(3,0.062,0.005))),
((mean(0.062,0.063,0.063)-rnorm(3,0.062,0.005))),
((mean(0.062,0.062,0.063)-rnorm(3,0.062,0.005))),
((mean(0.061,0.061,0.063)-rnorm(3,0.062,0.005))),
((mean(0.062,0.063,0.063)-rnorm(3,0.062,0.005))),
((mean(0.062,0.061,0.062)-rnorm(3,0.062,0.005))),
((mean(0.062,0.061,0.063)-rnorm(3,0.062,0.005))),
((mean(0.055,0.055,0.051)-rnorm(3,0.062,0.005))),
((mean(0.107,0.108,0.104)-rnorm(3,0.062,0.005))),
((mean(0.12,0.12,0.116)-rnorm(3,0.062,0.005))),
((mean(0.139,0.139,0.137)-rnorm(3,0.062,0.005))),
((mean(0.142,0.157,0.375)-rnorm(3,0.062,0.005))),
((mean(0.164,0.168,0.162)-rnorm(3,0.062,0.005))),
((mean(0.176,0.183,0.165)-rnorm(3,0.062,0.005))),
((mean(0.377,0.38,0.375)-rnorm(3,0.062,0.005))),
((mean(0.051,0.054,0.053)-rnorm(3,0.062,0.005))),
((mean(0.113,0.109,0.11)-rnorm(3,0.062,0.005))),
((mean(0.122,0.122,0.121)-rnorm(3,0.062,0.005))),
((mean(0.137,0.139,0.14)-rnorm(3,0.062,0.005))),
((mean(0.145,0.16,0.357)-rnorm(3,0.062,0.005))),
((mean(0.17,0.176,0.169)-rnorm(3,0.062,0.005))),
((mean(0.186,0.196,0.174)-rnorm(3,0.062,0.005))))
```

```

((mean(0.382,0.376,0.359)-r
((mean(0.052,0.054,0.053)-r
((mean(0.099,0.1,0.112)-mea
((mean(0.121,0.121,0.12)-me
((mean(0.134,0.134,0.137)-r
((mean(0.147,0.164,0.422)-r
((mean(0.183,0.192,0.181)-r
((mean(0.194,0.215,0.188)-r
((mean(0.509,0.562,0.426)-r
((mean(0.052,0.053,0.052)-r
((mean(0.101,0.104,0.113)-r
((mean(0.123,0.126,0.124)-r
((mean(0.132,0.137,0.137)-r
((mean(0.149,0.168,0.445)-r
((mean(0.181,0.194,0.184)-r
((mean(0.199,0.23,0.199)-me
((mean(0.525,0.519,0.471)-r

```

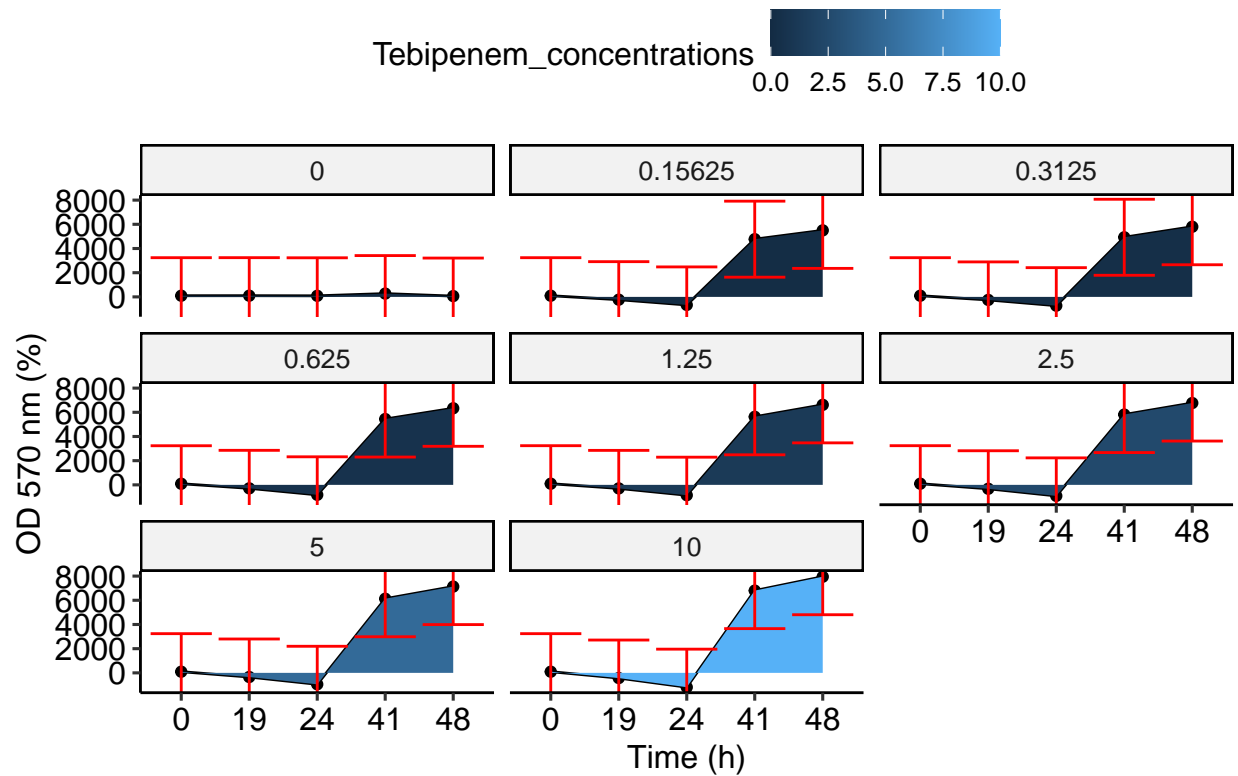
#Make a line graphs for changing in OD with time according to Tebipenem concentrations

```

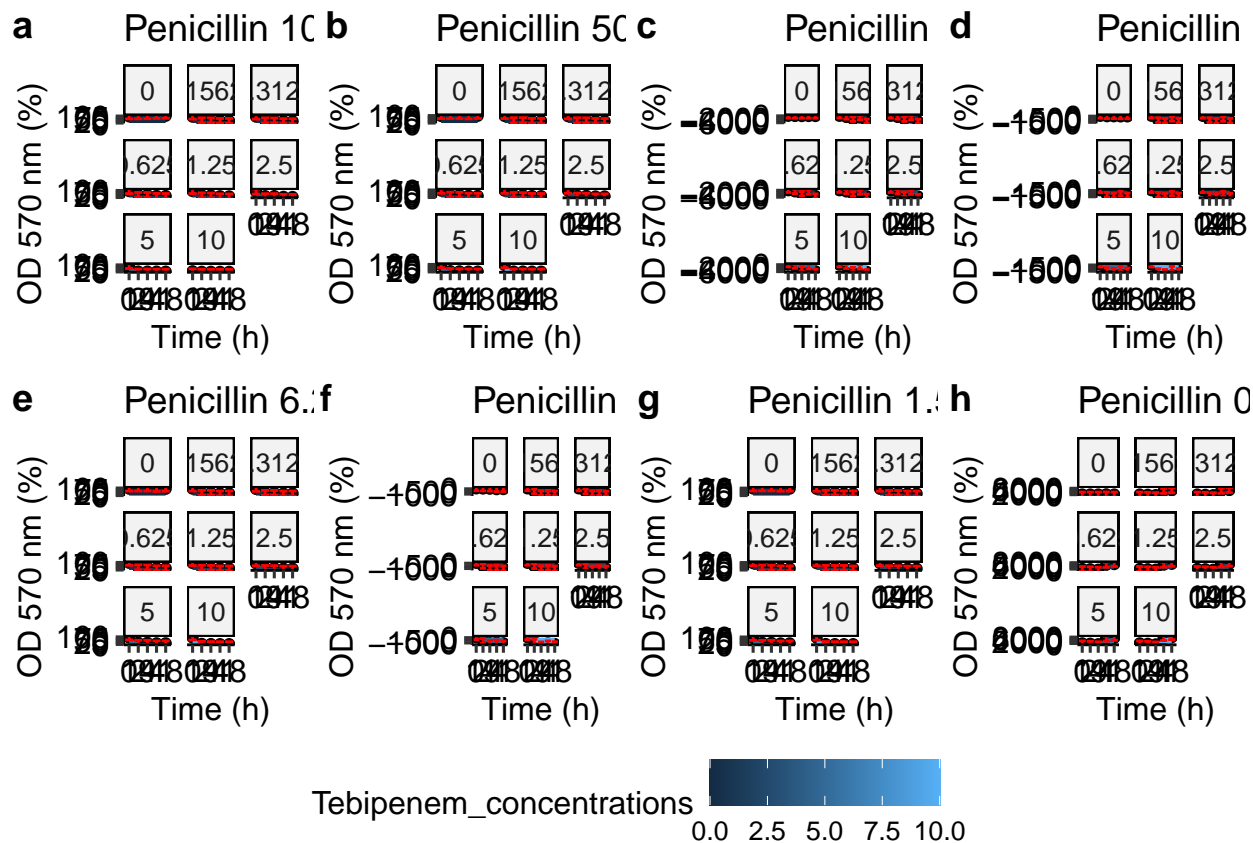
Pp8 <- Proteus_mirabilis_Oug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations)) +
  geom_line() +
  geom_point() +
  geom_area() +
  facet_wrap(~Tebipenem_concentrations) +
  ggtitle("Penicillin 0 ug/mL") +
  xlab("Time (h)") +
  ylab("OD 570 nm (%)") +
  geom_errorbar(ymin=Proteus_mirabilis_Oug_data$Optical_density_mean_values-sd(Proteus_mirabilis_Oug_data$Optical_density_mean_values),
               ymax=Proteus_mirabilis_Oug_data$Optical_density_mean_values+sd(Proteus_mirabilis_Oug_data$Optical_density_mean_values))
print(Pp8)

```

Penicillin 0 ug/mL



```
#Align all graphs together
library(ggplot2)
library(ggpubr)
theme_set(theme_pubr())
figure_2 <- ggarrange(Pp1,Pp2,Pp3,Pp4, Pp5, Pp6, Pp7, Pp8,
  labels=c("a","b","c","d","e","f","g","h"),
  ncol=4,nrow=2,
  common.legend = TRUE,legend = "bottom")
print(figure_2)
```



```
#Compare concentrations that inhibit the bacterial growth
Final_Proteus_data <- data.frame(Time_f2 =c("0","19","24","41","48"),
                                   Concentrations= c(rep("PenV+Tebipenem (100 ug/mL+10 ug/mL)",5),rep("PenV+Tebipenem (50 ug/mL+10 ug/mL)",5),rep("PenV+Tebipenem (6.25 ug/mL+10 ug/mL)",5),rep("PenV+Tebipenem (2.5 ug/mL+10 ug/mL)",5)),
                                   Optical_density=c((mean(0.04,0.06,0.806)-0.038)/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.04,0.049,0.051)-mean(0.038,0.037,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.04,0.048,0.043)-mean(0.038,0.037,0.038))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.041,0.049,0.039)-mean(0.038,0.036,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.041,0.048,0.036)-mean(0.038,0.036,0.036))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.06,0.061,0.061)-0.038)/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.05,0.06,0.054)-mean(0.038,0.037,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.051,0.052,0.051)-mean(0.038,0.037,0.038))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.053,0.053,0.051)-mean(0.038,0.036,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.051,0.051,0.052)-mean(0.038,0.036,0.036))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.06,0.06,0.04)-mean(0.035,0.036,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.046,0.048,0.194)-mean(0.035,0.036,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.049,0.051,0.239)-mean(0.037,0.038,0.038))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.05,0.052,0.239)-0.038)/(mean(0.0505,0.514,0.514)-0.038),
                                                       (mean(0.05,0.051,0.168)-0.038)/(mean(0.521,0.515,0.515)-0.038),
                                                       (mean(0.06,0.06,0.06)-mean(0.035,0.036,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.063,0.097,0.069)-mean(0.035,0.036,0.037))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.057,0.1,0.067)-mean(0.037,0.038,0.038))/(mean(0.064,0.063,0.063)-0.038),
                                                       (mean(0.054,0.082,0.056)-0.038)/(mean(0.505,0.514,0.514)-0.038),
                                                       (mean(0.056,0.083,0.061)-0.038)/(mean(0.521,0.515,0.515)-0.038),
                                                       (mean(0.062,0.063,0.061)-0.036)/(mean(0.064,0.065,0.065)-0.036)))
```

```

((mean(0.057,0.057,0.05)-mean(0.035,0.035,0.338))/(mean(0.05,0.051,0.05)-mean(0.035,0.037,0.366))/(mean(0.051,0.052,0.052)-mean(0.036,0.037,0.469))/(mean(0.051,0.052,0.055)-mean(0.036,0.037,0.49))/(mean(0.06,0.063,0.059)-0.036)/(mean(0.062,0.061,0.062)-0.036)/(mean(0.051,0.054,0.051)-0.036)/(mean(0.035,0.036,0.036)-0.036)/(mean(0.049,0.051,0.053)-mean(0.037,0.036,0.037))/(mean(0.052,0.053,0.053)-mean(0.037,0.037,0.036))/(0.052- mean(0.037,0.037,0.036))/(mean(0.51,0.503,0.503)-0.503)

print(Final_Proteus_data)

```

##	Time_f2	Concentrations	Optical_density
## 1	0	PenV+Tebipenem (100 ug/mL+10 ug/mL)	7.6923077
## 2	19	PenV+Tebipenem (100 ug/mL+10 ug/mL)	0.7067138
## 3	24	PenV+Tebipenem (100 ug/mL+10 ug/mL)	0.6430868
## 4	41	PenV+Tebipenem (100 ug/mL+10 ug/mL)	0.6833713
## 5	48	PenV+Tebipenem (100 ug/mL+10 ug/mL)	0.6578947
## 6	0	PenV+Tebipenem (100 ug/mL+5 ug/mL)	84.6153846
## 7	19	PenV+Tebipenem (100 ug/mL+5 ug/mL)	4.2402827
## 8	24	PenV+Tebipenem (100 ug/mL+5 ug/mL)	4.1800643
## 9	41	PenV+Tebipenem (100 ug/mL+5 ug/mL)	3.4168565
## 10	48	PenV+Tebipenem (100 ug/mL+5 ug/mL)	2.8508772
## 11	0	PenV+Tebipenem (50 ug/mL+10 ug/mL)	92.5925926
## 12	19	PenV+Tebipenem (50 ug/mL+10 ug/mL)	3.6666667
## 13	24	PenV+Tebipenem (50 ug/mL+10 ug/mL)	3.7037037
## 14	41	PenV+Tebipenem (50 ug/mL+10 ug/mL)	2.5695931
## 15	48	PenV+Tebipenem (50 ug/mL+10 ug/mL)	2.4844720
## 16	0	PenV+Tebipenem (50 ug/mL+5 ug/mL)	92.5925926
## 17	19	PenV+Tebipenem (50 ug/mL+5 ug/mL)	9.3333333
## 18	24	PenV+Tebipenem (50 ug/mL+5 ug/mL)	6.1728395
## 19	41	PenV+Tebipenem (50 ug/mL+5 ug/mL)	3.4261242
## 20	48	PenV+Tebipenem (50 ug/mL+5 ug/mL)	3.7267081
## 21	0	PenV+Tebipenem (6.25 ug/mL+10 ug/mL)	92.8571429
## 22	19	PenV+Tebipenem (6.25 ug/mL+10 ug/mL)	6.7484663
## 23	24	PenV+Tebipenem (6.25 ug/mL+10 ug/mL)	4.3731778
## 24	41	PenV+Tebipenem (6.25 ug/mL+10 ug/mL)	3.1578947
## 25	48	PenV+Tebipenem (6.25 ug/mL+10 ug/mL)	3.0800821
## 26	0	PenV+Tebipenem (1.5625 ug/mL+10 ug/mL)	92.3076923
## 27	19	PenV+Tebipenem (1.5625 ug/mL+10 ug/mL)	4.7770701
## 28	24	PenV+Tebipenem (1.5625 ug/mL+10 ug/mL)	3.6474164
## 29	41	PenV+Tebipenem (1.5625 ug/mL+10 ug/mL)	3.2397408
## 30	48	PenV+Tebipenem (1.5625 ug/mL+10 ug/mL)	3.1712474

```

#Make up a line graph
Final_Prot <- Final_Proteus_data %>%
  ggplot(aes(x=Time_f2, y=Optical_density,group=Concentrations, shape=Concentrations))+
  geom_line()+
  geom_point()+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Final_Proteus_data$Optical_density-sd(Final_Proteus_data$Optical_density),
                ymax=Final_Proteus_data$Optical_density+sd(Final_Proteus_data$Optical_density),
                width=.2)+

```

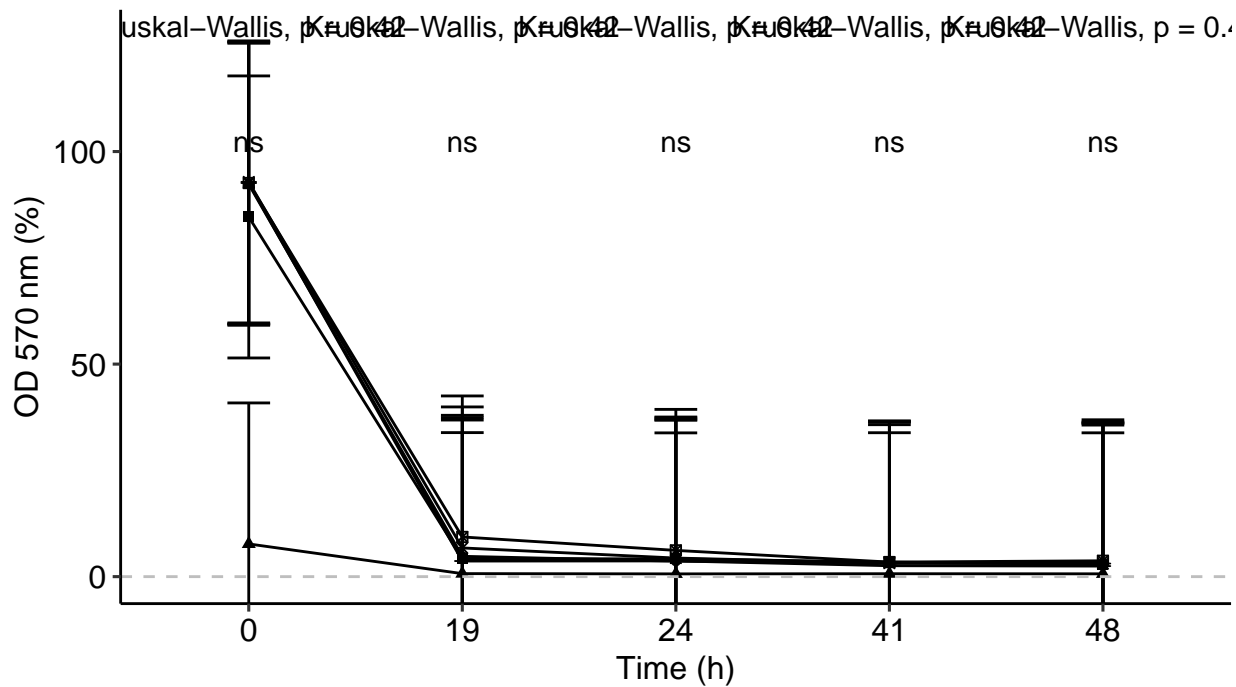


```

stat_compare_means(method = "kruskal.test", label.y = 127)+
stat_compare_means(label = "p.signif", label.y = c(100,100,100,100,100), label.x = 10)+
geom_hline(yintercept = 0, linetype="dashed", col="grey")
print(Final_Prot)

```

PenV+Tebipenem (1.5625 ug/mL+10 ug/mL) ■ PenV+Tebipenem (100 ug/mL+5 ug/mL) ▣ PenV+T
 PenV+Tebipenem (100 ug/mL+10 ug/mL) + PenV+Tebipenem (50 ug/mL+10 ug/mL) * PenV+T



```

#Mycobacterium smegmatis RESULTS AND PLOTS
#Penicillin 100 ug/ml
Mycobacterium_smegmatis_100ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8)),
  Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
  Optical_density_mean_values =c((mean(0.047,0.053,0.049)-mean(0.047,0.051,0.047))-mean(0.047,0.046,0.046))-mean(0.047,0.047,0.047))-mean(0.048,0.045,0.045))-mean(0.046,0.045,0.045))-mean(0.046,0.044,0.046))-mean(0.046,0.044,0.046))-mean(0.057,0.064,0.047))-mean(0.067,0.076,0.101))-mean(0.078,0.075,0.126))-mean(0.086,0.114,0.125))-mean(0.118,0.103,0.146))-mean(0.123,0.144,0.138))-mean(0.109,0.106,0.152))-mean(0.135,0.12,0.163))-mean

```

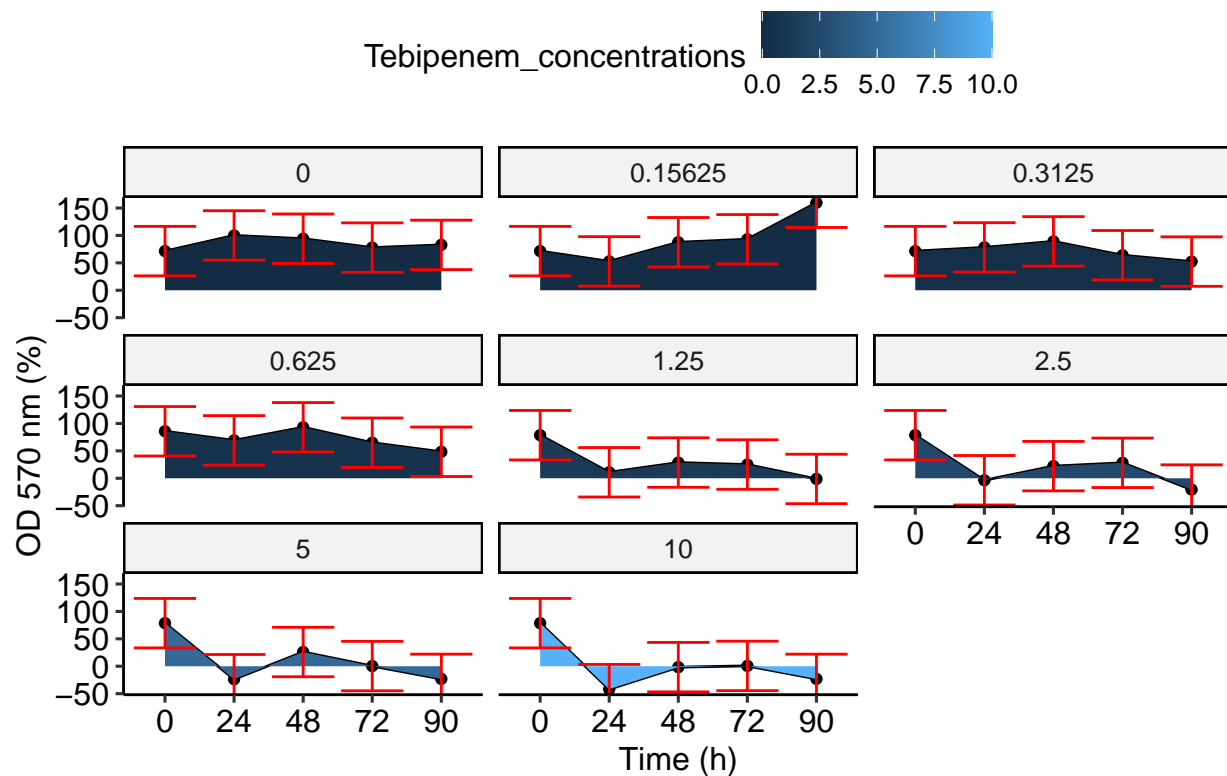
```

((mean(0.049,0.044,0.08)-mean(
((mean(0.1,0.065,0.119)-mean(
((mean(0.093,0.068,0.084)-mean(
((mean(0.105,0.226,0.182)-mean(
((mean(0.224,0.138,0.183)-mean(
((mean(0.217,0.263,0.163)-mean(
((mean(0.214,0.174,0.237)-mean(
((mean(0.226,0.201,0.25)-mean(
((mean(0.049,0.058,0.043)-mean(
((mean(0.048,0.044,0.128)-mean(
((mean(0.136,0.066,0.048)-mean(
((mean(0.126,0.32,0.153)-mean(
((mean(0.252,0.187,0.302)-mean(
((mean(0.249,0.368,0.209)-mean(
((mean(0.341,0.292,0.315)-mean(
((mean(0.293,0.326,0.34)-mean(
((mean(0.044,0.045,0.041)-mean(
((mean(0.044,0.046,0.14)-mean(
((mean(0.052,0.088,0.083)-mean(
((mean(0.115,0.587,0.137)-mean(
((mean(0.276,0.245,0.373)-mean(
((mean(0.289,0.44,0.281)-mean(
((mean(0.638,0.462,0.637)-mean(
((mean(0.388,0.418,0.498)-mean(

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp1 <- Mycobacterium_smegmatis_100ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations)) +
  geom_line() +
  geom_point() +
  geom_area() +
  facet_wrap(~Tebipenem_concentrations) +
  ggtitle("Penicillin 100 ug/mL") +
  xlab("Time (h)") +
  ylab("OD 570 nm (%)") +
  geom_errorbar(ymin=Mycobacterium_smegmatis_100ug_data $Optical_density_mean_values-sd(Mycobacterium_smegmatis_100ug_data $Optical_density_mean_values),
                ymax=Mycobacterium_smegmatis_100ug_data $Optical_density_mean_values+sd(Mycobacterium_smegmatis_100ug_data $Optical_density_mean_values))
print(Mp1)

```

Penicillin 100 ug/mL



#Penicillin 50 ug/mL

```
Mycobacterium_smegmatis_50ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
Optical_density_mean_values =c((mean(0.049,0.05,0.049),
((mean(0.048,0.048,0.06),
((mean(0.048,0.047,0.05),
((mean(0.048,0.047,0.04),
((mean(0.048,0.046,0.04),
((mean(0.048,0.046,0.04),
((mean(0.048,0.047,0.04),
((mean(0.047,0.047,0.04),
((mean(0.067,0.074,0.05),
((mean(0.082,0.082,0.05),
((mean(0.086,0.085,0.10),
((mean(0.092,0.101,0.14),
((mean(0.114,0.106,0.15),
((mean(0.125,0.106,0.15),
((mean(0.134,0.114,0.16),
((mean(0.129,0.142,0.17),
((mean(0.053,0.049,0.07),
((mean(0.1,0.063,0.088),
((mean(0.085,0.09,0.093),
((mean(0.121,0.151,0.17),
((mean(0.157,0.159,0.20),
((mean(0.196,0.169,0.16),
((mean(0.246,0.201,0.21)
```

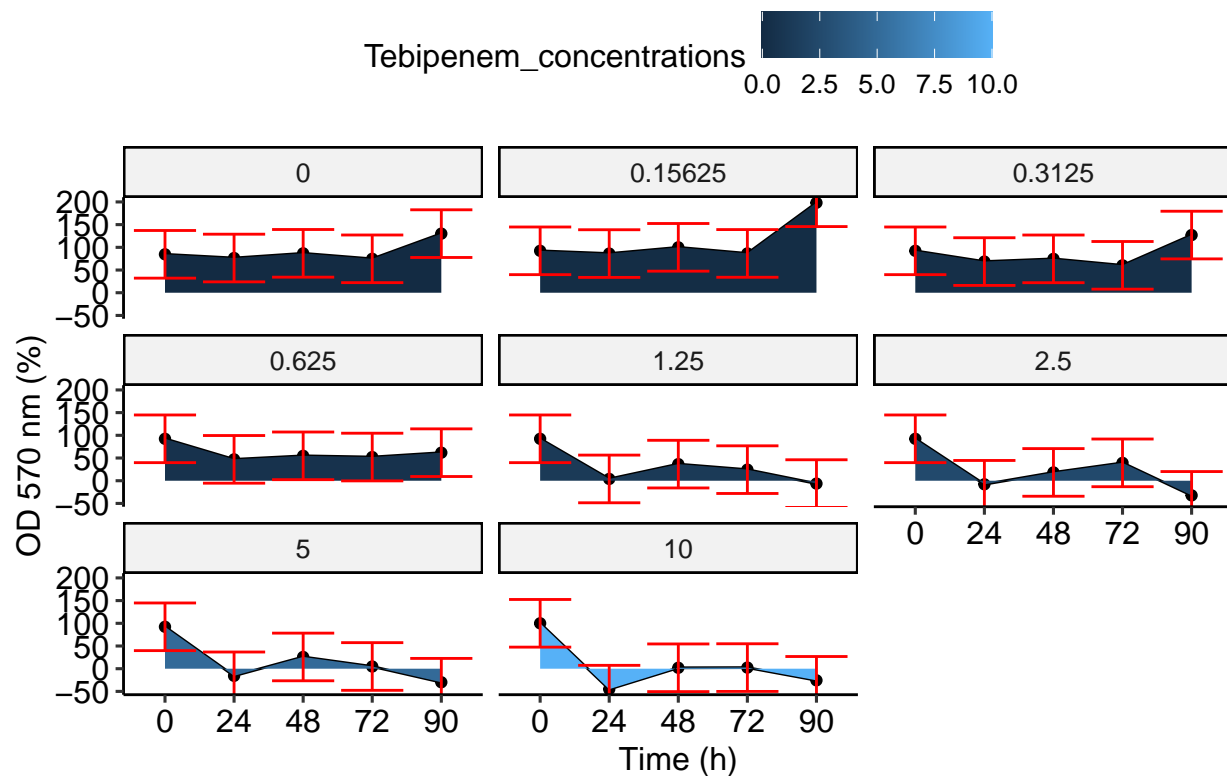
```

((mean(0.22,0.253,0.273)
((mean(0.057,0.051,0.053)
((mean(0.065,0.048,0.041)
((mean(0.178,0.074,0.054)
((mean(0.129,0.217,0.193)
((mean(0.22,0.209,0.278)
((mean(0.247,0.291,0.223)
((mean(0.333,0.299,0.303)
((mean(0.294,0.354,0.323)
((mean(0.062,0.061,0.041)
((mean(0.05,0.066,0.094)
((mean(0.043,0.043,0.073)
((mean(0.117,0.207,0.223)
((mean(0.311,0.272,0.243)
((mean(0.497,0.427,0.303)
((mean(0.7,0.498,0.581)
((mean(0.506,0.521,0.543)

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp2 <- Mycobacterium_smegmatis_50ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations)) +
  geom_line() +
  geom_point() +
  geom_area() +
  facet_wrap(~Tebipenem_concentrations) +
  ggtitle("Penicillin 50 ug/mL") +
  xlab("Time (h)") +
  ylab("OD 570 nm (%)") +
  geom_errorbar(ymin=Mycobacterium_smegmatis_50ug_data$Optical_density_mean_values-sd(Mycobacterium_smegmatis_50ug_data$Optical_density_mean_values),
               ymax=Mycobacterium_smegmatis_50ug_data$Optical_density_mean_values+sd(Mycobacterium_smegmatis_50ug_data$Optical_density_mean_values))
print(Mp2)

```

Penicillin 50 ug/mL



#Penicillin 25 ug/mL

```
Mycobacterium_smegmatis_25ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8),rep("90",8)),
  Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125,0.0390625,0.01953125,0.009765625,0.0048828125),
  Optical_density_mean_values =c((mean(0.044,0.044,0.044,0.044,0.044,0.044,0.044,0.044)),
    (mean(0.044,0.046,0.045,0.043,0.042,0.043,0.044,0.042)),
    (mean(0.044,0.044,0.043,0.043,0.042,0.043,0.044,0.042)),
    (mean(0.045,0.043,0.044,0.043,0.042,0.043,0.044,0.042)),
    (mean(0.045,0.044,0.043,0.043,0.042,0.043,0.044,0.042)),
    (mean(0.071,0.068,0.048,0.047,0.046,0.047,0.048,0.047)),
    (mean(0.079,0.085,0.062,0.061,0.06,0.061,0.062,0.061)),
    (mean(0.076,0.079,0.104,0.103,0.102,0.103,0.104,0.103)),
    (mean(0.084,0.089,0.111,0.11,0.109,0.11,0.111,0.11)),
    (mean(0.107,0.101,0.144,0.143,0.142,0.143,0.144,0.143)),
    (mean(0.11,0.102,0.133,0.132,0.131,0.132,0.133,0.132)),
    (mean(0.112,0.105,0.172,0.171,0.17,0.171,0.172,0.171)),
    (mean(0.127,0.127,0.163,0.162,0.161,0.162,0.163,0.162)),
    (mean(0.043,0.042,0.075,0.074,0.073,0.074,0.075,0.074)),
    (mean(0.086,0.053,0.106,0.105,0.104,0.105,0.106,0.105)),
    (mean(0.101,0.091,0.106,0.105,0.104,0.105,0.106,0.105)),
    (mean(0.103,0.147,0.127,0.126,0.125,0.126,0.127,0.126)),
    (mean(0.127,0.144,0.235,0.234,0.233,0.234,0.235,0.234)),
    (mean(0.225,0.187,0.144,0.143,0.142,0.143,0.144,0.143)),
    (mean(0.236,0.181,0.209,0.208,0.207,0.208,0.209,0.208))
  )
```

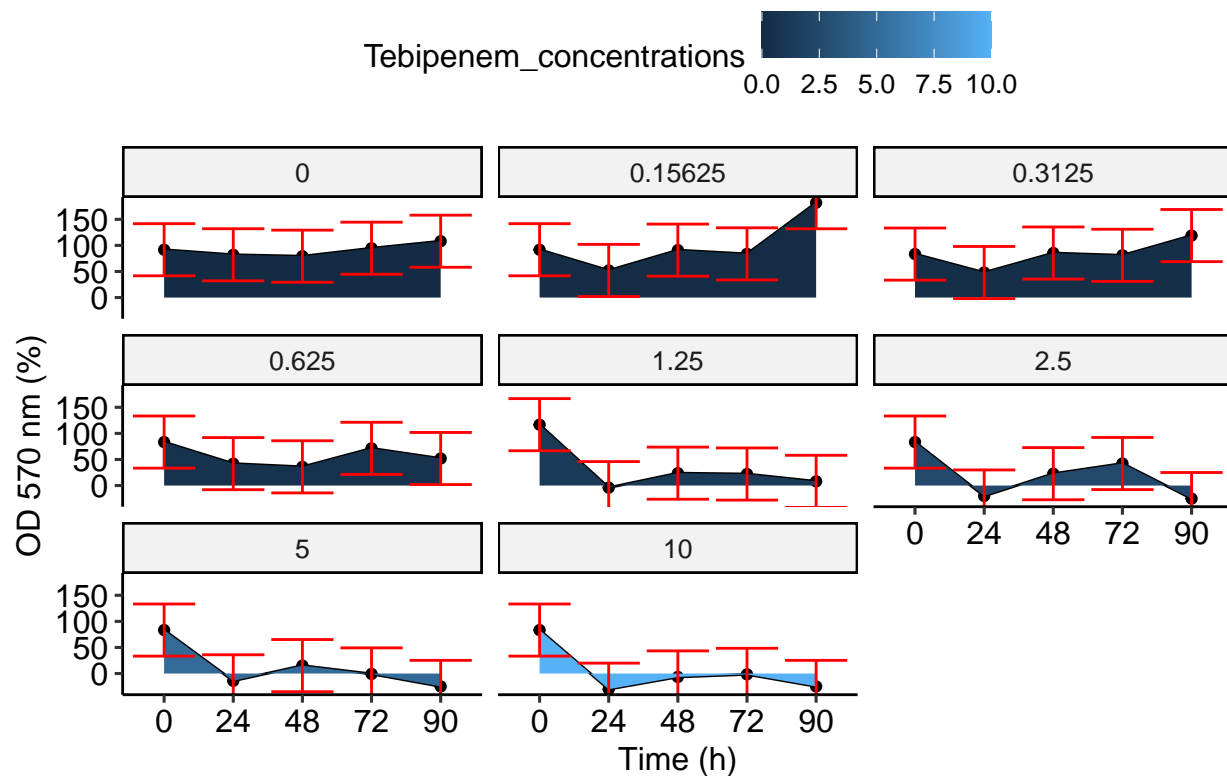
```

((mean(0.213,0.228,0.241)
((mean(0.051,0.052,0.049)
((mean(0.053,0.04,0.044)
((mean(0.164,0.041,0.054)
((mean(0.112,0.251,0.14)
((mean(0.239,0.187,0.311)
((mean(0.264,0.284,0.188)
((mean(0.271,0.297,0.256)
((mean(0.299,0.302,0.302)
((mean(0.041,0.046,0.05)
((mean(0.041,0.079,0.059)
((mean(0.04,0.04,0.057)-1
((mean(0.147,0.243,0.165)
((mean(0.289,0.294,0.677)
((mean(0.506,0.455,0.358)
((mean(0.71,0.486,0.542)
((mean(0.471,0.468,0.603)

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp3 <- Mycobacterium_smegmatis_25ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 25 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Mycobacterium_smegmatis_25ug_data$Optical_density_mean_values-sd(Mycobacterium_sme
                ymax=Mycobacterium_smegmatis_25ug_data$Optical_density_mean_values+sd(Mycobacterium_sme
print(Mp3)

```

Penicillin 25 ug/mL



```
#Penicillin 12.5 ug/mL
Mycobacterium_smegmatis_12.5ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8),rep("90",8)),
  Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.0),
  Optical_density_mean_values =c((mean(0.049,0.05,0.047),
    (mean(0.048,0.048,0.048),
    (mean(0.048,0.047,0.048),
    (mean(0.05,0.046,0.049),
    (mean(0.048,0.046,0.048),
    (mean(0.048,0.048,0.047),
    (mean(0.048,0.046,0.047),
    (mean(0.048,0.047,0.047),
    (mean(0.071,0.072,0.053),
    (mean(0.085,0.081,0.063),
    (mean(0.083,0.08,0.122),
    (mean(0.093,0.088,0.125),
    (mean(0.112,0.105,0.153),
    (mean(0.119,0.114,0.135),
    (mean(0.125,0.119,0.16),
    (mean(0.133,0.129,0.165),
    (mean(0.076,0.055,0.082),
    (mean(0.083,0.056,0.119),
    (mean(0.108,0.107,0.119),
    (mean(0.108,0.13,0.147),
    (mean(0.171,0.178,0.148),
    (mean(0.198,0.221,0.157),
    (mean(0.22,0.198,0.213))
```

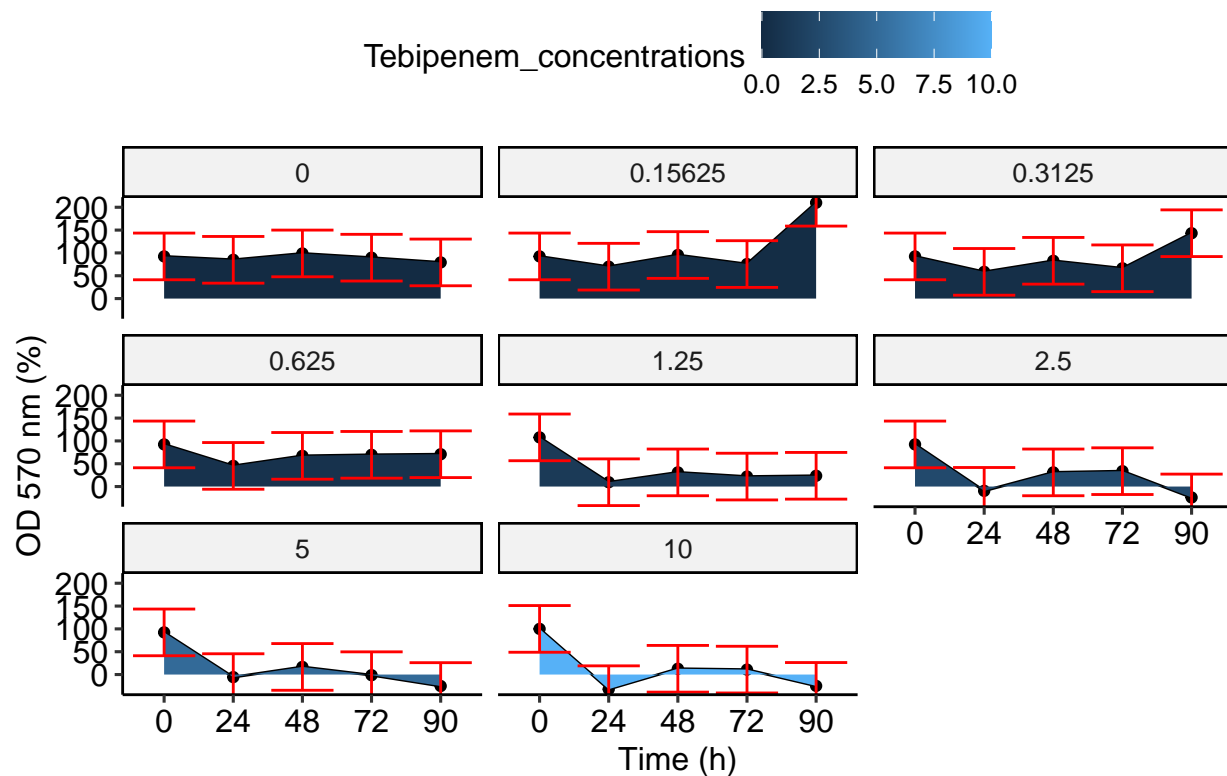
```

((mean(0.226,0.231,0.247)
((mean(0.083,0.05,0.048)
((mean(0.049,0.044,0.052)
((mean(0.147,0.048,0.065)
((mean(0.114,0.172,0.147)
((mean(0.247,0.293,0.258)
((mean(0.238,0.34,0.222)
((mean(0.264,0.316,0.266)
((mean(0.303,0.3,0.397)-1
((mean(0.046,0.061,0.048)
((mean(0.045,0.05,0.057)
((mean(0.049,0.08,0.048)
((mean(0.202,0.19,0.155)
((mean(0.354,0.304,0.433)
((mean(0.587,0.504,0.291)
((mean(0.802,0.45,0.489)
((mean(0.381,0.484,0.508)

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp4 <- Mycobacterium_smegmatis_12.5ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 12.5 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Mycobacterium_smegmatis_12.5ug_data$Optical_density_mean_values-sd(Mycobacterium_sm
                ymax=Mycobacterium_smegmatis_12.5ug_data$Optical_density_mean_values+sd(Mycobacterium_sm
print(Mp4)

```


Penicillin 12.5 ug/mL



```
#Penicillin 6.25 ug/mL
Mycobacterium_smegmatis_6.25ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8),rep("90",8)),
  Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
  Optical_density_mean_values =c((mean(0.049,0.048,0.047,0.046,0.045,0.044,0.043,0.042)),
    (mean(0.046,0.047,0.048,0.049,0.05,0.051,0.052,0.053)),
    (mean(0.047,0.045,0.043,0.041,0.039,0.037,0.035,0.033)),
    (mean(0.046,0.046,0.046,0.046,0.046,0.046,0.046,0.046)),
    (mean(0.047,0.046,0.045,0.044,0.043,0.042,0.041,0.04)),
    (mean(0.047,0.045,0.043,0.041,0.039,0.037,0.035,0.033)),
    (mean(0.047,0.045,0.043,0.041,0.039,0.037,0.035,0.033)),
    (mean(0.047,0.046,0.045,0.044,0.043,0.042,0.041,0.04)),
    (mean(0.073,0.071,0.069,0.067,0.065,0.063,0.061,0.059)),
    (mean(0.083,0.078,0.073,0.068,0.063,0.058,0.053,0.048)),
    (mean(0.081,0.081,0.1,0.11,0.12,0.13,0.14,0.15)),
    (mean(0.088,0.091,0.11,0.12,0.13,0.14,0.15,0.16)),
    (mean(0.111,0.114,0.12,0.13,0.14,0.15,0.16,0.17)),
    (mean(0.116,0.118,0.12,0.13,0.14,0.15,0.16,0.17)),
    (mean(0.121,0.121,0.12,0.13,0.14,0.15,0.16,0.17)),
    (mean(0.137,0.143,0.2,0.21,0.22,0.23,0.24,0.25)),
    (mean(0.05,0.048,0.07,0.068,0.066,0.064,0.062,0.06)),
    (mean(0.084,0.085,0.1,0.11,0.12,0.13,0.14,0.15)),
    (mean(0.108,0.104,0.11,0.12,0.13,0.14,0.15,0.16)),
    (mean(0.108,0.134,0.15,0.16,0.17,0.18,0.19,0.2)),
    (mean(0.136,0.179,0.19,0.2,0.21,0.22,0.23,0.24)),
    (mean(0.224,0.199,0.19,0.2,0.21,0.22,0.23,0.24)),
    (mean(0.216,0.221,0.2,0.21,0.22,0.23,0.24,0.25))
  )
```

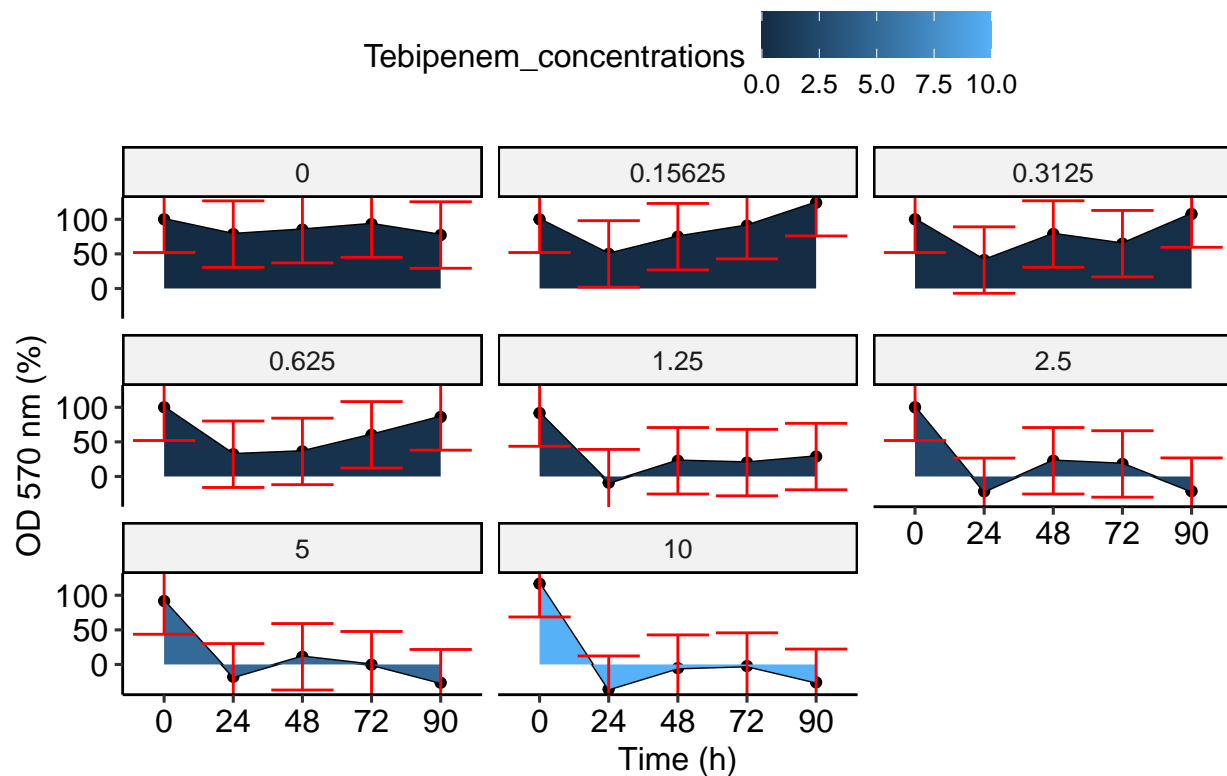
```

((mean(0.237,0.256,0.2
((mean(0.051,0.047,0.0
((mean(0.057,0.039,0.0
((mean(0.113,0.051,0.0
((mean(0.119,0.215,0.1
((mean(0.241,0.279,0.2
((mean(0.255,0.306,0.2
((mean(0.334,0.355,0.2
((mean(0.341,0.304,0.3
((mean(0.045,0.044,0.0
((mean(0.043,0.044,0.0
((mean(0.06,0.132,0.04
((mean(0.225,0.135,0.1
((mean(0.414,0.364,0.2
((mean(0.485,0.542,0.3
((mean(0.539,0.499,0.3
((mean(0.385,0.458,0.4

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp5 <- Mycobacterium_smegmatis_6.25ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations))+
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 6.25 ug/mL")+
  xlab("Time (h)") +
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Mycobacterium_smegmatis_6.25ug_data$Optical_density_mean_values-sd(Mycobacterium_smegmatis_6.25ug_data$Optical_density_mean_values),
                ymax=Mycobacterium_smegmatis_6.25ug_data$Optical_density_mean_values+sd(Mycobacterium_smegmatis_6.25ug_data$Optical_density_mean_values))+
  print(Mp5)

```

Penicillin 6.25 ug/mL



#Penicillin 3.125 ug/mL

```
Mycobacterium_smegmatis_3.125ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8),rep("90",8)),
  Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
  Optical_density_mean_values =c((mean(0.047,0.049,0.047,0.046,0.047,0.046,0.047,0.046),
    (mean(0.049,0.046,0.047,0.045,0.047,0.045,0.046,0.045),
    (mean(0.047,0.045,0.047,0.045,0.046,0.045,0.047,0.047),
    (mean(0.047,0.046,0.046,0.045,0.046,0.045,0.046,0.045),
    (mean(0.047,0.046,0.046,0.045,0.046,0.045,0.046,0.045),
    (mean(0.046,0.045,0.046,0.045,0.046,0.045,0.046,0.045),
    (mean(0.047,0.046,0.046,0.045,0.046,0.045,0.046,0.045),
    (mean(0.078,0.088,0.088,0.088,0.088,0.088,0.088,0.088),
    (mean(0.089,0.111,0.111,0.111,0.111,0.111,0.111,0.111),
    (mean(0.087,0.085,0.085,0.085,0.085,0.085,0.085,0.085),
    (mean(0.094,0.094,0.116,0.116,0.116,0.116,0.116,0.116),
    (mean(0.116,0.108,0.108,0.108,0.108,0.108,0.108,0.108),
    (mean(0.123,0.116,0.116,0.116,0.116,0.116,0.116,0.116),
    (mean(0.131,0.12,0.161,0.161,0.161,0.161,0.161,0.161),
    (mean(0.149,0.153,0.153,0.153,0.153,0.153,0.153,0.153),
    (mean(0.046,0.05,0.053,0.053,0.053,0.053,0.053,0.053),
    (mean(0.077,0.052,0.116,0.116,0.116,0.116,0.116,0.116),
    (mean(0.141,0.077,0.141,0.141,0.141,0.141,0.141,0.141),
    (mean(0.114,0.172,0.172,0.172,0.172,0.172,0.172,0.172),
    (mean(0.161,0.186,0.186,0.186,0.186,0.186,0.186,0.186),
    (mean(0.235,0.203,0.203,0.203,0.203,0.203,0.203,0.203),
    (mean(0.214,0.205,0.205,0.205,0.205,0.205,0.205,0.205))
```

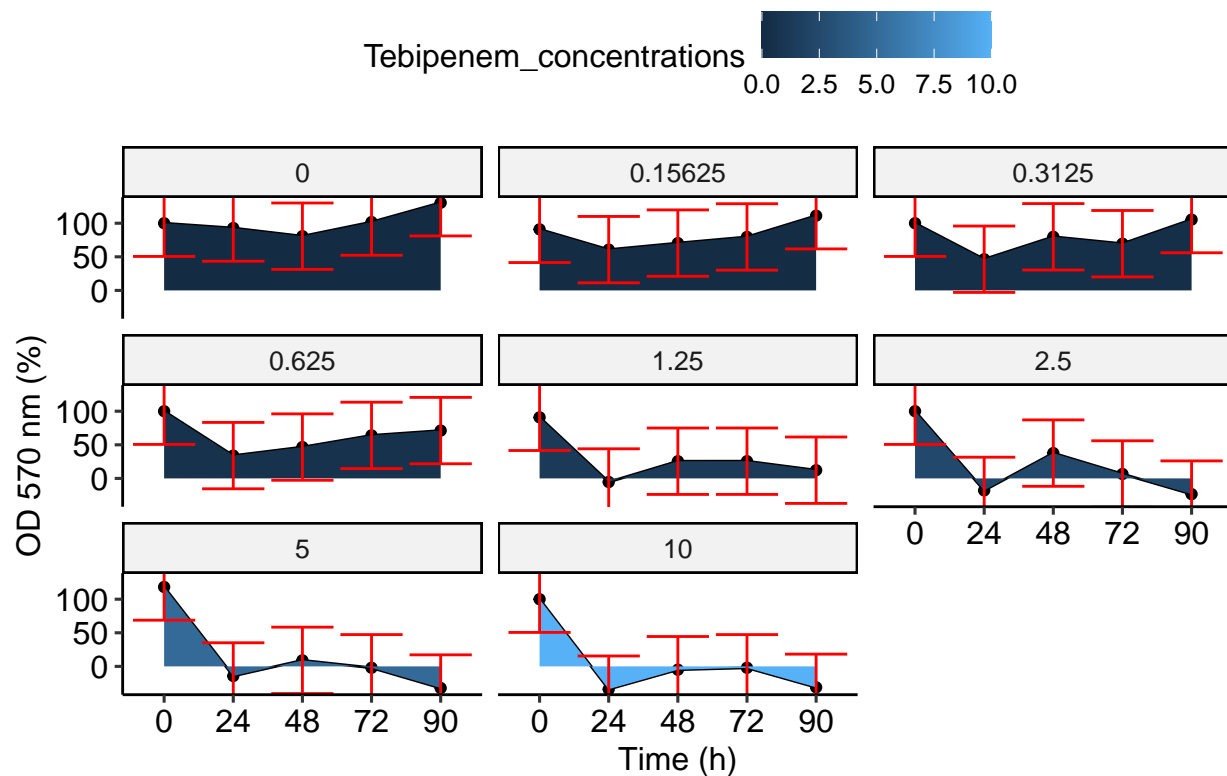
```

((mean(0.237,0.266,0.2
((mean(0.046,0.047,0.0
((mean(0.046,0.042,0.0
((mean(0.071,0.041,0.0
((mean(0.126,0.198,0.1
((mean(0.237,0.252,0.2
((mean(0.253,0.369,0.2
((mean(0.282,0.278,0.2
((mean(0.346,0.322,0.3
((mean(0.045,0.044,0.0
((mean(0.042,0.044,0.0
((mean(0.068,0.05,0.04
((mean(0.173,0.186,0.2
((mean(0.347,0.316,0.3
((mean(0.448,0.411,0.3
((mean(0.465,0.319,0.3
((mean(0.522,0.592,0.4

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp6 <- Mycobacterium_smegmatis_3.125ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations)) +
  geom_line() +
  geom_point() +
  geom_area() +
  facet_wrap(~Tebipenem_concentrations) +
  ggtitle("Penicillin 3.125 ug/mL") +
  xlab("Time (h)") +
  ylab("OD 570 nm (%)") +
  geom_errorbar(ymin=Mycobacterium_smegmatis_3.125ug_data$Optical_density_mean_values-sd(Mycobacterium_smegmatis_3.125ug_data$Optical_density_mean_values),
                ymax=Mycobacterium_smegmatis_3.125ug_data$Optical_density_mean_values+sd(Mycobacterium_smegmatis_3.125ug_data$Optical_density_mean_values))
print(Mp6)

```

Penicillin 3.125 ug/mL



```
#Penicillin 1.5625 ug/mL
Mycobacterium_smegmatis_1.5625ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
Optical_density_mean_values =c((mean(0.047,0.049,0.047,0.047,0.047,0.047,0.047,0.047),
(mean(0.047,0.047,0.047,0.047,0.047,0.047,0.047,0.047),
(mean(0.048,0.045,0.045,0.045,0.045,0.045,0.045,0.045),
(mean(0.047,0.047,0.047,0.047,0.047,0.047,0.047,0.047),
(mean(0.046,0.045,0.045,0.045,0.045,0.045,0.045,0.045),
(mean(0.047,0.045,0.045,0.045,0.045,0.045,0.045,0.045),
(mean(0.046,0.045,0.045,0.045,0.045,0.045,0.045,0.045),
(mean(0.068,0.07,0.07,0.07,0.07,0.07,0.07,0.07),
(mean(0.094,0.084,0.084,0.084,0.084,0.084,0.084,0.084),
(mean(0.081,0.081,0.081,0.081,0.081,0.081,0.081,0.081),
(mean(0.113,0.094,0.094,0.094,0.094,0.094,0.094,0.094),
(mean(0.111,0.111,0.111,0.111,0.111,0.111,0.111,0.111),
(mean(0.11,0.139,0.139,0.139,0.139,0.139,0.139,0.139),
(mean(0.121,0.12,0.12,0.12,0.12,0.12,0.12,0.12),
(mean(0.134,0.153,0.153,0.153,0.153,0.153,0.153,0.153),
(mean(0.053,0.048,0.048,0.048,0.048,0.048,0.048,0.048),
(mean(0.072,0.05,0.05,0.05,0.05,0.05,0.05,0.05),
(mean(0.131,0.105,0.105,0.105,0.105,0.105,0.105,0.105),
(mean(0.14,0.165,0.165,0.165,0.165,0.165,0.165,0.165),
(mean(0.14,0.201,0.201,0.201,0.201,0.201,0.201,0.201),
(mean(0.179,0.216,0.216,0.216,0.216,0.216,0.216,0.216),
(mean(0.222,0.222,0.222,0.222,0.222,0.222,0.222,0.222),
```

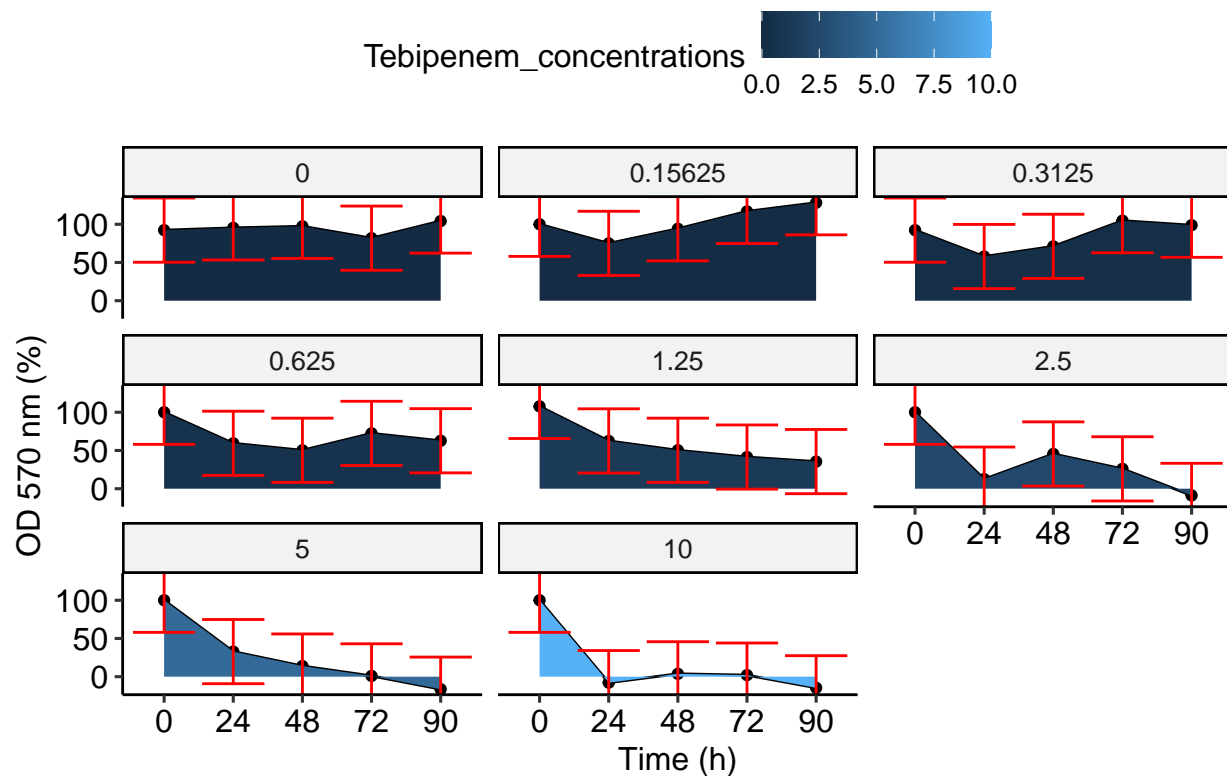
```

((mean(0.228,0.258,0.1
((mean(0.047,0.049,0.
((mean(0.044,0.042,0.
((mean(0.118,0.044,0.
((mean(0.164,0.209,0.
((mean(0.256,0.271,0.
((mean(0.352,0.296,0.
((mean(0.388,0.281,0.
((mean(0.284,0.284,0.
((mean(0.05,0.045,0.0
((mean(0.044,0.043,0.
((mean(0.069,0.042,0.
((mean(0.215,0.219,0.
((mean(0.305,0.322,0.
((mean(0.424,0.465,0.
((mean(0.521,0.322,0.4
((mean(0.442,0.349,0.

#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp7 <- Mycobacterium_smegmatis_1.5625ug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concentrations))+
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 1.5625 ug/mL")+
  xlab("Time (h)") +
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Mycobacterium_smegmatis_1.5625ug_data$Optical_density_mean_values-sd(Mycobacterium_smegmatis_1.5625ug_data$Optical_density_mean_values),
                ymax=Mycobacterium_smegmatis_1.5625ug_data$Optical_density_mean_values+sd(Mycobacterium_smegmatis_1.5625ug_data$Optical_density_mean_values))
print(Mp7)

```

Penicillin 1.5625 ug/mL



#Penicillin 0 ug/mL

```
Mycobacterium_smegmatis_0ug_data <- data.frame(Time= c(rep("0",8),rep("24",8),rep("48",8),rep("72",8),rep("96",8)),
Tebipenem_concentrations=c(10.0,5.0,2.5,1.25,0.625,0.3125,0.15625,0.078125),
Optical_density_mean_values =c((mean(0.05,0.052,0.054,0.056,0.058,0.06,0.062,0.064),
(mean(0.049,0.051,0.053,0.055,0.057,0.059,0.061,0.063),
(mean(0.049,0.049,0.049,0.049,0.049,0.049,0.049,0.049),
(mean(0.048,0.048,0.048,0.048,0.048,0.048,0.048,0.048),
(mean(0.048,0.047,0.047,0.047,0.047,0.047,0.047,0.047),
(mean(0.049,0.048,0.048,0.048,0.048,0.048,0.048,0.048),
(mean(0.048,0.046,0.046,0.046,0.046,0.046,0.046,0.046),
(mean(0.048,0.048,0.048,0.048,0.048,0.048,0.048,0.048),
(mean(0.07,0.084,0.098,0.112,0.126,0.14,0.154,0.168),
(mean(0.108,0.098,0.088,0.078,0.068,0.058,0.048,0.038),
(mean(0.094,0.093,0.092,0.091,0.09,0.089,0.088,0.087),
(mean(0.108,0.109,0.11,0.111,0.112,0.113,0.114,0.115),
(mean(0.125,0.118,0.111,0.104,0.097,0.09,0.083,0.076),
(mean(0.121,0.144,0.167,0.19,0.213,0.236,0.259,0.282),
(mean(0.12,0.127,0.134,0.141,0.148,0.155,0.162,0.169),
(mean(0.129,0.152,0.175,0.198,0.221,0.244,0.267,0.29),
(mean(0.051,0.052,0.053,0.054,0.055,0.056,0.057,0.058),
(mean(0.093,0.046,0.047,0.048,0.049,0.05,0.051,0.052),
(mean(0.125,0.064,0.065,0.066,0.067,0.068,0.069,0.07),
(mean(0.142,0.178,0.214,0.25,0.286,0.322,0.358,0.394),
(mean(0.161,0.179,0.197,0.215,0.233,0.251,0.269,0.287),
(mean(0.259,0.244,0.229,0.214,0.199,0.184,0.169,0.154),
(mean(0.267,0.229,0.191,0.153,0.115,0.077,0.039,0.001))
```

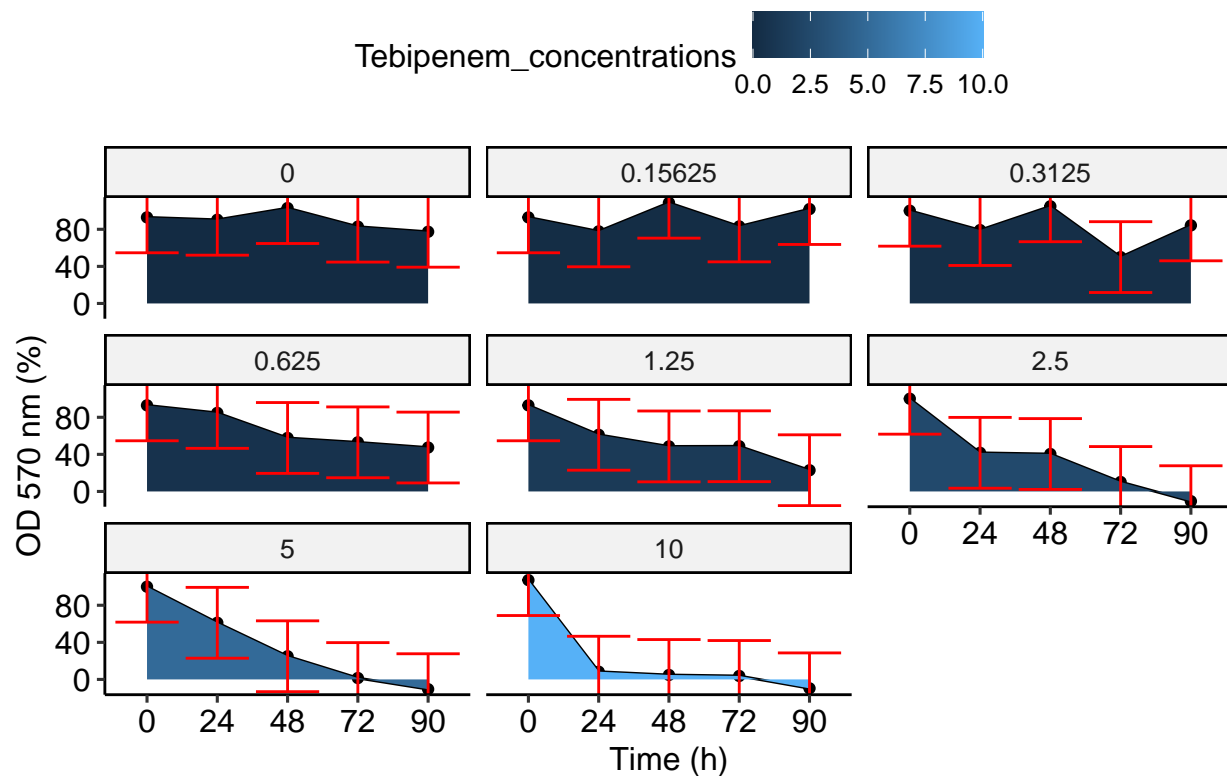
```

((mean(0.255,0.277,0
((mean(0.053,0.048,0
((mean(0.044,0.065,0
((mean(0.079,0.042,0
((mean(0.234,0.062,0
((mean(0.251,0.287,0
((mean(0.239,0.391,0
((mean(0.372,0.238,0
((mean(0.371,0.315,0
((mean(0.048,0.049,0
((mean(0.044,0.047,0
((mean(0.044,0.042,0
((mean(0.19,0.183,0.
((mean(0.297,0.297,0
((mean(0.458,0.447,0
((mean(0.535,0.454,0
((mean(0.428,0.521,0

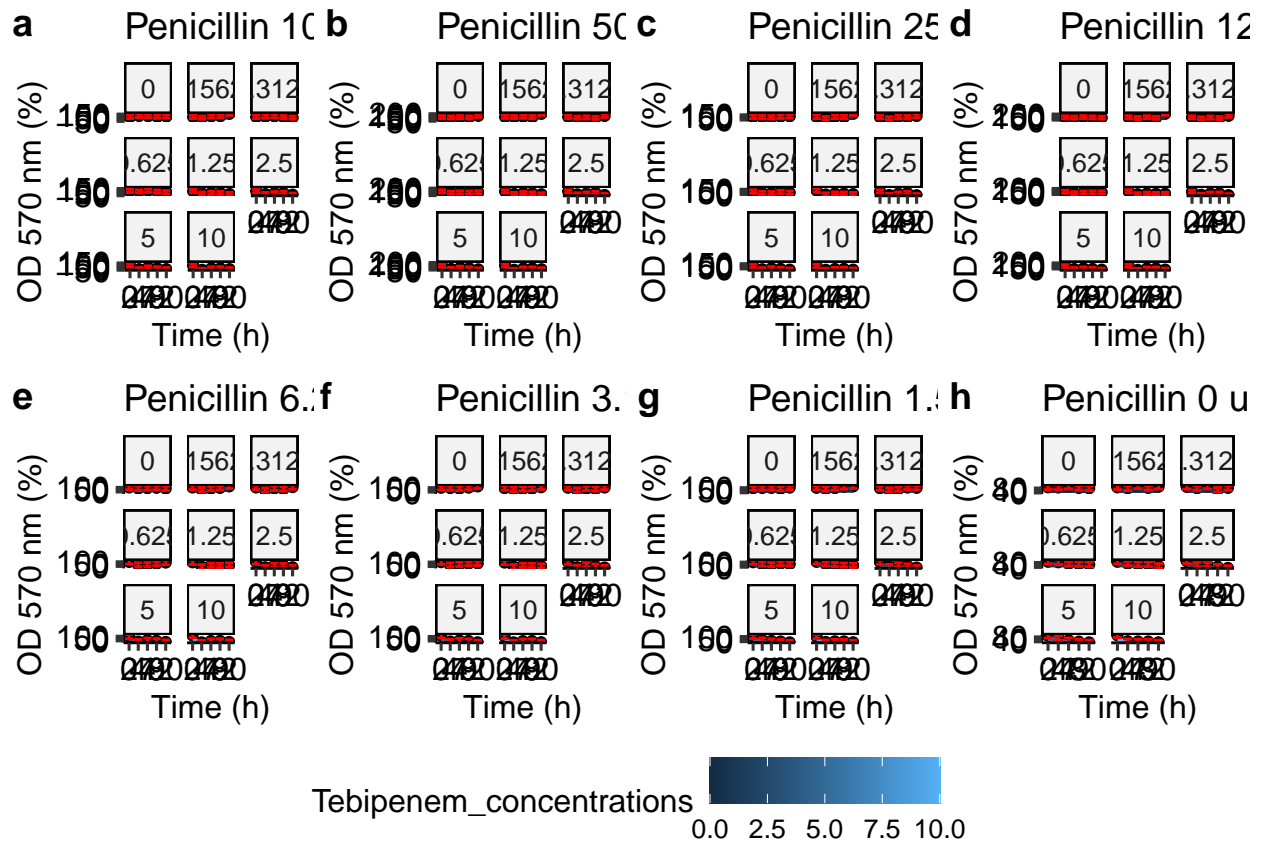
#Make a line graphs for changing in OD with time according to Tebipenem concentrations
Mp8 <- Mycobacterium_smegmatis_Oug_data %>%
  ggplot(aes(x=Time,y=Optical_density_mean_values,group=Tebipenem_concentrations, fill=Tebipenem_concen
  geom_line()+
  geom_point()+
  geom_area() +
  facet_wrap(~Tebipenem_concentrations)+
  ggtitle("Penicillin 0 ug/mL")+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Mycobacterium_smegmatis_Oug_data$Optical_density_mean_values-sd(Mycobacterium_smegm
                ymax=Mycobacterium_smegmatis_Oug_data$Optical_density_mean_values+sd(Mycobacterium_smegm
print(Mp8)

```


Penicillin 0 ug/mL



```
#Align all graphs together
library(ggplot2)
library(ggpubr)
theme_set(theme_pubr())
figure_3 <- ggarrange(Mp1,Mp2,Mp3,Mp4, Mp5, Mp6, Mp7, Mp8,
  labels=c("a","b","c","d","e","f","g","h"),
  ncol=4,nrow=2,
  common.legend = TRUE,legend = "bottom")
print(figure_3)
```



```

#Make up a line graph
Final_Myco<- Final_Myco_data %>%
  ggplot(aes(x=Time_f3, y=Optical_density_value,group=Concentrations, shape=Concentrations))+
  geom_line()+
  geom_point(size=2)+
  xlab("Time (h)")+
  ylab("OD 570 nm (%)")+
  geom_errorbar(ymin=Final_Myco_data$Optical_density_value-sd(Final_Myco_data$Optical_density_value),
                ymax=Final_Myco_data$Optical_density_value+sd(Final_Myco_data$Optical_density_value),
                width=.2)+
  stat_compare_means(method = "kruskal.test", label.y =140)+
  stat_compare_means(label = "p.signif", label.y = c(110,100,90,70,50))+
  geom_hline(yintercept = 0, linetype="dashed", col="grey")
print(Final_Myco)

```

Tebip 2.5 ug/mL ▲ PenicillinV 1.5625 ug/mL + Tebip 2.5 ug/mL ■ PenicillinV 100 ug/mL + Tebip 1.5625 ug/mL

