

# Data Science Workshop

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# Quizz

SQL is a ... language.

... clause is used to choose the columns

... clause is used to filter the rows

... gets rid of the duplicates

... is used to create aggregated summaries

A Primary key is ...

# Quizz

Please complete the Query:

```
SELECT Sales.*, Customers.*  
FROM Sales  
LEFT JOIN Customers  
... Customers.CustomerID = Sales.CustomerID
```

# Quizz

- {...} helps us connect to SQL
- {...} helps us handle data
- {...} helps us visualize data

```
pulsedIV <- pulsedIV ...  
  filter(Example==1)
```

# Quizz

```
ggplot(pulsedIV, aes(x=V2,  
                     y=I,  
                     ... = V1)) +  
  geom_point() +  
  geom_line()
```

# Quizz

```
pulsedIV_summary <- pulsedIV %>%  
  ... (V1) %>%  
  ... (maxI=max(I, na.rm = TRUE))
```

# Quizz

What is the difference between numpy and pandas?

Which libraries did we use to connect to SQL?

Which libraries did we use to make a plot?

Please finish the command

```
df1952 = ...
```

# Summary

We have seen SQL (a neat way to store data but not only).

We have seen 2 open source programming languages:

- We have seen R, packages, SQL connection, pipe, ggplot
- We have seen Python, libraries, SQL connection, seaborn

We add another building block today.



# Web Applications

What we are going to create today:

- Create a Web Application that displays the PCM data.
- Select one wafer from the list
- Make a button to apply log scale.

# Let's look at the data

```
library(readr)  
  
PCM <- read_csv("./Data/PCM2.csv")  
  
View(PCM)
```

# Let's visualize the data

Please filter the data according to this rule:

Wafer = 1

```
PCM_example <- PCM %>%  
  filter(Wafer == 1)
```

# Is this scalable?

```
ggplot(PCM_example,  
      aes(x=X_COORD,  
          y=Y_COORD,  
          fill= value)) +  
  geom_tile() +  
  scale_fill_gradient(low="red",high="green")
```

# Is this scalable?

What if I want to see another wafer? We can filter the data again, and visualize it.

```
PCM_example <- PCM %>%  
  filter(Wafer == 2)
```

We can apply a for loop that goes through the waferIDs one by one and generate .png charts for each one.

# Is this scalable?

or we can use this code:

```
WaferList <- c(1,2)
PCM_example <- PCM %>%
  filter(Wafer %in% WaferList)

ggplot(PCM_example, aes(x=X_COORD,
                        y=Y_COORD,
                        group= Wafer,
                        fill= value)) +

  geom_tile() +
  scale_fill_gradient(low="red",high="green") +
  facet_grid(.~Wafer)
```

# Is this scalable?

What if we have new data coming from additional tests?

We need to log in, generate the new plots...

# We need something else..

A web Application that is running 24/7. It checks for new data every time we launch it.



# Welcome to Shiny



**Figure 1:** <https://shiny.rstudio.com>

# Let's start

<https://shiny.rstudio.com/gallery/widget-gallery.html>

We need a selection button and a check box for log10 graphs.

# Let's develop a PCM app

Loading the usual suspects

```
library("readr")  
library("dplyr")  
library('ggplot2')  
library('shiny')
```

Loading the data

```
PCM <- read_csv('./Data/PCM2.csv')
```

# Let's develop a PCM app

```
WaferList <- c(1,2)
PCM_example <- PCM %>%
  filter(Wafer %in% WaferList)

ggplot(PCM_example, aes(x=X_COORD,
                        y=Y_COORD,
                        group= Wafer,
                        fill= value)) +
  geom_tile() +
  scale_fill_gradient(low="red",high="green") +
  facet_grid(.~Wafer)
```

# Let's develop the ui side

the UI side

```
ui <- fluidPage(  
  selectInput("Wafer", label = h3("Select Wafer"),  
              sort(WaferList)),  
  plotOutput('plot')  
)
```

# Let's develop the server side

the Server side

```
server <- function(input, output) {  
  WaferList <- c(1,2)  
  PCM_example <- PCM %>%  
    filter(Wafer %in% WaferList)  
  
  plot <- ggplot(PCM_example, aes(x=X_COORD,  
                                  y=Y_COORD,  
                                  group=Wafer,  
                                  fill= value)) +  
  
    geom_tile() +  
    scale_fill_gradient(low="red",high="green") +  
    facet_grid(.~Wafer)  
}
```

# Let's develop the server side

the Server side

```
server <- function(input, output) {  
  PCM_example <- reactive({PCM %>%  
    filter(Wafer %in% WaferList)  
  })  
  
  output$plot <- renderPlot({ggplot(PCM_example(), aes(x=X_COORD,  
                                                         y=Y_COORD,  
                                                         group=Wafer,  
                                                         fill= value)) +  
    geom_tile() +  
    scale_fill_gradient(low="red",high="green") +  
    facet_grid(.~Wafer)  
  })  
}
```

# Let's call the app

```
shinyApp(ui = ui, server = server)
```



## Let's continue working on the Server side

```
server <- function(input, output) {  
  PCM_example <- reactive({PCM %>%  
    filter(Wafer %in% WaferList)  
  })  
  
  output$plot <- renderPlot({ggplot(PCM_example(),  
                                     aes(x=X_COORD,  
                                           y=Y_COORD,  
                                           group=Wafer,  
                                           fill= value)) +  
    geom_tile() +  
    scale_fill_gradient(low="red",high="green") +  
    facet_grid(.~Wafer)  
  })  
}
```

# Let's continue working on the ui side

Let's add the ON/OFF button for Log10

```
ui <- fluidPage(  
  selectInput("Wafer",  
    label = h3("Select Wafer"),  
    sort(WaferList),  
    multiple = TRUE,  
    selected = WaferList[1]),  
  checkboxInput("checkbox", label = "log10", value = FALSE),  
  plotOutput('plot')  
)
```

## Let's continue working on the Server side

```
if (input$checkbox){  
  ggplot(PCM_example(), aes(x=X_COORD,  
                             y=Y_COORD,  
                             group=Wafer,  
                             fill= value)) +  
  
  geom_tile() +  
  scale_fill_gradient(low="red",  
                      high="green",  
                      trans = "log10") +  
  
  facet_grid(.~Wafer)  
}
```

## Let's continue working on the ui side

```
ui <- fluidPage(  
  selectInput("Wafer", label = h3("Select Wafer"),  
    sort(unique(PCM$Wafer)),  
    multiple = TRUE,  
    selected = WaferList[1]),  
  checkboxInput("checkbox", label = "log10", value = FALSE),  
  plotOutput('plot')  
)
```