MTT#1 Cell Density

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Tidying the data

First, I load the libraries needed and read the raw data from **Omega** in *.xlsx*. Then I create my **tidy data** selecting the proper values and assigning them to their corresponding **cell density**.

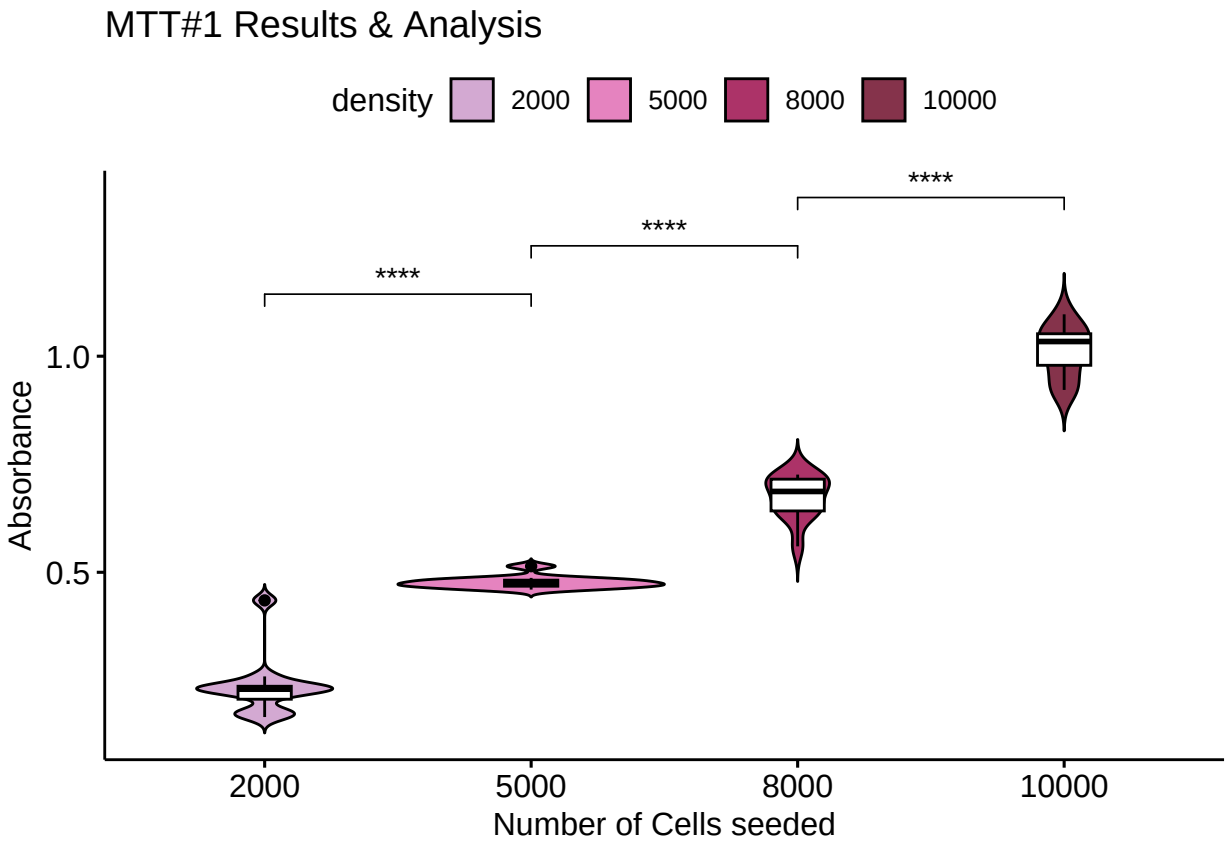
```
library(ggpubr)
library(readxl)
library(caret)
mtt_raw <- read_excel("C:\\Users\\andre\\OneDrive - unizar.es\\Laboratorio\\UCL ILDH 2023\\Results\\MTT
mtt_tidy<-data.frame(absorbance=unlist(mtt_raw[4:9,3:10]), density=0)
mtt_tidy<-mtt_tidy[1:45,] #This assigns the absorbances to the cell density
mtt_tidy[1:12, 2]<- 2000
mtt_tidy[13:24, 2]<- 5000
mtt_tidy[25:36, 2]<- 8000
mtt_tidy[37:45, 2]<- 10000
```

Plotting with ggplot

Violin plot with boxplot, adding a two sample *t test* for significance.

```
density_comparisons<-list( c("2000", "5000"),
                           c("5000", "8000"),c("8000", "10000"))
model<-lm(density~absorbance, mtt_tidy[1:36,])
violin<- ggviolin(mtt_tidy,
          x          = "density",
          y          = "absorbance",
          title      = "MTT#1 Results & Analysis",
          xlab       = "Number of Cells seeded",
          ylab       = "Absorbance",
          fill       = "density",
          palette = c("#c994c7", "#df65b0", "#980043", "#67001f"),
          alpha      = 0.8,
          add        = "boxplot",
          add.params = list(fill = "white")) +
  stat_compare_means(comparisons = density_comparisons,
                     label       = "p.signif", method="t.test")


violin
```



Density checking

While preparing the dilutions for the MTT I took less RPMI volume than I should have for the 10k cell density solution. Due to that, I could not fill all the wells, only having 9 compared to the 12 wells of the rest of the groups (2k, 5k, 8k). That means that there should be more than 10k cell per well. If I create a regression model trained with the 2k, 5k and 8k only, and then predict the cell density corresponding to the absorbance shown in the 10k well I should be able to ched whether the hypothesis is true.

```
model<-lm(density~absorbance, mtt_tidy[1:36,]) #I create the model
prediction<-predict(model, mtt_tidy[37:45,]) #I predict the density
print(paste(c(round(mean(prediction)),"> 10k"), collapse = " "))
```

```
## [1] "11969 > 10k"
```

```
#I print the mean of those predicted values
```

Indeed, *I seeded more cells per well in the 10k group than I should have.*