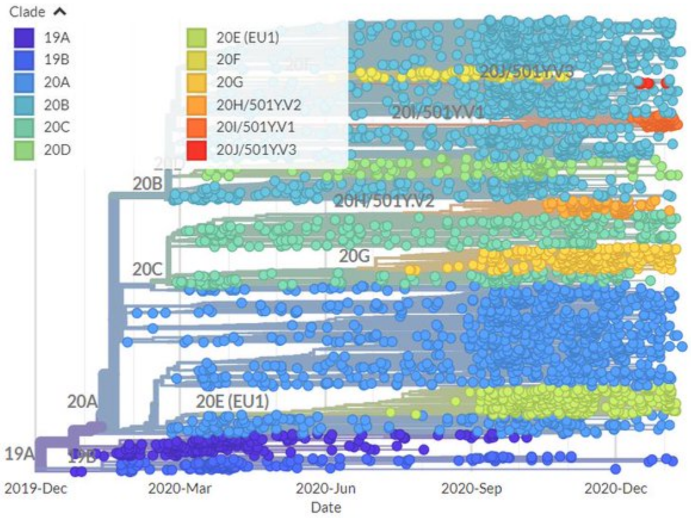
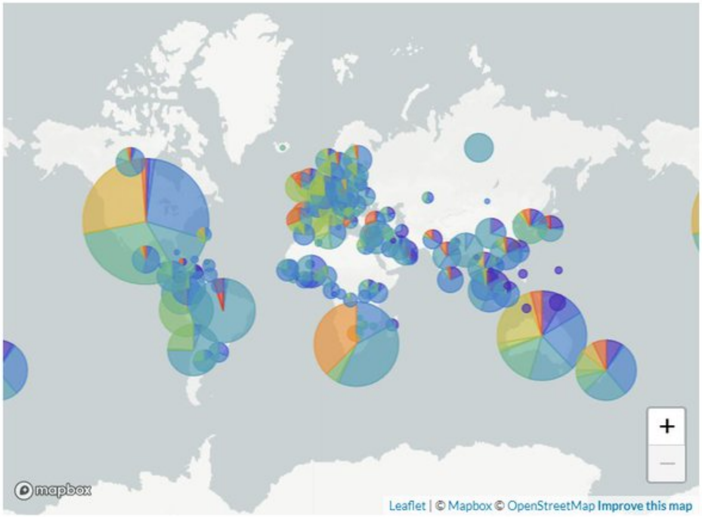
Twitter Thread by Nextstrain

Nextstrain
@nextstrain

We are always looking for ways to make things better, more intuitive, & more helpful at Nextstrain! Some of you may have already noticed that we recently added a bunch of great new features - but in case you didn't, let's explore them!

1/11



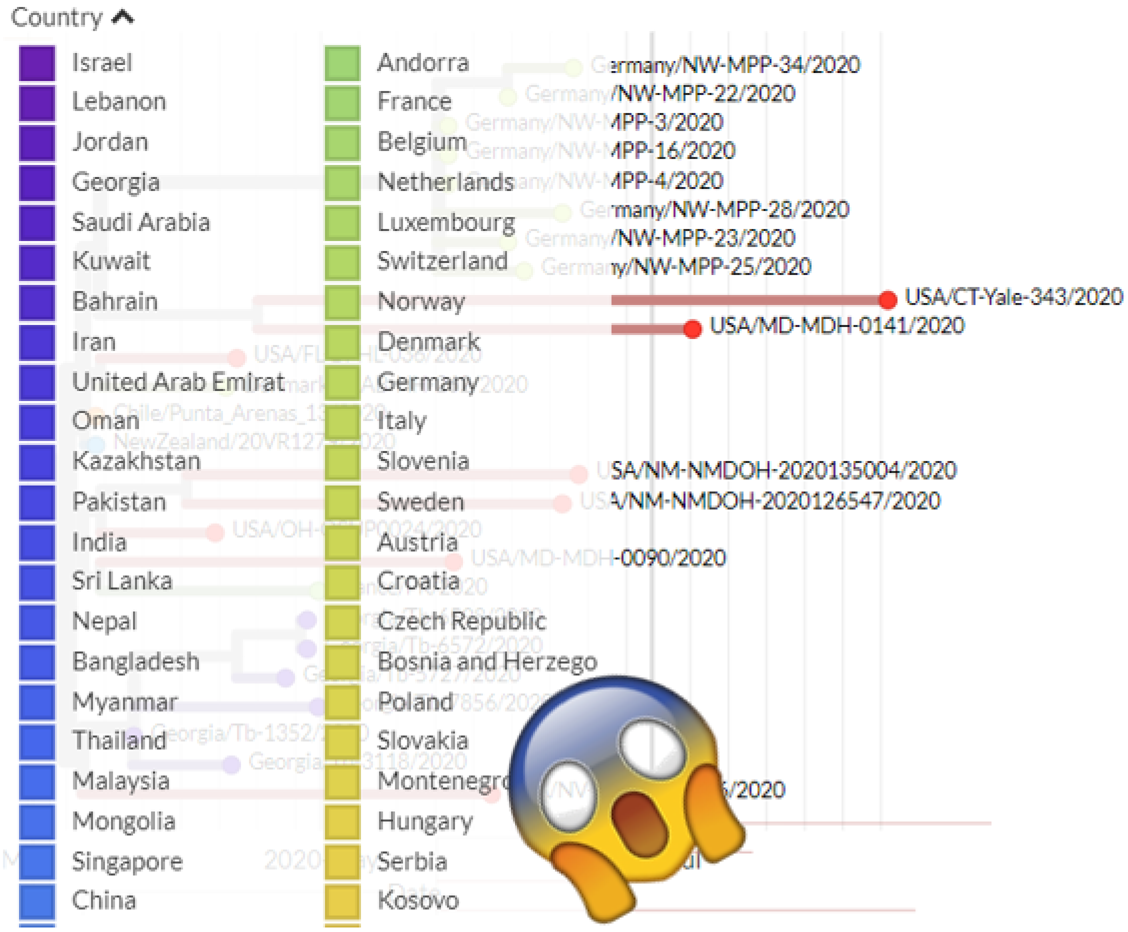


First, if you're a regular user you'll remember the fun of extra-long legends even when zoomed in...

Now, the legend will only show what's visible on the map, making it much more useful!

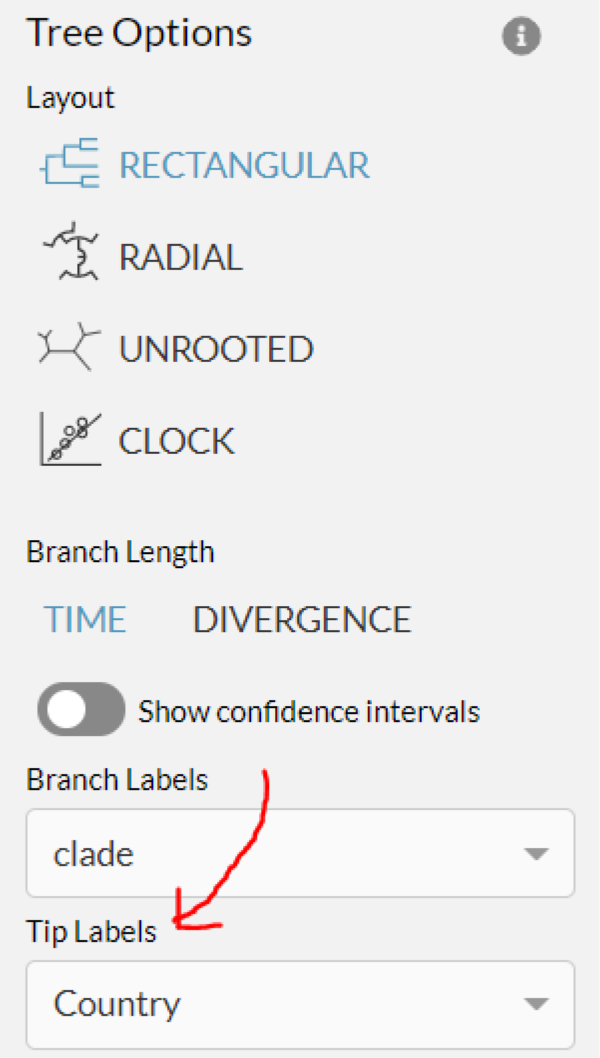
(Works with colourings like genotype, too!)

2/11



When using Nextstrain we often want to examine 2 things at once - until now that was sometimes difficult!

Now it's a little easier - you can change the tip-labels from the default 'strain', so that you can combine colouring & tip labels to show different things!



Tree Options

Layout

RECTANGULAR

RADIAL

UNROOTED

CLOCK

Branch Length

TIME DIVERGENCE

Show confidence intervals

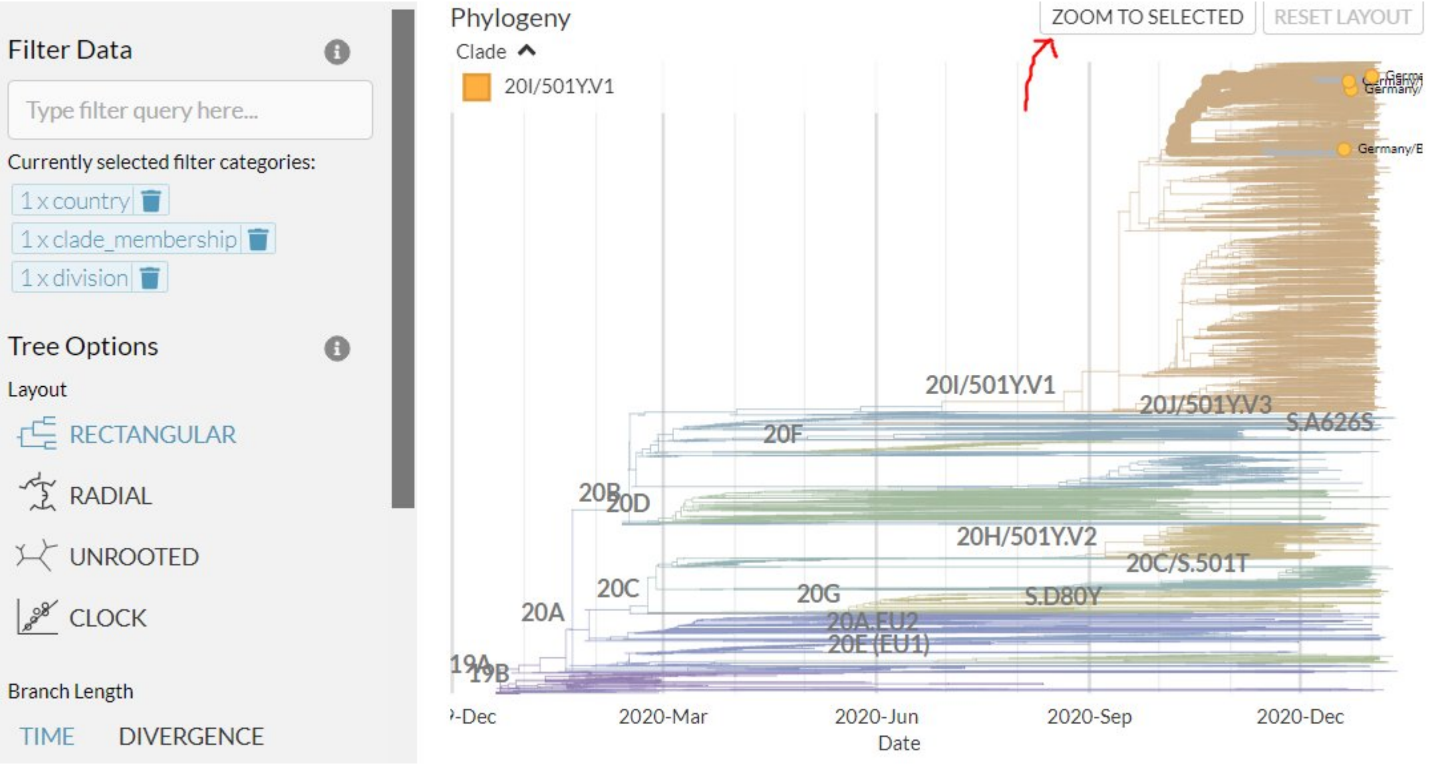
Branch Labels: clade

Tip Labels: Country

With the recent type-to-filter function it's easier than ever to narrow down to just the sequences you want - but you're often still very far away!

A new 'Zoom to Selected' button will take you right in close to exactly what you're interested in looking at!

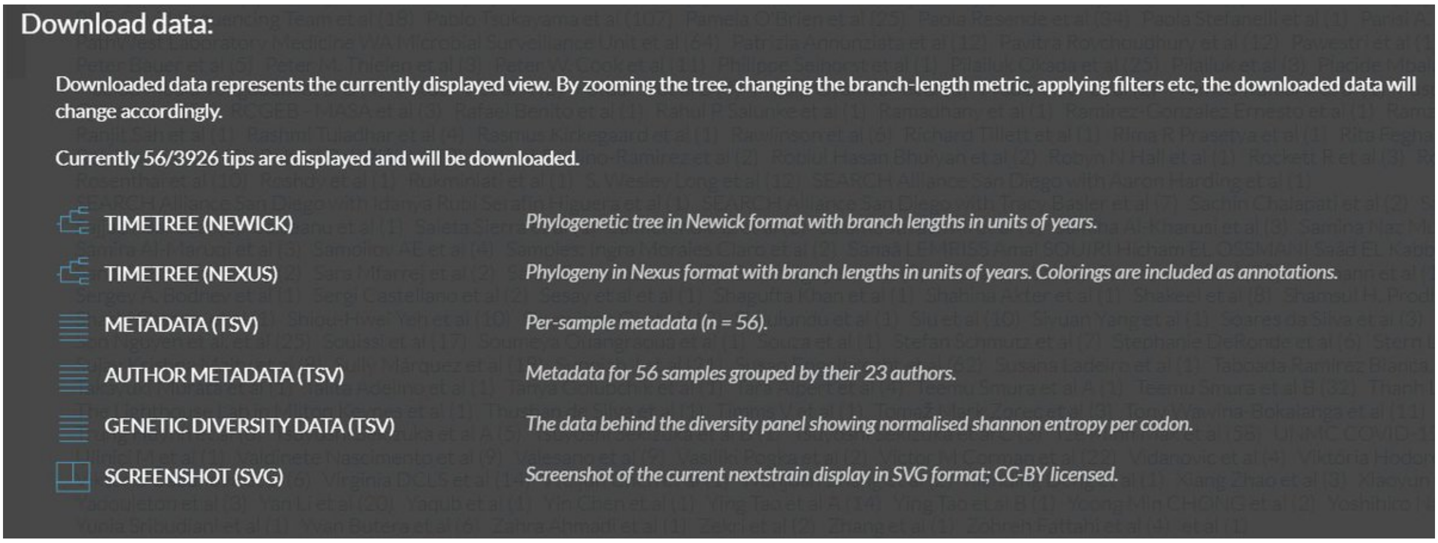
4/11



If you commonly download trees from Nextstrain you'll be happy to learn we've improved how this works!

Downloaded trees now reflect the subtree visible & you can now download annotated Nexus format that works in FigTree! (Note the view is 'upside down' between the 2 pics!)

5/11



Download data:

Downloaded data represents the currently displayed view. By zooming the tree, changing the branch-length metric, applying filters etc, the downloaded data will change accordingly.

Currently 56/3926 tips are displayed and will be downloaded.

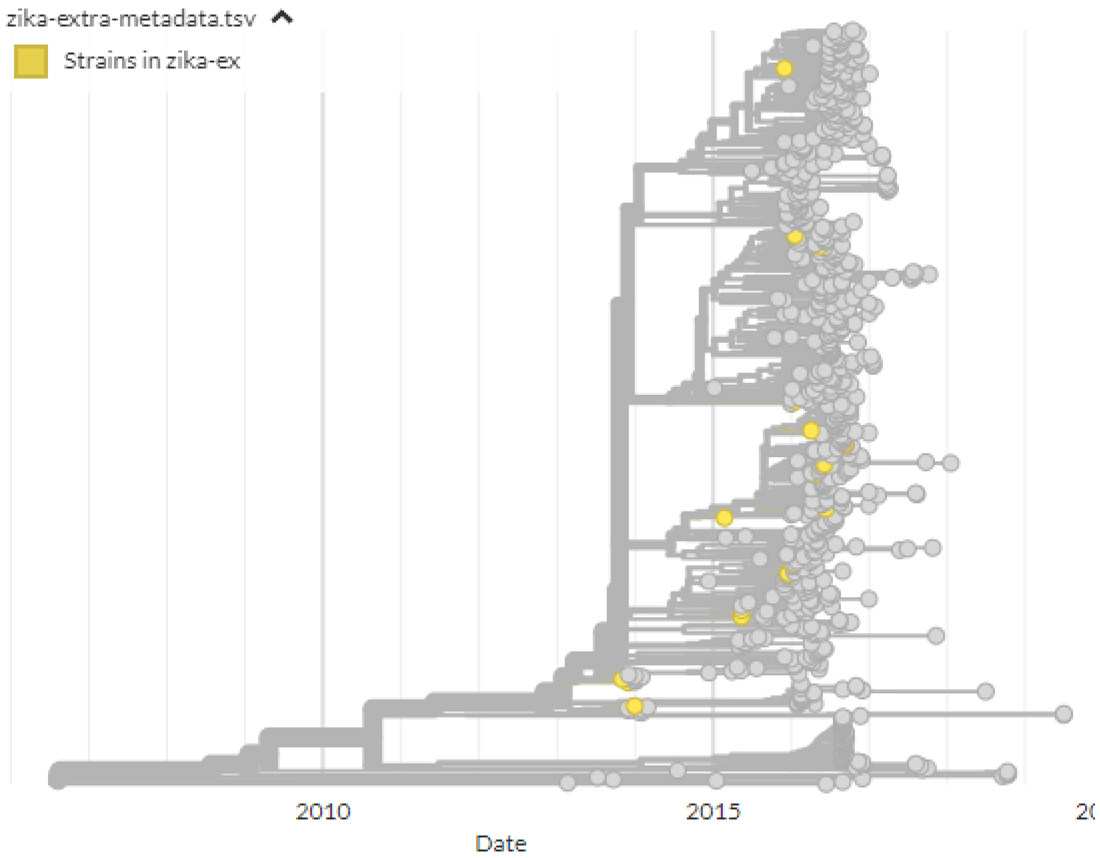
TIMETREE (NEWICK)	*Phylogenetic tree in Newick format with branch lengths in units of years.*
TIMETREE (NEXUS)	*Phylogeny in Nexus format with branch lengths in units of years. Colorings are included as annotations.*
METADATA (TSV)	*Per-sample metadata (n = 56).*
AUTHOR METADATA (TSV)	*Metadata for 56 samples grouped by their 23 authors.*
GENETIC DIVERSITY DATA (TSV)	*The data behind the diversity panel showing normalised shannon entropy per codon.*
SCREENSHOT (SVG)	*Screenshot of the current nextstrain display in SVG format; CC-BY licensed.*

Use drag-&-drop metadata to add extra info to builds? We've updated this too!

See the docs below for the details - it's now easier to see which tips added metadata & to add more types of data! (If you don't know about this feature - check it out!)

6/11

https://t.co/iseTa0qBrT

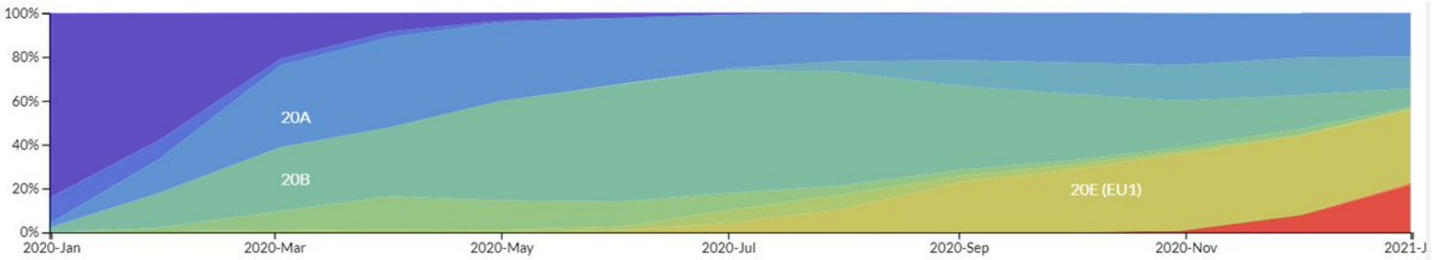


This is a little more subtle, but can still be very useful:

Previously, our frequency charts only had 1 point a month, sometimes leading to choppy graphs. We've improved this, so graphs are smoother & project less extremely into the future!

(Old on left, new on right!)

7/11



Finally, we've vastly improved how we can show off the many #SARSCoV2 Nextstrain builds people are maintaining, all over the world! See the new map (link below)!

Click to zoom in on regions with many builds & mouse-over dots to find out more!

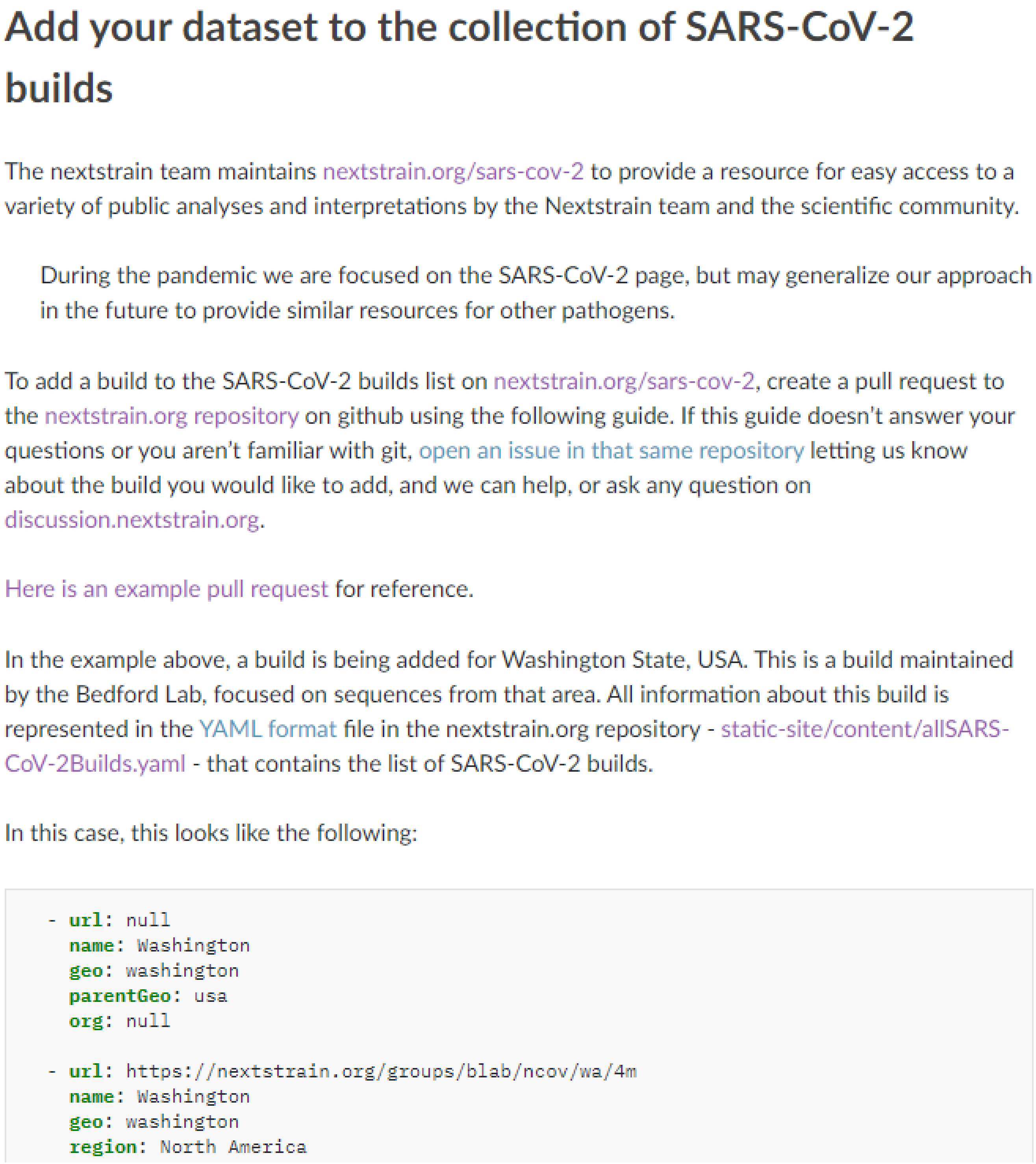
8/11

https://t.co/wYGQV3gprx

It's easy to add your own build to this map! (& we'd love to have it up to help others find it!) Just submit a Pull Request to our https://t.co/5Q05vfE2gm repository - you can find how to do this at the link below!

9/11

https://t.co/nMrgr3jj2x



Add your dataset to the collection of SARS-CoV-2 builds

The nextstrain team maintains nextstrain.org/sars-cov-2 to provide a resource for easy access to a variety of public analyses and interpretations by the Nextstrain team and the scientific community.

> During the pandemic we are focused on the SARS-CoV-2 page, but may generalize our approach in the future to provide similar resources for other pathogens.

To add a build to the SARS-CoV-2 builds list on nextstrain.org/sars-cov-2, create a pull request to the nextstrain.org repository on github using the following guide. If this guide doesn't answer your questions or you aren't familiar with git, open an issue in that same repository letting us know about the build you would like to add, and we can help, or ask any question on discussion.nextstrain.org.

Here is an example pull request for reference.

In the example above, a build is being added for Washington State, USA. This is a build maintained by the Bedford Lab, focused on sequences from that area. All information about this build is represented in the YAML format file in the nextstrain.org repository - static-site/content/allSARS-CoV-2Builds.yaml - that contains the list of SARS-CoV-2 builds.

In this case, this looks like the following:

```
- url: null
  name: Washington
  geo: washington
  parentGeo: usa
  org: null

- url: https://nextstrain.org/groups/blab/ncov/wa/4m
  name: Washington
  geo: washington
  region: North America
```

You can read about all of our latest updates in our Changelog (linked below).

We hope these updates make Nextstrain even more useful for your exploration, research, & analysis!

10/11

https://t.co/ykbEna5eYJ

These updates are thanks to great ideas & hard work from many Nextstrain team members, in particular from @hamesjadfield @wcassias @eliasharkins @trvrb & Jover Lee! ■■■

11/11