

COVID Model Projections

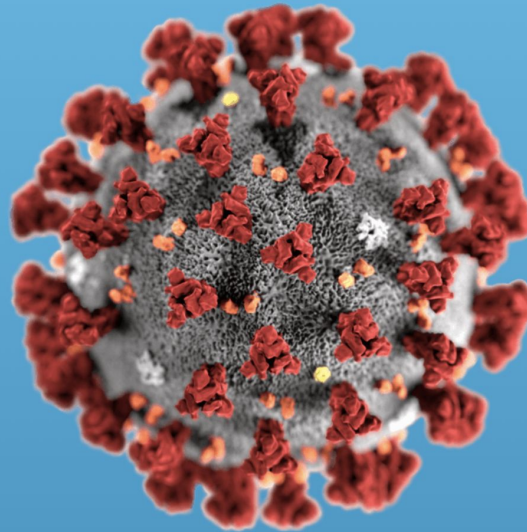
June 2, 2021

[BC COVID-19 Modelling Group](#)

About BC COVID-19 Modelling Group

The BC COVID-19 Modelling Group works on rapid response modelling of the COVID-19 pandemic, with a special focus on British Columbia and Canada.

The interdisciplinary Group was convened by [Caroline Colijn](#) (SFU) and [Dan Coombs](#) (UBC) with support from the [Pacific Institute for the Mathematical Sciences](#).



<https://bccovid-19group.ca>

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*Independent and freely offered advice,
using a diversity of modelling approaches.*

BC: Facing old and new variants of concern

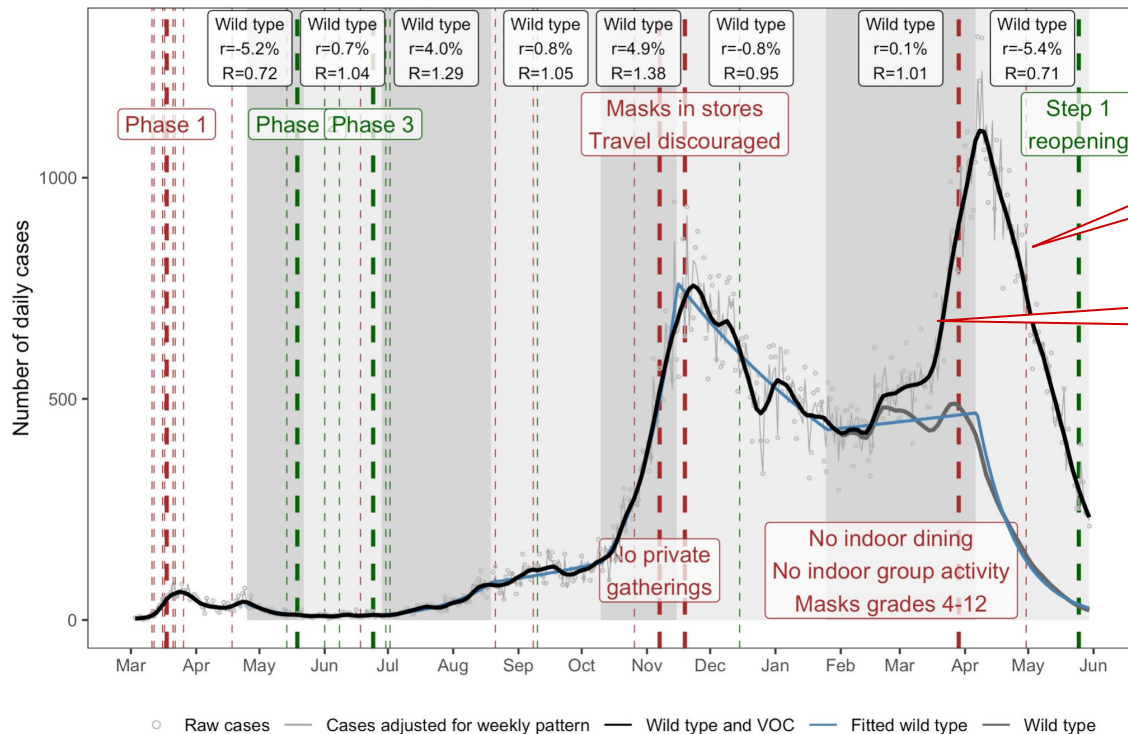
Key messages

- Cases in BC are currently dominated by B.1.1.7 and P.1 (>80% frequency).
- With these currently dominant strains, cases are projected to increase briefly and then turn around later in June, as vaccination levels rise.
- With these currently dominant strains, hospital and ICU occupancy are projected to continue to decline.
- The new variant of concern B.1.617.2 appears to be increasing in number in many jurisdictions, including BC. Its growth advantage is nearly double the advantage that B.1.1.7 had over non-variants.
- Projections have a large amount of uncertainty to them for the next couple of months
 - Vaccine effectiveness with B.1.617.2 with dosing schedule used in BC is unclear.
 - Current level of community spread in BC of B.1.617.2 is uncertain.
- Cases and hospitalization targets are the most reliable factors for determining reopening; higher vaccination targets will allow for a safer reopening.

State of the COVID-19 Pandemic in BC

Covid-19 daily new cases in British Columbia (up to Sun May 30)

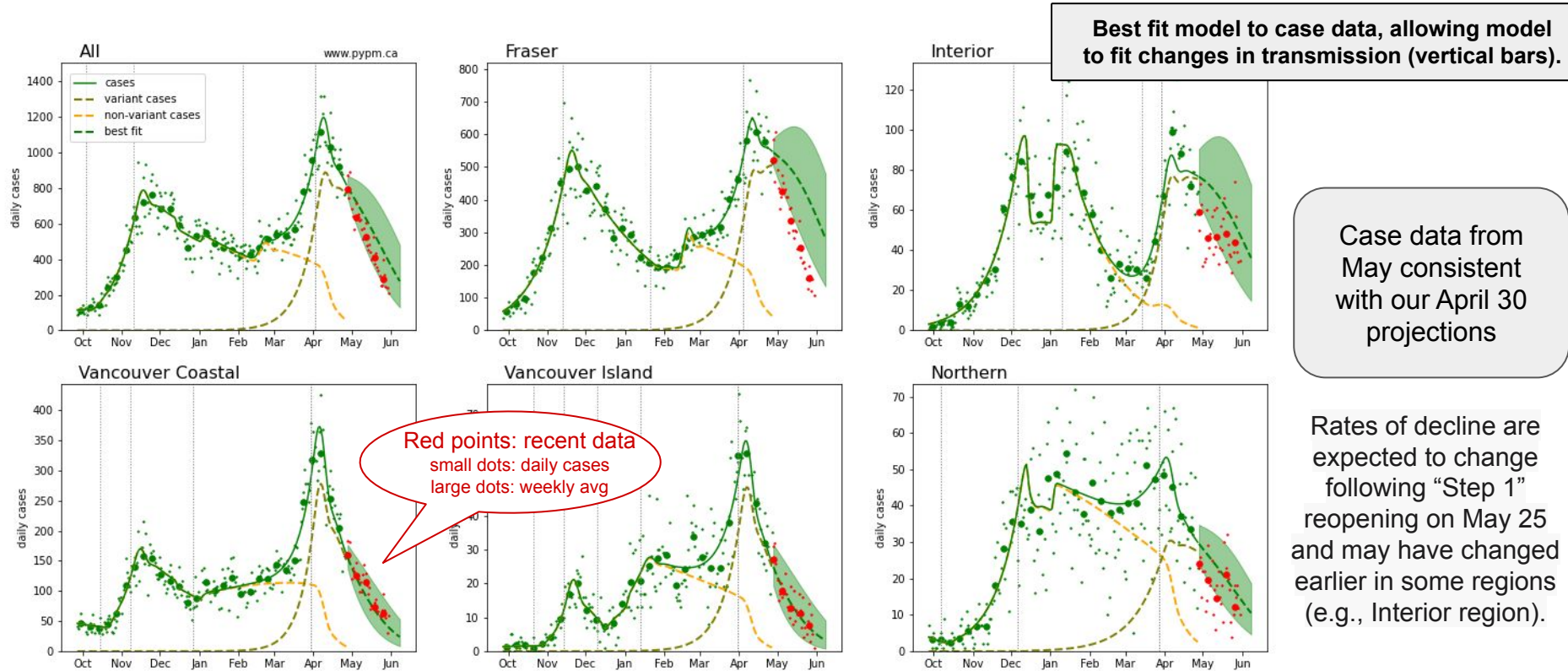
Timeline of **closure** and **reopening** events



MountainMath, Data: BCCDC

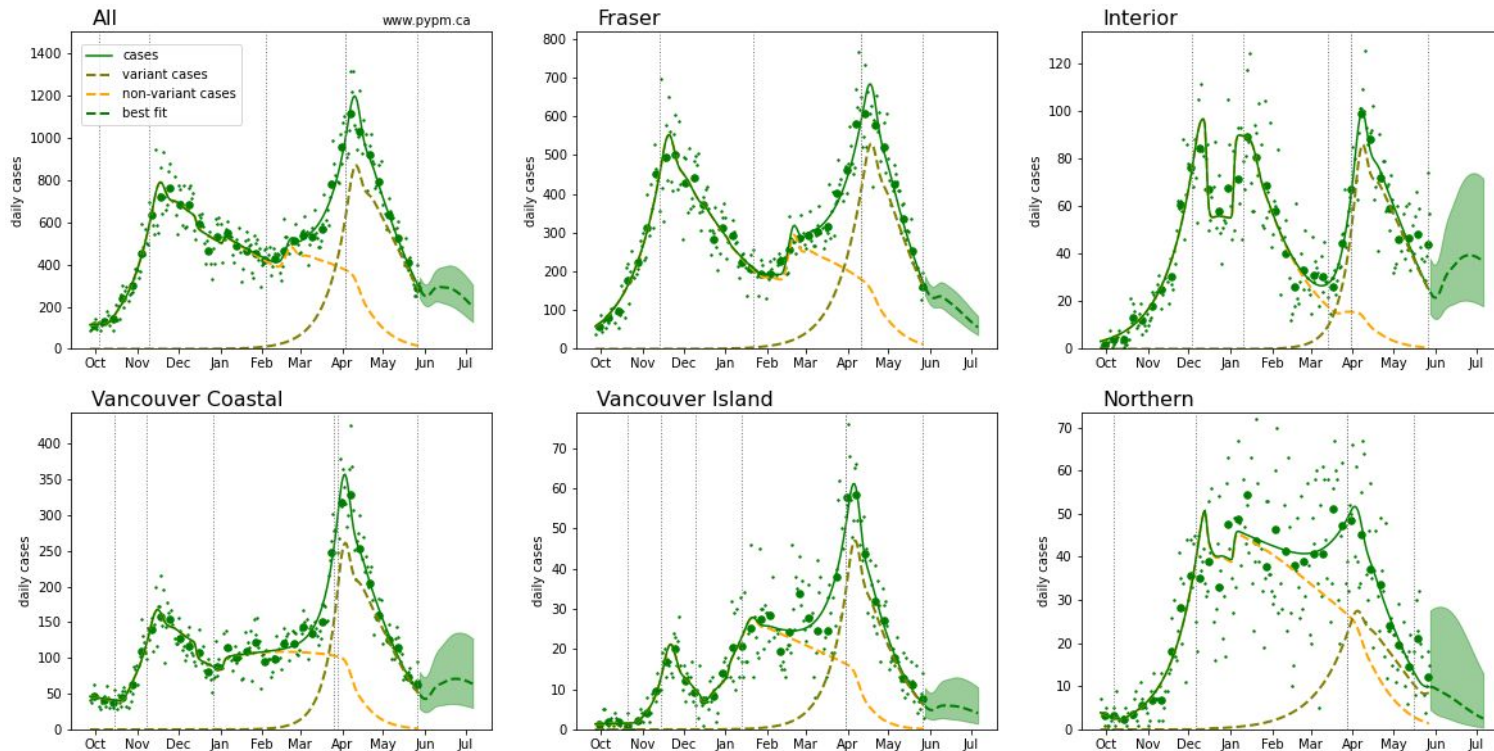
Source (J. von Bergmann) Case data from BC COVID-19 Database (<http://www.bccdc.ca/health-info/diseases-conditions/covid-19/data>). Vertical lines give dates of public health measures (major as thick lines, minor as thin lines). Grey dots are raw case counts, grey lines is cases abused for weekly pattern, black STL trend line and blue fitted periods of constant exponential growth.

April 30 model fit to case data by Health Authority



Source (D. Karlen). See www.pypm.ca. Assumed homogeneous mixing (no age structure). Assumed vaccination rate of 1st doses in May would be 35,000/day (vaccines given to all ages and in proportion to HA populations). Vaccination model benchmarked with data from Israel: see Appendix and [link](#). Assumed that “circuit breaker” health measures remained in force throughout May. Shaded bands indicate range of trajectories consistent with case data up to April 30 (68% CL).

Updated model fit to case data by Health Authority



To estimate the effect of May 25 relaxation of health measures, the transmission rates from Feb/March are applied to June.

**Not included:
B.1.617.2**

Source (D. Karlen). See www.pymp.ca. These models have no age structure. Assumes vaccination rate of 1st doses continues at 52,000/day (given to all ages and in proportion to HA populations until 75% of the population is vaccinated), ultimate 1st dose effectiveness is 90%. Vaccination model benchmarked with data from Israel: see Appendix and [link](#). Assumes current public health measures remain in place in June. Shaded bands indicate range of trajectories consistent with case data (68% CL).

New variant of concern from India (B.1.617.2)

Evidence is increasing from around the world that B.1.617.2 spreads at a faster rate than previous variants that took over in BC (B.1.1.7 and P.1).

The next few slides focus on the risk posed by this variant.

The World Health Organization has [proposed new names](#) for the four variants of concern.*

Lineage	New WHO name	Country of first spread
B.1.1.7	Alpha	United Kingdom
B.1.351	Beta	South Africa
P.1	Gamma	Brazil
B.1.617.2	Delta	India

* A variant of concern (VOC) has a demonstrated negative impact on COVID-19, increasing transmission, increasing severity (“virulence”), or reducing the efficacy of public health measures like vaccination.

New variant from India (B.1.617)

B.1.617 has been spreading in India and consists of three main sub-lineages, B.1.617.1, B.1.617.2, and B.1.617.3.

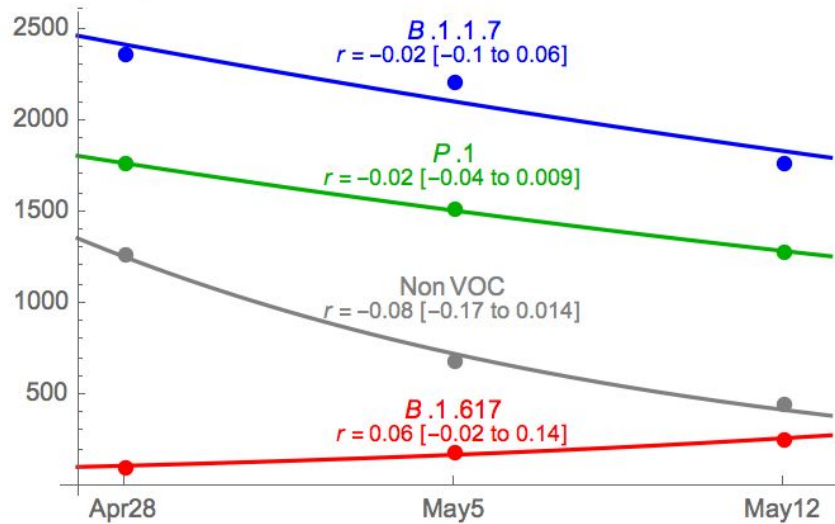
What do we know?

- With >400,000 cases and >4000 deaths per day at the peak in mid May, the rapid rise in cases in India has greatly challenged their health care system and caused enormous human suffering. B.1.617 lineages rose in frequency over this time period, but the extent to which the surge was due to this variant is unknown.
- In the UK, B.1.617.2 is [increasing in frequency](#) and has recently led to a [rise in cases](#) in several regions. B.1.617.1 and B.1.617.3 do not appear to be [spreading](#).
- The chance that an infected person passes COVID-19 onto a household member (“secondary household attack rate”) is about [50% higher](#) for B.1.617.2 than for B.1.1.7 [UK: 13.5% (95%CI:12.5-14.6%) vs 8.1% (95% CI: 7.9-8.3%)].
- A vaccine [study](#) found a lower real-world effectiveness 21 days after one dose (B.1.617.2: 33.5%; B.1.1.7: 51.1%), but more similar effectiveness after two doses (B.1.617.2: 80.9%; B.1.1.7: 86.8%). It is uncertain how effectiveness rises over time after one dose with a delayed second dose, which is important in a Canadian context.
- B.1.617.2 has a higher than expected number of [mutations](#), more than 96% of the other 1280 SARS-CoV-2 lineages, including many in [spike](#) (see appendix slide 22). B.1.617.1 and B.1.617.3 have fewer changes.

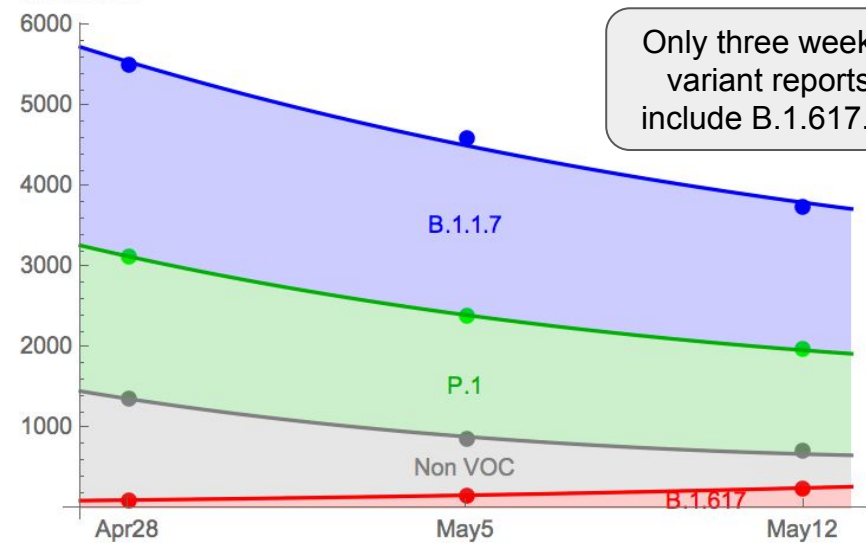
Spread in BC: New variant from India (B.1.617)

Whole genome sequencing of cases reported by the BCCDC from April 25 to May 15 indicates that all variants are declining except B.1.617, which was growing even before the partial re-opening on May 25.

Number of variant cases



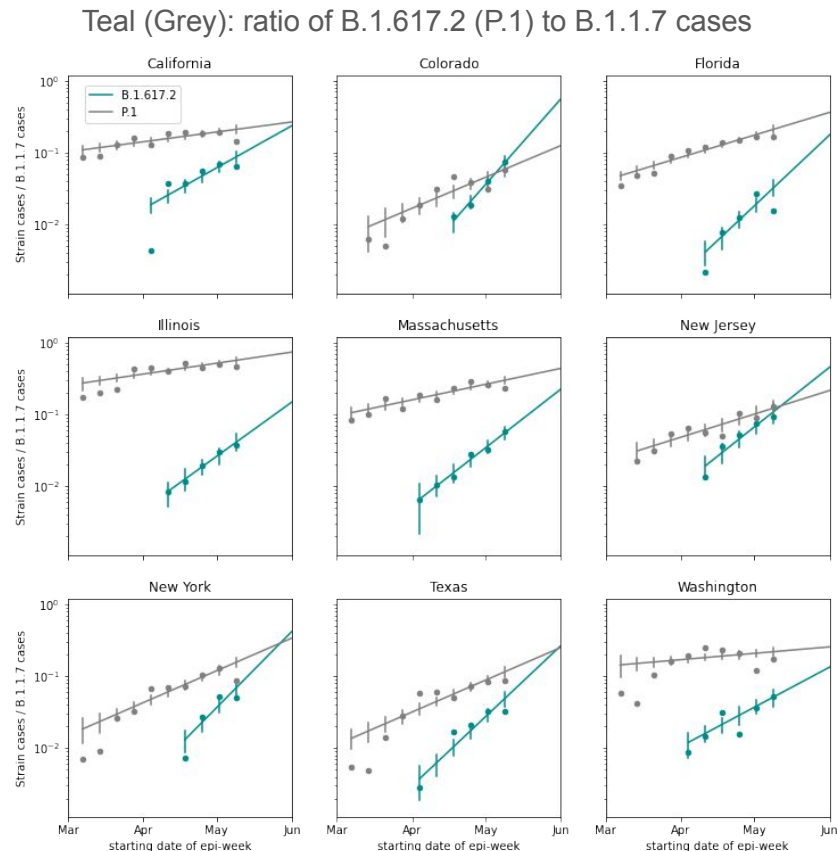
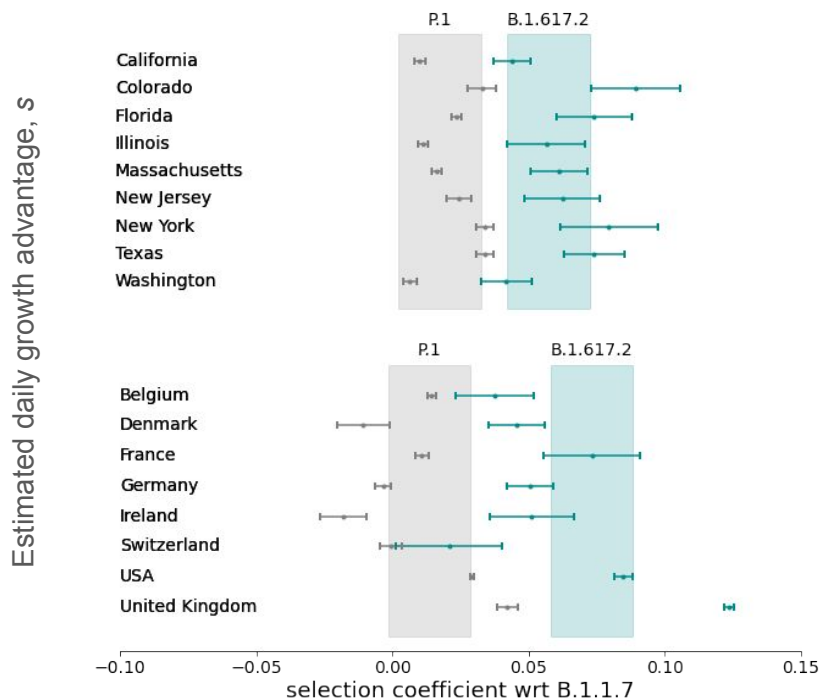
Total cases



Source (S. Otto). Fit to weekly [Variant report](#) from BCCDC (subtypes of B.1.617 not distinguished). Uses weekly cumulative case numbers for each epiweek (mid-date of epiweek shown on the x axis) and multiplies by the “Sample prevalence VOCs” to estimate the number of each variant in each week. Exponential model fit is used to estimate daily growth rate, r . Note that r estimates are highly uncertain with only three data points [95% CI in square brackets]. The selective advantage for B.1.617 relative to B.1.1.7 is $s = 0.08$ per day (the difference in their daily growth rates, consistent with other jurisdictions, next slide)

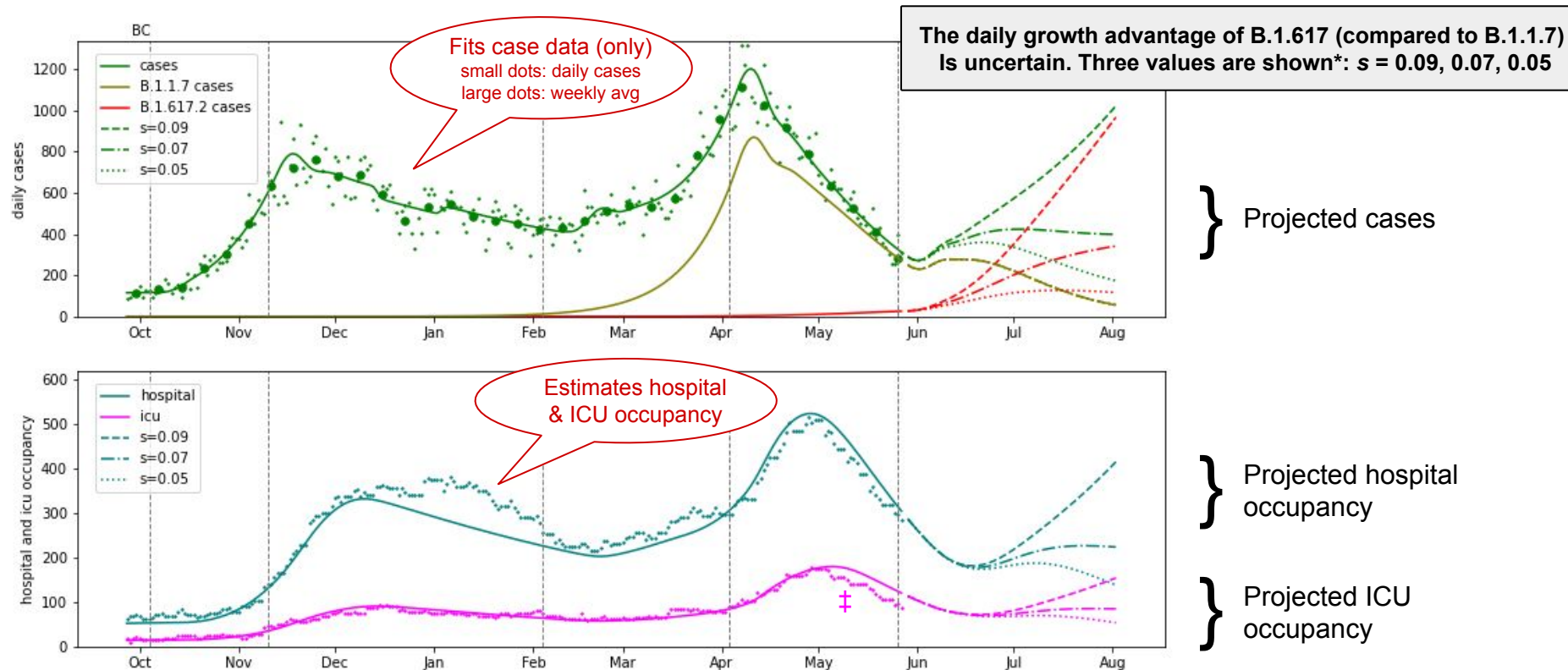
Estimating growth advantage of B.1.617.2

B.1.617.2 grows faster than B.1.1.7 and P.1 in many other jurisdictions.



Source (D. Karlen). Fit to GISAID data as compiled by covariants.org for Europe and by outbreak.info for USA. Growth advantage (“selection coefficient”, s) measures the daily rise in the frequency of a variant (B.1.617.2 or P.1) relative to the frequency of B.1.1.7.

Model projections with B.1.617.2 variant



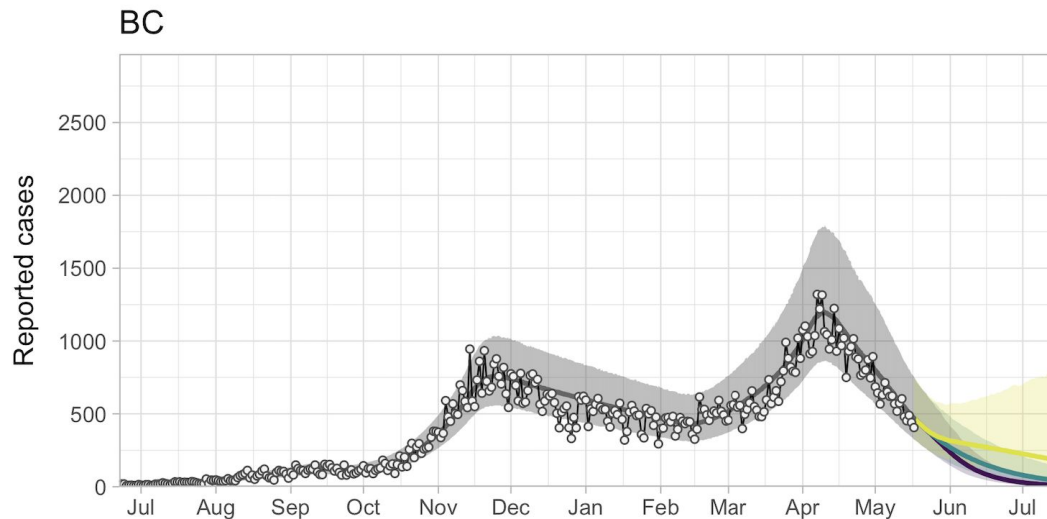
Source (D. Karlen). See www.pyppm.ca. Homogeneous mixing (no age structure). Vaccination rate assumption: 52,000/day until 75% vaccinated, with 90% asymptomatic effectiveness (see Appendix from [May 14 report](#) for comparison to real-world effectiveness). ‡ To better match ICU data, the fraction of cases leading to ICU admission is increased by 60% in early April. Assumes current public health measures remain in place. *Range of growth advantage (selection coefficient, s) for B.1.617.2 with respect to B.1.1.7 is based on genomic data from other jurisdictions (see previous slide).

BC incidence projections: contact and slight reopening

Incidence continues to decline, with vaccinations[§] contributing to that decline.

This decline is robust to a slight increase in contact rates* among those distancing (+30% in yellow, -30% in purple).

It is too early to determine impact of Step 1 of BC's reopening plan relative to these projections.

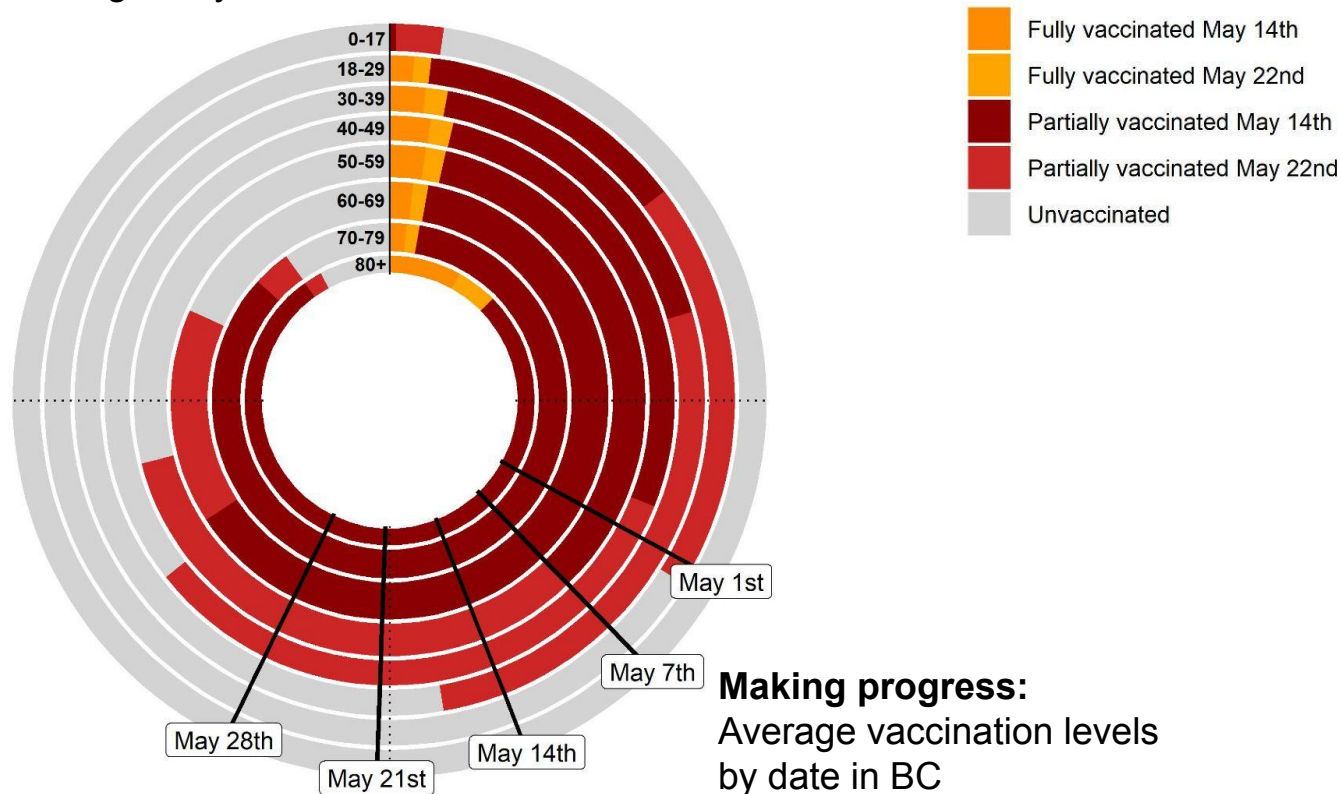


Yellow: 30% increase in contact*. Green: as now. Purple: 30% decrease in contact.

Source (E. Are, C. Colijn). Daily case numbers projected forward, accounting for B.1.1.7 and P.1 data from BCCDC variant reports. These data provide % of cases that were VOC by week (see appendix slide 23). These data were fit by a logistic function to estimate percent VOC by day (see Appendix of April 14 report). Assuming a 40% increase in transmissibility (consistent with the estimated selection s in the Appendix of April 14 report), the percent VOC is used to create an overall reproduction number R for the virus population. R changes in time as the VOC rises in frequency. The social distancing parameter (among others) is estimated to fit the data using the [‘covidseir’](#) R package (M. Irvine, S. Anderson). [§]Vaccination is incorporated by removing susceptibles at a rate accounting for contact by age, vaccination by age and susceptibility of contacts. * Measured as f , the relative contact rate among those willing and able to distance.

Closing the circle: Vaccination status by age

May 28 update includes data through May 22nd, 2021



Closing the circle: Vaccination status by age

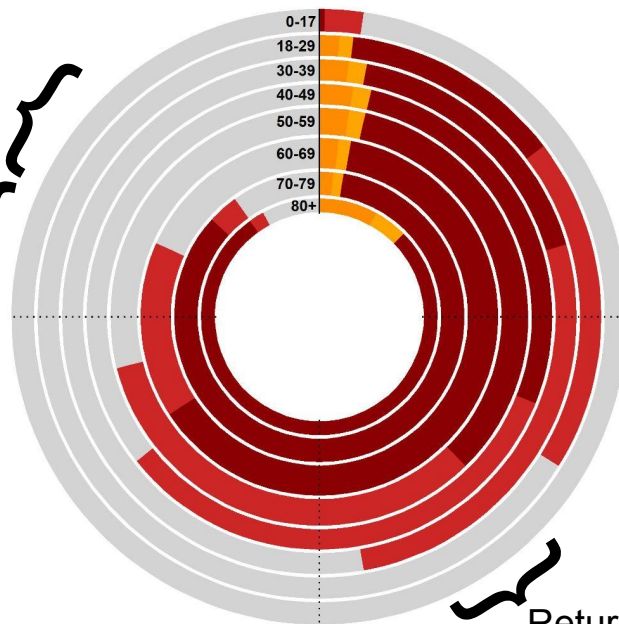
May 28 update includes data through May 22nd, 2021

If vaccines were 100% effective:

Herd immunity if $R_0 \sim 5-6$

Herd immunity if $R_0 \sim 4-5$

R_0 for B.1.617.2 unknown but may be ~ 4 to 7 given an R_0 for B.1.1.7 of ~ 2.8 to 5.4* without control measures



Herd immunity: the level of immunity in a population at which a disease starts to decline*

→ $(1-f) R < 1$ where f is level of immunity

Reproductive number (R): number of new cases per case, called R_0 in the absence of any control measures.

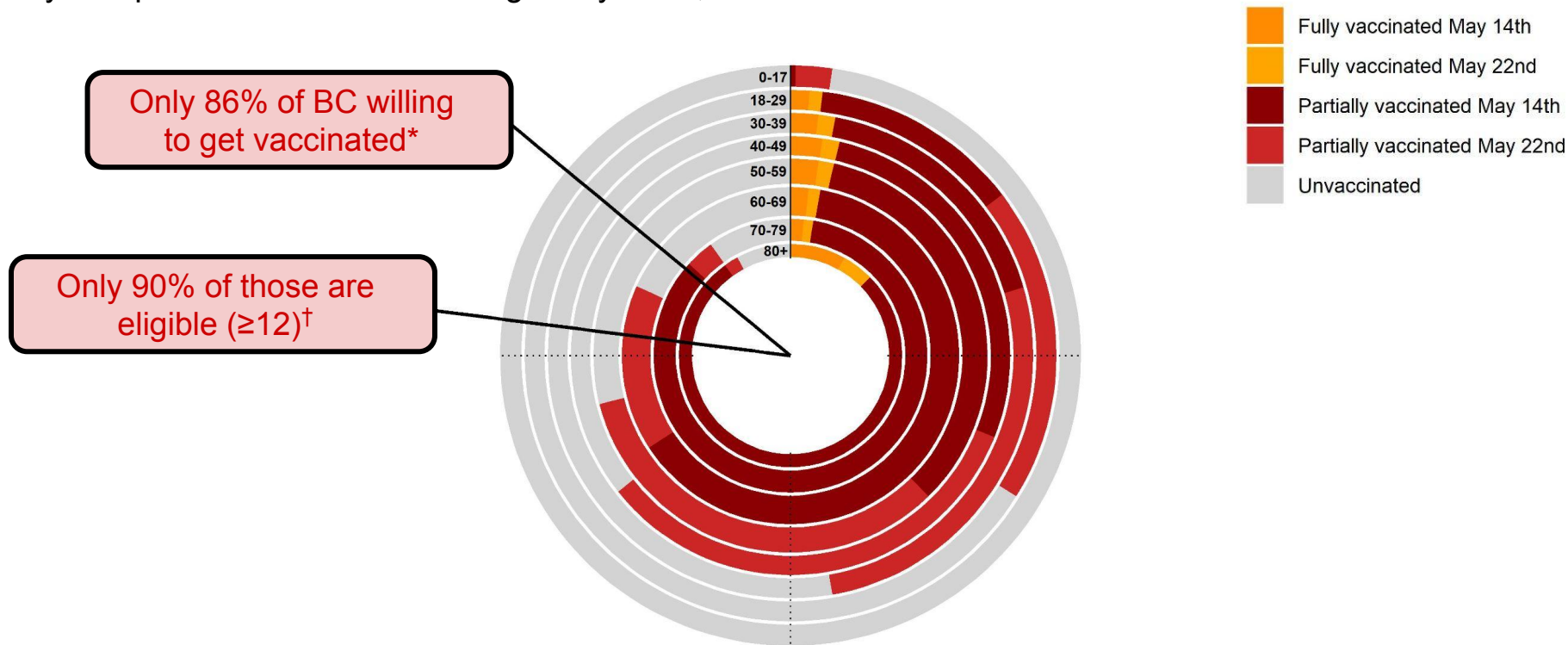
Return to Feb/March 2021 activities when $R \sim 1.7$ for B.1.1.7 & P.1 in BC[†]

Source (B. Wiley). Design by Blake Shaffer (https://blakeshaffer.shinyapps.io/app_vaccines/) [†]<https://bccovid-19group.ca/post/april-2021-report/>

*Public Health Ontario: <https://www.publichealthontario.ca/-/media/documents/ncov/covid-wwksf/2021/02/wwksf-herd-immunity.pdf>, assuming B.1.617.2 has a selective advantage of $s=0.05$ and using a 6.5 day generation time to translate to reproductive numbers (as in [Volz et al.](#)). *Typically assumes no or minimal control measures.

Closing the circle: Vaccination status by age

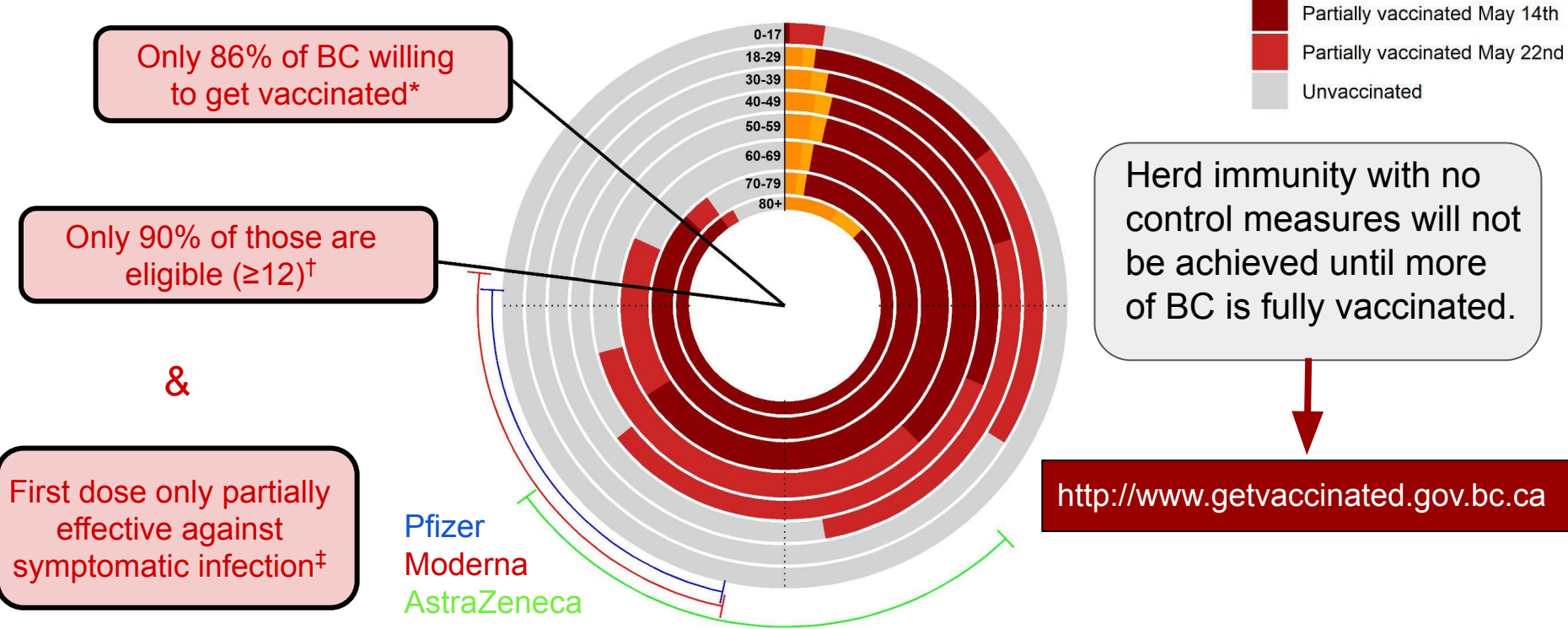
May 28 update includes data through May 22nd, 2021



Source (B. Wiley). Design by Blake Shaffer. *Angus Reid (April 26, 2021): <https://angusreid.org/vaccine-astrazeneca-johnson/>. [†]BCCDC (April 24, 2021) Epi-week 16 Situation Report. [‡]NACI "Recommendations on the use of COVID-19 vaccines" (May 3, 2021), Efficacy against symptoms >14 days after one dose (>21 days for AstraZeneca) but before two doses; Pfizer: 92.3% [95%CI: 69-98%]; Moderna: 92.1% [95%CI: 68.8-91.1%]; AstraZeneca: 71.3% [95%CI: 49.0-83.8%].

Closing the circle: Vaccination status by age

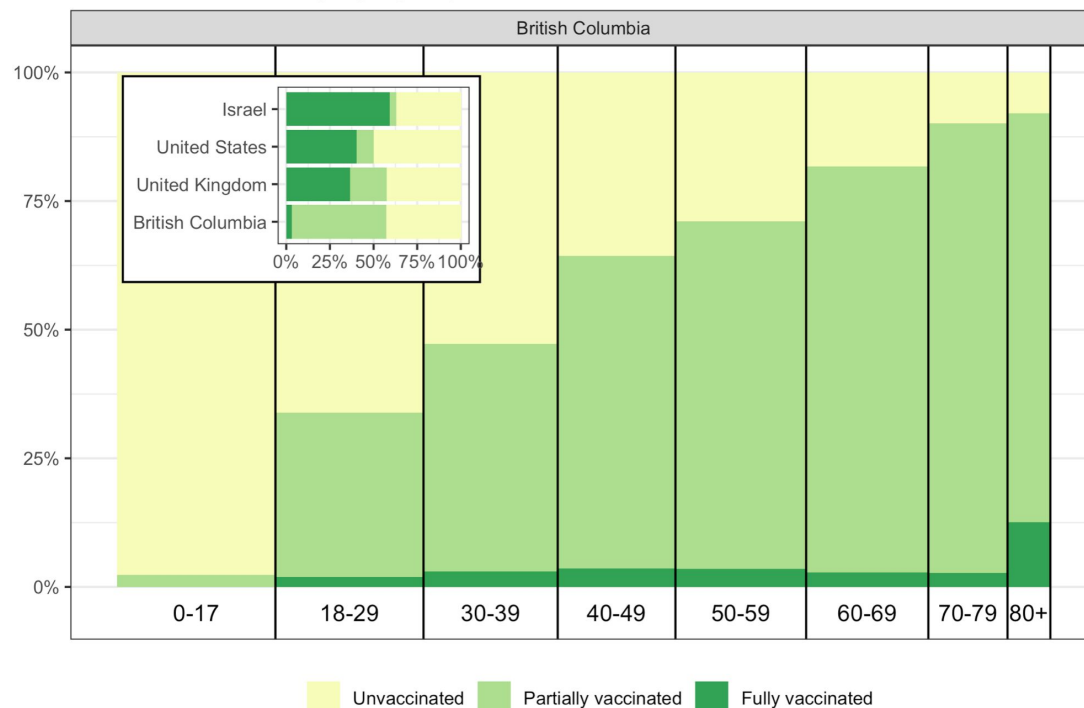
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Source (B. Wiley). Design by Blake Shaffer. *Angus Reid (April 26, 2021): <https://angusreid.org/vaccine-astrazeneca-johnson/>. [†]BCCDC (April 24, 2021) Epi-week 16 Situation Report. [‡]NACI "Recommendations on the use of COVID-19 vaccines" (May 3, 2021), Efficacy against symptoms >14 days after one dose (>21 days for AstraZeneca) but before two doses; Pfizer: 92.3% [95%CI: 69-98%]; Moderna: 92.1% [95%CI: 68.8-99.1%]; AstraZeneca: 71.3% [95%CI: 49.0-83.8%].

Vaccination status by age group

Last age-based BC data update May 22



PHAC, StatCan table 17-10-0005

Israel: 63% vaccinated (at least one dose, 59.2% fully vaccinated).

Schools fully reopened on Apr 26 with no restrictions; no restrictions on travel; immunity passports being used for indoor dining, gyms and sports; no restrictions on indoor/outdoor socialization in groups of 50 or less

UK: 57.6% vaccinated (at least one dose, 36.7% fully vaccinated).

Schools fully open with optional rapid testing available and masks for secondary students; travel is discouraged; indoor dining remains closed; outdoor socializing only, in groups of up to 6. Further reopening starting May 17.

Countries with high vaccination levels are reopening slowly

Data gap: Where are the genomes?



BC is a global leader in genomics, yet BC has not publicly shared the thousands of SARS-CoV-2 genomes sequenced in 2021.

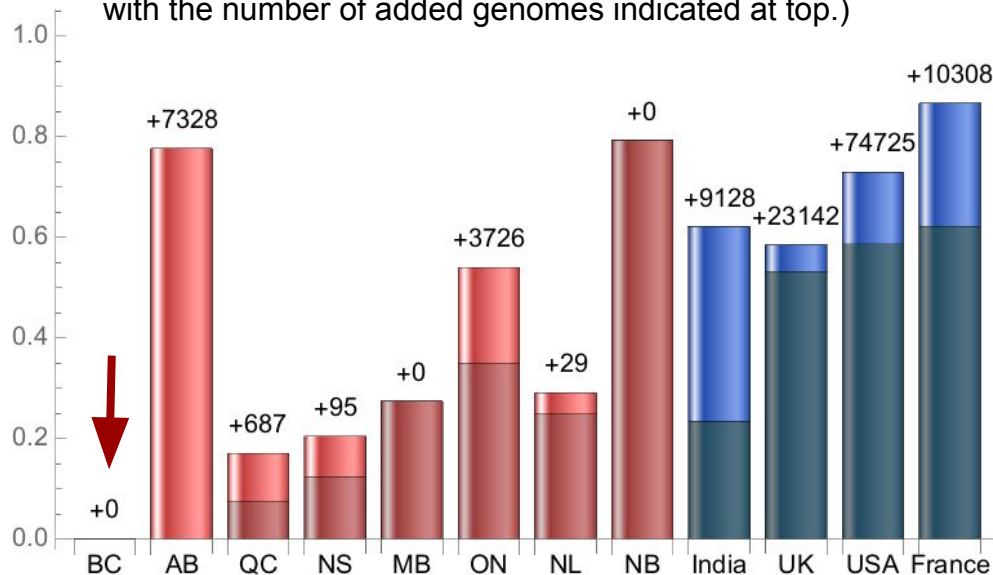
These sequences are needed for global analyses to:

- Identify new variants
- Estimate rates of spread
- Assess efficacy of restrictions
- Detect importations

Alberta has recently submitted over 7000 viral sequences from 2021!

Fraction of SARS-CoV-2 genomes in GISAID from samples collected in 2021

(Light bars indicate newly added 2021 sequences since May 14, with the number of added genomes indicated at top.)



2021 samples:	BC	AB	QC	NS	MB	ON	NL	NB	India	UK	USA	France
	11	7328	1217	242	369	10 605	199	303	14 671	251 922	382 240	36 585
All samples:	5876	9431	7112	1181	1344	19 626	683	382	23 608	430 477	523 800	42 197

Further messages

If B.1.617.2 remains contained, the Step 1 reopening* on May 25 is expected to lead to only a moderate increase in cases, which will decline as more people are vaccinated.

We should aim for more than 70% vaccination of 18+ (~60% of all ages) in order to allow more reopening safely, especially in light of newly emerging VOC, like B.1.617.2.

Spread of B.1.617.2 is consistent with it growing 5-10% faster *per day* relative to B.1.1.7.

Although data is limited to three weekly variant reports from BC's whole genome sequencing, these data indicate that B.1.617 was increasing in absolute numbers even before the May 25 reopening.

Data gaps identified in [last report](#) remain.

*Including restaurant reopenings, small indoor gatherings, allowance for low impact gym activities.

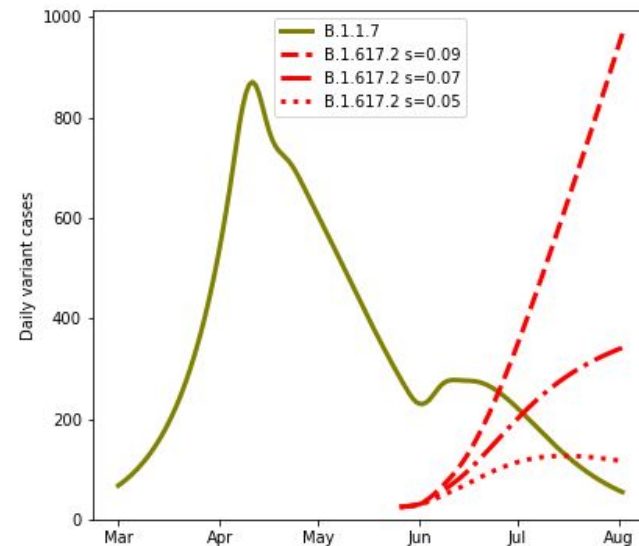
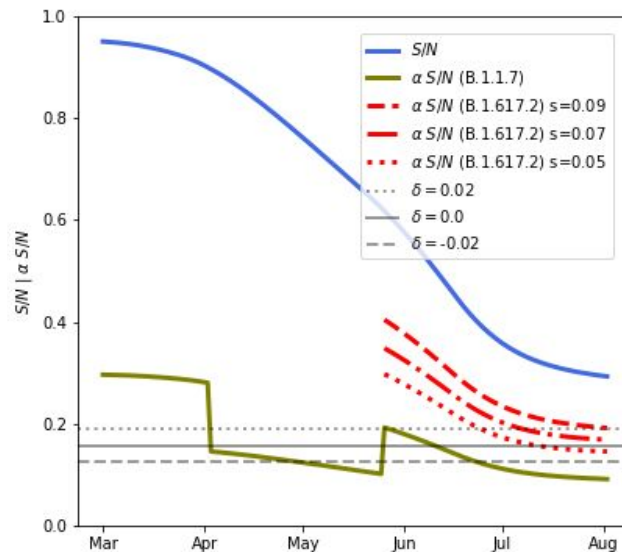
Appendix: Looking under the hood

The decline in the number of susceptible individuals (blue) due to vaccination leads to a reduction in the growth rates of B.1.1.7 (olive) and B.1.617.2 (red) in pypm model (slide 11)

The daily growth rate (δ) depends on the product of the transmission rate (α) and the susceptible fraction (S/N in blue). This product is shown for B.1.1.7 (olive) and B.1.617.2* (red).

The values for the product ($\alpha S/N$) that produce growth rates of $\delta = -0.02$, 0, and 0.02 are shown as grey horizontal lines.

The decline in the susceptible fraction stalls due to the incomplete vaccination of the population.



Appendix: Measuring growth of an epidemic

New cases/day and **New cases/day/100K population** are two common ways to think about epidemics but there are other measures:

- **$R(t)$ [Called the “reproduction number”]** estimates, at time t , how many new infections are generated from one case over the course of their infection. An $R(t) < 1$ implies the epidemic is shrinking; an $R(t) > 1$ implies it is growing. While conceptually useful, it is hard to measure $R(t)$ directly unless all cases can be tracked.
- **r [Called “little r ”]** is the daily growth rate in new cases (comparable to a daily interest rate, compounding over time), which can be more easily measured. The relationship between daily growth (“little r ”) and $R(t)$ depends on the model (e.g., see Figure for one example).
- **s [Called the “selection coefficient”]** is a measure of the daily growth rate advantage of one variant over another. So, if the growth rate for type A is 0.05 and for type B is -0.04, then $s = 0.09$ and the ratio of A to B (A/B) grows at 9% per day.

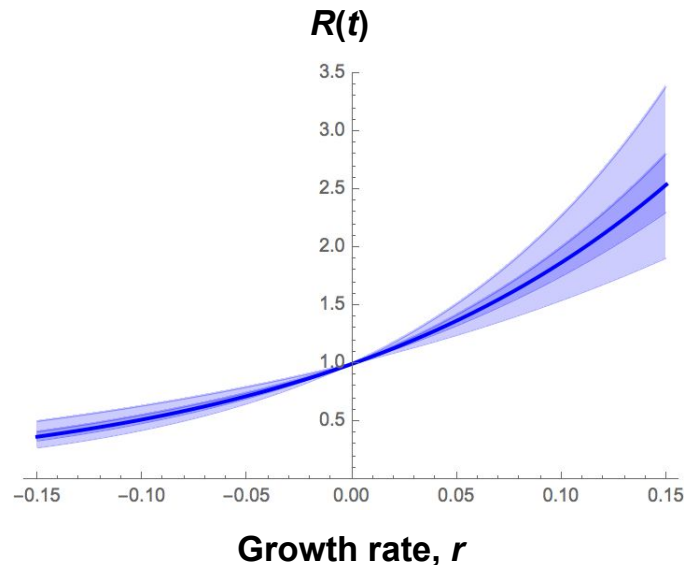


Figure translates between r and $R(t)$ using the renewal equation below, as used by [Volz et al.](#) to estimate $R(t)$ for B.1.1.7. Assumes infections last for an average of 6.4 ± 1 days, with infectivity rising and falling according to a gamma distribution, $g()$, with a coefficient of variation of 0.6. The bands describe 50% and 95% CI given the uncertainty in the length of the infectious period. Assumes no age structure or heterogeneity.

$$1 = R \int_{a=0}^{\infty} \exp(-r a) g(a) da$$

Appendix: SARS-CoV-2 evolution

- As COVID-19 spreads from person to person, the virus SARS-CoV-2 replicates, mutations occur, and the mutated virus can be passed along.
- The virus has an RNA genome with ~30,000 positions. Most mutations have little to no effect on the functioning of the virus, others harm the virus and are rapidly eliminated. Rare mutations, however, can change the virus in a way that is suspected (“variant of interest”) or demonstrated (“variant of concern”) to make the disease worse.
- Because strains can have more than one mutation, strains are given designations that indicate their ancestry, e.g. **B.1.1** and **B.1.1.7** arise from the earlier strain **B.1** (see figure).
- Some mutations change the amino acid structure of proteins. These mutations can be identified by the amino acid that was expected, the amino acid that was observed, and the position, e.g. S:N501Y refers to a mutation in the 501st position of spike (“S”) that changes an “N” amino acid to a “Y”.
- There are **1273** amino acids that make up the SARS-CoV-2 spike protein.
- Mutations in the spike protein are tracked closely because this protein is essential for the virus to get into our cells and is encoded by many vaccines.
- It is thought that many mutations in the virus are needed before vaccines will stop working, but partial vaccine “escape” mutations have been observed and are being closely monitored.

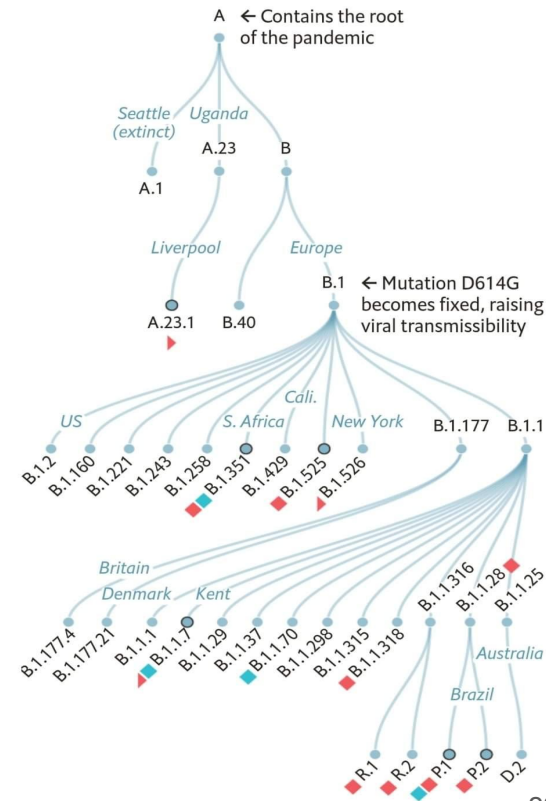


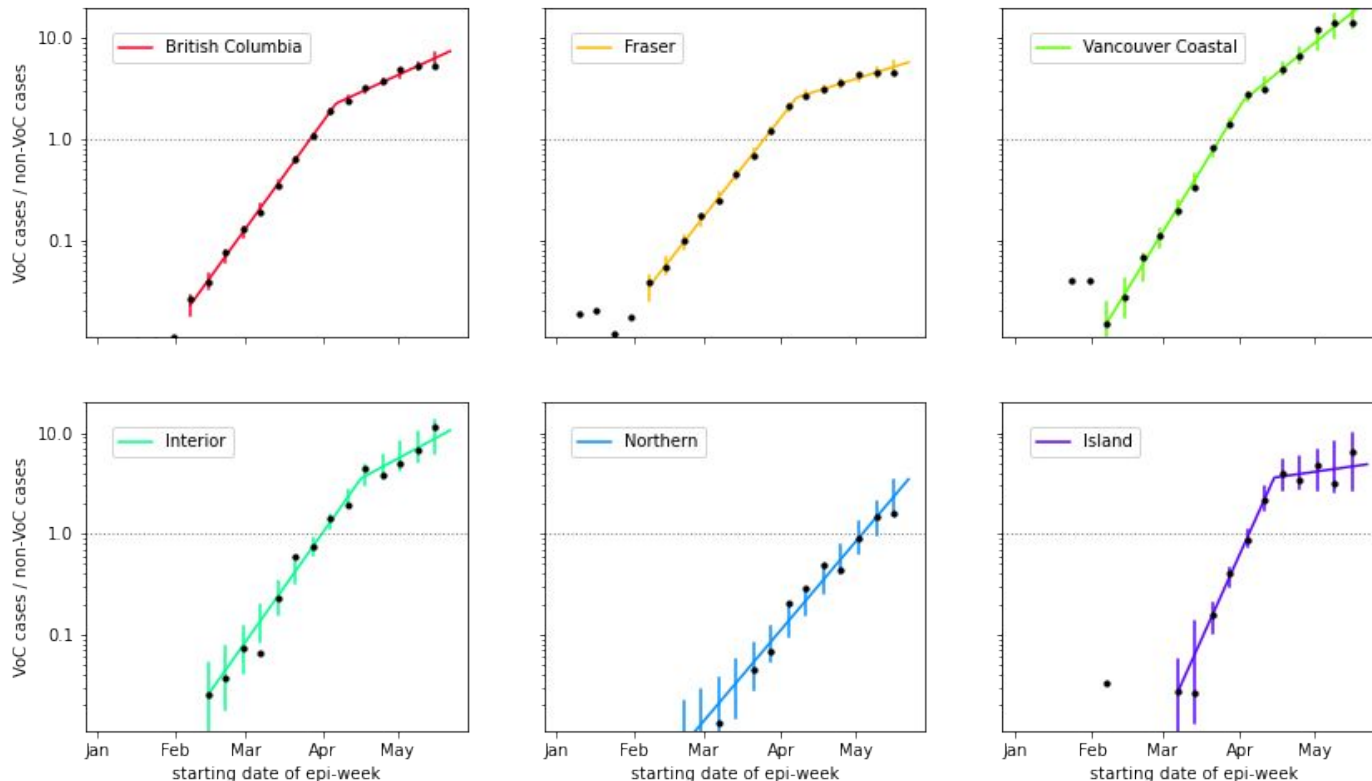
Figure source: [The Economist](#)

Appendix: Growth advantage of B.1.1.7 and P.1 in BC

B.1.1.7 and P.1 initially grew 8%/day faster than original strains (s)

The majority of BC's virus population now consists of these two VOC (>50% above horizontal line)

With “circuit breaker”, advantage reduced to 4%/day faster than original strains: measures had greater effect on B.1.1.7 and P.1 than on the original strains



Source (D. Karlen). Fit to weekly VoC and non-VoC case data from [bccdc](https://www.bccdc.ca). Except for Northern HA, a change to the daily growth advantage (selection coefficient, s) is apparent in early April, and fit estimates the change to occur near April 10. There are insufficient data in Northern and Island regions to accurately estimate the change.