Gene Expression - Karl 1

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#Inserting Code

```
data<-read_csv(here::here("raw-data", "Gene_Expression.csv"))
```

```
## Rows: 88 Columns: 5
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## chr (3): Cell_Line, Treatment, Cell Line_Treatment
## dbl (2): Concentration, Gene_Expression
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
data
```

```
## # A tibble: 88 x 5
##    Cell_Line Concentration Treatment Gene_Expression `Cell Line_Treatment`
##    <chr>             <dbl> <chr>               <dbl> <chr>
##  1 Wild Type             0 Placebo              5.51 Wild TypePlacebo
##  2 Wild Type             1 Placebo              6.41 Wild TypePlacebo
##  3 Wild Type             2 Placebo              5.71 Wild TypePlacebo
##  4 Wild Type             3 Placebo              7.94 Wild TypePlacebo
##  5 Wild Type             4 Placebo              6.87 Wild TypePlacebo
##  6 Wild Type             5 Placebo              7.29 Wild TypePlacebo
##  7 Wild Type             6 Placebo             10.0  Wild TypePlacebo
##  8 Wild Type             7 Placebo              8.85 Wild TypePlacebo
##  9 Wild Type             8 Placebo              8.91 Wild TypePlacebo
## 10 Wild Type             9 Placebo              9.68 Wild TypePlacebo
## # ... with 78 more rows
```

#Clean

```
skimr::skim_without_charts(data)
```

Table 1: Data summary

Name	data
Number of rows	88
Number of columns	5
Column type frequency:	
character	3
numeric	2
Group variables	None

Variable type: character

skim_variable	n_missing	complete_rate	min	max	empty	n_unique	whitespace
Cell_Line	0	1	9	13	0	2	0
Treatment	0	1	7	20	0	2	0
Cell Line_Treatment	0	1	16	33	0	4	0

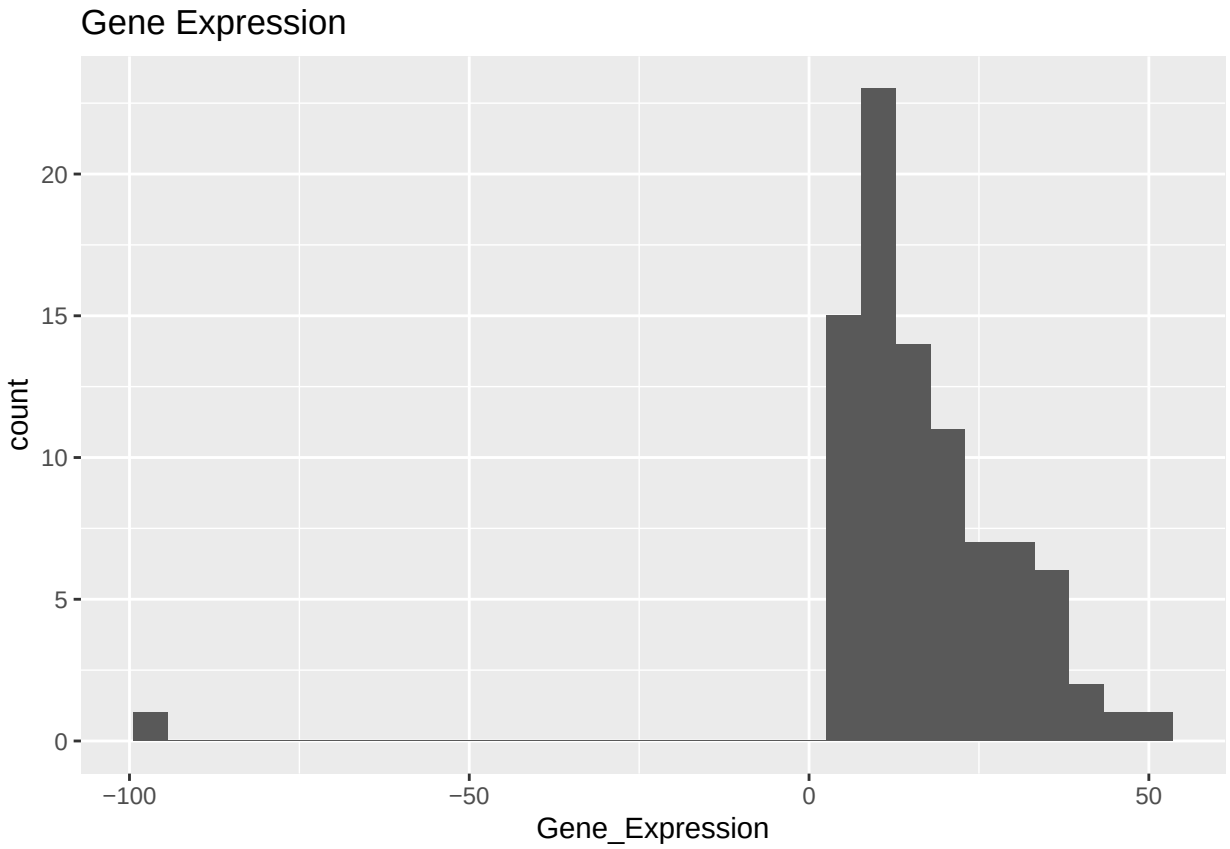
Variable type: numeric

skim_variable	n_missing	complete_rate	mean	sd	p0	p25	p50	p75	p100
Concentration	0	1	5.00	3.18	0	2.00	5.00	8.00	10.00
Gene_Expression	0	1	16.14	16.45	-99	8.96	14.82	24.28	48.96

#Investigate gene expression

```
data |> ggplot(aes(x=Gene_Expression)) + geom_histogram() + ggtitle("Gene Expression")
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



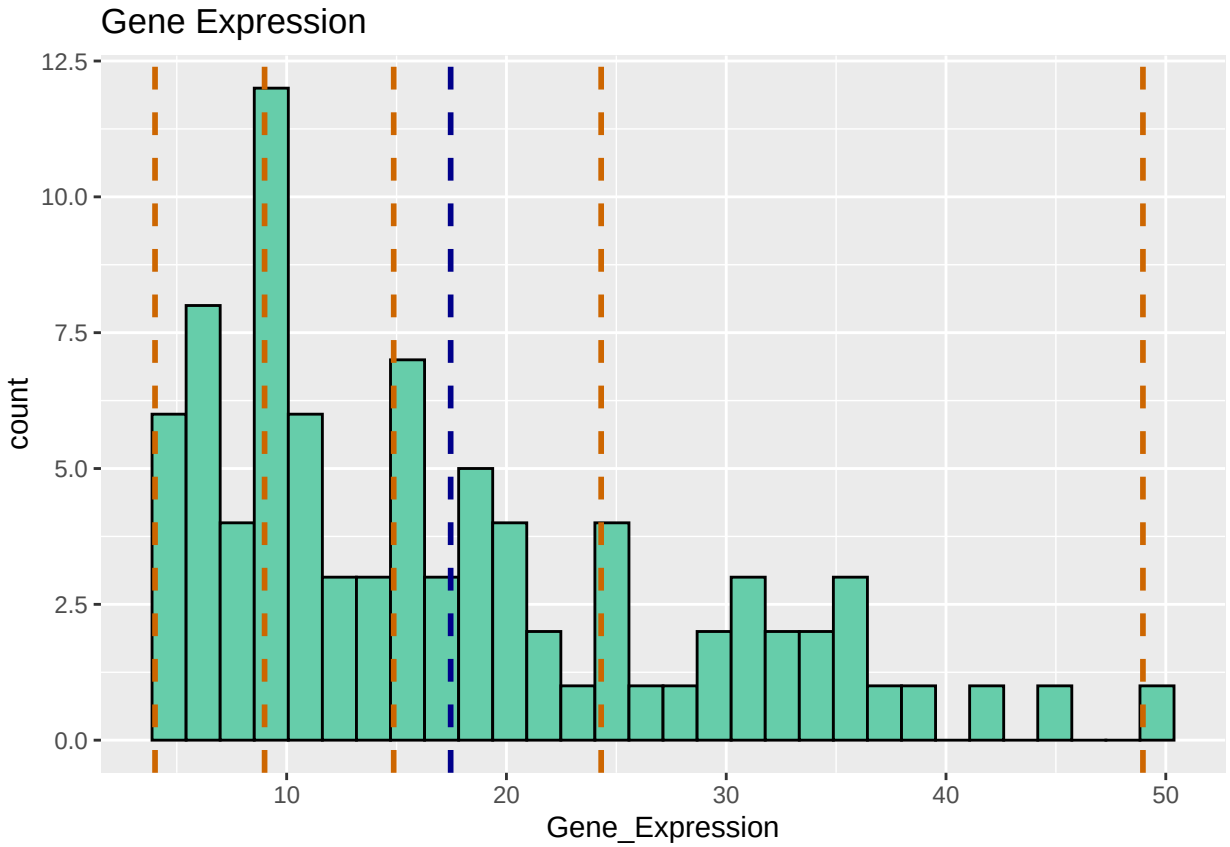

```
#We can see there is a value of -99 which has been entered incorrectly - we will set this to NA

data <- data |> filter(Gene_Expression>0)

five<- fivenum(data$Gene_Expression)
```

```
data |> ggplot(aes(x=Gene_Expression)) +
  geom_histogram(fill="mediumaquamarine", col="black") +
  ggtitle("Gene Expression") +
  geom_vline(aes(xintercept=mean(Gene_Expression)),col="darkblue",linetype="dashed",size=1)  +
  scale_color_brewer(palette="Dark2") +
  geom_vline(aes(xintercept=five[1]),col="darkorange3",linetype="dashed",size=1) +
  geom_vline(aes(xintercept=five[2]),col="darkorange3",linetype="dashed",size=1) +
  geom_vline(aes(xintercept=five[3]),col="darkorange3",linetype="dashed",size=1) +
  geom_vline(aes(xintercept=five[4]),col="darkorange3",linetype="dashed",size=1) +
  geom_vline(aes(xintercept=five[5]),col="darkorange3",linetype="dashed",size=1)
```

```
## `stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```



#Investigate cell line

```
class(data$Cell_Line)
```

```
## [1] "character"
```

```
table(data$Cell_Line)
```

```
##
## Cell Type 101     Wild Type
##            44            43
```

#Investigate Concentration

```
class(data$Concentration)
```

```
## [1] "numeric"
```

```
table(data$Concentration)
```

```
##
##  0  1  2  3  4  5  6  7  8  9 10
##  8  8  8  8  8  7  8  8  8  8  8
```

#Investigate Treatment

```
class(data$Treatment)
```

```
## [1] "character"
```

```
table(data$Treatment)
```

```
##
## Activating Factor 42              Placebo
##                   43                   44
```

#Gene Expression box plot + points

```
data |> ggplot(aes(x=Gene_Expression, fill=Treatment)) +
  geom_dotplot(dotsize=1.2) +
  scale_fill_manual(values=c("Placebo" = "deepskyblue1",
                             "Activating Factor 42"="magenta1")) +
  ggtitle("Dot Plot of Gene Expression coloured by Treatment")
```

```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```


```
data |> ggplot(aes(x=Gene_Expression, fill=Cell_Line)) +
  geom_dotplot(dotsize=1.2) +
  scale_fill_manual(values=c("Wild Type" = "springgreen3",
```

```
                                "Cell Type 101"="darkorchid2")) +
  ggtitle("Dot Plot of Gene Expression coloured by Cell Line")
```

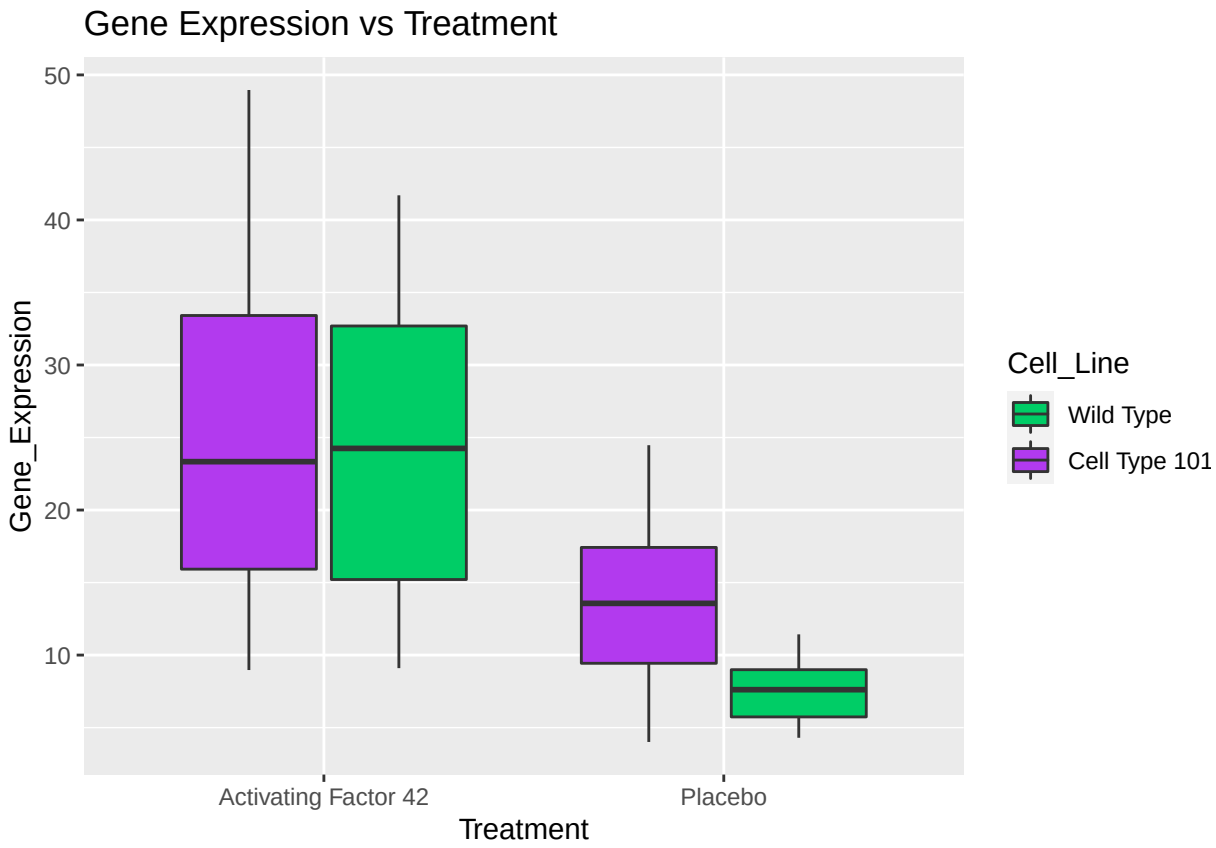
```
## Bin width defaults to 1/30 of the range of the data. Pick better value with `binwidth`.
```

#Plots

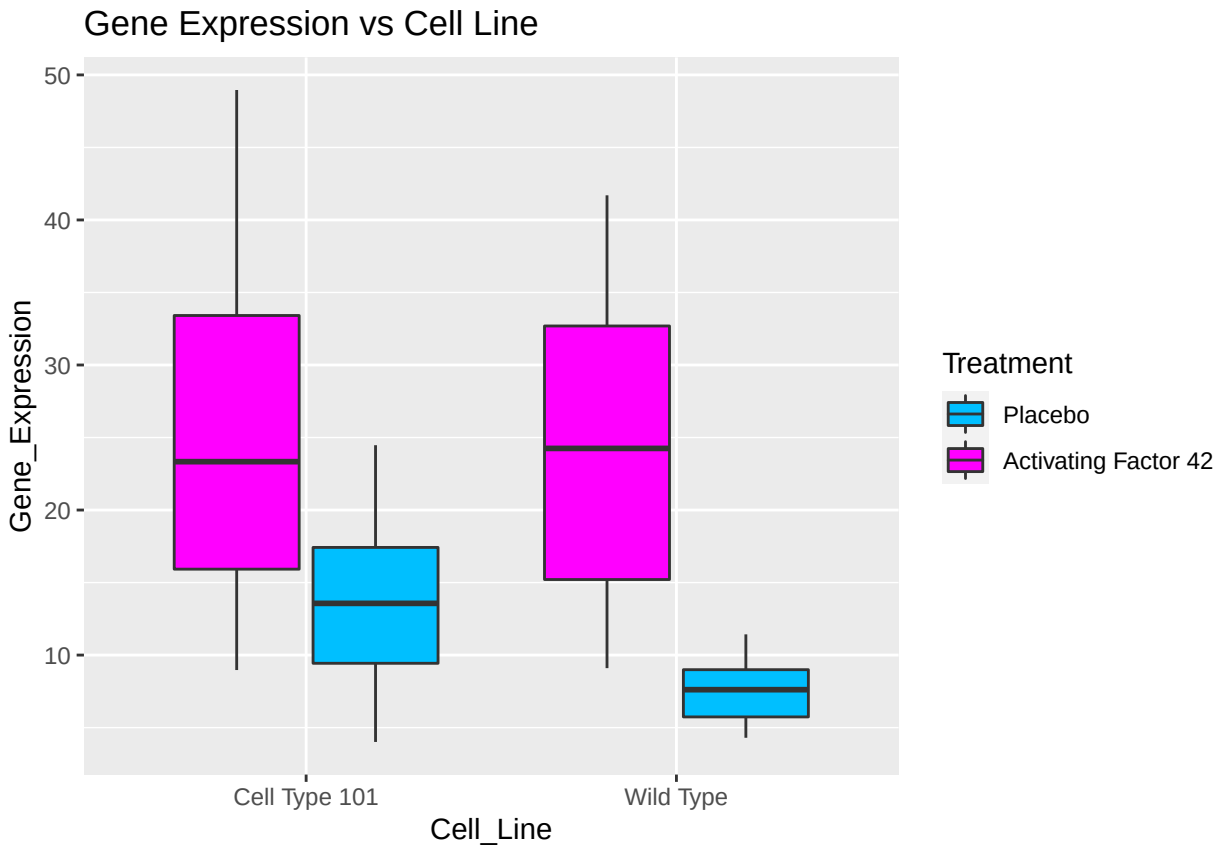
```
sum <- data |> group_by(Cell_Line) |> summarize(min=fivenum(Gene_Expression)[1],
                                                Q1=fivenum(Gene_Expression)[2],
                                                Med=fivenum(Gene_Expression)[3],
                                                Q3=fivenum(Gene_Expression)[4],
                                                max=fivenum(Gene_Expression)[5])
sum
```

```
## # A tibble: 2 x 6
##   Cell_Line       min    Q1   Med    Q3   max
##   <chr>         <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Cell Type 101  4.01 11.6   17.0  24.4  49.0
## 2 Wild Type      4.3   7.62  10.0  24.0  41.7
```

```
data |> ggplot(aes(x=Treatment, y=Gene_Expression,fill=Cell_Line)) +
  geom_boxplot() +
  scale_fill_manual(values=c("Wild Type" = "springgreen3",
                             "Cell Type 101"="darkorchid2")) + ggtitle("Gene Expression vs Treatment")
```




```
data |> ggplot(aes(x=Cell_Line, y=Gene_Expression,fill=Treatment)) +
  geom_boxplot() +
  scale_fill_manual(values=c("Placebo" = "deepskyblue1",
                             "Activating Factor 42"="magenta1")) +
  ggtitle("Gene Expression vs Cell Line")
```




```
sum2 <- data |> group_by(Treatment,Cell_Line) |> summarize(min=fivenum(Gene_Expression)[1],
                                                           Q1=fivenum(Gene_Expression)[2],
                                                           Med=fivenum(Gene_Expression)[3],
                                                           Q3=fivenum(Gene_Expression)[4],
                                                           max=fivenum(Gene_Expression)[5])
```

```
## `summarise()` has grouped output by 'Treatment'. You can override using the
## `.groups` argument.
```

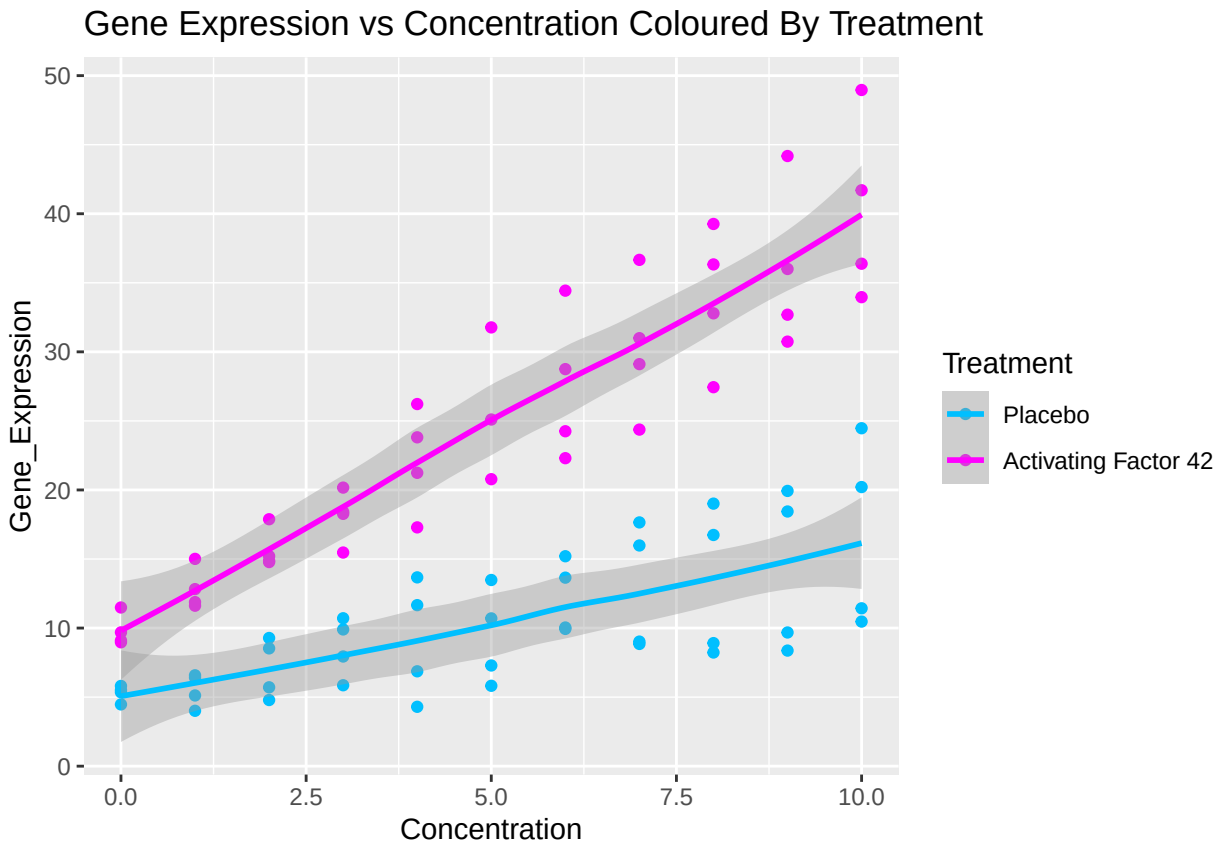
```
sum2
```

```
## # A tibble: 4 x 7
## # Groups:   Treatment [2]
##   Treatment            Cell_Line       min    Q1   Med    Q3   max
##   <chr>                <chr>         <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 Activating Factor 42 Cell Type 101  8.97 15.5  23.3  34.0   49.0
## 2 Activating Factor 42 Wild Type      9.1  15.2  24.2  32.7   41.7
## 3 Placebo              Cell Type 101  4.01  9.28 13.6  17.6   24.5
## 4 Placebo              Wild Type      4.3   5.71  7.62  9.02  11.4
```

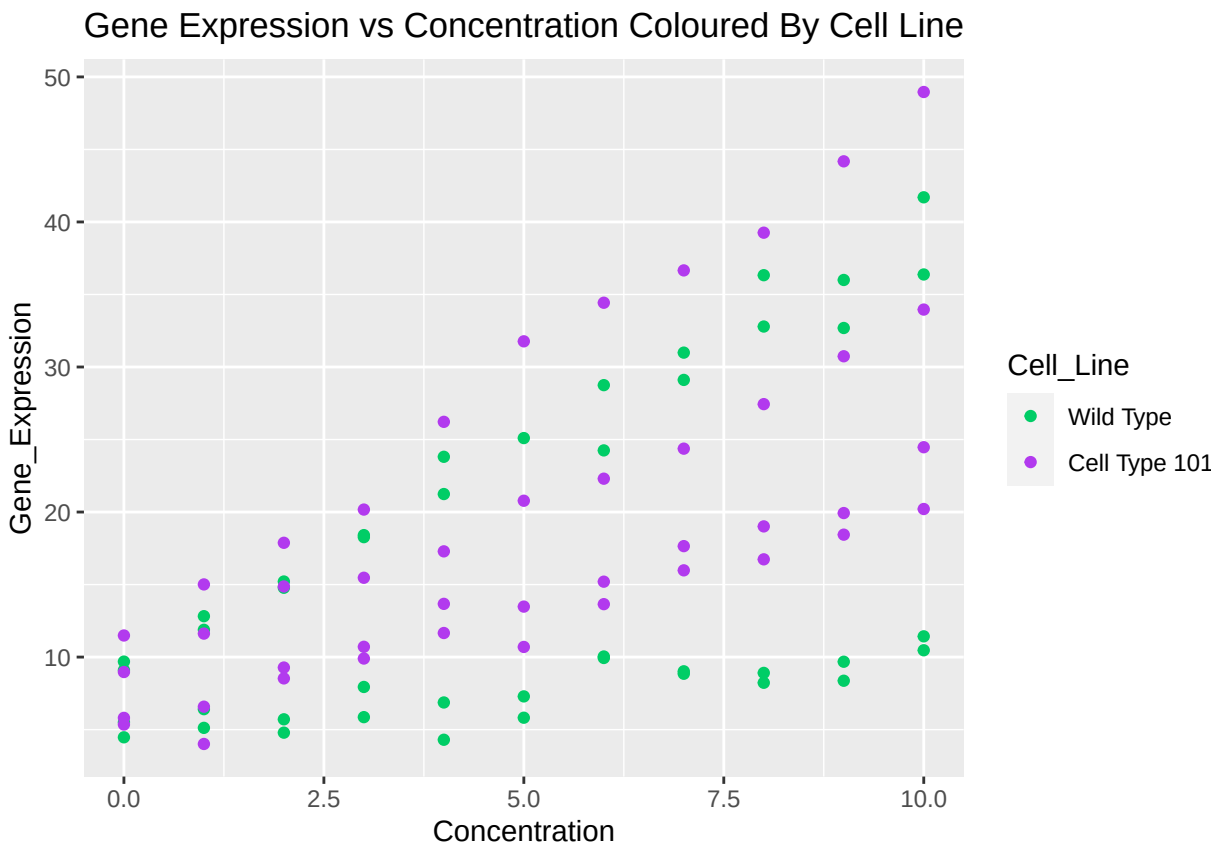
```
data |> ggplot(aes(x=Concentration, y=Gene_Expression, col=Treatment)) +
  geom_point(line="black") + geom_smooth() +
  scale_colour_manual(values=c("Placebo" = "deepskyblue1",
                               "Activating Factor 42"="magenta1")) +
  ggtitle("Gene Expression vs Concentration Coloured By Treatment")
```

```
## Warning: Ignoring unknown parameters: line
```

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

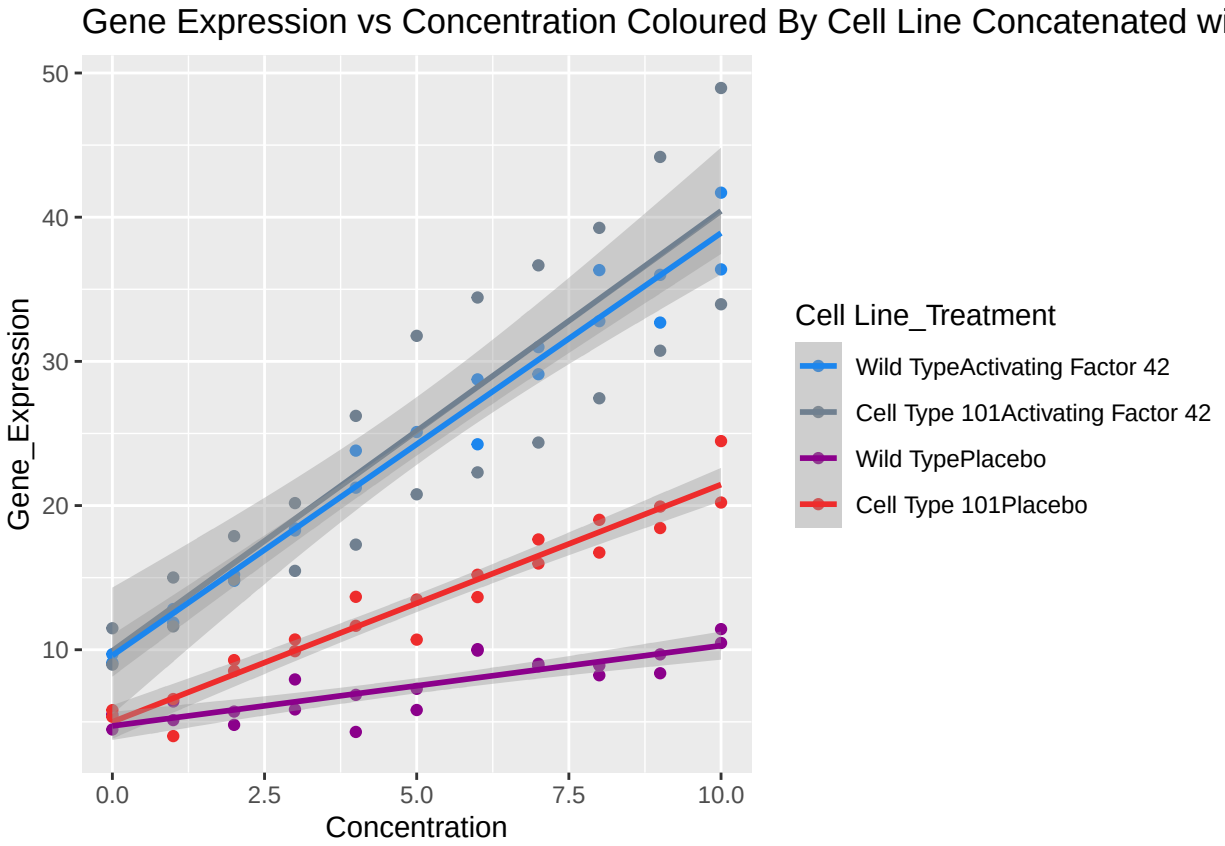



```
data |> ggplot(aes(x=Concentration, y=Gene_Expression, col=Cell_Line)) +
  geom_point() +
  scale_colour_manual(values=c("Wild Type" = "springgreen3",
                               "Cell Type 101"="darkorchid2")) +ggtitle("Gene Expression vs Concentrati
```




```
data |> ggplot(aes(x=Concentration, y=Gene_Expression, col=`Cell Line_Treatment`)) +
  geom_point() + geom_smooth(method=lm) +
  ggtitle("Gene Expression vs Concentration Coloured By Cell Line Concatenated with Treatment") +
  scale_colour_manual(values=c("Wild TypeActivating Factor 42"="dodgerblue2",
                               "Cell Type 101Activating Factor 42"="slategray",
                               "Wild TypePlacebo"="darkmagenta",
                               "Cell Type 101Placebo"="firebrick2"))
```

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



#Make a table

```
Cell1<-data |>
  group_by(Cell_Line) |>
  summarise(Mean=mean(Gene_Expression), SD=sd(Gene_Expression))

gt_data1<-
  gt(Cell1) |>
  tab_header(title="Table 1: Mean of Gene Expression for each Cell Line")
gt_data1 |>
cols_label(Cell_Line="Cell Line",Mean="Mean", SD="Standard Deviation")
```

Table 1: Mean of Gene Expression for each Cell Line

Cell Line	Mean	Standard Deviation
Cell Type 101	19.20000	10.57852
Wild Type	15.68209	10.97189

#Make a table 2

```
Treat1<-data |>
  group_by(Treatment) |>
  summarise(Mean=mean(Gene_Expression), SD=sd(Gene_Expression))

gt_data2<-
  gt(Treat1) |>
  tab_header(title="Table 2: Mean of Gene Expression for each Treatment")
```

```
gt_data2 |>
cols_label(Mean="Mean", SD="Standard Deviation")
```

Table 2: Mean of Gene Expression for each Treatment

Treatment	Mean	Standard Deviation
Activating Factor 42	24.72419	10.421329
Placebo	10.36341	5.036591

#Make a table 3

```
five_num<-data |>
  group_by(Treatment) |>
  summarise(fivenum=fivenum(Gene_Expression))
```

```
## `summarise()` has grouped output by 'Treatment'. You can override using the
## `.groups` argument.
```

```
five_num
```

```
## # A tibble: 10 x 2
## # Groups:   Treatment [2]
##    Treatment            fivenum
##    <chr>                  <dbl>
##  1 Activating Factor 42    8.97
##  2 Activating Factor 42   15.3
##  3 Activating Factor 42   24.2
##  4 Activating Factor 42   32.7
##  5 Activating Factor 42   49.0
##  6 Placebo                 4.01
##  7 Placebo                 6.14
##  8 Placebo                 9.15
##  9 Placebo                13.6
## 10 Placebo                24.5
```