

Udoma_Supplementary

Usman

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R Markdown

Udoma's Supplementary

```
# Analysis for Interferon gamma as Udoma

st.tst_gamma<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF"))%>%
  dunn_test(ifn_gamm_avrg~diagnosis,p.adjust.method="none")%>%
  add_xy_position(x="diagnosis")

cause_ifn<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF", "UTI"="UI"))%>%
  ggplot(aes(x=diagnosis,y=ifn_gamm_avrg))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(st.tst_gamma, label = "p.adj.signif",hide.ns = TRUE,
                    tip.length = 0.01,color = "darkblue",size = 10,
                    y.position = c(500,520))+
  labs(y = expression(bold("Interferon-~*gamma~"(pg/mL))),
       x=expression(bold("Clinical daignostic cause of Infertility")))+
  theme_minimal()

# Analysis for Interleukin 10

st.tst_10<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF", "UTI"="UI"))%>%
  dunn_test(il_10_avrg~diagnosis,p.adjust.method="none")%>%
  add_xy_position(x="diagnosis")

cause_il<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF", "UTI"="UI"))%>%
  ggplot(aes(x=diagnosis,y=il_10_avrg))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(st.tst_10, label = "p.adj.signif",hide.ns = TRUE,
                    tip.length = 0.01,color = "darkblue",size = 10,y.position = c(625)
                    )+
  labs(y = expression(bold("Interleukin-10 (pg/mL)")),
       x=expression(bold("Clinical daignosis of Infertility")))+
  theme_minimal()

# Ct-HSP60 titer response along clinical diagnostic cause of infertility
```

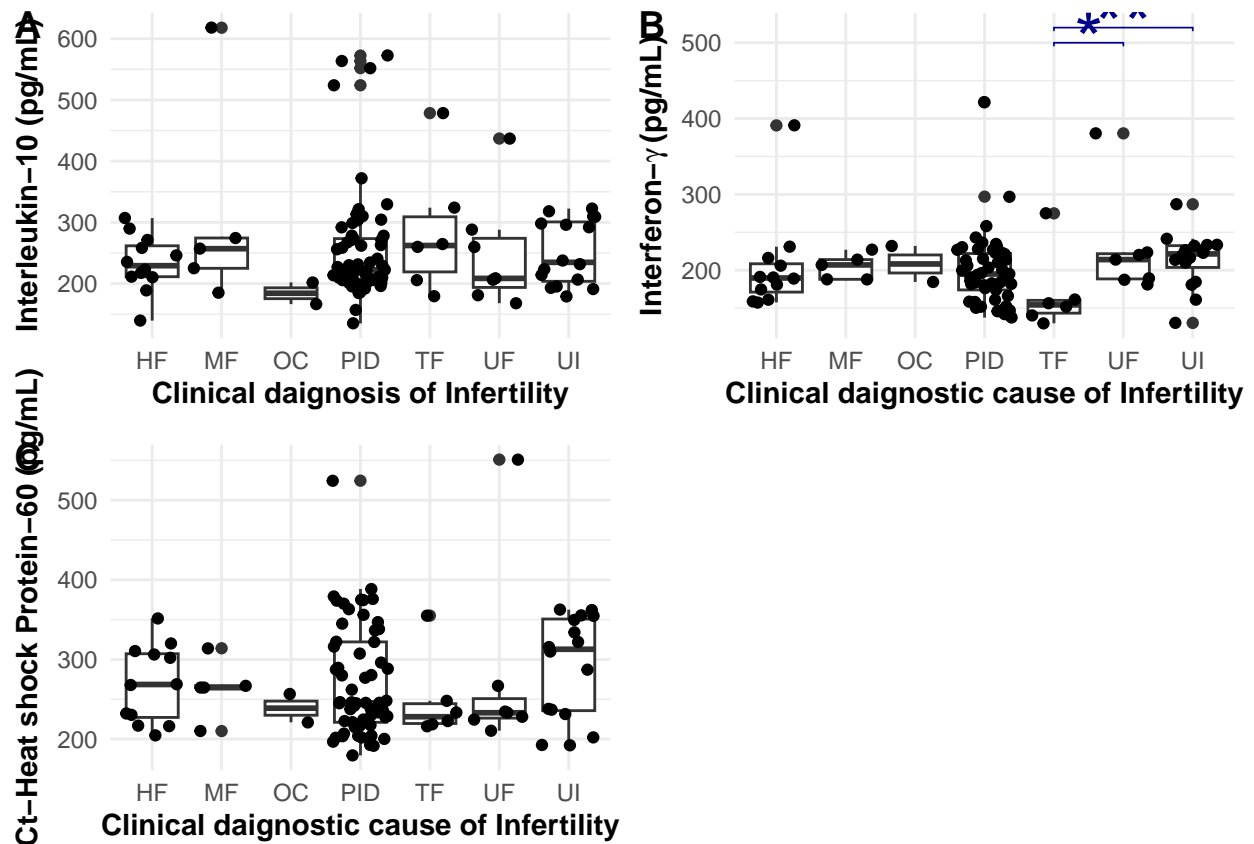
```

st.tst_hsp60<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF","UTI"="UI"))%>%
  dunn_test(hsp_60_avrg~diagnosis,p.adjust.method="none")%>%
  add_xy_position(x="diagnosis")

cause_hsp<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF","UTI"="UI"))%>%
  ggplot(aes(x=diagnosis,y=hsp_60_avrg))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(st.tst_hsp60, label = "p.adj.signif",hide.ns = TRUE,
                    tip.length = 0.01,color = "darkblue",size = 10,y.position = c(450))+
  labs(y = expression(bold("Ct-Heat shock Protein-60 (pg/mL)")),
       x=expression(bold("Clinical daignostic cause of Infertility")))+
  theme_minimal()

ggarrange(cause_il,cause_ifn,cause_hsp,labels = c("A","B","C"))

```



Including Plots

```

stat_oudeur<-newdata%>%group_by(group)%>%
  dunn_test(il_10_avrg~oudeur,p.adjust.method="none")%>%
  add_xy_position(x="oudeur",group = "group")
stat_oudeur

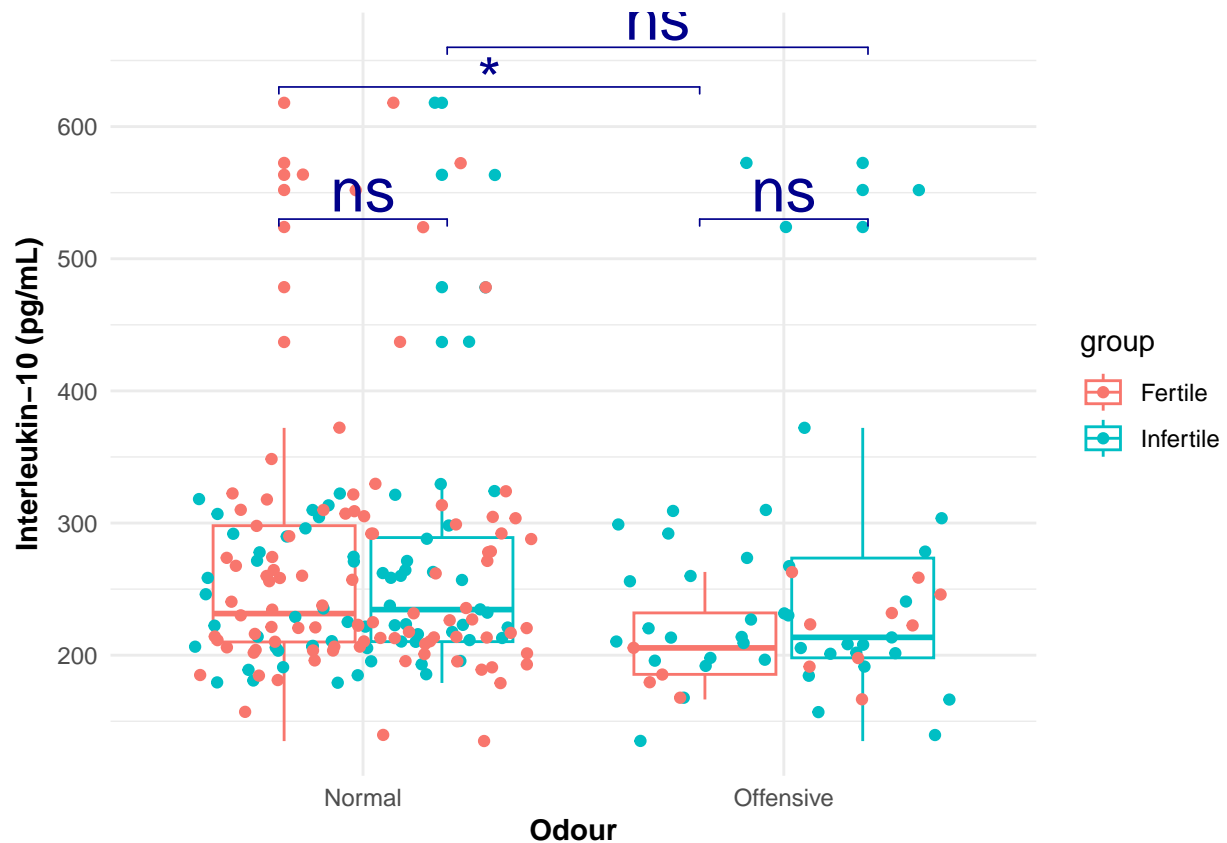
```

```
## # A tibble: 2 x 14
##   group      .y.   group1 group2    n1    n2 statistic      p  p.adj p.adj.signif
##   <chr>      <chr> <chr>  <chr>  <int> <int>    <dbl>  <dbl>  <dbl> <chr>
## 1 Fertile   il_1~ Normal Offen~    93    13    -2.46 0.0139 0.0139 *
## 2 Infertile il_1~ Normal Offen~    67    41    -1.60 0.111  0.111  ns
## # i 4 more variables: y.position <dbl>, groups <named list>, xmin <dbl>,
## #   xmax <dbl>
```

```
stat_odour_1<-newdata%>%
  group_by(odour)%>%
  dunn_test(il_10_avrg~group,p.adjust.method="none")%>%
  add_xy_position(x="odour")
stat_odour_1
```

```
## # A tibble: 2 x 15
##   odour      .y.   group1 group2    n1    n2 statistic      p  p.adj p.adj.signif
##   <chr>      <chr> <chr>  <chr>  <int> <int>    <dbl>  <dbl>  <dbl> <chr>
## 1 Normal   il_10~ Ferti~ Infer~    93    67    -0.104 0.917 0.917  ns
## 2 Offensive il_10~ Ferti~ Infer~    13    41     1.21 0.225 0.225  ns
## # i 5 more variables: y.position <dbl>, groups <named list>, x <dbl>,
## #   xmin <dbl>, xmax <dbl>
```

```
A_i<-newdata%>%ggplot(aes(x=odour,y=il_10_avrg,color=group))+
  geom_boxplot()+
  geom_point(position=position_jitter()+
  stat_pvalue_manual(stat_odour, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "darkblue",
    y.position = c(630,660))+
  stat_pvalue_manual(stat_odour_1,
    label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "darkblue",size = 8,y.position = c(5
A_i
```



```
stat_odour_ifn<-newdata%>%group_by(group)%>%
  dunn_test(ifn_gamm_avrg~odour,p.adjust.method="none")%>%
  add_xy_position(x="odour",group = "group")
stat_odour_ifn
```

```
## # A tibble: 2 x 14
##   group   .y.  group1 group2    n1    n2 statistic      p  p.adj p.adj.signif
##   <chr>   <chr> <chr>  <chr>  <int> <int>    <dbl> <dbl> <dbl> <chr>
## 1 Fertile ifn_~ Normal Offen~    93    13   -0.453 0.651 0.651 ns
## 2 Infertile ifn_~ Normal Offen~    67    41   -1.84 0.0654 0.0654 ns
## # i 4 more variables: y.position <dbl>, groups <named list>, xmin <dbl>,
## #   xmax <dbl>
```

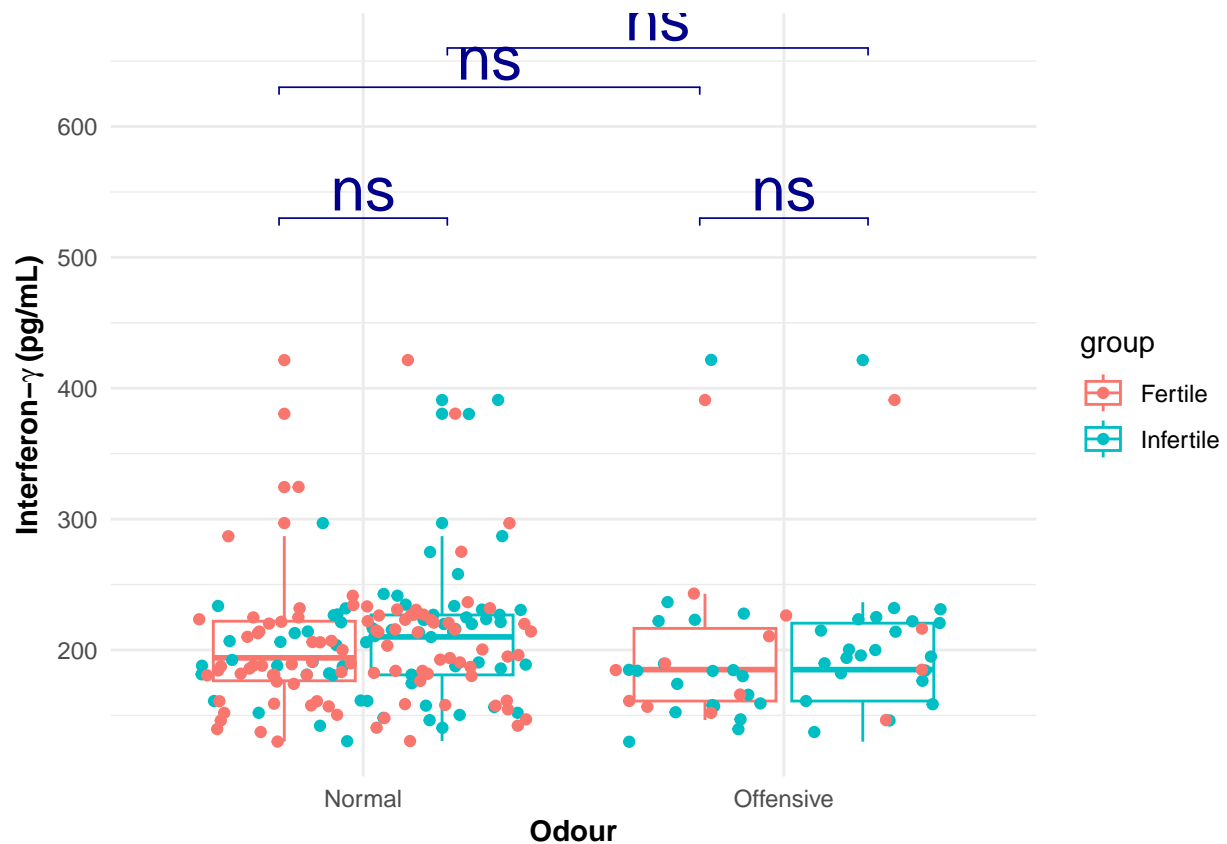
```
stat_odour_ifn1<-newdata%>%
  group_by(odour)%>%
  dunn_test(ifn_gamm_avrg~group,p.adjust.method="none")%>%
  add_xy_position(x="odour")
stat_odour_ifn1
```

```
## # A tibble: 2 x 15
##   odour   .y.  group1 group2    n1    n2 statistic      p  p.adj p.adj.signif
##   <chr>   <chr> <chr>  <chr>  <int> <int>    <dbl> <dbl> <dbl> <chr>
## 1 Normal ifn_ga~ Ferti~ Infer~    93    67    1.12 0.261 0.261 ns
## 2 Offensive ifn_ga~ Ferti~ Infer~    13    41   -0.111 0.911 0.911 ns
## # i 5 more variables: y.position <dbl>, groups <named list>, x <dbl>,
```

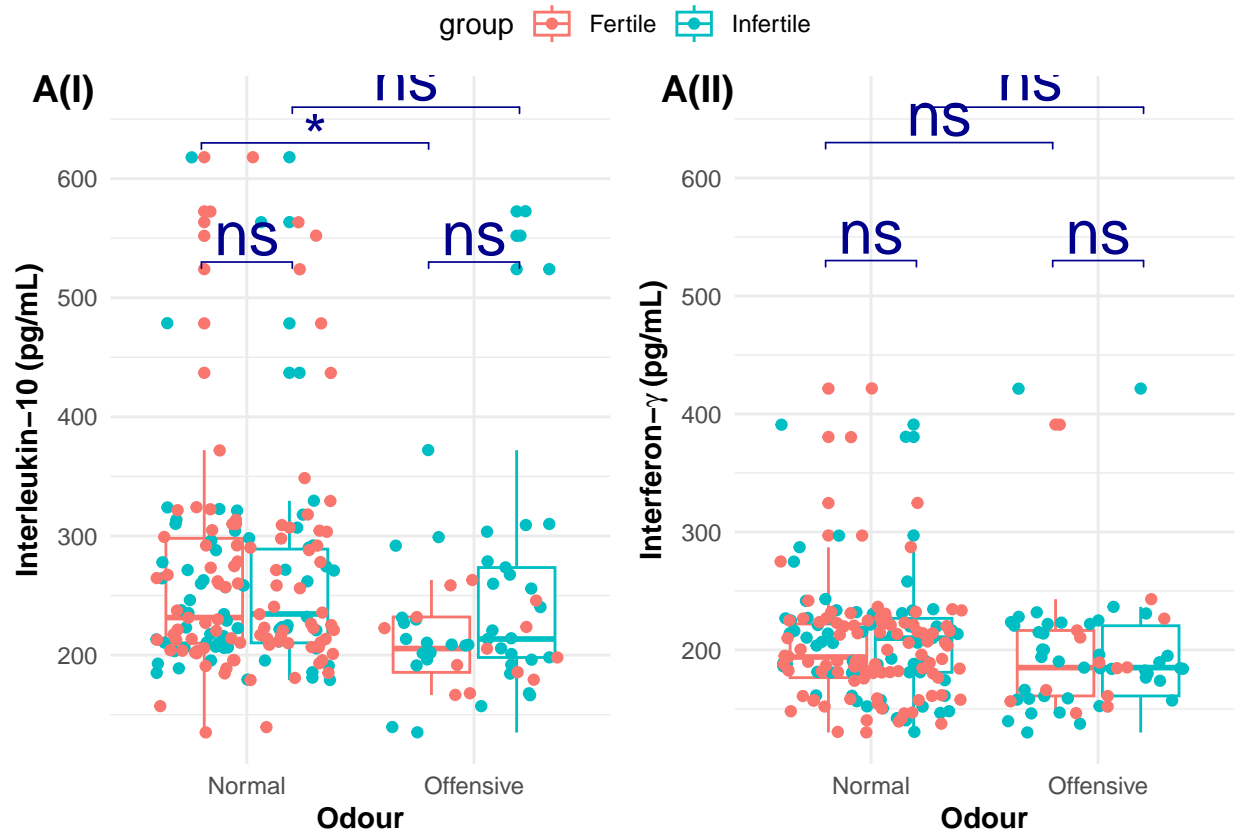
```
## #   xmin <dbl>, xmax <dbl>
```

```
A_ii<-newdata%>%
  ggplot(aes(x=odour,y=ifn_gamm_avrg,color=group))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(stat_odour_ifn, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "darkblue",
                    y.position = c(630,660))+
  stat_pvalue_manual(stat_odour_ifn1,
                    label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "darkblue",size = 8,y.position = c(530,560)),
  labs(y = expression(bold("Interferon- $\gamma$ "*gamma ~"(pg/mL)")),x=expression(bold("Odour")))+theme_minimal()
```

A_ii



```
ggarrange(A_i,A_ii,labels = c("A(I)","A(II)"),common.legend = TRUE)
```



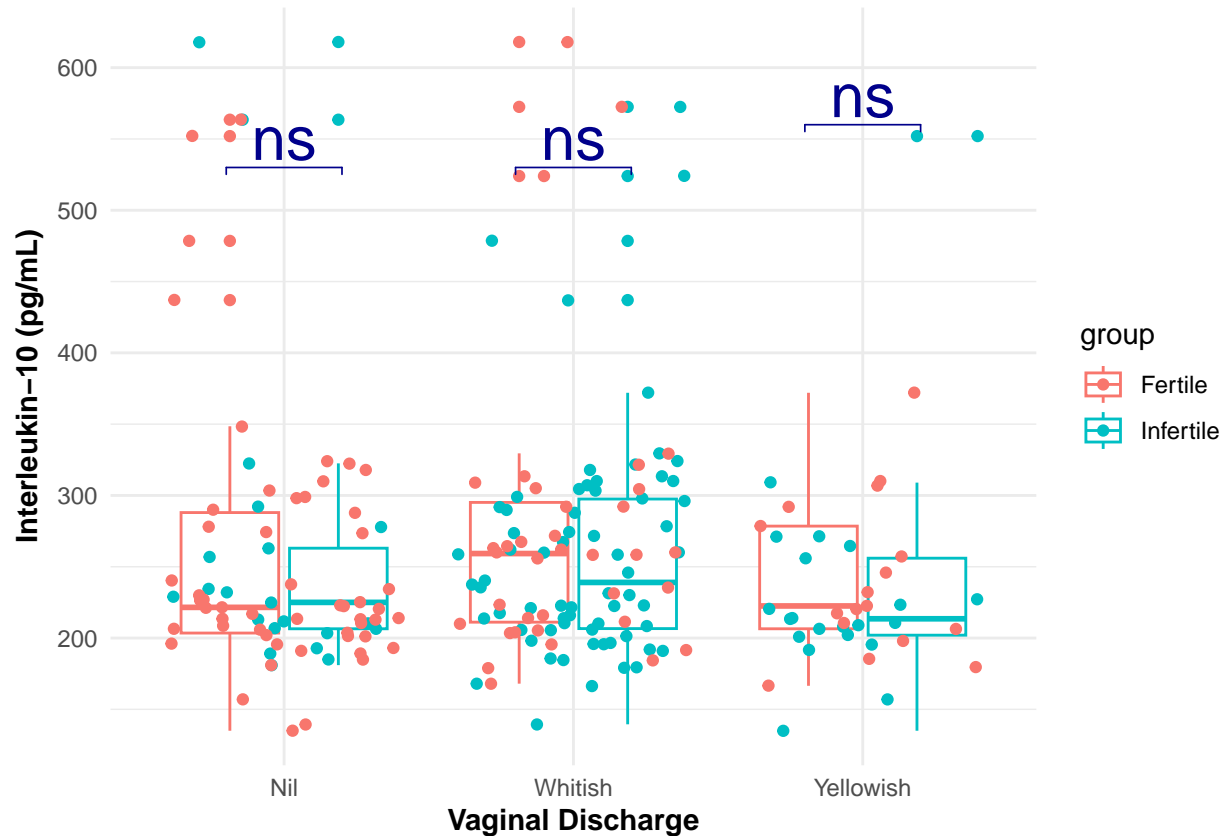
```
# stat_discharge<-newdata%>%group_by(group)%>%
#dunn_test(il_10_avrg~
#vaginal_discharge1,p.adjust.method="none")%>%
#add_xy_position(x="vaginal_discharge1")
# stat_discharge
stat_discharge_1<-newdata%>%
  group_by(vaginal_discharge1)%>%
  dunn_test(il_10_avrg~group,p.adjust.method="none")%>%
  add_xy_position(x="vaginal_discharge1",group = "group")
stat_discharge_1
```

```
## # A tibble: 3 x 15
##   vaginal_discharge1 .y.      group1 group2   n1    n2 statistic    p p.adj
##   <chr>              <chr>    <chr>  <chr> <int> <int>    <dbl> <dbl> <dbl>
## 1 Nil              il_10_avrg Fertile Infer~   53   21  -0.0540 0.957 0.957
## 2 Whitish          il_10_avrg Fertile Infer~   36   66  -0.476  0.634 0.634
## 3 Yellowish        il_10_avrg Fertile Infer~   17   21  -0.822  0.411 0.411
## # i 6 more variables: p.adj.signif <chr>, y.position <dbl>,
## #   groups <named list>, x <dbl>, xmin <dbl>, xmax <dbl>
```

```
B_i<-newdata%>%
  ggplot(aes(x=vaginal_discharge1,y=il_10_avrg,color=group))+
  geom_boxplot()+
  geom_point(position=position_jitter())+
  # stat_pvalue_manual(stat_discharge_1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color
```

```
stat_pvalue_manual(stat_discharge_1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color =
labs(y = expression(bold("Interleukin-10 (pg/mL)")),x=expression(bold("Vaginal Discharge")))+theme_minimal())
```

B_i



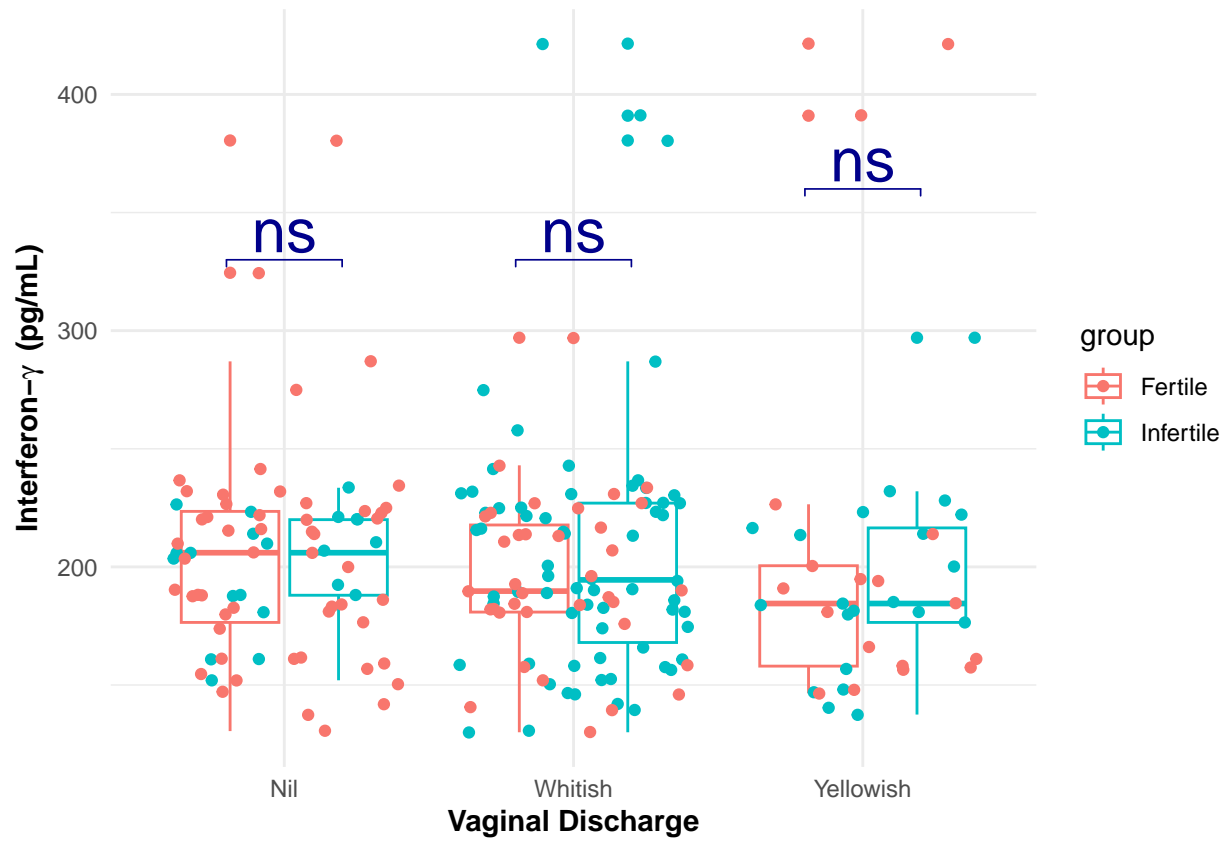
```
# Interferon gamma levels according vaginal discharge
stat_discharge_ifn1<-newdata%>%
  group_by(vaginal_discharge1)%>%
  dunn_test(ifn_gamm_avrg~group,p.adjust.method="none")%>%
  add_xy_position(x="vaginal_discharge1",group = "group")
stat_discharge_ifn1
```

```
## # A tibble: 3 x 15
##   vaginal_discharge1 .y.      group1 group2    n1    n2 statistic    p p.adj
##   <chr>              <chr>    <chr>  <chr>  <int>  <int>    <dbl> <dbl> <dbl>
## 1 Nil              ifn_gamm_a~ Ferti~ Infer~    53    21  -0.0120 0.990 0.990
## 2 Whitish          ifn_gamm_a~ Ferti~ Infer~    36    66   0.742  0.458 0.458
## 3 Yellowish         ifn_gamm_a~ Ferti~ Infer~    17    21   0.220  0.826 0.826
## # i 6 more variables: p.adj.signif <chr>, y.position <dbl>,
## #   groups <named list>, x <dbl>, xmin <dbl>, xmax <dbl>
```

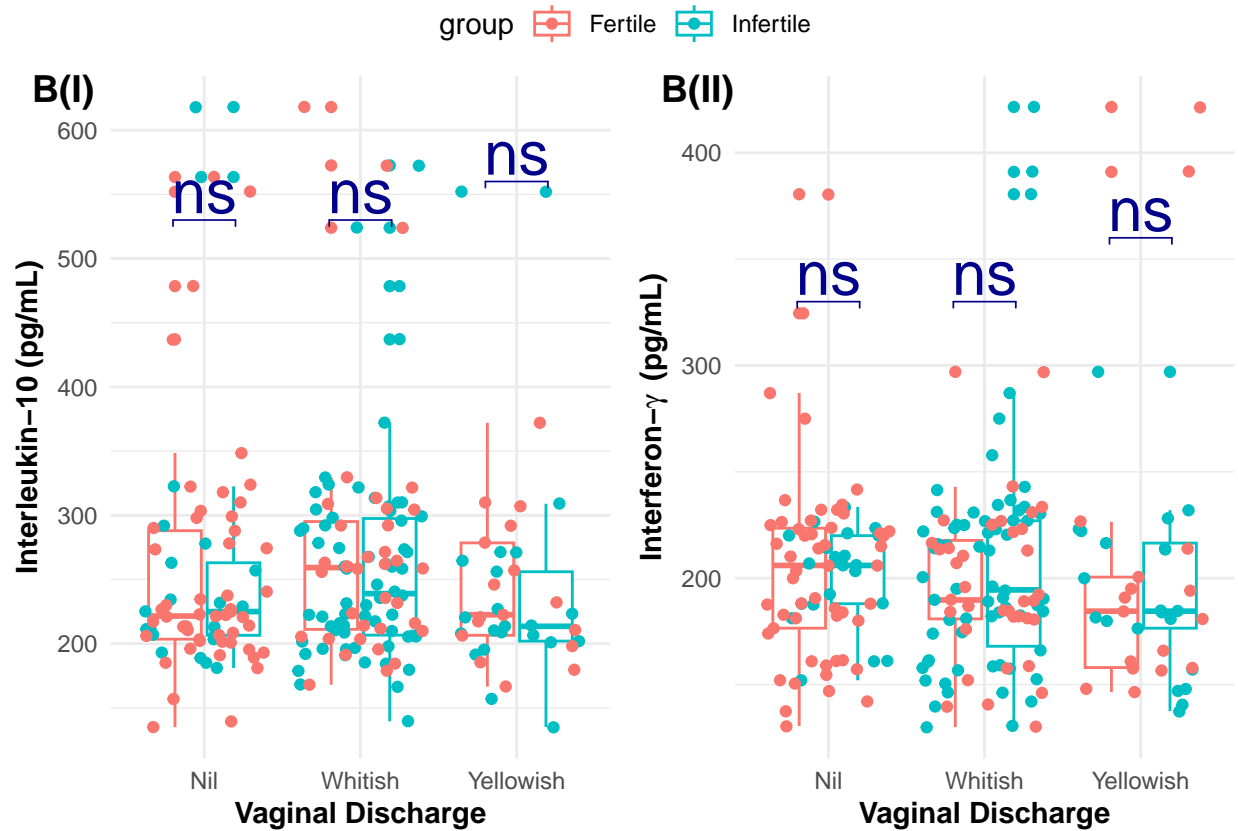
```
B_ii<-newdata%>%
  ggplot(aes(x=vaginal_discharge1,y=ifn_gamm_avrg,color=group))+
  geom_boxplot()+geom_point(position=position_jitter())+
```

```
# stat_pvalue_manual(stat_discharge_1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "darkblue",
stat_pvalue_manual(stat_discharge_ifn1,
label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "darkblue",size = 8,y.position = c(3,
labs(y = expression(bold("Interferon- $\gamma$ " (pg/mL))),x=expression(bold("Vaginal Discharge")))+
theme_minimal()
```

B_ii



```
ggarrange(B_i,B_ii,labels = c("B(I)","B(II)"),common.legend = TRUE)
```

level of interferon-10 and Interferon gamma stratified according to discomfort Clinical presentation

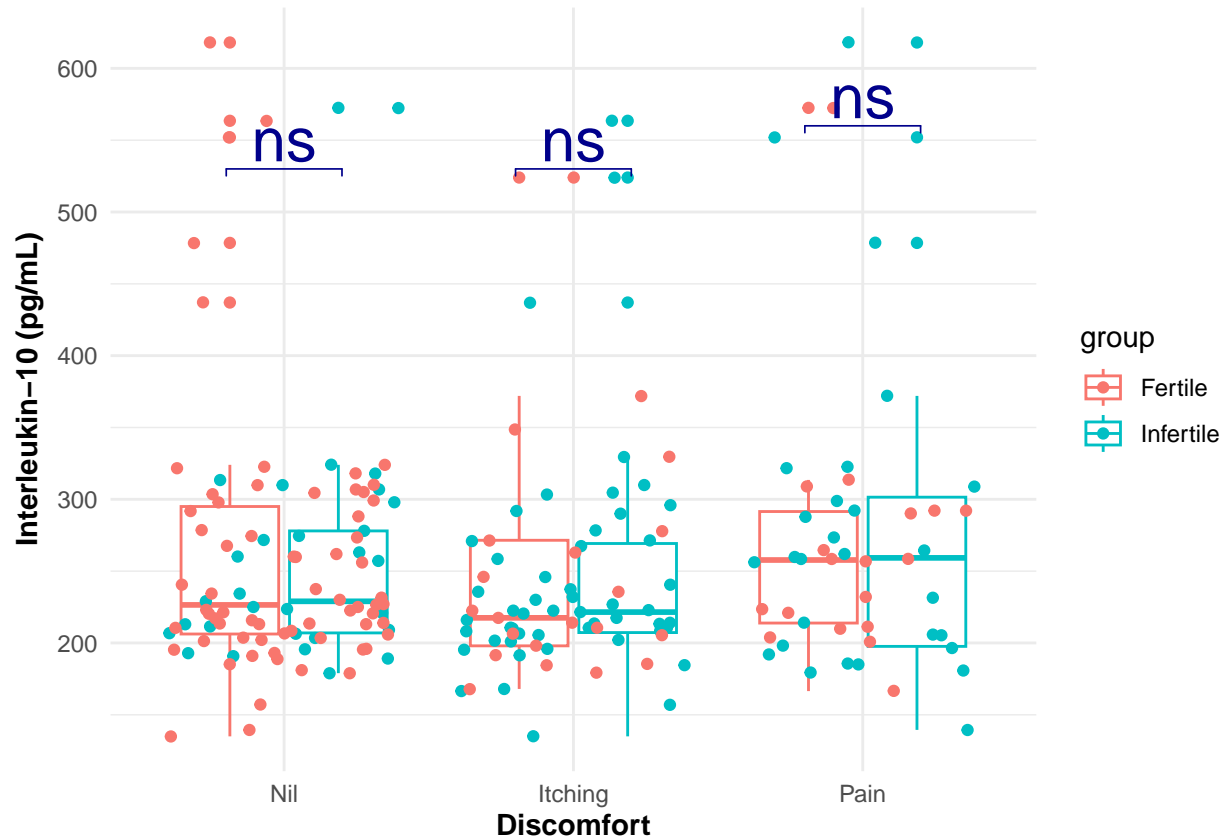
```
# stat_discomfort<-newdata%>%group_by(group)%>%dunn_test(il_10_avrg~vaginal_discharge1,p.adjust.method=
# stat_discharge
stat_discomfort_1<-newdata%>%
  group_by(discomfort1)%>%
  dunn_test(il_10_avrg~group,p.adjust.method="none")%>%
  add_xy_position(x="discomfort1",group = "group")
stat_discomfort_1
```

```
## # A tibble: 3 x 15
##   discomfort1 .y. group1 group2 n1 n2 statistic p p.adj p.adj.signif
##   <chr> <chr> <chr> <chr> <int> <int> <dbl> <dbl> <dbl> <chr>
## 1 Itching il_1~ Ferti~ Infer~ 21 51 0.173 0.862 0.862 ns
## 2 Nil il_1~ Ferti~ Infer~ 67 29 0.108 0.914 0.914 ns
## 3 Pain il_1~ Ferti~ Infer~ 18 28 -0.0901 0.928 0.928 ns
## # i 5 more variables: y.position <dbl>, groups <named list>, x <dbl>,
## # xmin <dbl>, xmax <dbl>
```

```
C_i<-newdata%>%ggplot(aes(x=discomfort1,y=il_10_avrg,color=group))+
  geom_boxplot()+geom_point(position=position_jitter())+
  # stat_pvalue_manual(stat_discharge_1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color
```

```
stat_pvalue_manual(stat_discomfort_1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "blue",
  labs(y = expression(bold("Interleukin-10 (pg/mL)")),x=expression(bold("Discomfort"))))+theme_minimal()
```

C_i



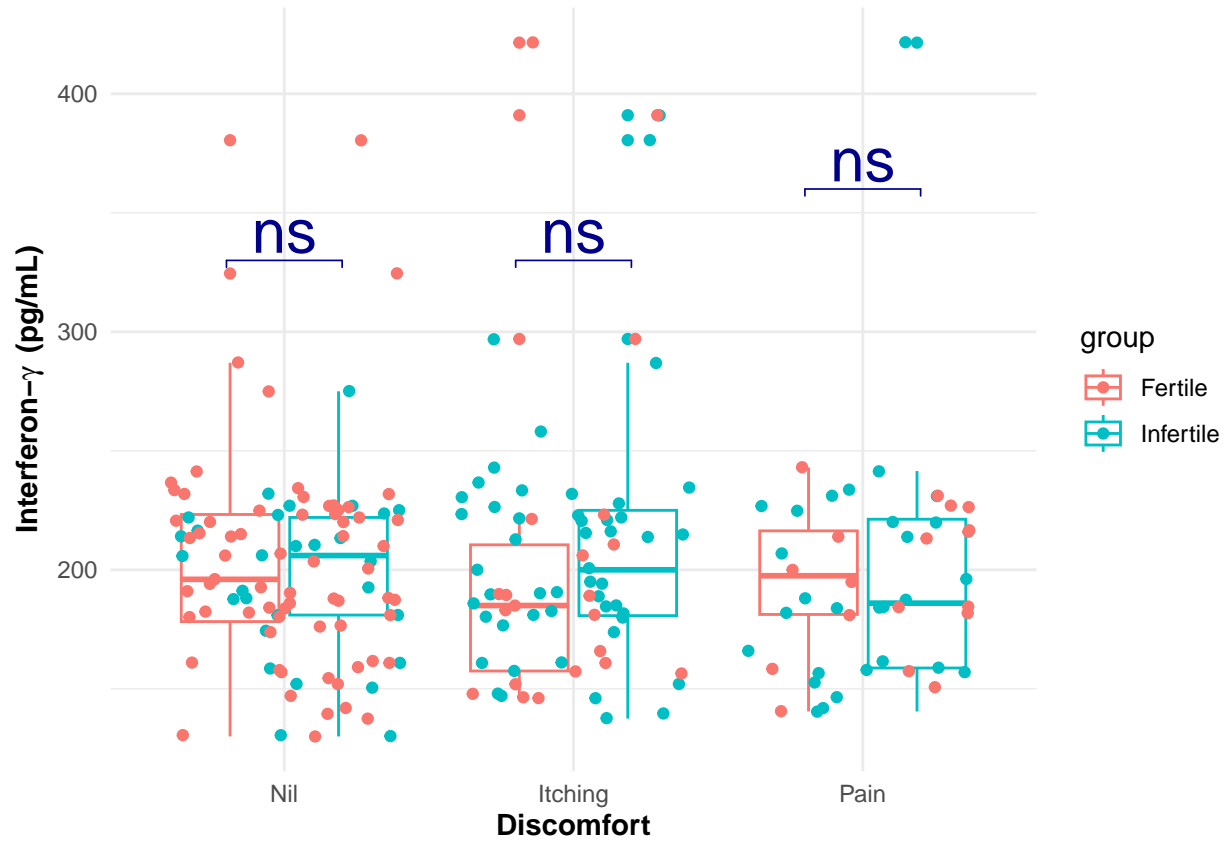
```
# Interferon gamma levels according vaginal discharge
stat_discomfort_ifn1<-newdata%>%
  group_by(discomfort1)%>%
  dunn_test(ifn_gamm_avrg~group,p.adjust.method="none")%>%
  add_xy_position(x = "discomfort1")
stat_discomfort_ifn1
```

```
## # A tibble: 3 x 15
##   discomfort1 .y. group1 group2 n1 n2 statistic p p.adj p.adj.signif
##   <chr> <chr> <chr> <chr> <int> <int> <dbl> <dbl> <dbl> <chr>
## 1 Itching ifn_~ Ferti~ Infer~ 21 51 1.33 0.185 0.185 ns
## 2 Nil ifn_~ Ferti~ Infer~ 67 29 -0.176 0.861 0.861 ns
## 3 Pain ifn_~ Ferti~ Infer~ 18 28 -0.338 0.736 0.736 ns
## # i 5 more variables: y.position <dbl>, groups <named list>, x <dbl>,
## # xmin <dbl>, xmax <dbl>
```

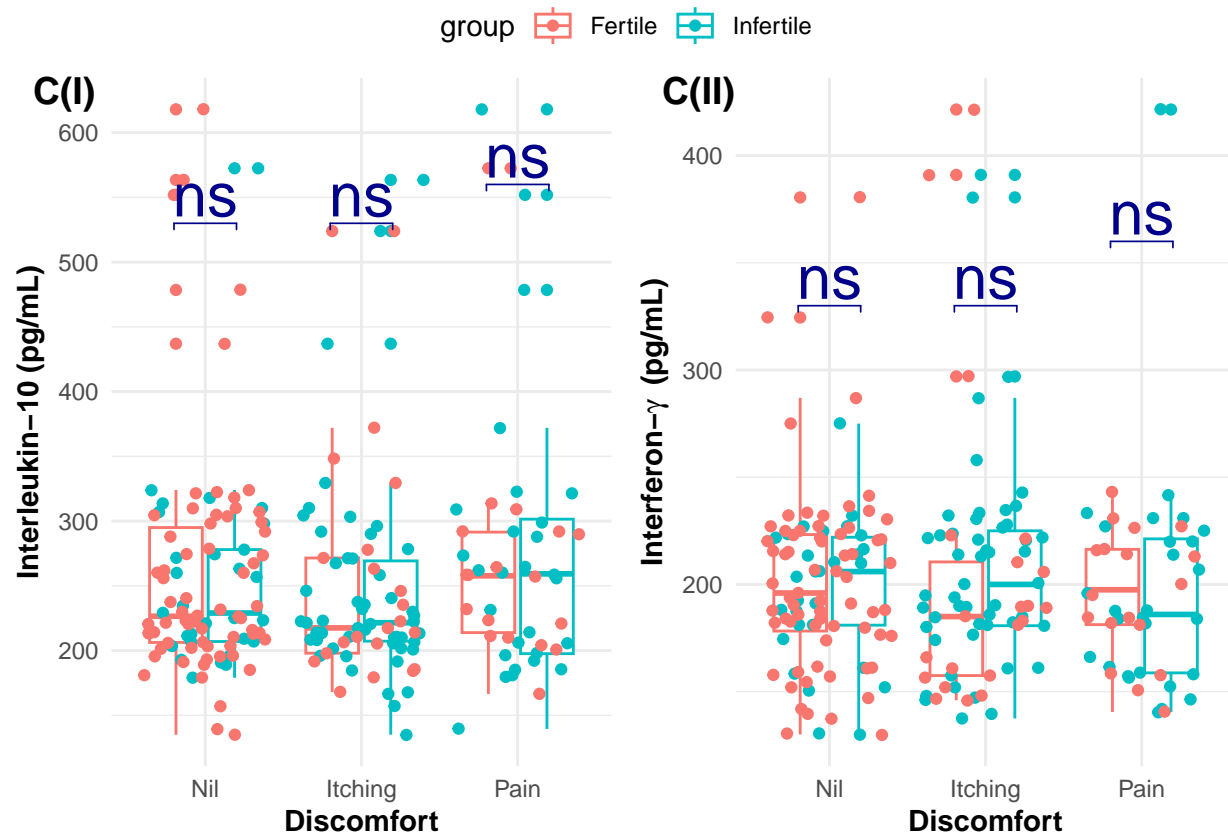
```
C_ii<-newdata%>%ggplot(aes(x=discomfort1,y=ifn_gamm_avrg,color=group))+
  geom_boxplot()+geom_point(position=position_jitter())+
  # stat_pvalue_manual(stat_discharge_1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color = "blue")
```

```
stat_pvalue_manual(stat_discomfort_ifn1, label = "p.adj.signif",hide.ns = FALSE,tip.length = 0.01,color
  labs(y = expression(bold("Interferon- $\gamma$ " (pg/mL))),x=expression(bold("Discomfort")))+theme_min
```

C_ii



```
ggarrange(C_i,C_ii,labels = c("C(I)","C(II)"),common.legend = TRUE)
```

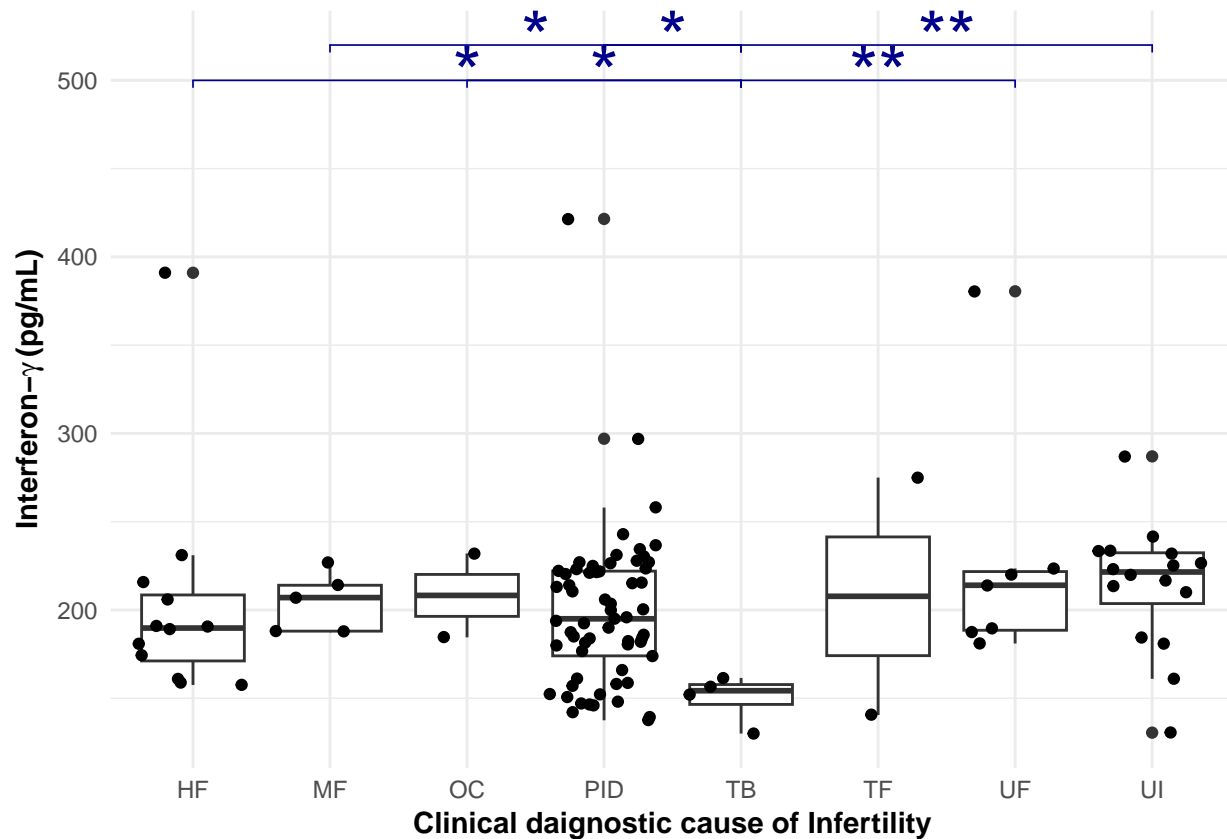


```
clinical_diagnostic_infertility_type<-Infertile_type[c(1:109),,]%>%mutate(diagnosis=recode(diagnosis,"TB
```

```
# Analysis for Interferon gamma as Udoma
```

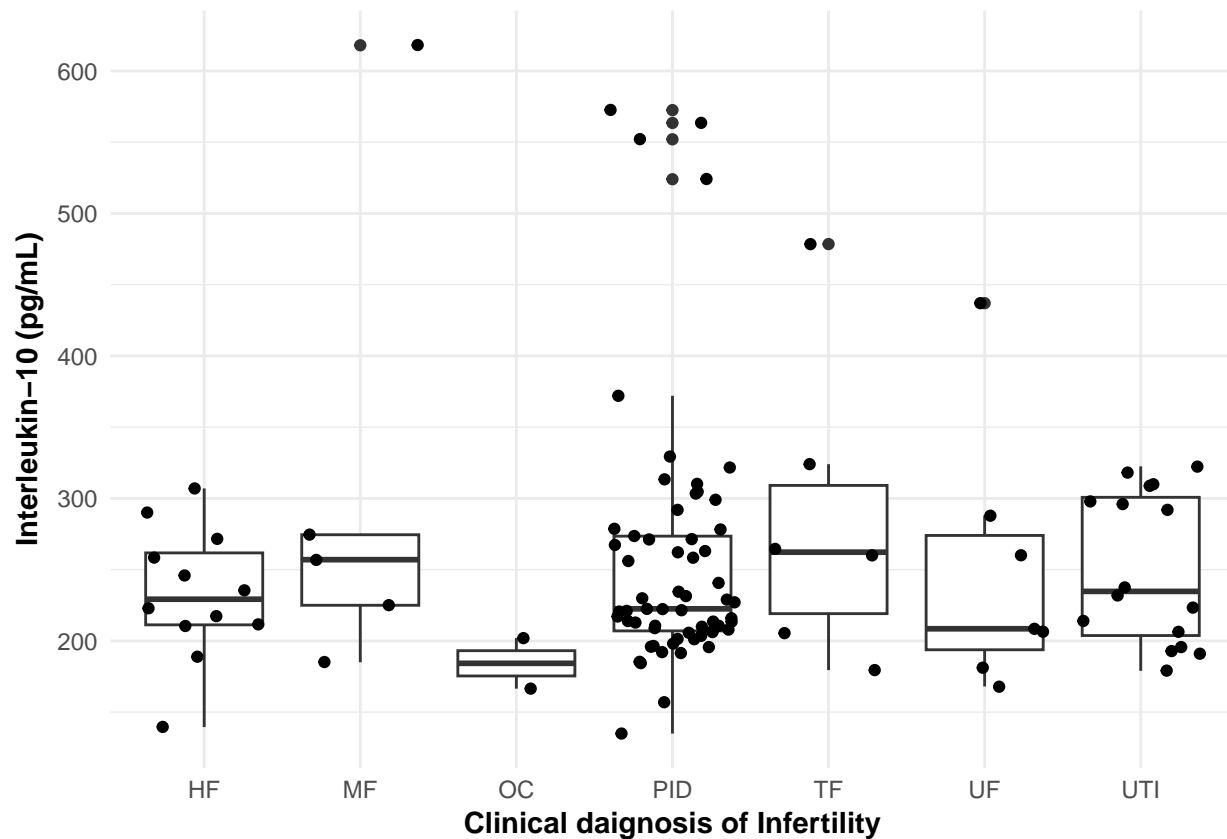
```
st.tst_gamma<-Infertile_type[c(1:109),,]%>%
  dunn_test(ifn_gamm_avrg~diagnosis,p.adjust.method="none")%>%
  add_xy_position(x="diagnosis")

Infertile_type[c(1:109),,]%>%mutate(diagnosis=recode(diagnosis,"UTI"="UI"))%>%
  ggplot(aes(x=diagnosis,y=ifn_gamm_avrg))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(st.tst_gamma, label = "p.adj.signif",hide.ns = TRUE,
                    tip.length = 0.01,color = "darkblue",size = 10,
                    y.position = c(500,520))+
  labs(y = expression(bold("Interferon- $\gamma$ "*(pg/mL)))),
       x=expression(bold("Clinical daignostic cause of Infertility")))+
  theme_minimal()
```



```
# Analysis for Interleukin 10
st.tst_10<-Infertile_type[c(1:109),]%>%
# st.tst_10<-Infertile_type[c(1:109),]%>%
# st.tst_10<-Infertile_type[c(1:109),]%>%
# st.tst_10<-Infertile_type[c(1:109),]%>%
st.tst_10<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF"))%>%
  dunn_test(il_10_avrg~diagnosis,p.adjust.method="none")%>%
  add_xy_position(x="diagnosis")

Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF"))%>%
  ggplot(aes(x=diagnosis,y=il_10_avrg))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(st.tst_10, label = "p.adj.signif",hide.ns = TRUE,
                    tip.length = 0.01,color = "darkblue",size = 10,y.position = c(625)
  )+
  labs(y = expression(bold("Interleukin-10 (pg/mL)")),
       x=expression(bold("Clinical daignosis of Infertility")))+
  theme_minimal()
```



Ct-HSP60 titer response along clinical diagnostic cause of infertility

```
st.tst_hsp60<-Infertile_type[c(1:109),]%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF"))%>%
  dunn_test(hsp_60_avrg~diagnosis,p.adjust.method="none")%>%
  add_xy_position(x="diagnosis")

Infertile_type[c(1:109),]%>%mutate(diagnosis=recode(diagnosis,"UTI"="UI"))%>%
  mutate(diagnosis=recode(diagnosis,"TB"="TF"))%>%
  ggplot(aes(x=diagnosis,y=hsp_60_avrg))+
  geom_boxplot()+geom_point(position=position_jitter())+
  stat_pvalue_manual(st.tst_hsp60, label = "p.adj.signif",hide.ns = TRUE,
    tip.length = 0.01,color = "darkblue",size = 10,y.position = c(450))+
  labs(y = expression(bold("Ct-Heat shock Protein-60 (pg/mL)")),
    x=expression(bold("Clinical daignostic cause of Infertility")))+
  theme_minimal()
```

