# Bioinformatics First Year Exam Q15

Mirte Ciz Marieke Kuijpers

2022-06-16

## Set Up

First packages and the data need to be loaded into the R working environment.

```
# Load data
data <- read.csv("covid19_variants.csv", header = T)

# Check data
head(data, n = 2)
```

```
##         date       area area_type variant_name specimens percentage
## 1 2021-01-01 California     State        Total        59     100.00
## 2 2021-01-01 California     State        Alpha         1       1.69
##   specimens_7d_avg percentage_7d_avg
## 1               NA                NA
## 2               NA                NA
```

```
tail(data, n = 2)
```

```
##            date       area area_type variant_name specimens percentage
## 5059 2022-05-21 California     State       Lambda         0          0
## 5060 2022-05-21 California     State        Alpha         0          0
##      specimens_7d_avg percentage_7d_avg
## 5059                0                 0
## 5060                0                 0
```

```
summary(data)
```

```
##      date               area            area_type         variant_name
##  Length:5060        Length:5060        Length:5060        Length:5060
##  Class :character   Class :character   Class :character   Class :character
##  Mode  :character   Mode  :character   Mode  :character   Mode  :character
##
##
##
##
##    specimens         percentage     specimens_7d_avg   percentage_7d_avg
##  Min.   :   0.00   Min.   :  0.00   Min.   :   0.000   Min.   :  0.0000
##  1st Qu.:   0.00   1st Qu.:  0.00   1st Qu.:   0.000   1st Qu.:  0.0000
##  Median :   0.00   Median :  0.00   Median :   0.571   Median :  0.0862
##  Mean   : 179.93   Mean   : 20.00   Mean   : 181.336   Mean   : 20.0000
##  3rd Qu.:  37.25   3rd Qu.: 13.51   3rd Qu.:  40.143   3rd Qu.: 12.7339
##  Max.   :5776.00   Max.   :100.00   Max.   :3255.429   Max.   :100.0000
##                                     NA’s   :60         NA’s   :60
```

```
# Load packages
library("ggplot2")
```

```
## Warning: package ’ggplot2’ was built under R version 4.1.3
```

```
library("dplyr")
```

```
## Warning: package ’dplyr’ was built under R version 4.1.3
```

```
##
## 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
```

```
library("lubridate")
```

```
##
## Attaching package: ’lubridate’
```

```
## The following objects are masked from ’package:base’:
##
##     date, intersect, setdiff, union
```

## Format data

Note that `summary` shows us that `R` is treating the date column data as character data. This should be changed so that `R` can recognize this as time/date information.

```
# State of date before fixing
class(data$date)
```

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

```
# Use a Lubridate function to tell R that the date column holds dates not characters
data$date <- ymd(data$date)

# Check this was successful
class(data$date)
```

```
## [1] "Date"
```

Another thing to check is whether the variants present in the data match those in the plot I am trying to recreate, and remove any inappropriate categories.

```
# Check the variants present in the data
unique(data$variant_name)
```

```
##  [1] "Total"   "Alpha"   "Beta"    "Mu"      "Delta"   "Gamma"   "Lambda"
##  [8] "Epsilon" "Omicron" "Other"
```

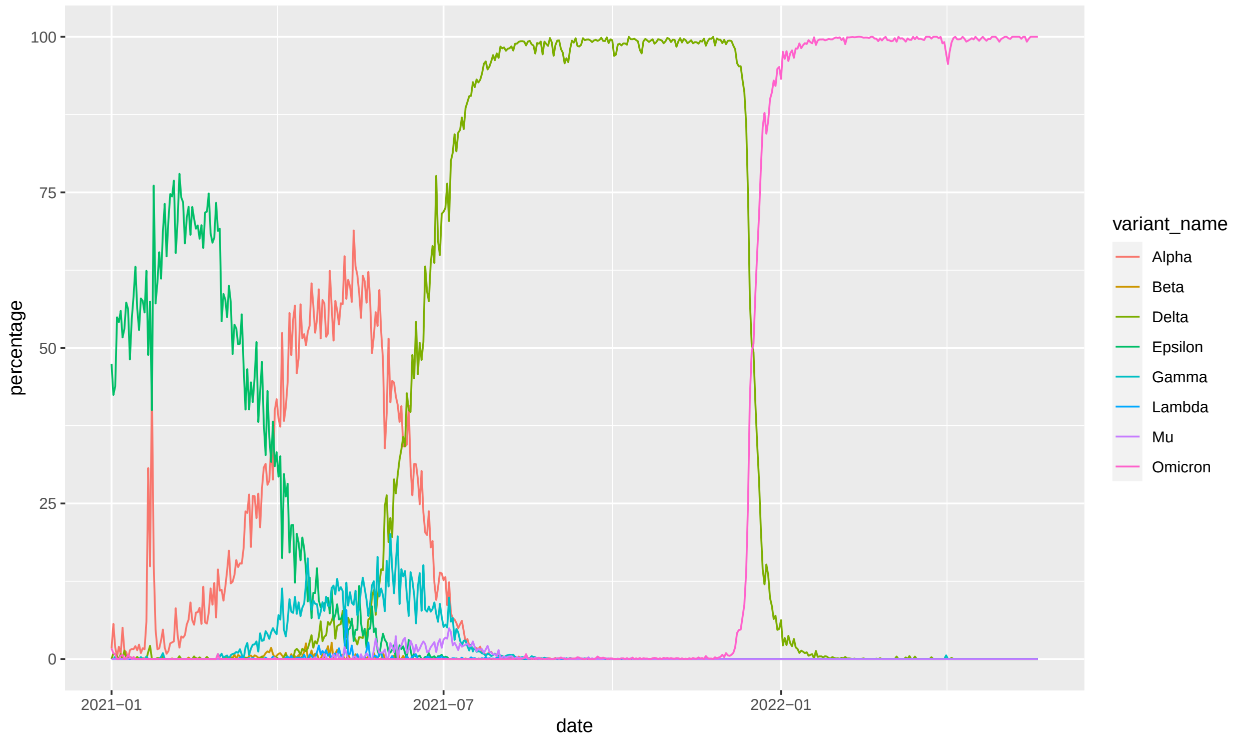
```
# Remove "Total" and "Other", which are not in the template plot
#### not (!) rows with Other or Total in the variant column
dat <- data[!data$variant_name %in% c("Other", "Total"), ]

# Check if successful
unique(dat$variant_name)
```

```
## [1] "Alpha"   "Beta"    "Mu"      "Delta"   "Gamma"   "Lambda"  "Epsilon"
## [8] "Omicron"
```

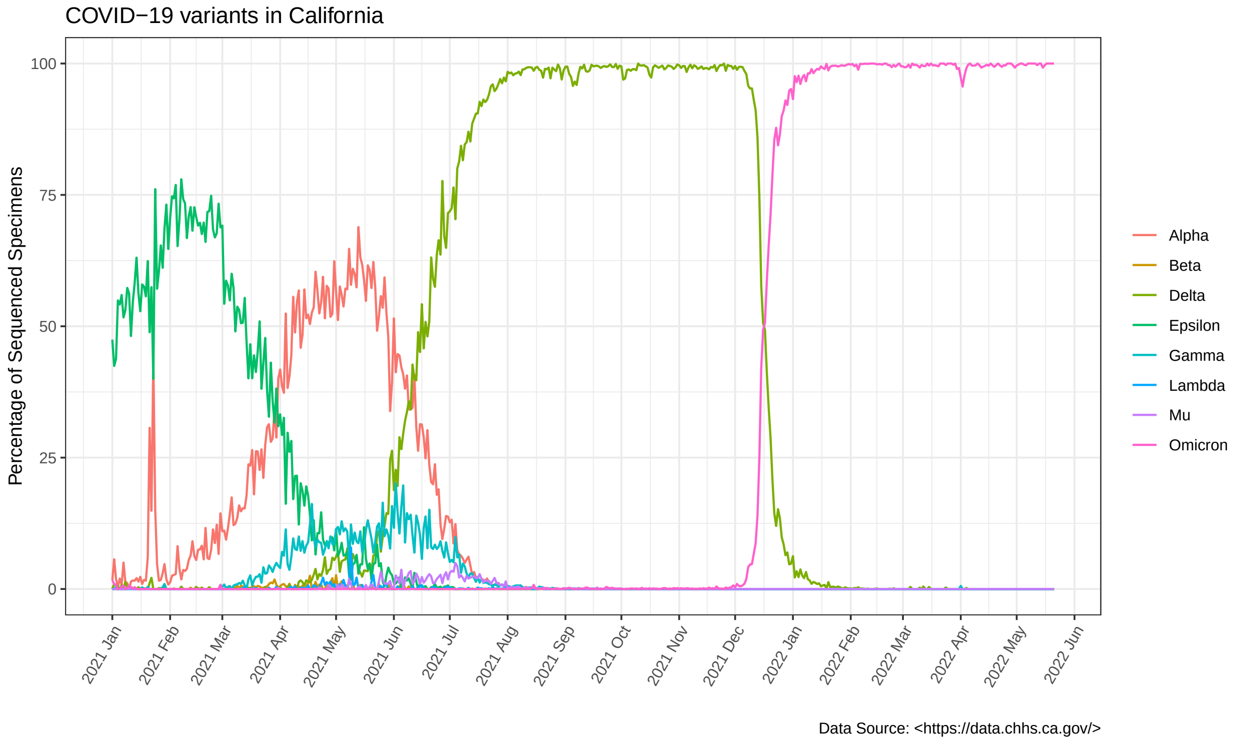
## Plot data

Now that the data has been properly formatted it is possible to plot it. I will focus on first plotting the data correctly, and when this is complete I will make a secondary plot with appropriate aesthetics.

```
# Basic plot
ggplot(dat, aes(date, percentage, col = variant_name)) +
  geom_line()
```



```r
# Plot with aesthetics
ggplot(dat, aes(date, percentage, col = variant_name)) +
  geom_line(cex = 0.6) +
  theme_bw() + # basic theme to build upon
  scale_x_date(date_labels = "%Y %b", date_breaks = "1 month") + # format axis
  theme(axis.text.x=element_text(angle=60, hjust=1)) + # customize bw theme
  labs(x = "", y = "Percentage of Sequenced Specimens",
       title = "COVID-19 variants in California", col = "",
       caption = "Data Source: <https://data.chhs.ca.gov/>")
```

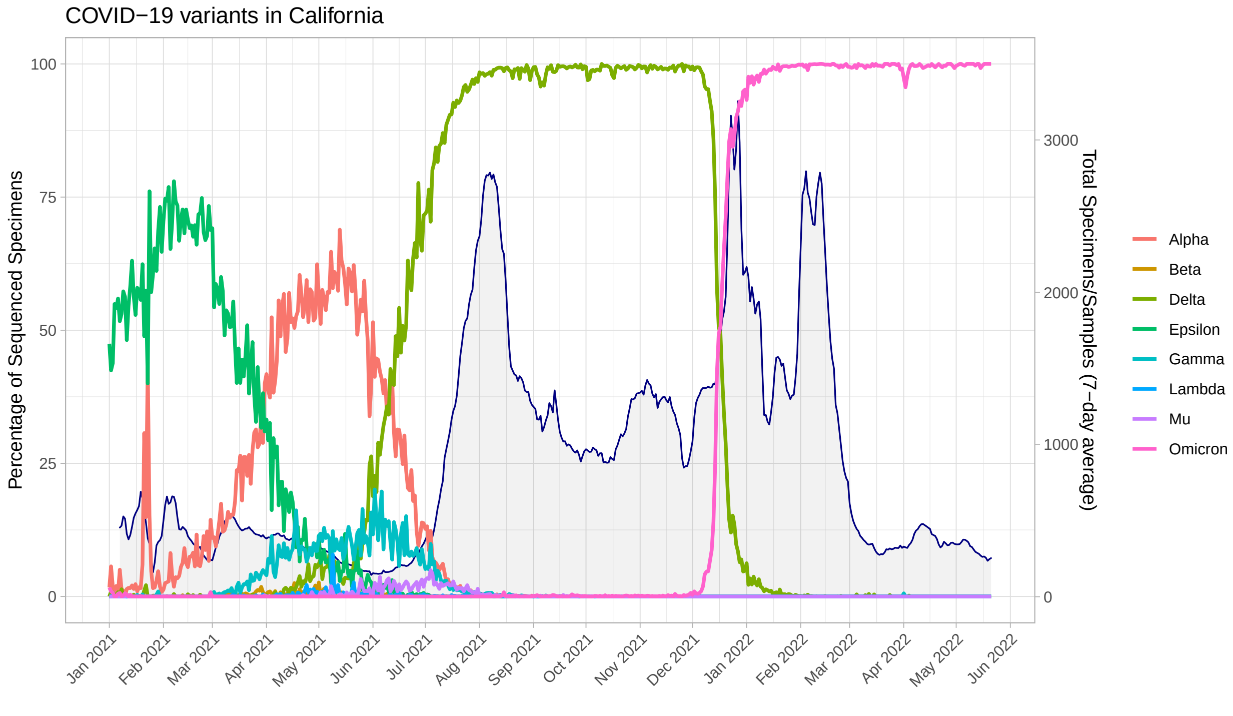


Note that within the "{r}" of this code chunk I added the following `fig.width=10, fig.height= 6` to ensure that the plots were knitted at a reasonable size into the final document. Without this customization they were a little smaller than I thought they should be.

Now that the template plot has been replicated I can also play around with my own styles.

```r
# Subset the data for just the total numbers
tot <- data[data$variant_name == "Total",]

# My plot
ggplot(dat, aes(x = date, col = variant_name)) +
  geom_area(data = tot, aes(x = date, y = specimens_7d_avg/35), col = "navy",
            cex = 0.45, alpha = 0.05, fill = "black") +
  geom_line(aes(y = percentage), cex = 1) +
  scale_y_continuous(
    # Features of the first axis
    name = "Percentage of Sequenced Specimens",
    # Add a second axis and specify its features
    sec.axis = sec_axis( trans=~.*35, name="Total Specimens/Samples (7-day average)")
  ) +
  theme_light() + # basic theme to build upon
  scale_x_date(date_labels = "%b %Y", date_breaks = "1 month") + # format axis
  theme(axis.text.x=element_text(angle=45, hjust=1)) + # customize bw theme
  labs(x = "", title = "COVID-19 variants in California", col = "",
       caption = "Data Source: <https://data.chhs.ca.gov/>")
```

```
## Warning: Removed 6 rows containing missing values (position_stack).
```



Data Source: <https://data.chhs.ca.gov/>

I chose to overlay the COVID-19 variant data over the 7-day average of specimen numbers. I choose this 3rd variable because the more samples sequenced the more likely rare variants are sampled. Therefore, the 100% levels of Delta and Omicron during there peaks can be stated with more confidence when one notes that the sampling levels are high during these peaks. I chose the 7 day average because using all the specimen data (from the `specimen` column) led the eye away from the trend due to the many peaks and troughs of the higher resolution data. A more interesting metric here, rather than sample frequency, might be case frequency, although this could also be misleading, as the ability to detect and report cases, as well as the reliability of data collection and reporting has improved over the course of the pandemic.

# Session Information

```
sessionInfo()
```

```
## R version 4.1.2 (2021-11-01)
## Platform: x86_64-w64-mingw32/x64 (64-bit)
## Running under: Windows 10 x64 (build 22000)
##
## Matrix products: default
```

```
##
## locale:
## [1] LC_COLLATE=English_United Kingdom.1252
## [2] LC_CTYPE=English_United Kingdom.1252
## [3] LC_MONETARY=English_United Kingdom.1252
## [4] LC_NUMERIC=C
## [5] LC_TIME=English_United Kingdom.1252
##
## attached base packages:
## [1] stats     graphics  grDevices utils     datasets  methods   base
##
## other attached packages:
## [1] lubridate_1.8.0 dplyr_1.0.9     ggplot2_3.3.6
##
## loaded via a namespace (and not attached):
##  [1] highr_0.9        pillar_1.7.0     compiler_4.1.2   tools_4.1.2
##  [5] digest_0.6.29    evaluate_0.15    lifecycle_1.0.1  tibble_3.1.7
##  [9] gtable_0.3.0     pkgconfig_2.0.3  rlang_1.0.2      cli_3.2.0
## [13] DBI_1.1.2        rstudioapi_0.13  yaml_2.3.5       xfun_0.29
## [17] fastmap_1.1.0    withr_2.5.0      stringr_1.4.0    knitr_1.39
## [21] generics_0.1.2   vctrs_0.4.1      grid_4.1.2       tidyselect_1.1.2
## [25] glue_1.6.2       R6_2.5.1         fansi_1.0.3      rmarkdown_2.14
## [29] farver_2.1.0     purrr_0.3.4      magrittr_2.0.3   scales_1.2.0
## [33] ellipsis_0.3.2   htmltools_0.5.2  assertthat_0.2.1 colorspace_2.0-3
## [37] labeling_0.4.2   utf8_1.2.2       stringi_1.7.6    munsell_0.5.0
## [41] crayon_1.5.1
```