

# Modelling COVID-19 from a physicist's perspective

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European COVID-19 Modelling Hub  
July 6, 2021

# My background

- Professor in Particle Physics at the University of Victoria holding a joint appointment with the TRIUMF Laboratory (BC – Canada)
  - Build experiments and analyze data in large international collaborations
  - I teach data analysis to physicists
- Since April 2020, using a model based on a physicists perspective:
  - Incorporate the fundamental workings of the system.
  - Keep it as simple as possible. A model is never “perfect” (always wrong!)
  - Focus on its main purpose: interpret data to learn about the spread of COVID
  - The model ([www.pypm.ca](http://www.pypm.ca)) has served that purpose well
  - Engaged in regular discussions with academics in epidemiology in BC
- Since July 2020, participating in the US CDC COVID-19 forecasting group
  - US case/hospitalization/death data are very useful to challenge models
  - Led to joining the German forecast-hub later in 2020 → European hub

# Overview

- Introducing the pypm model
- Insights:
  - Piece-wise constant transmission rates:
    - describe case, hospitalization, death time series reasonably well
    - give models an ability to forecast the spread of COVID-19
  - Variants and Vaccination have large impact on the spread:
    - models that incorporate these have an improved ability to forecast
- Summary
  - comments on data access/collaboration/forecasts and public policy

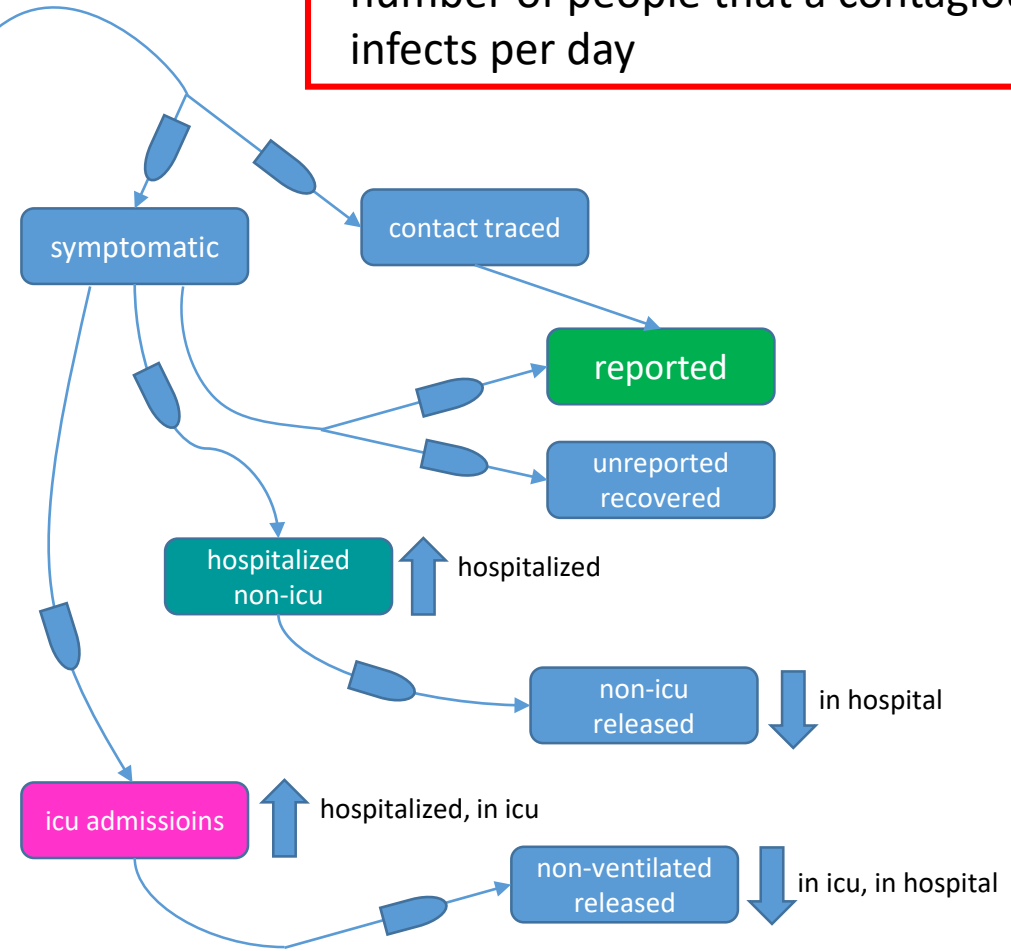
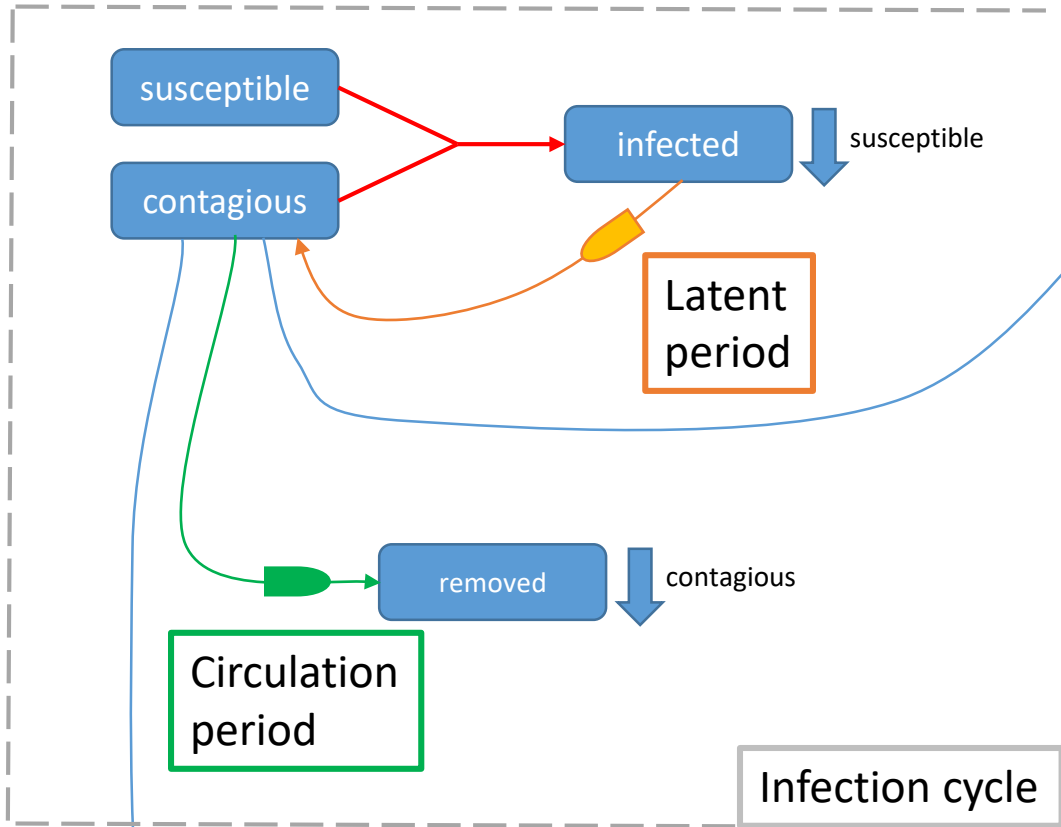
# pyPM.ca: python Population Modeller

- A general framework for building population models: pypmca
  - Based on finite time-difference equations
    - allows for arbitrary time delay distributions (not limited to exponential)
    - choose  $\Delta t = 1$  day to match data sources
  - Model objects are built from “population” objects and “connection” objects
    - Separates model design from numerical implementation: simplifies model construction and modification
  - Model objects can evolve expectation values and can produce simulated data
    - Simulated data essential to evaluate parameter estimators and to report quantiles
- A technical graphical user interface for jupyter notebook: ipypm
  - interact with data and models, explore parameter space
  - model parameters are estimated by fitting to cumulative case data (no ML)
- Open source on pypi/github
  - See: [www.pypm.ca](http://www.pypm.ca)
  - Single click startup

# Basic pyPM.ca model

$$E[\Delta I_{t+1}] = \alpha \frac{E[S_t]}{E[N_t]} E[C_t]$$

$\alpha$ : transmission rate. Initially, the average number of people that a contagious person infects per day



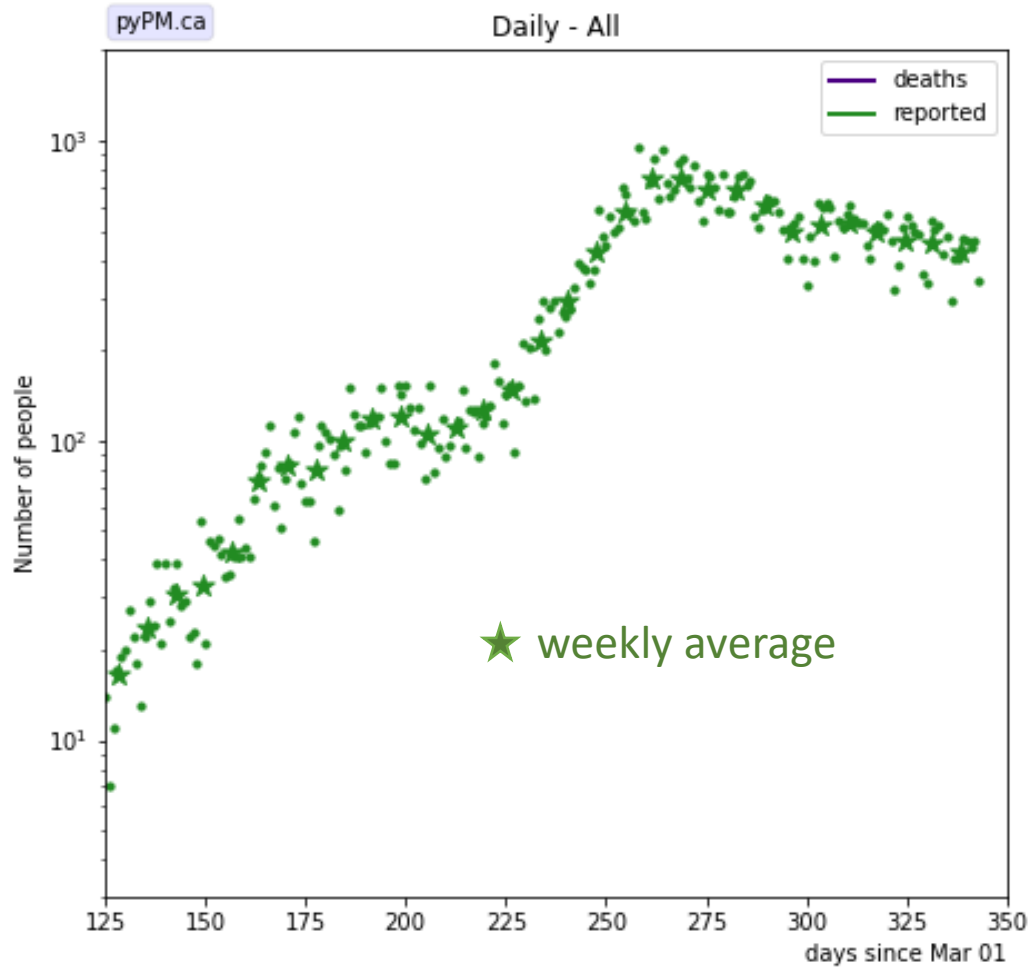
# Epidemic growth

- The “steady state” solution to the infection cycle equations (with constant susceptible fraction) is exponential growth (or decline): characterized by  $\delta$ :

$$E[C_{t+1}] = (1 + \delta)E[C_t]$$

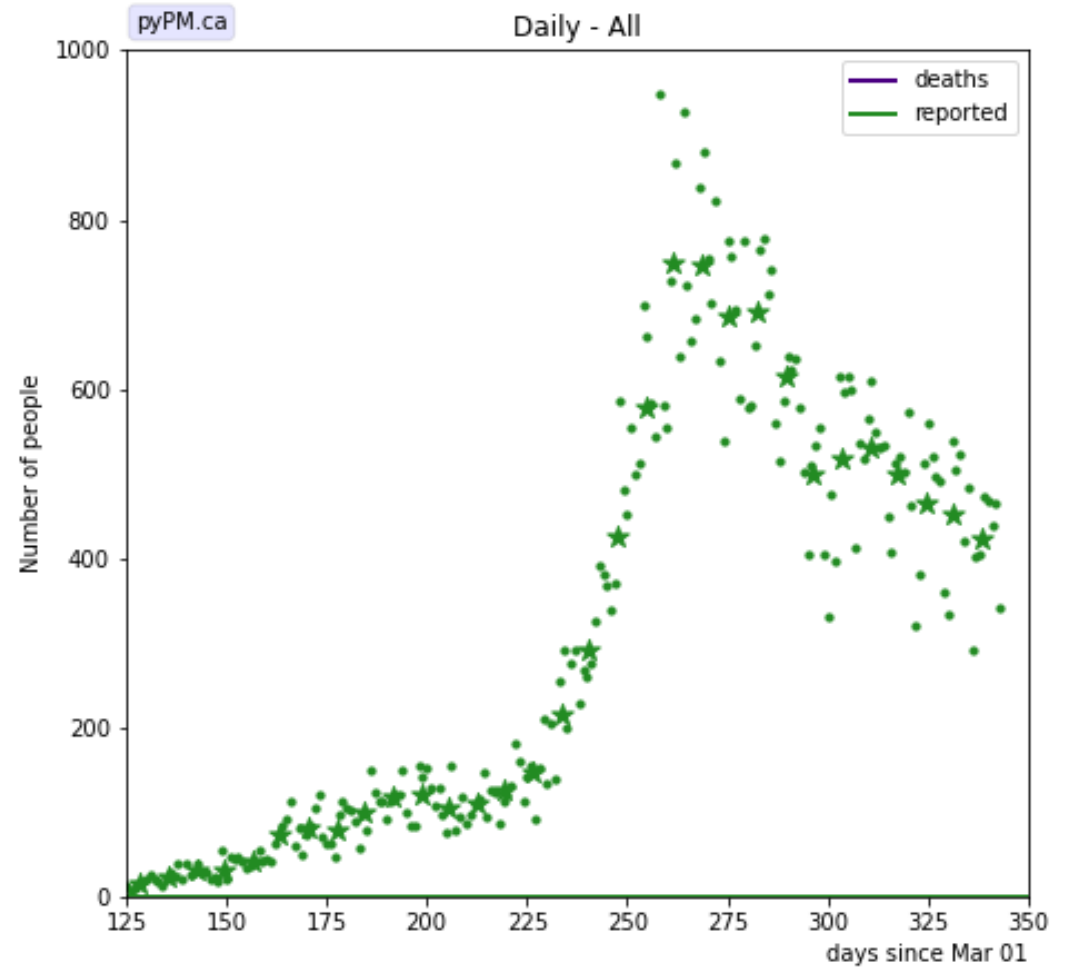
- $C_t$ : size of the circulating contagious population on day  $t$
- Imposing lockdown measures, reduces social contacts (reducing  $\alpha$ ), thereby reducing  $\delta$ 
  - Use case data to determine the transmission rate and when it changes
- Transmission rates alone do not determine the growth ( $\delta$ )
  - In the pyPM model: also depends on the latent and circulation period delays
  - In my analyses I keep these delays fixed, so the estimated values for  $\alpha$  are “effective transmission rates”

# Example: BC-Canada case data (July 2020 – Feb 2021)

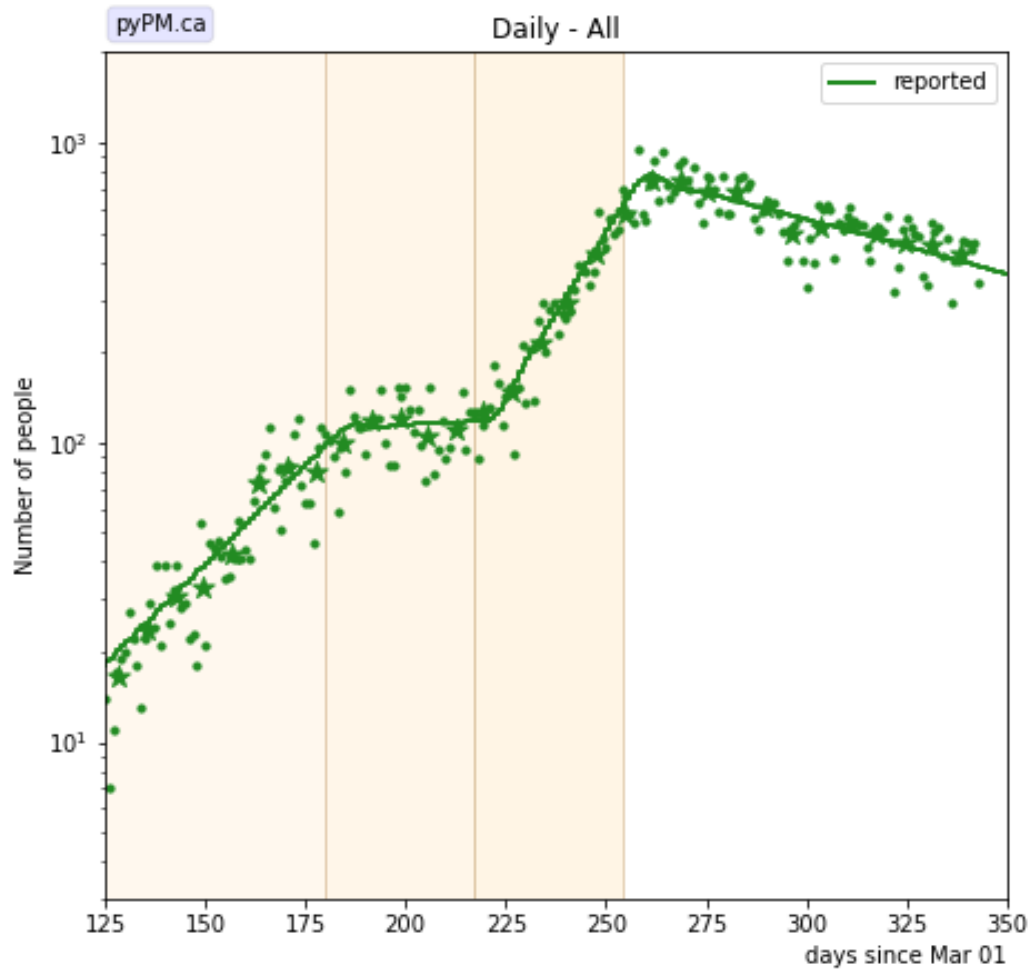


Jul 1, 2020

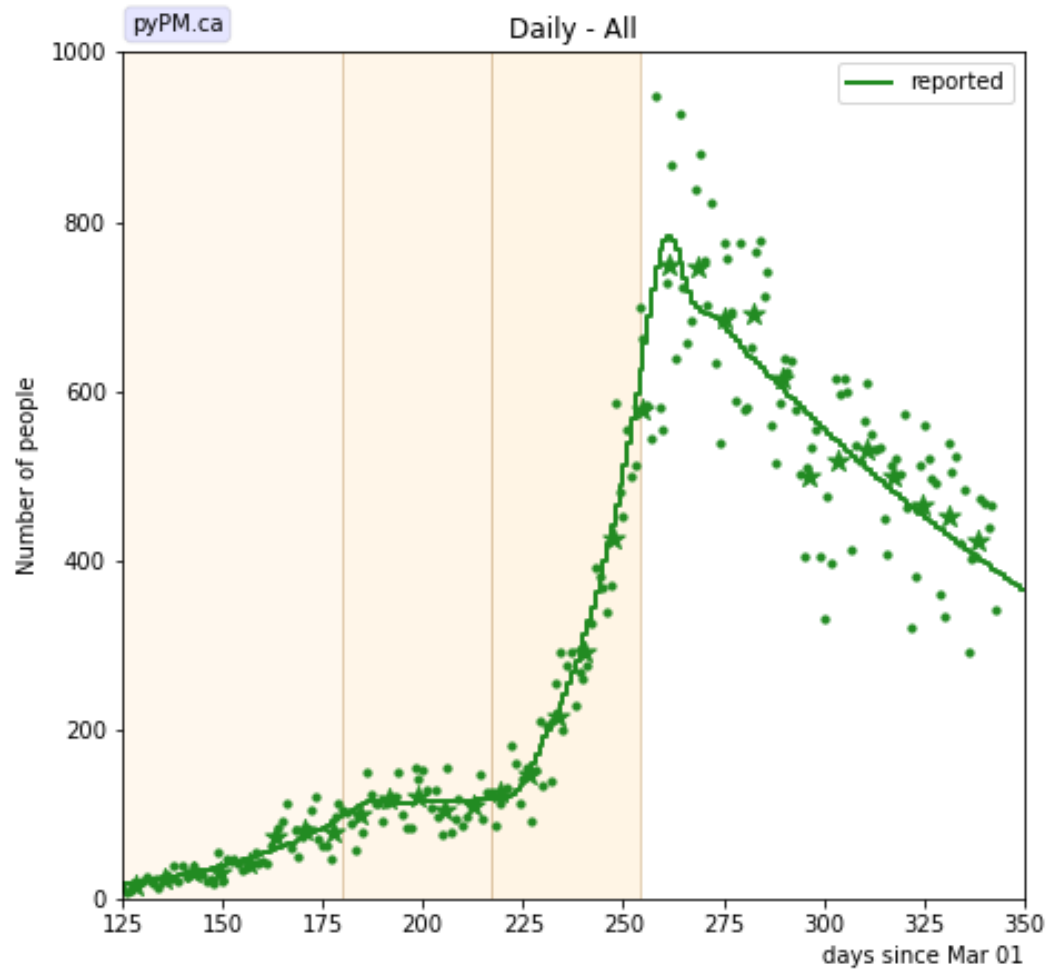
Feb 9, 2021



# BC-Canada case data (with model)



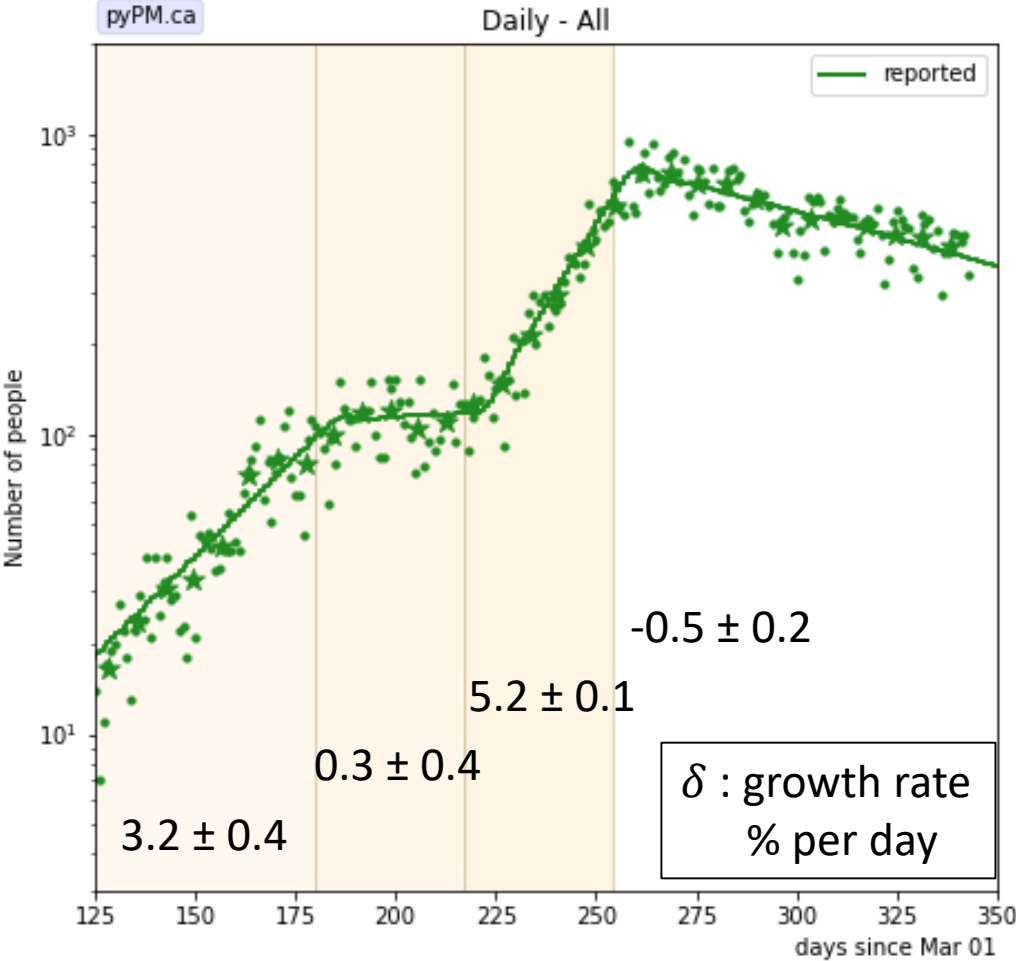
Jul 1 Aug 28 Oct 04 Nov 10 Feb 9



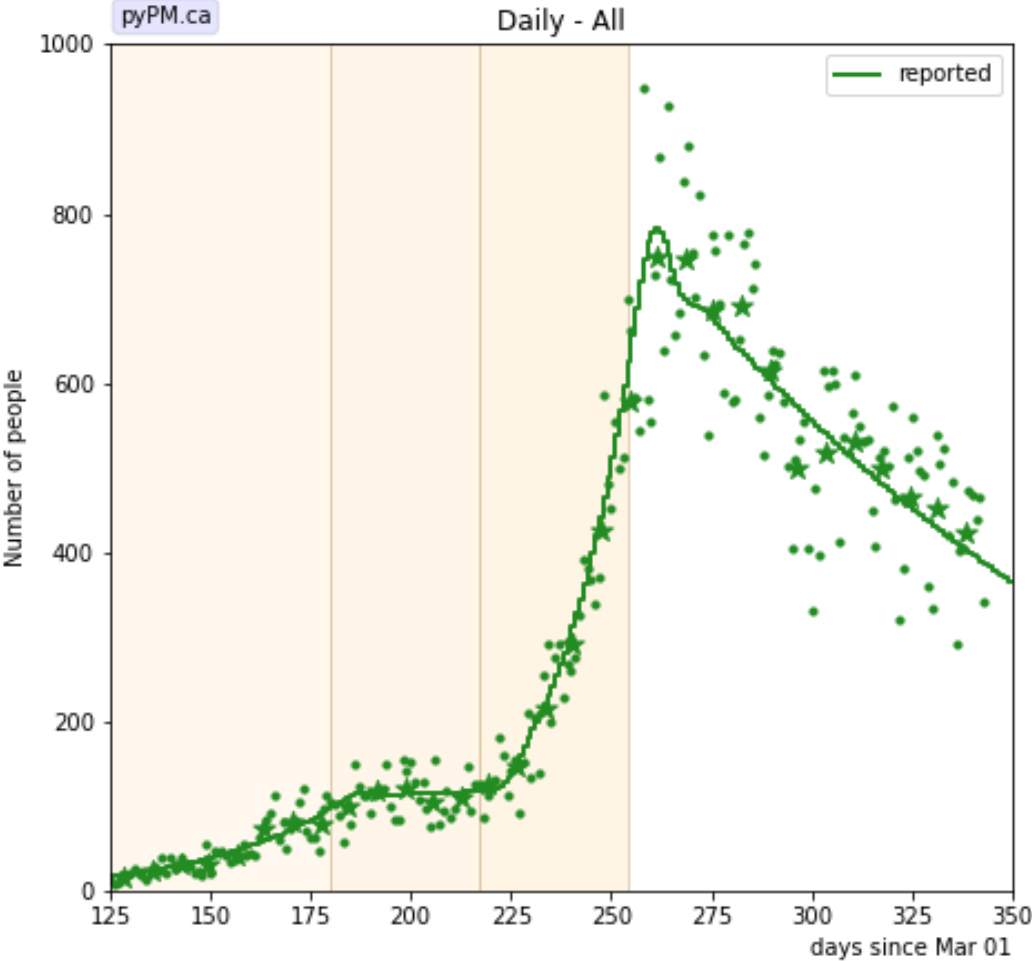
The spread of COVID-19 can be characterized by long periods of constant growth or decline.



# BC case data (with model)



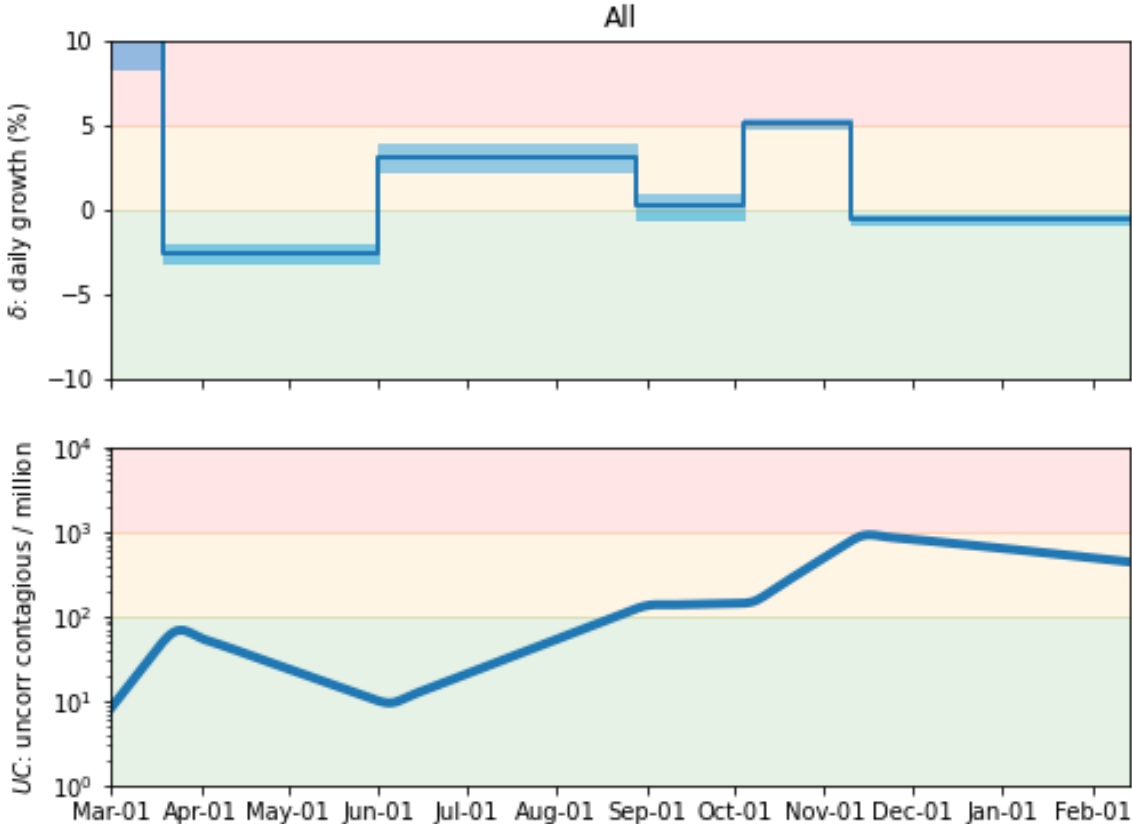
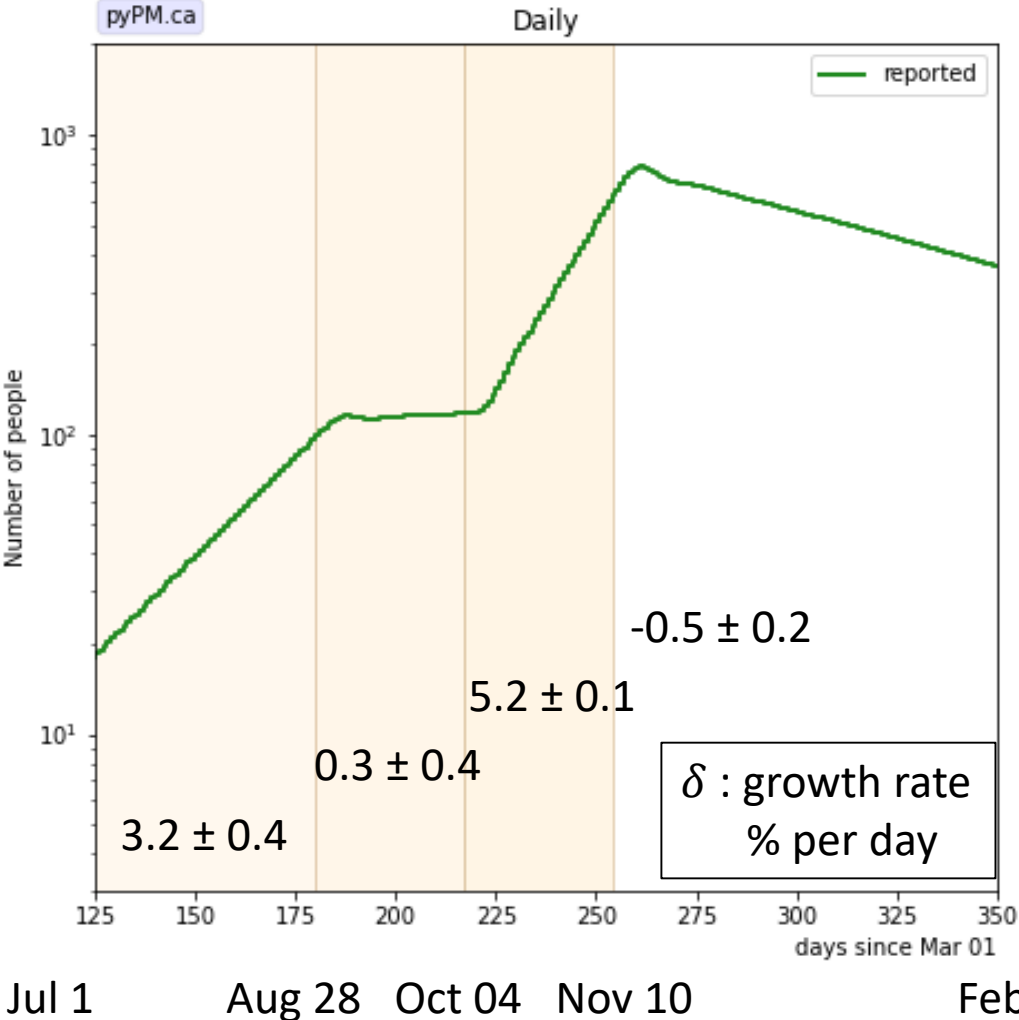
Jul 1      Aug 28    Oct 04    Nov 10                      Feb 9



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# BC model

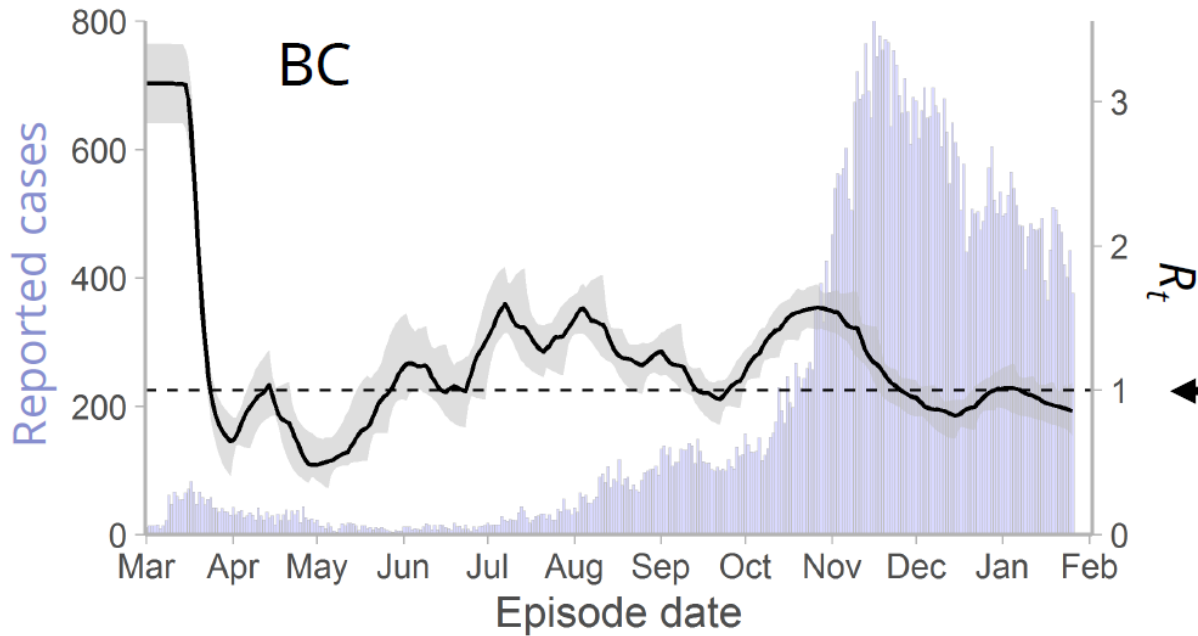
BC case history characterized by just a few “model independent” quantities.



The spread of COVID-19 can be characterized by long periods of constant growth or decline.

# Dynamic Compartmental Modeling: Recent Trends

Provincially, our model-based estimate of  $R_t$  (average daily number of new infections generated per case) continues to hover near 1.



Whenever  $R_t$  is  $> 1$ , there is a risk that the number of new cases could grow rapidly.

*Solid black line: median  $R_t$  based on data up to Feb 2, 2021; Grey band: 5%-95% credible interval; Purple bars: all reported cases. Due to a lag from symptom onset to reporting, the most recent cases are not shown.*

## COVID-19 IN BC

Many epidemiologists do not use this approach

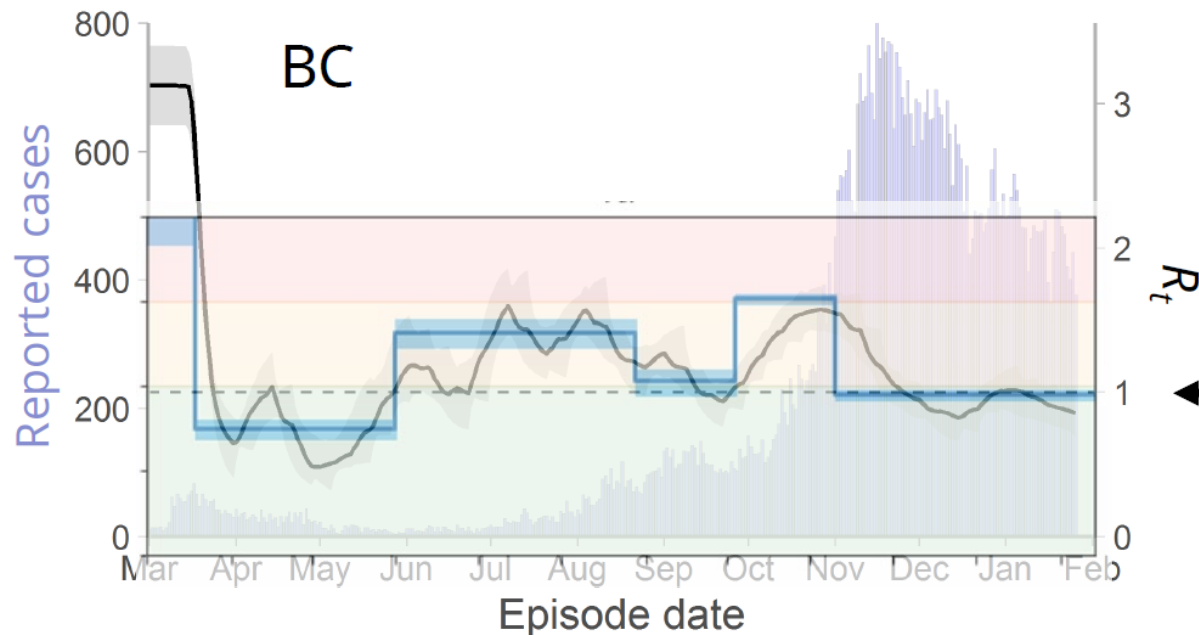
RIUMF

The spread of COVID-19 can be characterized by long periods of constant growth or decline.

21

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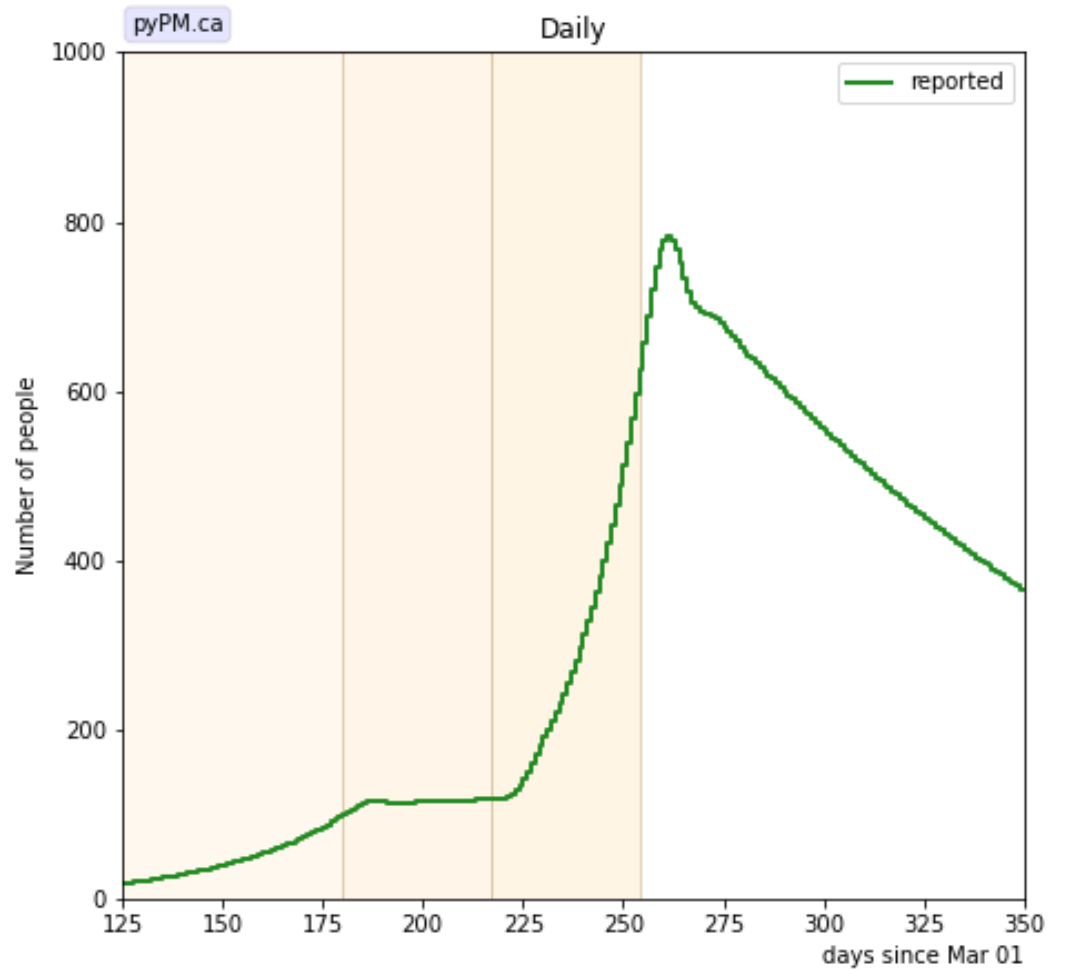
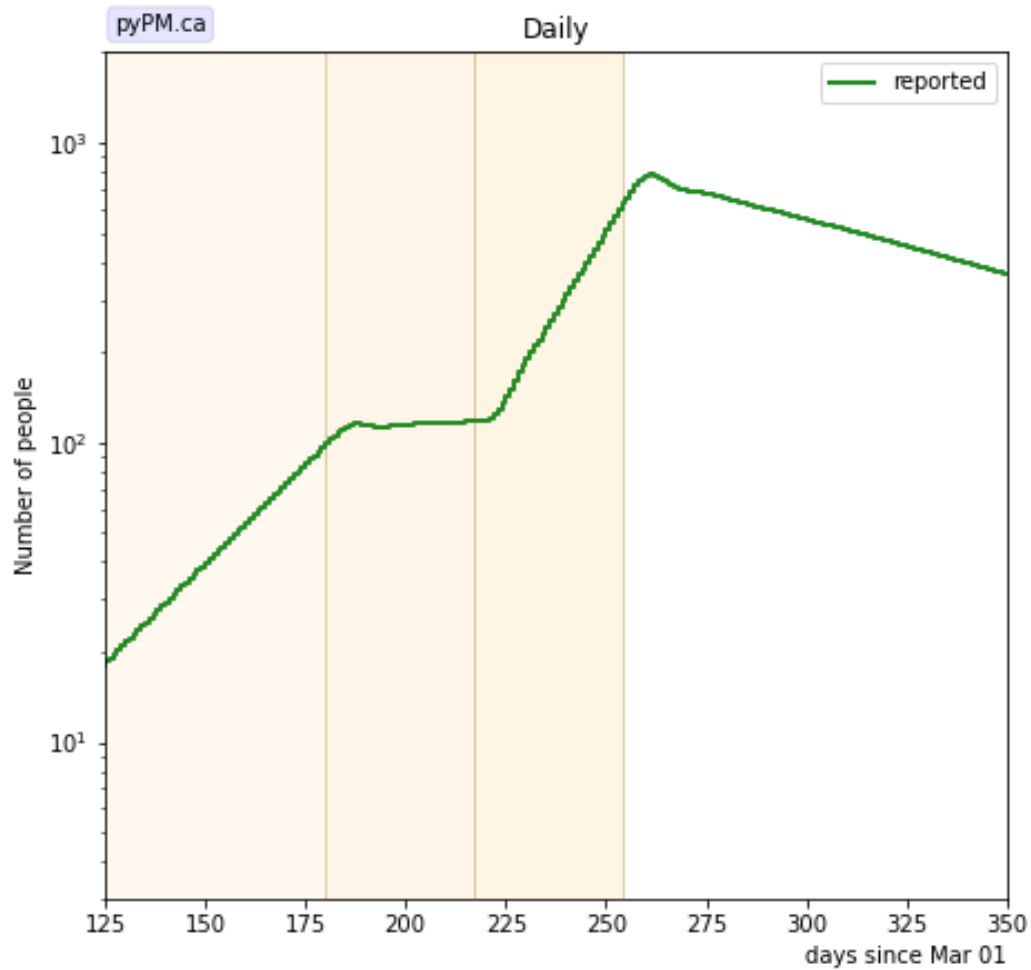
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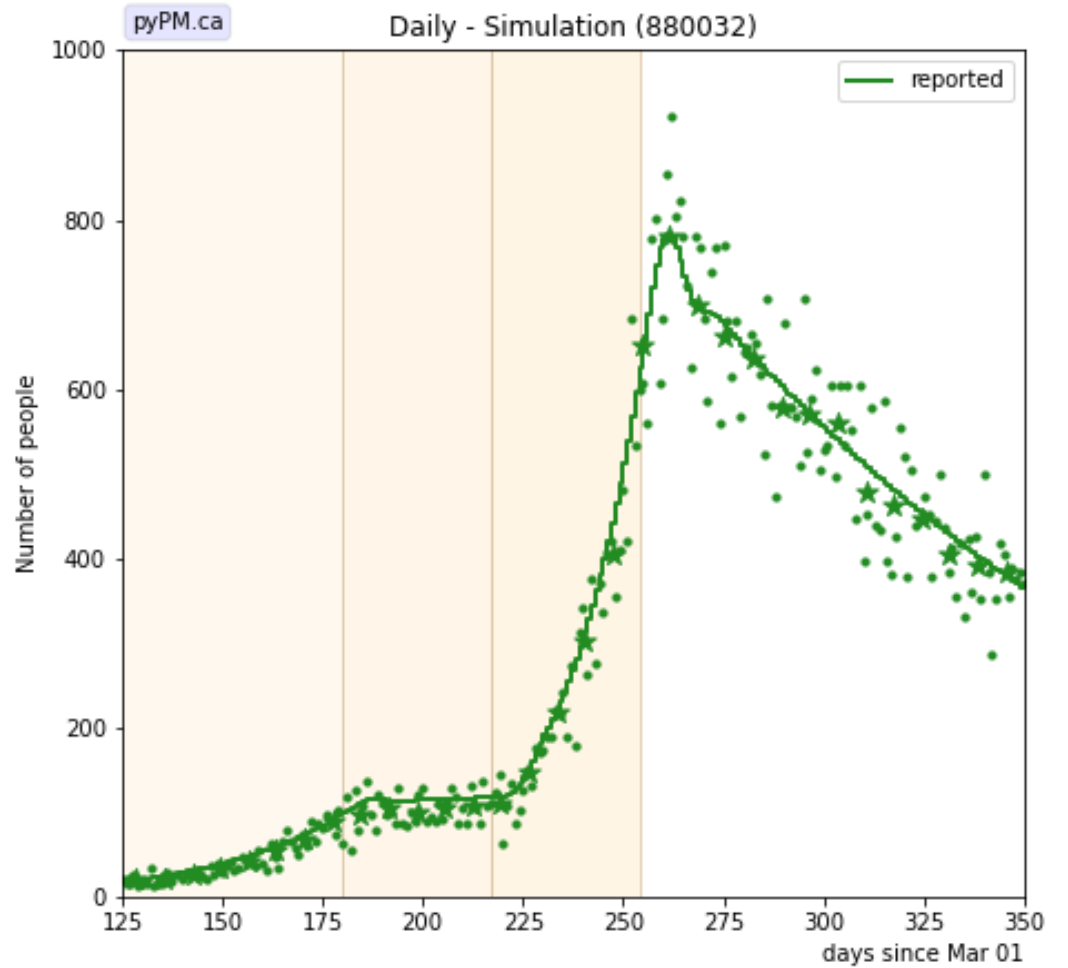
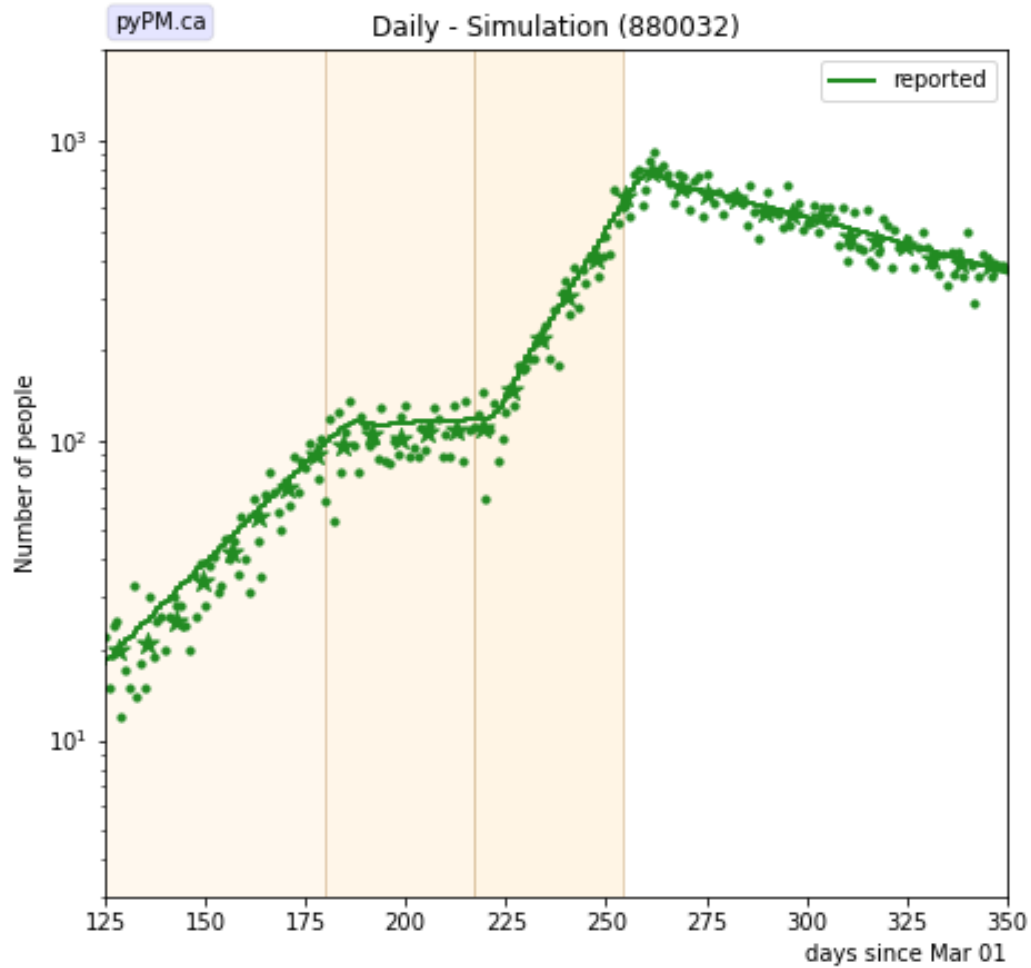
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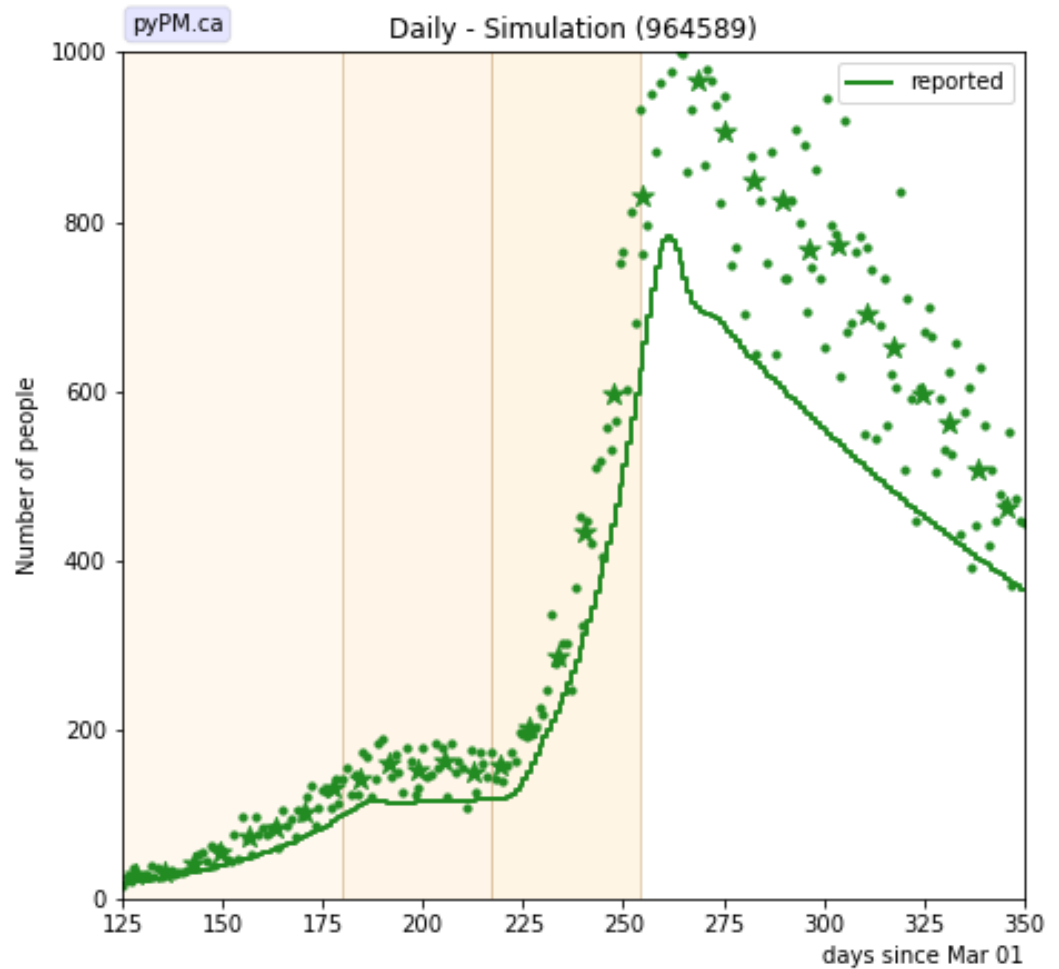
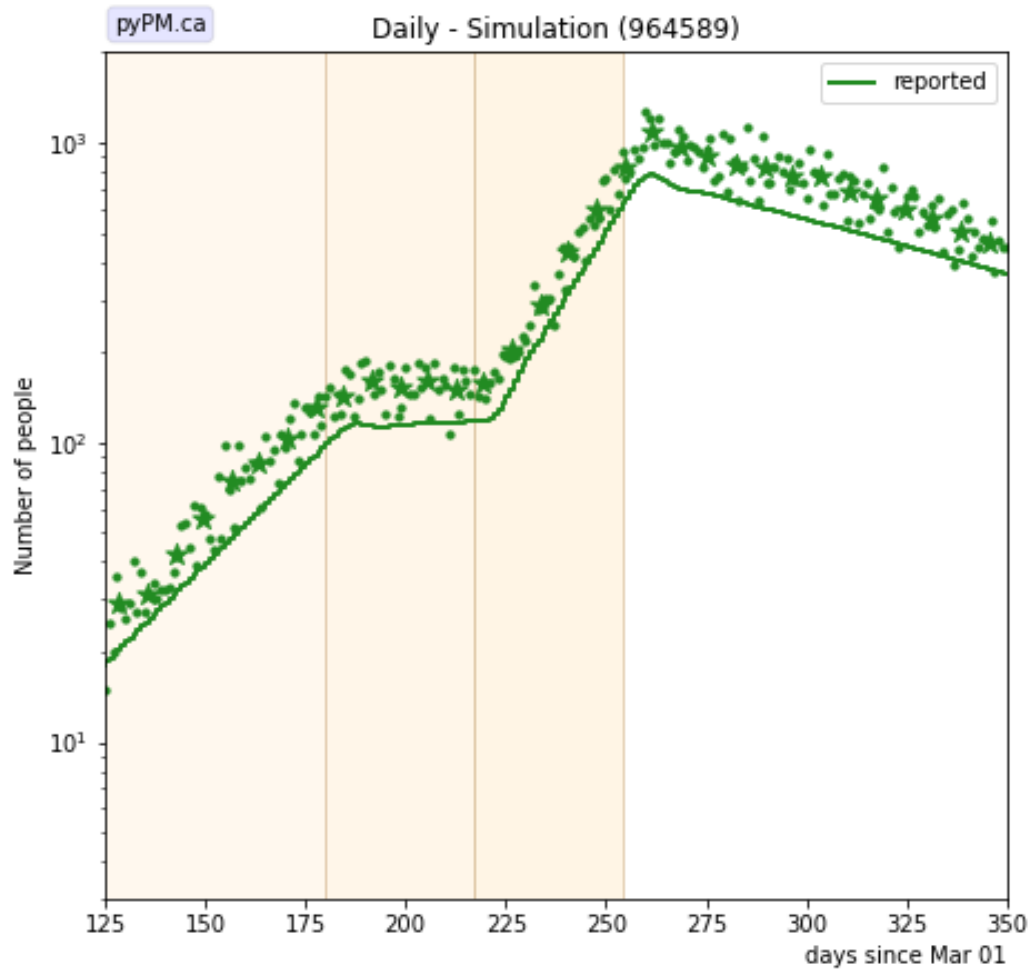
# Modelling variation: BC model



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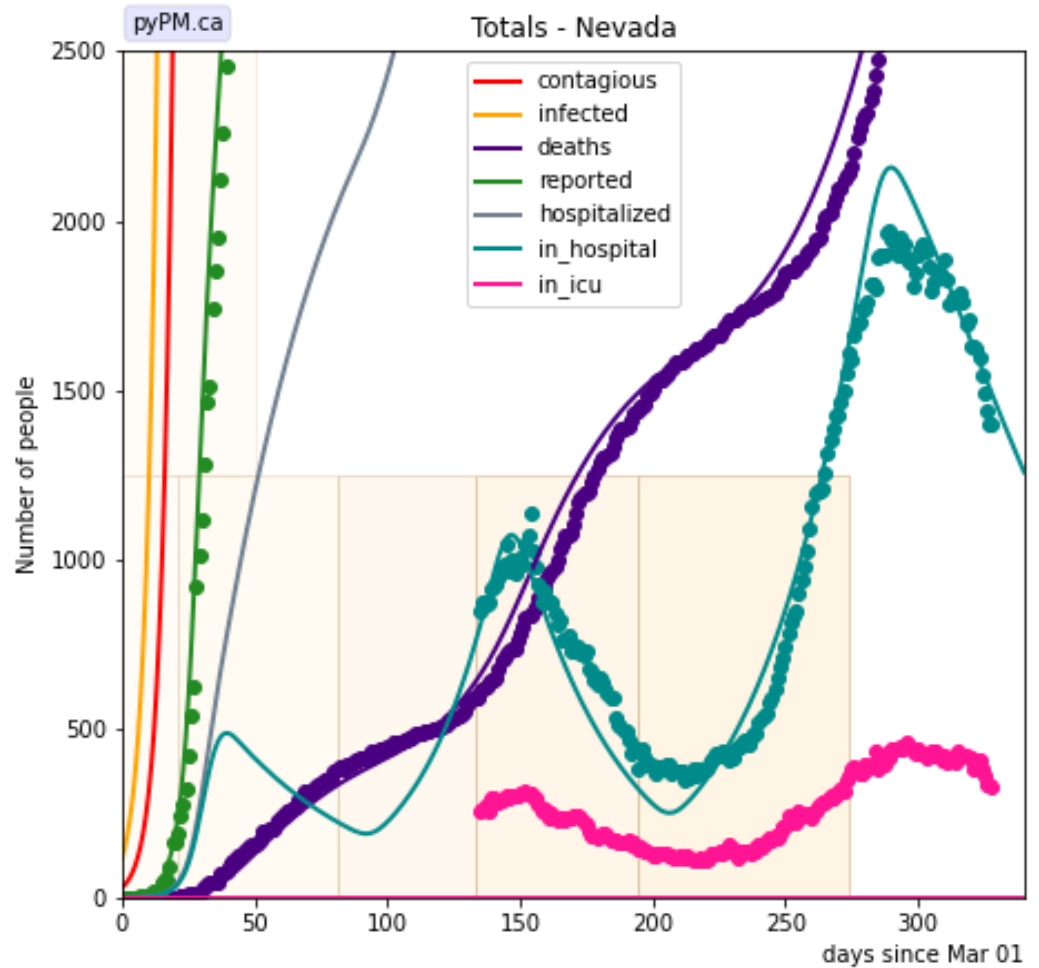
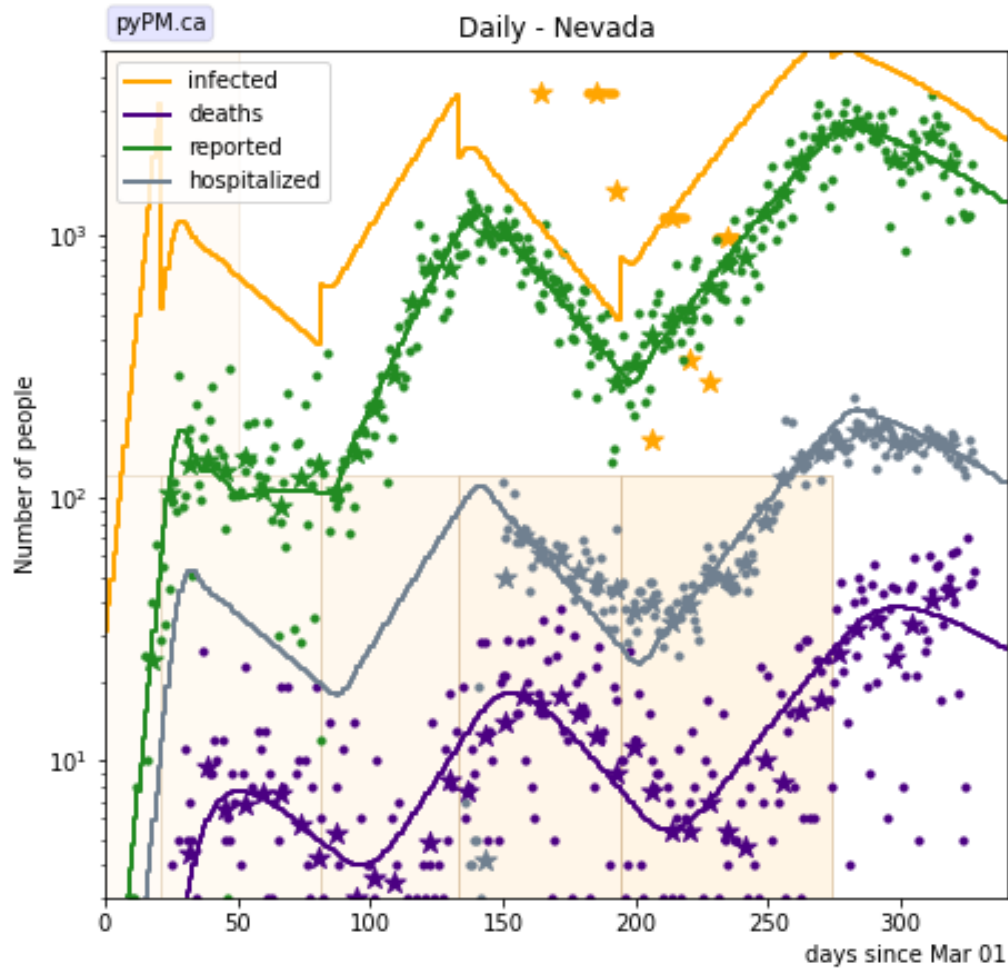


# Modelling variation: BC model



Modelling variation is essential to analyze data.

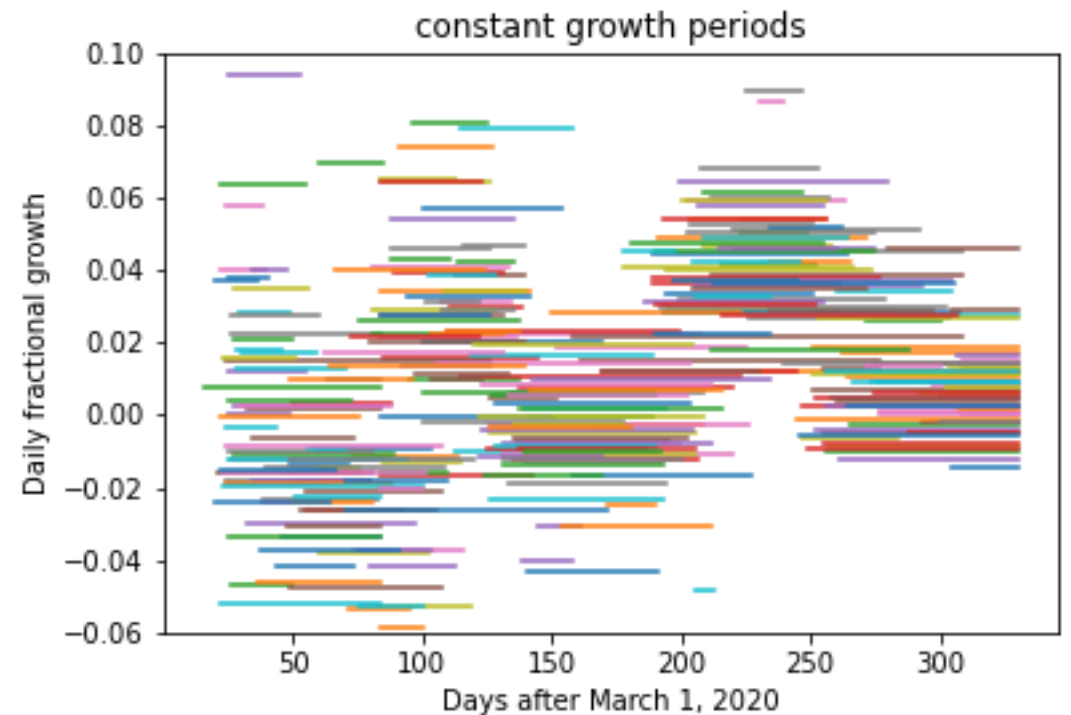
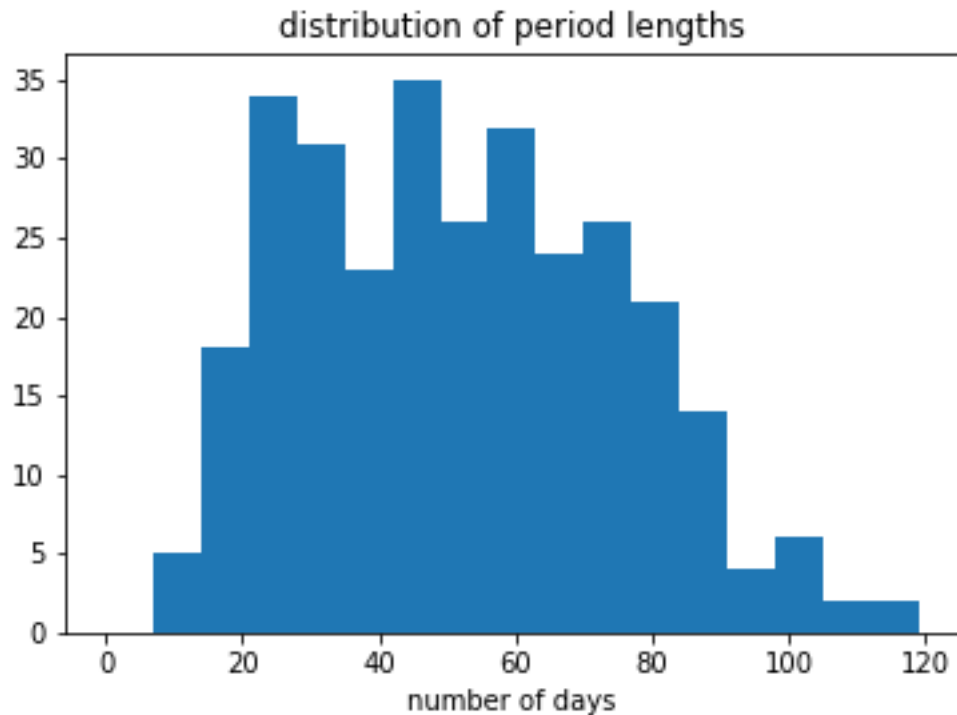
# Example: Nevada (US)





# Periods of constant transmission are long

- Mean length almost 2 months (for US states)



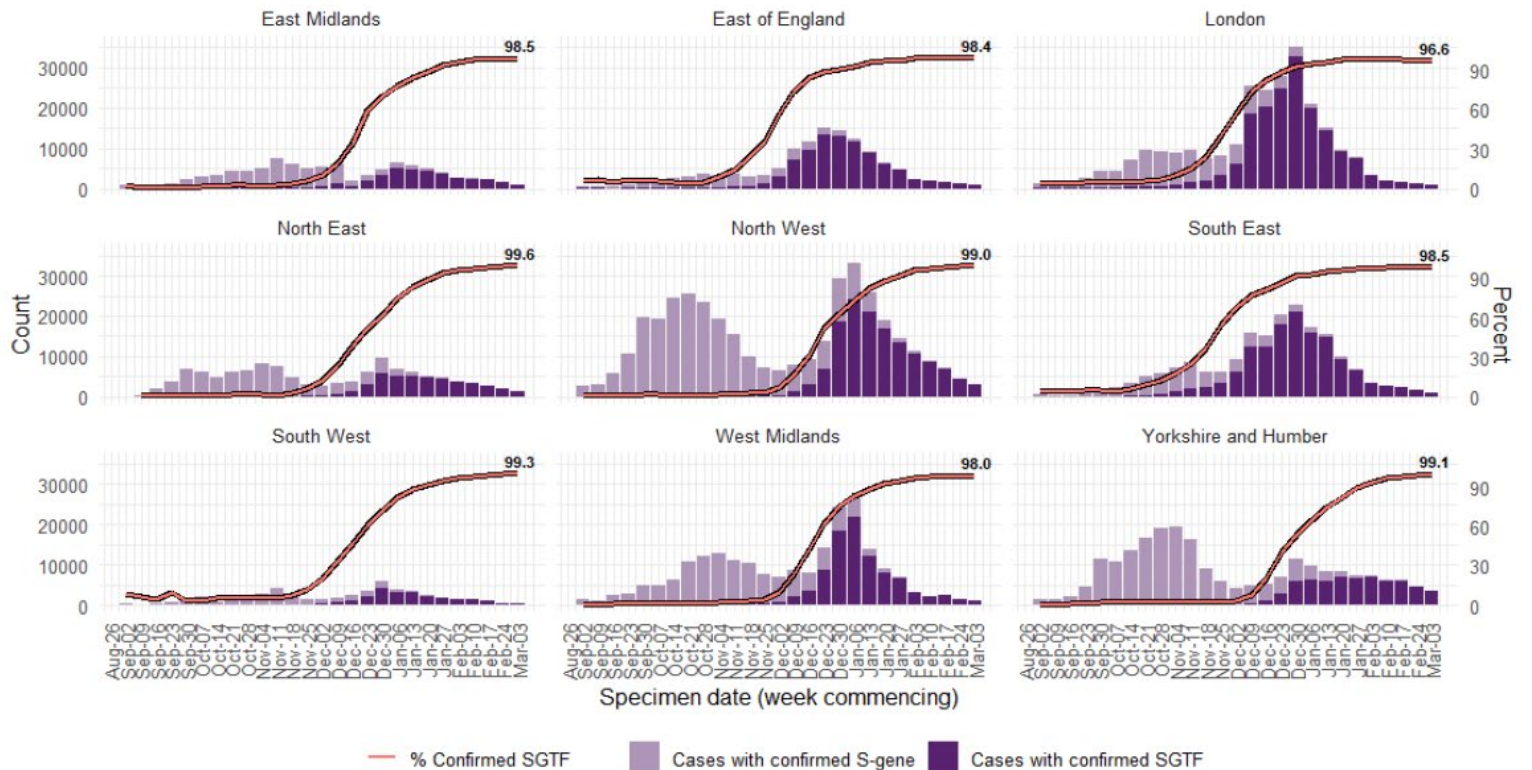
# Forecasting the spread of COVID

- In 2020, models had some ability to forecast the future, thanks to long periods of constant transmission rate
- Changes to transmission rate (timing and amount) difficult to predict:
  - difficult to model effectiveness of NPI from first principles
  - difficult to model human behaviour
- Starting in 2021 – models could predict changes in the spread of COVID due to:
  - Variants – solution: add second (and third) infection cycle to model
    - properties of the variants known from genomic sampling
  - Immunity – solution: reduce susceptible fraction according to infections and vaccination
    - vaccination rate and effectiveness reasonably well known

# The alpha variant

- Rapid case growth in the UK (shortly after relaxation measures)
- Their PCR test at the time targeted 3 genes to identify SARS-CoV-2
- Saw rapid growth in cases in which one of the genes was not present: S-gene
  - Referred to such cases as SGTF (S-gene target failure)
- A fortuitous indicator to identify the first “Variant of Concern”: B.1.1.7 (alpha)

Figure 11. Weekly number and proportion of England Pillar 2 COVID-19 cases with SGTF among those tested with the TaqPath assay and with S gene detection results, by region of residence (1 September 2020 to 9 March 2021)



# Modeling a rapidly spreading variant

- Consider steady-state exponential growth of two strains: their ratio

$$\frac{N_v(t)}{N_{nv}(t)} = \frac{N_{v0}e^{r_v t}}{N_{nv0}e^{r_{nv} t}} = ae^{[r_v - r_{nv}]t} = ae^{st} = e^{s(t-t_0)}$$

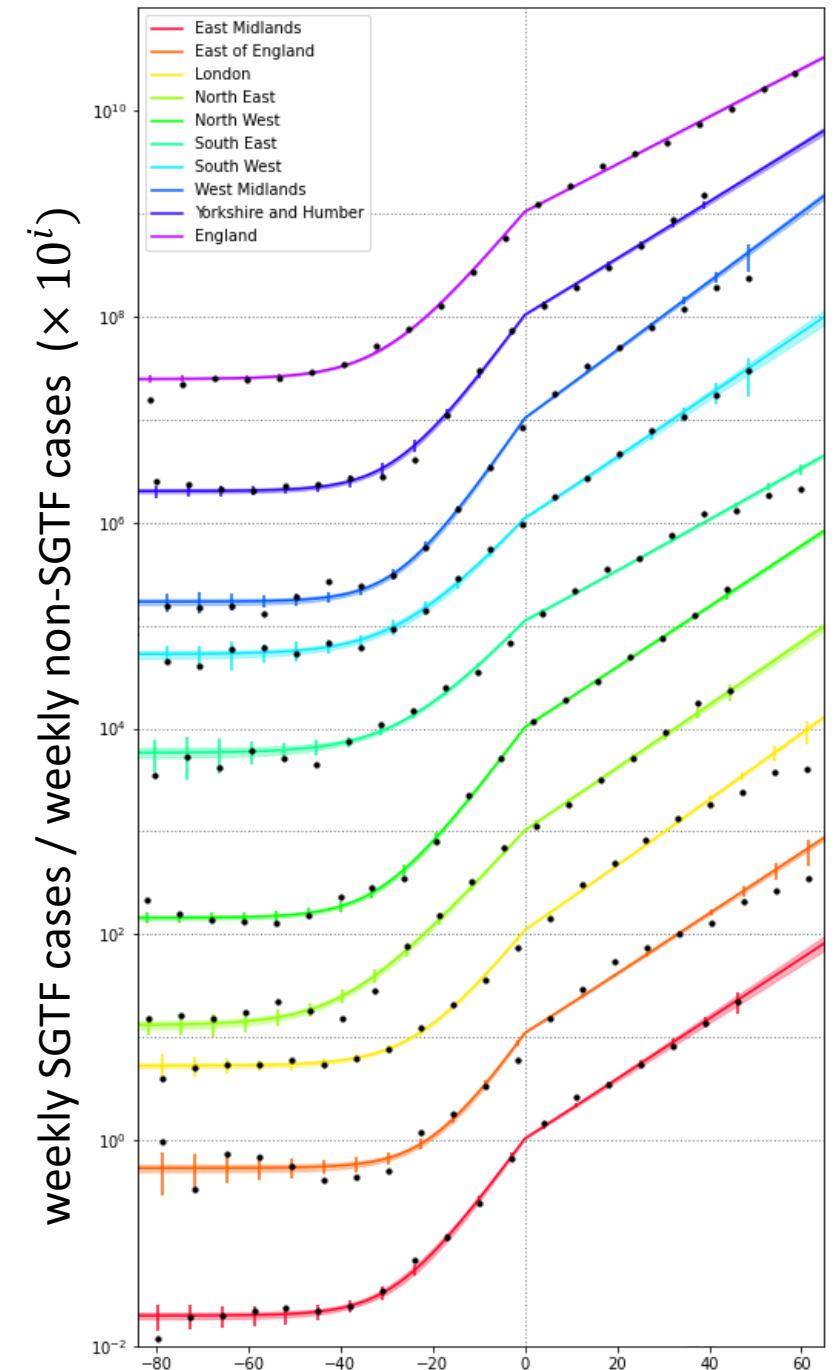
- In population modelling,  $s$  is called the “selection coefficient”
- The relation might be a good approximation in more dynamic situations, provided:

$$r_v(t) - r_{nv}(t) = s(t) \cong s$$

# UK SGTF/non-SGTF ratio

- day = 0: date when ratio = 1 (crossover day)
- s1: selection coefficient prior to crossing
- s2: selection coefficient after crossing
- w: SGTF false identification for B.1.1.7

region	s1	s2	w
East Midlands	0.141 +/- 0.003	0.067 +/- 0.001	0.019 +/- 0.001
East of England	0.147 +/- 0.004	0.068 +/- 0.000	0.051 +/- 0.002
London	0.127 +/- 0.002	0.074 +/- 0.000	0.051 +/- 0.001
North East	0.112 +/- 0.002	0.070 +/- 0.001	0.013 +/- 0.001
North West	0.137 +/- 0.002	0.068 +/- 0.000	0.014 +/- 0.000
South East	0.108 +/- 0.002	0.058 +/- 0.000	0.055 +/- 0.003
South West	0.111 +/- 0.004	0.070 +/- 0.001	0.050 +/- 0.002
West Midlands	0.148 +/- 0.002	0.077 +/- 0.001	0.017 +/- 0.001
Yorkshire and Humber	0.140 +/- 0.002	0.064 +/- 0.001	0.020 +/- 0.000
England	0.122 +/- 0.000	0.054 +/- 0.000	0.024 +/- 0.000

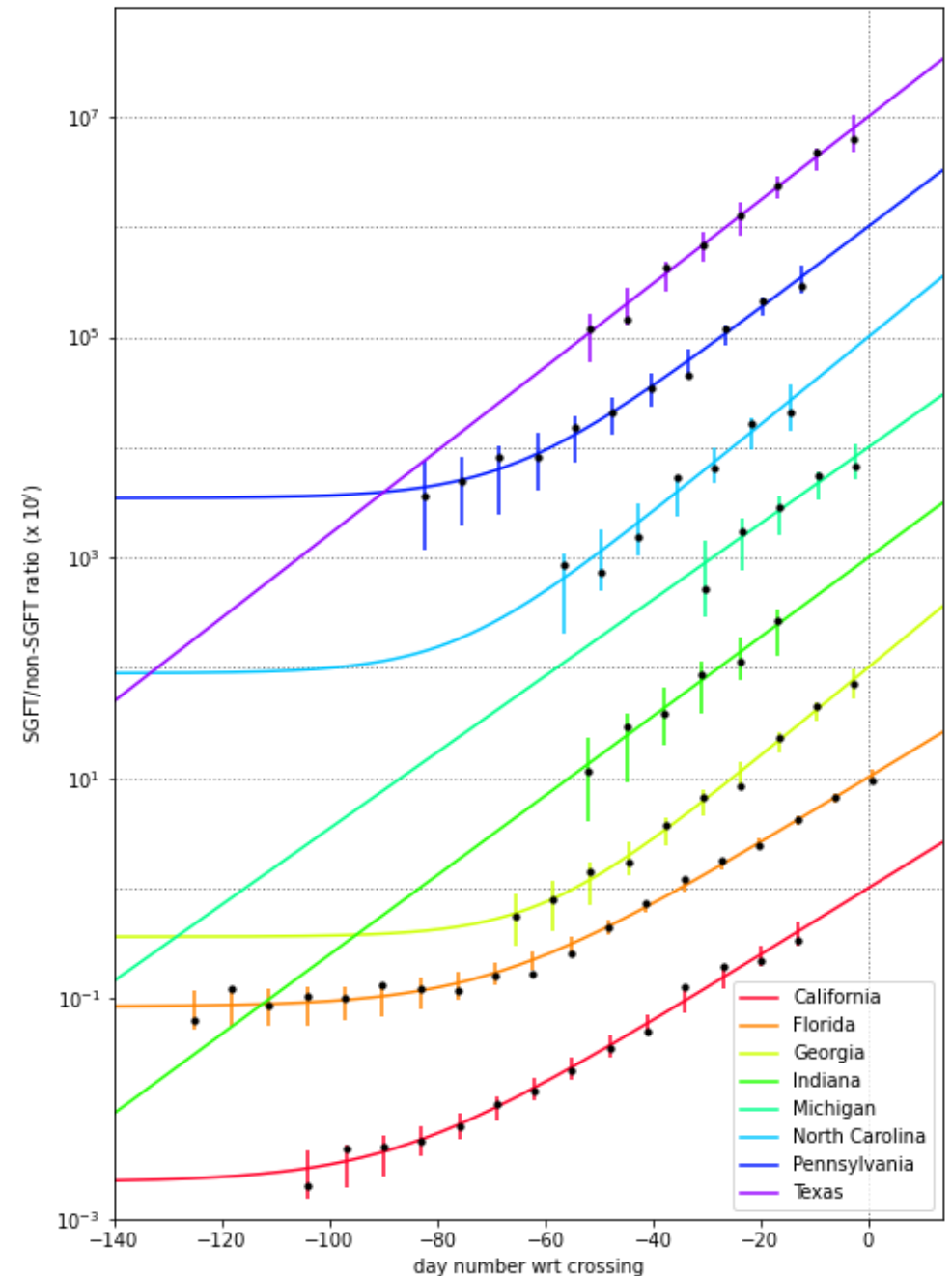


# Alpha in USA (mid-March)

- Sufficient data available from 8 states
  - $f_v$ : fraction of cases from variant on Mar 13
  - growth advantage remains, despite vaccination immunity

region	s	w	$f_v$ (Mar 13)
California	$0.070 \pm 0.004$	$0.002 \pm 0.012$	$0.381 \pm 0.007$
Florida	$0.069 \pm 0.001$	$0.008 \pm 0.001$	$0.614 \pm 0.007$
Georgia	$0.093 \pm 0.002$	$0.004 \pm 0.001$	$0.578 \pm 0.011$
Indiana	$0.083 \pm 0.010$	$0.000 \pm 0.000$	$0.288 \pm 0.044$
Michigan	$0.080 \pm 0.010$	$0.000 \pm 0.000$	$0.573 \pm 0.045$
North Carolina	$0.092 \pm 0.004$	$0.001 \pm 0.003$	$0.313 \pm 0.008$
Pennsylvania	$0.085 \pm 0.002$	$0.003 \pm 0.001$	$0.366 \pm 0.004$
Texas	$0.087 \pm 0.004$	$0.000 \pm 0.000$	$0.572 \pm 0.028$

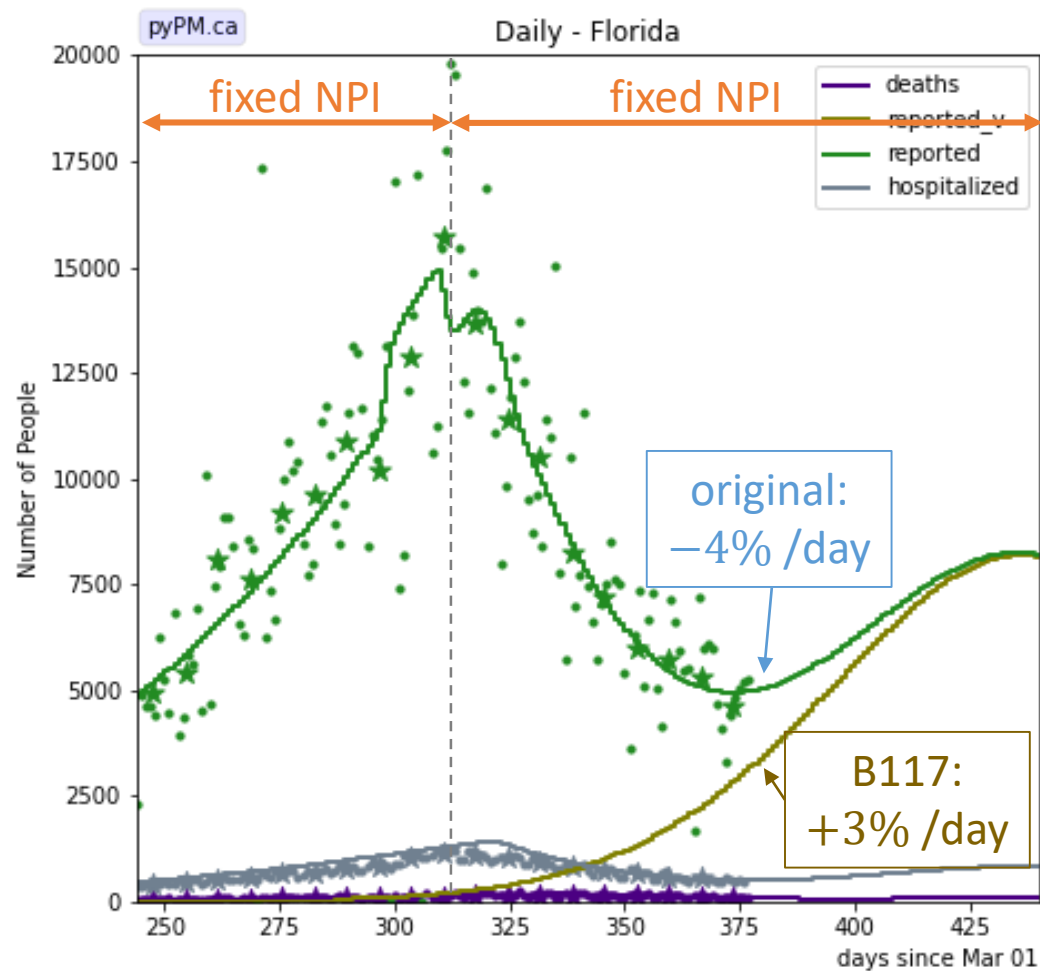
<https://www.helix.com/pages/helix-covid-19-surveillance-dashboard>



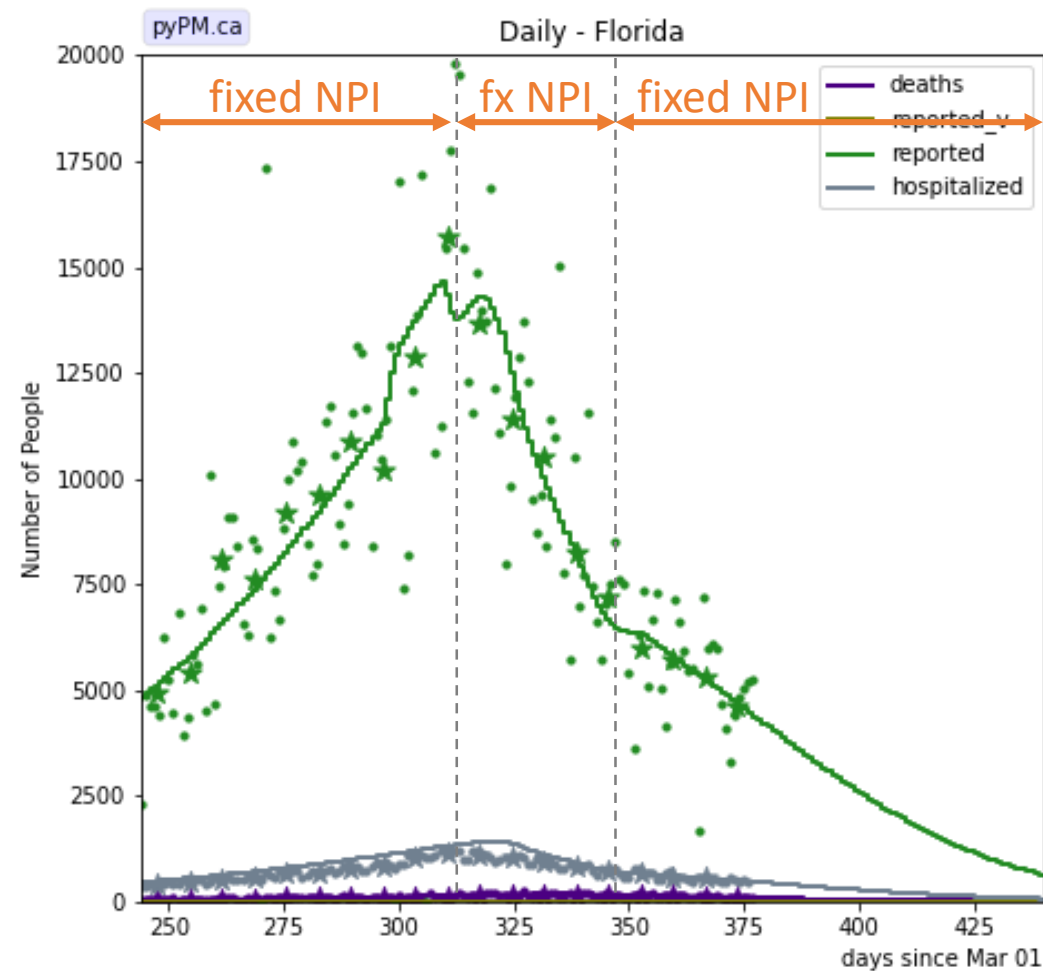
# Florida

Data fit with B.1.1.7

Data fit without B.1.1.7: change in NPI



Oct 1



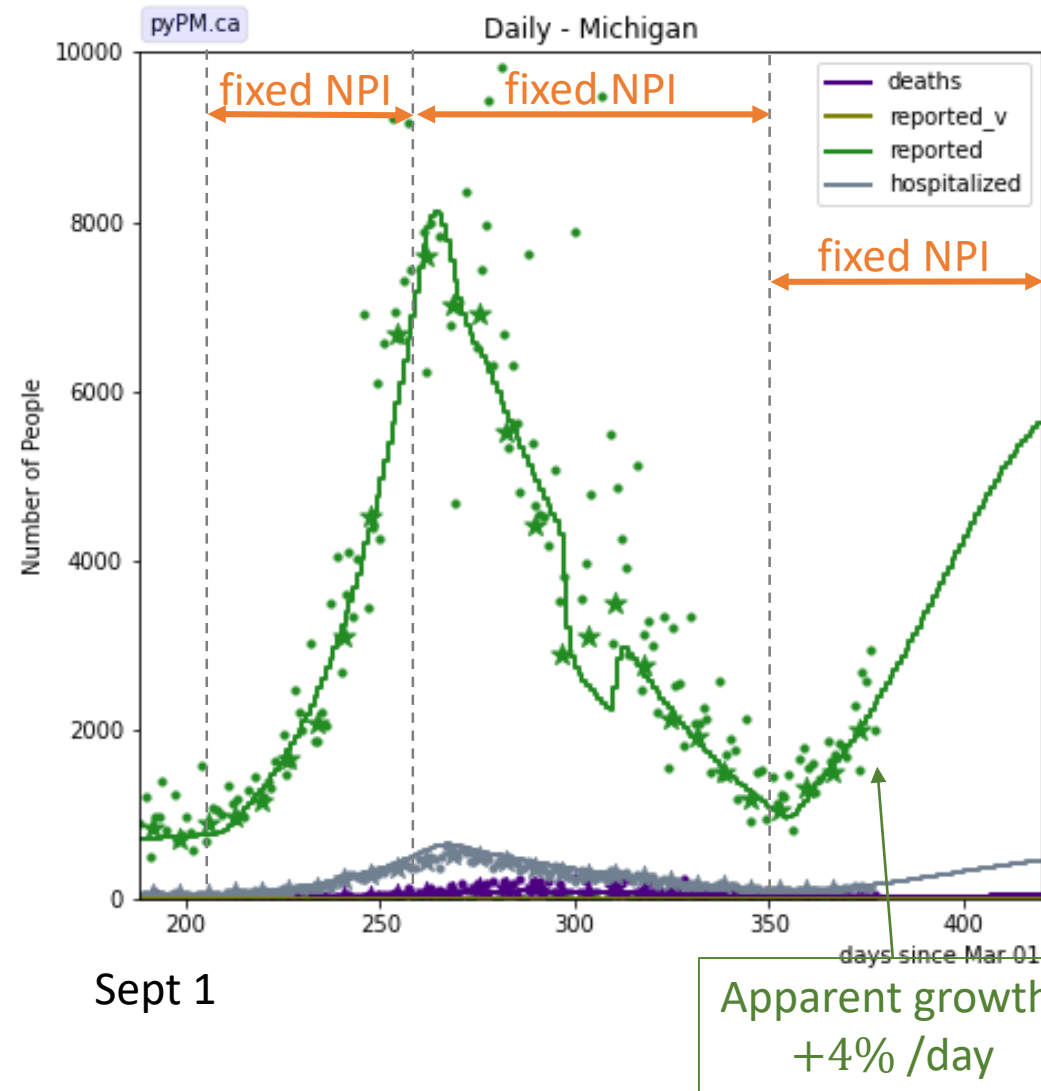
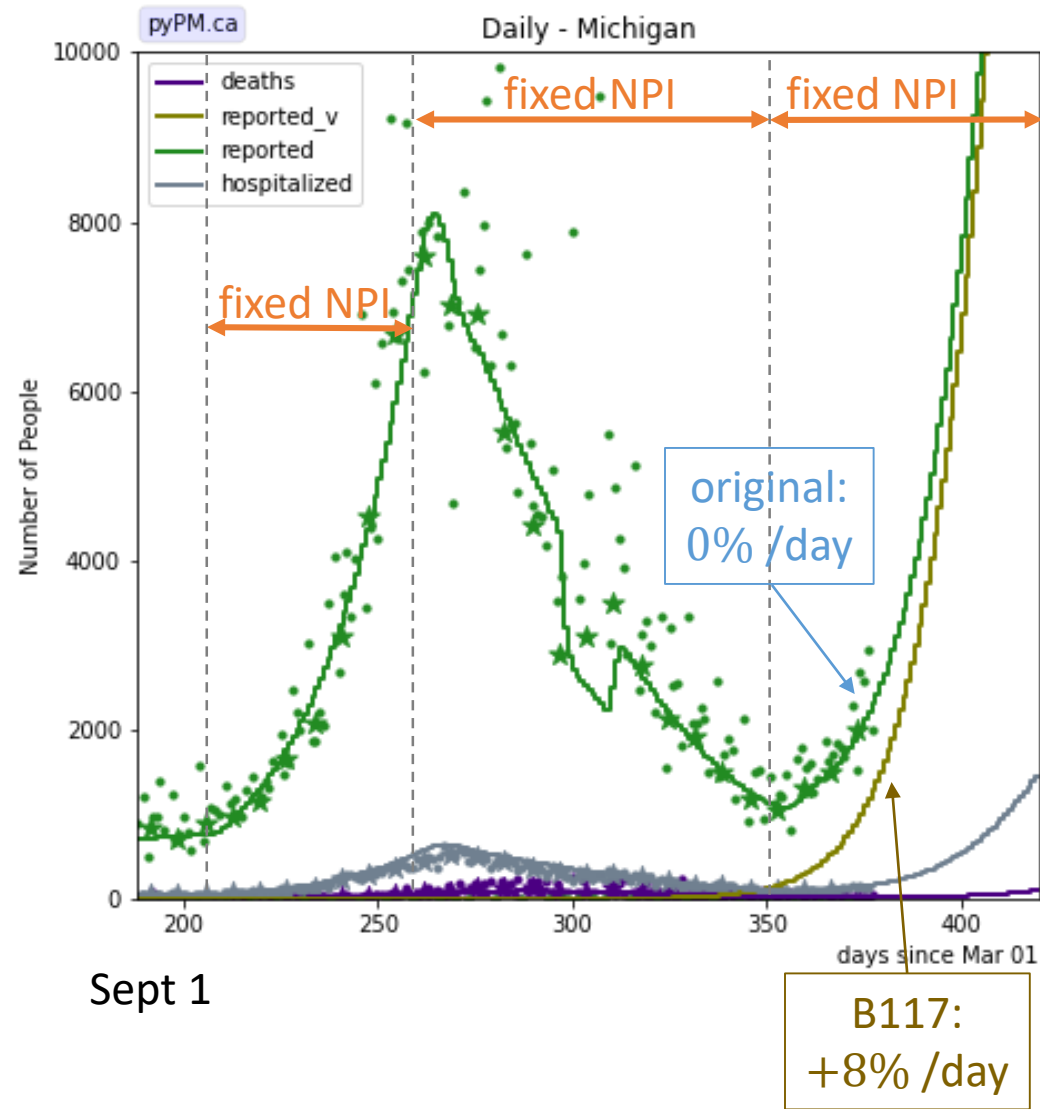
Oct 1



# Michigan

Data fit with B.1.1.7

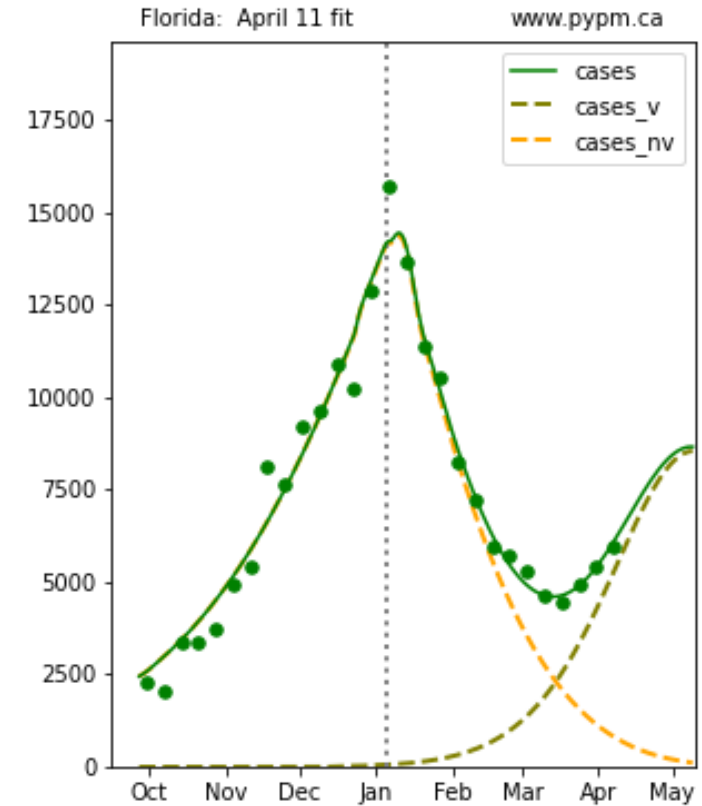
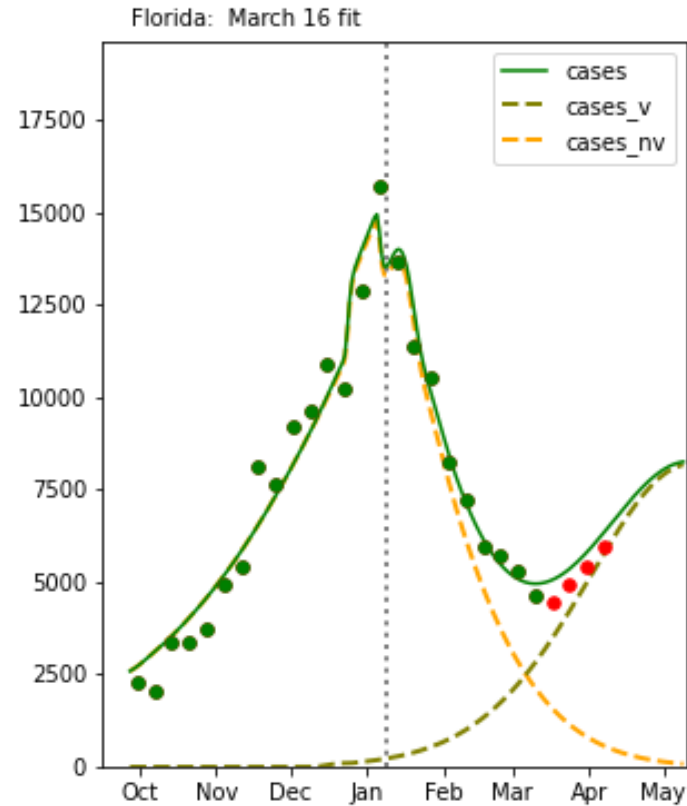
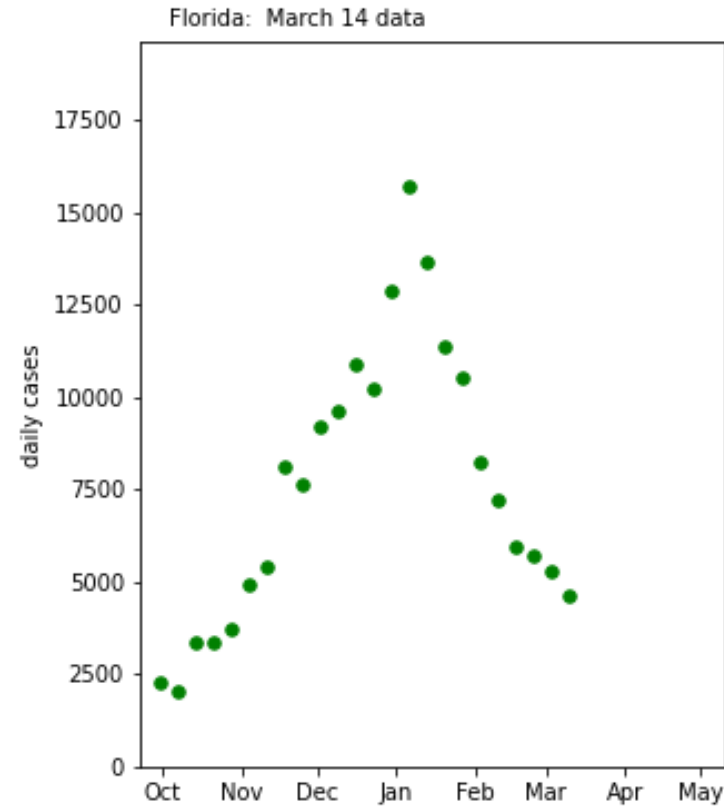
Data fit without B.1.1.7: only change in NPI





# Florida

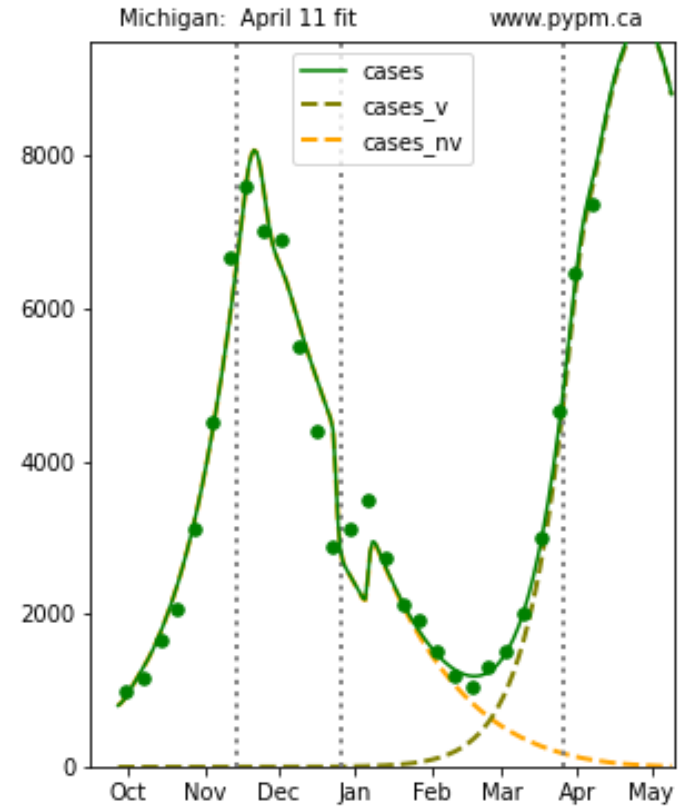
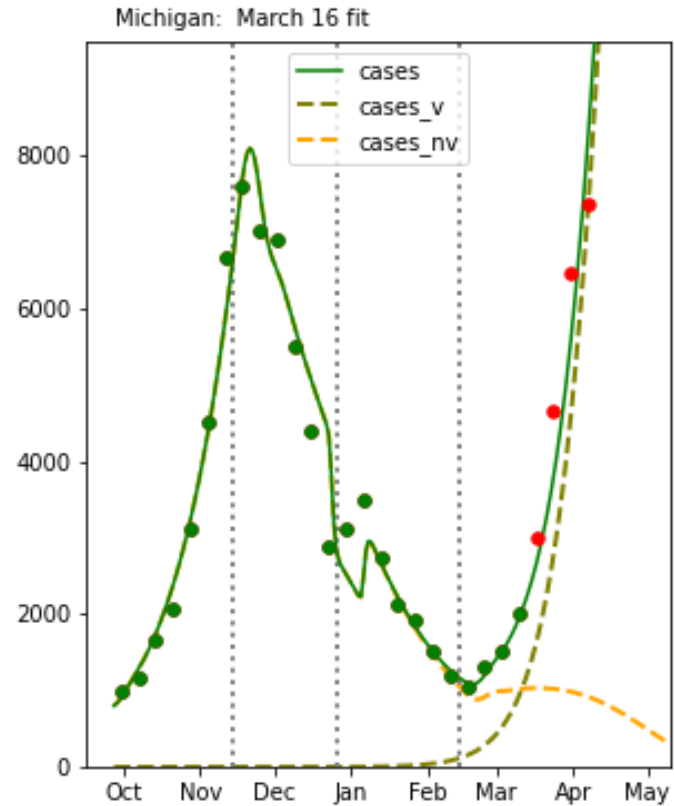
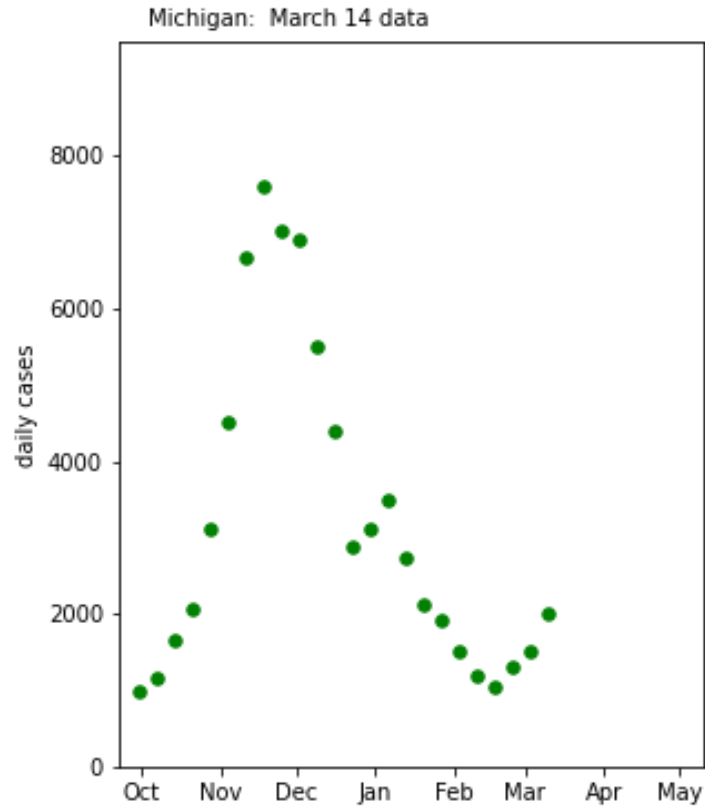
curve: March 16 fit  
red points: 4 weeks  
data following



Models had some ability to predict a change in the spread of COVID-19

# Michigan

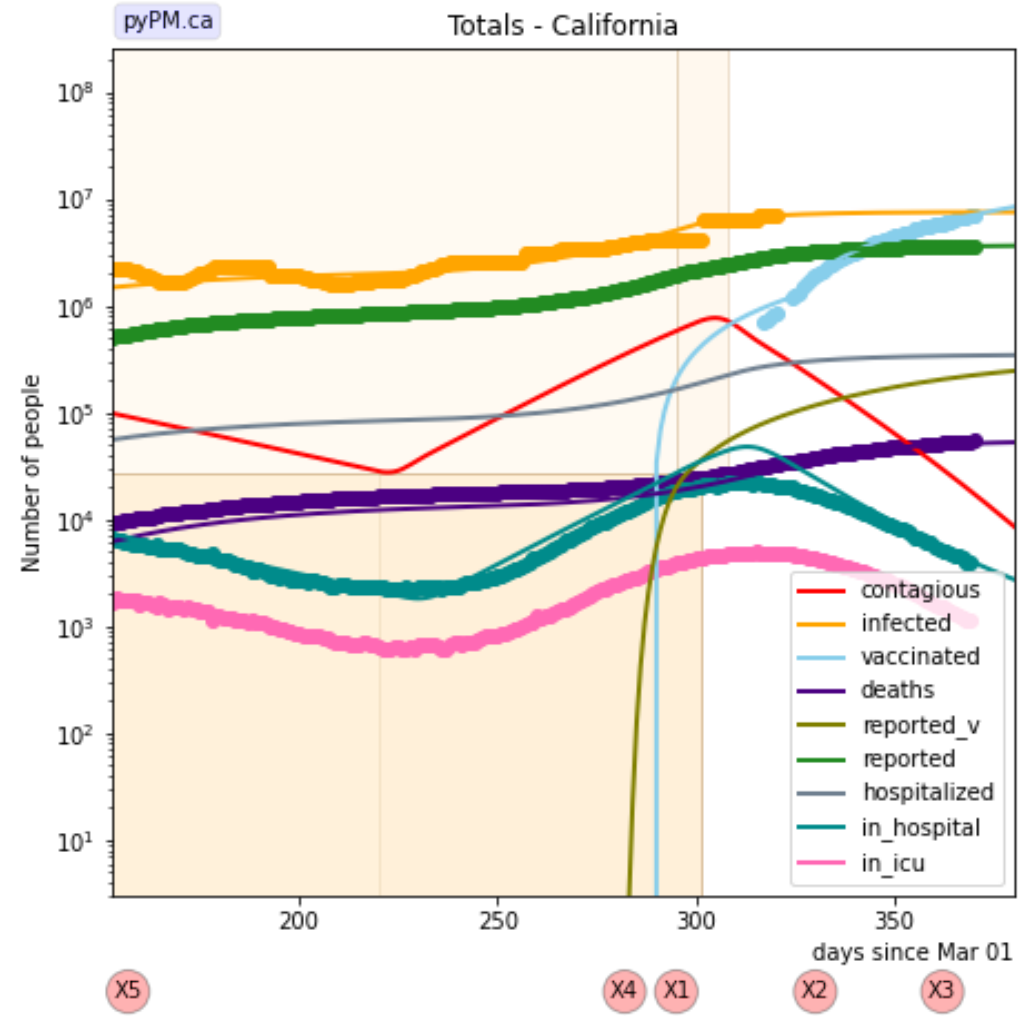
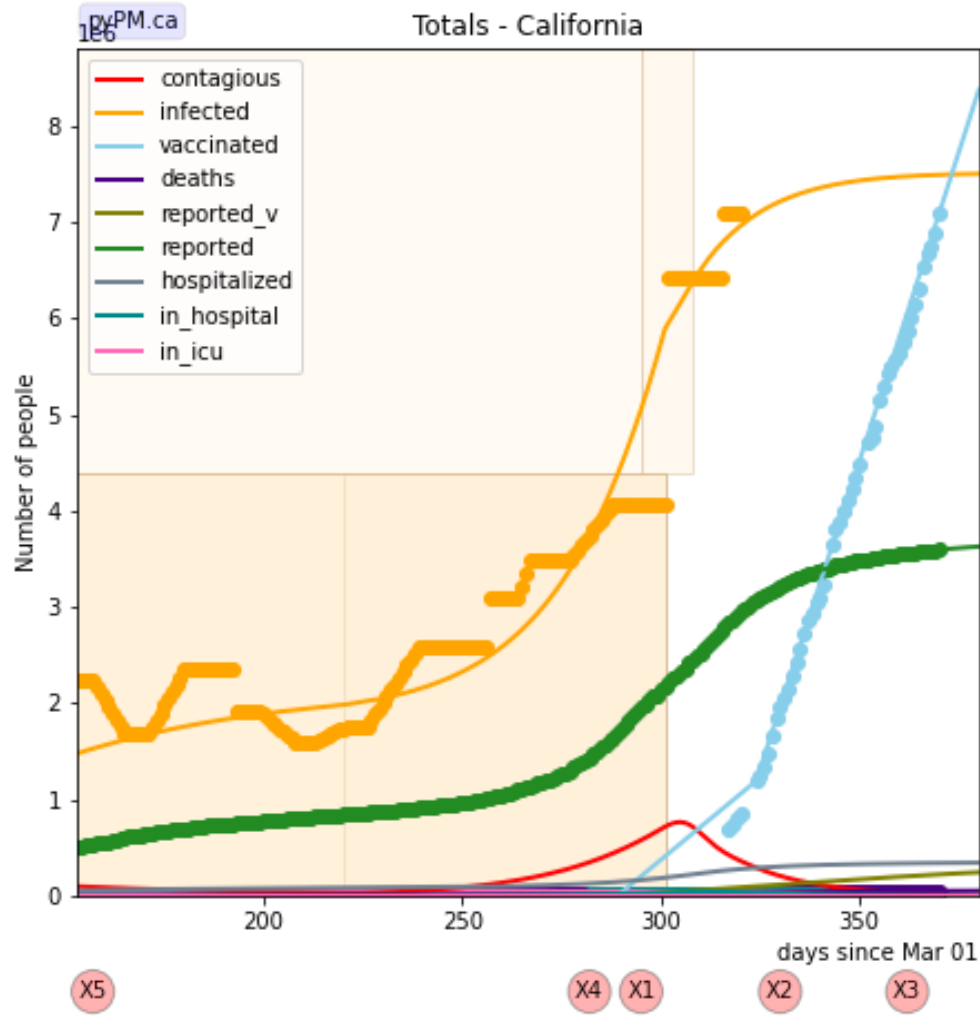
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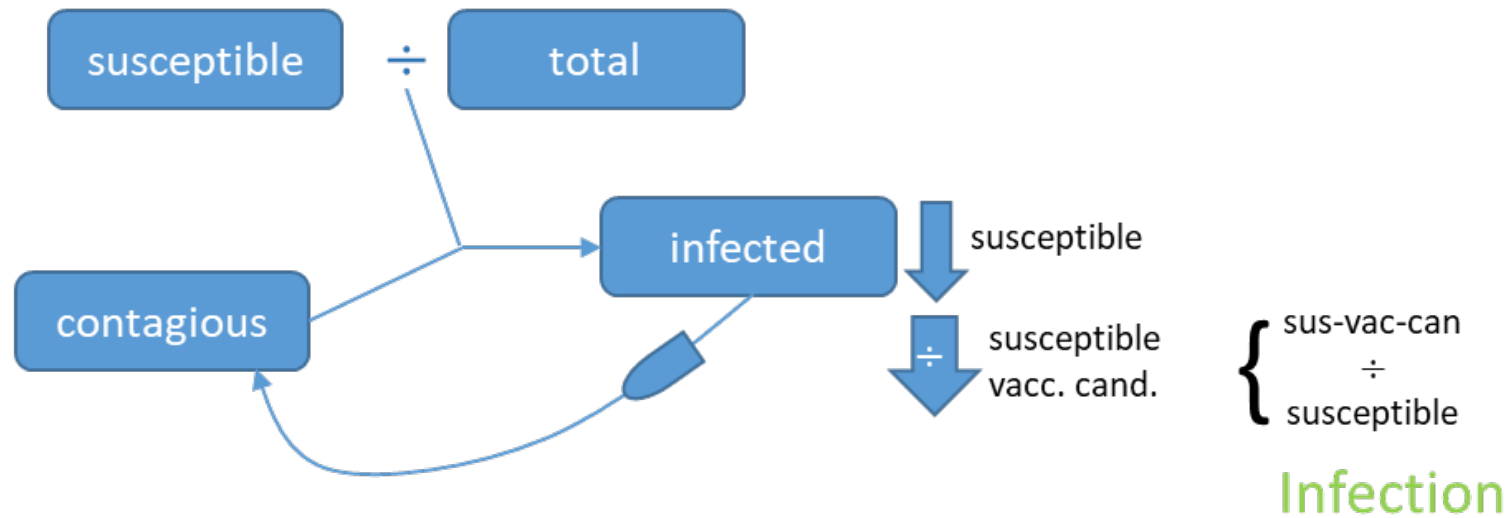
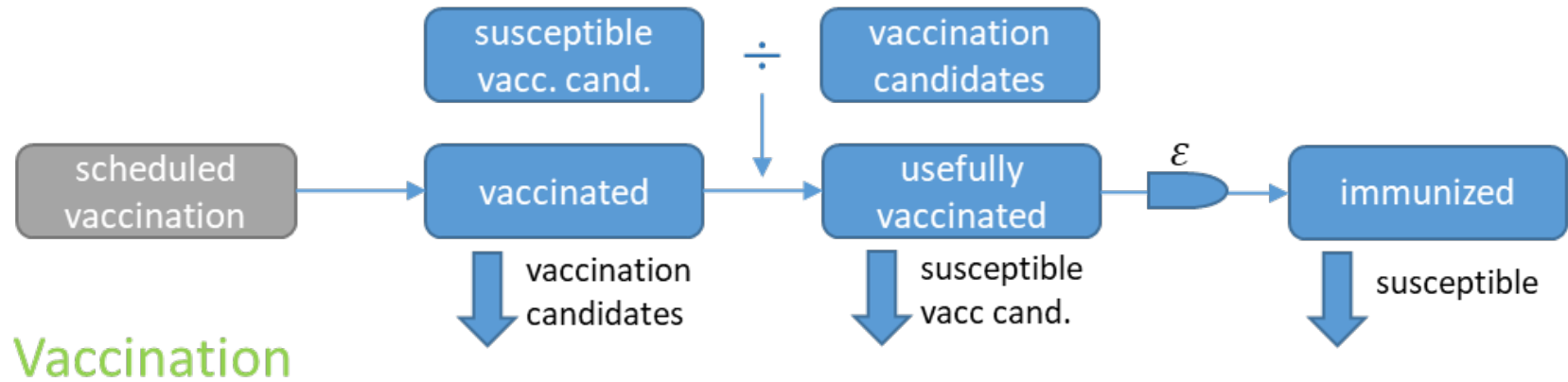
# Immunity

- Natural immunity:
  - In early 2020 the fraction of infections that were reported not well known
  - In US – seroprevalence data was very useful to estimate that fraction
- Vaccination immunity:
  - Israel provided the earliest population-level data to benchmark vaccination immunity models

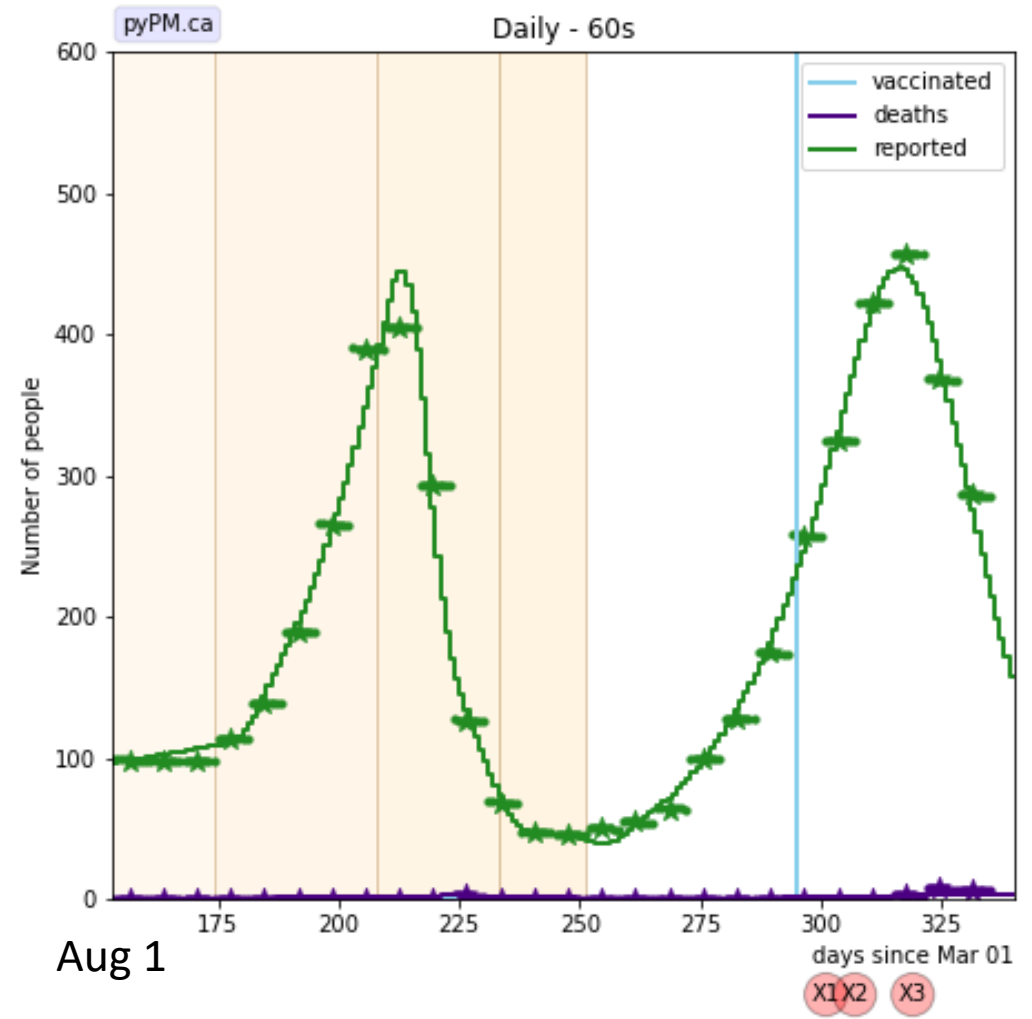
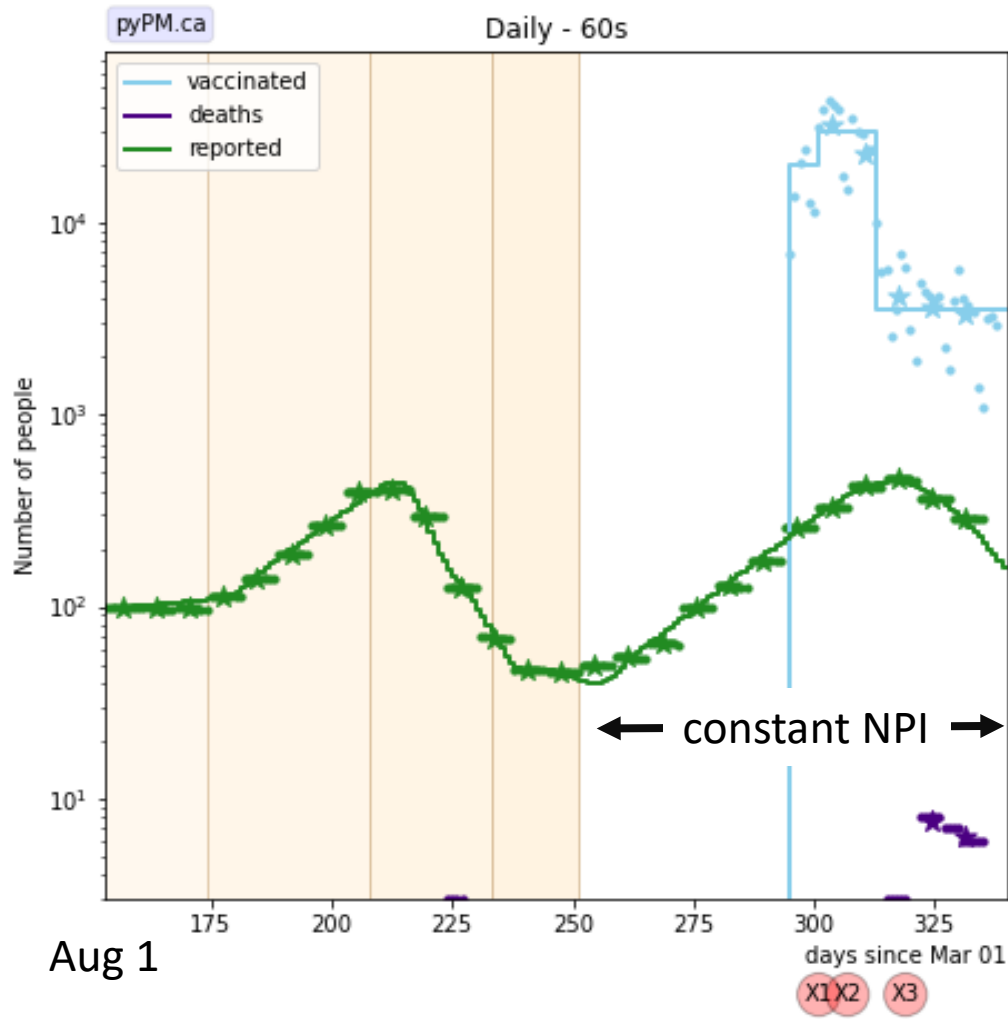
# California



# The Vaccination Model

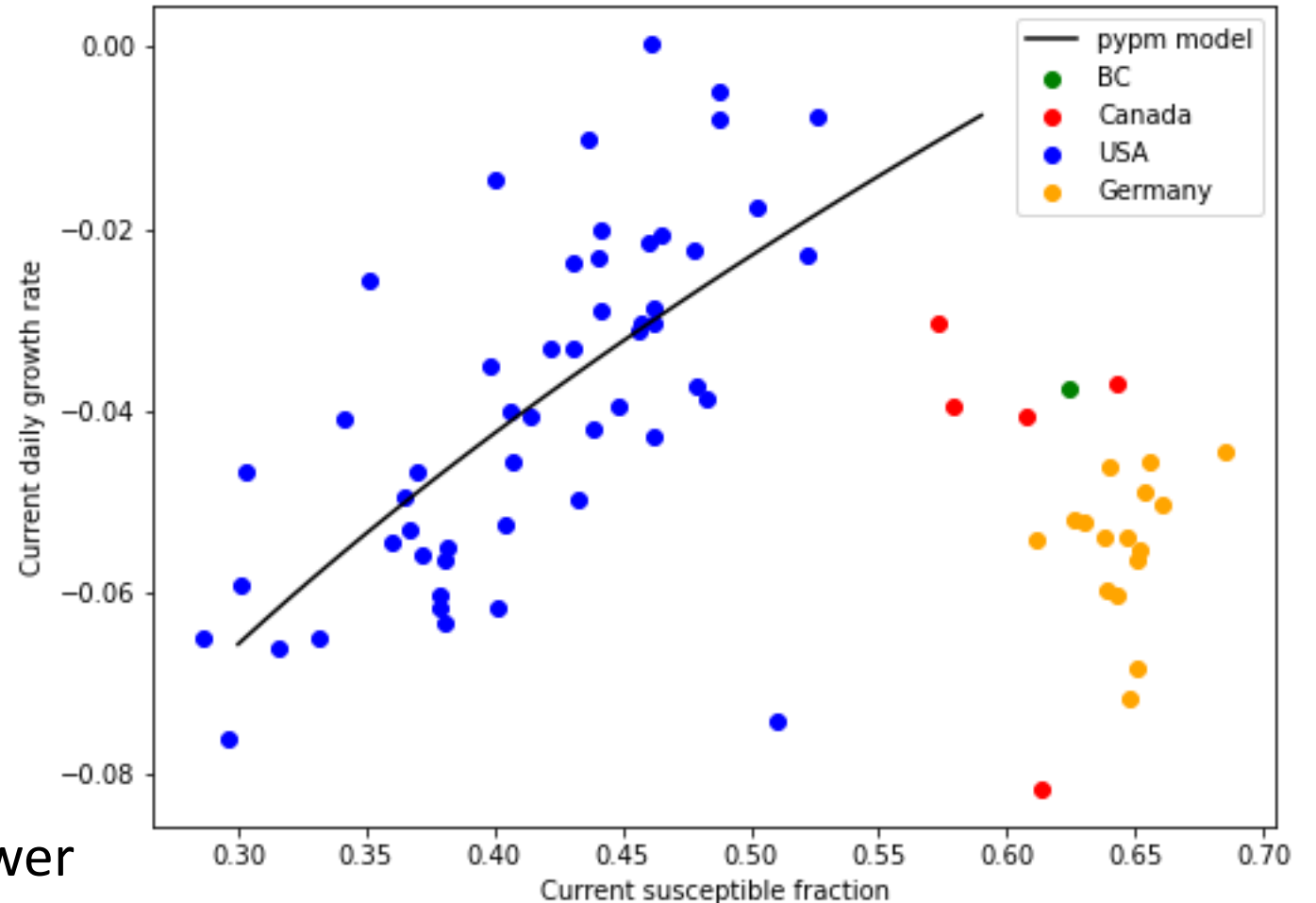


# 60-69



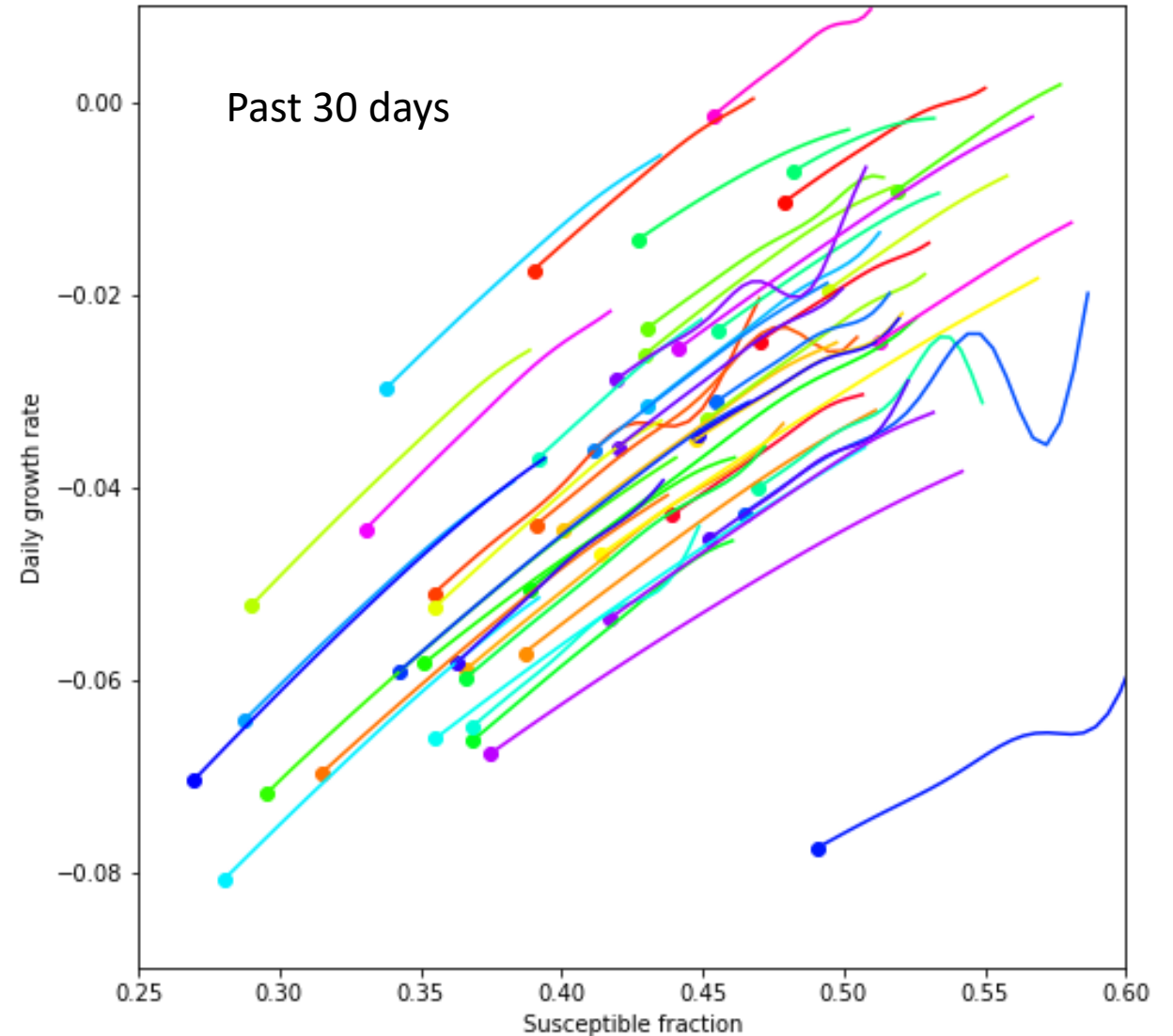
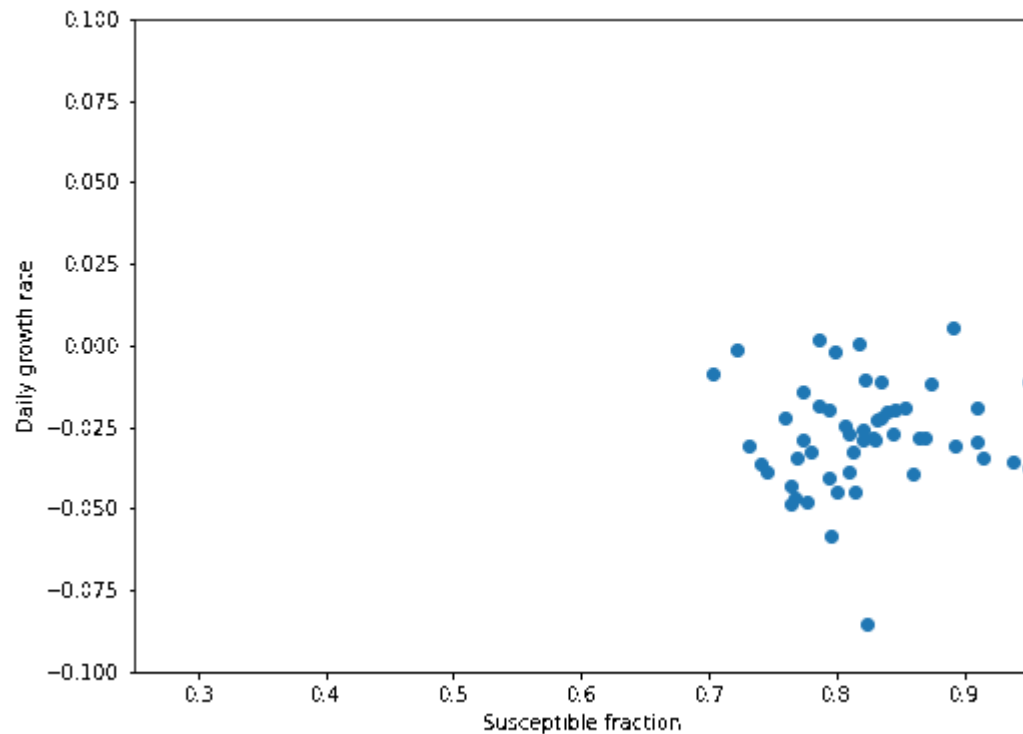
# Declining growth rate with increasing immunity

- Currently in the US, the most important factor that determines growth rate is the susceptible fraction
  - wide immunity distribution
  - variation in transmission rates produces less variation in growth
- Transmission rates lower in Canada and Germany than in US
  - immunity distribution narrower



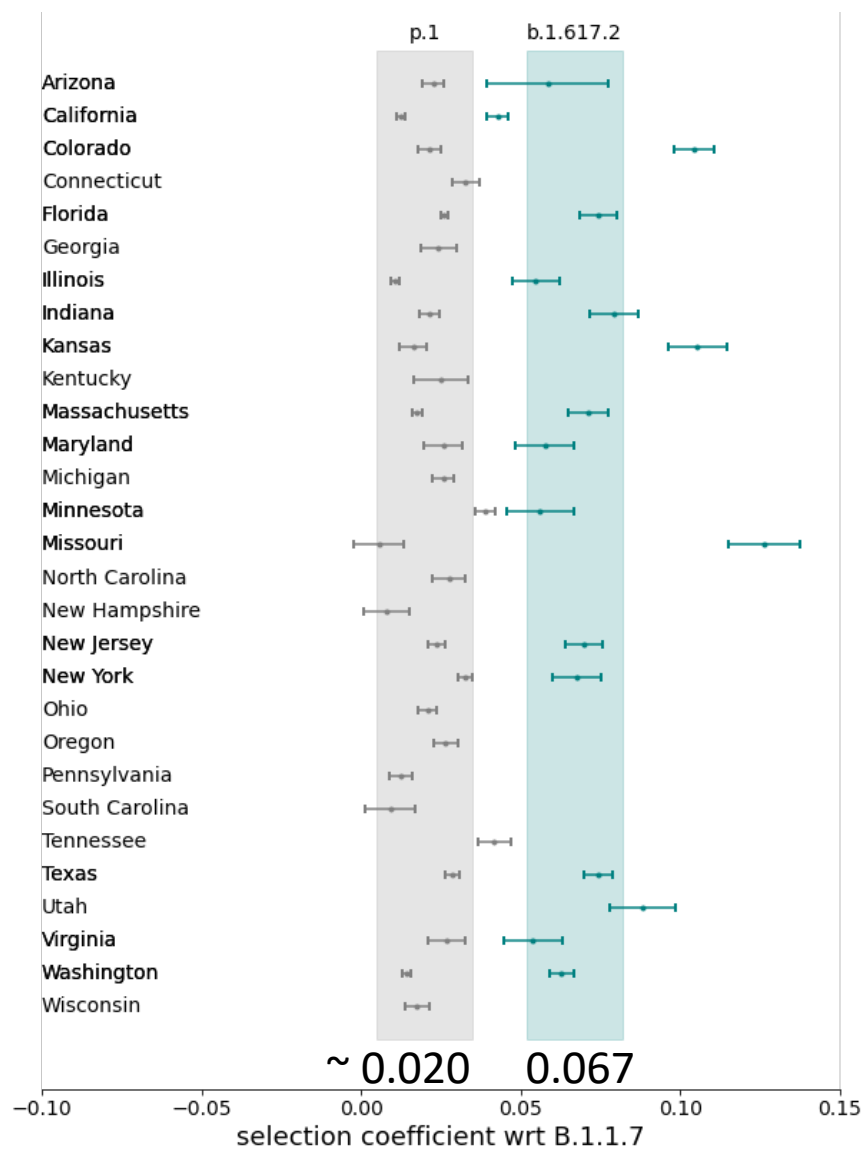
# Declining growth rate with increasing immunity

- Animation: from Jan 15 – now
  - post Xmas decline, variant growth, variant turnaround, decline from immunity

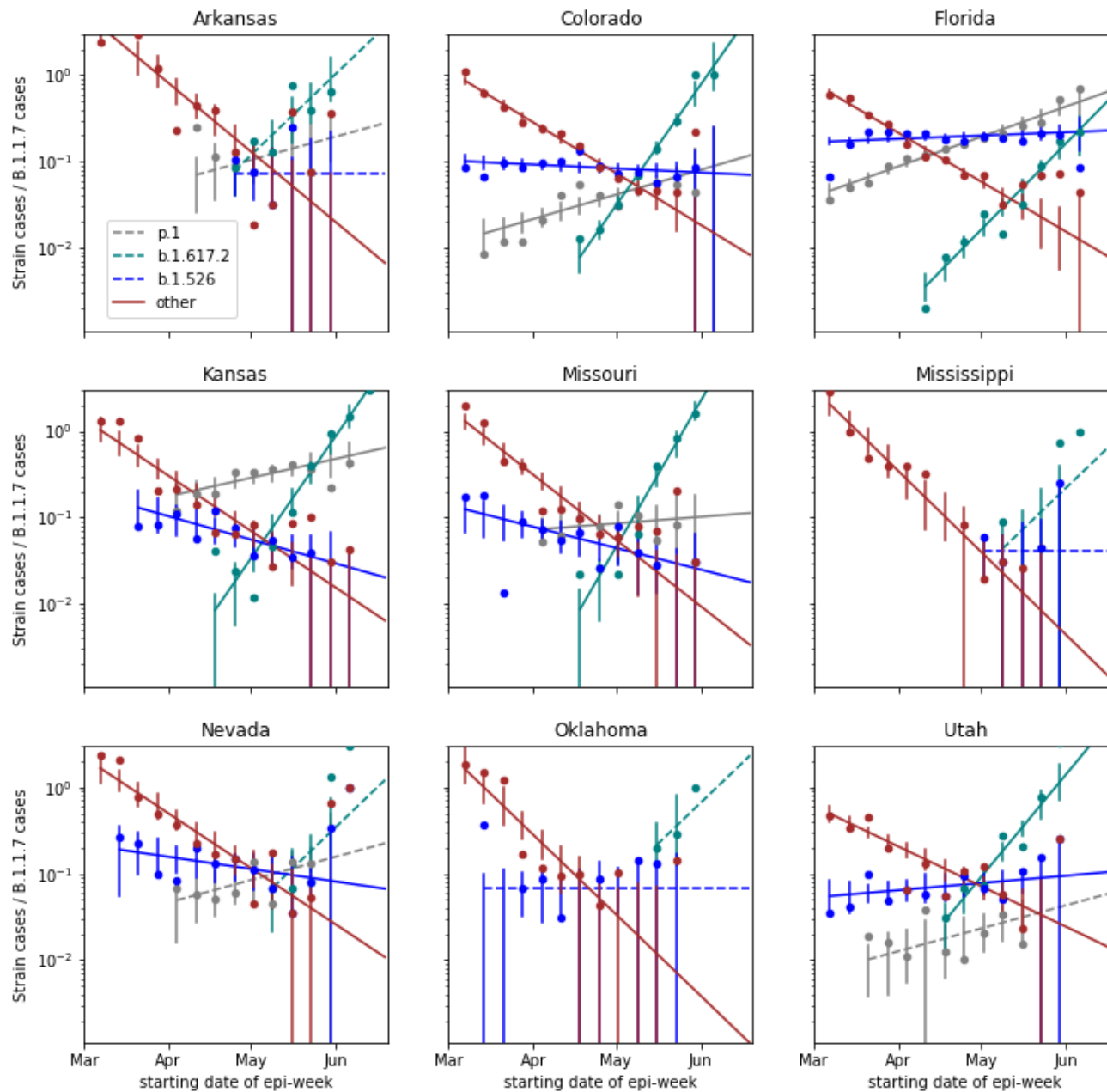




# Delta in the USA



2021-06-22

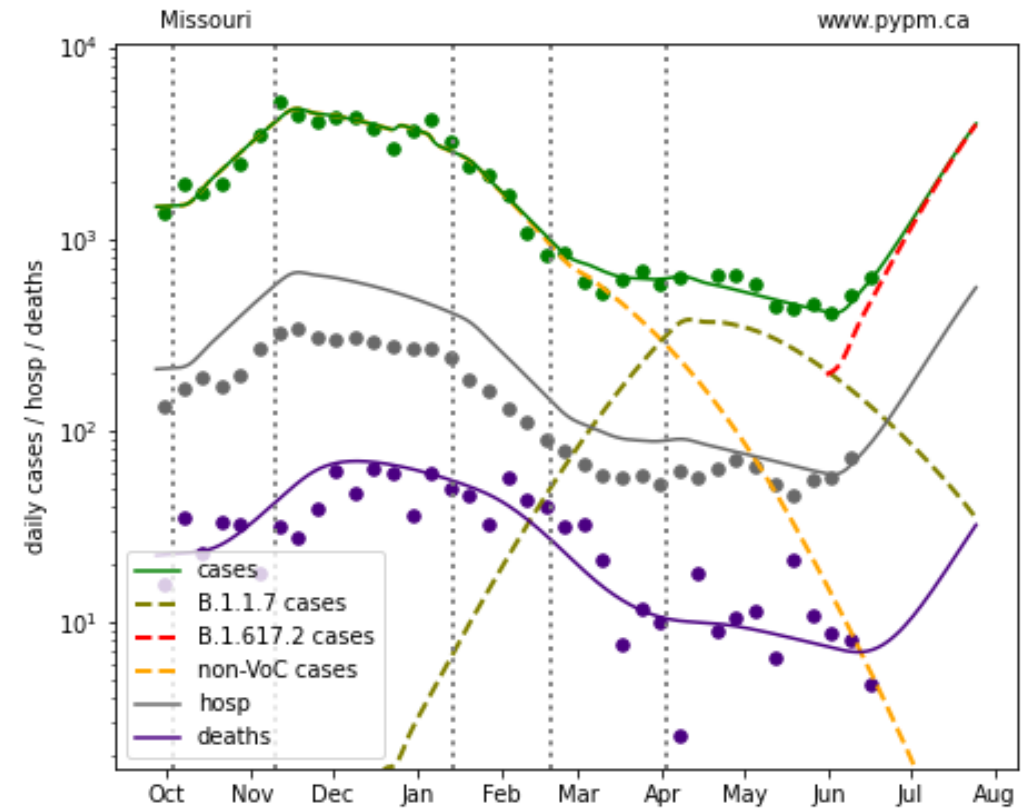
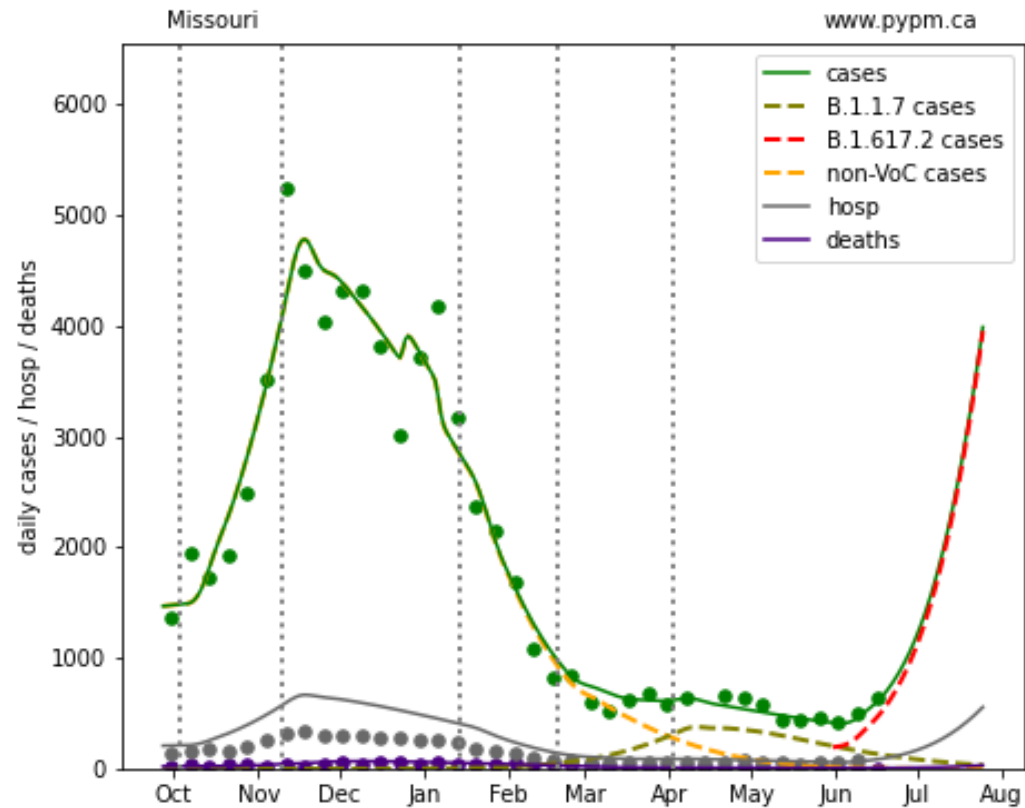


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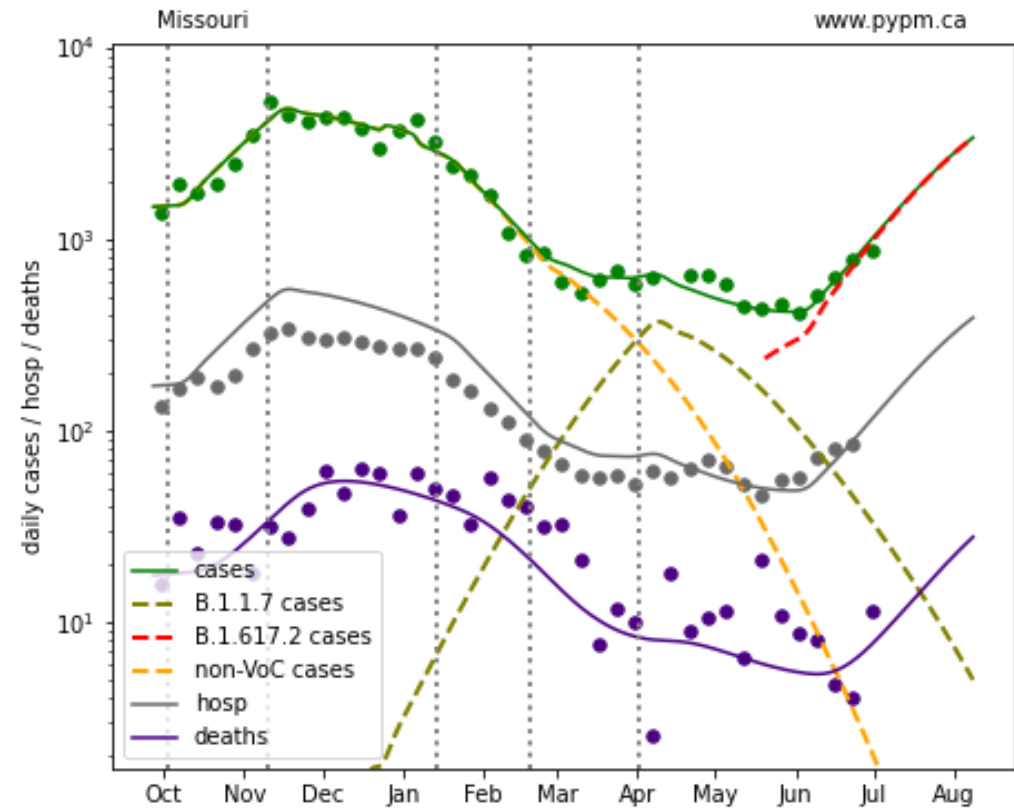
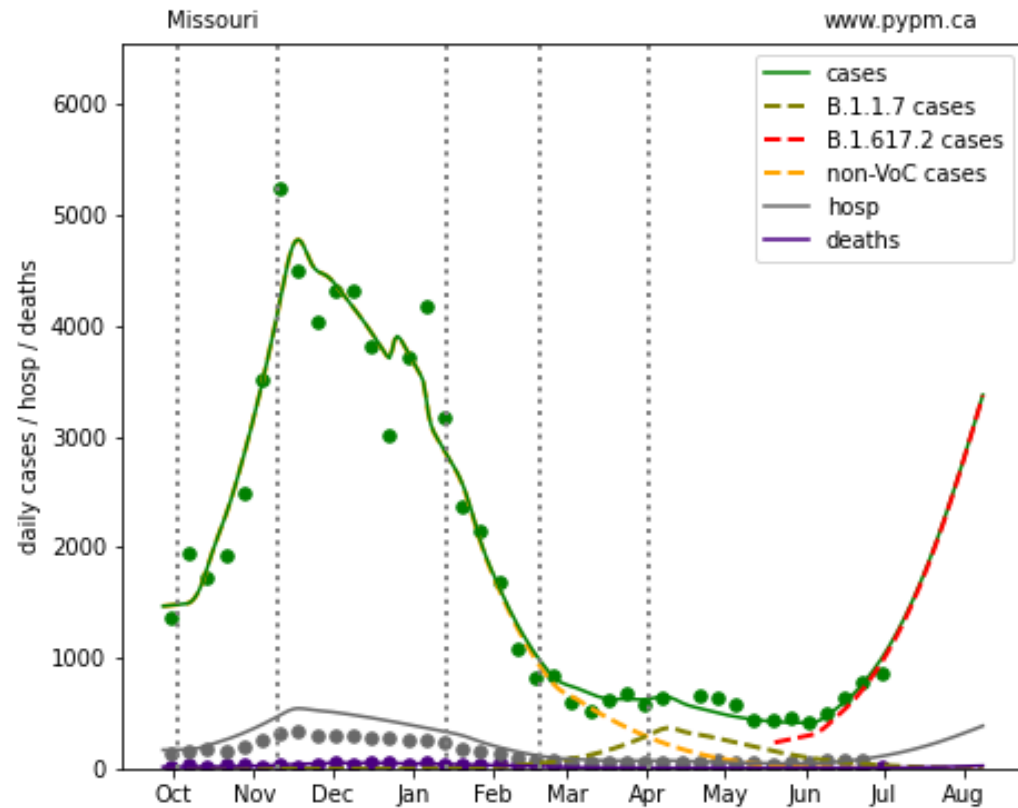
dashed: insufficient data to estimate  $s$  33

# Missouri (June 20 fit)

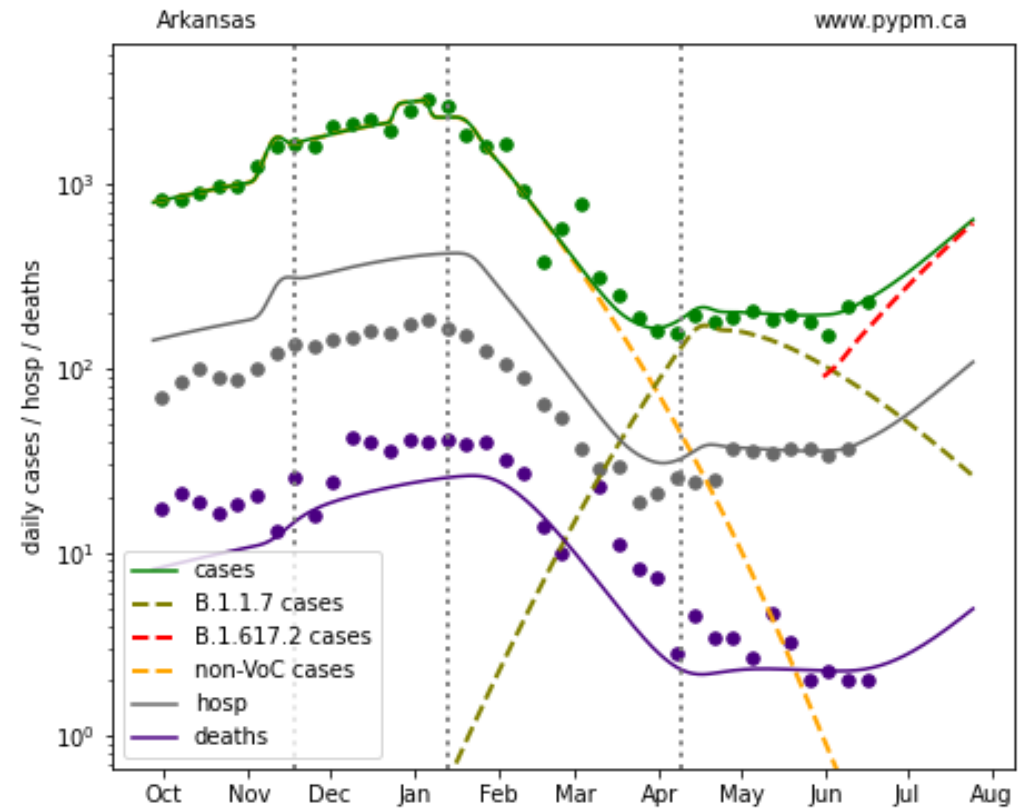
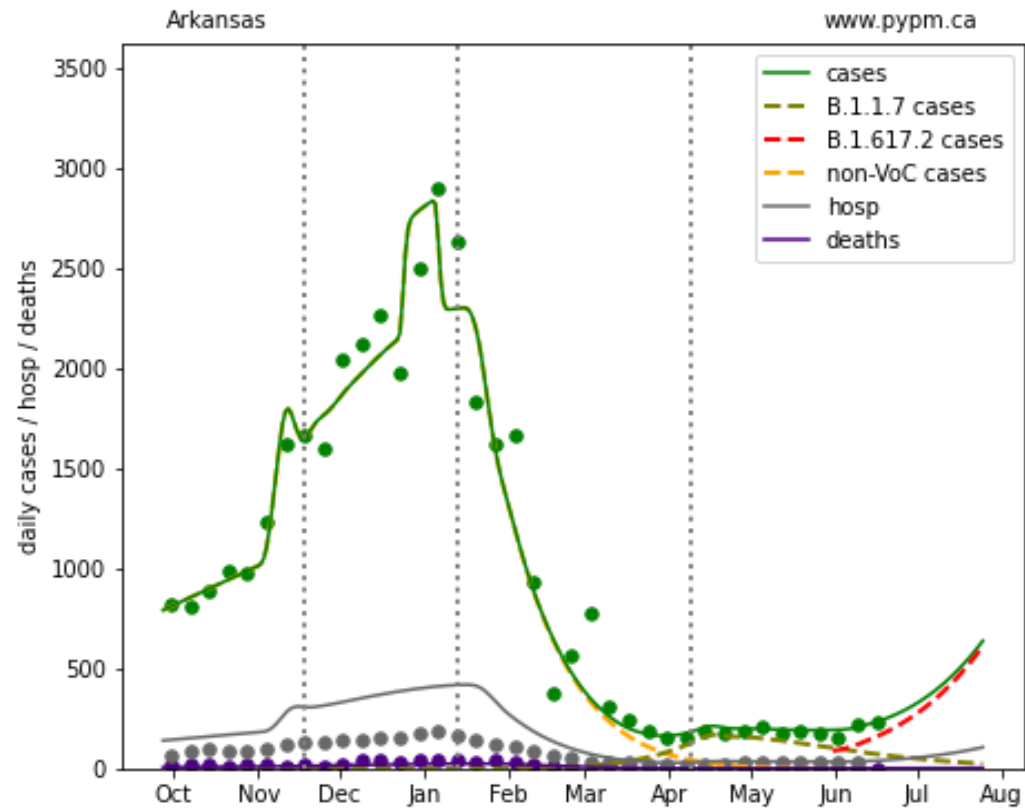
Fit assumes constant NPI since April 1



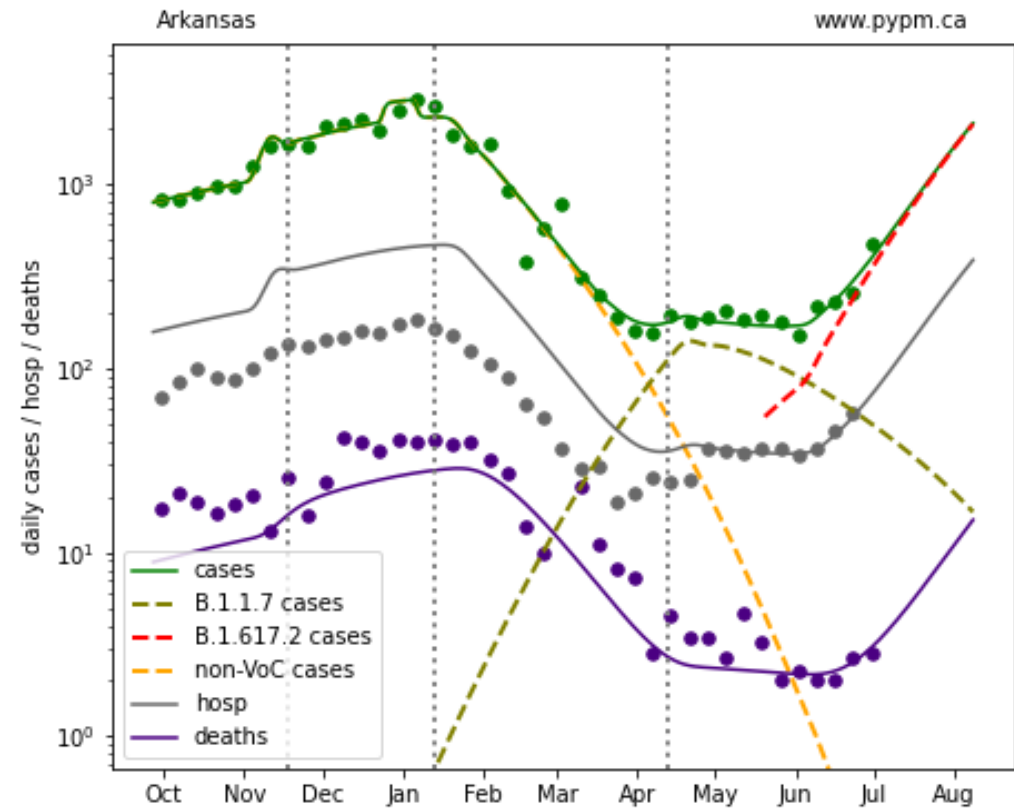
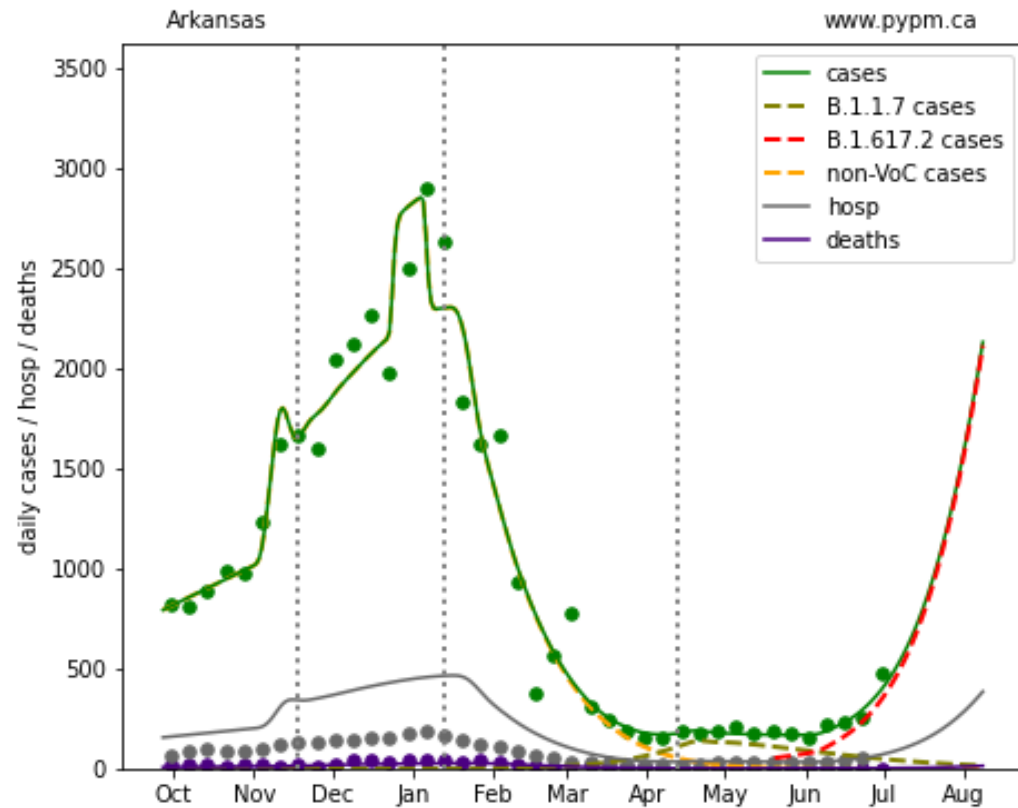
# Missouri (July 4 fit)



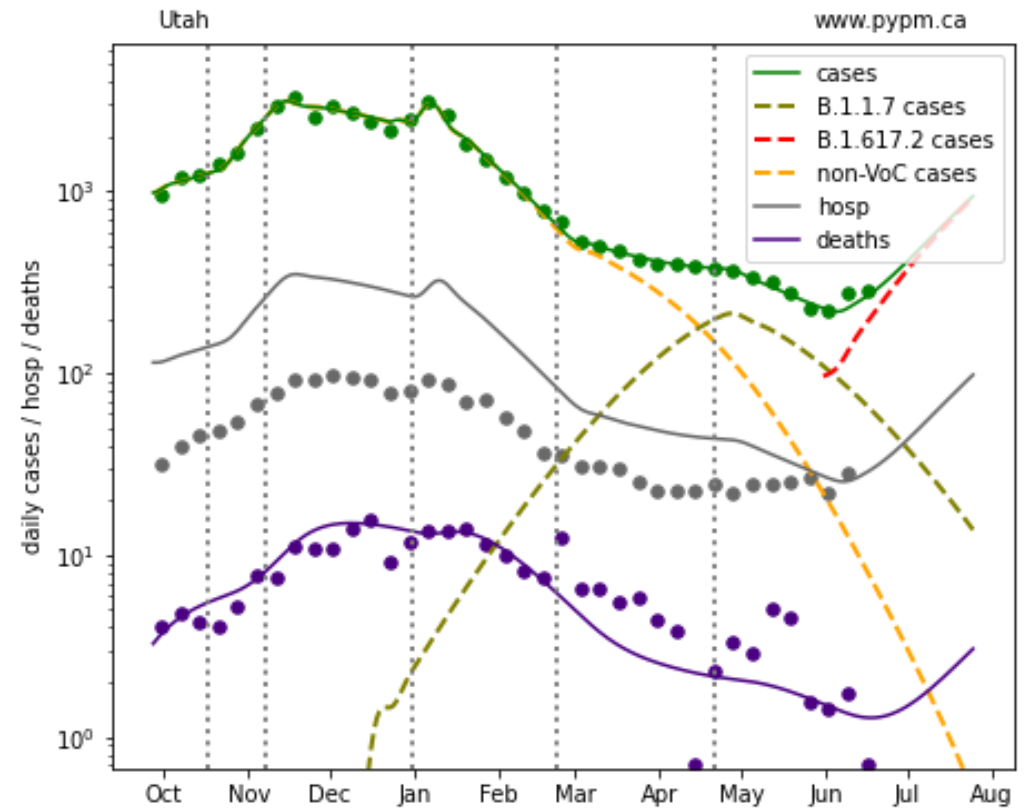
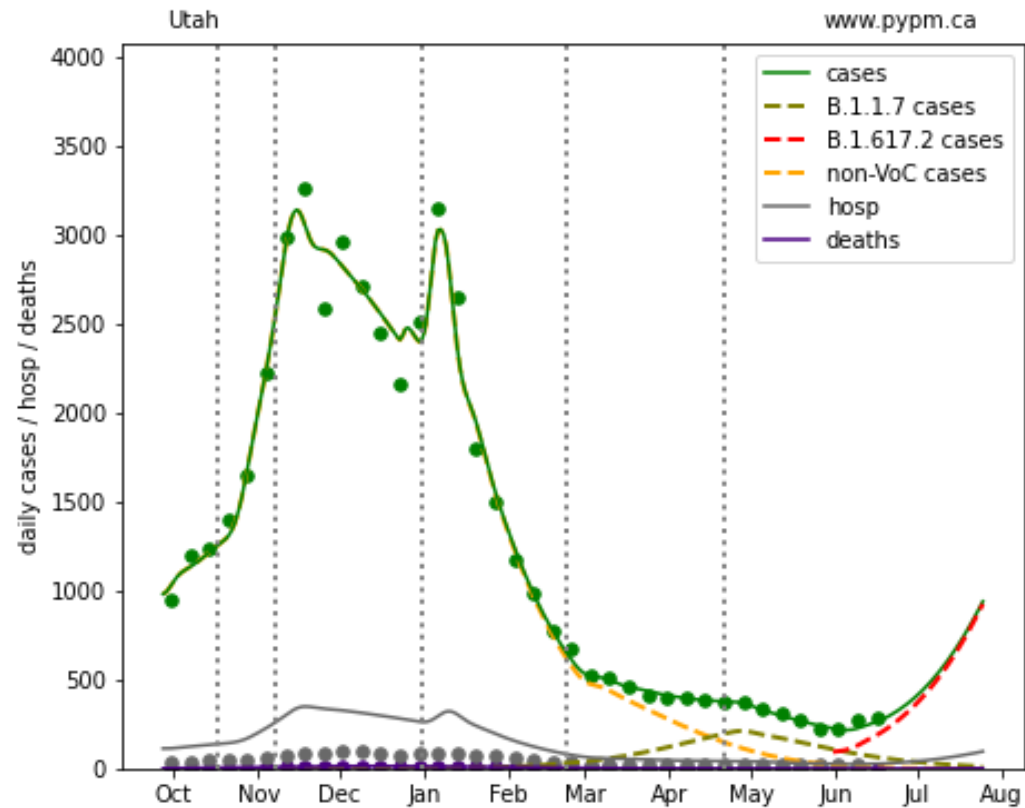
# Arkansas (June 20 fit)



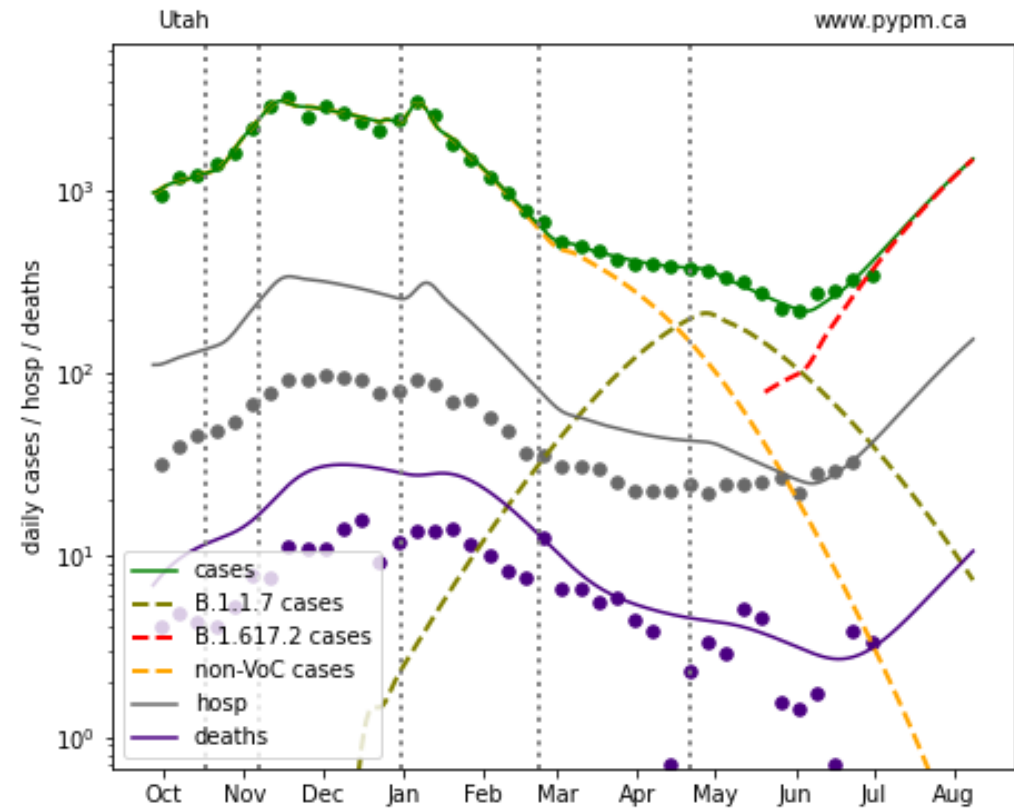
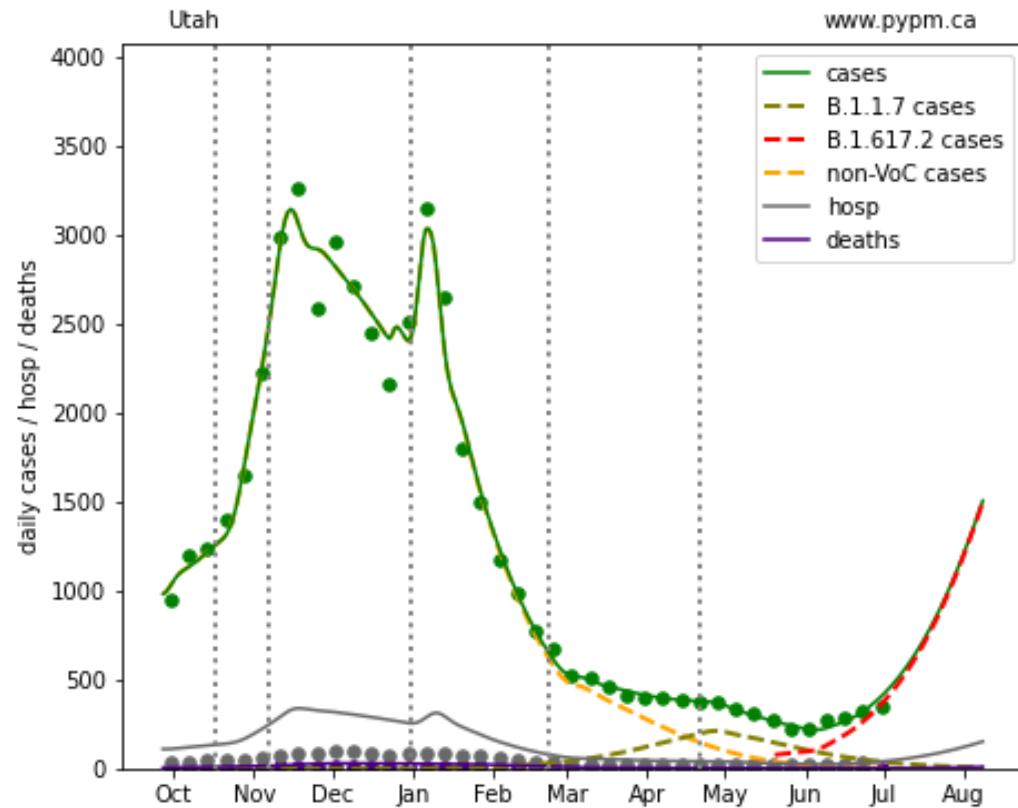
# Arkansas (July 4 fit)



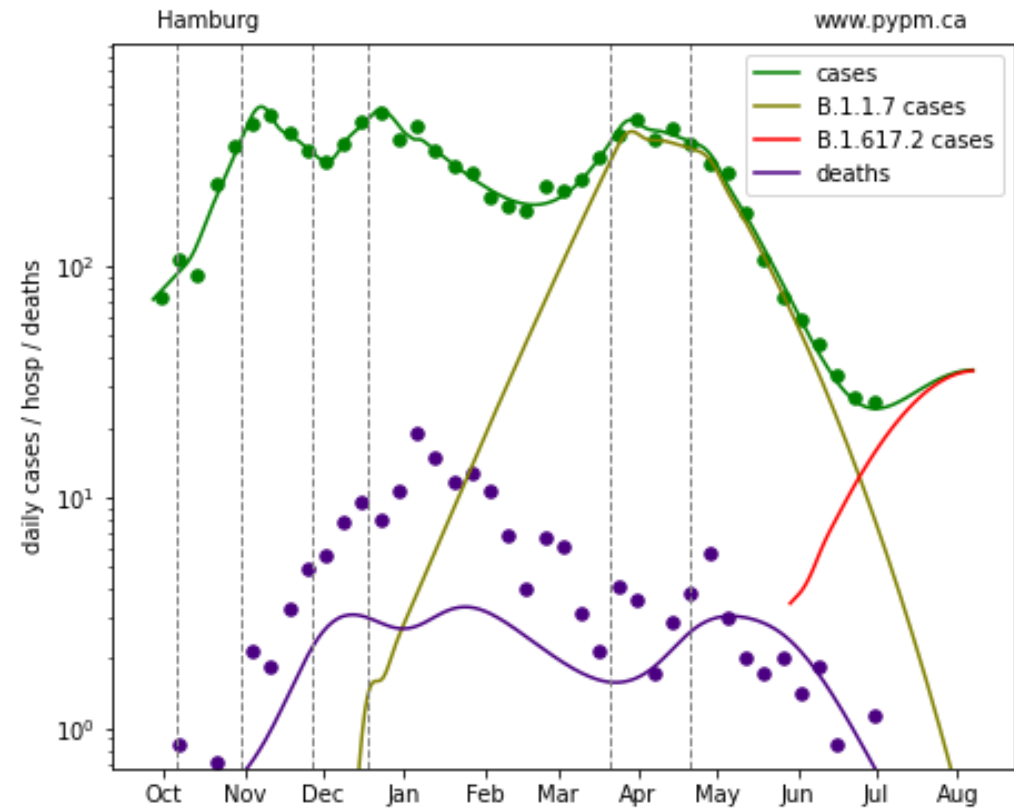
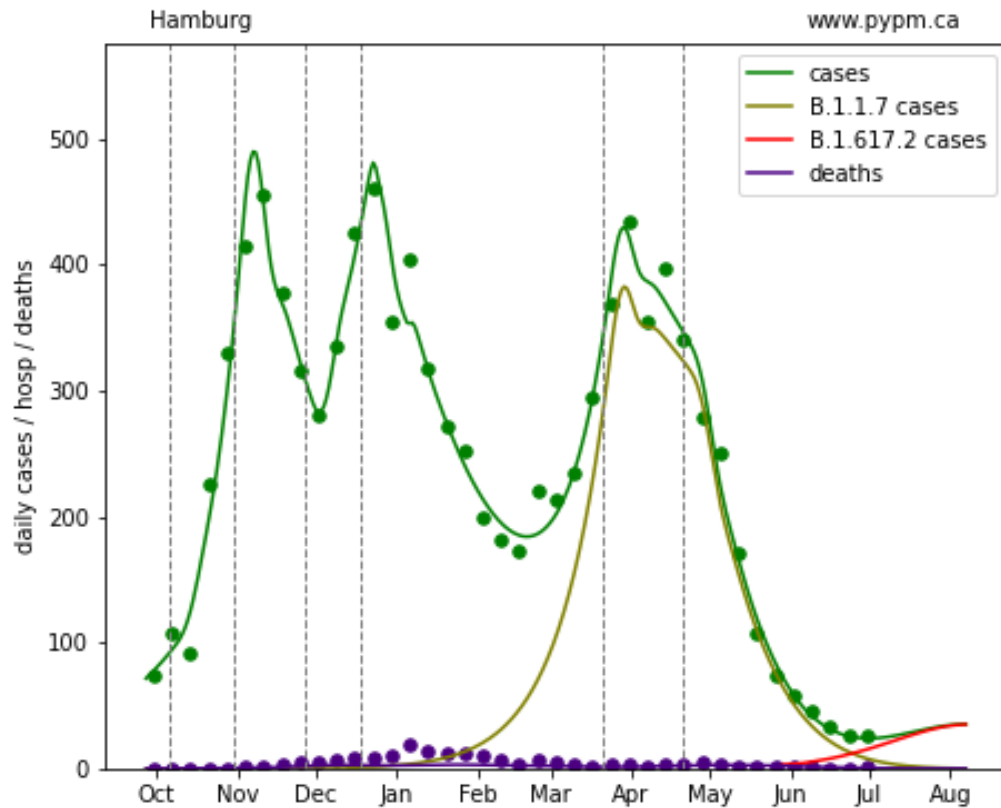
# Utah (June 20 fit)



# Utah (July 4 fit)

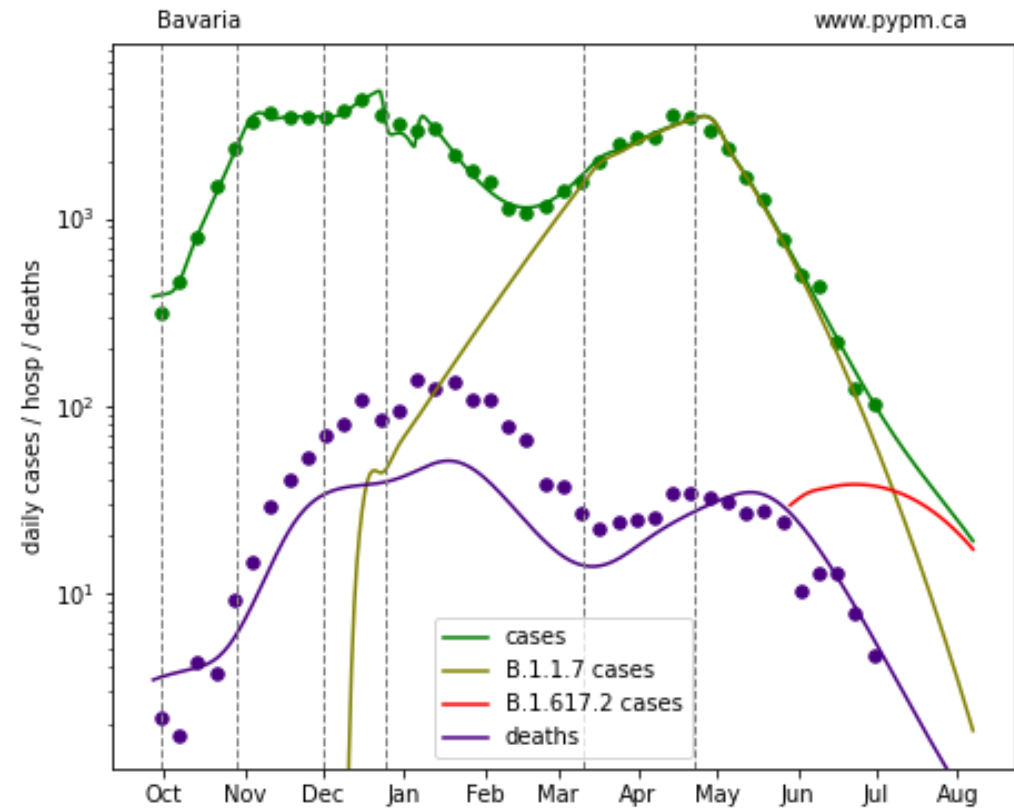
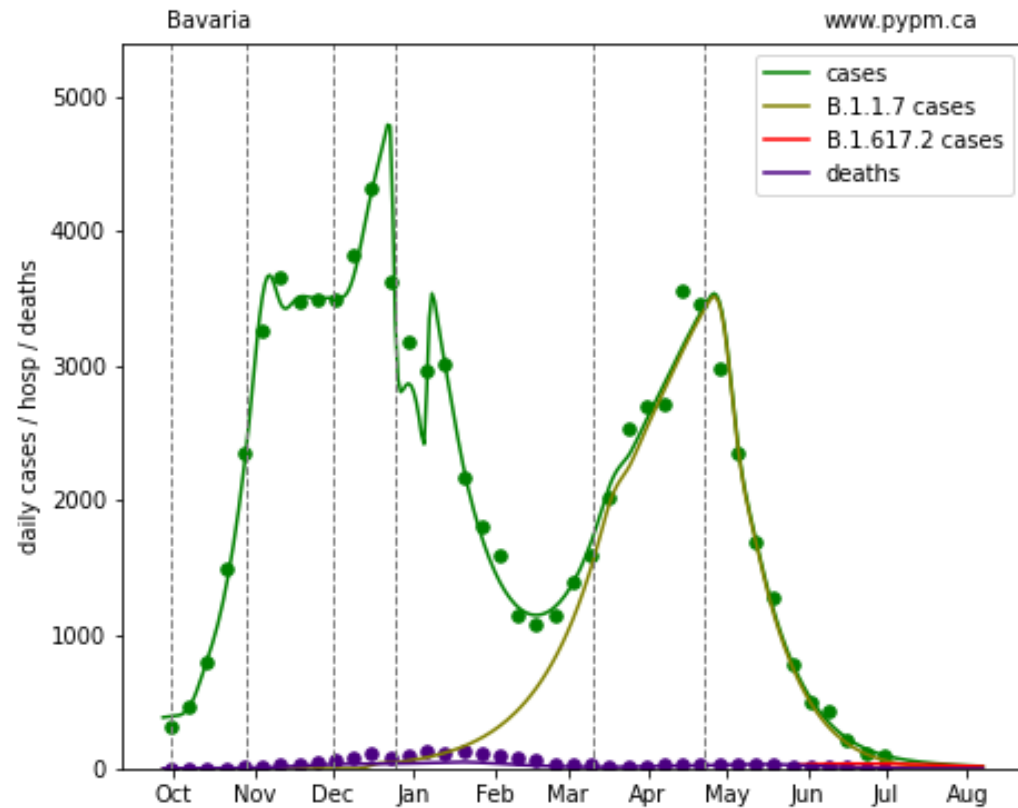


# Hamburg (July 4 fit)





# Bavaria (July 4 fit)



# Summary

- It has been an interesting year being engaged in COVID modelling as an “outsider”
- Some general concerns/points for discussion
  - data access issues have stalled several analyses
    - in Canada, genomic data was slow to be released, often in an unusable form
  - there is limited amount of true collaboration across borders
    - working together on large problems by developing common frameworks/tools
  - public policy only weakly influenced by models
    - in Canada, the coming Alpha storm was not acted upon like a coming hurricane!
- For more information about this work, see: [www.pypm.ca](http://www.pypm.ca)