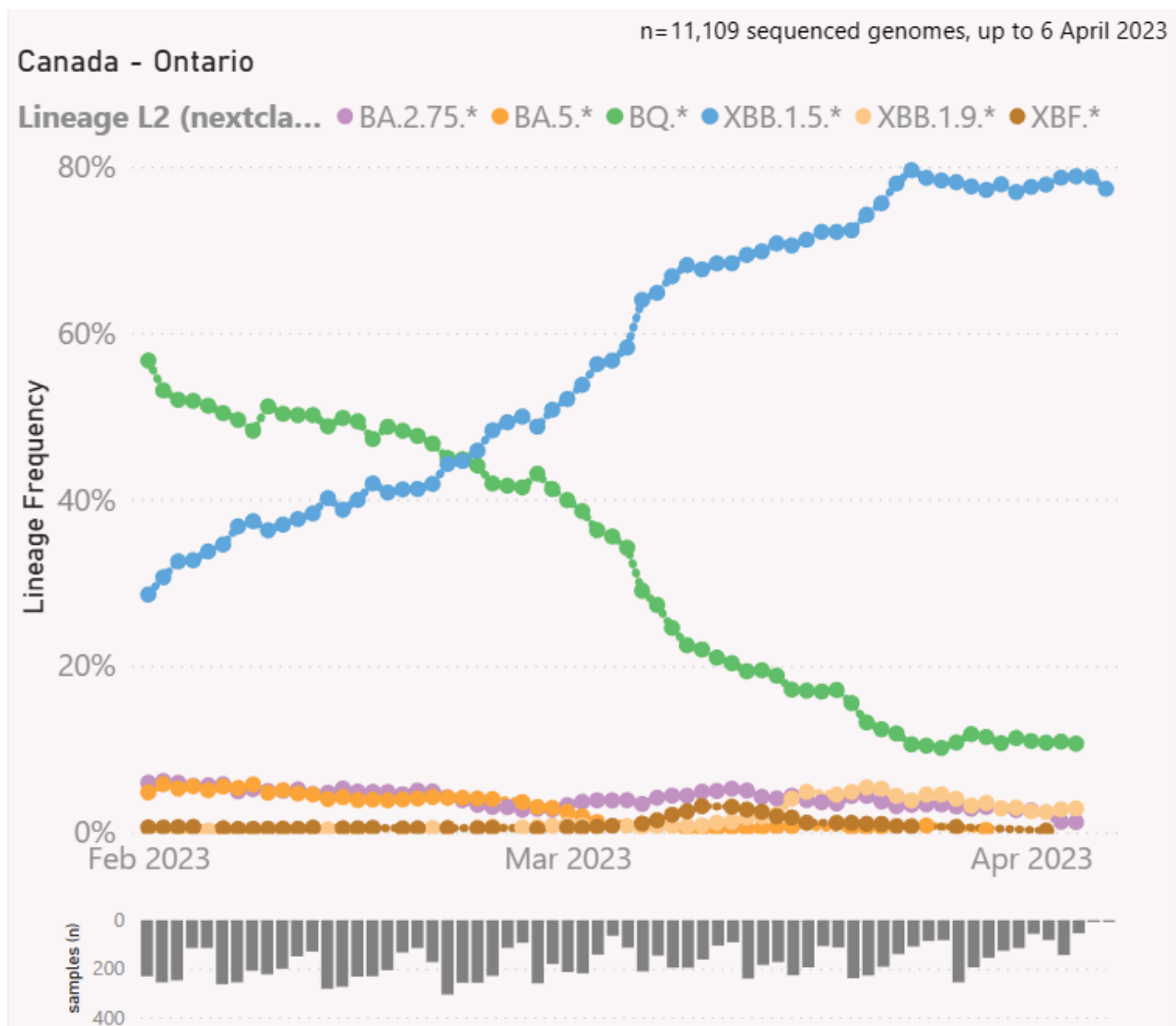


## More from @jeffgilchrist

[pingthread.com/thread/1647232148397498368](https://pingthread.com/thread/1647232148397498368)

How To: See what variants are circulating in your country/province/State

This thread will walk you through how to see which variants are circulating in your area using @Mike\_Honey\_'s visualization tool. 🧵 1/

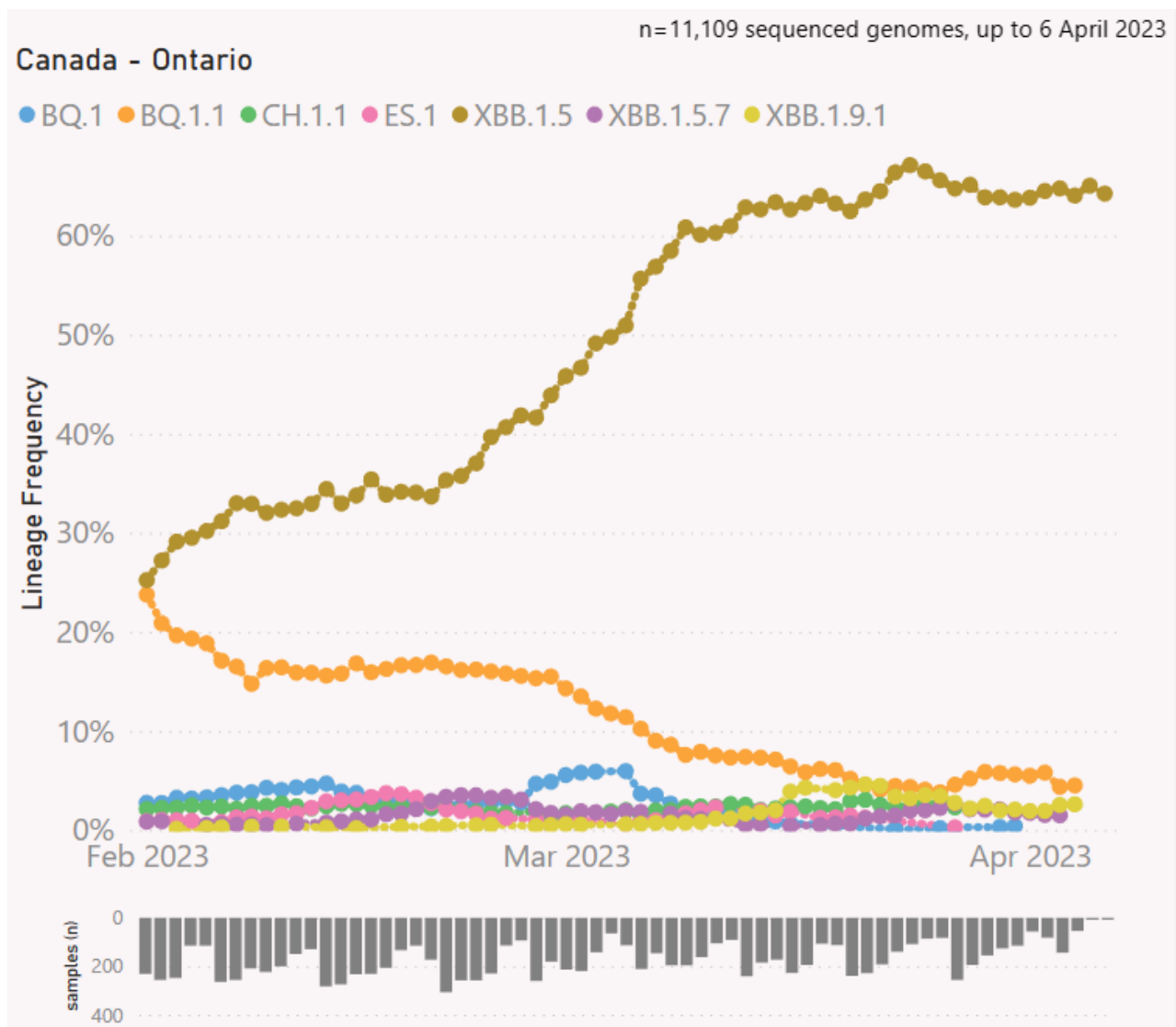


An unrolled one-page web view for this long thread that may be easier to read or share can be found here ( ). 2/

The link for the unrolled one-page version of the "How To: See what variants are circulating in your country/province/State" thread can be found in the next tweet once it is posted. 🙌

— Jeff Gilchrist (@jeffgilchrist) [April 15, 2023](#)

Step 1: Go to Mike's variant visualization tool: [app.powerbi.com/view?r=eyJrIjojN...](https://app.powerbi.com/view?r=eyJrIjojN...) 3/

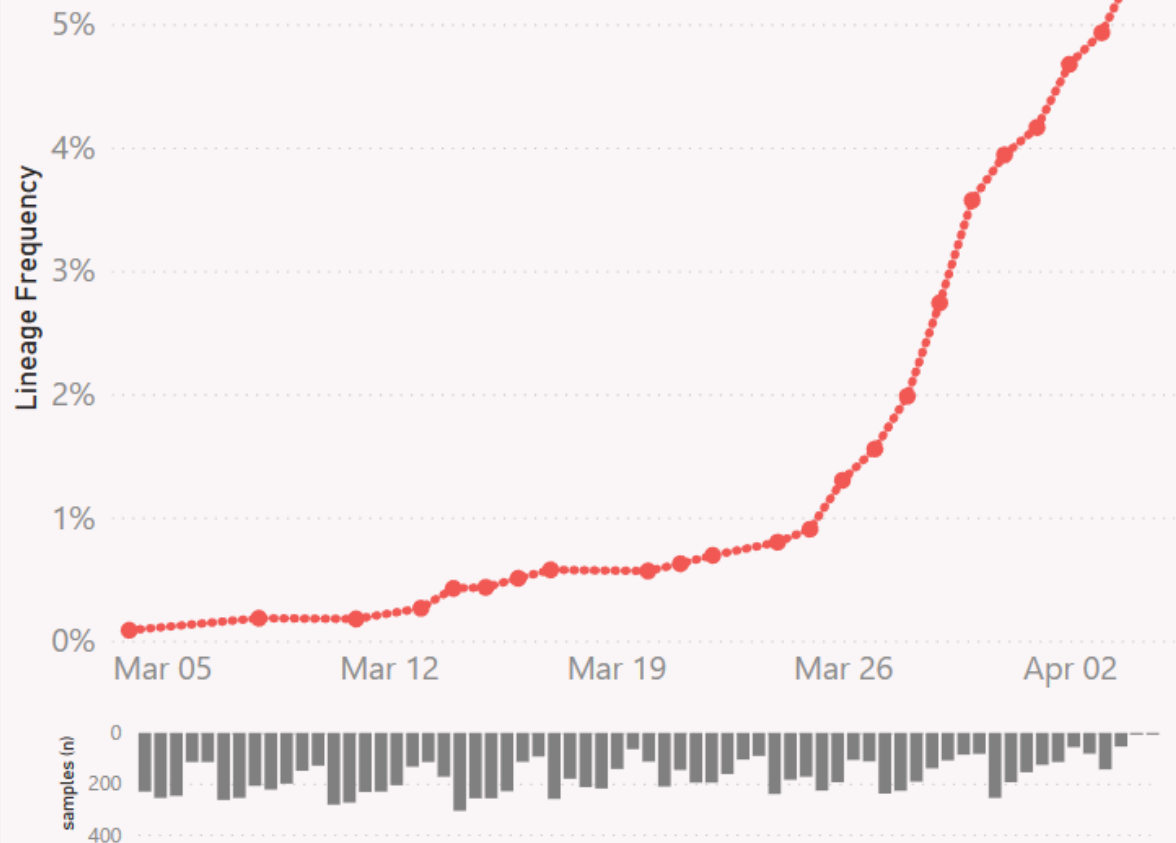


You should see something like this show up. By default, Australia is chosen which you can see in the red circled area in the top left. The last time the database was updated is shown in the red circled area in the top right (2023-04-14). 4/

## Canada - Ontario

n=11,109 sequenced genomes, up to 6 April 2023

● XBB.1.16

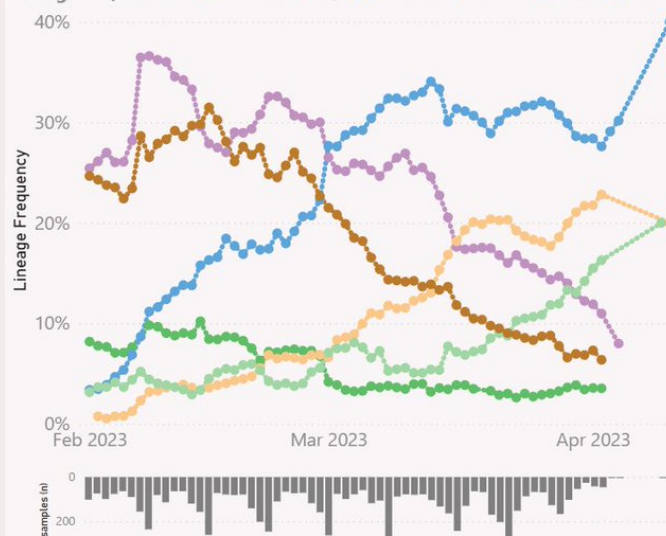


Last Update: 2023-04-14 11:46 (UTC)

## Australia

n=7,167 sequenced genomes, up to 10 April 2023

Lineage L2 (nextclade) ● BA.2.75.\* ● BQ.\* ● XBB.1.5.\* ● XBB.1.9.\* ● XBC.\* ● XBF.\*



Date

2/1/2023

4/30/2023

Host

Human

Continent, Country, Location

Oceania (Continent) + Australia (Country)

Lineage L2, Lineage (nextclade)

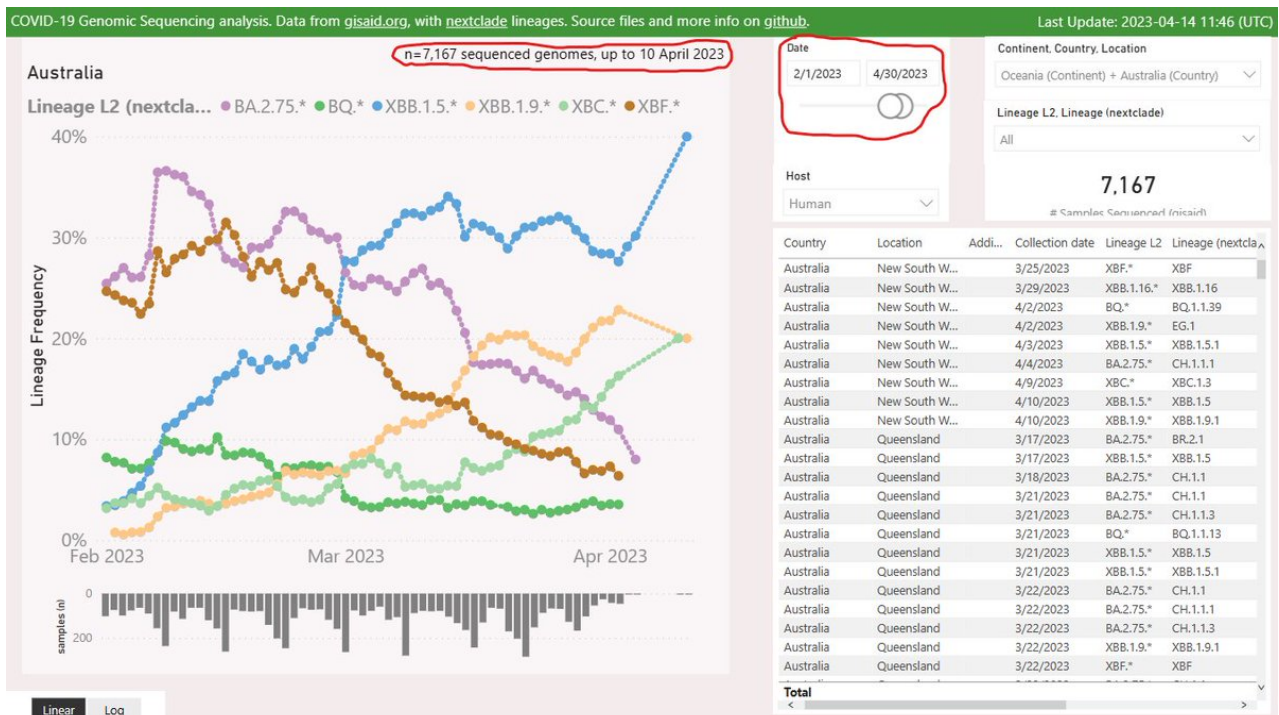
All

7,167

# Samples (n) (

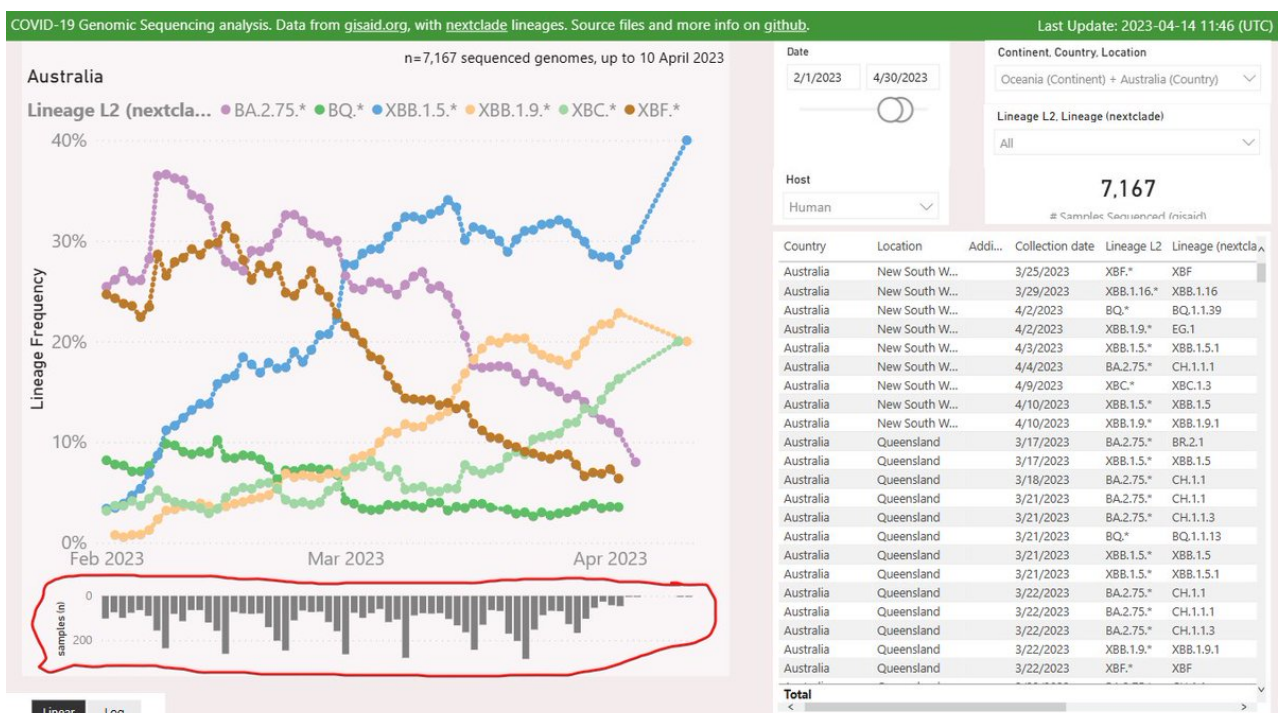
The red circled section in the middle shows how many sequences were found from the start date up to the latest dated sequence, in this case 7,167 sequences up to 10 April 2023.

5/



Just to the right of that is the display date range which shows the from date on the left (2/1/2023) and the to date (4/30/2023) on the right. 6/

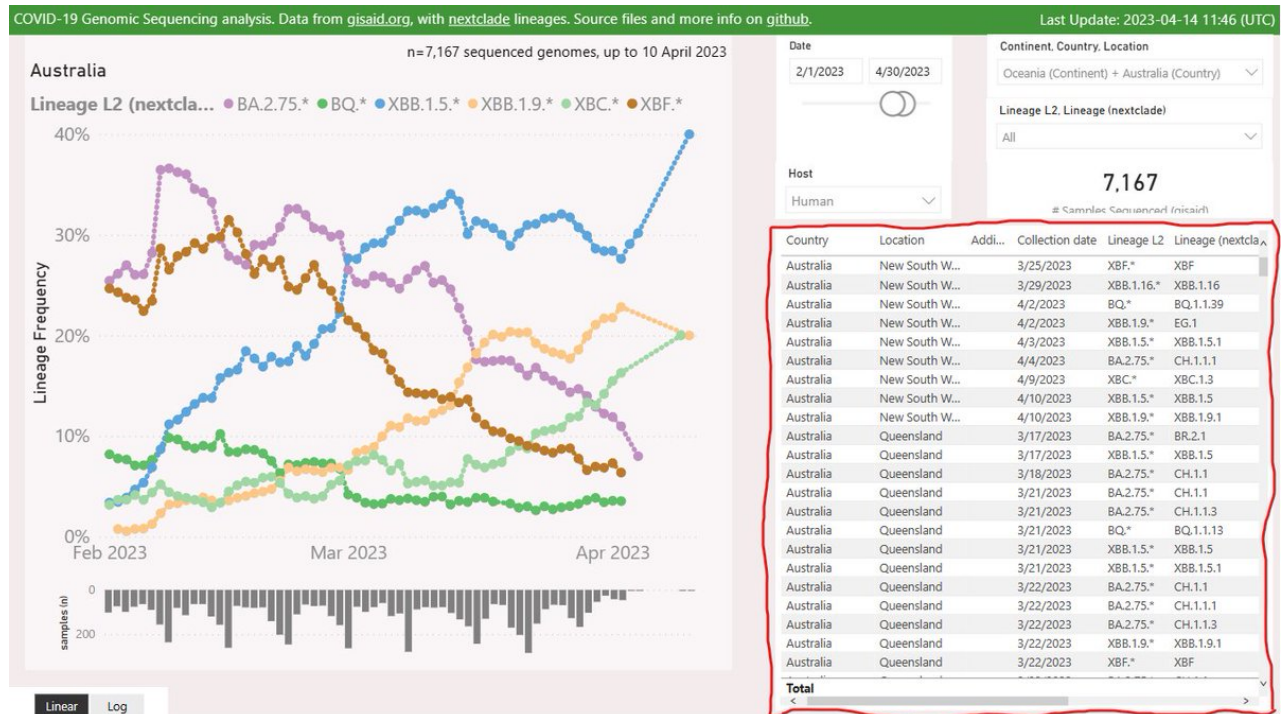
Note, there are usually delays from the time a PCR test sample is taken, to the time it is sequenced and uploaded to GISAID. You can see in the red circled area at the bottom of the graph how many sequences were reported for each day. 7/





There may only be a small number of sequences in the last several days so the % of lineage frequency may change for those last few days as more sequences are uploaded and become more accurate over time. 8/

The table on the bottom right shows information about the # of sequences of different variants collected on various dates. 9/



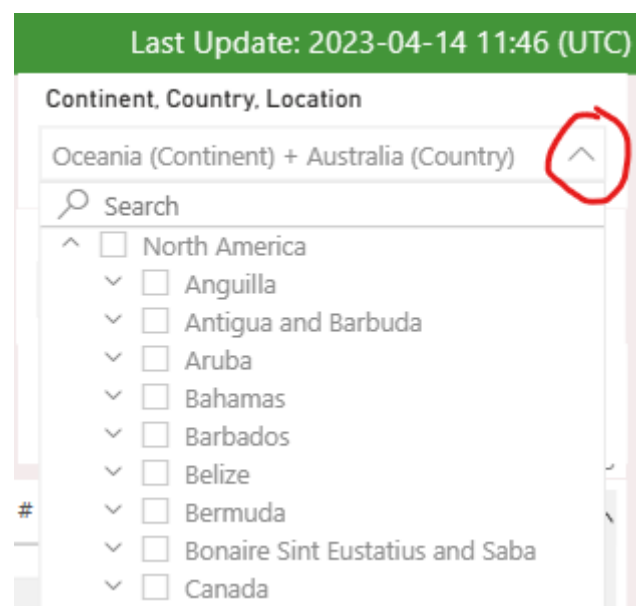
How do you pick your location to see what variants are circulating in your specific country or province/state? 10/

Click on the V to the right of the current Continent, County, Location which by default is "Oceania + Australia" and you will see a drop-down list of continents and countries. Scroll down until you find your continent and then country of interest. 11/

Under "North America" you can see multiple countries including Canada. There is also "V" beside Canada which means you can drill down further into provinces of Canada if you want. 12/

Click on the "V" to expand further choices and if you wanted to pick variants from Ontario, Canada, you would click on the white box beside "Ontario" as shown in the image. 13/

After a few seconds while the tool loads the sequences from your newly selected location, the graph will be updated and



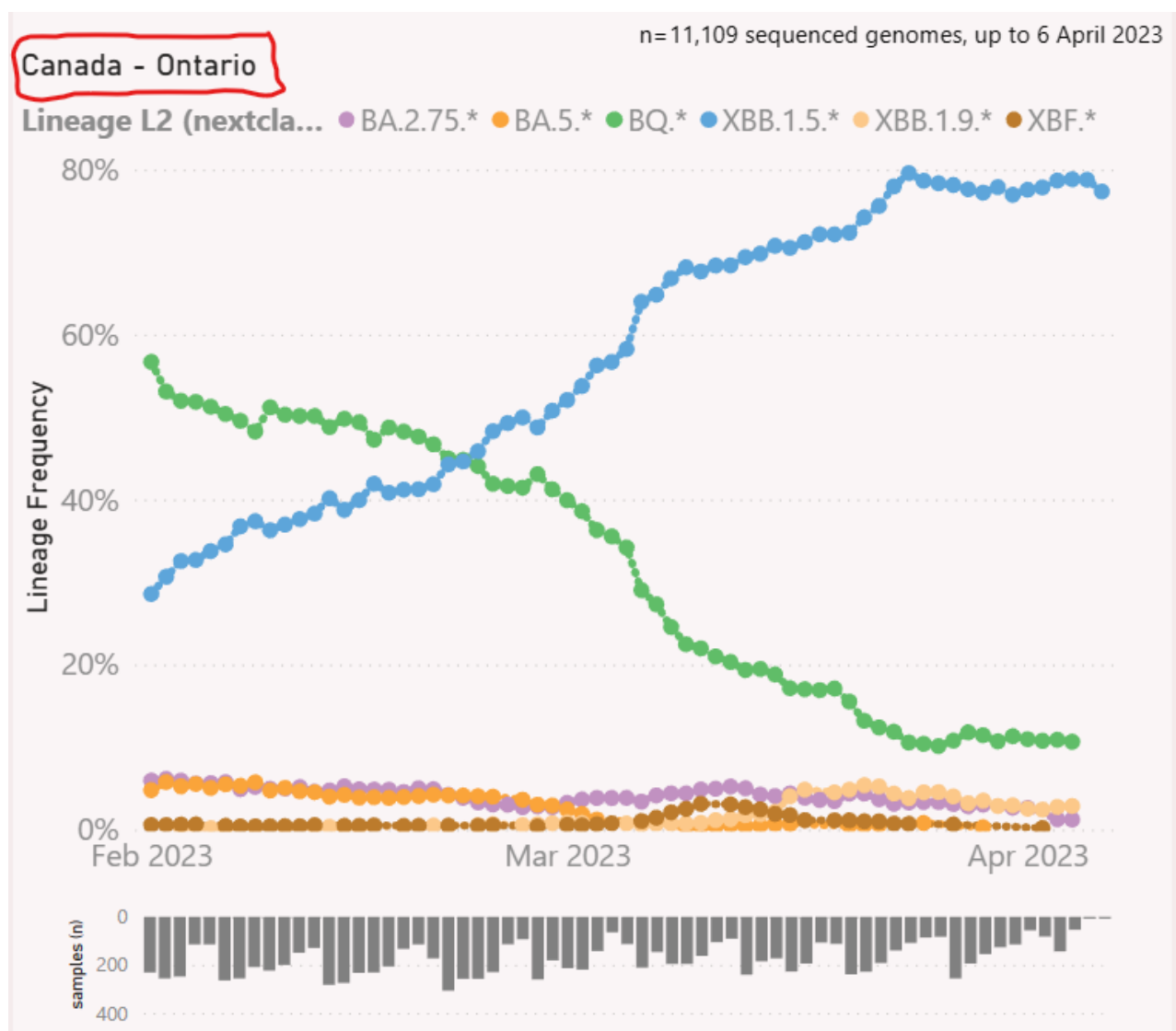
now display the variant families for your location over the past 2 months (see Date selector box for exact range). 14/

#### Continent, Country, Location

North America (Continent) + Canada (Coun... ^

Search

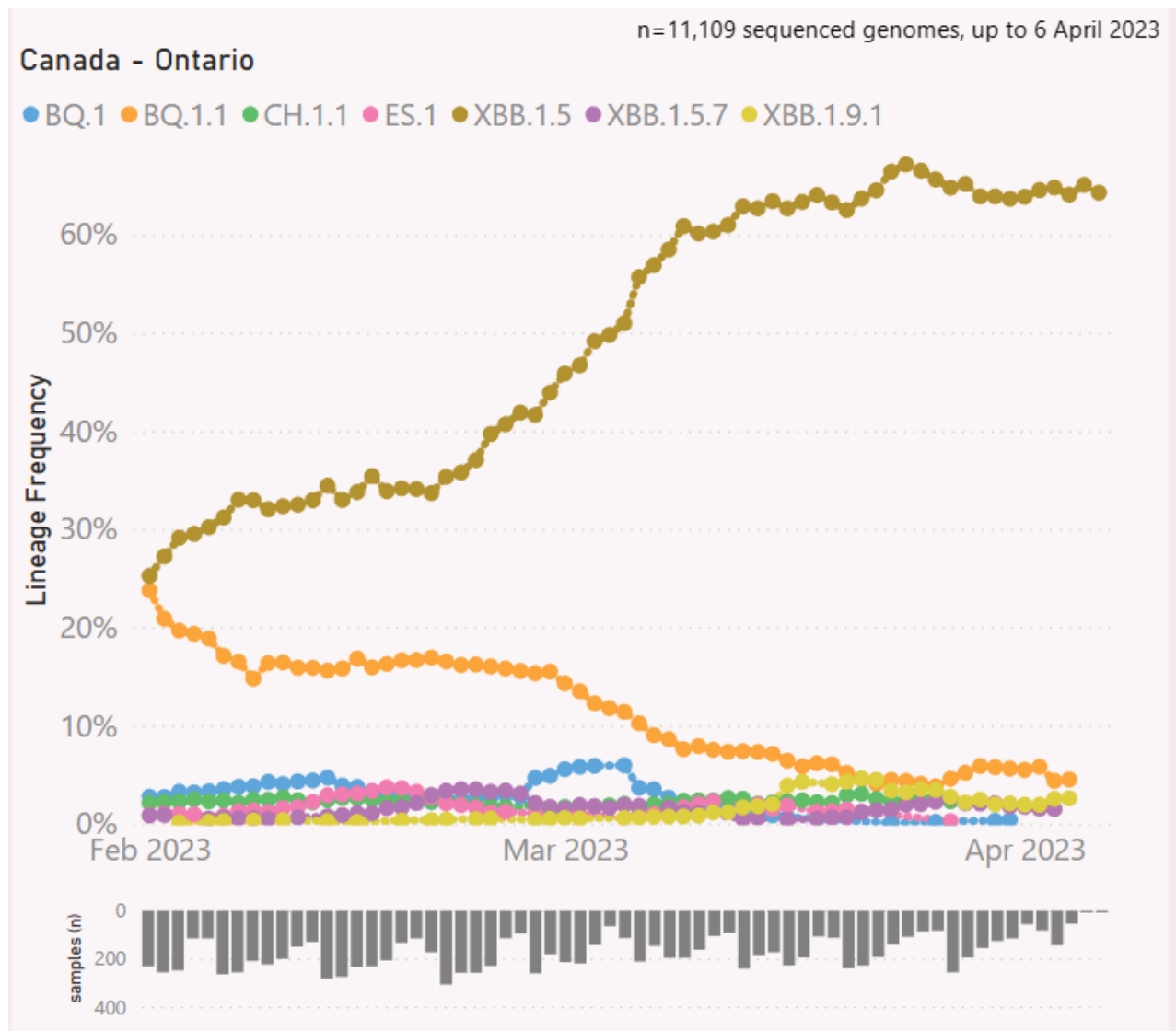
- ☒ Canada
  - ☐ (Blank)
  - ☐ Alberta
  - ☐ British Columbia
  - ☐ Gran Canaria
  - ☐ Manitoba
  - ☐ New Brunswick
  - ☐ Newfoundland and Labrador
  - ☐ Nova Scotia
  - ☒ Ontario



In this case the XBB.1.5.\* family (the \* means all variants of XBB.1.5 and any children of that variant such as XBB.1.5.1, XBB.1.5.15, etc..) is the vast majority if sequences hovering around the 80% mark while the other top 6 lineages are much lower. 15/

This is just page #1 of the visualization tool. At the very bottom you can see there are 31 pages of reports. You can click on the right arrow to scroll through the various pages of information to see what else is available. 16/

Click on the right arrow to go to page 2. Instead of displaying variant families, it shows you the top 7 specific variants in the location over the entire time period selected. 17/



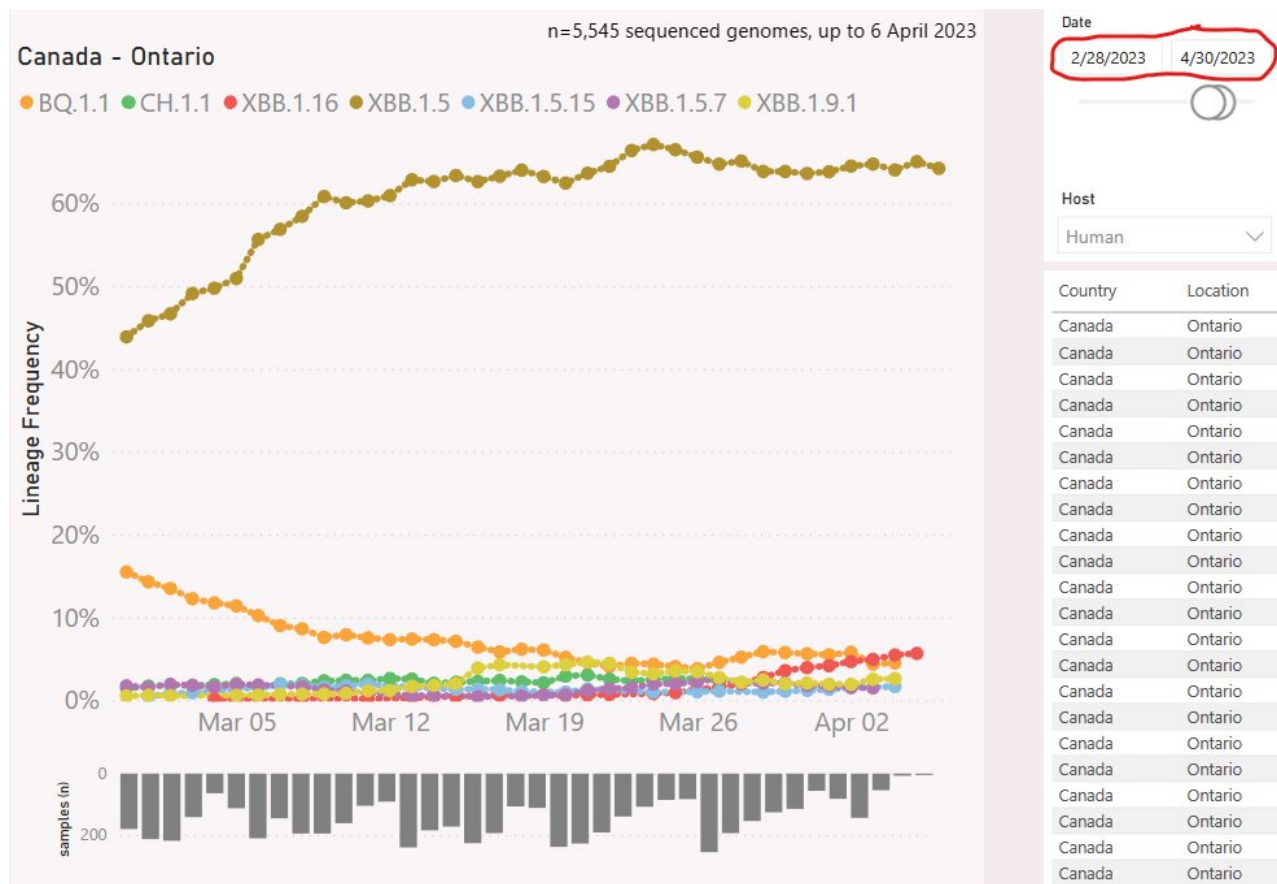
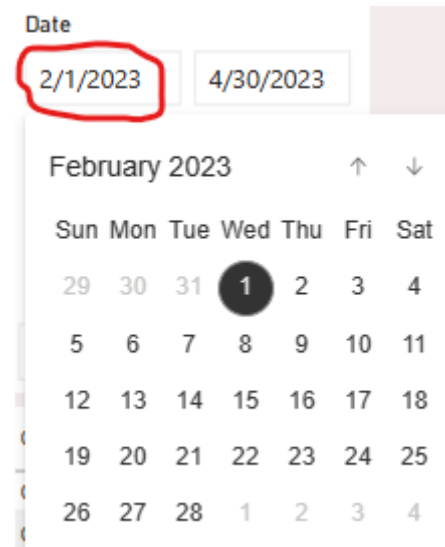
Now you can see that XBB.1.5 on its own commands about 65% of sequences and in second place is BQ.1.1 which has mostly vanished now at 4.5%. It is important to note that the display only shows the top 7 variants, there are many other variants circulating as well. 18/

The top 7 calculation is done over the entire period so in this case Feb 1, 2023 to Apr. 30, 2023. If new variants are starting to increase rapidly, but only recently they might not be displayed because other variants that have been around longer. 19/

That is actually the case right now with XBB.1.16 "Arcturus" which is growing rapidly. How can we change the date range of the graph? Just click on the date you want to update. 20/

For the start date in this example click on 2/1/2023 as shown in the image which will open a calendar view and then select the date. Let's pick Feb. 28th so we are showing the last 2 weeks of sequences. Click on the "28" in the calendar to make your selection. 21/

Now with the updated date range you can see that BQ.1 and ES.1 are no longer displayed but replaced with XBB.1.5.15 and XBB.1.16 "Arcturus" which is actually now in 2nd place at 5.6%. 22/



What if you are interested in just a specific variant or family of variants? You can filter one or more variants to be displayed using the Lineage selector at the top right of the page. Click on the "V" to the right of "All" to display a dropdown select to select. 23/

Since XBB.1.16 is new and the 2nd highest variant being sequenced in Ontario, let's take a look at that. Click on the white box to the left of XBB.1.16.\* to filter only on that variant family. 24/



Now the graph is only displaying variants in the XBB.1.16.\* family and you can see just how fast this variant is growing in Ontario.  
25/

#### Continent, Country, Location

North America (Continent) + Canada (Coun... ▼

#### Lineage L2, Lineage (nextclade)

All

Search

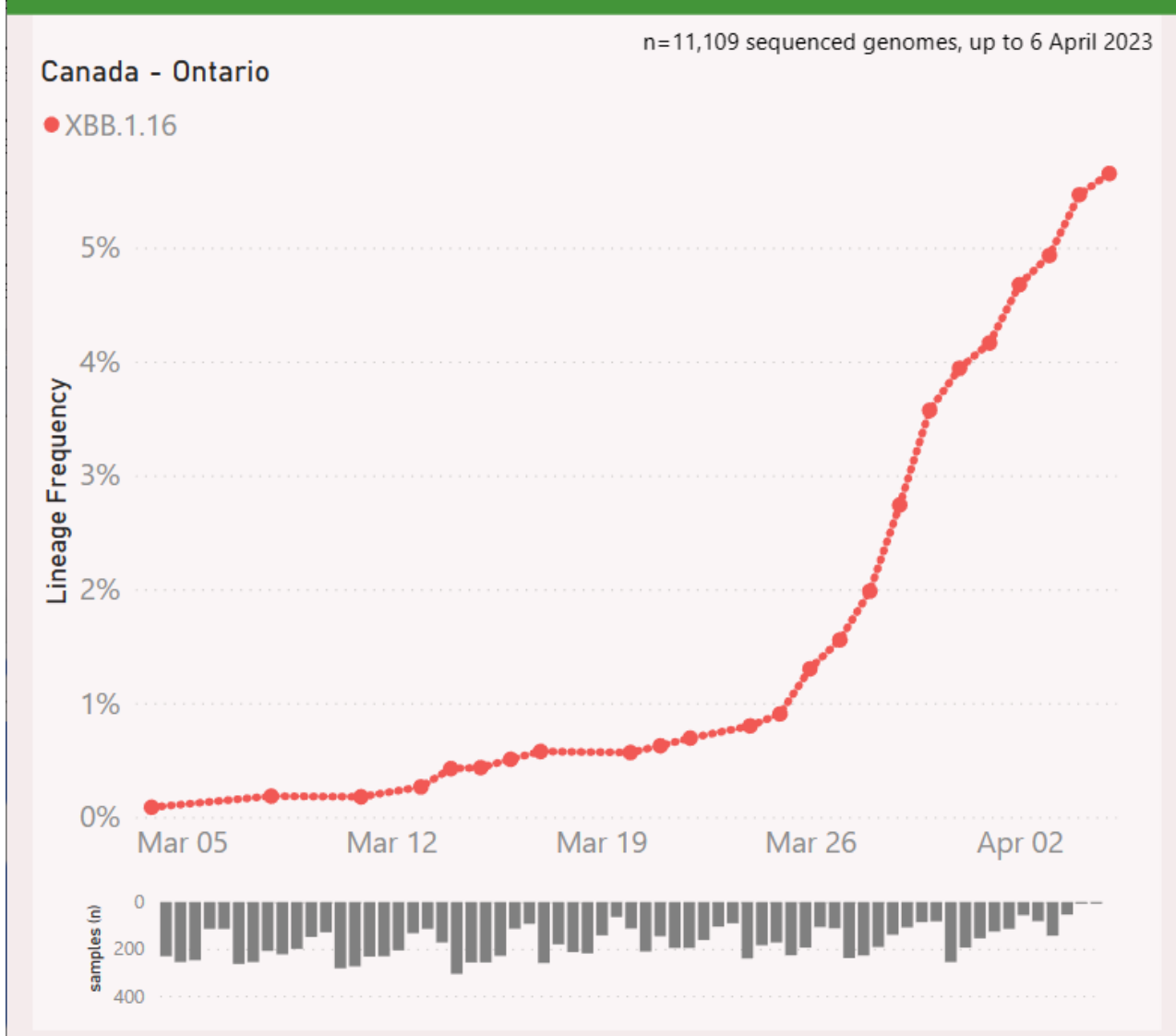
- ☐ Select all
- ▼ ☐ BA.1.\*
- ▼ ☐ BA.2.\*
- ▼ ☐ BA.2.75.\*
- ▼ ☐ BA.5.\*
- ▼ ☐ BQ.\*
- ▼ ☐ XBB.\*
- ▼ ☐ XBB.1.16.\*
- ▼ ☐ XBB.1.5.\*
- ▼ ☐ XBB.1.9.\*

#### Lineage L2, Lineage (nextclade)

XBB.1.16.\*

Search

- ☒ Select all
- ▼ ☐ BA.1.\*
- ▼ ☐ BA.2.\*
- ▼ ☐ BA.2.75.\*
- ▼ ☐ BA.5.\*
- ▼ ☐ BQ.\*
- ▼ ☐ XBB.\*
- ▼ ☒ XBB.1.16.\*
- ▼ ☐ XBB.1.5.\*
- ▼ ☐ XBB.1.9.\*



You can also select multiple variants if you wish to compare specific ones. Each variant family has a "V" dropdown in the list so you can also pick specific variants within a family. 26/

Generally I just use the first 2 pages to look at my specific location, but there are many other pages of information that compare specific variants in many countries and other analysis that you can explore. 27/

If you ever get yourself into a spot where you don't know how to undo a change or filter, just refresh the web page in your browser or close the tab and open a new one and browser back to: [app.powerbi.com/view?r=eyJrIjojN...](https://app.powerbi.com/view?r=eyJrIjojN...) 28/

Big shoutout to [@Mike\\_Honey\\_](#) for building this visualization tool so that people anywhere in the world can see what variants are circulating in their location or elsewhere. He is also on the M platform here ( [aus.social/@mike\\_honey\\_...](https://aus.social/@mike_honey_...) ). 29/

He also makes his code available on GitHub: [github.com/Mike-Honey/covid-19-g...](https://github.com/Mike-Honey/covid-19-g...) 30/

Is this thread incomplete? [Refresh Thread](#)

Jun. 17, 2021

## **Jeff Gilchrist**

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COVID-19: Pfizer and Moderna vaccines reverse engineered In Canada you can mix mRNA (Moderna/Pfizer) vaccines for first and second doses, so can be treated as equivalent. They both use an mRNA platform but the contents of the vaccine are not identical. 🧵 1/

Jan. 28, 2022

## **Jeff Gilchrist**

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COVID-19: Air quality sensors in all Boston public schools Boston's public schools have implemented the ability measure indoor air quality to help ensure the safety of students and provide them with the best learning environment (. 🧵 1/ @DavidElfstrom

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