

Situational analysis of COVID-19 in Bangladesh

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Food and Agriculture
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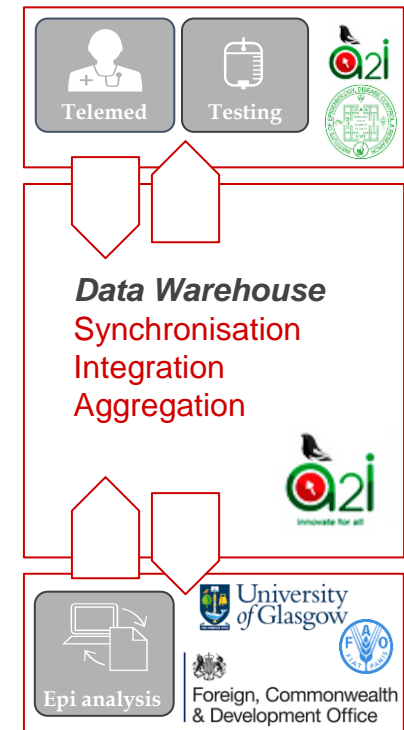
Lecture roadmap – hopefully 1 hour!

- Introduction to situational analysis (5 mins)
- Short overview of pandemic in Bangladesh (15 mins)
- Re-visit lecture with the R code!
 - Bangladesh timeseries - 10 mins
 - Bangladesh maps - 10 mins
 - Calculating R - 10 mins
 - Some annotation and other bits and pieces - 10 mins

What routine local/ national data can be used to better understand the COVID-19 trajectory?



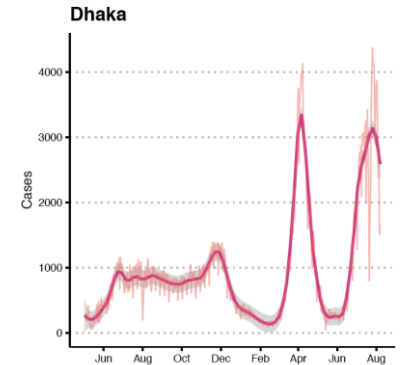
- Cases (PCR positives)
- Deaths (confirmed COVID-19)
- Testing (Tests performed & results)



How to use these routine local/ national data?

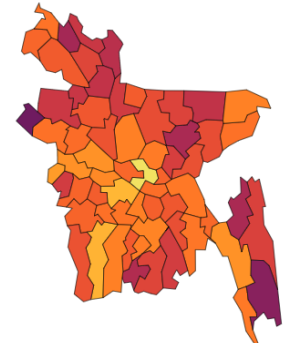
Visualize:

- Incidence of cases (and deaths) over time
- Map by locality e.g. district/ division
- Normalize by population and consider spatial scale



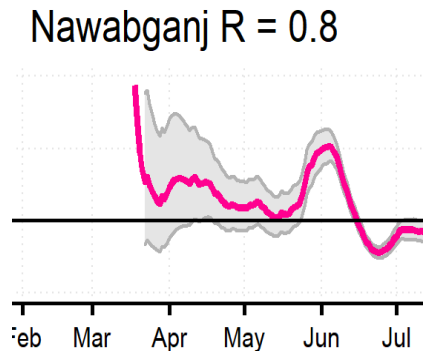
Examine test positivity

- Consider capacity (tests available, speed of turnaround) & epidemiological situation (incidence & severity – note variants)

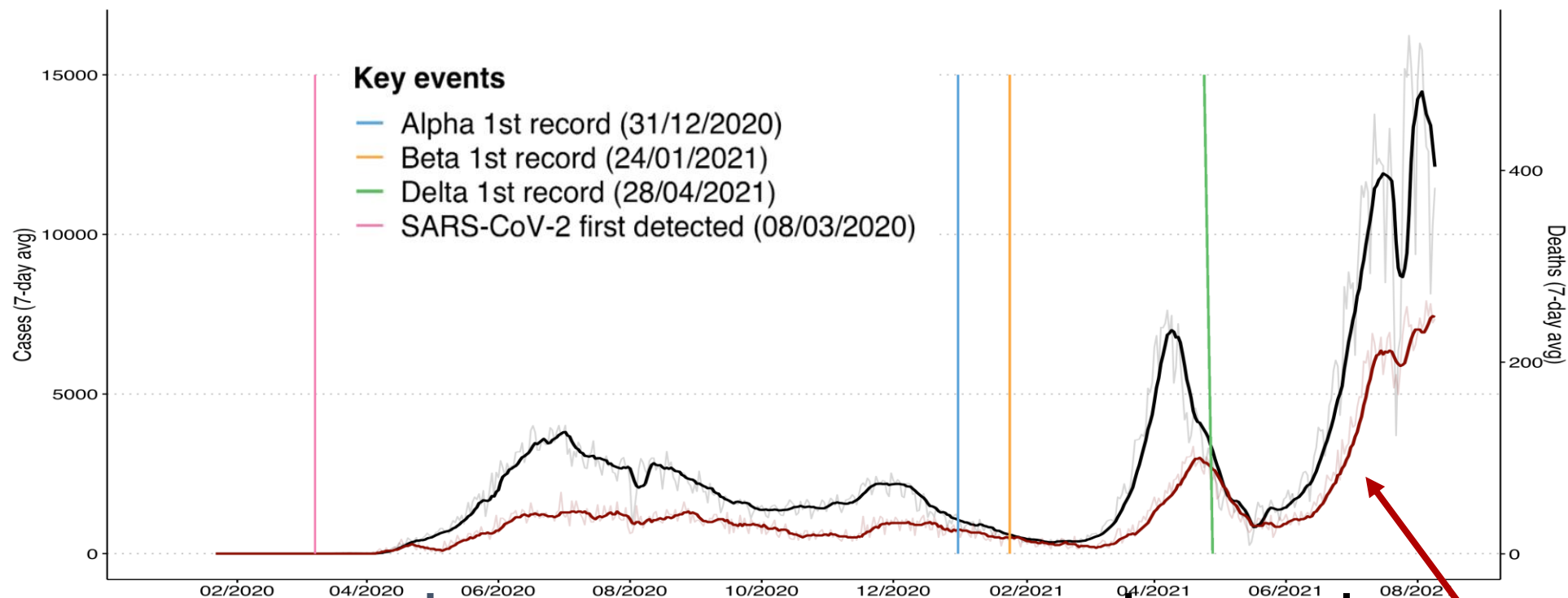


Estimate R_t (reproduction number at time t)

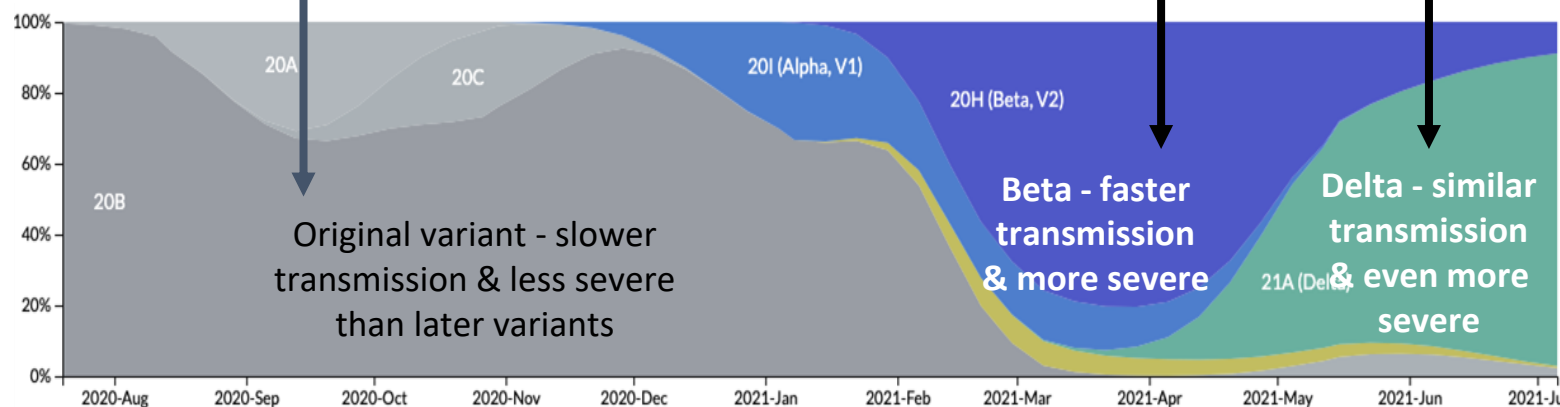
- Growth rate that determines if epidemic is increasing ($R > 1$) or declining ($R < 1$)
- Average secondary infections per case in a population with both susceptible and immune individuals (due to infection or vaccination), and control measures in place e.g. non-pharmaceutical interventions.



What is the overall picture of COVID-19 in Bangladesh?



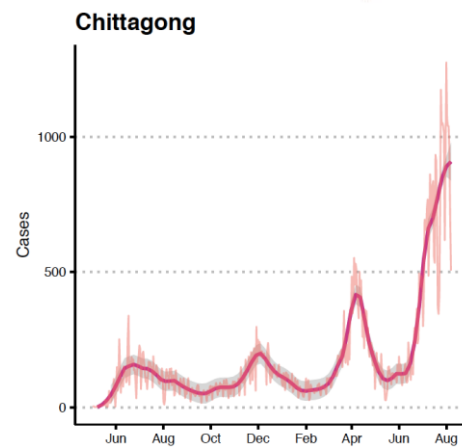
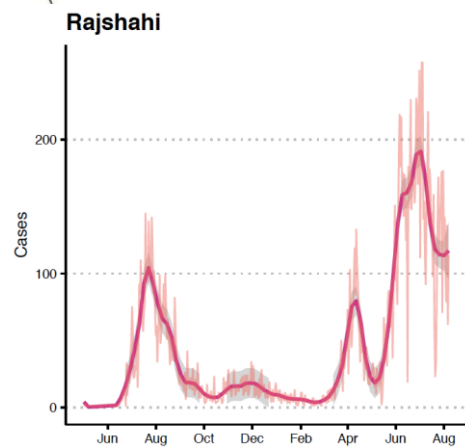
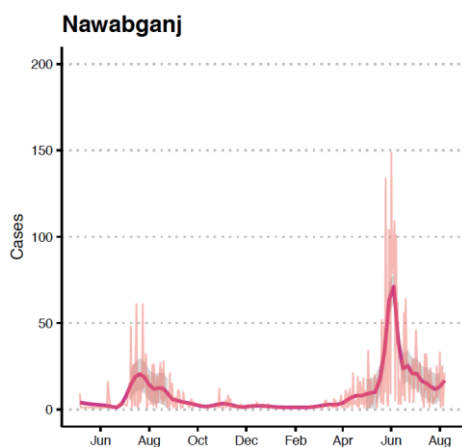
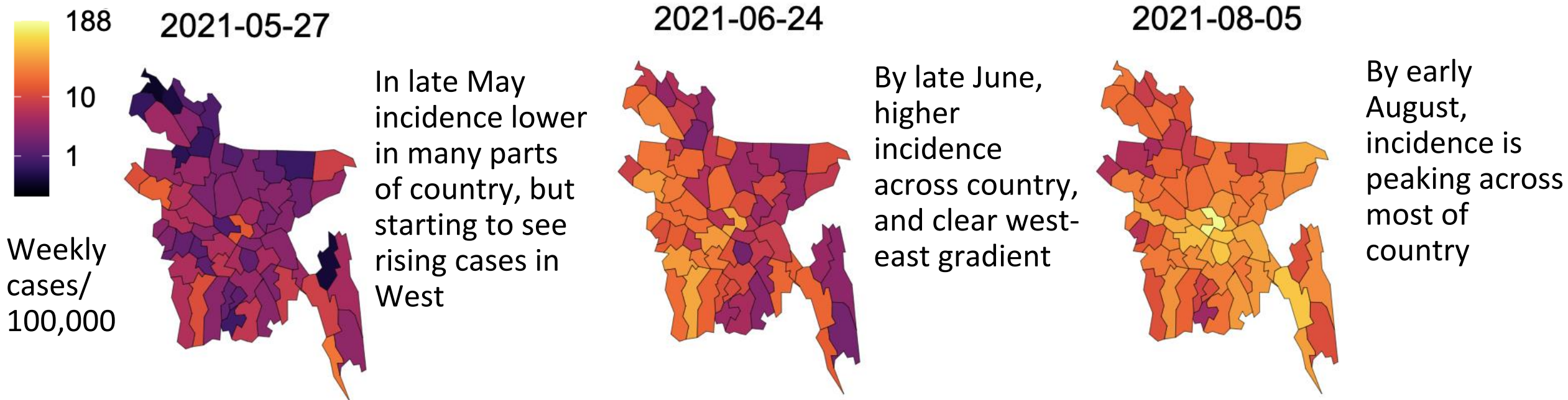
Each epidemic wave has been driven by new variants



Note that we expect deaths (& hospital occupancy) to lag cases

What is the overall picture of COVID-19 in Bangladesh?

Incidence has varied over time and by location



Epidemics in urban areas longer due to:

1. More imports seeding spread
2. Larger populations maintaining infection
3. Rural cases seeking care in urban health facilities

Current wave driven by Delta variant

Community transmission began in districts bordering India, but rapidly spread eastwards

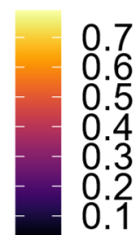
6 May - community transmission in Rajshahi

In May 2021, cases predominantly in Dhaka (declining 2nd wave from Beta), **but Delta had been detected in several localities**

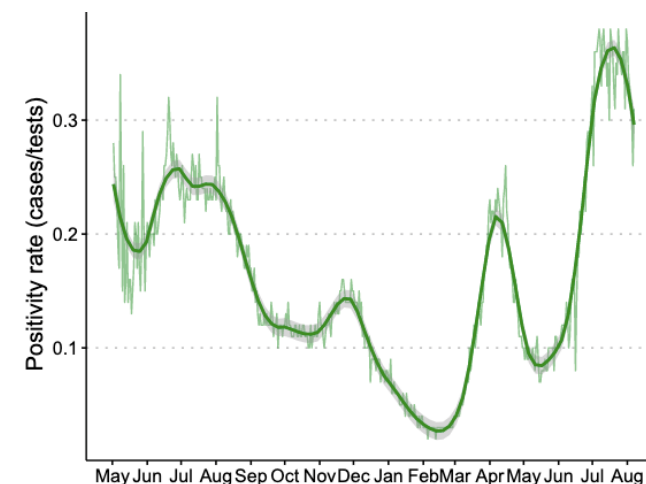
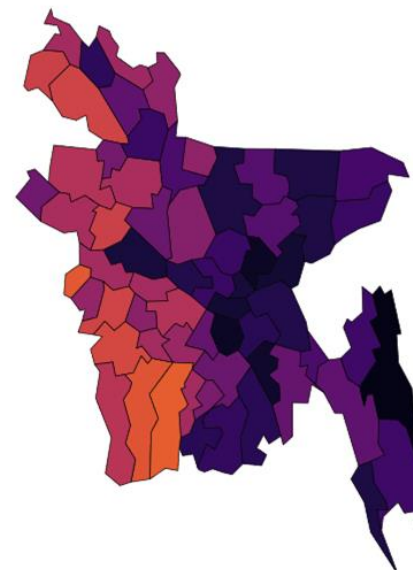
29 April – Rangpur, exposure in India

28 April – Barishal, exposure in India

Weekly positivity (cases/tests)



2021-06-24



Test positivity has tracked the epidemic waves, and was dramatically skewed West to East with the spread of Delta

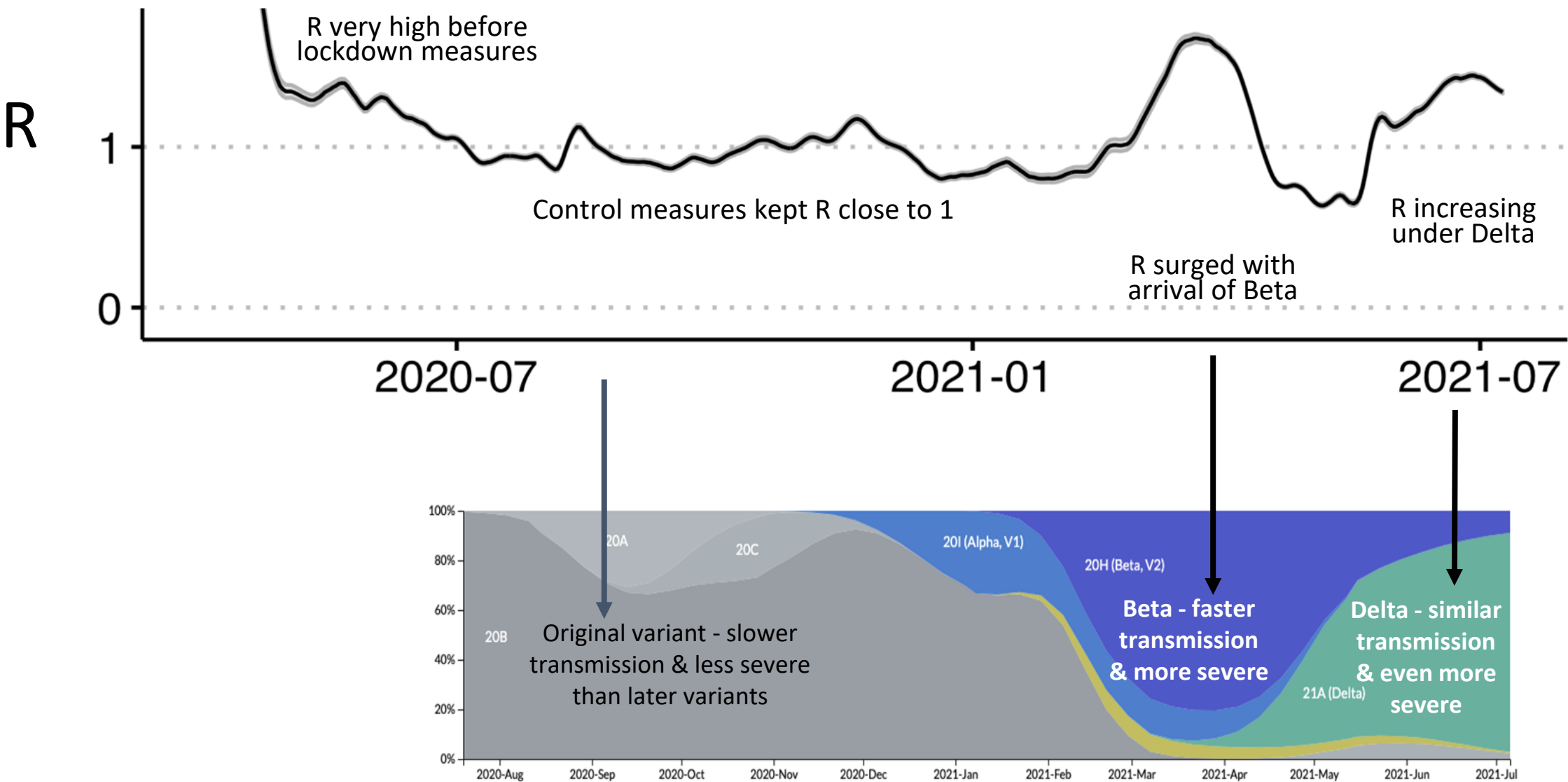
100

10

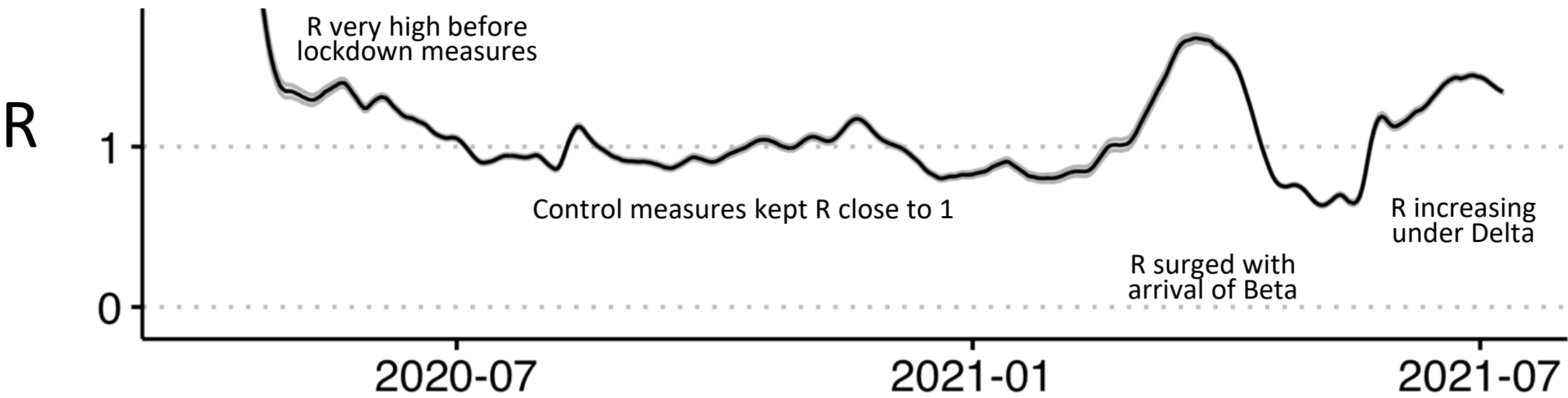
1

Weekly cases per 100,000

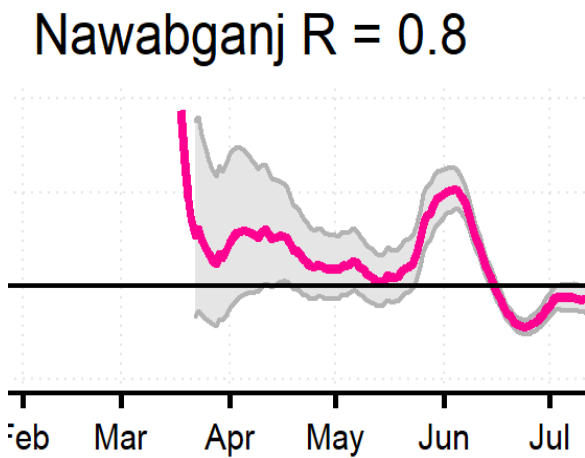
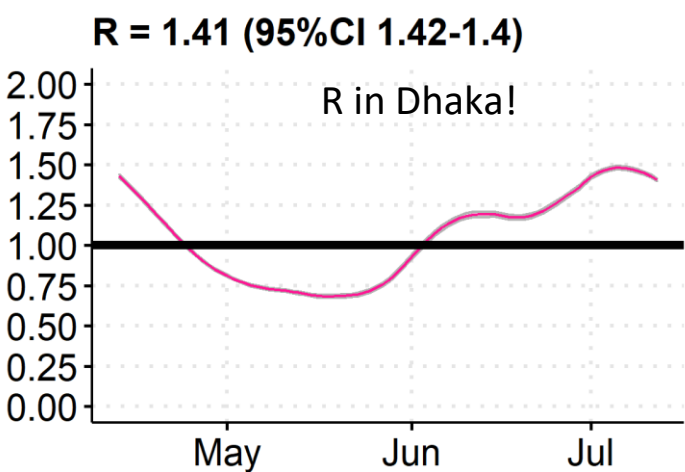
R for all of Bangladesh follows the overall epidemiological trajectory
(with each variant associated with different epidemiological characteristics)



R for all of Bangladesh follows the overall epidemiological trajectory with each variant associated with different epidemiological characteristics)



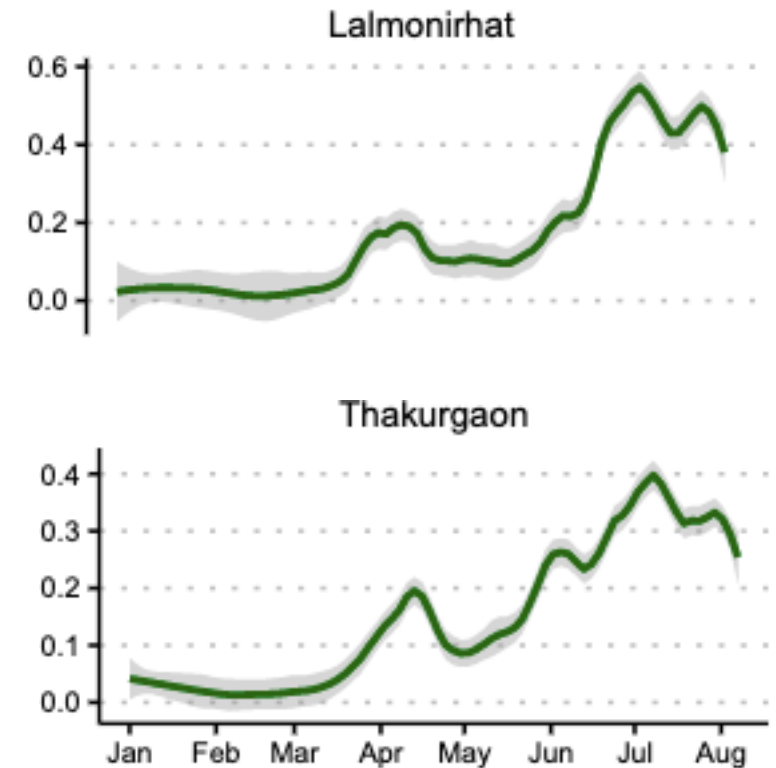
But since most cases are in Dhaka, the trajectory of R is mainly tracking Dhaka!



R is already much lower in several western rural districts

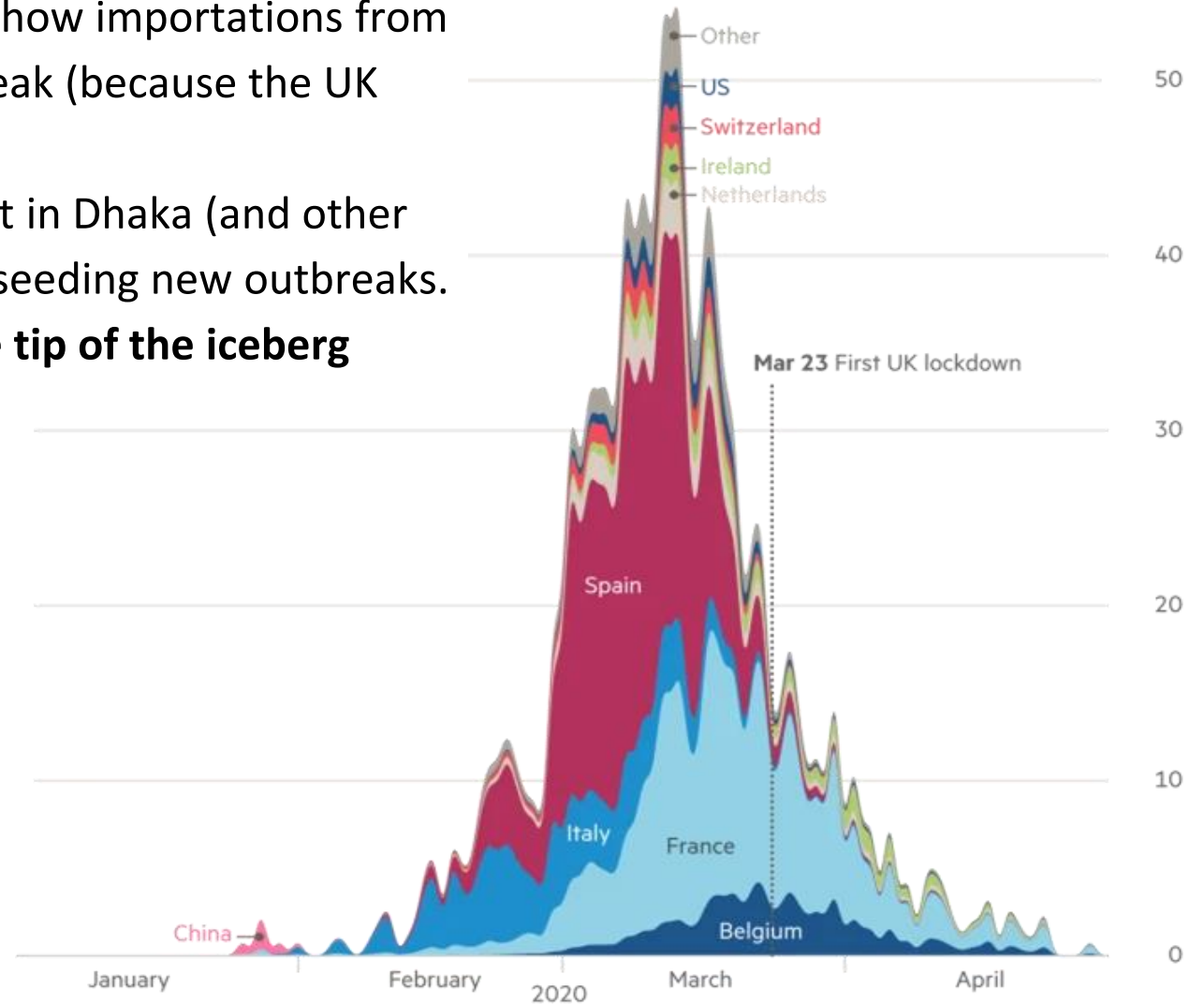
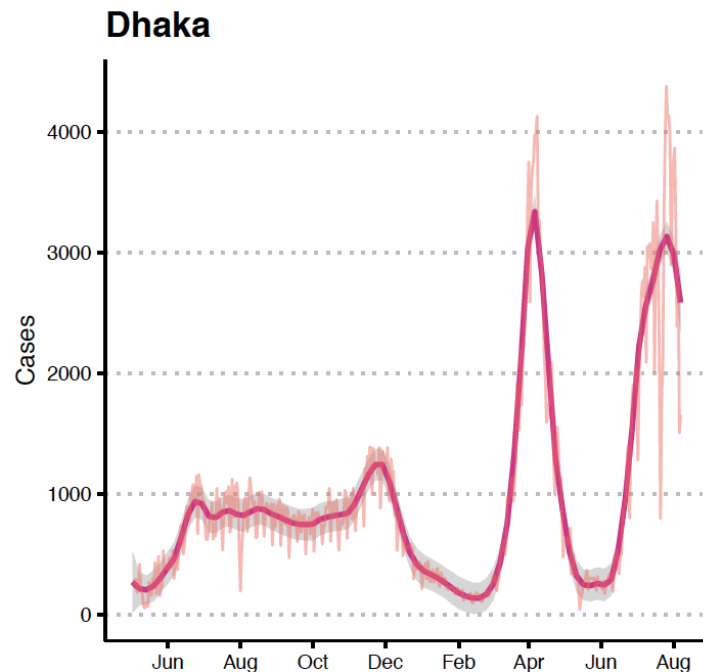
Additional epidemiological interpretation:

- Total case numbers are affected by testing capacity
 - Test capacity has increased over time and become more decentralized
 - However test capacity has frequently been saturated
 - Patterns of test results also reflect sociocultural factors e.g. Eid
- Even given caveats, test positivity is a very useful indicator
- Comparing R and test positivity is useful to consolidate interpretation
 - R helps to explain outbreak duration etc

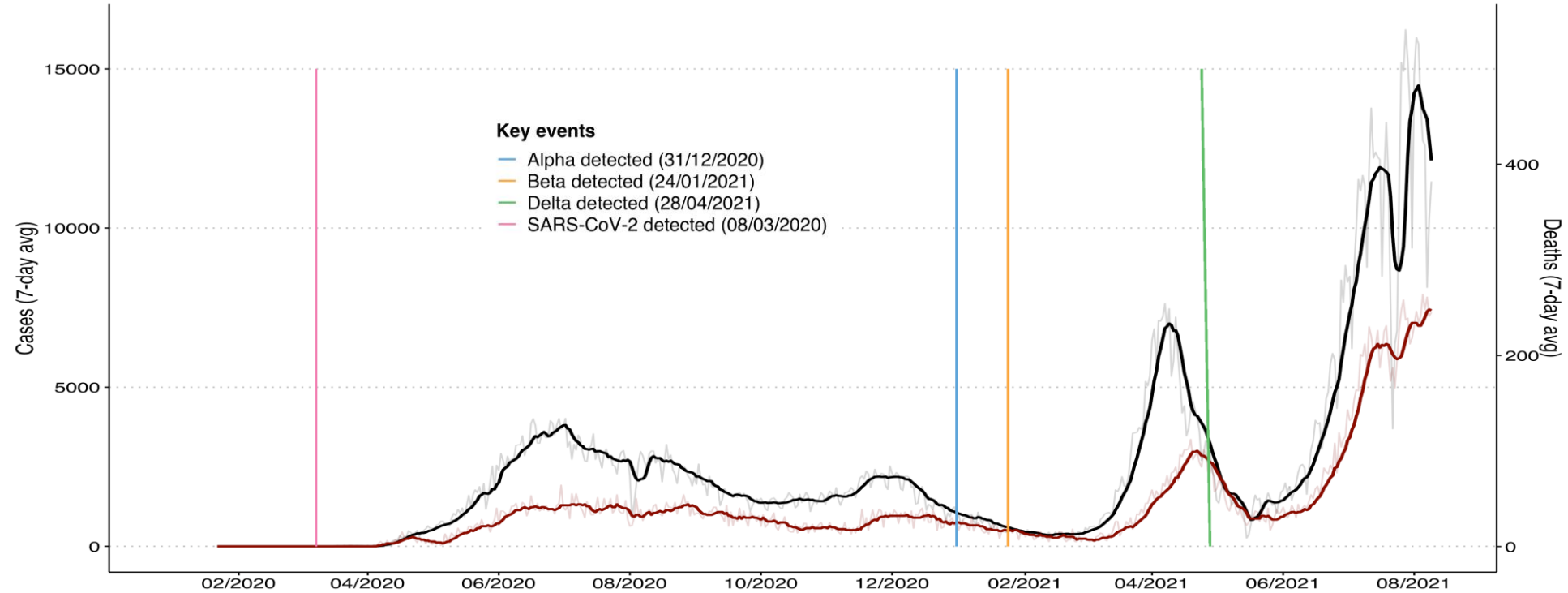


Importations seed new outbreaks that compound epidemic growth

- This example from the first wave in the UK shows how importations from around the world led to an extremely large outbreak (because the UK was far too slow to lockdown)
- The same process is occurring for the Delta variant in Dhaka (and other cities) as infections brought from other areas are seeding new outbreaks.
- **The early Delta sequences in April/May were the tip of the iceberg**



Let's revisit using R code!



```
## Load libraries
# devtools::install_github("RamiKrispin/coronavirus")
library(tidyverse)
library(coronavirus); #update_dataset()
library(zoo)
library(ggthemes)
library(lubridate)
```

Let's revisit using R code!

1. Obtain the data, select for Bangladesh and arrange for plotting:

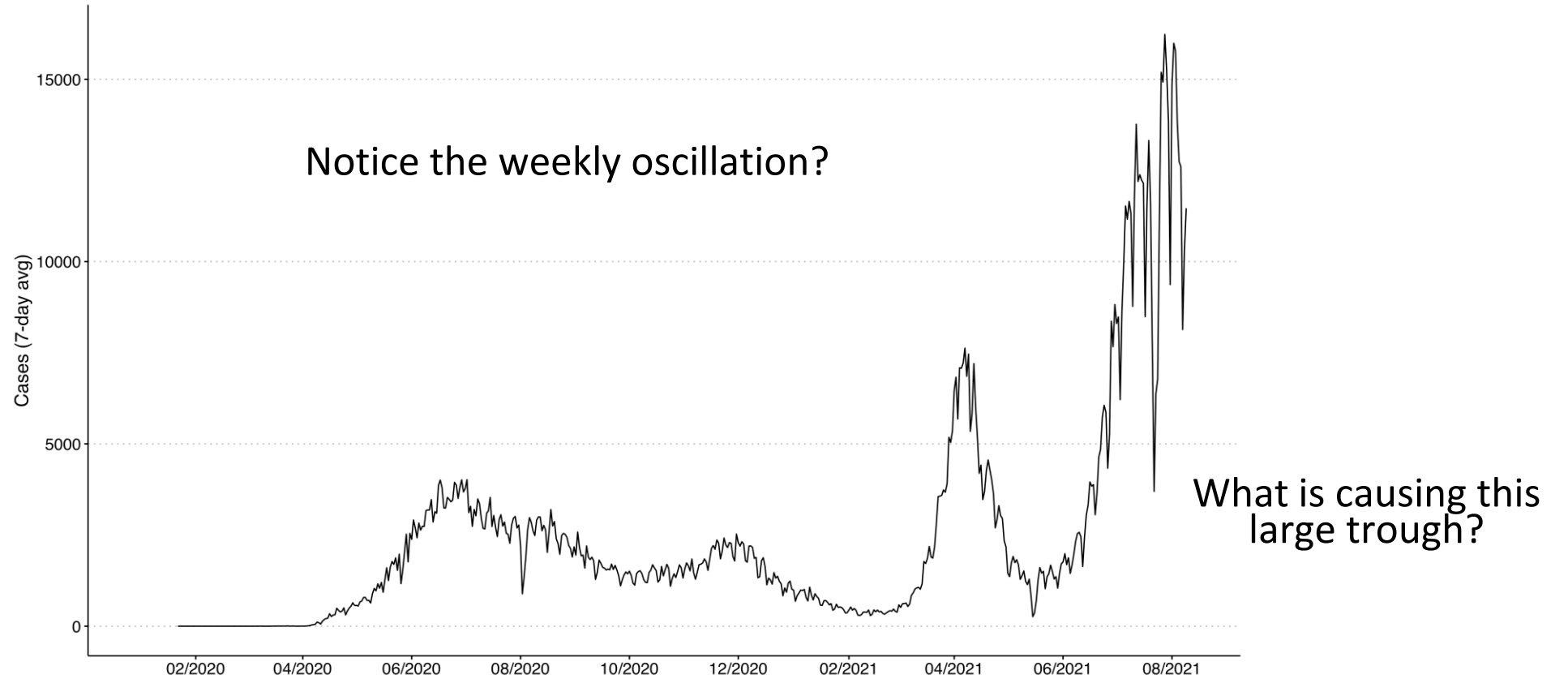
```
# pull data from John Hopkins repository - using installed package
data("coronavirus")
covid19_df <- refresh_coronavirus_jhu()

data <- covid19_df %>%
  filter(location == "Bangladesh") %>% # Select Bangladesh
  spread(data_type, value) %>%
  arrange(date) %>%
  mutate(deaths = deaths_new, cases = cases_new) %>% # rename variables
  # calculate 7-day rolling means - for cases and deaths
  mutate(cases_07 = floor(rollmean(cases, k = 7, fill=NA, align="right")),
         deaths_07 = floor(rollmean(deaths, k = 7, fill=NA, align="right"))) %>%
  ungroup()
```

2. Obtain the data, select for Bangladesh and arrange for plotting:

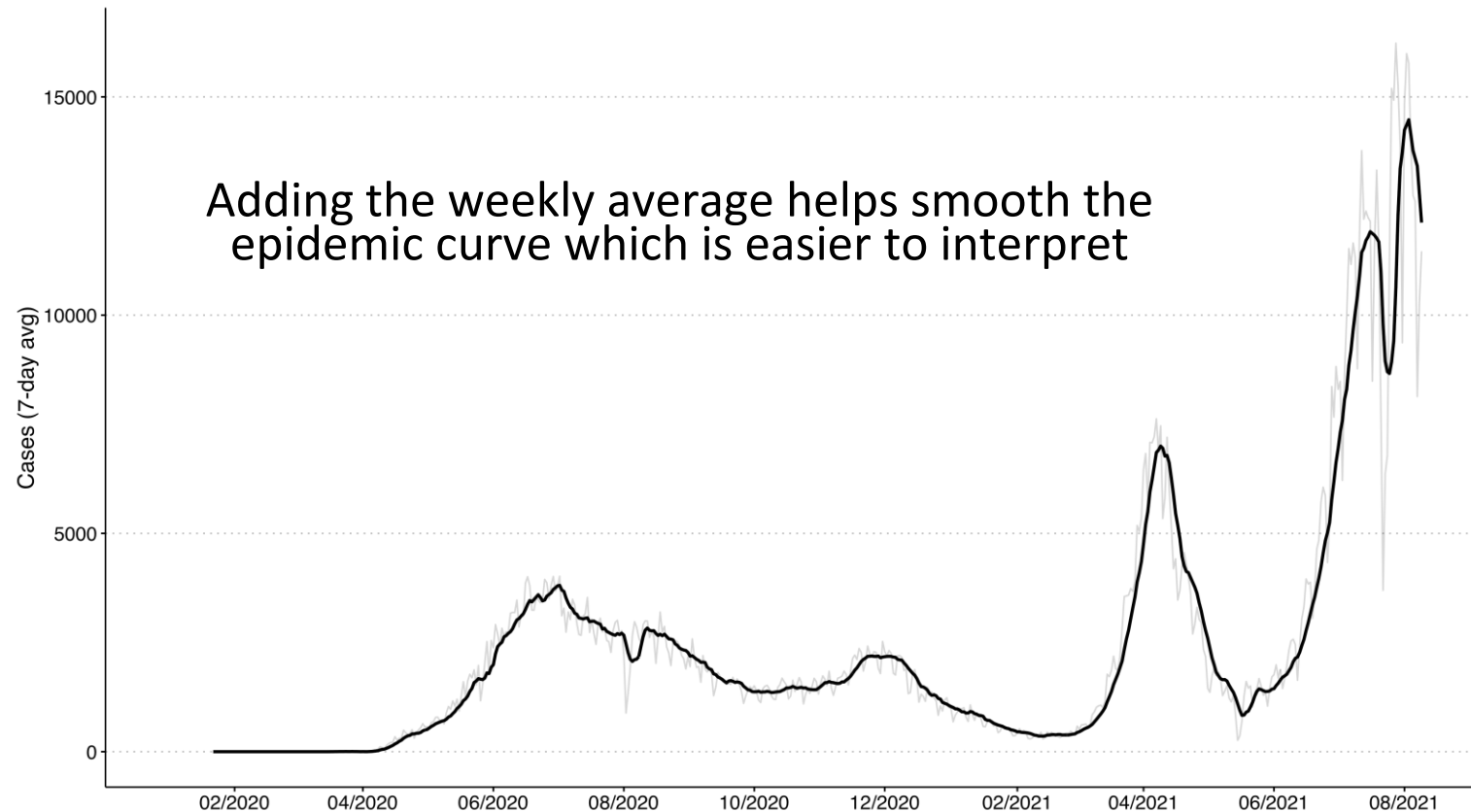
```
p1 <- ggplot(data, aes(x=date)) +
  geom_line(data = data, aes(y = cases), color="black") +
  scale_x_date(limits=c(startdate, enddate), date_breaks="2 month", date_labels = "%m/%Y") +
  labs(x="", y="Cases (7-day avg)") + theme
p1
```

Let's revisit using R code!



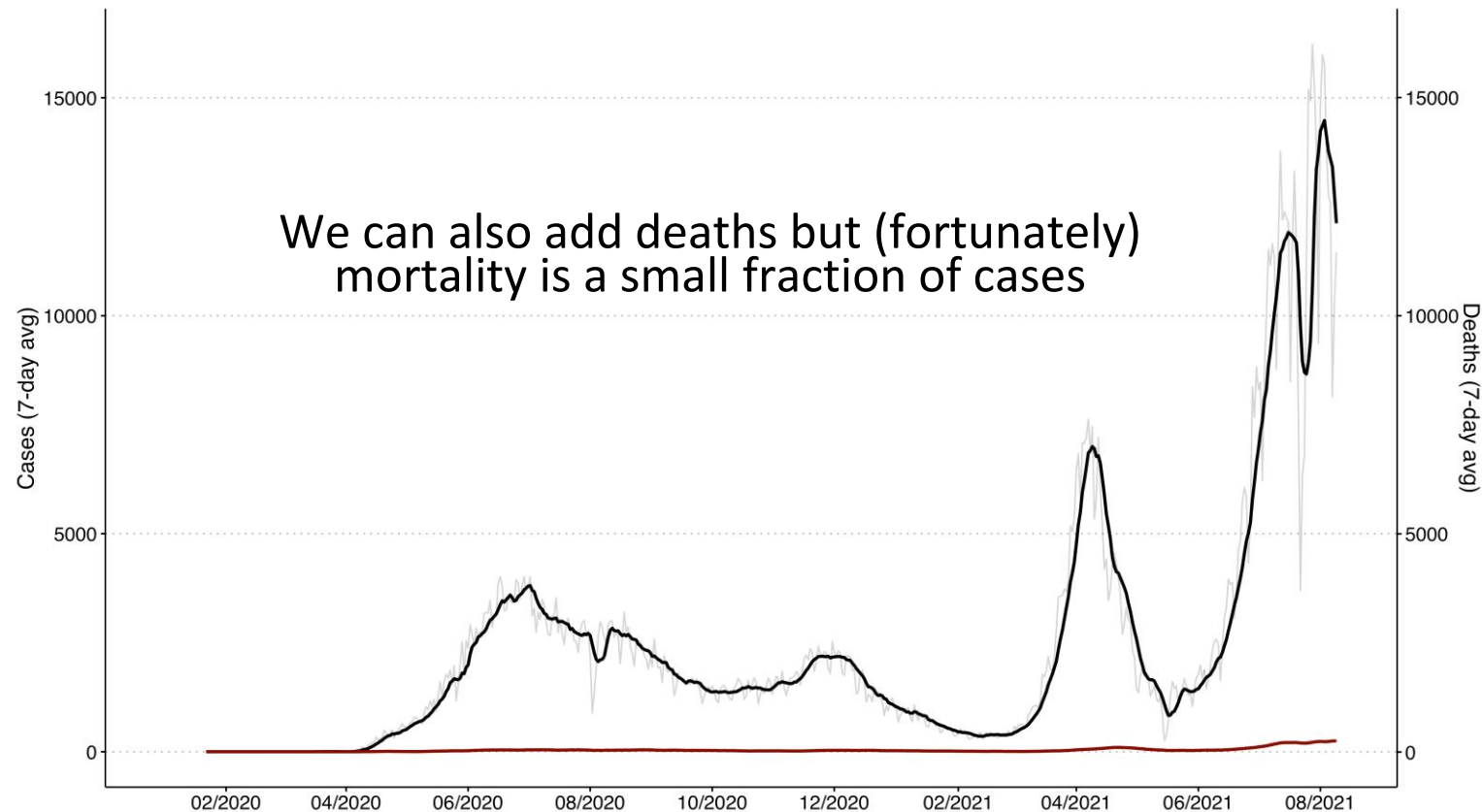
Its not quite ready for a government report yet.....

Let's revisit using R code!



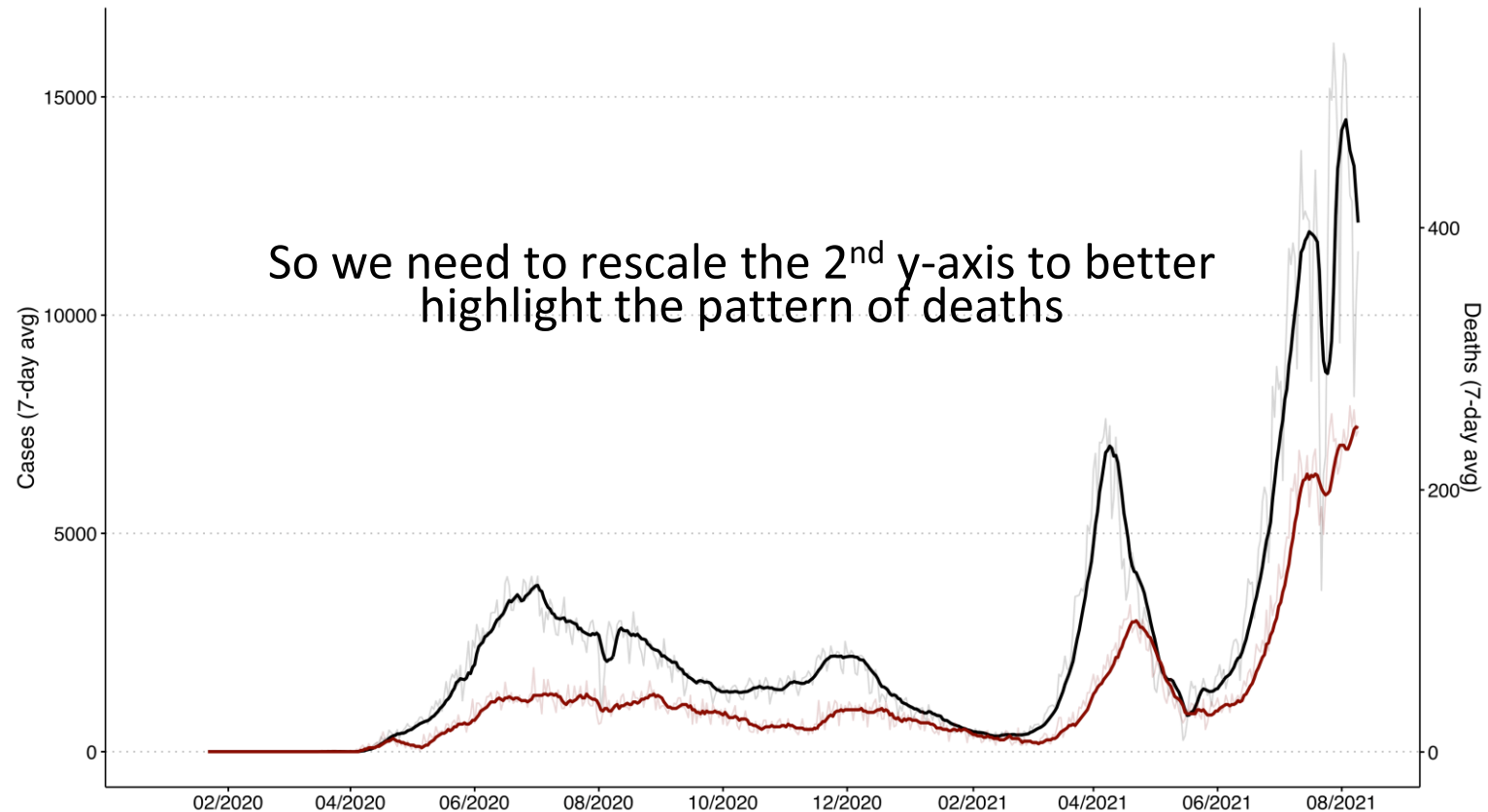
```
# 2. reduce colour of daily cases and add 7-day rolling mean
p2 <- ggplot(data, aes(x=date)) +
  geom_line(data = data, aes(y = cases), color="black", alpha=0.2) +
  geom_line(aes(y = cases_07), color="black", alpha=1, size=1) +
  scale_x_date(limits=c(startdate, enddate), date_breaks="2 month", date_labels = "%m/%Y") +
  labs(x="", y="Cases (7-day avg)") + theme
```


Let's revisit using R code!



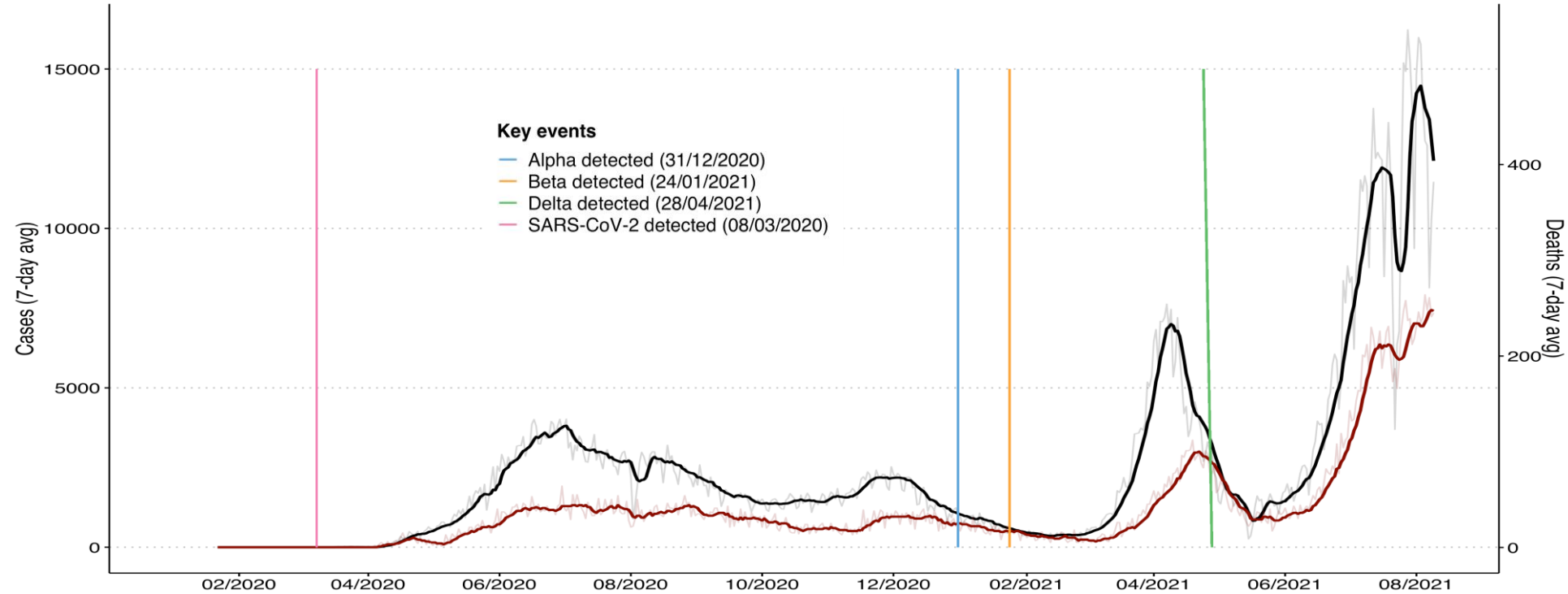
```
p3 <- ggplot(data, aes(x=date)) +  
  geom_line(data = data, aes(y = cases), color="black", alpha=0.2) +  
  geom_line(aes(y = cases_07), color="black", alpha=1, size=1) +  
  geom_line(aes(y = deaths), color="darkred", alpha=0.2) +  
  geom_line(aes(y = deaths_07), color="darkred", alpha=1, size=1) +  
  scale_x_date(limits=c(startdate, enddate), date_breaks="2 month", date_labels = "%m/%Y") +  
  scale_y_continuous(sec.axis = sec.axis(~., name = "Deaths (7-day avg)")) +  
  labs(x="", y="Cases (7-day avg)") + theme
```

Let's revisit using R code!



```
geom_line(aes(y = deaths*30), color="darkred", alpha=0.2) +  
geom_line(aes(y = deaths_07*30), color="darkred", alpha=1, size=1) +  
scale_x_date(limits=c(startdate, enddate), date_breaks="2 month", date_labels = "%m/%Y") +  
scale_y_continuous(sec.axis = sec_axis(~ ./30, name = "Deaths (7-day avg)")) +
```

Let's revisit using R code!



And finally we add on other annotation regarding detection of each variant

```
geom_segment(aes(x = ymd("2020-03-08"), y = 15000, xend = ymd("2020-03-08"), yend = 0, color="SARS-CoV-2 detected (08/03/2020)", size=0.6, linetype = "solid")) +  
geom_segment(aes(x = ymd("2020-12-31"), y = 15000, xend = ymd("2020-12-31"), yend = 0, color="Alpha detected (31/12/2020)", size=0.7, linetype = "solid")) +  
geom_segment(aes(x = ymd("2021-01-24"), y = 15000, xend = ymd("2021-01-24"), yend = 0, color="Beta detected (24/01/2021)", size=0.7, linetype = "solid")) +  
geom_segment(aes(x = ymd("2021-04-24"), y = 15000, xend = ymd("2021-04-28"), yend = 0, color="Delta detected (28/04/2021)", size=0.7, linetype = "solid")) +  
  
scale_x_date(limits=c(startdate, enddate), date_breaks="2 month", date_labels = "%m/%Y") +  
scale_y_continuous(sec.axis = sec_axis(~ ./30, name = "Deaths (7-day avg)")) +  
ggthemes::scale_color_few() +  
labs(x="", y="Cases (7-day avg)", color="Key events") + theme
```

By coding this in R we can quickly generate time series for every district:

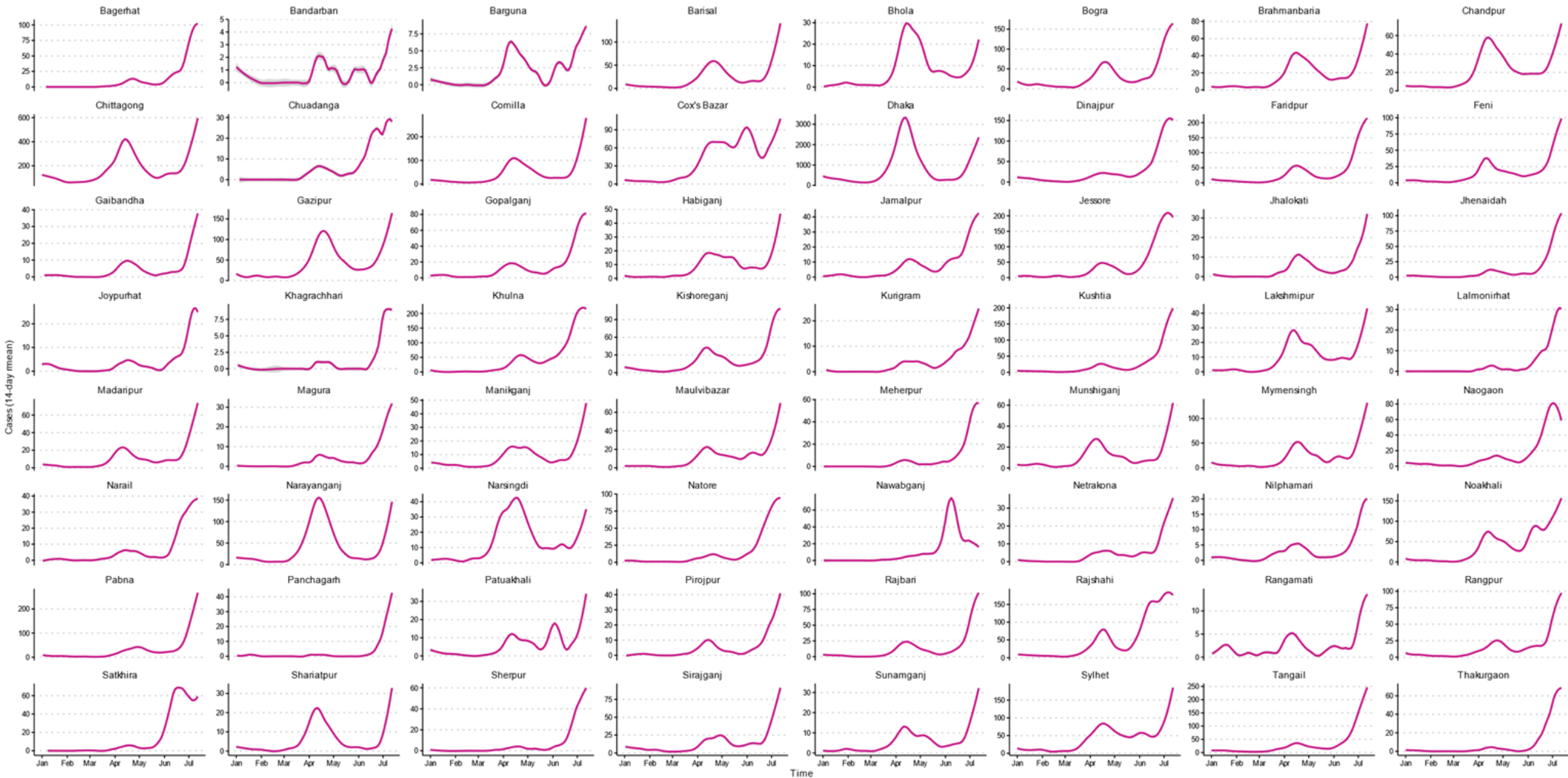
1. First organize the data, grouping it by district

```
data.daily <- data.daily %>% arrange(date) %>% group_by(district) %>% arrange(date) %>%  
  mutate(cum_cases = cumsum(cases),  
         cum_tests = cumsum(tests),  
         cases_07 = floor(rollmean(cases, k = 7, fill = NA, align="right")),  
         tests_07 = floor(rollmean(tests, k = 7, fill = NA, align="right"))) %>%  
  mutate(positivity = round(cases/tests, 2),  
         positivity_07 = round(cases_07/tests_07, 2),  
         cases.100k_07 = round((cases_07/pop)*100000,2),  
         tests.100k_07 = round((tests_07/pop)*100000,2)) %>% na.omit()
```

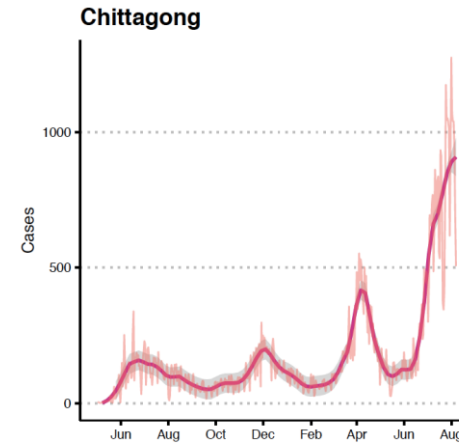
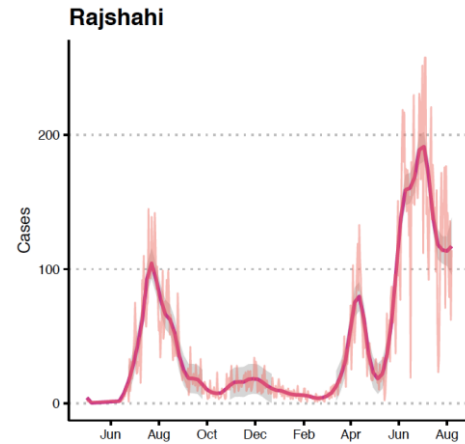
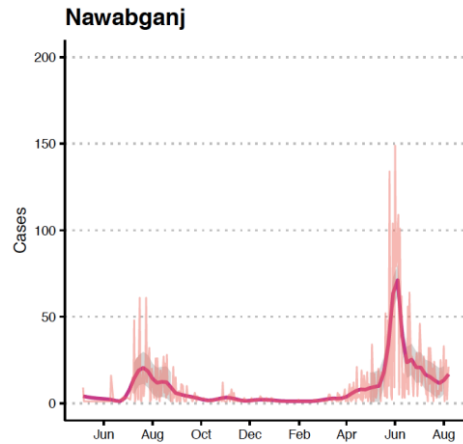
2. Then plot using the facet_wrap tool to show a panel for each district

```
p4 <- ggplot(data.daily, aes(x=date)) +  
  geom_smooth(aes(y = cases), color="mediumvioletred", span=0.1) +  
  theme +  
  facet_wrap(~district, scales="free_y") +  
  scale_x_date(limits = c(dmy("01-01-2021"), max(data.daily$date)), date_breaks="1 month", date_labels = "%b") +  
  labs(x="", y="Cases", color="Legend")
```

By coding this in R we can quickly generate time series for every district:



But perhaps that is too much!
We can also plot one at a time... but this requires a “for loop”



```
for(i in 1:length(districts)){  
  data <- subset(data.daily, district == districts[i])  
  
  print(  
    ggplot(data, aes(x=date)) +  
      geom_smooth(aes(y = cases), color="mediumvioletred", span=0.1) +  
      geom_line(aes(y = cases, color="mediumvioletred"), alpha=0.5) +  
      theme +  
      scale_x_date(date_breaks="2 month", date_labels = "%b") +  
      ylim(0, max(200, max(data$cases))) +  
      labs(x="", y="Cases", color="Legend", title = districts[i]) +  
      theme(legend.position = "none")  
  )  
}
```

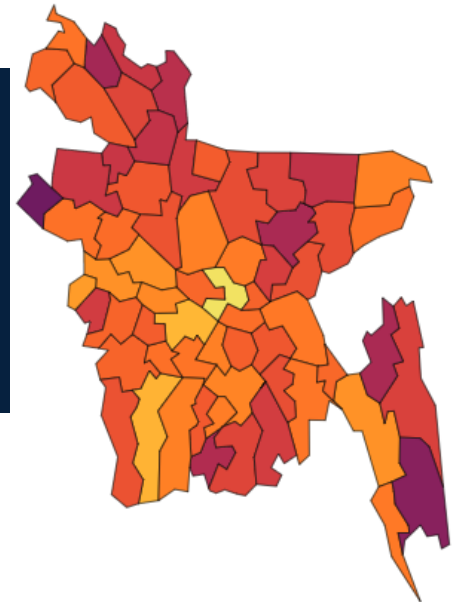
We can make maps in a similar way

- But we need to understand how to work with shapefiles (argh!)

```
# import district shapefile
district.shp <- read_sf(paste0(git.path, "observingcovidprocesses/BGD_COVID_mapping/processed_data/simplified_BGD_dist
  transmute(district = DISTNAME) %>% st_transform(crs=4326)
format(object.size(district.shp), units="Mb")
```

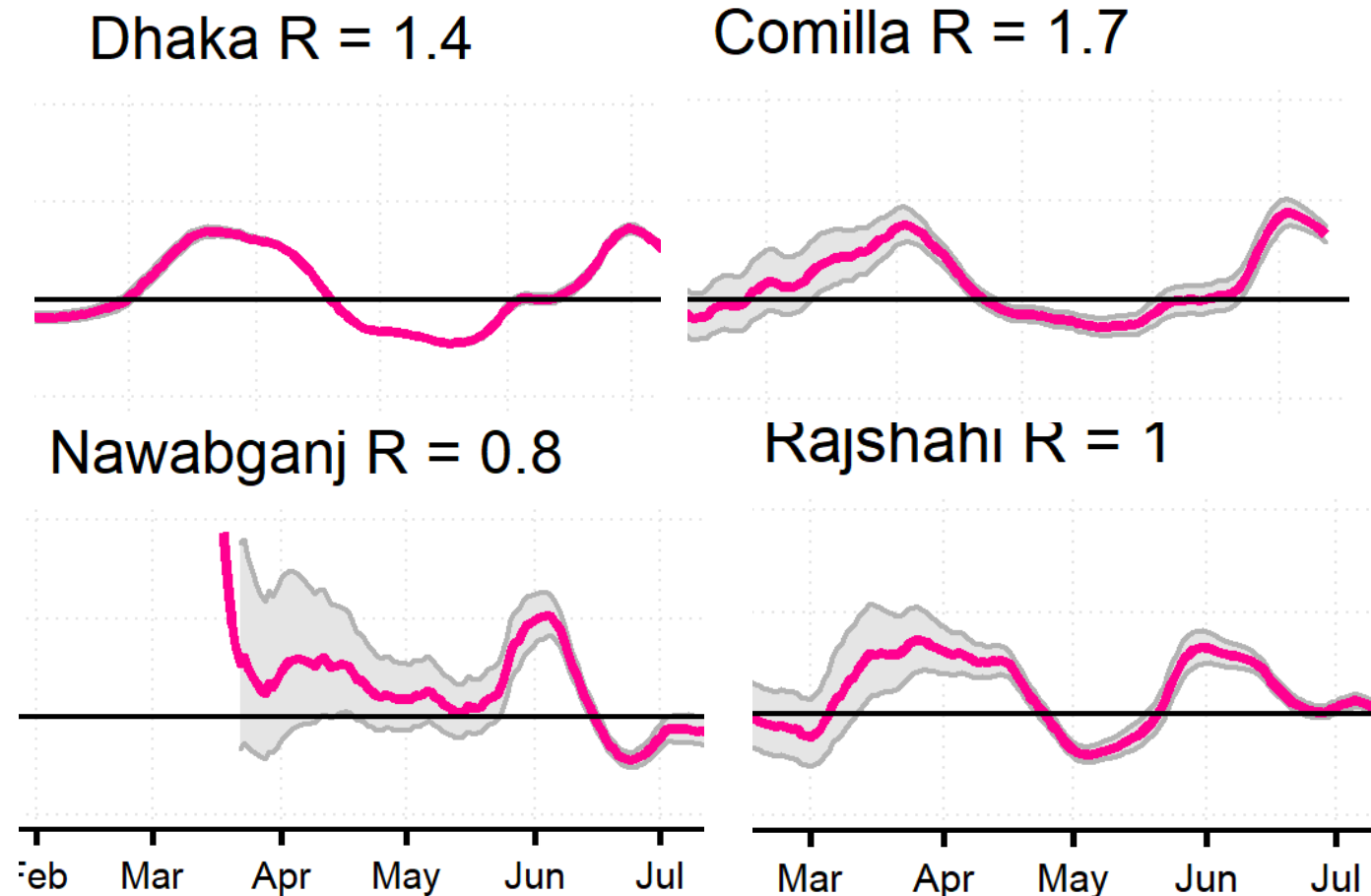
2021-07-13

```
p1 <- ggplot(data=data.daily, aes(fill = cases)) +
  geom_sf(color="black", size = 0.1) +
  scale_fill_viridis(trans="log", option = "C",
    breaks = c(0, 10, 100, data.daily$cases[which.max(data.daily$cases)]),
    labels = c(0, 10, 100, data.daily$cases[which.max(data.daily$cases)])) +
  facet_wrap(~date, nrow = 2, ncol = 3) +
  theme + labs(x = "", y = "", fill="Daily cases")
```



Calculating R is conceptually difficult, but thanks to some handy R packages is relatively simple to do:

- We need to parameterize the serial interval first!
- Select a time window for estimation
- Use the `estimate_R` function
- Store our estimate and 95% confidence intervals
- We also should recognize why R might go awry!



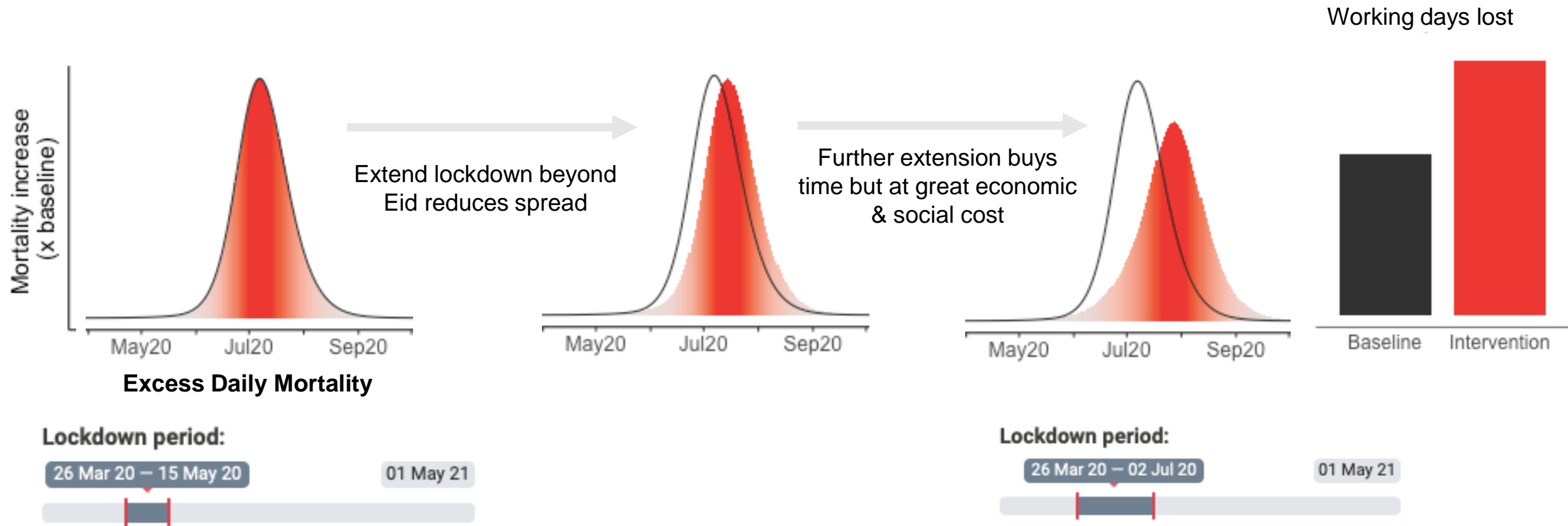
What other things can we do...

A lot!

- Saving useful outputs (pdfs, jpegs, html files - what do you need for your presentation or report?)
- Making interactive outputs – do you want to share outputs that stakeholders can explore?

COVID-19 Epi-Econ Decision Support (CEEDS) tool

http://boydorr.gla.ac.uk/BGD_Covid-19/CEEDS/

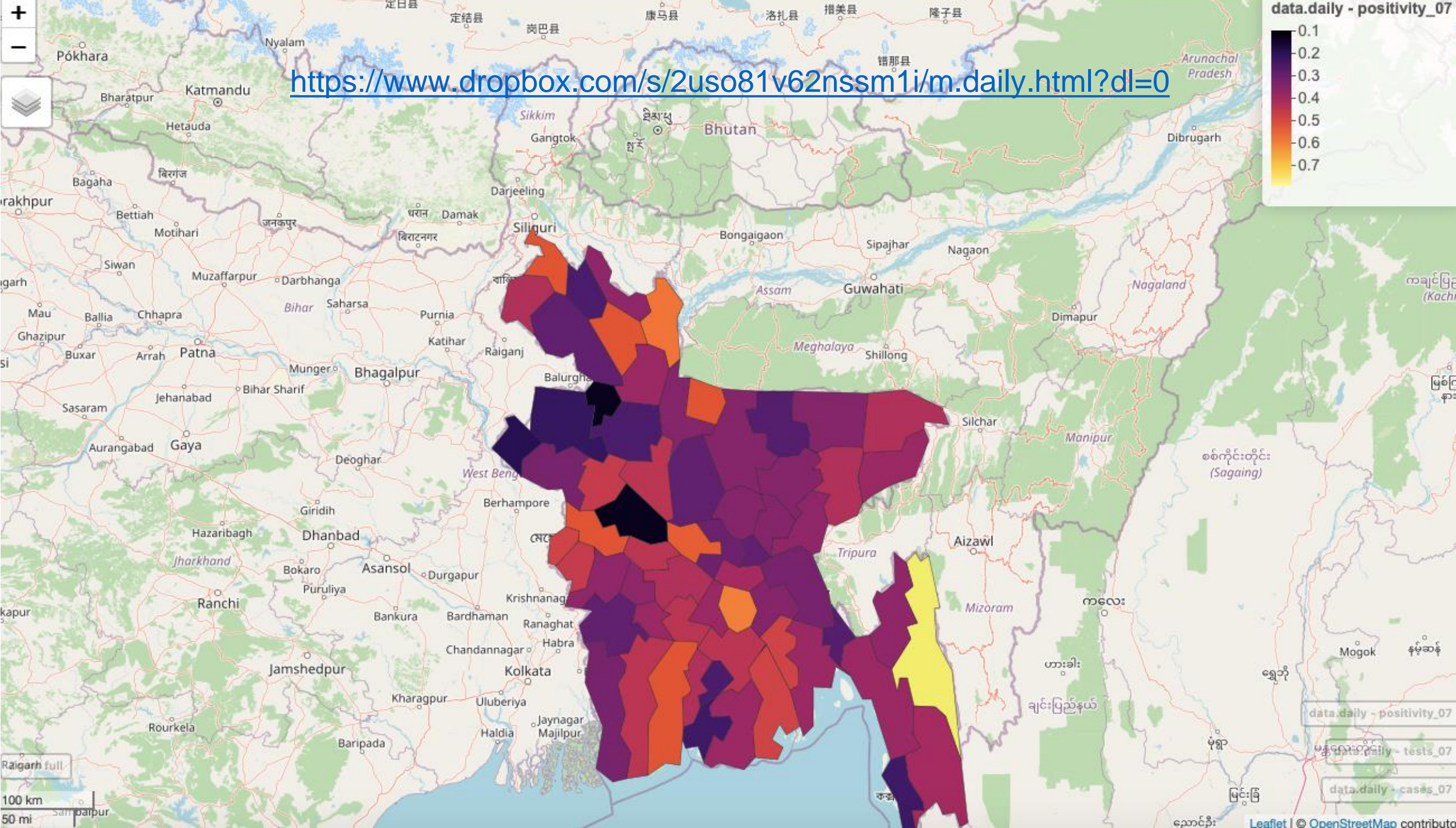
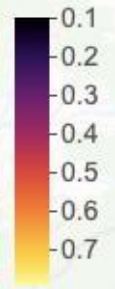


- Initial modeling & case data indicated introductions in early February
- Lockdown from 23rd March but challenges to sustaining given precarity & food security
- Extended lockdown beyond EEID to buy time and prevent massive dissemination



<https://www.dropbox.com/s/2uso81v62nssm1i/m.daily.html?dl=0>

data.daily - positivity_07



data.daily - positivity_07

data.daily - tests_07

data.daily - cases_07

R is very powerful! But it is a *steep* learning curve

- If you want to understand this lecture in more depth, come to the extra sessions planned
- Bangladesh needs budding quantitative epidemiologists able to lead this work!
- **We are looking to support IEDCR and DGHS to further develop and adapt these situation reports for the future**

