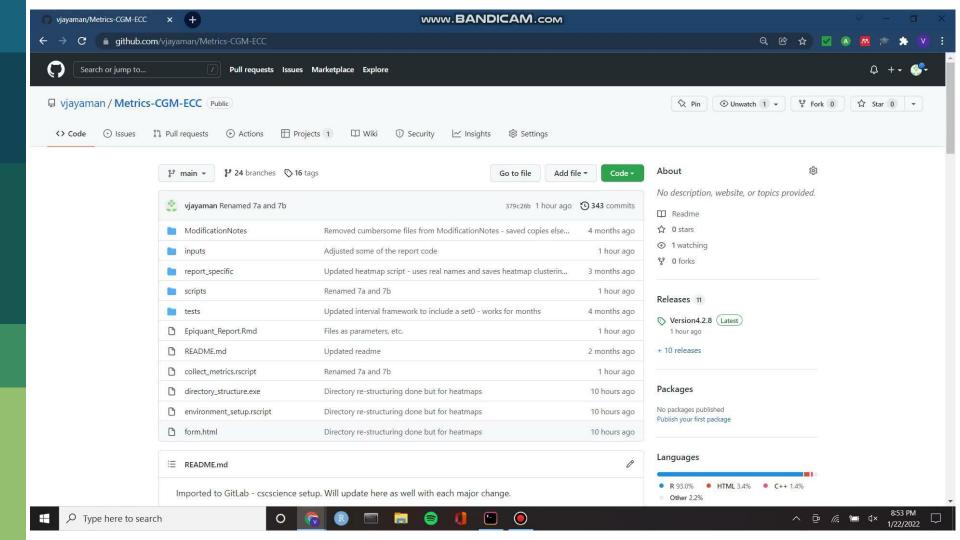
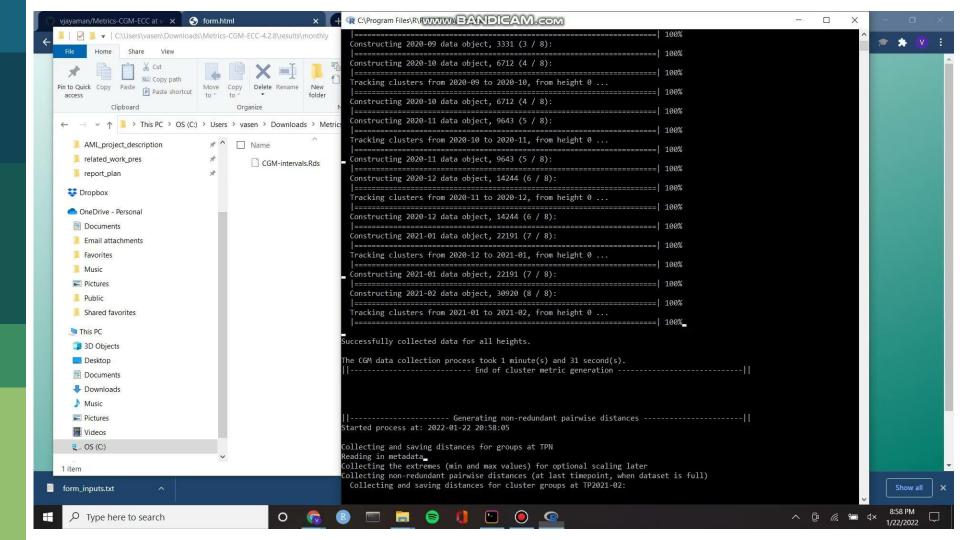
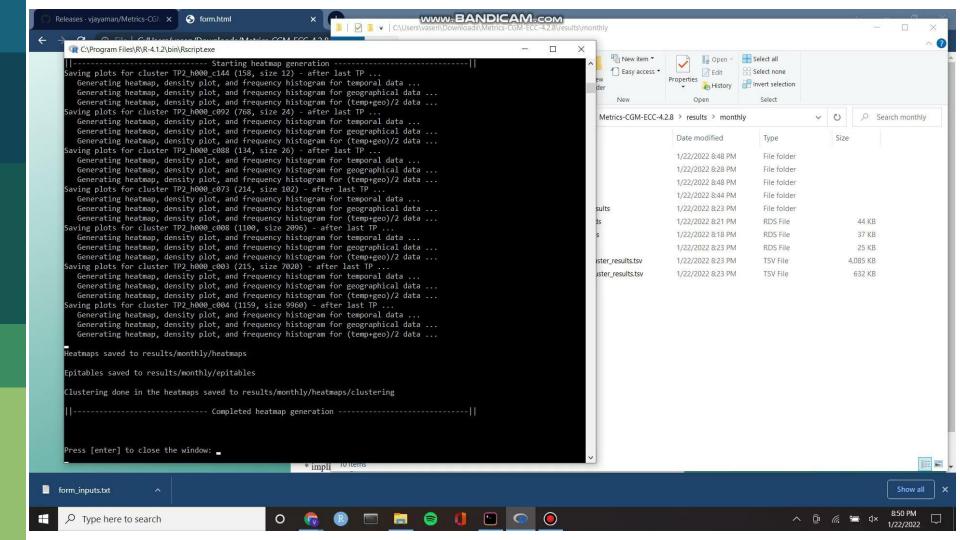
## Progress: Campy-COVID Project Metrics generation

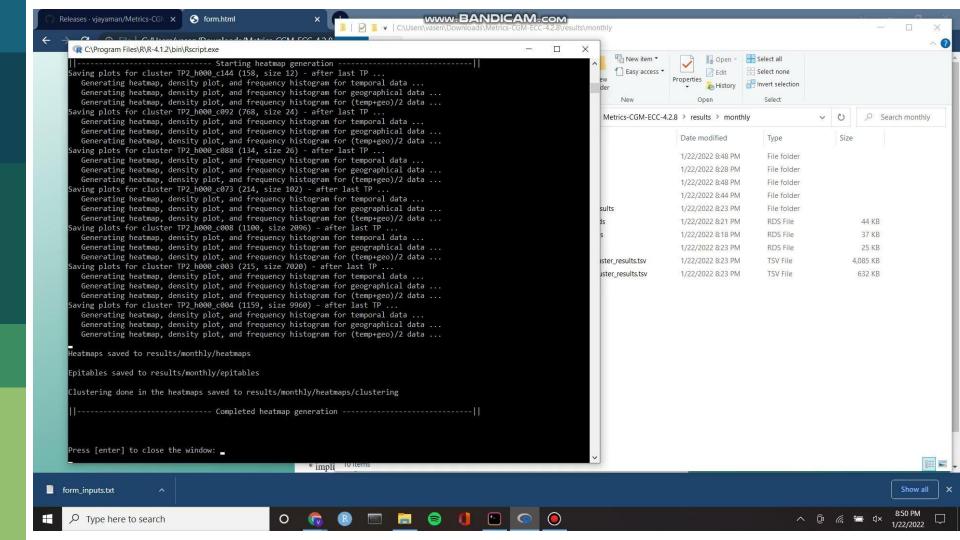
## **Steps**

simply click to run!









```
Epiquant_Report.Rmd
            ■ Knit on Save
                                                                                                   ○ - 1 I Run - - =
    1 ----
    2 title: "SARS CoV2 EpiQuant Analysis Report"
        bookdown::html document2:
      params:
    6
         strain results: "Merged strain results"
        long file dir: "multiset"
   10
        vector file: "inputs/Vector Order.csv"
   11
   12
         epitables dir: "results/monthly/epitables"
   13 - ---
   14
                                                                                                                             *
   15 {r setup, include=FALSE}
   16
   17 knitr::opts chunk$set(echo = FALSE,message = FALSE,warning = FALSE,eval=TRUE)
   18
   19 -
   20
   21
   24
   25
   26
   27
   28
      y <- lapply(libs, require, character.only = TRUE); rm(libs); rm(v)
   29
   30
   31 ## for tables
      pacman::p load(
   33
   34
        here,
   35
        skimr,
   36
        tidyverse,
   37
         gtsummary,
   38
   39
```

```
Epiquant_Report.Rmd
🛑 🕽 🔚 🤚 🖪 Knit on Save 🗎 🔍 🌌 Knit 🔻 🌣 🔻
                                                                                        Oc - ↑ ↓ Run - 2 - =
  1)/ 4. ELL direction classes vs compass rose (see |rigure 4.4|(#rig.4.4-11nk))
  158
  159 \\ \r\
  161
  162
  163 #
                        long_file_dir = "multiset",
  164 #
  165
  166
  167
  168
  169
       Lineages <- read csv(params$lineage file) %>%
  170
         filter (T0 != "#N/A") %>% select("Strain", "T0.original", "Pango lineage")
  171
  172
       ECC long base <- file.path("results", params$long file dir, params$strain results) %>%
  173
         list.files(., full.names = TRUE, pattern = "tsv") %>%
  174
  175
         map(read tsv) %>% reduce(rbind)
  176
  177
       ECC Month base <- file.path("results", "monthly", params$strain results) %>%
  178
  179
         list.files(., full.names = TRUE, pattern = "tsv") %>%
  180
         map(read tsv) %>% reduce(rbind)
  181
       first monthday <- grep("set0", ECC Month base$interval, value = TRUE) %>% unique() %>%
  182
         as.character() %>% gsub("set0-",
       ECC Month base$interval <- gsub('set0', first monthday, ECC Month base$interval)
  183
       ECC Month base <- ECC Month base %>% separate(interval, into = c('Month 1', 'Month 2'), sep = 8)
  184
  185
       ECC Month base <- merge(x = ECC Month base, y = Lineages, by = "Strain", all.x = TRUE)
  186
  187
       ECC Week <- file.path("results", "weekly", params$strain results) %>%
  188
         list.files(., full.names = TRUE, pattern = "tsv") %>%
  189
  190
         map(read tsv) %>% reduce(rbind)
  191
```

```
Epiquant_Report.Rmd
Oc - ↑ ↓ | ■ Run - | - - | = |
      ECC Week <- file.path("results", "weekly", params$strain results) %>%
  188
         list.files(., full.names = TRUE, pattern = "tsv") %>%
  189
  190
         map(read tsv) %>% reduce(rbind)
  191
       ECC Week <- ECC Week %>%
  192
  193
  194
                Year Week = strftime(ECC Week$Date, format = "%G-%V")) %>%
  195
  196
         merge(x = ., y = Lineages, by = "Strain", all.x = TRUE) %>%
         mutate if(is.numeric, ~ round(., digit = 2))
  197
  198
  199
  200
       ECC Week <- ECC Week %>%
  201
         mutate(Multistrain_Cluster = ifelse(ECC_Week$`TP2 cluster size (1)` > 2,"Multistrain","Singleton" ),
  202
                Cluster Size = ECC Week TP2 cluster size (1),
  203
                Geo_ECC = ECC_Week$TP2_ECC.0.0.1, Temp_ECC=ECC_Week$TP2_ECC.0.1.0,
  204
                Delta Geo ECC = ECC Week$delta ECC 0.0.1,
  205
                Delta Temp ECC=ECC Week$delta ECC 0.1.0,
                Cluster Size1 = ECC Week$`TP1 cluster size + 1 (2)`,
  206
  207
                Geo ECC1 = ECC Week$TP1 ECC.0.0.1,
  208
                Temp ECC1 = ECC Week$TP1 ECC.0.1.0,
  209
                "Cluster growth by size"=ECC Week$`Actual cluster growth (TP2 size - TP1 size)`,
  210
                "Novel growth by rate"=ECC Week$ Novel growth = (TP2 size) / (TP2 size - number of novels) )
  211
  212
  213 WX <- list.files(params$epitables dir, full.names = TRUE)
  214 Whisker Data <- lapply(WX[3:5], function(x i) {
  215
         cluster name <- strsplit(x i, split = "/") %>% unlist() %>% extract2(4) %>% gsub(".Rds", "", .)
  216
         readRDS(x i) %>% add column(Cluster = cluster name)
  217 - }) %>% bind rows() %>% select(Cluster, Temp.Dist, Geog.Dist) %>%
  218
         separate(Cluster, sep = 13, into = c("Cluster", "Cluster1"))
  219
  220
       country code <- read csv(params$country code file)
  221
      Vector Order <- read csv(params$vector file)
  222
  223
  224 - #
  225 • # HOW TO READ IN THE ORIGINAL CLUSTER NAMES and collect cluster sizes: -----
  227 # tpn <- readRDS("inputs/processed/allTP2.Rds")
  228 # Lineages <- as.data.table(tpn$original[,c("Strain","T0")]) %>%
```

## Progress: Campy-COVID Project Metrics generation