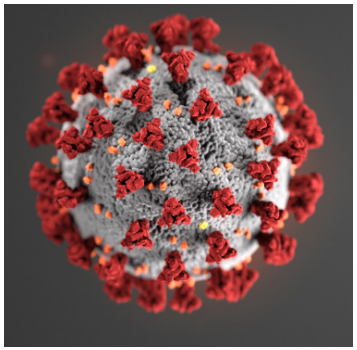
New Emergency Management in a Resilience Era Facing Health, Climate and Energy Challenges

6th to 10th December 2021

Modeling the Delta and Omicron Variants of COVID-19

Dr. George Markowsky

Missouri University of Science & Technology



Modeling the Delta and Omicron Variants of COVID-19

Prof. George Markowsky

Department of Computer Science

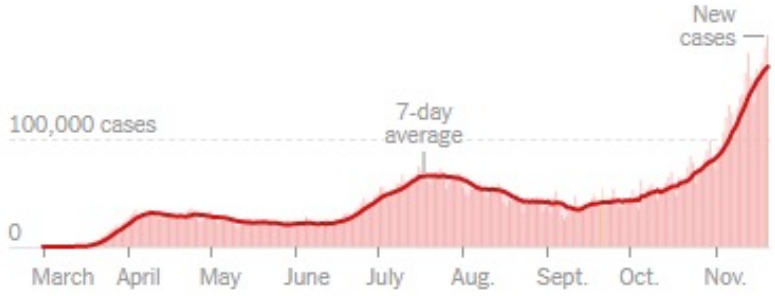
Missouri University of Science & Technology

Introduction

- At last year's TIEMS Annual Conference I presented a talk entitled *Modeling and Battling COVID-19*
- We have learned a lot about COVID-19 since that talk, but many of the concepts presented in that talk are the foundation for the analysis that we present in this talk
- Before we review the concepts from the previous talk, I want to take a high-level view of where we are right now compared to where we were back in November 2020

By The New York Times Updated November 21, 2020, 12:17 A.M. E.T.

Leer en español



	TOTAL REPORTED	ON NOV. 20	14-DAY CHANGE
Cases	12 million+	198,537	+67% ↗
Deaths	254,320	1,947	+63% ↗
Hospitalized		82,178	+50% ↗

Day with data reporting anomaly.

Hospitalization data from the Covid Tracking Project; 14-day change trends use 7-day averages.

We still have a difficult battle ahead of us to control this pandemic!

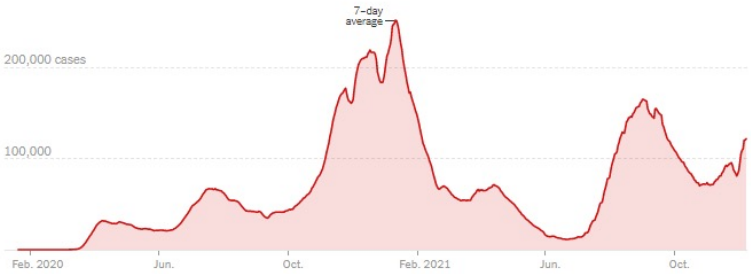
Coronavirus in the U.S.: Latest Map and Case Count

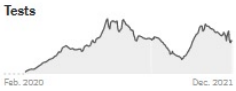
Updated Dec. 9, 2021

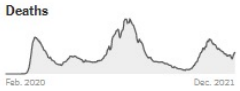
Get the latest updates on the Omicron variant.

New reported cases

All time | Last 90 days







	DAILY AVG. ON DEC. 8	14-DAY CHANGE	TOTAL REPORTED
Cases	121,311	+27%	49,505,304
Tests	1,152,160	Flat	—
Hospitalized	61,936	+20%	—
Deaths	1,275	+12%	791,933

Vaccinations

	AT LEAST ONE DOSE	FULLY VACCINATED
All ages	71%	60%
12 and up	82%	70%
65 and up	>99%	87%

See more details ›

About this data

State of the virus

Update for Dec. 9

- More than 120,000 coronavirus cases are emerging each day as conditions continue to worsen, especially in the Great Lakes region and in the Northeast.
- Cases, deaths and hospitalizations are rising nationally, but remain below the levels seen during the summer and during last winter's peak.
- New Hampshire leads the country in recent cases per capita. More coronavirus patients are hospitalized in that state than at any other point in the pandemic.

	Nov 21, 2020 US	Dec 9, 2021 US	Dec 8, 2021 World
Cases	12 million	50 million	267 million
Hospitalized	82,178	61,936	???
Deaths	254,320	791,933	5.27 million
Fatalities	2.12%	1.58%	1.97%

How much progress have we made?
How can we do better?
What are the obstacles?

We still have a difficult battle ahead of us to control this pandemic!

These numbers are all Delta numbers

Changes Since 2020

- A lot has changed since that talk that was given in November 2020

1. We now have vaccines
2. We now have breakthrough and repeat infections!
3. We now have new variants of COVID-19

- These are 3 things that we did not have to deal with in our simple 2020 model
- We will consider how each of these 3 factors affects our model and describe some of the changes that need to be made
- The time constraints of this talk will not let us get into the equations so we will primarily give a qualitative treatment
- A quantitative treatment will be presented in a future, longer paper
- Let's review some of the key ideas of our simple model

Compartmental Models

- In a compartmental model, we partition the members of our group into compartments and establish rules on how individuals move from one compartment to another
- We assume that the behavior of all individuals in a given compartment is the same
- Usually, the more compartments we establish, the more accurate the model
- We want to create a short-term model, so we will ignore events such as births and immigration

The SIR Model

- The SIR model is one of the simplest of the compartmental models and gets its name from the three compartments (S, I, R) that it divides the entire population into
- The model was first proposed by William Kermack and Anderson McKendrick in a series of 3 papers written between 1927 and 1933
- The SIR model forms the basis for many of the models in use today
- It assumes that population does not change during the modeling period and that there are three compartments of people – Susceptible, Infectious, and Recovered

The S, I, and R Compartments

- You might think that you understand the nature of the S, I, and R compartments from their names and you would be mostly correct, but there are subtleties associated with these definitions
- One thing that might strike you as strange is that there do not seem to be any dead people in this model
- Actually, the dead people are in the Recovered compartment
- The term recovered is a bit misleading, since what we are really talking about is people who can no longer infect other people
- It might have been better to call this compartment U for uninfectious

Infectious People

- Note also, that we refer to the compartment I as consisting of **infectious** people and not infected people
- For the sake of the model, we care primarily whether a person can infect other people and not whether they are infected or not
- For example, suppose a disease typically takes a person 15 days to recover from, but the person only produces particles that can infect other people on the first day of the disease, then we would put the person into the Recovered group after 1 day and not after 15 days
- Similarly, if a person is infectious for 15 days, but after day 5 the person goes into quarantine and can no longer infect other people they would go into the Recovered compartment as soon as they are quarantined even though they might still be sick
- Also, a person might get sick and end up with kidney failure but stop being infectious
- In this case, we classify that person as recovered but not everyone would apply the term “recovered” to this person

Recovered People

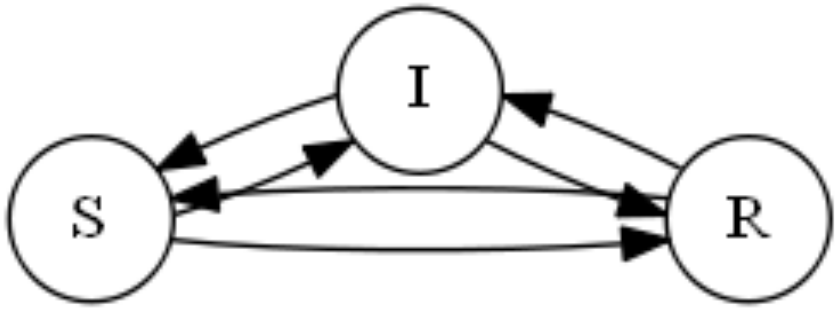
- The language is a bit tricky here
- Usually, when we say that someone recovered from the flu we mean that they are no longer sick and are back to “normal”
- If someone died from the flu, we would not normally say that “they recovered from the flu”
- The important thing to understand here is that recovered means that the people in question can no longer infect other people
- Another tricky instance is if a person had genetic immunity to the disease that person should be considered recovered even though that person was never infected
- Also, if an infectious person is quarantined so that they can no longer infect anyone, we would move them to the Recovered compartment even though they are still sick and could potentially infect people
- Because dead people are placed in the Recovered compartment, we can say that the population does not change during the modeling

Susceptible People

- A susceptible person is a person who is not infected, but who could become infectious by exposure to infectious people

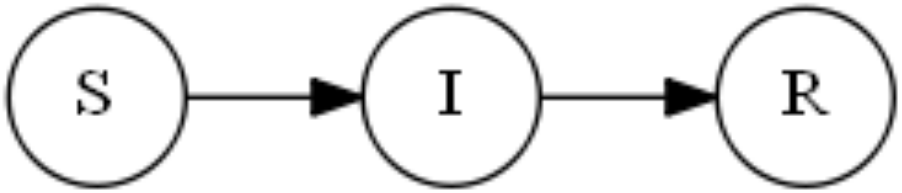
Relationships Between Compartments

- In modeling an epidemic, we want to understand how people move from one compartment to another
- In general, we can envisage a diagram such as the one to the right in which there are circumstances under which people can move directly from one compartment to any other compartment
- In the simple 2020 model we restricted the movement of people as shown on the next slide



Simplifying the Diagram

- At this time, it is still not completely known exactly what type of immunity "recovered" COVID-19 victims maintain
- This is not an idle question since we know there is enough mutation among other Corona viruses (e.g., the common cold) so that people can get reinfected, even in the same cold season
- Needless to say, the more arrows we have in the model linking the compartments the more complex the model
- To simplify our discuss, we will assume that we have the diagram to the right which we will call the S→I→ R diagram



The S→I→R Diagram

The Fundamental Equations

- We discussed how to make the equations not dependent on the actual population, but described numbers as a percentage of the population
- This permitted us to write equations that applied to all populations

1. $\frac{ds(t)}{dt} = -bci(t)s(t)$
2. $\frac{di(t)}{dt} = bci(t)s(t) - ai(t)$
3. $\frac{dr(t)}{dt} = ai(t)$

- Where s(t), i(t), and r(t) are the percentages of the population that are susceptible, infectious, and recovered (respectively)
- The constants a, b, and c are the rate at which people recover, the probability of being infected by a contact, and the number of contacts per day

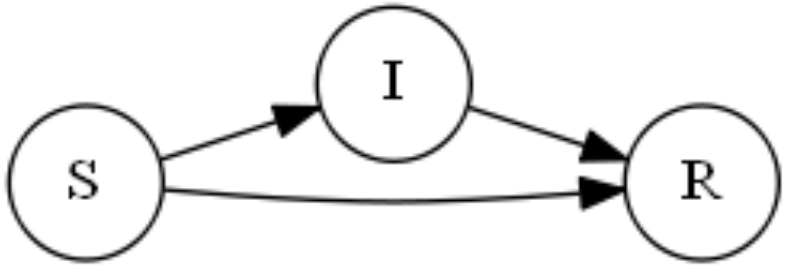
Modeling Vaccinations

- Your model changes depending on how vaccinations affect infections
- We will consider some assumptions that need to be discussed when discussion vaccinations

1. Assume that vaccinated people are never infectious (this does not mean that they are never sick)
2. Assume that vaccinated people become infectious at a lower rate than non-vaccinated people
3. Assume that vaccinated people recover faster than non-vaccinated people

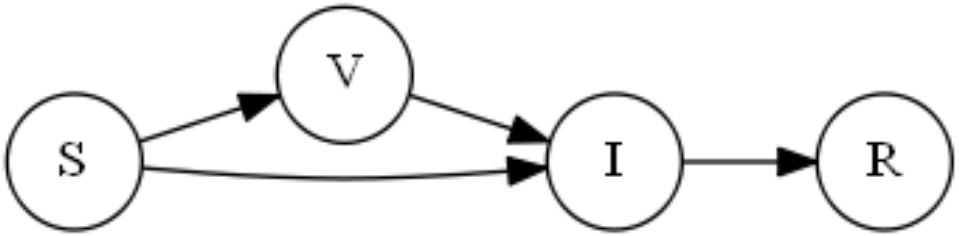
If Vaccinated People are Never Infectious

- If vaccinated people are never infectious, they go directly from the S compartment to the R compartment
- They might very well get sick, but they are never infectious
- This requires a direct link from S to R with appropriate terms added to the equations shown before
- There are additional constants involved which reflect the rate at which susceptible people are vaccinated



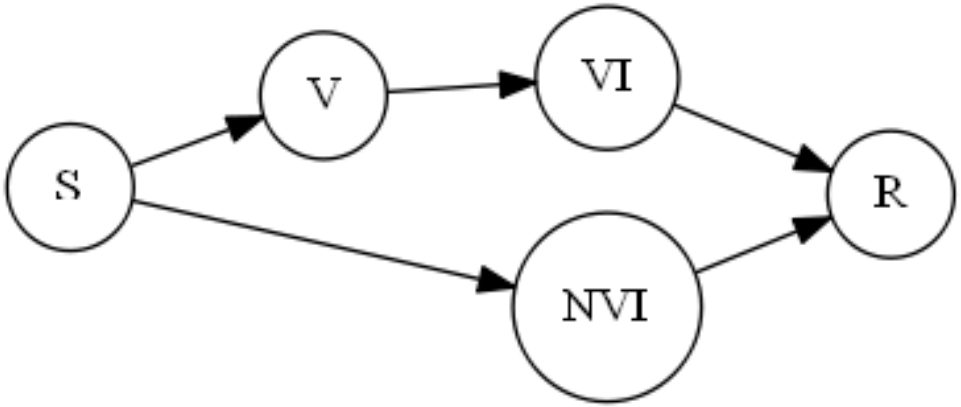
If Vaccinated People Become Infectious at a Lower Rate

- If vaccinated people become infectious at a lower rate than unvaccinated people, we need to introduce a new compartment V which holds the vaccinated people
- We need to add new equations to reflect how people move from S to V and from both S and V to I



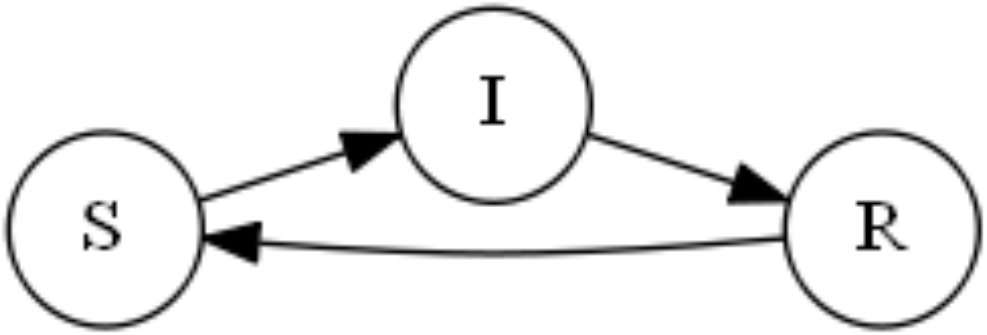
If Vaccinated People Recover Faster

- If vaccinated people can become infectious but recover at a faster rate than unvaccinated people, we need to replace the I compartment by two compartments VI (vaccinated infectious) and NVI (nonvaccinated infectious)
- We need to add new equations to reflect how people move between compartments



How to Model Breakthrough or Repeat Infections

- Breakthrough or repeat infections can be modeled in a variety of ways depending on the assumptions you make
- The simplest assumption is shown in the diagram to the right, and it deals with just people returning to the pool of susceptible people at a particular rate
- If you want to model having previously vaccinated people being reinfected at a different rate from unvaccinated people who were infected, you would have to add compartments similar to the ones that we just discussed
- We will not discuss further variations in this talk because of time constraints

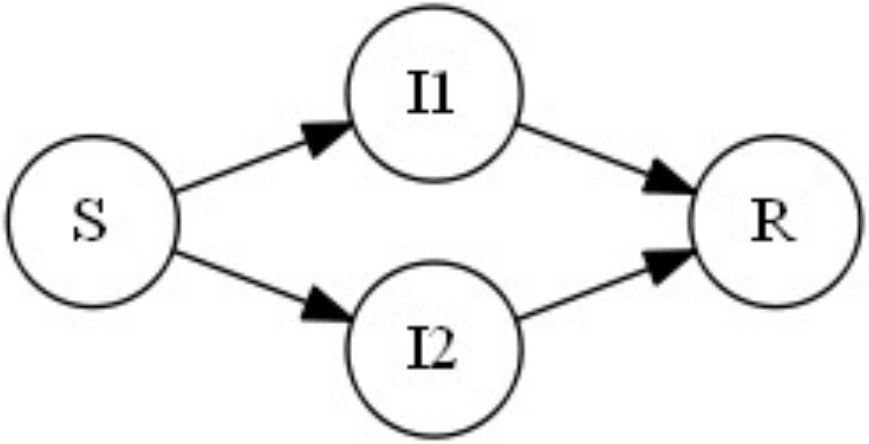


Modeling Variants

- Over the past two years, there have been several variants of COVID-19 with different characteristics
- Typically, one variant is replaced by another if the newer variant is more infectious than the current variant
- Originally, this talk was entitled "Modeling the Delta variant of COVID-19", but even as we speak it appears that the Omicron variant is on its way to replace the Delta variant around the world, which is why we changed the title of this presentation
- The jury is still out about whether Omicron is more deadly than Delta, but the evidence seems clear that it is significantly more contagious and readily infects many vaccinated people, especially if some time has elapsed since people have been immunized

Modeling Variants

- To understand the modeling of variants we need to consider a graph at least as complicated as the one shown to the right
- I1 is the compartment of infectious people infected with variant 1 and I2 is the compartment of infectious people infected with variant 2



Modeling Variants

- The previous diagram is oversimplified because it assumes that there are only two variants active
- There could be more than two variants active at one time which would lead to a more complicated diagram
- There are even possibilities that people who were infected and recovered from one variant might be immune to one variant but not to another
- Variants might also react differently to vaccines so our models can get much more complicated
- There is a website that deserves mention that displays a tremendous amount of information about the variants of COVID-19 – https://covariants.org/
- We will conclude this talk by revieing this website, which also includes the programs used to make the graphs – https://github.com/hodcroftlab/covariants
- Many thanks to Emma Hodcroft for making the programs available

CoVariants

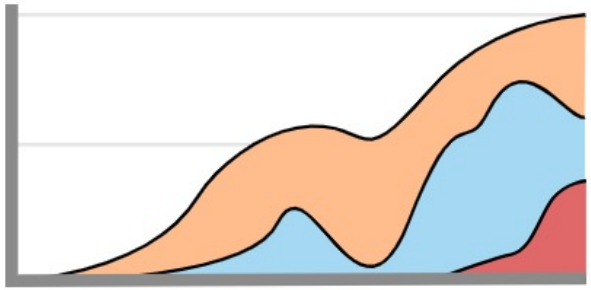
Variant

- 20I (Alpha, V1)
- 20H (Beta, V2)
- 20J (Gamma, V3)
- 21A (Delta)
- 21I (Delta)
- 21J (Delta)
- 21K (Omicron)
- 21G (Lambda)

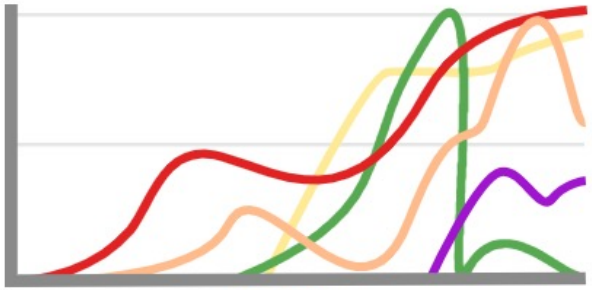
Click on a variant button to start exploring!

CoVariants provides an overview of SARS-CoV-2 variants and mutations that are of interest. Here, you can find out what mutations define a variant, what impact they might have (with links to papers and resources), where variants are found, and see the variants in Nextstrain builds!

Click one of the colored buttons to look at a particular Variant - to read information, see graphs and the protein structure, and link out to focused Nextstrain builds. To look at many variants at once, check out the Per Variant and Per Country pages, where you can view a lot of data in the same place, and compare variants and countries!



Per Country

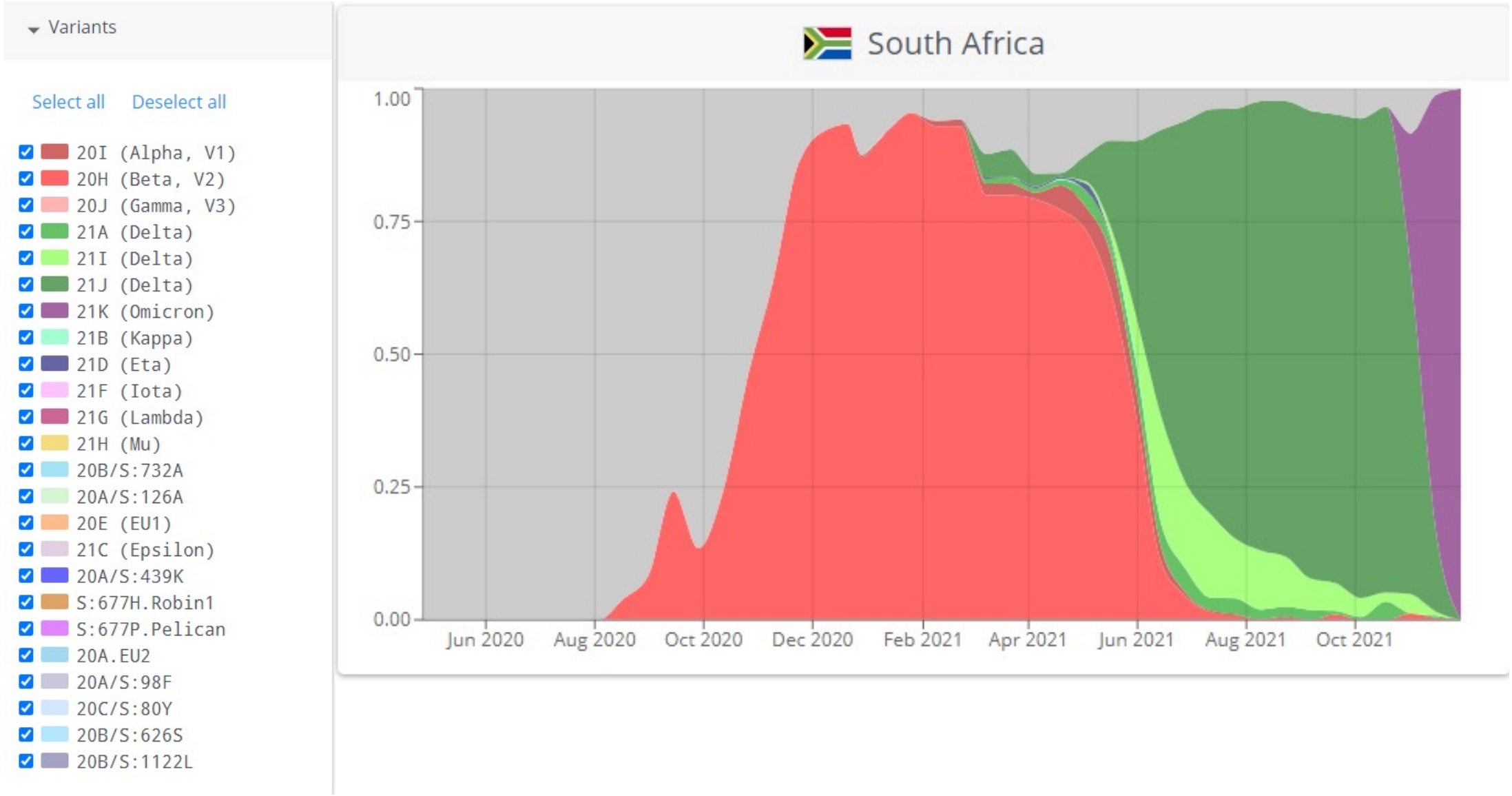


Per Variant

What do the names mean?

CoVariants uses the Nextstrain naming system for variants (read more here). However, the fact that there's multiple naming systems is confusing! See the table below to help find the variant you're interested in.

Nextstrain Clade	Pango Lineage	WHO Label	Other
20I (Alpha, V1)	B.1.1.7	α Alpha	VOC 202012/01
20H (Beta, V2)	B.1.351	β Beta	501Y.V2
20J (Gamma, V3)	P.1	γ Gamma	
21A (Delta)	B.1.617.2	δ Delta	
21I (Delta)		δ Delta	
21J (Delta)		δ Delta	
21B (Kappa)	B.1.617.1	κ Kappa	
21C (Epsilon)	B.1.427, B.1.429	ε Epsilon	CAL.20C
21D (Eta)	B.1.525	η Eta	
21F (Iota)	B.1.526	ι Iota	(Part of Pango lineage)
21G (Lambda)	C.37	λ Lambda	
21H (Mu)	B.1.621	μ Mu	
21K (Omicron)	B.1.1.529	ο Omicron	
20E (EU1)	B.1.177		EU1
20B/S:732A	B.1.1.519		
20A/S:126A	B.1.620		
20A.EU2	B.1.160		
20A/S:439K	B.1.258		
20A/S:98F	B.1.221		
20C/S:80Y	B.1.367		
20B/S:626S	B.1.1.277		
20B/S:1122L	B.1.1.302		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Variants

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- 20E (EU1)
- 21C (Epsilon)
- 20A/S:439K
- S:677H.Robin1
- S:677P.Pelican
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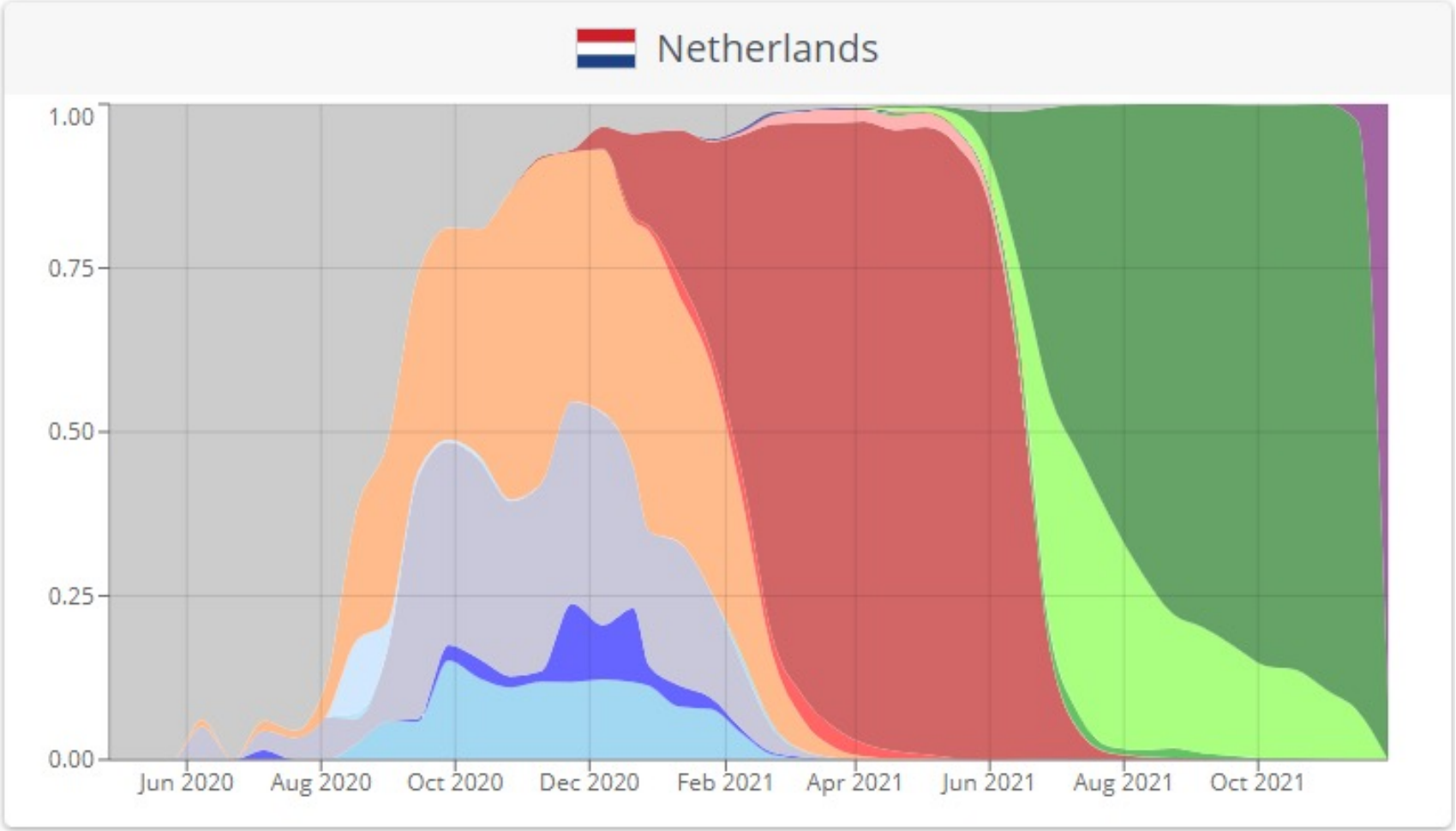

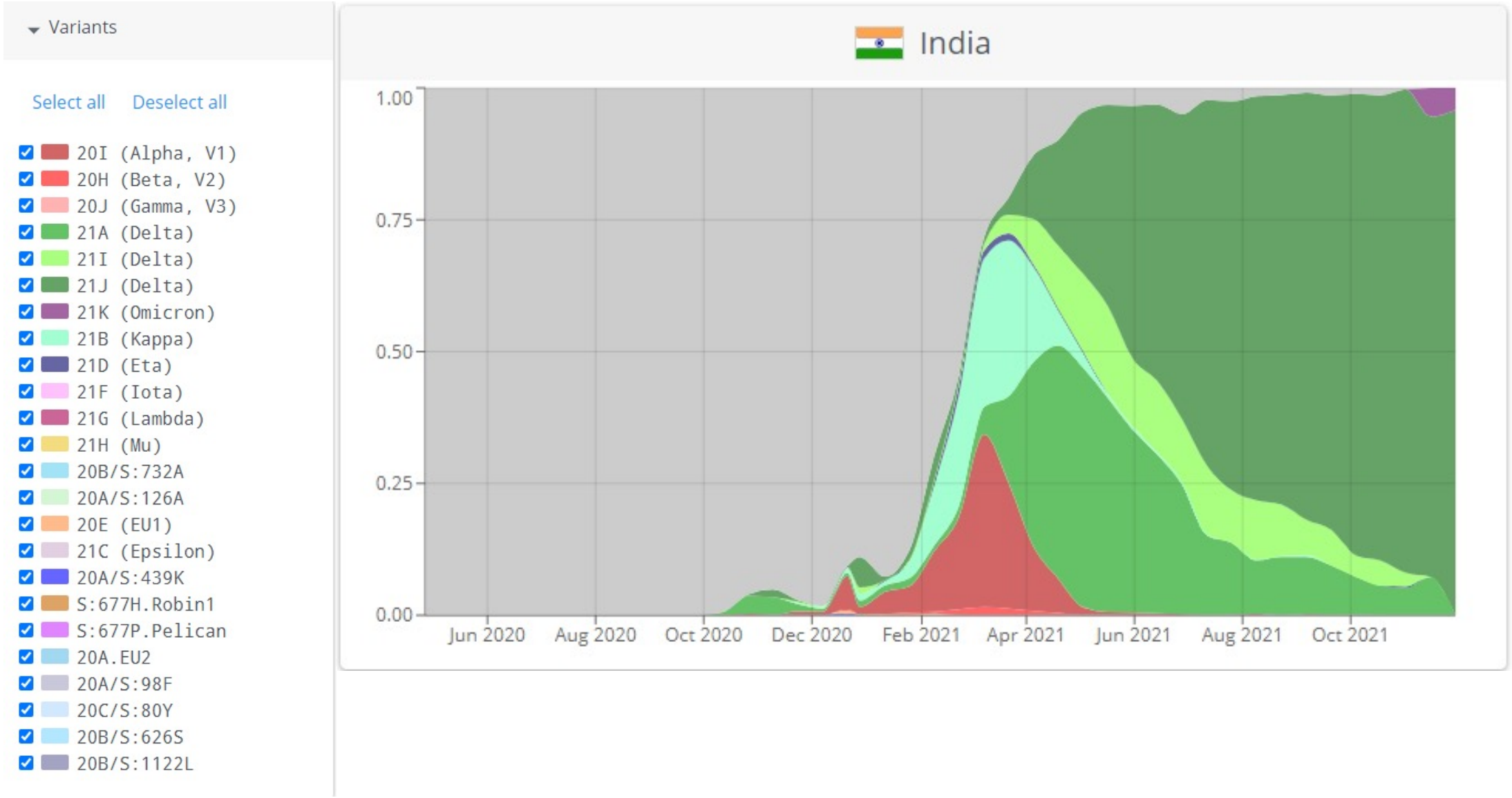
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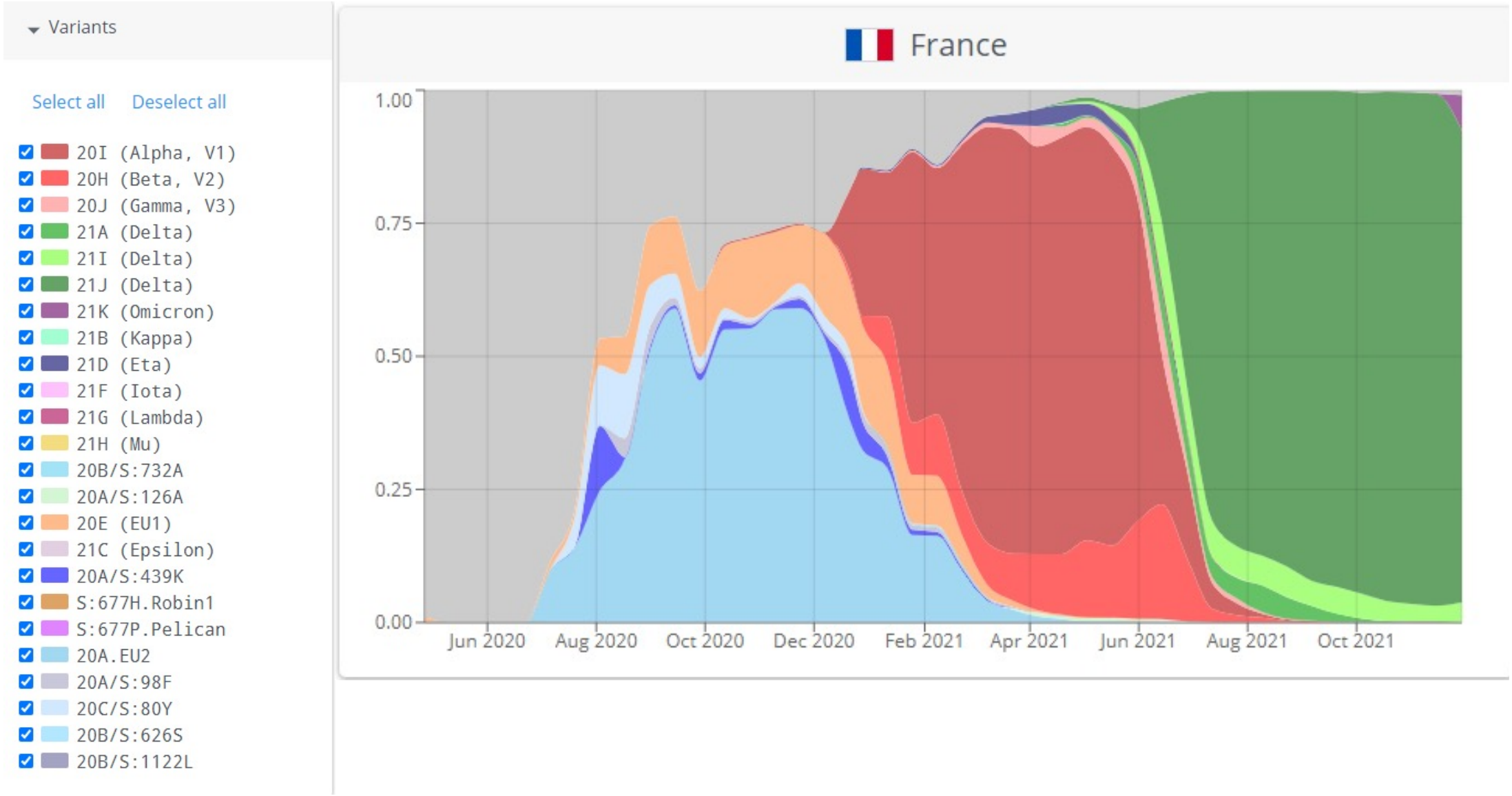
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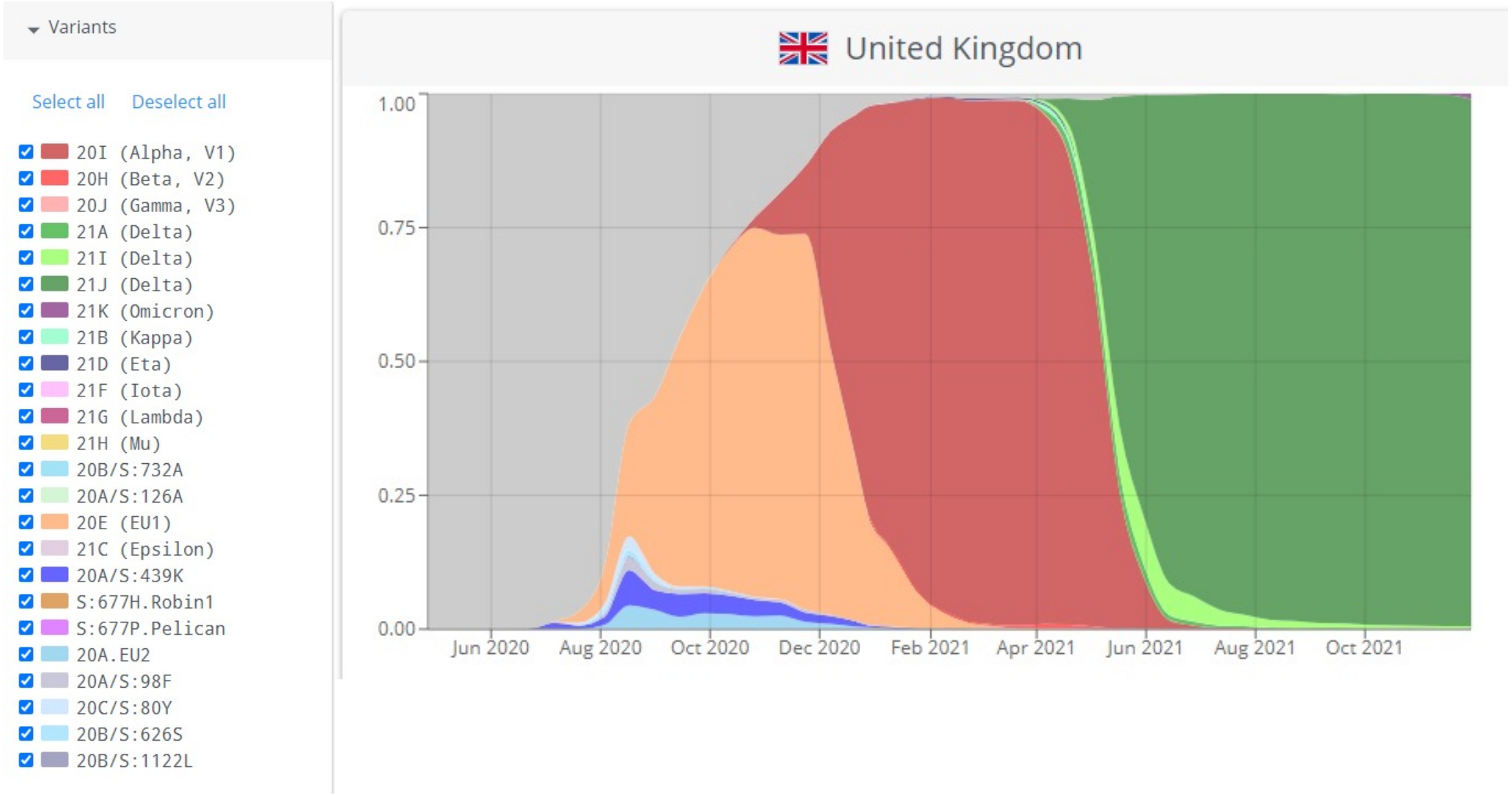
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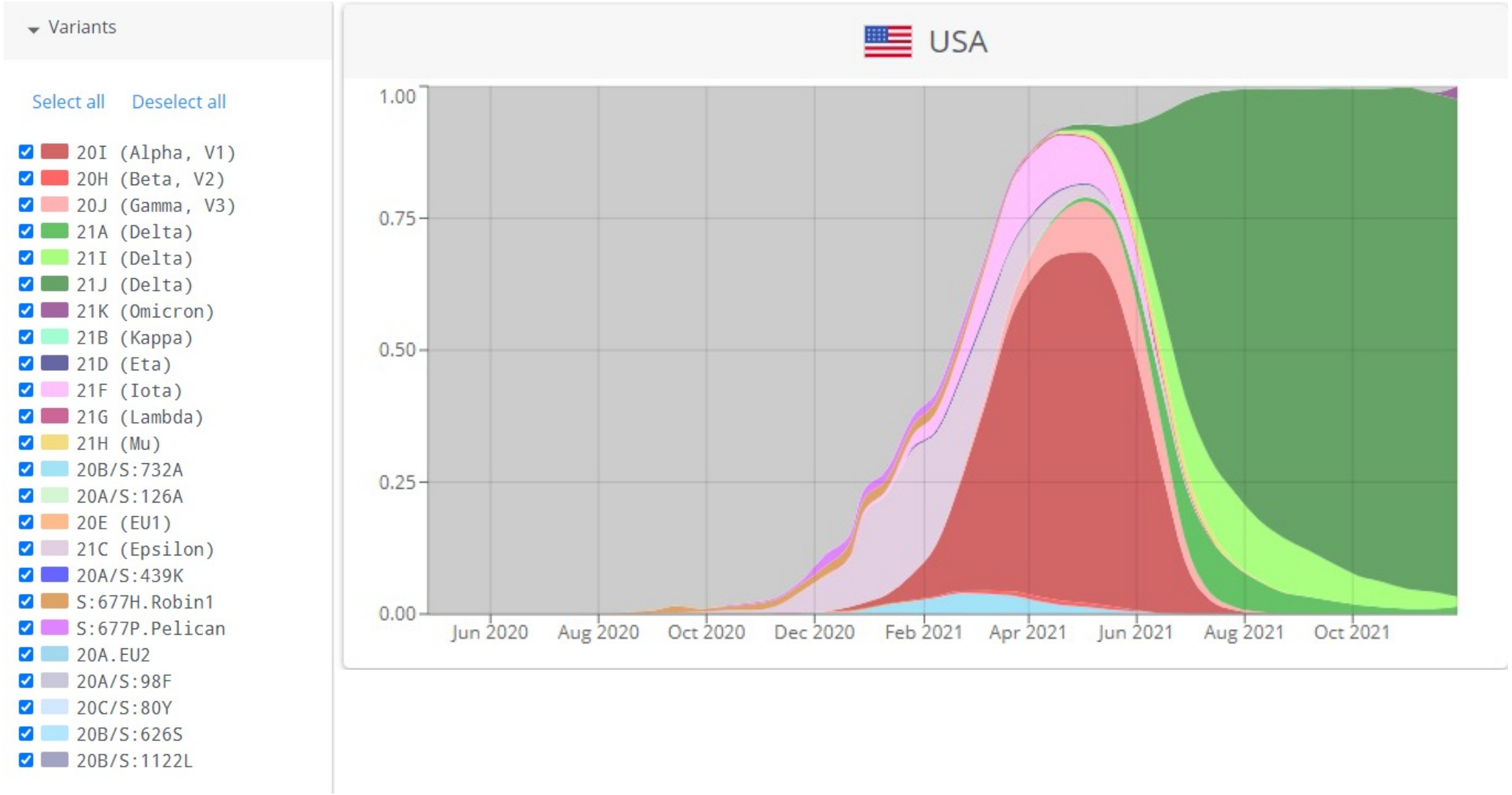
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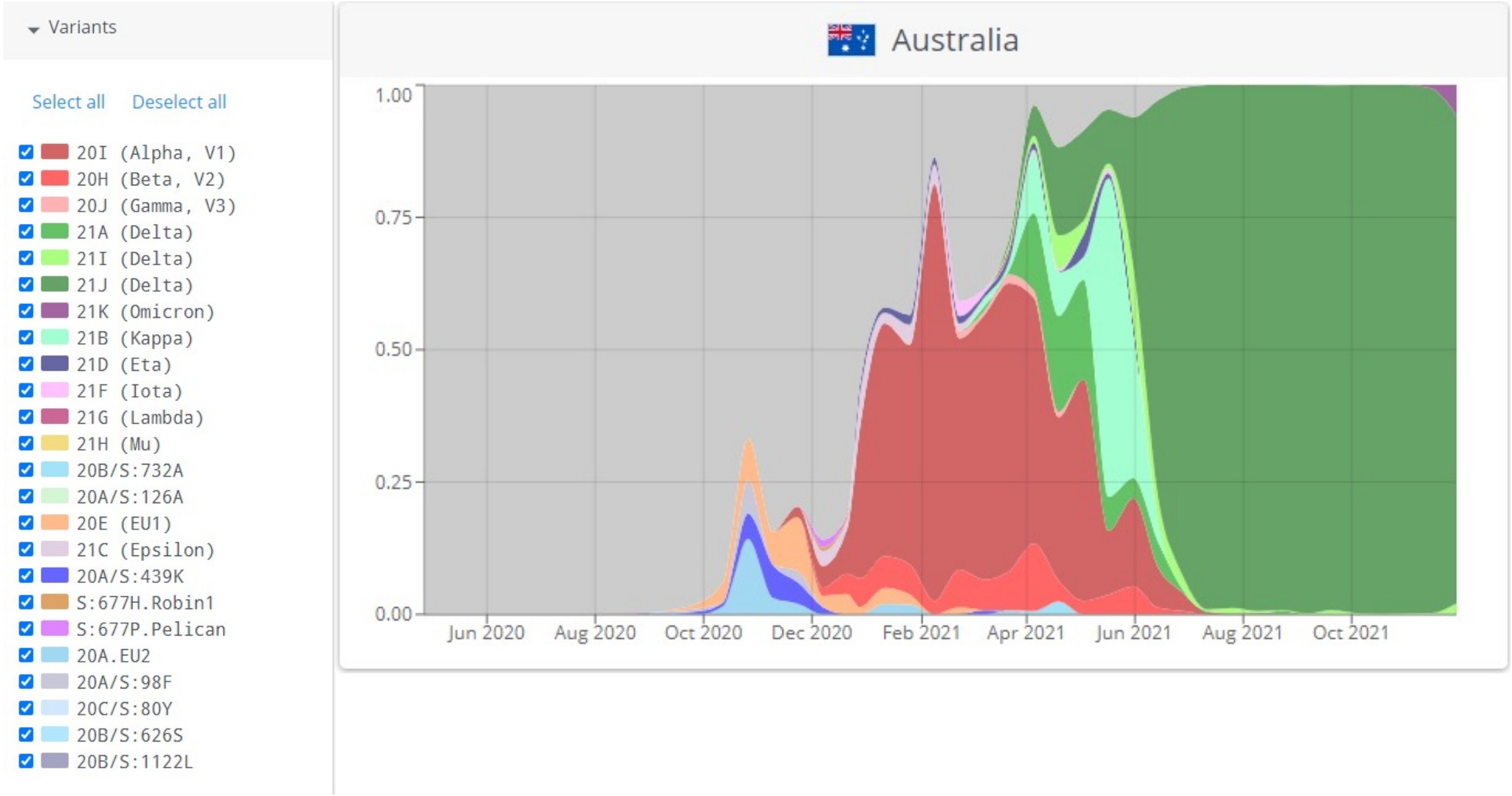
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Deselect all
20I (Alpha, V1)
20H (Beta, V2)
20J (Gamma, V3)
21A (Delta)
21I (Delta)
21J (Delta)
21K (Omicron)
21B (Kappa)
21D (Eta)
21F (Iota)
21G (Lambda)
21H (Mu)
20B/S:732A
20A/S:126A
20E (EU1)
21C (Epsilon)
20A/S:439K
S:677H.Robin1
S:677P.Pelican
20A.EU2
20A/S:98F
20C/S:80Y
20B/S:626S
20B/S:1122L
Australia
1.00
0.75
0.50
0.25
0.00
Jun 2020
Aug 2020
Oct 2020
Dec 2020
Feb 2021
Apr 2021
Jun 2021
Aug 2021
Oct 2021

Some Conclusions

- Omicron seems much more contagious than Delta
- It takes over rapidly from Delta
- It seems to be less affected by vaccines than Delta
- Its lethality compared to Delta is not yet known although people are working to answer that question
- It seems likely that within a month or two Omicron will dominate the world
- We could be in for a very difficult time if Omicron proves to be at least as lethal as Delta
- I urge everyone not to relax their precautions until we know more about Omicron