

## corr interro 2

```
library(SummarizedExperiment)
library(tidyverse)

se <- readRDS("data/se.rds")

rowData(se)

## DataFrame with 8 rows and 2 columns
##           gene      location
##      <character> <character>
## Gene1      Gene1      Nucleus
## Gene2      Gene2      Nucleus
## Gene3      Gene3      Nucleus
## Gene4      Gene4      Nucleus
## Gene5      Gene5      Nucleus
## Gene6      Gene6      Nucleus
## Gene7      Gene7      Nucleus
## Gene8      Gene8      Nucleus

cbind(assay(se), rowData(se)) %>%
  as_tibble() %>%
  pivot_longer(names_to = "samples", values_to = "gene_expression", -c(gene, location)) %>%
  full_join(as_tibble(colData(se))) %>%
  ggplot(aes(x = group, y = gene_expression)) +
  geom_boxplot() +
  facet_wrap(~ gene)

## Joining, by = "samples"
```

