DATA 606 Data Project Proposal

Libraries Imported

```
library(tidyverse)
```

```
## Warning: package 'tidyverse' was built under R version 4.1.3
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --
```

```
## v ggplot2 3.3.5     v purrr   0.3.4
## v tibble  3.1.2     v dplyr   1.0.7
## v tidyr   1.1.3     v stringr 1.4.0
## v readr   1.4.0     v forcats 0.5.1
```

```
## Warning: package 'ggplot2' was built under R version 4.1.2
```

```
## Warning: package 'stringr' was built under R version 4.1.2
```

```
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```
library(dplyr)
library(plotly)
```

```
## Warning: package 'plotly' was built under R version 4.1.3
```

```
##
## Attaching package: 'plotly'
```

```
## The following object is masked from 'package:ggplot2':
##
##     last_plot
```

```
## The following object is masked from 'package:stats':
##
##     filter
```

```
## The following object is masked from 'package:graphics':
##
##     layout
```

```
library(tidyr)
library(stringr)
library(psych)
```

```
## Warning: package 'psych' was built under R version 4.1.2
```

```
##
## Attaching package: 'psych'
```

```
## The following objects are masked from 'package:ggplot2':
##
##     %+%, alpha
```

```
library(ggplot2)
```

Data Preparation

```
metadata_df <- read.delim("https://raw.githubusercontent.com/rfpoulos/pymaceuticals/master/data/Mouse_m
head(metadata_df)
```

load dataset1

```
##   Mouse.ID Drug.Regimen    Sex Age_months Weight..g.
## 1     k403     Ramicane   Male         21         16
## 2     s185    Capomulin Female          3         17
## 3     x401    Capomulin Female         16         15
## 4     m601    Capomulin   Male         22         17
## 5     g791     Ramicane   Male         11         16
## 6     s508     Ramicane   Male          1         17
```

Grouping by Drug.Regimen

```
df <- metadata_df %>%
  group_by(Drug.Regimen)

head(df)
```

```
## # A tibble: 6 x 5
## # Groups:   Drug.Regimen [2]
##   Mouse.ID Drug.Regimen Sex    Age_months Weight..g.
##   <chr>    <chr>        <chr>       <int>      <int>
## 1 k403     Ramicane     Male           21         16
## 2 s185     Capomulin    Female          3         17
## 3 x401     Capomulin    Female         16         15
## 4 m601     Capomulin    Male           22         17
## 5 g791     Ramicane     Male           11         16
## 6 s508     Ramicane     Male            1         17
```

Load dataset2

```
results_df <- read.delim("https://raw.githubusercontent.com/rfpoulos/pymaceuticals/master/data/Study_re
head(results_df)
```

```
##   Mouse.ID Timepoint Tumor.Volume..mm3. Metastatic.Sites
## 1     b128         0                 45                0
## 2     f932         0                 45                0
## 3     g107         0                 45                0
## 4     a457         0                 45                0
## 5     c819         0                 45                0
## 6     h246         0                 45                0
```

Introduction:

Pymaceuticals Inc., a fictional burgeoning pharmaceutical company based out of San Diego, CA, specializes in drug-based, anti-cancer pharmaceuticals.They have provided the data to test the efficacy of potential drug treatments for squamous cell carcinoma. In this study, 249 mice identified with Squamous cell carcinoma (SCC) tumor growth, kind of skin cancer, were treated through a variety of drug regimens. Over the course of 45 days, tumor development was observed and measured.The objective is to analyze the data to show how four treatments (Capomulin, Infubinol, Ketapril, and Placebo) compare.

Research question:

You should phrase your research question in a way that matches up with the scope of inference your dataset allows for.

Question 1: Is Capomulin more or less effective in reducing the tumor size than Infubinol, or Ketapril drugs categories?

Question 2: Is there a correlation between the age, weight and the tumor size growth for each drug category?

Hypothesis Test

Null Hypothesis: There is no difference between the mean percent change in tumor volume for the four drug categories.

Alternate Hypothesis: There is a difference between the mean percent change in tumor volume for the four drug categories.

Approach for answering the research question will be:

1- Calculate the mean percent change in tumor volume for the four drug categories.

2- Perform the Hypothesis test to find out whether or not the difference exist between the mean tumor size for all four drug categories.

3- Perform linear regression to study the correlation between various variables by calculating the correlation coefficient.

4- Finally analyze the results to find out if Capomulin more or less effective in reducing the tumor size of sample mice than Infubinol, or Ketapril drugs categories.

Cases:

What are the cases? How many different drug treatments are there? How many total sample size as well as the sample size by drug treatments are there?

Answer: The metadata_df contain 249 unique mouse id and so are the number of cases that treated with variety of drug regimem .The results_df dataset holds the tumor growth measurments observed for each Mouse ID and carries 1,893 rows results. There are 10 different drug treatments. The total sample size of mouse_id for four treatments (Capomulin, Infubinol, Ketapril, and Placebo) is 100 and the sample size of mouse_id by drug treatments is 25 each.

Data collection:

Describe the method of data collection.

Answer: Data is collected by the fictitious pharmaceutical company who was testing the efficacy of potential drug treatments for squamous cell carcinoma. I import the data into my .Rmd file from github.

Type of study:

What type of study is this (observational/experiment)?

Answer: This is a experimental study.A group of 249 mice were monitored after administration of a variety of drug regimens over a 45-day treatment period. The impact of Capomulin on tumor growth, metastasis and survival rates were monitored, along with Infubinol, Ketapril, and Placebo.

Data Source:

If you collected the data, state self-collected. If not, provide a citation/link.

Answer: The citation and data collection links are as follows.

In my search for the experimental datasets, I found the Mouse_metadata and the Study_results on the GitHub link provided below:

https://raw.githubusercontent.com/rfpoulos/pymaceuticals/master/data/Mouse_metadata.csv

https://raw.githubusercontent.com/rfpoulos/pymaceuticals/master/data/Study_results.csv

Upon further research in finding the original source of the the dataset, I found that these datasets are provided by Pymaceuticals Inc., a fictional burgeoning pharmaceutical company based out of San Diego, CA, specializes in drug-based, anti-cancer pharmaceuticals. Below is the link for the original source of the datasets.

https://c-l-nguyen.github.io/web-design-challenge/index.html

Response

What is the response variable, and what type is it (numerical/categorical)?

Answer: The response variable is the size of tumor, "Tumor.Volume..mm3." and it holds a numerical data.

Explanatory

What is the explanatory variable, and what type is it (numerical/categorical)?

Answer: The explanatory variable is the "Drug.Regimen" and it holds a categorical data and "Timepoint" which holds numerical data. The 'Timepoint' unit is 'days'.

Relevant summary statistics: (Tables and Charts)

Provide summary statistics relevant to your research question. For example, if you're comparing means across groups provide means, SDs, sample sizes of each group. This step requires the use of R, hence a code chunk is provided below. Insert more code chunks as needed.

```
summary(metadata_df)
```

```
##    Mouse.ID         Drug.Regimen           Sex              Age_months
##  Length:249         Length:249         Length:249         Min.   : 1.00
##  Class :character   Class :character   Class :character   1st Qu.: 6.00
##  Mode  :character   Mode  :character   Mode  :character   Median :13.00
##                                                           Mean   :12.73
##                                                           3rd Qu.:19.00
##                                                           Max.   :24.00
##    Weight..g.
##  Min.   :15.00
##  1st Qu.:25.00
##  Median :27.00
##  Mean   :26.12
##  3rd Qu.:29.00
##  Max.   :30.00
```

Summary Statistic

```
summary(results_df)
```

```
##    Mouse.ID           Timepoint     Tumor.Volume..mm3. Metastatic.Sites
##  Length:1893        Min.   : 0.00   Min.   :22.05      Min.   :0.000
##  Class :character   1st Qu.: 5.00   1st Qu.:45.00      1st Qu.:0.000
##  Mode  :character   Median :20.00   Median :48.95      Median :1.000
##                     Mean   :19.57   Mean   :50.45      Mean   :1.022
##                     3rd Qu.:30.00   3rd Qu.:56.29      3rd Qu.:2.000
##                     Max.   :45.00   Max.   :78.57      Max.   :4.000
```

Sample Sizes for metadata_df

```
nrow(metadata_df)
```

```
## [1] 249
```

Sample Sizes for results_df

```
nrow(results_df)
```

```
## [1] 1893
```

How many drug treatments are there?

```
drug_count <- unique(metadata_df$Drug.Regimen)

drug_count
```

```
##  [1] "Ramicane"  "Capomulin" "Infubinol" "Placebo"   "Ceftamin"  "Stelasyn"
##  [7] "Zoniferol" "Ketapril"  "Propriva"  "Naftisol"
```

```
length(drug_count)
```

```
## [1] 10
```

Sample sizes of mouse_id by drug treatment

```
capomulin_df <- filter(metadata_df, Drug.Regimen=="Capomulin")

head(capomulin_df)
```

```
##   Mouse.ID Drug.Regimen    Sex Age_months Weight..g.
## 1     s185    Capomulin Female          3         17
## 2     x401    Capomulin Female         16         15
## 3     m601    Capomulin   Male         22         17
## 4     f966    Capomulin   Male         16         17
## 5     u364    Capomulin   Male         18         17
## 6     y793    Capomulin   Male         17         17
```

```
nrow(capomulin_df)
```

```
## [1] 25
```

```
infubinol_df <- filter(metadata_df, Drug.Regimen=="Infubinol")

nrow(infubinol_df)
```

```
## [1] 25
```

```
ketapril_df <- filter(metadata_df, Drug.Regimen=="Ketapril")

nrow(ketapril_df)
```

```
## [1] 25
```

```
placebo_df <- filter(metadata_df, Drug.Regimen=="Placebo")

nrow(placebo_df)
```

```
## [1] 25
```

Performing full outer join, so that no data is lost

```
merge_df <- merge(x = metadata_df, y = results_df, all = TRUE)

head(merge_df)
```

```
##   Mouse.ID Drug.Regimen    Sex Age_months Weight..g. Timepoint
## 1     a203    Infubinol Female         20         23        20
## 2     a203    Infubinol Female         20         23        25
## 3     a203    Infubinol Female         20         23        15
## 4     a203    Infubinol Female         20         23        10
## 5     a203    Infubinol Female         20         23        35
## 6     a203    Infubinol Female         20         23         0
##   Tumor.Volume..mm3. Metastatic.Sites
## 1           55.17334                1
## 2           56.79321                1
## 3           52.77787                1
## 4           51.85244                1
## 5           61.93165                2
## 6           45.00000                0
```

```
glimpse(merge_df)
```

```
## Rows: 1,893
## Columns: 8
## $ Mouse.ID           <chr> "a203", "a203", "a203", "a203", "a203", "a203", "a2~
## $ Drug.Regimen       <chr> "Infubinol", "Infubinol", "Infubinol", "Infubinol",~
## $ Sex                <chr> "Female", "Female", "Female", "Female", "Female", "~
## $ Age_months         <int> 20, 20, 20, 20, 20, 20, 20, 20, 20, 20, 21, 21, 21,~
## $ Weight..g.         <int> 23, 23, 23, 23, 23, 23, 23, 23, 23, 23, 25, 25, 25,~
## $ Timepoint          <int> 20, 25, 15, 10, 35, 0, 30, 5, 45, 40, 5, 40, 35, 45~
## $ Tumor.Volume..mm3. <dbl> 55.17334, 56.79321, 52.77787, 51.85244, 61.93165, 4~
## $ Metastatic.Sites   <int> 1, 1, 1, 1, 2, 0, 1, 0, 2, 2, 0, 1, 1, 1, 1, 1, 1, ~
```

Dropping the NA rows

```
merge_df <- merge_df %>% drop_na()

head(merge_df)
```

```
##   Mouse.ID Drug.Regimen    Sex Age_months Weight..g. Timepoint
## 1     a203    Infubinol Female         20         23        20
## 2     a203    Infubinol Female         20         23        25
## 3     a203    Infubinol Female         20         23        15
## 4     a203    Infubinol Female         20         23        10
## 5     a203    Infubinol Female         20         23        35
## 6     a203    Infubinol Female         20         23         0
##   Tumor.Volume..mm3. Metastatic.Sites
## 1           55.17334                1
## 2           56.79321                1
## 3           52.77787                1
## 4           51.85244                1
## 5           61.93165                2
## 6           45.00000                0
```

Change colnames of some columns

assigning new names to the columns of the merged data frame

Colnames(df)[2] <- "new_col2"

```
colnames(merge_df)[1] <- c("Mouse_Id")
colnames(merge_df)[2] <- c("Drug_Regimen")
colnames(merge_df)[5] <- c("Weight_g")
colnames(merge_df)[7] <- c("Tumor_Volume_mm3")
colnames(merge_df)[8] <- c("Metastatic_Sites")

head(merge_df)
```

```
##   Mouse_Id Drug_Regimen    Sex Age_months Weight_g Timepoint Tumor_Volume_mm3
## 1     a203    Infubinol Female         20       23        20         55.17334
## 2     a203    Infubinol Female         20       23        25         56.79321
## 3     a203    Infubinol Female         20       23        15         52.77787
## 4     a203    Infubinol Female         20       23        10         51.85244
## 5     a203    Infubinol Female         20       23        35         61.93165
## 6     a203    Infubinol Female         20       23         0         45.00000
##   Metastatic_Sites
## 1                1
## 2                1
## 3                1
## 4                1
## 5                2
## 6                0
```

```
merge_df %>% group_by(Mouse_Id, Timepoint)
```

```
## # A tibble: 1,893 x 8
## # Groups:   Mouse_Id, Timepoint [1,888]
##    Mouse_Id Drug_Regimen Sex    Age_months Weight_g Timepoint Tumor_Volume_mm3
##    <chr>    <chr>        <chr>       <int>    <int>     <int>            <dbl>
##  1 a203     Infubinol    Female         20       23        20             55.2
##  2 a203     Infubinol    Female         20       23        25             56.8
##  3 a203     Infubinol    Female         20       23        15             52.8
##  4 a203     Infubinol    Female         20       23        10             51.9
##  5 a203     Infubinol    Female         20       23        35             61.9
##  6 a203     Infubinol    Female         20       23         0             45
##  7 a203     Infubinol    Female         20       23        30             59.5
##  8 a203     Infubinol    Female         20       23         5             48.5
##  9 a203     Infubinol    Female         20       23        45             68.0
## 10 a203     Infubinol    Female         20       23        40             63.6
## # ... with 1,883 more rows, and 1 more variable: Metastatic_Sites <int>
```

```
head(merge_df)
```

```
##   Mouse_Id Drug_Regimen    Sex Age_months Weight_g Timepoint Tumor_Volume_mm3
## 1     a203    Infubinol Female         20       23        20         55.17334
## 2     a203    Infubinol Female         20       23        25         56.79321
## 3     a203    Infubinol Female         20       23        15         52.77787
## 4     a203    Infubinol Female         20       23        10         51.85244
## 5     a203    Infubinol Female         20       23        35         61.93165
## 6     a203    Infubinol Female         20       23         0         45.00000
##   Metastatic_Sites
## 1                1
## 2                1
## 3                1
## 4                1
## 5                2
## 6                0
```

```
df1 <- select(merge_df, Drug_Regimen, Tumor_Volume_mm3, Age_months, Weight_g)
head(df1)
```

```
##   Drug_Regimen Tumor_Volume_mm3 Age_months Weight_g
## 1    Infubinol         55.17334         20       23
## 2    Infubinol         56.79321         20       23
## 3    Infubinol         52.77787         20       23
## 4    Infubinol         51.85244         20       23
## 5    Infubinol         61.93165         20       23
## 6    Infubinol         45.00000         20       23
```

```
df1 <- group_by(df1, Drug_Regimen)
head(df1)
```

```
## # A tibble: 6 x 4
## # Groups:   Drug_Regimen [1]
```

```
##   Drug_Regimen Tumor_Volume_mm3 Age_months Weight_g
##   <chr>                   <dbl>      <int>    <int>
## 1 Infubinol                55.2         20       23
## 2 Infubinol                56.8         20       23
## 3 Infubinol                52.8         20       23
## 4 Infubinol                51.9         20       23
## 5 Infubinol                61.9         20       23
## 6 Infubinol                45           20       23
```

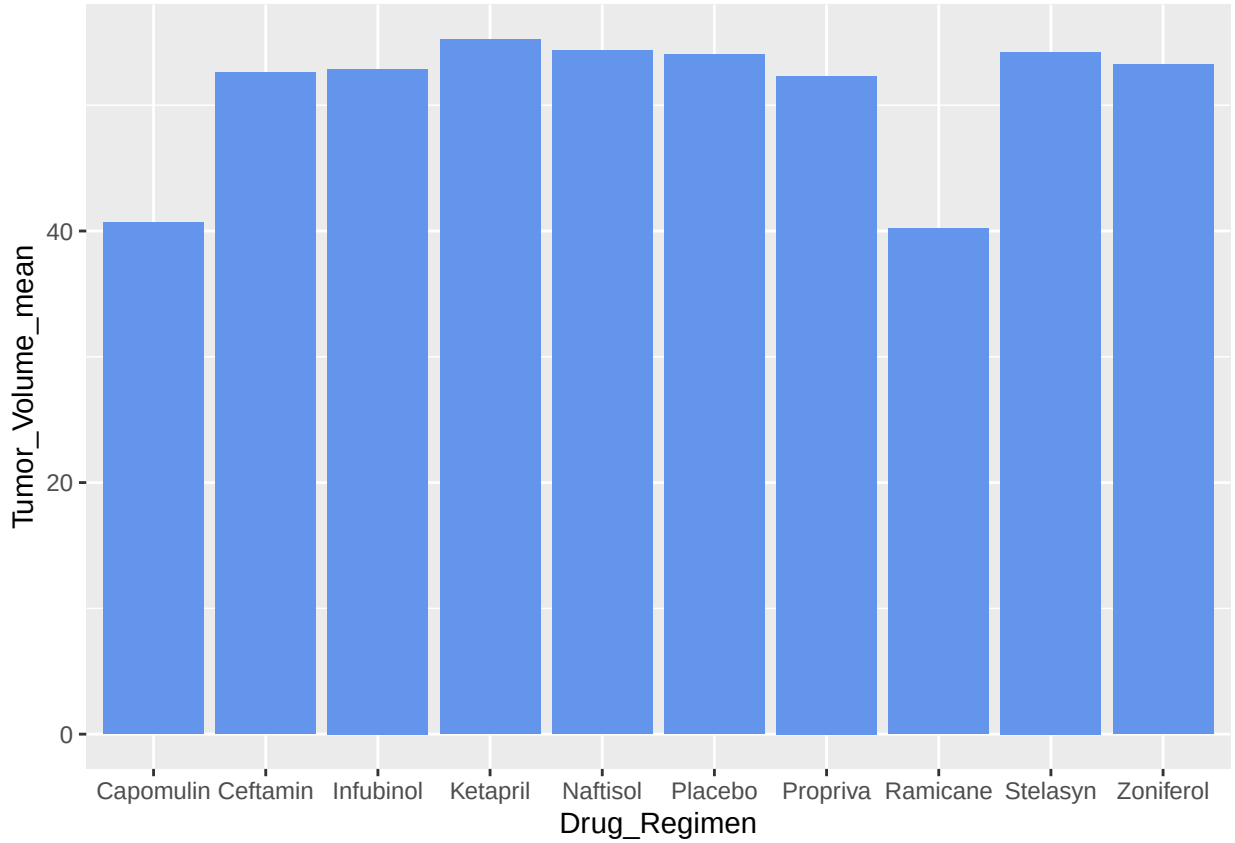
Finding the summary statistics of Tumor_Volume

```
stats_df <- df1 %>% summarise(
  Tumor_Volume_mean = mean(Tumor_Volume_mm3), Tumor_Volume_median = median(Tumor_Volume_mm3), Tumor_Volu

head(stats_df)
```

```
## # A tibble: 6 x 5
##   Drug_Regimen Tumor_Volume_me~ Tumor_Volume_me~ Tumor_Volume_sd Tumor_Volume_se
##   <chr>                   <dbl>            <dbl>           <dbl>           <dbl>
## 1 Capomulin                40.7             41.6            4.99           0.329
## 2 Ceftamin                 52.6             51.8            6.27           0.470
## 3 Infubinol                52.9             51.8            6.57           0.492
## 4 Ketapril                 55.2             53.7            8.28           0.604
## 5 Naftisol                 54.3             52.5            8.13           0.596
## 6 Placebo                  54.0             52.3            7.82           0.581
```

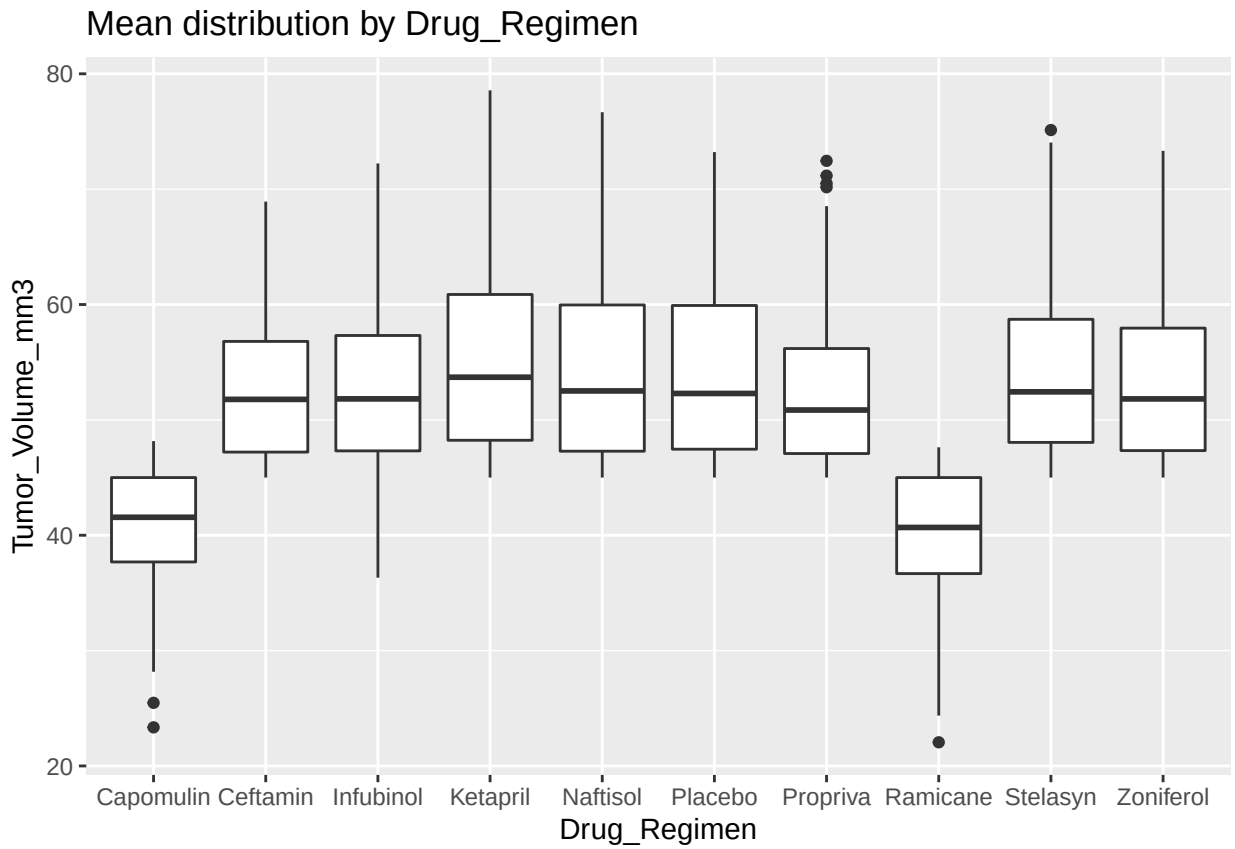
Comparing means of tumor size by drug treatment.

```
library(ggplot2)

# plot mean salaries
ggplot(stats_df,
       aes(x = Drug_Regimen,
           y = Tumor_Volume_mean)) +
  geom_bar(stat = "identity",  fill = "cornflowerblue")
```



Side-by-side box plots are very useful for comparing groups (i.e., the levels of a categorical variable) on a numerical variable. Outliers are prominent for Drug_Regimen Capomulin, Propriva, Ramicane and Stelasyn.

```
ggplot(merge_df,
       aes(x = Drug_Regimen,
           y = Tumor_Volume_mm3)) +
  geom_boxplot() +
  labs(title = "Mean distribution by Drug_Regimen")
```



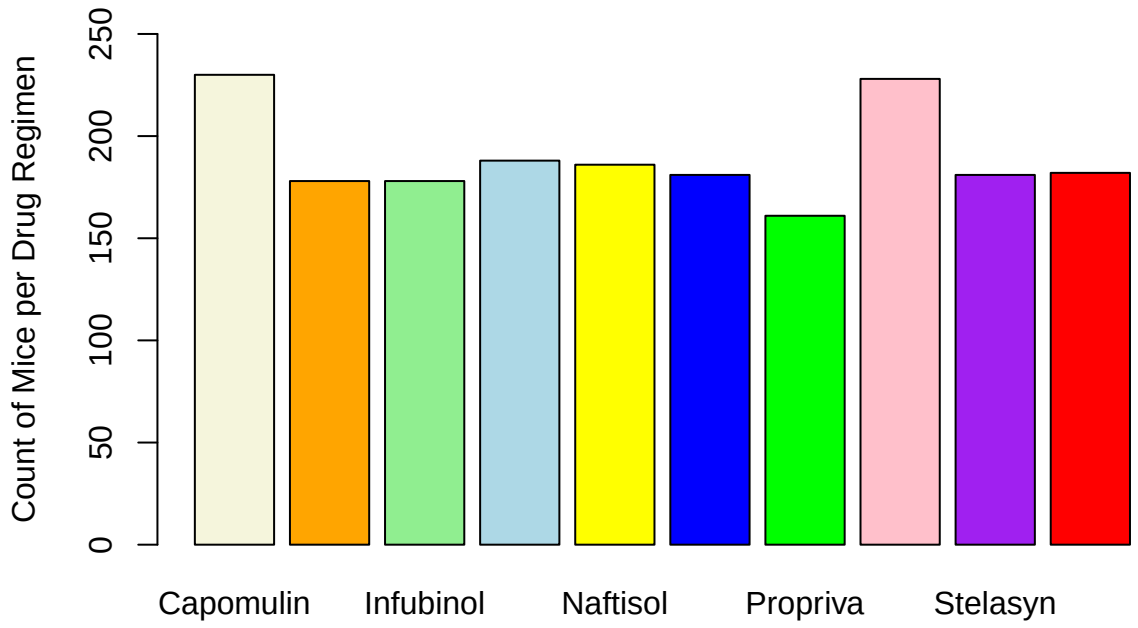
Finding the mice count of each Drug Regimen

```
count_df <- df1 %>% count(Drug_Regimen)

count_df
```

```
## # A tibble: 10 x 2
## # Groups:   Drug_Regimen [10]
##    Drug_Regimen     n
##    <chr>        <int>
##  1 Capomulin      230
##  2 Ceftamin       178
##  3 Infubinol      178
##  4 Ketapril       188
##  5 Naftisol       186
##  6 Placebo        181
##  7 Propriva       161
##  8 Ramicane       228
##  9 Stelasyn       181
## 10 Zoniferol      182
```

Ploting the number of mice in each drug regimen

```
barplot(c(230, 178, 178, 188, 186, 181, 161, 228, 181, 182),
        names.arg=c("Capomulin","Ceftamin","Infubinol","Ketapril","Naftisol", "Placebo", "Propriva", "Ra
        ylim=c(0,250),
        col=c("beige","orange","lightgreen","lightblue","yellow", "blue", "green", "pink", "purple", "re
        ylab="Count of Mice per Drug Regimen")
```



Remove duplicate rows across entire data frame

```
merge_df <- merge_df[!duplicated(merge_df), ]

head(merge_df)
```

```
##   Mouse_Id Drug_Regimen    Sex Age_months Weight_g Timepoint Tumor_Volume_mm3
## 1     a203    Infubinol Female         20       23        20         55.17334
## 2     a203    Infubinol Female         20       23        25         56.79321
## 3     a203    Infubinol Female         20       23        15         52.77787
## 4     a203    Infubinol Female         20       23        10         51.85244
## 5     a203    Infubinol Female         20       23        35         61.93165
## 6     a203    Infubinol Female         20       23         0         45.00000
##   Metastatic_Sites
```

```
## 1                1
## 2                1
## 3                1
## 4                1
## 5                2
## 6                0
```

filter by Capomulin, Infubinol, Ketapril, and Placebo

```
capomulin_df <- filter(merge_df, Drug_Regimen == "Capomulin")
infubinol_df <- filter(merge_df, Drug_Regimen == "Infubinol")
ketapril_df <- filter(merge_df, Drug_Regimen == "Ketapril")
placebo_df <- filter(merge_df, Drug_Regimen == "Placebo")


head(capomulin_df)
```

```
##   Mouse_Id Drug_Regimen    Sex Age_months Weight_g Timepoint Tumor_Volume_mm3
## 1     b128    Capomulin Female          9       22         5         45.65133
## 2     b128    Capomulin Female          9       22        25         43.26214
## 3     b128    Capomulin Female          9       22        35         37.96764
## 4     b128    Capomulin Female          9       22        10         43.27085
## 5     b128    Capomulin Female          9       22         0         45.00000
## 6     b128    Capomulin Female          9       22        40         38.37973
##   Metastatic_Sites
## 1                0
## 2                1
## 3                1
## 4                0
## 5                0
## 6                2
```

To generate a scatter plot of average tumor volume vs. mouse weight for all mice in the Capomulin regimen.

First we calculate the final tumor volume of each mouse_id across four of the treatment regimens:

(Capomulin, Infubinol, Ketapril, and Placebo)

Since not all mice lived until timepoint 45, we start by getting the last (greatest) timepoint for each mouse

capomulin_df:

```
capo_df1 <- select(capomulin_df, Mouse_Id, Timepoint, Tumor_Volume_mm3) %>%
  group_by(Mouse_Id) %>%
  filter(Timepoint == max(Timepoint, na.rm=TRUE))

head(capo_df1)
```

```
## # A tibble: 6 x 3
## # Groups:   Mouse_Id [6]
##   Mouse_Id Timepoint Tumor_Volume_mm3
##   <chr>        <int>            <dbl>
## 1 b128            45             39.0
## 2 b742            45             38.9
## 3 f966            20             30.5
## 4 g288            45             37.1
## 5 g316            45             40.2
## 6 i557            45             47.7
```

Find the average weight by mice_id in Capomulin_df

```
capo_df2 <- select(capomulin_df, Mouse_Id, Weight_g) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_weight = mean(Weight_g, na.rm=TRUE))

head(capo_df2)
```

```
## # A tibble: 6 x 2
##   Mouse_Id Average_weight
##   <chr>             <dbl>
## 1 b128                 22
## 2 b742                 21
## 3 f966                 17
## 4 g288                 19
## 5 g316                 22
## 6 i557                 24
```

Joining the two df's for adding average weight

```
capo_df <- capo_df1 %>% inner_join(capo_df2, by = "Mouse_Id")

head(capo_df)
```

```
## # A tibble: 6 x 4
## # Groups:   Mouse_Id [6]
##   Mouse_Id Timepoint Tumor_Volume_mm3 Average_weight
##   <chr>        <int>            <dbl>          <dbl>
## 1 b128            45             39.0             22
## 2 b742            45             38.9             21
## 3 f966            20             30.5             17
## 4 g288            45             37.1             19
## 5 g316            45             40.2             22
## 6 i557            45             47.7             24
```

Find the average age by mice_id in Capomulin_df

```
capo_df3 <- select(capomulin_df, Mouse_Id, Age_months) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_age = mean(Age_months, na.rm=TRUE))

head(capo_df3)
```

```
## # A tibble: 6 x 2
##   Mouse_Id Average_age
##   <chr>          <dbl>
## 1 b128               9
## 2 b742               7
## 3 f966              16
## 4 g288               3
## 5 g316              22
## 6 i557               1
```

Joining the two df's for adding average age

```
capo_df <- capo_df %>% inner_join(capo_df3, by = "Mouse_Id")

head(capo_df)
```

```
## # A tibble: 6 x 5
## # Groups:   Mouse_Id [6]
##   Mouse_Id Timepoint Tumor_Volume_mm3 Average_weight Average_age
##   <chr>        <int>            <dbl>          <dbl>       <dbl>
## 1 b128            45             39.0             22           9
## 2 b742            45             38.9             21           7
## 3 f966            20             30.5             17          16
## 4 g288            45             37.1             19           3
## 5 g316            45             40.2             22          22
## 6 i557            45             47.7             24           1
```

summerize the Tumor_Volume_mm3

```
capo_df$Tumor_Volume_mm3 %>%
  summary()
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   23.34   32.38   38.13   36.67   40.16   47.69
```

Standard Deviation

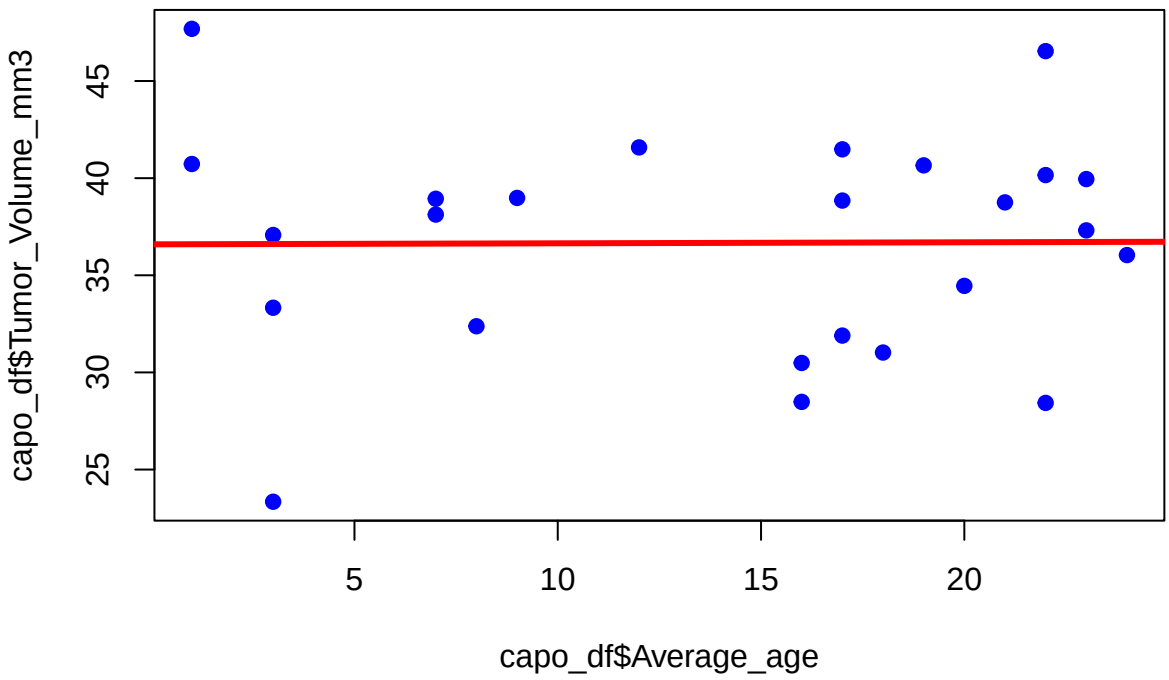
```
capo_df$Tumor_Volume_mm3 %>% sd()
```

```
## [1] 5.715188
```

For project proposal, plotting correlation matrices with all the relevant variables for Capomulin drug to analyze.

capomulin_df Vs Age_months

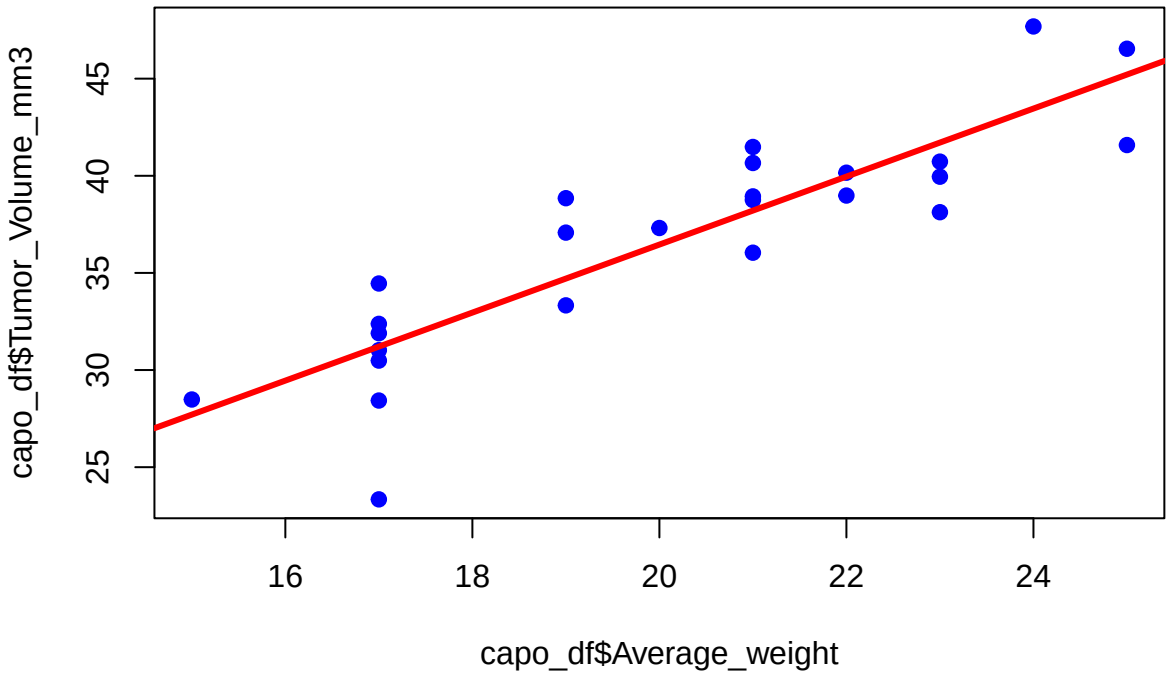
```
# Creating the plot
plot(capo_df$Average_age, capo_df$Tumor_Volume_mm3, pch = 19, col = "blue")

# Regression line
abline(lm(capo_df$Tumor_Volume_mm3 ~ capo_df$Average_age), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(capo_df$Average_age, capo_df$Tumor_Volume_mm3), 2)), x = 25, y = 95
```



capomulin_df Vs Weight_g

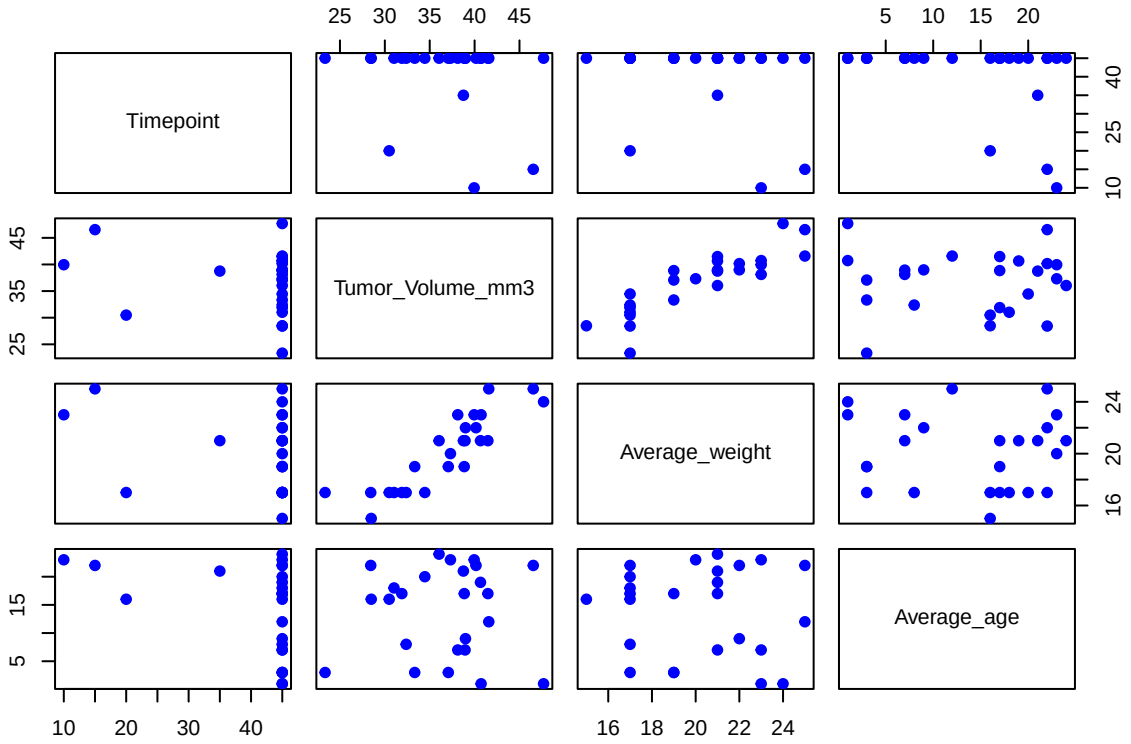
```
# Creating the plot
plot(capo_df$Average_weight, capo_df$Tumor_Volume_mm3, pch = 19, col = "blue")

# Regression line
abline(lm(capo_df$Tumor_Volume_mm3 ~ capo_df$Average_weight), col = "red", lwd = 3)
```

```
# Pearson correlation
text(paste("Correlation:", round(cor(capo_df$Average_weight, capo_df$Tumor_Volume_mm3), 2)), x = 25, y =
```



Correlation Matrix

```
pairs(capo_df[,2:5], pch = 19, col = "blue")
```



Infubinol_df:

```
infu_df1 <- select(infubinol_df, Mouse_Id, Timepoint, Tumor_Volume_mm3) %>%
  group_by(Mouse_Id) %>%
  filter(Timepoint == max(Timepoint, na.rm=TRUE))

### Find the average weight by mice_id in Infubinol_df


infu_df2 <- select(infubinol_df, Mouse_Id, Weight_g) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_weight = mean(Weight_g, na.rm=TRUE))

### Joining the two df's for adding average weight

infu_df <- infu_df1 %>% inner_join(infu_df2, by = "Mouse_Id")

### Find the average age by mice_id in Capomulin_df

infu_df3 <- select(infubinol_df, Mouse_Id, Age_months) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_age = mean(Age_months, na.rm=TRUE))

### Joining the two df's for adding average age
```

```r
infu_df <- infu_df %>% inner_join(infu_df3, by = "Mouse_Id")

head(infu_df)
```

```
## # A tibble: 6 x 5
## # Groups:   Mouse_Id [6]
##   Mouse_Id Timepoint Tumor_Volume_mm3 Average_weight Average_age
##   <chr>        <int>            <dbl>          <dbl>       <dbl>
## 1 a203            45             68.0             23          20
## 2 a251            45             65.5             25          21
## 3 a577            30             57.0             25           6
## 4 a685            45             66.1             30           8
## 5 c139            45             72.2             28          11
## 6 c326             5             36.3             25          18
```

summerize the Tumor_Volume_mm3

```r
infu_df$Tumor_Volume_mm3 %>%
  summary()
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   36.32   54.05   60.17   58.18   65.53   72.23
```

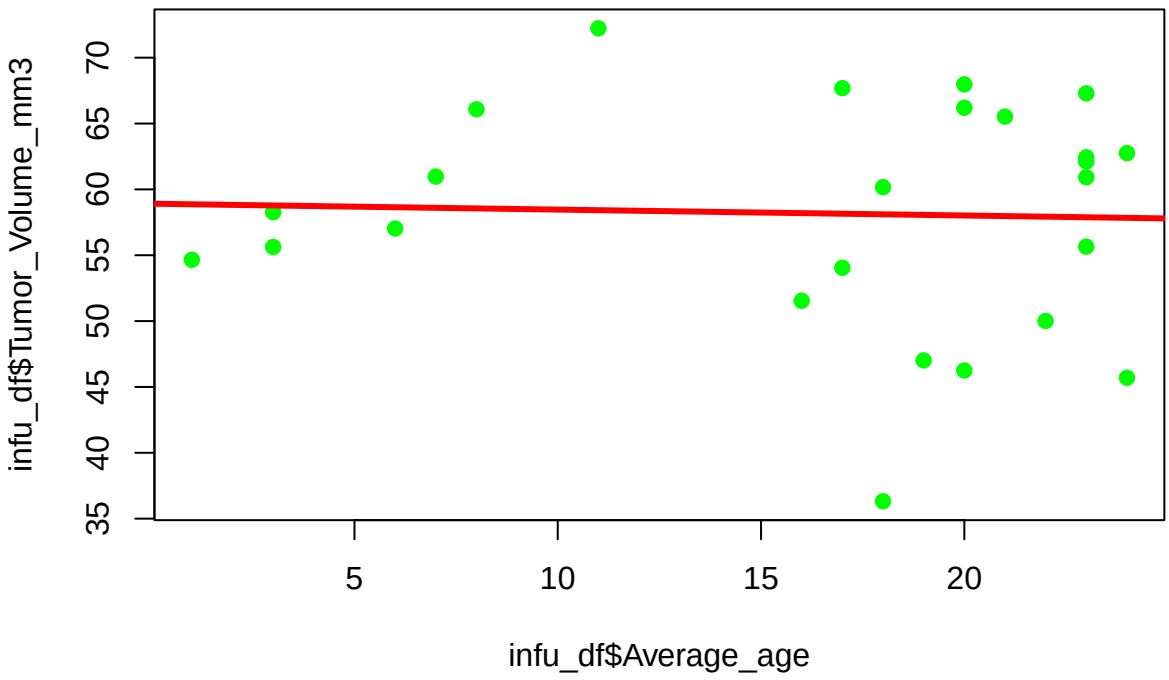
Standard Deviation

```r
infu_df$Tumor_Volume_mm3 %>% sd()
```

```
## [1] 8.602957
```

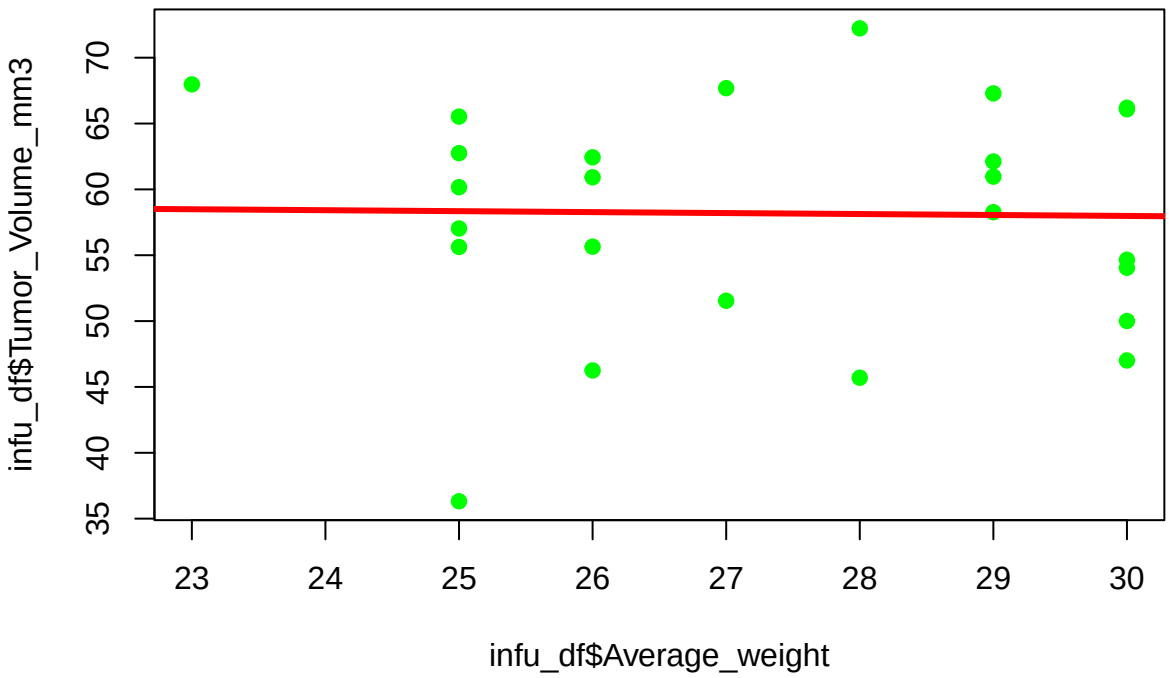
infubinol_df Vs Age_months

```r
# Creating the plot
plot(infu_df$Average_age, infu_df$Tumor_Volume_mm3, pch = 19, col = "green")

# Regression line
abline(lm(infu_df$Tumor_Volume_mm3 ~ infu_df$Average_age), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(infu_df$Average_age, infu_df$Tumor_Volume_mm3), 2)), x = 25, y = 95
```

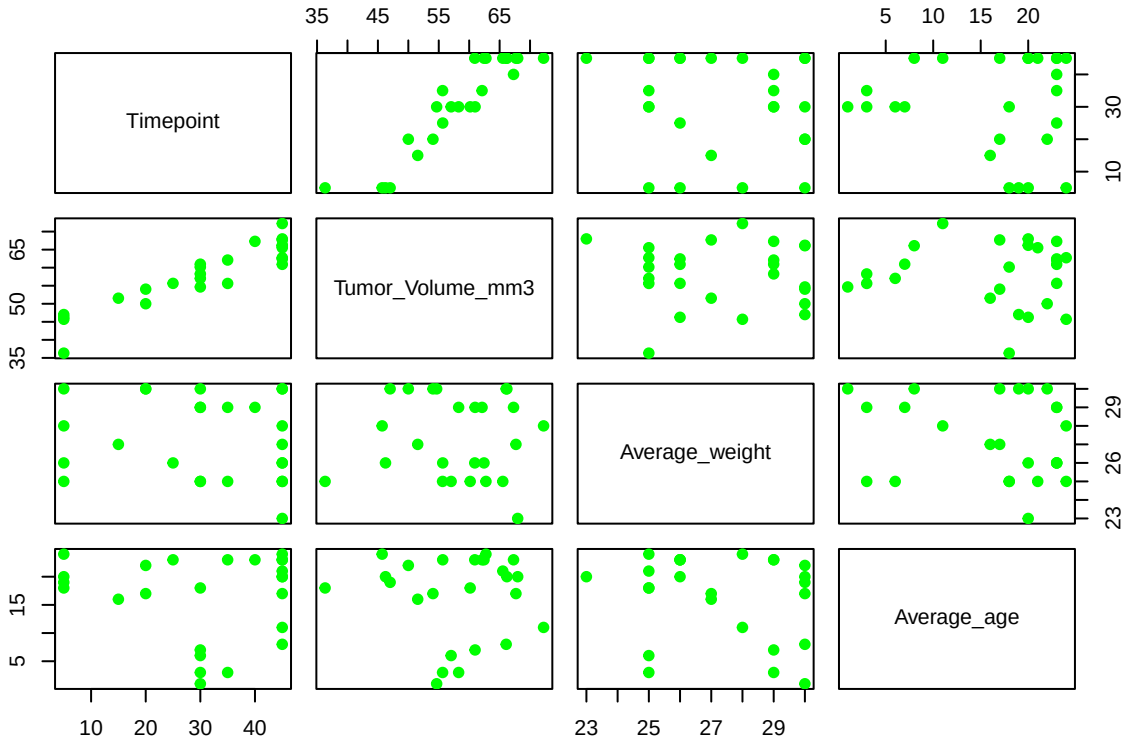


infubinol_df Vs Weight_g

```
# Creating the plot
plot(infu_df$Average_weight, infu_df$Tumor_Volume_mm3, pch = 19, col = "green")

# Regression line
abline(lm(infu_df$Tumor_Volume_mm3 ~ infu_df$Average_weight), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(infu_df$Average_weight, infu_df$Tumor_Volume_mm3), 2)), x = 25, y =
```




```
pairs(infu_df[,2:5], pch = 19, col = "green")
```



ketapril_df:

```
keta_df1 <- select(ketapril_df, Mouse_Id, Timepoint, Tumor_Volume_mm3) %>%
  group_by(Mouse_Id) %>%
  filter(Timepoint == max(Timepoint, na.rm=TRUE))

### Find the average weight by mice_id in Infubinol_df


keta_df2 <- select(ketapril_df, Mouse_Id, Weight_g) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_weight = mean(Weight_g, na.rm=TRUE))

### Joining the two df's for adding average weight

keta_df <- keta_df1 %>% inner_join(keta_df2, by = "Mouse_Id")

### Find the average age by mice_id in Capomulin_df

keta_df3 <- select(ketapril_df, Mouse_Id, Age_months) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_age = mean(Age_months, na.rm=TRUE))

### Joining the two df's for adding average age
```

```r
keta_df <- keta_df %>% inner_join(keta_df3, by = "Mouse_Id")

head(keta_df)
```

```
## # A tibble: 6 x 5
## # Groups:   Mouse_Id [6]
##   Mouse_Id Timepoint Tumor_Volume_mm3 Average_weight Average_age
##   <chr>        <int>            <dbl>          <dbl>       <dbl>
## 1 a457            10             49.8             30          11
## 2 c580            30             58.0             25          22
## 3 c819            40             62.2             25          21
## 4 c832            45             65.4             29          18
## 5 d474            40             60.2             27          18
## 6 f278             5             48.2             30          12
```

summerize the Tumor_Volume_mm3

```r
keta_df$Tumor_Volume_mm3 %>%
  summary()
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   45.00   56.72   64.49   62.81   69.87   78.57
```

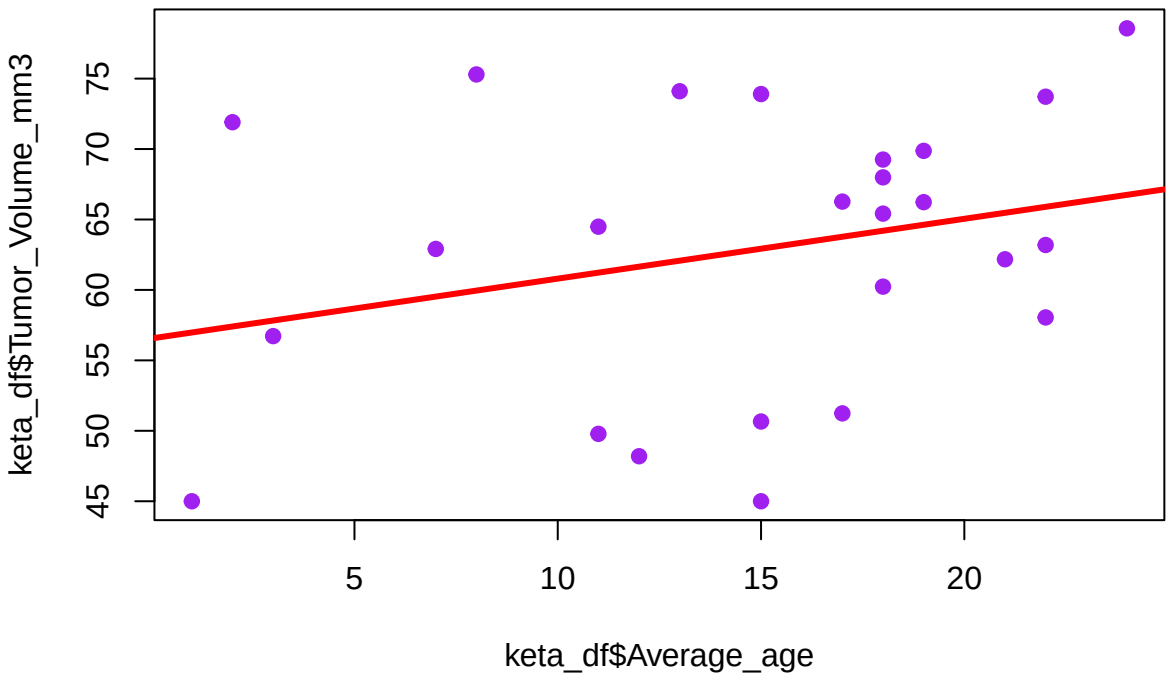
Standard Deviation

```r
keta_df$Tumor_Volume_mm3 %>% sd()
```

```
## [1] 9.94592
```

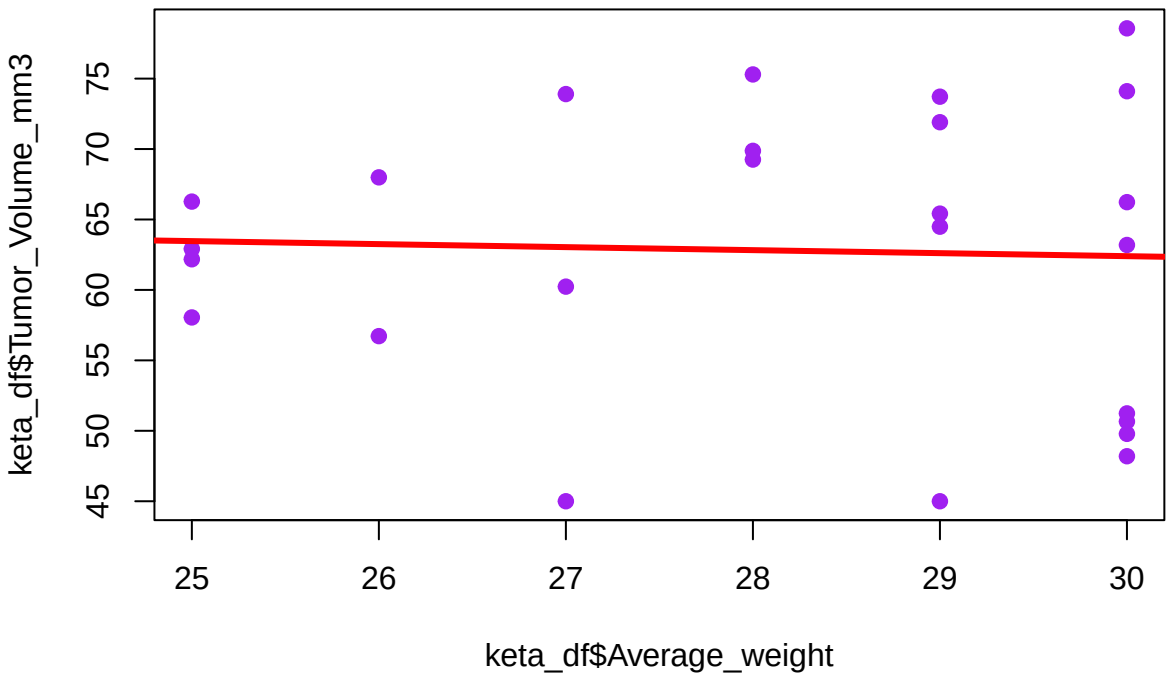
ketapril_df Vs Age_months

```r
# Creating the plot
plot(keta_df$Average_age, keta_df$Tumor_Volume_mm3, pch = 19, col = "purple")

# Regression line
abline(lm(keta_df$Tumor_Volume_mm3 ~ keta_df$Average_age), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(keta_df$Average_age, keta_df$Tumor_Volume_mm3), 2)), x = 25, y = 95
```

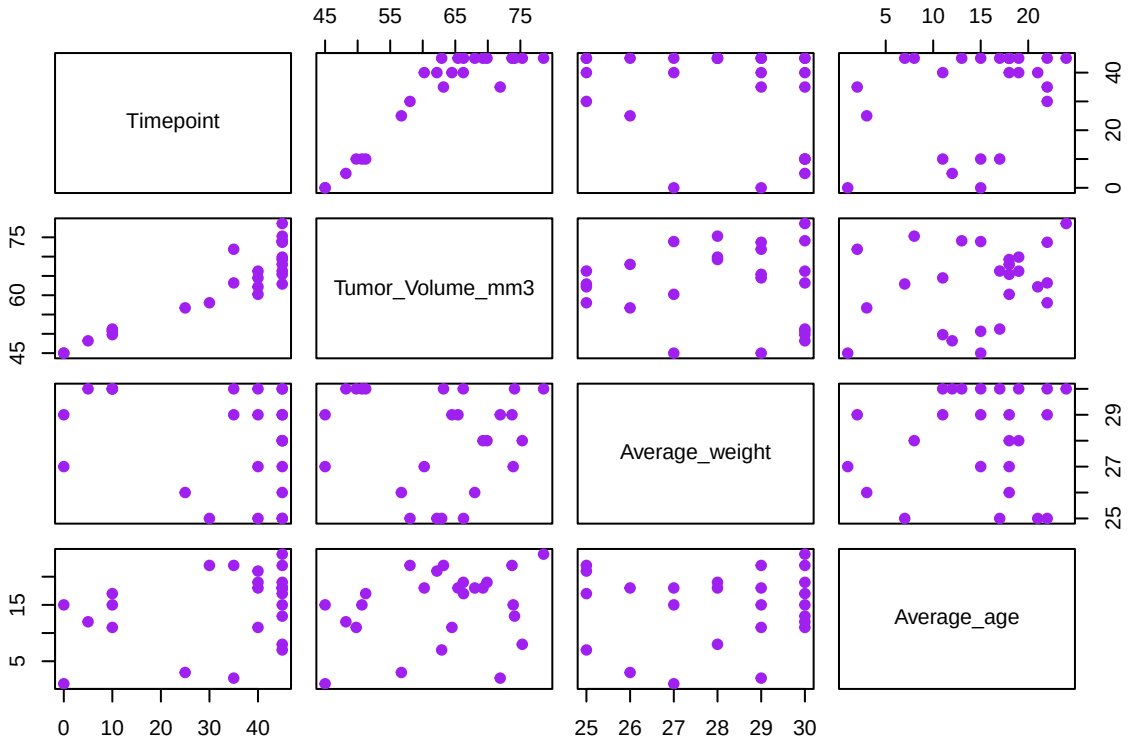


ketapril_df Vs Weight_g

```
# Creating the plot
plot(keta_df$Average_weight, keta_df$Tumor_Volume_mm3, pch = 19, col = "purple")

# Regression line
abline(lm(keta_df$Tumor_Volume_mm3 ~ keta_df$Average_weight), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(keta_df$Average_weight, keta_df$Tumor_Volume_mm3), 2)), x = 25, y =
```




```
pairs(keta_df[,2:5], pch = 19, col = "purple")
```



placebo_df:

```
plac_df1 <- select(placebo_df, Mouse_Id, Timepoint, Tumor_Volume_mm3) %>%
  group_by(Mouse_Id) %>%
  filter(Timepoint == max(Timepoint, na.rm=TRUE))

### Find the average weight by mice_id in Infubinol_df


plac_df2 <- select(placebo_df, Mouse_Id, Weight_g) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_weight = mean(Weight_g, na.rm=TRUE))

### Joining the two df's for adding average weight

plac_df <- plac_df1 %>% inner_join(plac_df2, by = "Mouse_Id")

### Find the average age by mice_id in Capomulin_df

plac_df3 <- select(placebo_df, Mouse_Id, Age_months) %>%
  group_by(Mouse_Id) %>%
 summarise(Average_age = mean(Age_months, na.rm=TRUE))

### Joining the two df's for adding average age
```

```r
plac_df <- plac_df %>% inner_join(plac_df3, by = "Mouse_Id")

head(plac_df)
```

```
## # A tibble: 6 x 5
## # Groups:   Mouse_Id [6]
##   Mouse_Id Timepoint Tumor_Volume_mm3 Average_weight Average_age
##   <chr>        <int>            <dbl>          <dbl>       <dbl>
## 1 a262            45             70.7             29          17
## 2 a897            45             72.3             28           7
## 3 c282            45             65.8             27          12
## 4 c757            45             69.0             27           9
## 5 c766            45             69.8             26          13
## 6 e227            45             73.2             30           1
```

summerize the Tumor_Volume_mm3

```r
plac_df$Tumor_Volume_mm3 %>%
  summary()
```

```
##    Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
##   45.00   52.94   62.03   60.51   68.13   73.21
```

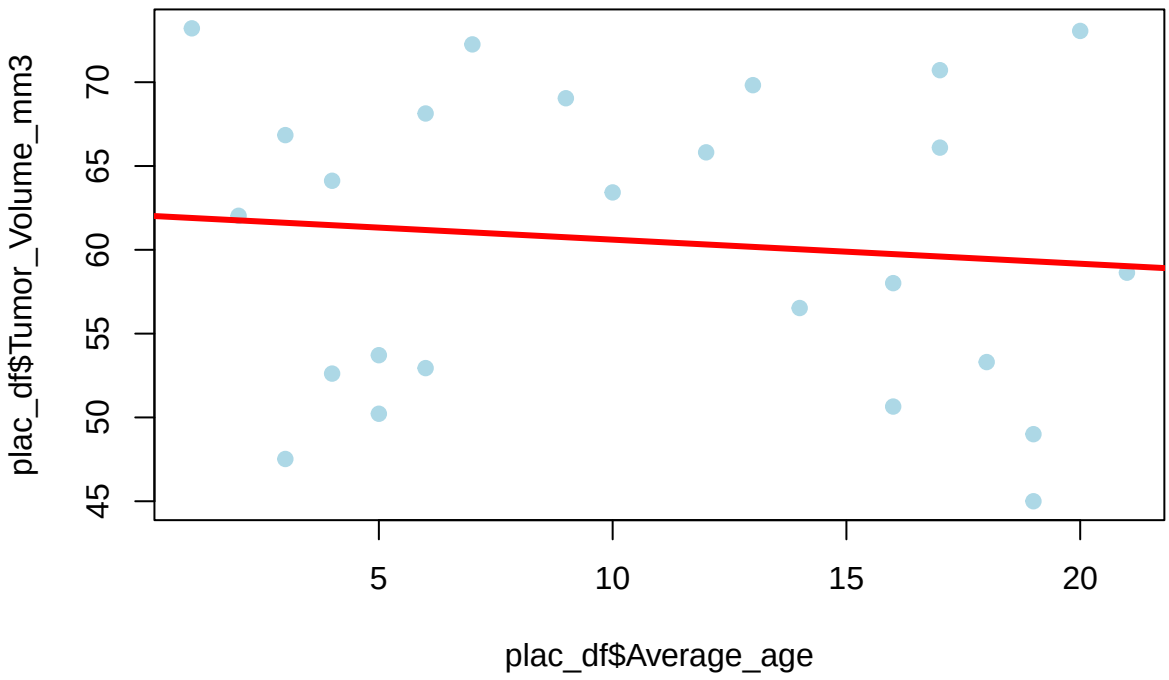
Standard Deviation

```r
plac_df$Tumor_Volume_mm3 %>% sd()
```

```
## [1] 8.874672
```

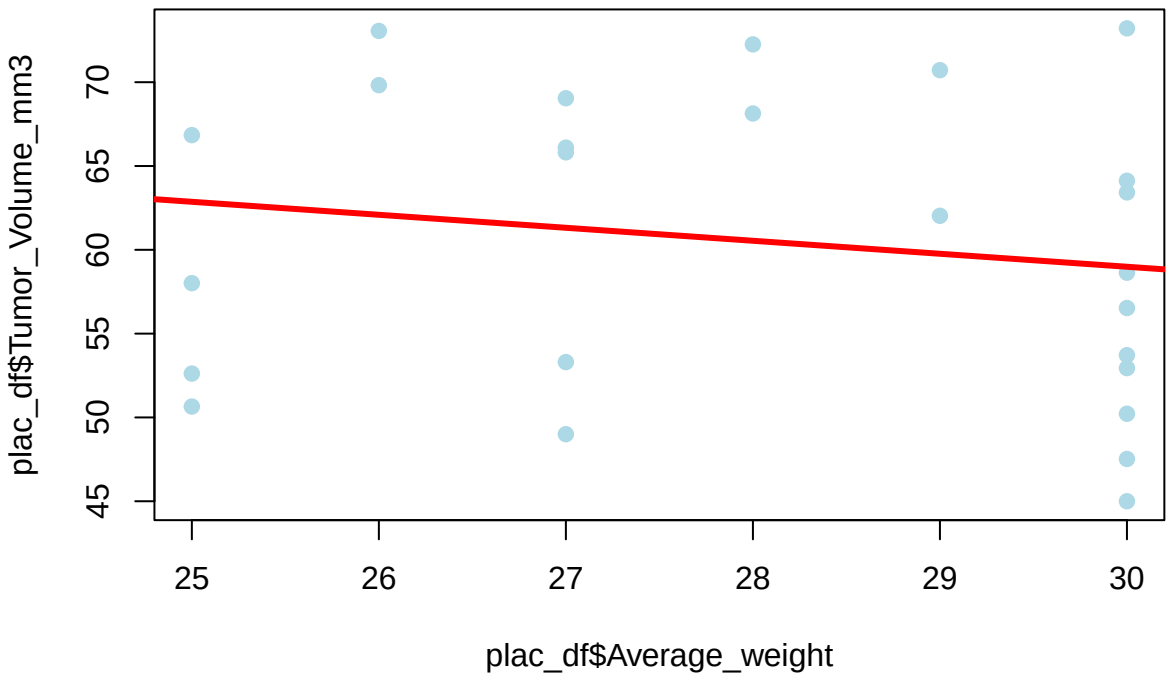
placebo_df Vs Age_months

```r
# Creating the plot
plot(plac_df$Average_age, plac_df$Tumor_Volume_mm3, pch = 19, col = "lightblue")

# Regression line
abline(lm(plac_df$Tumor_Volume_mm3 ~ plac_df$Average_age), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(plac_df$Average_age, plac_df$Tumor_Volume_mm3), 2)), x = 25, y = 95
```

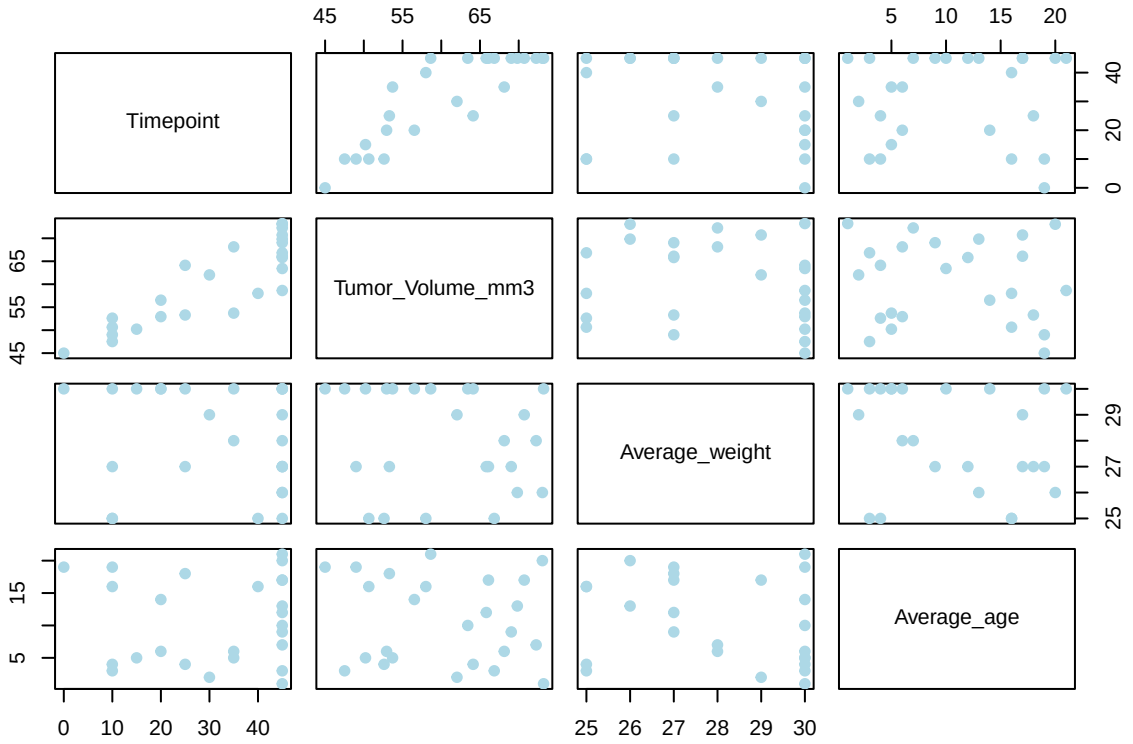


placebo_df Vs Weight_g

```
# Creating the plot
plot(plac_df$Average_weight, plac_df$Tumor_Volume_mm3, pch = 19, col = "lightblue")

# Regression line
abline(lm(plac_df$Tumor_Volume_mm3 ~ plac_df$Average_weight), col = "red", lwd = 3)

# Pearson correlation
text(paste("Correlation:", round(cor(plac_df$Average_weight, plac_df$Tumor_Volume_mm3), 2)), x = 25, y =
```




```
pairs(plac_df[,2:5], pch = 19, col = "lightblue")
```



Conclusion:

From the plots above, there seems a correlation between weight and Tumor size for capomulin drug regimen but will be checked by calculating the correlation coefficient.