My challenge was that in Connecticut counties aren't really an especially useful geographic entity (no offense to any county officials). It's just not how many of us think of the state and apart from that many decisions for things like school openings, and voting are based at the town level. In our quaint New England way (and

I should confess I was born elsewhere) we think about about things at a level called "town" (notwithstanding the cliche "quaint New England village"). That's where the title comes from – a play on "it takes a village".

This post chronicles the journey of taking Nathan's great work and modifying it to fit Connecticut as well as making a few other tweaks that I think help the overall presentation.

I know tl;dr get to the code Chuck that's why we're here.

Setup and libraries

I won't apologize but yes there are a lot of libraries invloved and yes I am going to suppress all the various start-up messages.

```
######
library(dplyr)
library(tidyr)
library(forcats)
library(purrr)
library(lubridate) # Date wrangling
library(ggplot2)
theme set(theme bw())
library(scales) # Pretty axis labels
library(tigris)
options(tigris_use_cache = TRUE)
library(gganimate) # GIF production
library(tidycensus) # Population estimates
library(transformr) # used by gganimate
library(ggthemes) # map themes
library(viridis) # Heatmap color palette
library(zoo) # rollapply
```

Initial data and wrangling

Nathan got his data from the COVID-19 Data Repository by the Center for Systems Science and Engineering (CSSE) at Johns Hopkins University, which is maintained

on Github.

Because I may choose to do some further analyses I'm going to grab the data from Connecticut Open Data which has a wealth of information about the state, including a daily set of information about Covid19 which is located at

https://data.ct.gov/Health-and-Human-Services/COVID-19-Tests-Cases-and-Deaths-By-Town-/28fr-iqnx.

The Connecticut COVID data starts on March 24th which is of course not

when this all started but will work for our purposes.

To make my life easier I've saved the file locally and renamed it to

To make my life easier I've saved the file locally and renamed it to include a date stamp.

As noted by comments in the code the first step is to convert Last.update.date to a true date format and convert Town into a factor. Once that's done it's easy to plot the obvious charts – raw cumulative cases for the state over time as well as the same information by Town for all 169 towns.

Applying scales::breaks pretty to our date axis makes easy work of

```
how granular we want the axis to be (monthly for now).
##### Get the data here
## https://data.ct.gov/Health-and-Human-Services/COVID-19-Tests-Cases-and-Deaths-By-
Town-/28fr-ignx
## change name to COVID19 CT By Town Oct15.csv
ct covid <- read.csv("COVID19 CT By Town Oct16.csv")
## Convert to date and factor
ct covid <-
   ct covid %>%
   mutate(Last.update.date = lubridate::as date(Last.update.date,
                                                   format = "%m/%d/%y"))
응>응
   mutate(Town = factor(Town))
# raw cases over time
ct covid %>%
   group by(Last.update.date) %>%
   summarise(cases = sum(Total.cases)) %>%
   ggplot(aes(x = Last.update.date, y = cases, group = 1)) +
   geom line() +
   scale x date(breaks = scales::breaks pretty(n = 10)) +
   scale_y_continuous(labels = scales::label_number(big.mark = ",")) +
   labs(
      title = "COVID-19 cases in Connecticut",
      x = "Month",
      y = "Cases",
      caption = paste0("Image generated: ",
                        Sys.time(), "\n",
                        "Data source: https://data.ct.gov/Health-and-Human-
Services/COVID-19-Tests-Cases-and-Deaths-By-Town-/28fr-iqnx")
```

COVID-19 cases in Connecticut 40,000 20,000

Month
Image generated: 2020-10-20 12:22:30
Data source: https://data.ct.gov/Health-and-Human-Services/COVID-19-Tests-Cases-and-Deaths-By-Town-/28ft-ignx

```
# raw cases by town over time
ct covid %>%
   group_by(Town, Last.update.date) %>%
   ggplot(aes(x = Last.update.date, y = Total.cases, group = Town,
color = Town)) +
   geom line(show.legend = FALSE) +
   scale_x_date(breaks = scales::breaks_pretty(n = 10)) +
   scale_y_continuous(labels = scales::label_number(big.mark = ",")) +
   labs(
      title = "COVID-19 cases in Connecticut by town",
      x = "Month",
      y = "Cases",
      caption = paste0("Image generated: ",
                        Sys.time(), "\n",
                        "Data source: https://data.ct.gov/Health-and-Human-
Services/COVID-19-Tests-Cases-and-Deaths-By-Town-/28fr-iqnx")
   )
```

COVID-19 cases in Connecticut by town

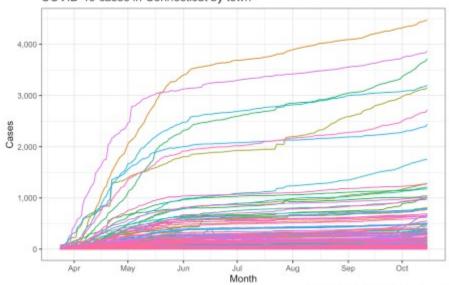


Image generated: 2020-10-20 12:22:30 Data source: https://data.ct.gov/Health-and-Human-Services/COVID-19-Tests-Cases-and-Deaths-By-Town-/28fr-ignx

Onward and upward

That was easy, but pretty uninformative. I guess there's solace in knowing that our 60,000+ cases are but a fraction of the US 8 million but it doesn't tell us much about the trend other than seeing the "bend" starting in June and what appears to be an increasing trend starting in September. The by town plot is rendered rather useless by having 169 lines and the fact that towns have very disparate populations. That's why many many towns are clustered under 500, they don't have large populations to begin with We need to address both of these issues in our final product.

To address the issue of different population levels by town we'll grab the 2010 Census data on a by town basis. CT data provides those numbers as well but by using tidycensus we'll get information about town by county as well as the all important GEOID which will enable us to put the data about population on a map.

tidycensus::get_decennial gets us the raw data we need (I checked and the population numbers match those the state provides – no surprise). The second step uses some tidyverse magic to clean and filter the data. The grep1 removes some rows that acknowledge the county boundaries but have zero population. The census data has Town, County and State in one column we use tidyr::separate to break them apart. States vary but for CT the towns are known as "county subdivision" in census parlance and variables = "P001001" gets us the total population for the town in 2010 according to the census.

```
ct town pops <-
  tidycensus::get decennial(geography = "county subdivision",
                          variables = "P001001",
                           state = "Connecticut")
ct town pops <-
  ct town pops %>%
  filter(!grepl("not defined", NAME)) %>%
  rename (population = value, name cty st = NAME) %>%
  select (-variable) %>%
  tidyr::separate(col = name cty st,
                 into = c("Town", "County", "State"),
                 sep = ",") %>%
  mutate(Town = gsub("town$", "\\1", Town),
         County = trimws(County, which = "both")) %>%
  select(-State)
ct town pops
## # A tibble: 169 x 4
## GEOID Town
                        County population
##
## 1 0900118500 Danbury Fairfield County
                                              80893
## 2 0900104720 Bethel Fairfield County
                                              18584
## 3 0900108070 Bridgeport Fairfield County 144229
## 4 0900108980 Brookfield Fairfield County
                                              16452
## 5 0900118850 Darien Fairfield County
                                              20732
```

```
## 6 0900123890 Easton Fairfield County 7490
## 7 0900126620 Fairfield Fairfield County 59404
## 8 0900133620 Greenwich Fairfield County 61171
## 9 0900148620 Monroe Fairfield County 19479
## 10 0900150580 New Canaan Fairfield County 19738
## # ... with 159 more rows
range(ct_town_pops$population)
## [1] 854 144229
```

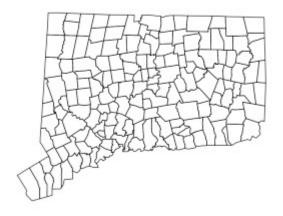
Finally we use good old range to show the smallest town population is 854 and the largest is 1.4422910^{5}.

Next we use tigris::county_subdivisions to get the geographic information about the shape of each town so we can map it. The package accesses the geographic shapefiles the

census bureau provides.

Once again grep1

helps us remove rows we don't want. A call to base plot confirms we're on track. A right_join allows us to marry the town shapes with the town populations into one object called ct town data.



```
ct town data <- right join(ct town pops, ct town shapes)
```

Let's roll

The plot looks good even with no special directives and renders both the shoreline and "the notch" well.

We now have two important objects <code>ct_covid</code> and <code>ct_town_data</code>, we still need to move from cumulative cases to rolling averages over time while adjusting for population size by making it **per capita**. For those of you that just live for long <code>dplyr</code> pipelines that do major transformations of the data here we go.

We will

- 1. Group by town (so we do all the math by Town)
- 2. Put yesterdays total case count into prev count with a lag
- 3. Therefore the increase in cases from day to day is Total.cases prev_count which we'll call new cases
- 4. Use zoo::rollapply to compute the mean (average) new cases over the last 7 days all call it roll cases.
- 5. After we ungroup we can join the population data to the case count data with a left join.
- 6. Now that evey row of our tibble has Total.cases, new_cases, and roll_cases we can create a column for each of those "per capita"

The most common per capita method used in public health is per 100,000 residents so the math is cases divided by population * 100,000 and voila. A tail gives you a glimpse of what selected columns look like.

```
roll ct covid <- ct covid %>%
   arrange(Last.update.date) %>%
   group by (Town) %>%
  mutate(prev count = lag(Total.cases, default = 0)) %>%
  mutate(new cases = Total.cases - prev count) %>%
   mutate(roll cases = zoo::rollapply(new cases,
                                             7,
                                            mean,
                                             fill = 0,
                                             align = "right",
                                             na.rm = TRUE)) %>%
  ungroup() %>%
  left join(
     ct town pops
   ) 응>응
  mutate(
     cases capita = Total.cases / population * 100000, # cases
per capita residents
     new capita = new cases / population * 100000, # cases per capita
residents
     roll capita = roll cases / population * 100000 # rolling new
cases per_capita residents
```

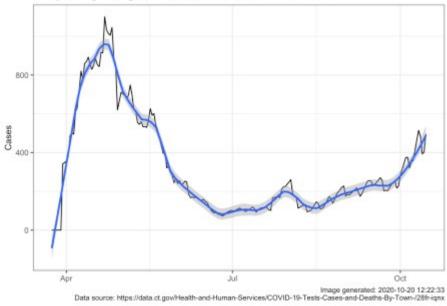
```
tail(roll ct covid %>%
       select (Last.update.date, Town, population, Total.cases,
new cases, roll cases, roll capita))
## # A tibble: 6 x 7
    Last.update.date Town population Total.cases new cases roll cases
roll capita
##
## 1 2020-10-15
                  Wind...
                                                    5
                                                          3.14
                         29044
                                        692
10.8
## 2 2020-10-15
                   Wind...
                            12498
                                         163
                                                    1
                                                          1
8.00
## 3 2020-10-15
                   Wolc... 16680
                                         159
                                                    2
                                                          1.71
10.3
## 4 2020-10-15
                   Wood...
                            8990
                                         155
                                                    0
                                                          0.286
3.18
## 5 2020-10-15
                                                    2
                   Wood...
                             9975
                                          71
                                                          0.571
5.73
## 6 2020-10-15
                   Wood...
                              7964
                                          40
                                             0
                                                          0.429
5.38
```

Before we go too much farther let's see what the trend is when we use the 7 day rolling average for new cases across the entire state.

```
roll agg ct cases <-
   roll ct covid %>%
   group by (Last.update.date) %>%
   summarize(roll cases = sum(roll cases))
roll agg ct cases %>%
   ggplot(aes(Last.update.date, roll cases)) +
   geom line() +
   geom smooth(span = .15) +
   labs(
      title = "7-Day Rolling Average of New COVID-19 Cases in
Connecticut",
      y = "Cases",
      caption = paste0("Image generated: ",
                        Sys.time(), "\n",
                        "Data source: https://data.ct.gov/Health-and-Human-
Services/COVID-19-Tests-Cases-and-Deaths-By-Town-/28fr-iqnx")
   ) +
   theme bw() +
   theme (
      title = element text(size = 10),
      axis.title.x = element blank()
```

)





Ah, now there's a much more informative plot. The black line shows the actual data with all its jags and sub peaks. The blue line applies <code>geom_smooth(span = .15)</code> which gives us a smoothing algorithm. Either line tells the same story. April 20-26 was the high point and by late June we were in much better shape. Summer was pretty flat but by September we were climbing and in October we're climbing faster. Unless you ignore the news completely you probably knew this but the state level picture can be very useful.

Show me the map

I know, I know I promised you a map by Town. First a little more clean-up.

A rolling average of 7 days requires seven days of data so the first day we can plot is six days from the first date in our data. The state doesn't publish data on the weekends or holidays so lets add some rows that basically just fill in the weekends and holidays from the day before. The tidyr::complete and tidyr::fill handle that for us.

There are rare cases where the total.cases go down by say one. Probably correcting a small error. In the unlikely event things turn negative let's just call it zero. We'll do that with a couple of ifelse.

```
### first date in dataset +6 is when rolling can go above zero
first_date <-
    ct_covid %>%
    pull(Last.update.date) %>%
    min() + 6

roll_ct_covid <-
    roll_ct_covid %>%
    group_by(Town) %>%
    tidyr::complete(Last.update.date = seq.Date(from = min(Last.update.date),
```

Okay now we need to do two more big things and one small thing. First we need to join the town "shapes" to the town COVID data before we can make a map. We'll take our temp object and our ct_town_shapes and inner join them.

Unlike Nathan's map I want to take the rolling average of new cases per capita roll_capita and put them in discrete "buckets" instead of a continuous variable. We'll make 11 buckets evenly spaced from 0 to 49.99999 by increments of 5 plus a final bucket with everything over 50. We'll do that with cut then forcats::fct_lump_n and lastly some gsub magic to make the factor levels pretty.

```
temp sf <- inner join(temp, ct town shapes) %>%
   select (GEOID, Town, Last.update.date, roll cases,
County:roll capita, geometry)
temp sf$roll cap levels <-</pre>
   temp sf$roll capita %>%
   cut width (width = 5,
             center = 2.5) %>%
   factor()
temp_sf$roll_cap_levels <-</pre>
   forcats::fct lump n(temp sf$roll cap levels,
                        n = 10,
                        other level = ">50")
temp sf$roll cap levels <-</pre>
   temp sf$roll cap levels %>%
   fct relabel(~ gsub(",[0-9]{1,2}",
                       " to ",
                       .x)) %>%
   fct relabel(~ gsub("\\[|\\]|\\(",
                       "",
                       .x))
```

A tiny bit of chicanery will allow us to center Town names on our map. sf::st_centroid and sf::st_coordinates will get us x and y coordinates to use to place the names near the geographic center of the town. Then we can make a pretty map of population by town labeled and with a nice scale. Because 169 towns is a lot of labels and because town boundaries are irregular we'll use ggrepel::geom text repel to declutter.

We'll use viridis to ensure that our colors are viewable for those with challenges seeing certain colors (colorblindness) and print well in gray scale. We'll shade the map so that more heavily populated areas show darkest and with an oversize scale under the map to show population numbers.

```
temp sf <- temp sf %>%
  mutate(
      CENTROID = purrr::map(geometry, sf::st centroid),
      COORDS = map(CENTROID, sf::st coordinates),
      COORDS X = map \ dbl (COORDS, 1),
      COORDS Y = map dbl(COORDS, 2)
   )
temp sf %>%
   filter(Last.update.date == "2020-03-30") %>%
   ggplot() +
   geom sf(aes(geometry = geometry, fill = population), size = 0.25) +
   ggrepel::geom text repel(
      mapping = aes(
        x = COORDS X,
        y = COORDS Y,
         label = Town),
      size = 2,
      min.segment.length = .5,
      point.padding = NA,
      segment.color = "grey50",
      force = .5,
      box.padding = .15,
      fontface = "bold") +
   scale fill viridis(alpha = .7,
                      direction = -1,
                      discrete = FALSE,
                      labels = comma,
                      breaks = seq.int(10000, 150000, 40000)) +
   ggthemes::theme map() +
   theme(legend.position = "bottom",
         legend.justification = "center",
         legend.key.size = unit(3, "lines"),
         legend.text = element text(size = 6)) +
      title = "Connecticut town populations",
      subtitle = "Census 2010 data",
```

```
caption = paste0("Image generated: ", Sys.time()))

Cornectout town populations

Carness 2010 data

Cornectour town populations

Carness 2010 data

Cornectour town populations

Carness 2010 data
```

Put it all together

The final step is to make the animation. This essentially means making a <code>ggplot</code> object in more or less the usual way. The initial lines should look quite familiar to the previous plot if you have been following along. Then comes:

```
gganimate::transition_time(Last.update.date) + enter_fade() +
exit fade()
```

which warns <code>gganimate</code> that our frames, our transitions, will be based on <code>Last.update.date</code>. <code>gganimate</code> does not support parallel processing unfortunately so it does take quite some time to run if we attempt to process a lot of dates. We'll create two animations

one with the full span

of data,

all 200 days (all_data), and another quicker one with just the last month (last_30_days).

In both cases the darker colors indicates low numbers (good for us) and "hot spots" are readily apparent as bright spots.

```
days <-
   temp_sf %>%
   pull(Last.update.date) %>%
   n_distinct()
days
## [1] 200
days2 <-
   temp_sf %>%
   filter(Last.update.date >= "2020-09-17") %>%
   pull(Last.update.date) %>%
   n distinct()
```

```
days2
## [1] 29
all data <- ggplot(temp sf) +
   geom sf(aes(fill = roll cap levels, geometry = geometry), size =
0.25) +
  viridis::scale fill viridis(name = "New cases 7 day average: ",
                               discrete = TRUE) +
   ggthemes::theme map() +
   theme(legend.position = "bottom",
         legend.justification = "center",
         legend.text = element text(size = 6)) +
   guides(fill = guide legend(nrow = 1,
                              title.position = "top",
                              label.position = "bottom",
                              label.hjust = 0,
                              title.hjust = 0.5,
                              byrow = TRUE)) +
   labs(
      title = paste0("Connecticut 7-day rolling average of new COVID
cases per ",
                     scales::comma(100000),
                     " residents by town"),
      subtitle = "Date: {frame time}",
      caption = paste0("Image generated: ", Sys.time(),
                       " Data updated ", max(ct covid$Last.update.date)
, "\n",
                       "Data source: https://data.ct.gov/ -- Connecticut Open
Data")
  ) +
   gganimate::transition_time(Last.update.date) +
  enter fade() +
  exit fade()
last 30 days <-
   temp sf %>% filter(Last.update.date >= "2020-09-17") %>%
   ggplot() +
   geom sf(aes(fill = roll cap levels, geometry = geometry), size =
0.25) +
   viridis::scale fill viridis(name = "New cases 7 day average: ",
                               discrete = TRUE) +
   ggthemes::theme map() +
   theme(legend.position = "bottom",
         legend.justification = "center",
         legend.text = element text(size = 6)) +
   guides(fill = guide_legend(nrow = 1,
                              title.position = "top",
                              label.position = "bottom",
                              label.hjust = 0,
                              title.hjust = 0.5,
                              byrow = TRUE)) +
```

Animate it

The call to <code>gganimate::animate</code> is relatively straight-forward, we feed it the name of the <code>ggplot</code> object we created above <code>all_data</code> or <code>last_30_days</code> how many frames to create (one per day plus the fade in and fade out) and optionally information about size and resolution. On my older Mac it takes approximately 14 minutes for the 200 days, and under 2 minutes for the month.

There is a function to save the animation as a **gif** which is what I have done for the larger file.

```
Sys.time()
## [1] "2020-10-20 12:23:02 EDT"
anim <- gganimate::animate(</pre>
  all data,
   nframes = days + 20,
   fps = 2,
   start pause = 5,
   end pause = 15,
   res = 96,
   width = 800,
  height = 600,
  units = "px"
)
gganimate::anim save("ct covid rolling Oct16.gif", animation = anim)
Sys.time()
## [1] "2020-10-20 12:35:47 EDT"
# anim
```

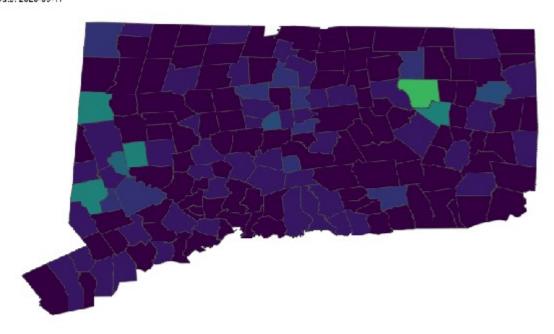
The smaller one I'll include directly in this blog post

```
Sys.time()
## [1] "2020-10-20 12:35:47 EDT"
anim2 <- gganimate::animate(
    last_30_days,
    nframes = days2 + 20,</pre>
```

```
fps = 1,
    start_pause = 5,
    end_pause = 15,
    res = 96,
    width = 800,
    height = 600,
    units = "px"
)

gganimate::anim_save("last_30_days.gif", animation = anim2)
Sys.time()
## [1] "2020-10-20 12:37:00 EDT"
anim2
```

Connecticut 7-day rolling average of new COVID cases per 100,000 residents by town Da.e: 2020-09-17





Done