Home work 1

Homework 1 - to be done as groups

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Group: 3

For deadlines etc, see absalon.

You have to supply botbh the answer (whatever it is: numbers, a table, plots or combinations thereof), as well as the R or Linux code you used to make the plots. This should be done using this R markdown template: we want both the R markdown file and a resulting PDF. For PDF output, you may have to install some extra programs - R studio will tell you.

Note that:

1. If the R code gives different results than your results, you will get severe point reductions or even 0 points for the exercise
2. Some questions may request you to use R options we have not covered explicitly in the course: this is part of the challenge
3. While this is a group work, we expect that everyone in the group will have understood the group solution: similar or harder question might show up in the individual homework. So, if something is hard, it means you need to spend more time on it
4. The results should be presented on a level of detail that someone else could replicate the analysis.

For statistical tests, you have to:

1) Motivate the choice of test
2) State exactly what the null hypothesis is (depends on test!)
3) Comment the outcome: do you reject the null hypothesis or not, and what does this mean for the actual question we wanted to answer (interpretation)?

Question 1

Install the package babynames and look at the data babynames:

```r
install.packages("babynames")
```

```r
library(babynames)
head(babynames)
```

```
## # A tibble: 6 x 5
##    year sex   name          n   prop
##   <dbl> <chr> <chr>     <int>  <dbl>
## 1  1880 F     Mary       7065 0.0724
## 2  1880 F     Anna       2604 0.0267
## 3  1880 F     Emma       2003 0.0205
## 4  1880 F     Elizabeth  1939 0.0199
## 5  1880 F     Minnie     1746 0.0179
## 6  1880 F     Margaret   1578 0.0162
```

a) List the top 5 female baby names starting with P, regardless of year, as a table.

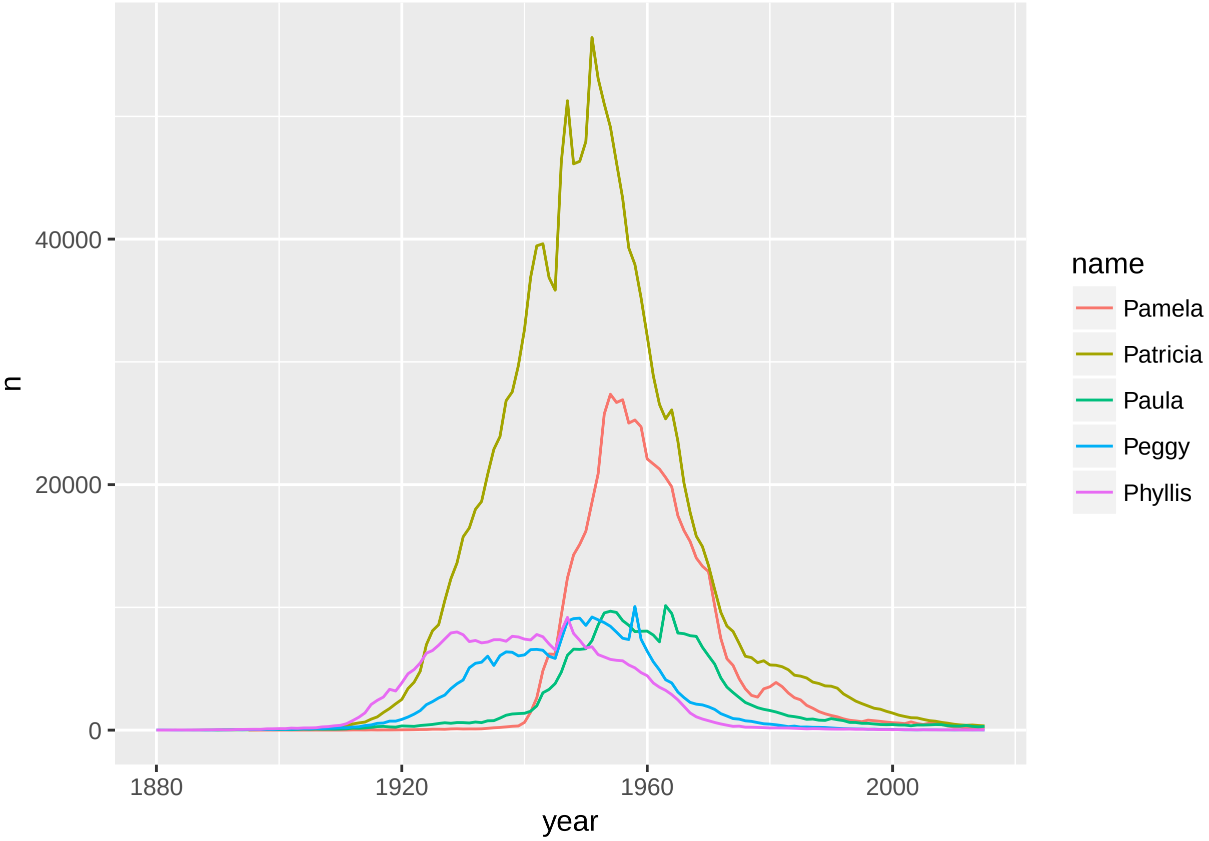
```
filter(babynames, str_detect(name, "^P"), sex=='F' ) %>%
  group_by(name) %>%
  summarise(count = sum(n)) %>%
  arrange(desc(count)) -> tableQ1
tableQ1[1:5,]
```

```
## # A tibble: 5 x 2
##   name        count
##   <chr>       <int>
## 1 Patricia 1570954
## 2 Pamela    593837
## 3 Phyllis   322316
## 4 Peggy     292535
## 5 Paula     277326
```

b) Using the results from a, plot their occurrences as a function of year using a line plot. Comment on your results. If you get strange results, explain them and/or improve the plot.

```
P_names_full<-filter(babynames, name %in% tableQ1$name[1:5], sex=='F')

ggplot(P_names_full)+geom_line(data=P_names_full, mapping = aes(x=year, y=n, col=name))
```



In the question we were asked to explain the reason for getting strange results. We think that we do not see any strange result because since we saw that some of the names correspond to both male and female, we have already filter by ‘sex=F’ and thus, the ‘strange lines’ disapeared.

Question 2

In the same dataset, is the name Arwen significantly more (or less) common in 2004 vs 1990? Is the change significant? What is the likely cause? Do not use hard-coding.

```
name_filter = 'Arwen'
year1='1990'
year2='2004'

arwen_1990<-filter(babynames, name==name_filter, year==year1)$n
arwen_2004<-filter(babynames, name==name_filter, year==year2)$n

no_arwen_2004<-filter(babynames, name!=name_filter, year==year2)
n_no_arwen_2004<-sum(no_arwen_2004$n)

no_arwen_1990<-filter(babynames, name!=name_filter, year==year1)
n_no_arwen_1990<-sum(no_arwen_1990$n)

table_names<-matrix(c(arwen_1990, n_no_arwen_1990, arwen_2004, n_no_arwen_2004), nrow = 2)
rownames(table_names)<-c('Arwen', 'No Arwen')
colnames(table_names)<-c(year1, year2)
fisher.test(table_names)
```

```
##
##  Fisher's Exact Test for Count Data
##
## data:  table_names
## p-value < 2.2e-16
## alternative hypothesis: true odds ratio is not equal to 1
## 95 percent confidence interval:
##  0.02737561 0.10976830
## sample estimates:
## odds ratio
## 0.05820022
```

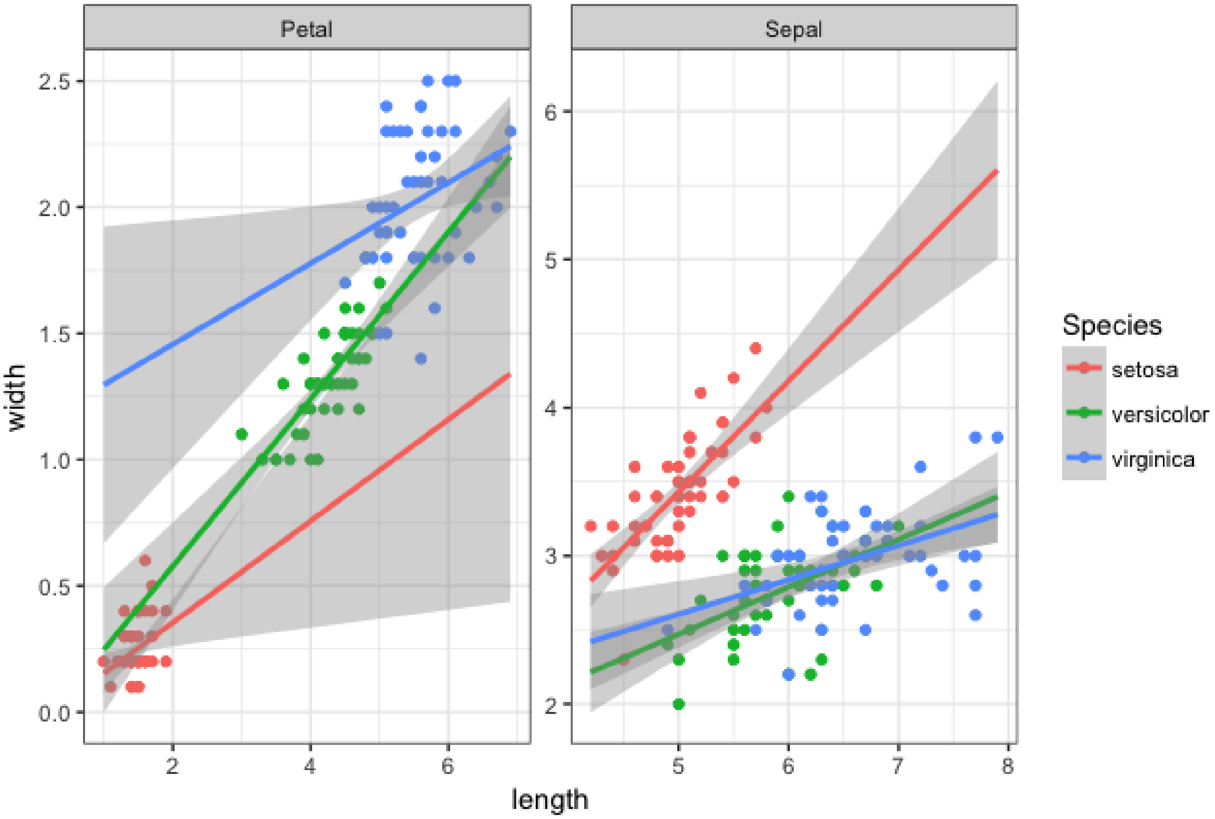
```
p_value_Q2<-fisher.test(table_names)$'p.value'
```

We use the Fisher test, since we want to test proportions on counts: the null hypothesis is there is no relation between row and columns, i.e. there is no relation beween number of babies named Arwen and the year.

With a p-value < 2.2e-16, we can reject the null hypothesis. Arwen is the name of one of the characters from "The Lord of The Rings" trilogy, which last film was released in 2003. It is likely that the popularity of the name Arwen increased after this release, given the huge popularity of the trilogy.

Question 3

Produce the following plot starting from the flowers dataset. A potentially useful function that you may not have seen: bind_rows(): merges two tibbles by rows so that the joint tibble becomes longer, not wider



For the exercise we will transform the dataset so that we will only have “width” and “length” features plus an extra one called “category” which can take values “Sepal” or “Petal” and will indicate to which part of the flower the width and length reffers to. To do that we first split the original dataset into one for petal features and one for sepal features using “transmutate”, then they must be joined using “bind_rows()”. Finally the plot is made splitting by “category” with “facet_wrap” and include the plot layers, “geom_point” for the scatter plots and “geom_smooth” for the linear model regression with a range (light grey shade).

```
data_flowers <- read_tsv("data/flowers.txt")
```

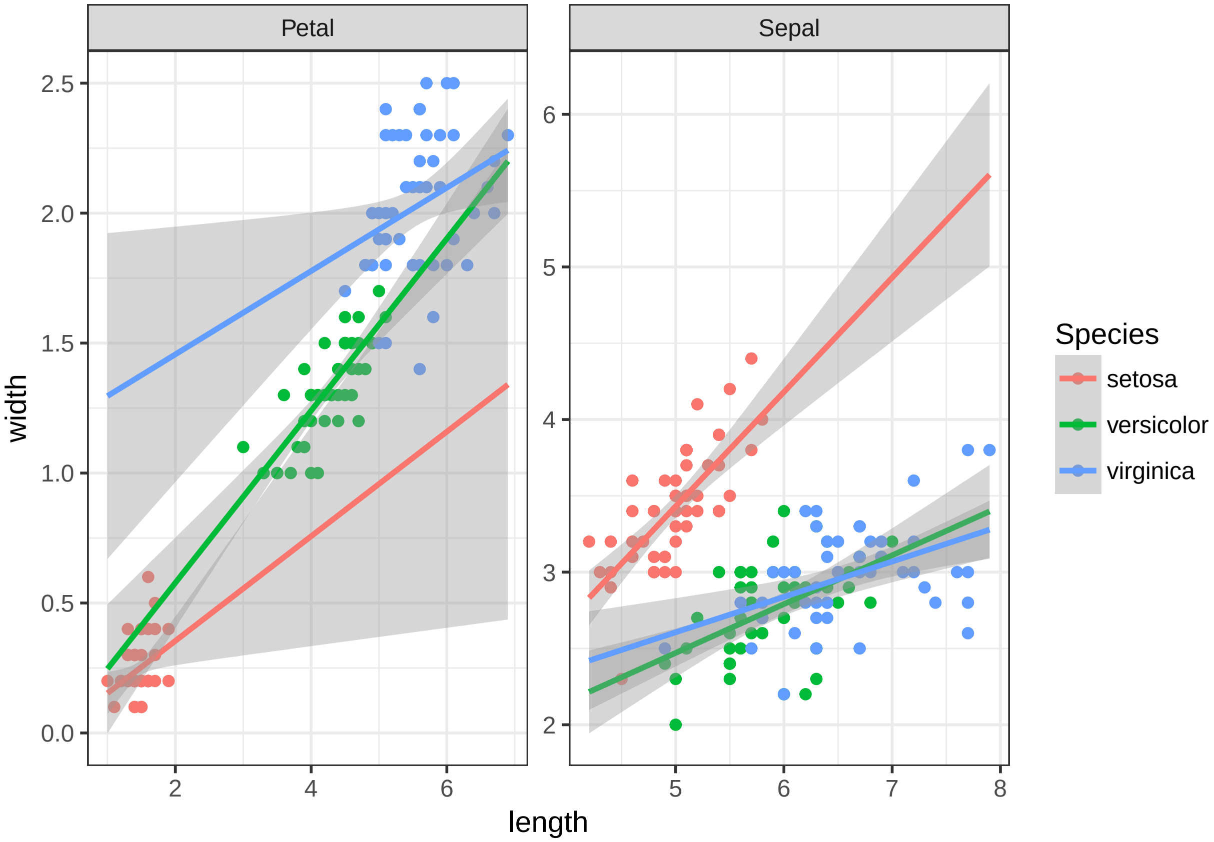
```
## Parsed with column specification:
## cols(
##   Sepal.Length = col_double(),
##   Sepal.Width = col_double(),
##   Petal.Length = col_double(),
##   Petal.Width = col_double(),
##   Species = col_character()
## )
```

```
flowers_petal <- transmute(data_flowers,  length = data_flowers$Petal.Length,
                           width = data_flowers$Petal.Width, Species =
                            as.factor(data_flowers$Species), category = "Petal")

flowers_sepal <- transmute(data_flowers, length = data_flowers$Sepal.Length,
                           width = data_flowers$Sepal.Width, Species =
                           as.factor(data_flowers$Species), category = "Sepal")

flowers_exp <- bind_rows(flowers_petal, flowers_sepal)

flowers_exp %>% ggplot(aes(x=length, y=width, col = Species)) +  geom_point() +
facet_wrap(~category, scales = "free") + theme_bw() + geom_smooth(method = "lm",
                                                                  fullrange = TRUE)
```



Question 4

We are given a file with binding sites of a certain transcription factor, made with the ChIP-seq technique (you will hear a lot more about the technique later in the course) by a collaborator. In the homework directory, there is a data file 'chip_mm5.txt' from the collaborator, representing binding sites from a Chip-chip experiment, with a column for chromosome, start, end, and score, where score is how 'good' the binding is. Our collaborator has two hypotheses:

1: Binding scores are dependent on chromosome

2: Binding site widths (end-start) are dependent on chromosome

Can you prove/disprove these two hypotheses statistically?

We first collect data from the Chip-chip experiment

```
chip<-read_tsv("data/chip_mm5.txt") #read data
```

```
## Parsed with column specification:
## cols(
##   chr = col_character(),
##   start = col_integer(),
##   end = col_integer(),
##   score = col_double()
## )
```

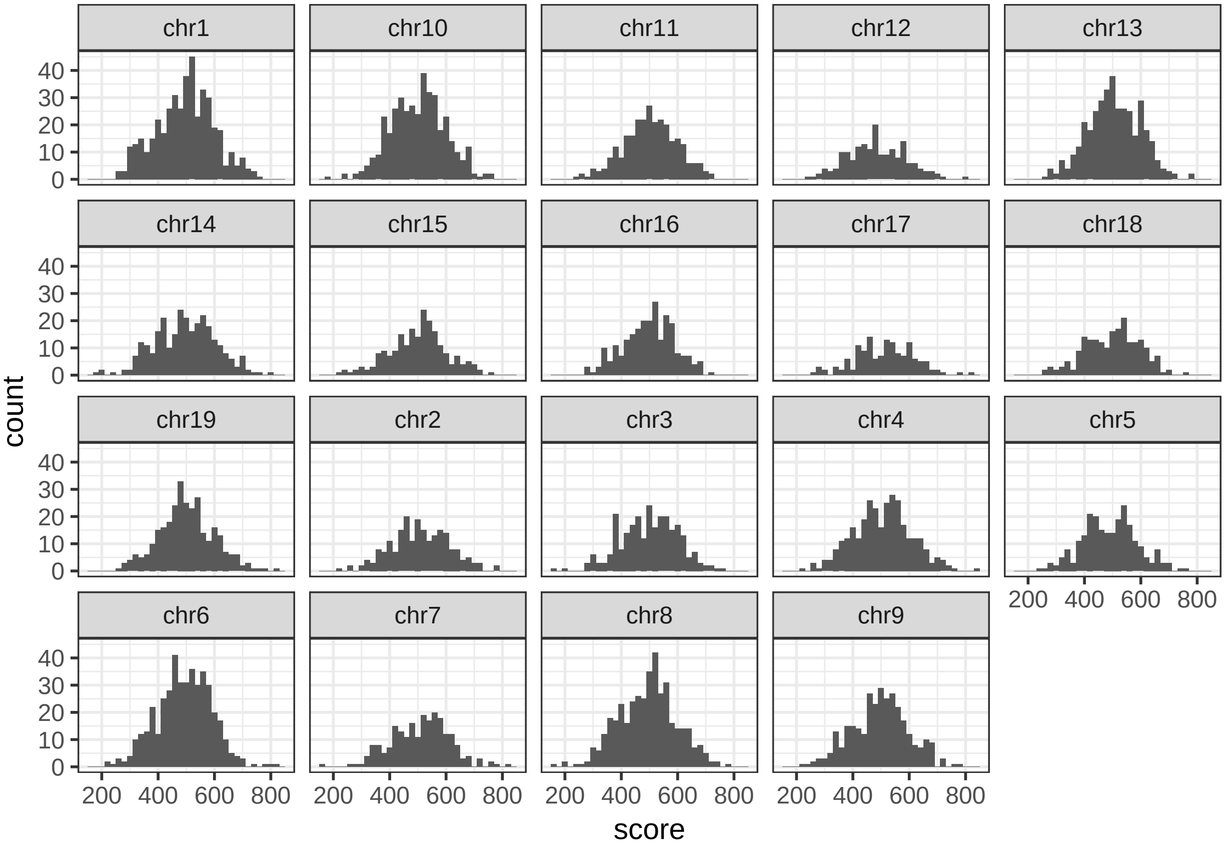
```
head(chip) #show data
```

```
## # A tibble: 6 x 4
##   chr      start     end score
##   <chr>    <int>   <int> <dbl>
## 1 chr1   4437288 4437576  606.
## 2 chr1   4437624 4437845  506.
## 3 chr1   4682247 4682767  616.
## 4 chr1   4779329 4779612  469.
## 5 chr1   6227828 6228473  512.
## 6 chr1   9699267 9699761   NA
```

In order to assertain which test to utilize, we plot the score in a historgram to see whether we can observe a normal distibution of the data.

```
ggplot(chip) + geom_histogram(aes(x=score),binwidth = 20) + facet_wrap(~chr) + theme_bw() # plot distri
```

```
## Warning: Removed 5 rows containing non-finite values (stat_bin).
```



The 5 removed rows were NA's.

We observe a normal distribution of score in each chromosome. In order to test whether there is a significant difference in binding score in the chromosomes, we utilize an one-way ANOVA test. H0: there is no significant difference in means of binding score for each chromosome. H1: there is a significant difference in means of binding score for each chromosome.

```
oneway.test(score ~ as.factor(chr), data=chip) #Anova test for significance difference between score va
```

```
##
```

```
##  One-way analysis of means (not assuming equal variances)
##
## data:  score and as.factor(chr)
## F = 1.0228, num df = 18.0, denom df = 1797.5, p-value = 0.4298
```

We cannot reject our null hypothesis since the calculated p-value > 0.05, therefore we do not observe that there is a difference in mean binding score across chromosomes.

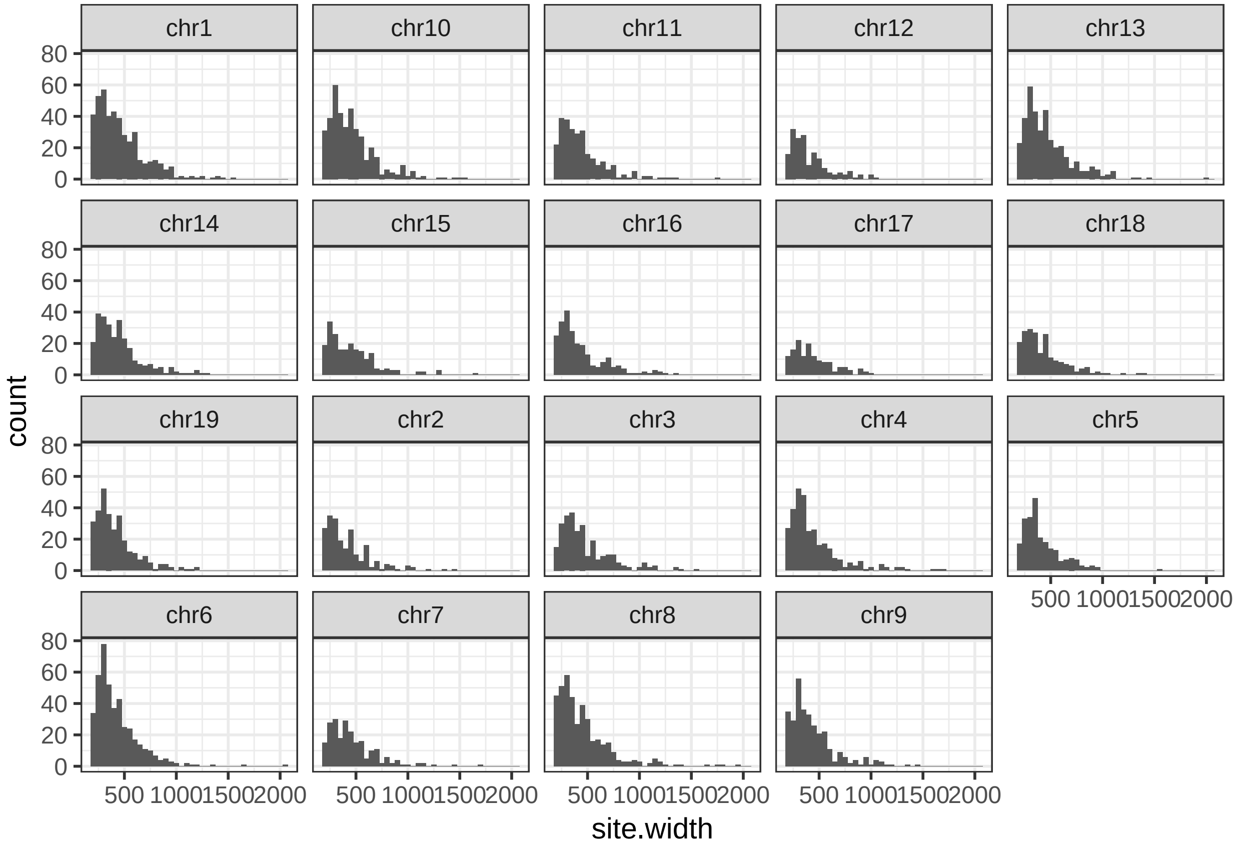
To test the other hypothesis, we need to modify our data set to include binding site width.

```
new_chip<-mutate(chip, site.width = end - start) #create site.width (end - start)
head(new_chip) #new data
```

```
## # A tibble: 6 x 5
##   chr      start     end score site.width
##   <chr>    <int>   <int> <dbl>      <int>
## 1 chr1   4437288 4437576  606.        288
## 2 chr1   4437624 4437845  506.        221
## 3 chr1   4682247 4682767  616.        520
## 4 chr1   4779329 4779612  469.        283
## 5 chr1   6227828 6228473  512.        645
## 6 chr1   9699267 9699761   NA         494
```

We plot the binding site width in a histogram to ascertain whether the data is normally distributed

```
ggplot(new_chip) + geom_histogram(aes(x=site.width),binwidth = 50) + facet_wrap(~chr) + theme_bw() # pl
```



The binding site width is not normal distributed in the chromosomes. We utilize a Kruskal-Wallis test to test our null hypothesis. H0: there is no significant difference in the mean binding site width for each chromosome. H1: there is a significant difference in the mean binding site width for each chromosome.

```
kruskal.test(site.width ~ as.factor(chr), data=new_chip) #Kruskal test for significance difference betw
```

```
##
##  Kruskal-Wallis rank sum test
##
## data:  site.width by as.factor(chr)
## Kruskal-Wallis chi-squared = 38.536, df = 18, p-value = 0.003288
```

Calculated p-value < 0.05 therefore we can reject our null hypothesis. The alternative hypothesis is proven and there is a significant difference in binding site width across the chromosomes.