Q15 - First Year Exam

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Load the data and packages

```
df <- read.csv("covid19_variants.csv")
library(ggplot2)
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
```

```
library(lubridate)
```

```
##
## Attaching package: 'lubridate'
```

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

Look at data

```
head(df)
```

```
##       date       area area_type variant_name specimens percentage
## 1 1/1/2021 California     State        Alpha         1       1.69
## 2 1/1/2021 California     State         Beta         0       0.00
## 3 1/1/2021 California     State           Mu         0       0.00
## 4 1/1/2021 California     State        Gamma         0       0.00
## 5 1/1/2021 California     State        Total        59     100.00
## 6 1/1/2021 California     State      Omicron         1       1.69
```

```
##   specimens_7d_avg percentage_7d_avg
## 1               NA                NA
## 2               NA                NA
## 3               NA                NA
## 4               NA                NA
## 5               NA                NA
## 6               NA                NA
```

Format Data

Remove 'Total' and 'Other' variants since these aren't in the plot given to us

```
df <- df[!df$variant_name %in% c("Other", "Total"), ]
head(df)
```

```
##       date       area area_type variant_name specimens percentage
## 1 1/1/2021 California     State        Alpha         1       1.69
## 2 1/1/2021 California     State         Beta         0       0.00
## 3 1/1/2021 California     State           Mu         0       0.00
## 4 1/1/2021 California     State        Gamma         0       0.00
## 6 1/1/2021 California     State      Omicron         1       1.69
## 7 1/1/2021 California     State      Epsilon        28      47.46
##   specimens_7d_avg percentage_7d_avg
## 1               NA                NA
## 2               NA                NA
## 3               NA                NA
## 4               NA                NA
## 6               NA                NA
## 7               NA                NA
```

Change the date to a 'date' variable rather than a 'character' variable using the 'lubridate' package

```
# observe column variable in wrong format
class(df$date)
```

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

```
df$date[1]
```

```
## [1] "1/1/2021"
```

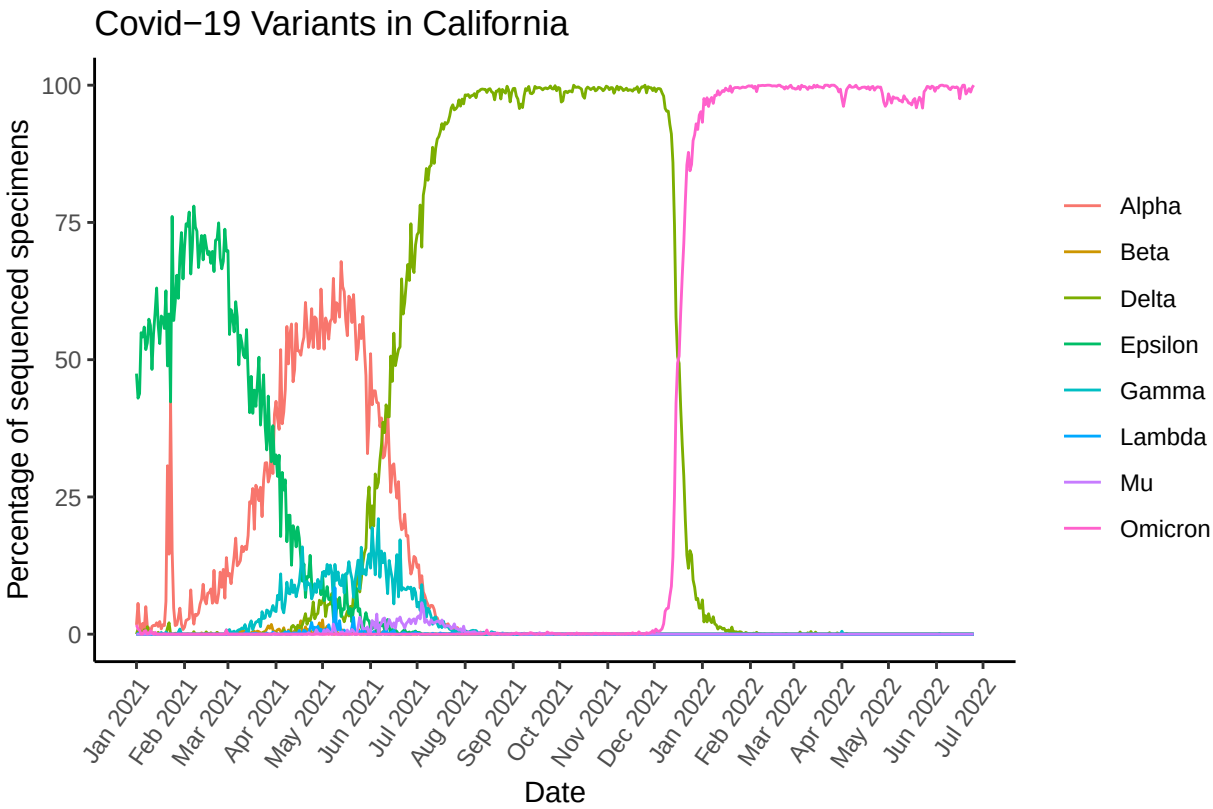
```
# fix above, make new column and add to df


df$new_date <- mdy(df$date)
head(df)
```

```
##       date       area area_type variant_name specimens percentage
## 1 1/1/2021 California     State        Alpha         1       1.69
## 2 1/1/2021 California     State         Beta         0       0.00
```

```
## 3 1/1/2021 California     State           Mu         0       0.00
## 4 1/1/2021 California     State        Gamma         0       0.00
## 6 1/1/2021 California     State      Omicron         1       1.69
## 7 1/1/2021 California     State      Epsilon        28      47.46
##   specimens_7d_avg percentage_7d_avg   new_date
## 1               NA                NA 2021-01-01
## 2               NA                NA 2021-01-01
## 3               NA                NA 2021-01-01
## 4               NA                NA 2021-01-01
## 6               NA                NA 2021-01-01
## 7               NA                NA 2021-01-01
```

Plot Data

```
ggplot(df, aes(new_date,percentage)) +
# group by variant (hence excluding total and other)
  geom_line(aes(color = variant_name)) +
# set theme
  theme_classic() +
# now, format axes
  scale_x_date(date_labels = "%b %Y", date_breaks = "1 month") +
# add axes titles
  ylab("Percentage of sequenced specimens") +
  xlab("Date") +
# make x axis readable (rotate), remove legend title
  theme(axis.text.x = element_text(angle = 55,
                                   hjust = 1),
        legend.position = "right",
        legend.title = element_blank()) +
# title plot
  ggtitle("Covid-19 Variants in California") +
# add caption to include website where data was found
  labs(caption = "Data Source: <https://data.chhs.ca.gov/dataset/covid-19-variant-data>")
```



Data Source: <https://data.chhs.ca.gov/dataset/covid−19−variant−data>