```r
library(readxl)
```

```
## Warning: package 'readxl' was built under R version 4.2.3
```

```r
setwd("D:/freelancer/data analysis/mahmoud werby/zewail project")
data <-  read_excel("D:/freelancer/data analysis/mahmoud werby/zewail project/inflammatory cytokines co
```

```r
##loading packages
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.2.3
```

```r
library(dplyr)
```

```
## Warning: package 'dplyr' was built under R version 4.2.3
```

```r
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.2.3
```

```
## Warning: package 'tibble' was built under R version 4.2.3
```

```
## Warning: package 'tidyr' was built under R version 4.2.3
```

```
## Warning: package 'readr' was built under R version 4.2.3
```

```
## Warning: package 'purrr' was built under R version 4.2.3
```

```
## Warning: package 'stringr' was built under R version 4.2.3
```

```
## Warning: package 'forcats' was built under R version 4.2.3
```

```
## Warning: package 'lubridate' was built under R version 4.2.3
```

```r
###releveling groups
data$group <- factor(data$group, levels = c("Untreated","Rifampicin", "Uio-66", "Rif@Uio-66", "LysB/Rif

#visualization of action of different drugs on different groups over time
ggplot(data = data, aes(x = group, y = lab ))+
  stat_summary(fun = "mean",geom = "bar", aes(fill =group ))+
  stat_summary(fun.data = "mean_sdl", geom = "errorbar", aes(color = group) )+
  facet_grid(inflam_mediator ~ time, scales = "free_y",switch = "y" ) +
  theme(panel.background  = element_blank(),
        panel.grid = element_blank(),
        axis.text.x = element_text(angle = 90,face = "bold"),
        text = element_text(size = 14, face = "bold"),
        axis.text.y.left = element_text(size = 10,face = "bold"),
        legend.text = element_text(size = 12, face = "bold"),
```

```
        strip.background.y = element_blank(),
        strip.background.x = element_blank(),
        strip.text.x = element_text(size = 16),
        strip.placement = "outside")+
  ylab("Concentration (pg/mL)") +
  xlab("Different Groups")
```
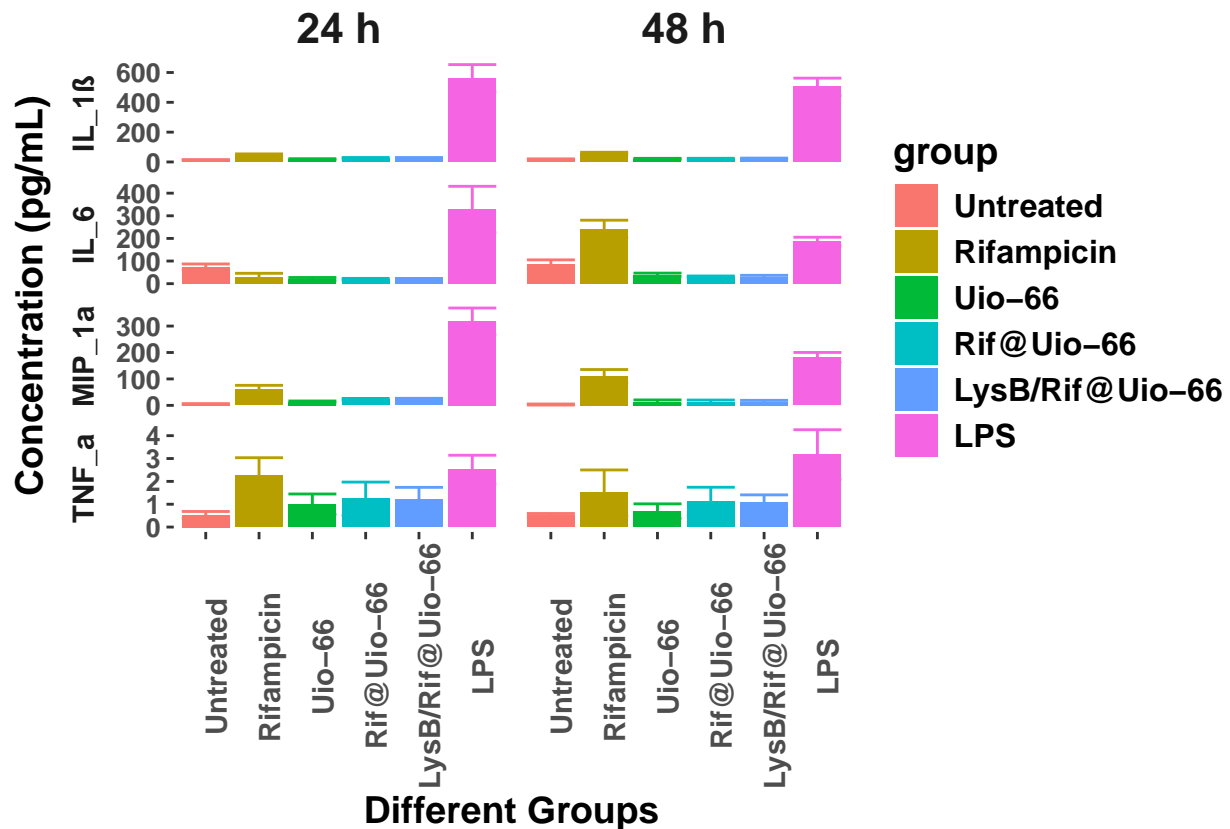


```
library(readxl)
setwd("D:/freelancer/data analysis/mahmoud werby/zewail project")
distribution <-  read_excel("D:/freelancer/data analysis/mahmoud werby/zewail project/distribution.xlsx
```
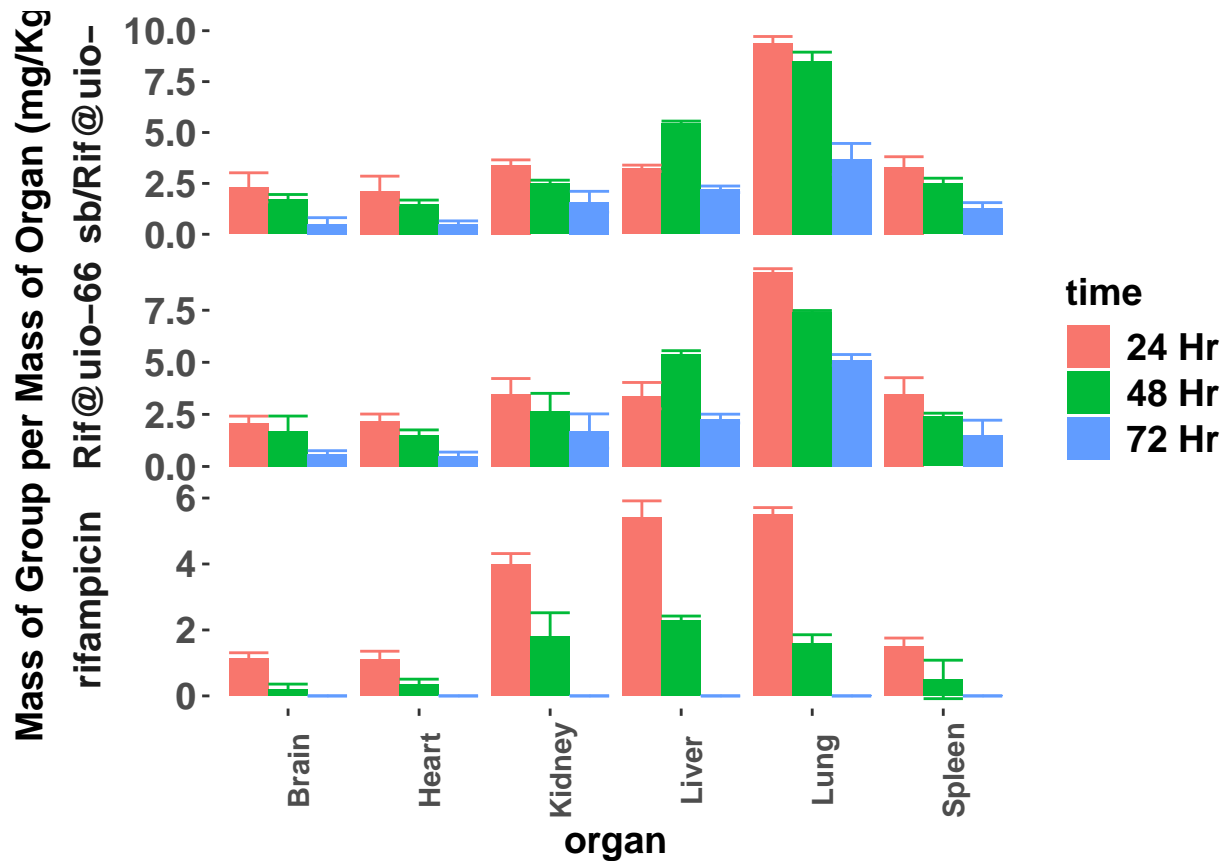
```
library(ggplot2)

ggplot(data= distribution, aes(x = organ, y = labs))+
  stat_summary(fun = "mean",geom = "bar", aes(fill = time ), position = "dodge")+
  stat_summary(fun.data = mean_sdl, geom = "errorbar", aes(color = time), position = "dodge" )+
  facet_grid(groups~., scales = "free_y",switch = "y") +
  theme(text = element_text(size = 14, face = "bold"),
    panel.background  = element_blank(),
        panel.grid = element_blank(),
        axis.text.x = element_text(angle = 90,face = "bold"),
        axis.text.y.left = element_text(size = 14,face = "bold"),
        legend.text = element_text(size = 14, face = "bold"),
        strip.background.y = element_blank(),
        strip.background.x = element_blank(),
```

```
        strip.placement = "outside",
        strip.text.y = element_text(size = 14 , face = "bold")) +
  ylab("Mass of Group per Mass of Organ (mg/Kg)")
```



```
library(ggplot2)

ggplot(data= distribution, aes(x = organ, y = labs))+
  stat_summary(fun = "mean",geom = "bar", aes(fill = organ ))+
  stat_summary(fun.data = mean_sdl, geom = "errorbar", aes(color = organ))+
  facet_grid(groups~.) +
  theme(panel.background  = element_blank(),
        panel.grid = element_blank(),
        axis.text.x = element_text(angle = 90,face = "bold"),
        text = element_text(size = 14, face = "bold"),
        axis.text.y.left = element_text(size = 14,face = "bold"),
        legend.text = element_text(size = 14, face = "bold"),
        strip.background.y = element_blank(),
        strip.background.x = element_blank())+
  ylab("Concentration (pg/mL)") +
  xlab("Different Organs")
```
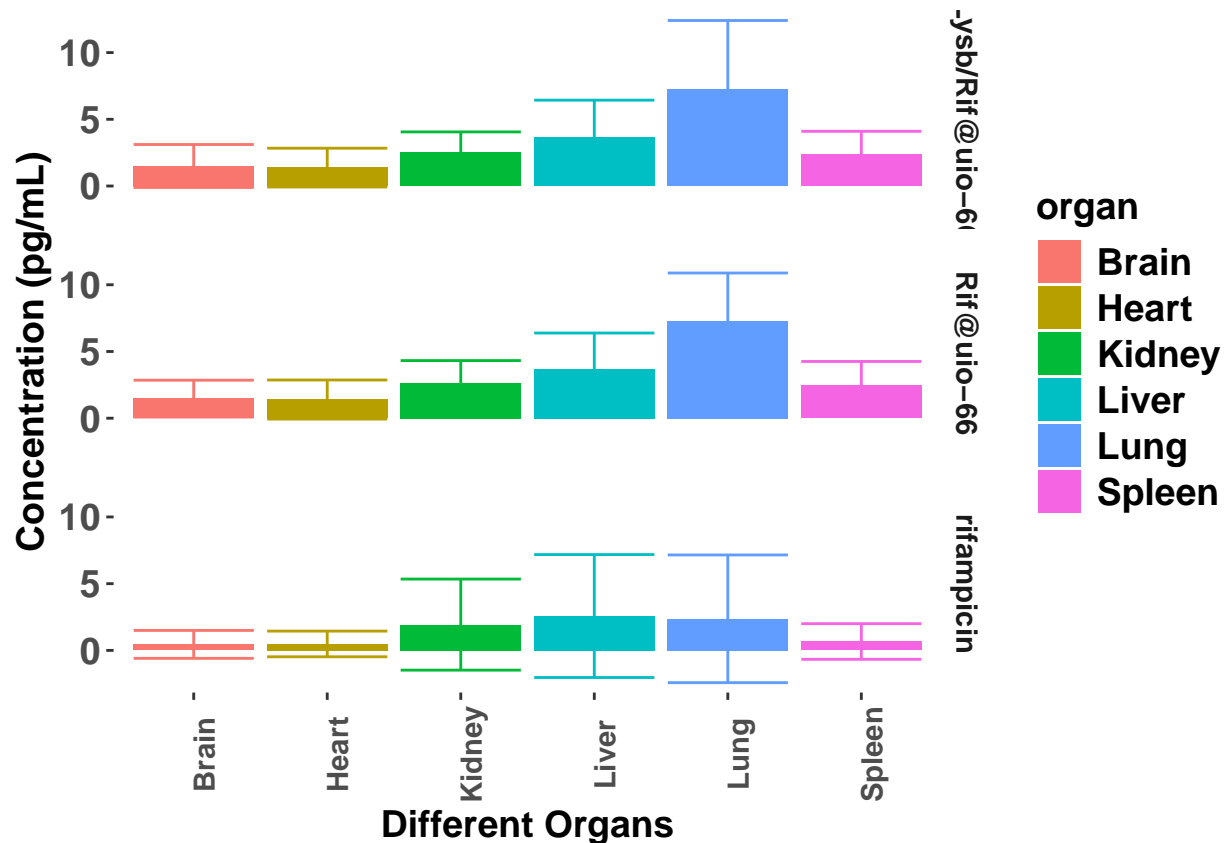
```
library(readxl)
setwd("D:/freelancer/data analysis/mahmoud werby/zewail project")
cell_viability <- read_excel("D:/freelancer/data analysis/mahmoud werby/zewail project/cell viability.x
```
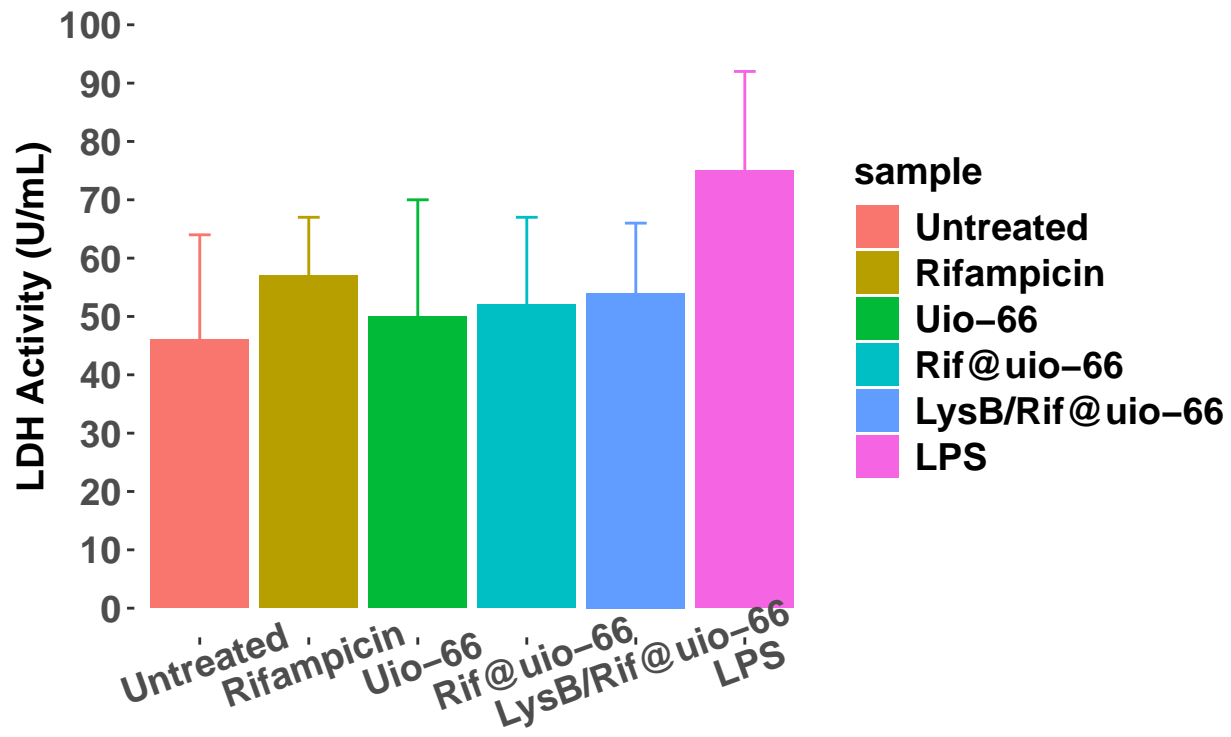
```
library(ggplot2)
ggplot(data = cell_viability, aes(x = factor(conc), y = viab)) +
  stat_summary(fun = "mean",geom = "bar", aes(fill = sample ), position = "dodge")+
  geom_errorbar(aes(ymin = viab -sd, ymax = viab + sd, color = sample ), width = 0.2) +
  facet_grid(~sample, scales = "free_y",switch = "x") +
  scale_y_continuous(limits = c(0,120), breaks = seq(0,120,10))+
  theme(text = element_text(size = 14, face = "bold"),
    panel.background  = element_blank(),
        panel.grid = element_blank(),
        axis.text.x = element_text(angle = 90,face = "bold"),
        axis.text.y.left = element_text(size = 14,face = "bold"),
        legend.text = element_text(size = 14, face = "bold"),
        strip.background.y = element_blank(),
        strip.background.x = element_blank(),
        strip.placement = "outside",
        strip.text.y = element_text(size = 14 , face = "bold")) +
  ylab("Cell Viability (%)")+
  xlab("Concentration")
```
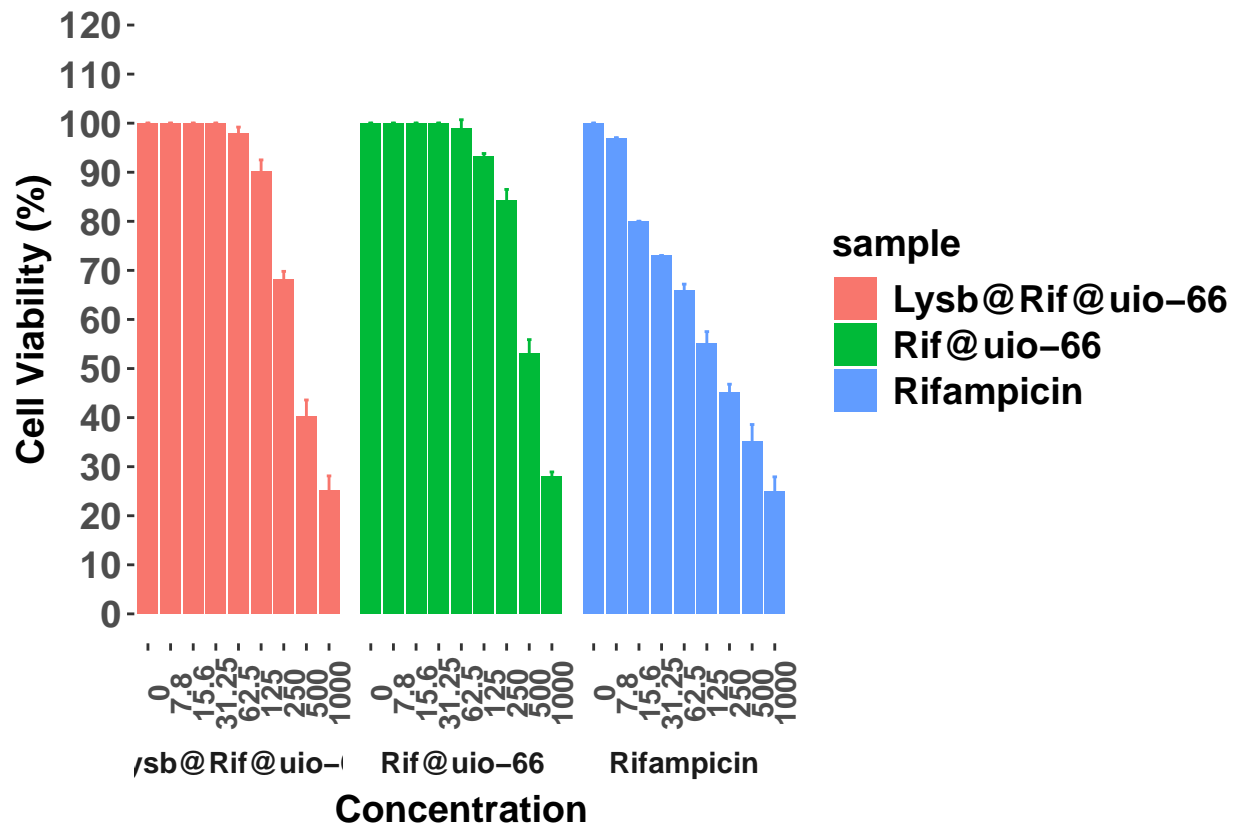
```
###import bal fluids
library(readxl)
bal <- read_excel("BAL fluid.xlsx")


bal$sample <- factor(bal$sample , levels = c("Untreated","Rifampicin", "Uio-66", "Rif@uio-66", "LysB/Ri

library(ggplot2)
ggplot(data = bal, aes(x = sample, y = ldh_activ)) +
  stat_summary(fun = "mean",geom = "bar", aes(fill = sample ), position = "dodge")+
  geom_errorbar(aes(ymin = ldh_activ - activ_sd, ymax = ldh_activ + activ_sd, color = sample ), width =
  theme(text = element_text(size = 14, face = "bold"),
    panel.background  = element_blank(),
        panel.grid = element_blank(),
        axis.text.x = element_text(angle = 20,face = "bold", size = 14),
        axis.text.y.left = element_text(size = 14,face = "bold"),
        legend.text = element_text(size = 14, face = "bold"),
        strip.background.y = element_blank(),
        strip.background.x = element_blank(),
        strip.placement = "outside",
        strip.text.y = element_text(size = 14 , face = "bold")) +
ylab("LDH Activity (U/mL)")+
xlab(" ")+
scale_y_continuous(limits = c(0,100), breaks = seq(0,100,10))
```

```r
bal$sample <- factor(bal$sample , levels = c("Untreated","Rifampicin", "Uio-66", "Rif@uio-66", "LysB/Ri

library(ggplot2)
 ggplot(data = bal, aes(x = sample, y = protein_conc)) +
  stat_summary(fun = "mean",geom = "bar", aes(fill = sample ), position = "dodge")+
  geom_errorbar(aes(ymin = protein_conc - conc_sd, ymax = protein_conc + conc_sd, color = sample ), widt
  theme(text = element_text(size = 14, face = "bold"),
    panel.background  = element_blank(),
       panel.grid = element_blank(),
       axis.text.x = element_text(angle = 20,face = "bold", size = 14),
       axis.text.y.left = element_text(size = 14,face = "bold"),
       legend.text = element_text(size = 14, face = "bold"),
       strip.background.y = element_blank(),
       strip.background.x = element_blank(),
       strip.placement = "outside",
       strip.text.y = element_text(size = 14 , face = "bold")) +
  ylab("Protein Concentration (mcg/mL)")+
  xlab(" ") +
  scale_y_continuous(breaks = seq(0,1000,100))
```