

Bioinformatics First Year Exam

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```
##Load packages into library
```

```
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
```

```
library(ggplot2)
```

```
library(tibble)
```

Data taken from <https://data.chhs.ca.gov/dataset/covid-19-variant-data>

```
##Reading CSV file and naming it as "covid.data"
```

```
covid.data <- read.csv("covid19_variants.csv")
```

```
##Loading data from .csv file into ggplot to create a line graph
```

```
##Taking data from covid.data and used the following the format for a line graph to plot the data with .
ggplot(data = covid.data, aes(x=date, y=percentage, group=variant_name, color=variant_name) )+
  ##insert line graph
  geom_line() +
  ## Label x-axis
  xlab("Date Range: 01/01/2021-06/25/2022") +
  ##Label y-axis
  ylab("Percentage of Sequenced Specimens") +
  ##Label Legend Title
  labs(colour= "Variant Name") +
  ##Label graph title
  ggtitle("Covid 19 Variants in California, USA")
```

