

Gráfica de dispersión

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```
library("pacman")
```

```
p_load("readr",  
      "dplyr",  
      "ggplot2")
```

```
PCR <- read_csv(file="https://raw.githubusercontent.com/ManuelLaraMVZ/Transcript-mica/main/datos_miRNAs.csv")  
head(PCR)
```

```
##           Gen Condicion  Cx1  Cx2  Cx3  T1  T2  T3  
## 1 U6 snRNA-001973 Control 13.7904 11.7446 11.9293 13.1954 12.9566 12.6417  
## 2 ath-miR159a-000338 Target 35.0000 35.0000 35.0000 35.0000 35.0000 35.0000  
## 3 hsa-let-7a-000377 Target 20.4943 21.0031 21.0073 20.3820 19.5925 20.9335  
## 4 hsa-let-7b-002619 Target 18.3545 19.0325 19.1368 18.2551 17.4500 18.9675  
## 5 hsa-let-7c-000379 Target 22.1791 23.6921 23.7763 22.9127 21.9639 23.9877  
## 6 hsa-let-7d-002283 Target 22.1898 22.6786 21.8660 21.9711 21.2081 21.9410
```

```
Referencia <- PCR %>%  
  filter(Condicion=="Control") %>%  
  select(-2)%>%  
  filter(Gen == "U6 snRNA-001973")  
head(Referencia)
```

```
##           Gen  Cx1  Cx2  Cx3  T1  T2  T3  
## 1 U6 snRNA-001973 13.7904 11.7446 11.9293 13.1954 12.9566 12.6417
```

```
Genes <- PCR %>%  
  filter(Condicion == "Target") %>%  
  select(-2)  
head(Genes)
```

```
##           Gen  Cx1  Cx2  Cx3  T1  T2  T3  
## 1 ath-miR159a-000338 35.0000 35.0000 35.0000 35.0000 35.0000 35.0000  
## 2 hsa-let-7a-000377 20.4943 21.0031 21.0073 20.3820 19.5925 20.9335  
## 3 hsa-let-7b-002619 18.3545 19.0325 19.1368 18.2551 17.4500 18.9675  
## 4 hsa-let-7c-000379 22.1791 23.6921 23.7763 22.9127 21.9639 23.9877  
## 5 hsa-let-7d-002283 22.1898 22.6786 21.8660 21.9711 21.2081 21.9410  
## 6 hsa-let-7e-002406 17.9679 18.3915 18.4673 18.0119 17.2932 18.5586
```

```
Mean_Ref <- Referencia %>%  
  mutate(Mean_Cx = (Cx1+Cx2+Cx3)/3,  
         Mean_Tx = (T1+T2+T3)/3) %>%  
  select("Gen", "Mean_Cx", "Mean_Tx")  
head(Mean_Ref)
```

```
##           Gen Mean_Cx Mean_Tx
## 1 U6 snRNA-001973 12.4881 12.93123
```

```
Mean_Gen <- Genes %>%
  mutate(Mean_Cx = (Cx1+Cx2+Cx3)/3,
         Mean_Tx = (T1+T2+T3)/3) %>%
  select("Gen", "Mean_Cx", "Mean_Tx")
head(Mean_Gen)
```

```
##           Gen Mean_Cx Mean_Tx
## 1 ath-miR159a-000338 35.00000 35.00000
## 2 hsa-let-7a-000377 20.83490 20.30267
## 3 hsa-let-7b-002619 18.84127 18.22420
## 4 hsa-let-7c-000379 23.21583 22.95477
## 5 hsa-let-7d-002283 22.24480 21.70673
## 6 hsa-let-7e-002406 18.27557 17.95457
```

```
Analisis <- Mean_Gen %>%
  mutate(DCt_Cx = Mean_Gen$Mean_Cx-Mean_Ref$Mean_Cx,
         DCt_Tx = Mean_Gen$Mean_Tx-Mean_Ref$Mean_Tx,
         DosDCt_Cx = 2^-(DCt_Cx),
         DosDCt_Tx = 2^-(DCt_Tx),
         DosDDCt = DosDCt_Tx/DosDCt_Cx)

head(Analisis)
```

```
##           Gen Mean_Cx Mean_Tx DCt_Cx DCt_Tx DosDCt_Cx
## 1 ath-miR159a-000338 35.00000 35.00000 22.511900 22.068767 1.672025e-07
## 2 hsa-let-7a-000377 20.83490 20.30267 8.346800 7.371433 3.071587e-03
## 3 hsa-let-7b-002619 18.84127 18.22420 6.353167 5.292967 1.223225e-02
## 4 hsa-let-7c-000379 23.21583 22.95477 10.727733 10.023533 5.896991e-04
## 5 hsa-let-7d-002283 22.24480 21.70673 9.756700 8.775500 1.155954e-03
## 6 hsa-let-7e-002406 18.27557 17.95457 5.787467 5.023333 1.810502e-02
##           DosDCt_Tx DosDDCt
## 1 2.273208e-07 1.359554
## 2 6.039173e-03 1.966141
## 3 2.550693e-02 2.085221
## 4 9.607620e-04 1.629241
## 5 2.281977e-03 1.974107
## 6 3.074865e-02 1.698349
```

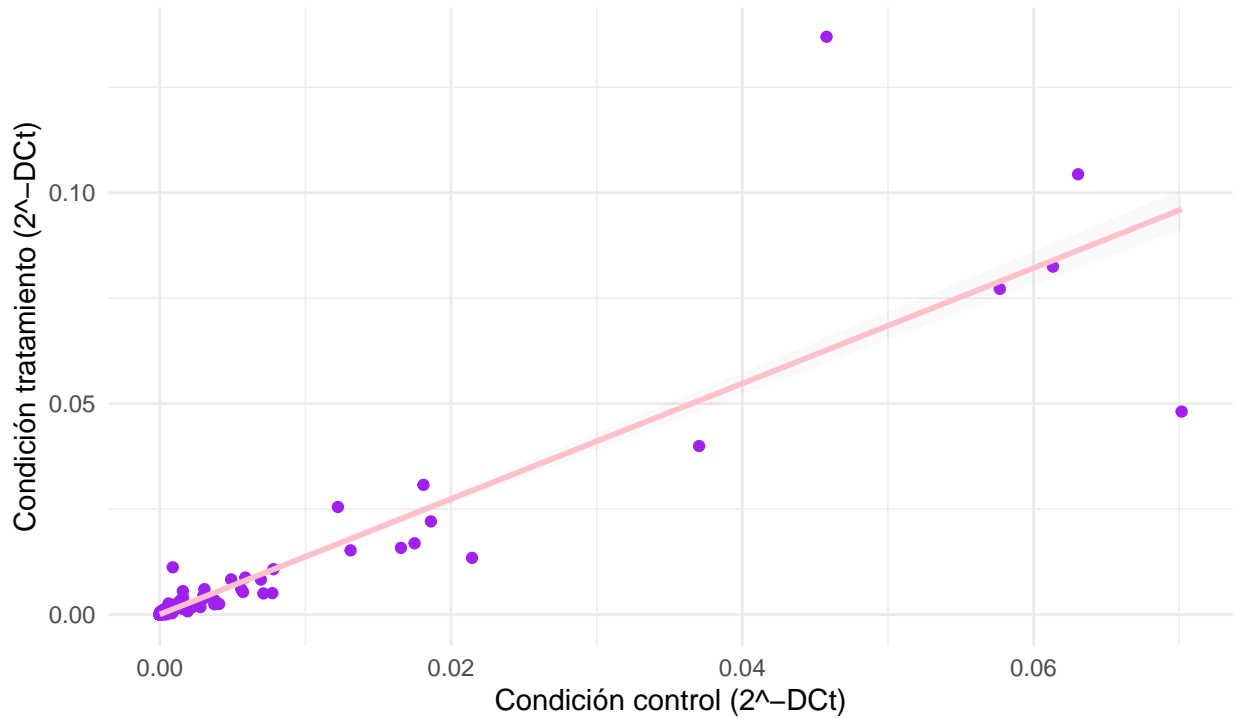
```
#####Gráfica
Grafica_1 <-ggplot(Analisis,
                  mapping = aes(x=DosDCt_Cx, y=DosDCt_Tx))+
  geom_point(color="purple")+
  labs(title= "Análisis de datos miRNAs",
       subtitle="Grafica de dispersión",
       x="Condición control (2^-DCt)",
       y="Condición tratamiento (2^-DCt)",
       caption="Creo Aranza Ugalde")+
  theme_minimal()+
  geom_smooth(method="lm",
             alpha=0.05,
             linewidth=1,
             span=1,
             color="pink")
```

Grafica_1

```
## `geom_smooth()` using formula = 'y ~ x'
```

Analisis de datos miRNAs

Grafica de dispersión



Creo Aranza Ugalde