A5_LI_ZHIJUN_Analysis.Rmd

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Import the Sequences.csv file

```
Data <- read.csv("A5_LI_ZHIJUN_Sequences.csv")
```

```
library(rentrez)
library(dplyr)
```

```
##
## Attaching package: 'dplyr'

## The following objects are masked from 'package:stats':
##
##     filter, lag

## The following objects are masked from 'package:base':
##
##     intersect, setdiff, setequal, union
```

Print out each sequence.

```
print(Data$Sequence)
```

```
## [1] "AGCATGCAAGTCAAACGAGATGTAGCAATACATCTAGTGGCGAACGGGTGAGTAACGCGTGGATGATCTACCTATGAGATGGGGATAACTATTAG
## [2] "AGCATGCAAGTCAAACGGGATGTAGCAATACATTCAGTGGCGAACGGGTGAGTAACGCGTGGATGATCTACCTATGAGATGGGGATAACTATTAG
## [3] "AGCATGCAAGTCAAACGAGATGTAGTAATACATCTAGTGGCGAACGGGTGAGTAACGCGTGGATGATCTACCTATGAGATGGGGATAACTATTAG
```

Count the number of each base pair (A, T, C and G), in each of the three sequences

```
#convert each sequence from a character to a vector of base pairs
Seq1 <- strsplit(Data$Sequence, "")[[1]]
Seq2 <- strsplit(Data$Sequence, "")[[2]]
Seq3 <- strsplit(Data$Sequence, "")[[3]]

#count the number
Count_A1 = sum(grepl("A", Seq1))
Count_T1 = sum(grepl("T", Seq1))
Count_G1 = sum(grepl("G", Seq1))
Count_C1 = sum(grepl("C", Seq1))

Count_A2 = sum(grepl("A", Seq2))
Count_T2 = sum(grepl("T", Seq2))
Count_G2 = sum(grepl("G", Seq2))
```

```
Count_C2 = sum(grepl("C", Seq2))

Count_A3 = sum(grepl("A", Seq3))
Count_T3 = sum(grepl("T", Seq3))
Count_G3 = sum(grepl("G", Seq3))
Count_C3 = sum(grepl("C", Seq3))
```

Print out the number as a table

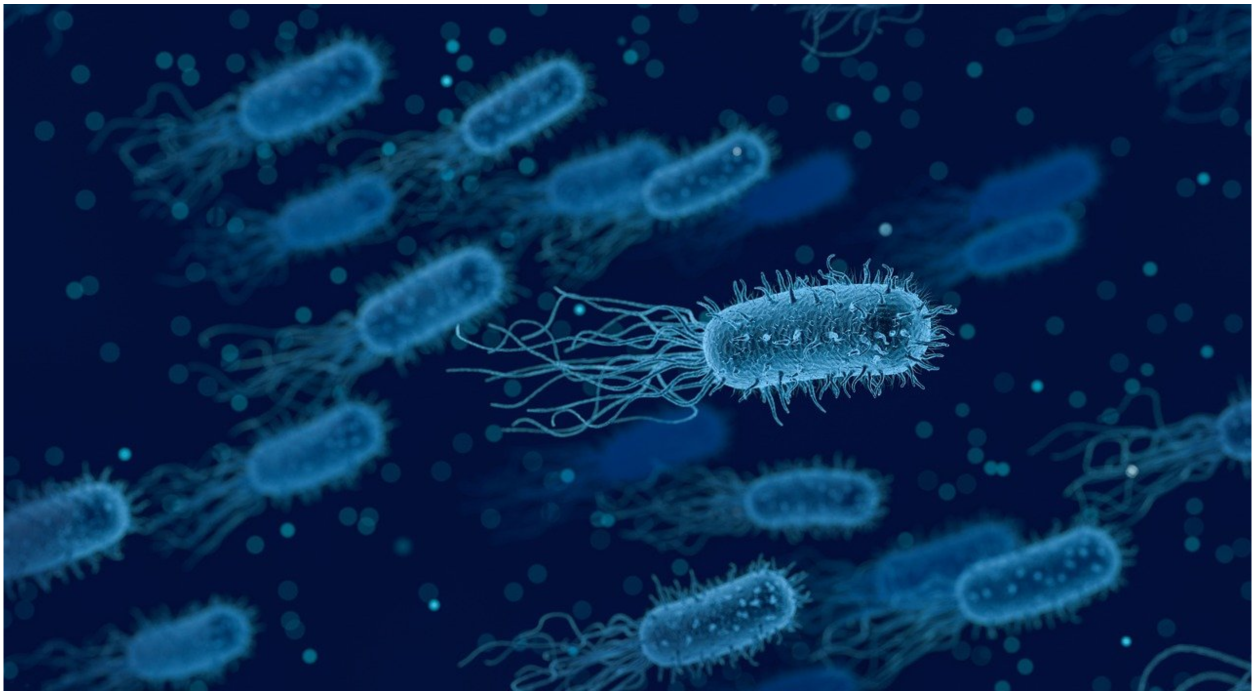
```
Name1 = gsub("(HQ433692.1).*", "\\1", Data$Name)[[1]]
Name2 = gsub("(HQ433694.1).*", "\\1", Data$Name)[[2]]
Name3 = gsub("(HQ433691.1).*", "\\1", Data$Name)[[3]]

Count_Table <- data.frame(Sequence_ID = c(Name1, Name2, Name3),
                          A = c(Count_A1, Count_A2, Count_A3),
                          T = c(Count_T1, Count_T2, Count_T3),
                          C = c(Count_C1, Count_C2, Count_C3),
                          G = c(Count_G1, Count_G2, Count_G3))

Count_Table
```

```
##   Sequence_ID   A   T  C   G
## 1 >HQ433692.1 154 114 82 131
## 2 >HQ433694.1 155 114 81 131
## 3 >HQ433691.1 154 115 81 131
```

Include an image of a bacteria from the internet, and a link to the Wikipedia page about Borrelia burgdorferi



Link: Wikipedia for Borrelia burgdorferi

Calculate GC Content and create a final table showing GC content for each sequence ID

```
library(formattable) #this package helps format the output

Count_Table %>%
  group_by(Sequence_ID) %>%
  summarise(GC_Content = (G+C)/(A+T+C+G)) %>%
  mutate(GC_Content = formattable::percent(GC_Content))
```

```
## # A tibble: 3 x 2
##   Sequence_ID GC_Content
##   <chr>       <formttbl>
## 1 >HQ433691.1 44.07%
## 2 >HQ433692.1 44.28%
## 3 >HQ433694.1 44.07%
```