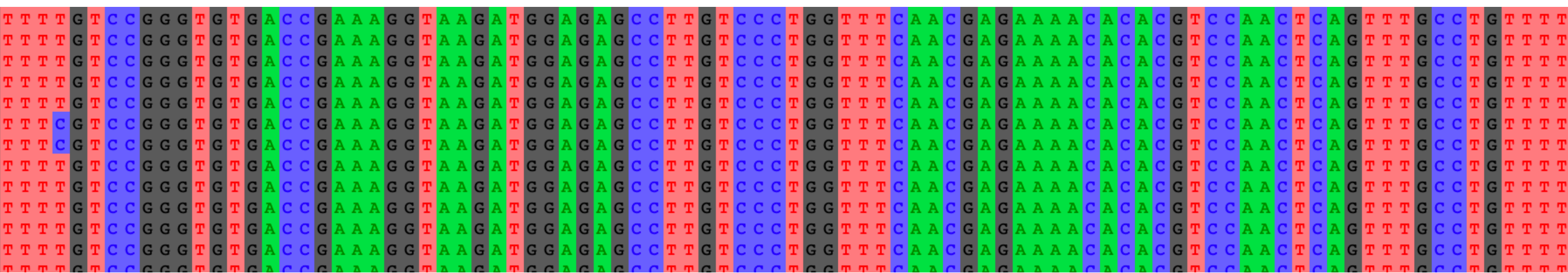


Genomic surveillance of SARS-CoV-2 in Switzerland

Sarah Nadeau

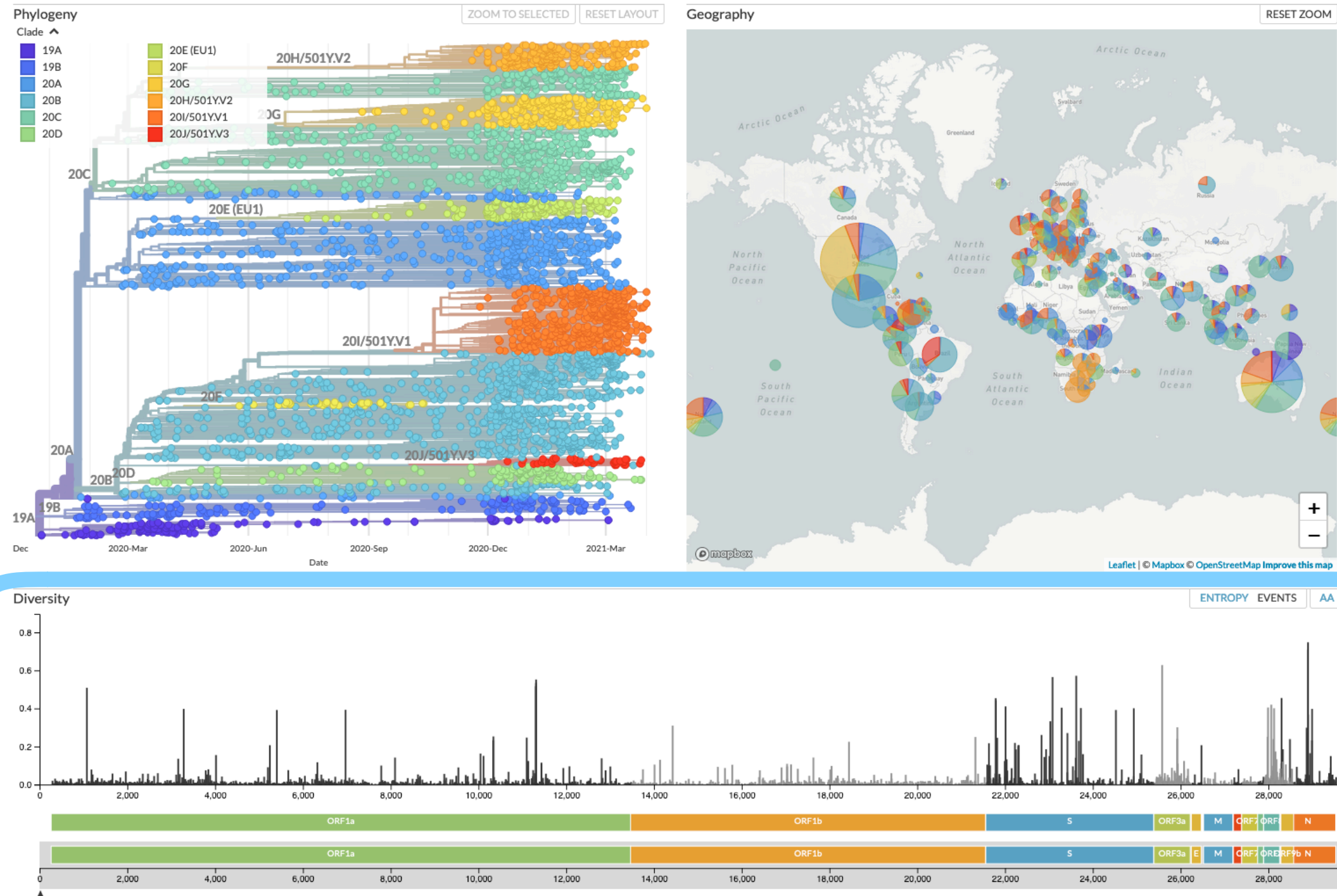


Agenda

- **Genomic epidemiology: definition and motivation**
- Genomic surveillance in Switzerland
- Results:
 - Swiss transmission chains
 - Estimating R_e from transmission chains

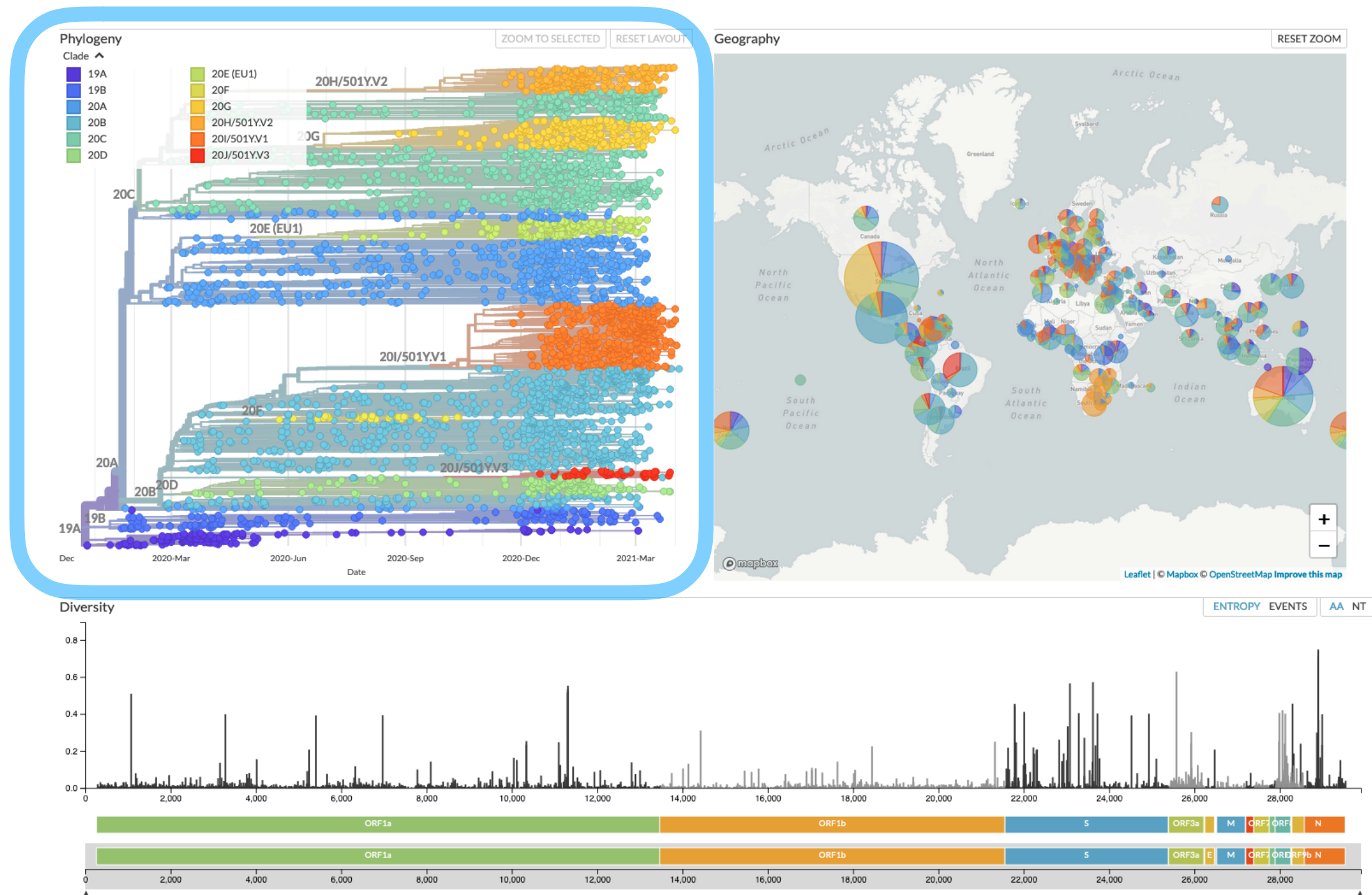
SARS-CoV-2 is evolving on the same time-scale as the pandemic

<https://nextstrain.org/>



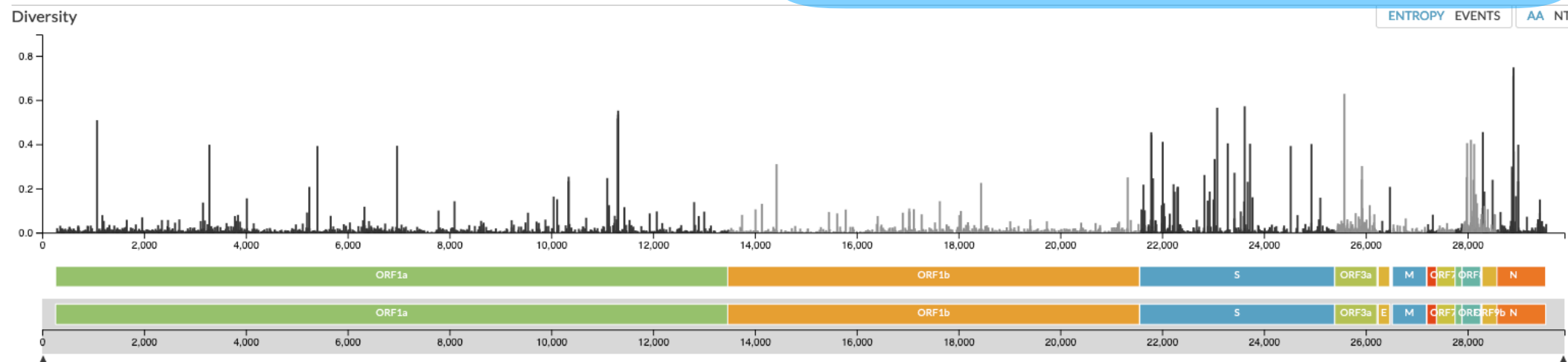
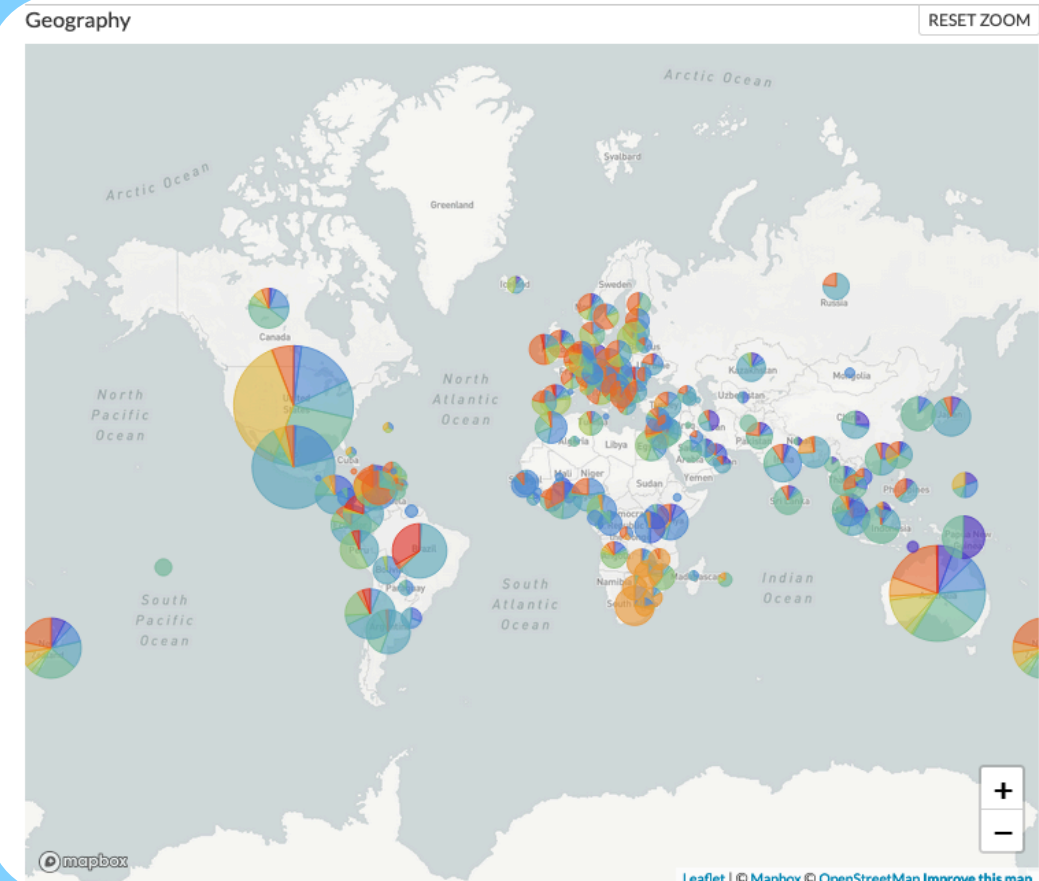
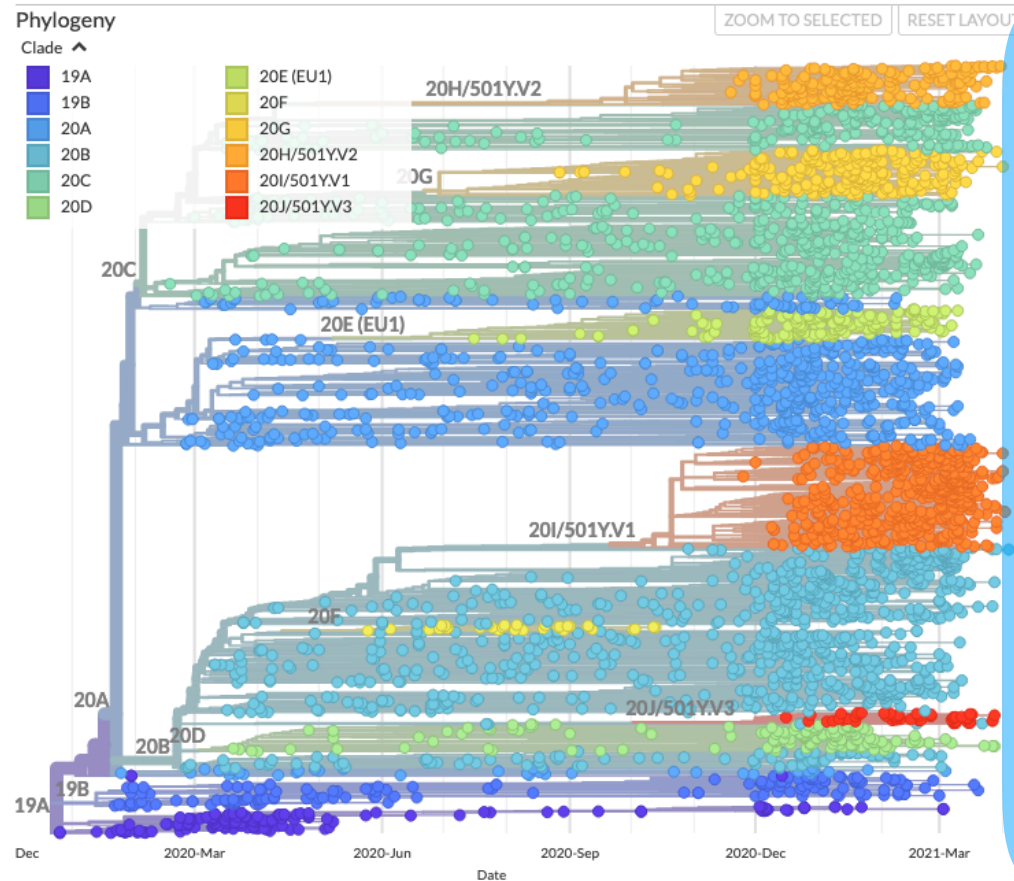
SARS-CoV-2 is evolving on the same time-scale as the pandemic

<https://nextstrain.org/>



Genomic epidemiology: using mutations as clues for how the virus spreads

<https://nextstrain.org/>



Example 1: Viruses from the first COVID-19 patients were very similar

📌 **Phylodynamic Analysis | 176 genomes | 6 Mar 2020**

 SARS-CoV-2 coronavirus  nCoV-2019 Genomic Epidemiology



arambaut  ARTIC Network

50  Jan '20

Phylogenetic analysis of nCoV-2019 genomes

→ a recent, single introduction into humans

Example 2: Early cases in the US and Europe carried viruses with distinct mutational signatures

Science

RESEARCH ARTICLES

Cite as: M. Worobey *et al.*, *Science*
10.1126/science.abc8169 (2020).

The emergence of SARS-CoV-2 in Europe and North America

Michael Worobey^{1*}, Jonathan Pekar^{2,3}, Brendan B. Larsen¹, Martha I. Nelson⁴, Verity Hill⁵, Jeffrey B. Joy^{6,7,8}, Andrew Rambaut⁵, Marc A. Suchard^{9,10,11*}, Joel O. Wertheim^{12*}, Philippe Lemey^{13*}

→ the first cases in these regions were separate introductions and not community spread

Example 3: B.1.1.7 variant rose in frequency across the UK

Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations

SARS-CoV-2 coronavirus | nCoV-2019 Genomic Epidemiology

 arambaut ARTIC Network 9 Dec '20 Dec 2020

Preliminary genomic characterisation of an emergent SARS-CoV-2 lineage in the UK defined by a novel set of spike mutations

Report written by: Andrew Rambaut¹, Nick Loman², Oliver Pybus³, Wendy Barclay⁴, Jeff Barrett⁵, Alesandro Carabelli⁶, Tom Connor⁷, Tom Peacock⁴, David L Robertson⁸, Erik Volz⁴, on behalf of COVID-19 Genomics Consortium UK (CoG-UK)⁹.

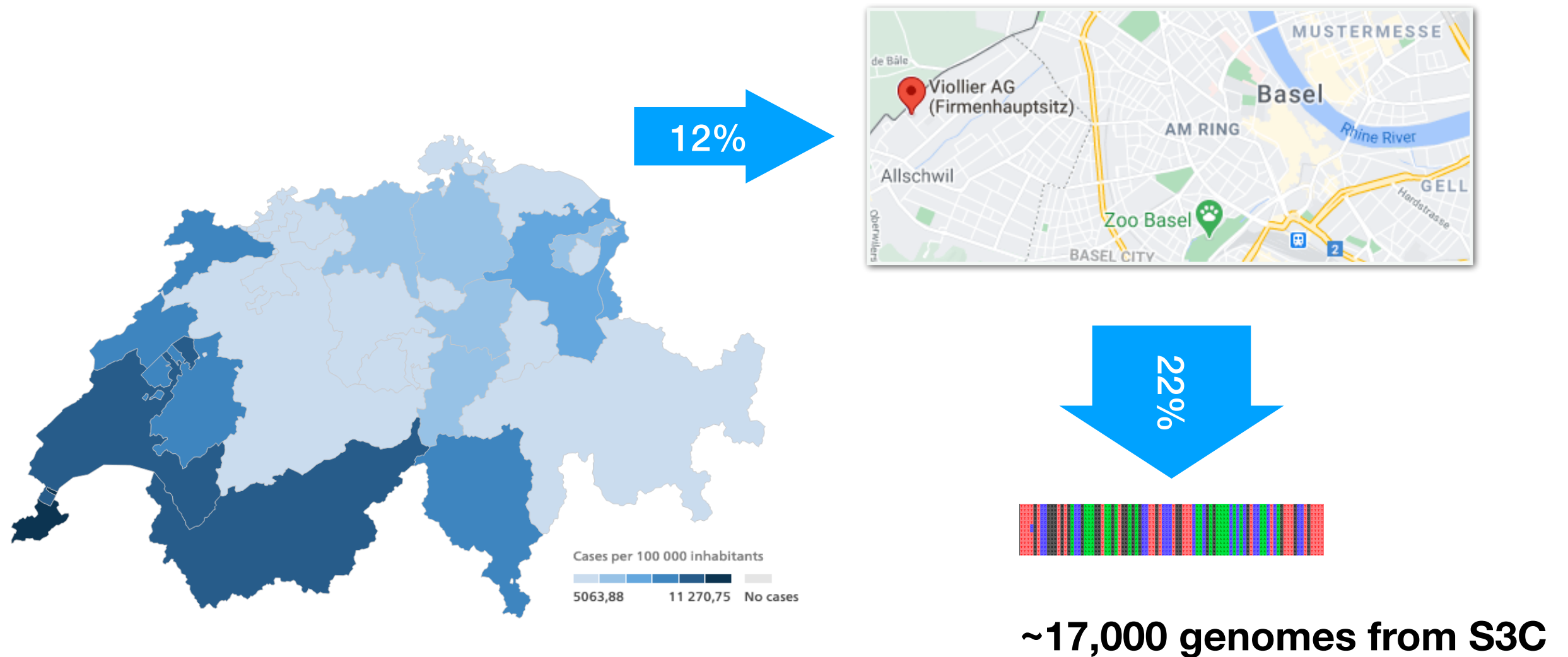
1 / 5
Dec 2020

→ genomic surveillance helps identify variants of concern

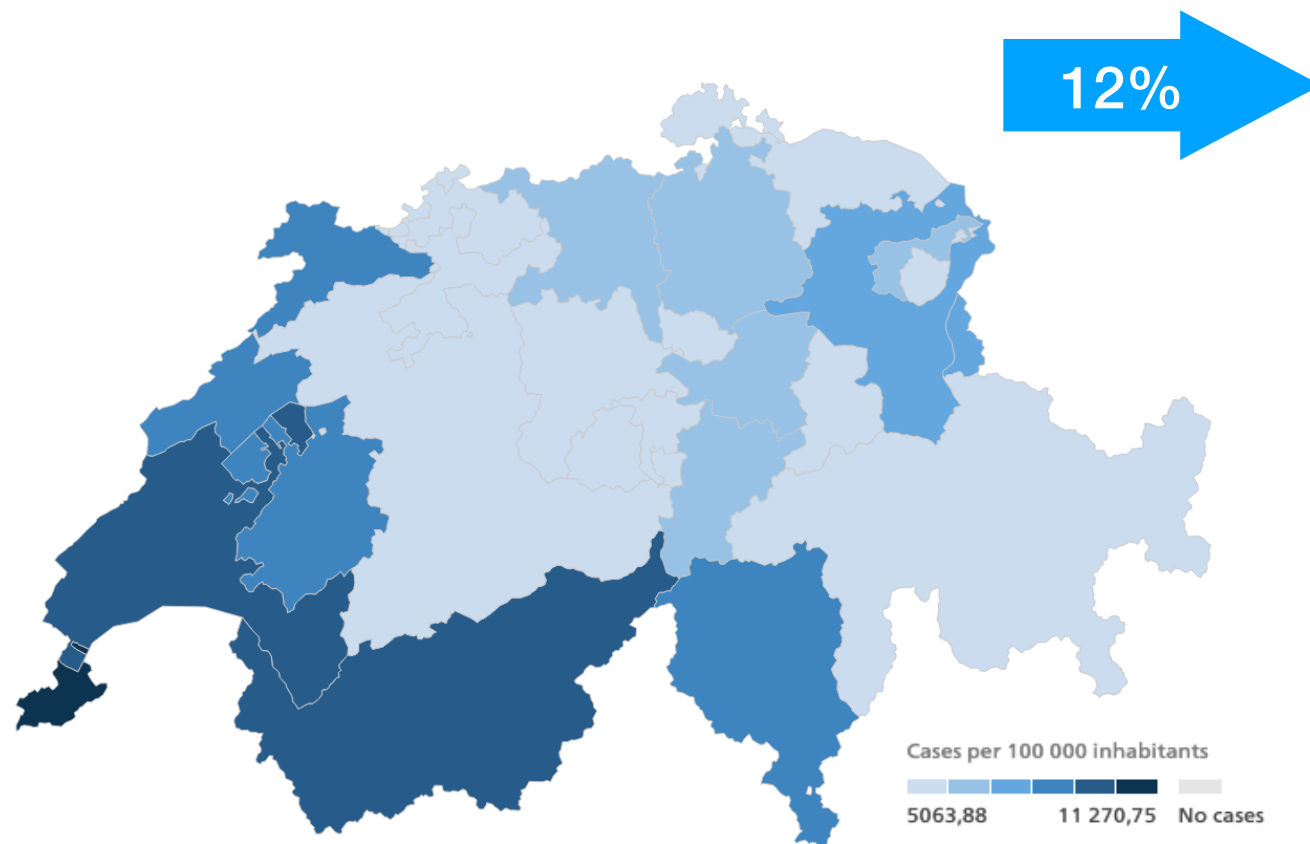
Agenda

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Swiss SARS-CoV-2 Sequencing Consortium (S3C) sequences from tests performed by Viollier AG



Switzerland ranked 7th globally for whole-genome sequence contribution to GISAID



~17,000 genomes from S3C
~ 7,000 genomes from others

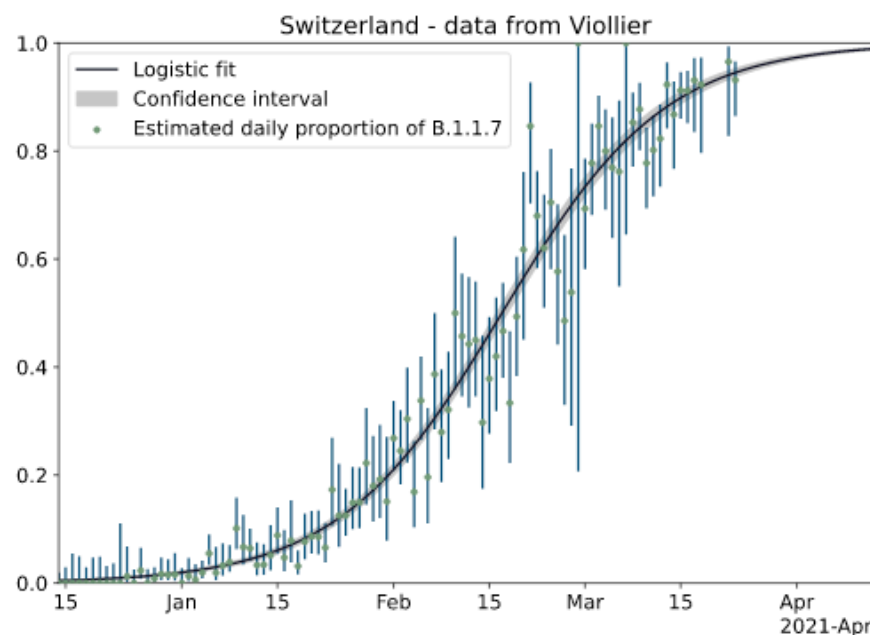
**7% of weekly confirmed cases
7th globally on GISAID**

The genome sequences are used for several purposes

Variant identification & tracking

Transmission chain estimation

B.1.1.7 (or S.501Y.V1) Variant



Import vs. local spread

Reproductive number estimation

<https://cevo-public.github.io/Quantification-of-the-spread-of-a-SARS-CoV-2-variant/>

A phylogenetic tree shows the relationships between genomes (and cases)

- Maximum-likelihood tree: the most likely tree best groups sequences with common mutations
- Branching events in the tree are transmissions events

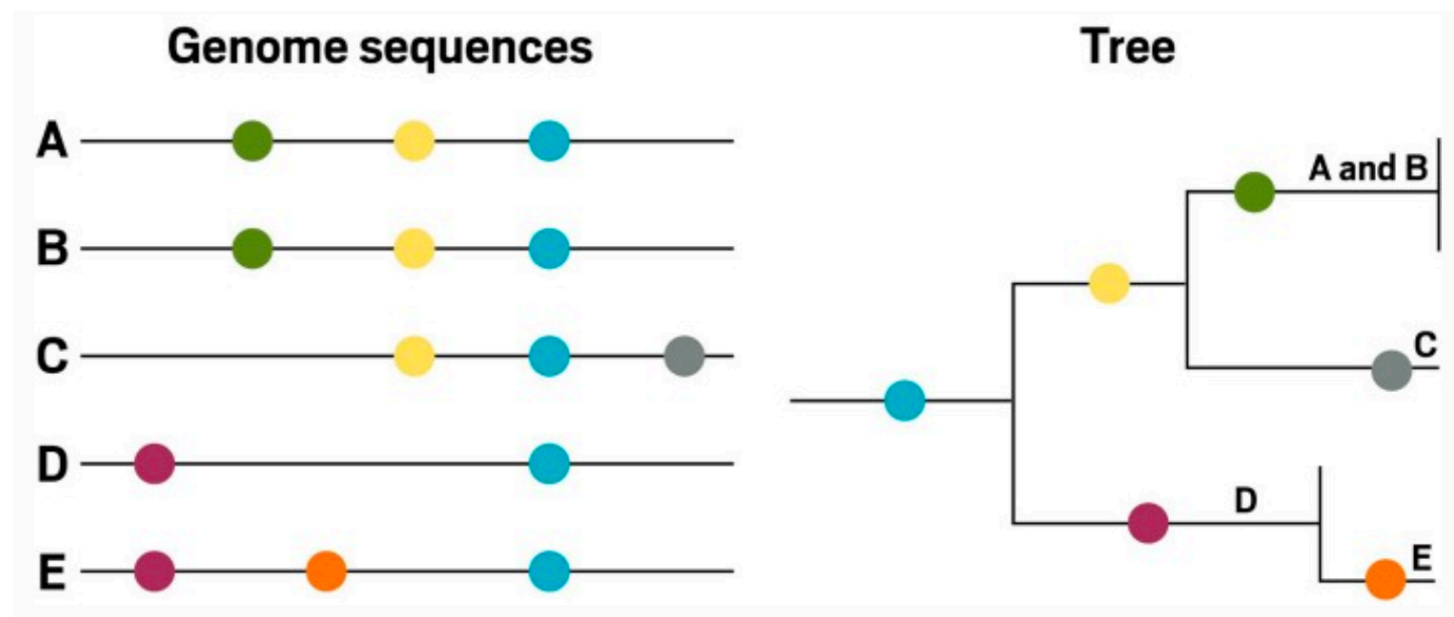
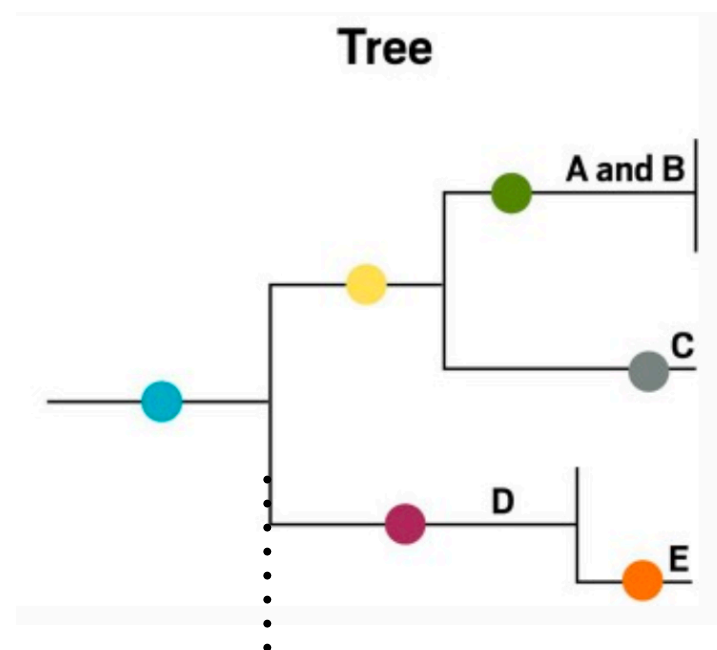


Image credit: Chemical & Engineering News, adapted from Nextstrain.org

A phylogenetic tree shows the relationships between genomes (and cases)

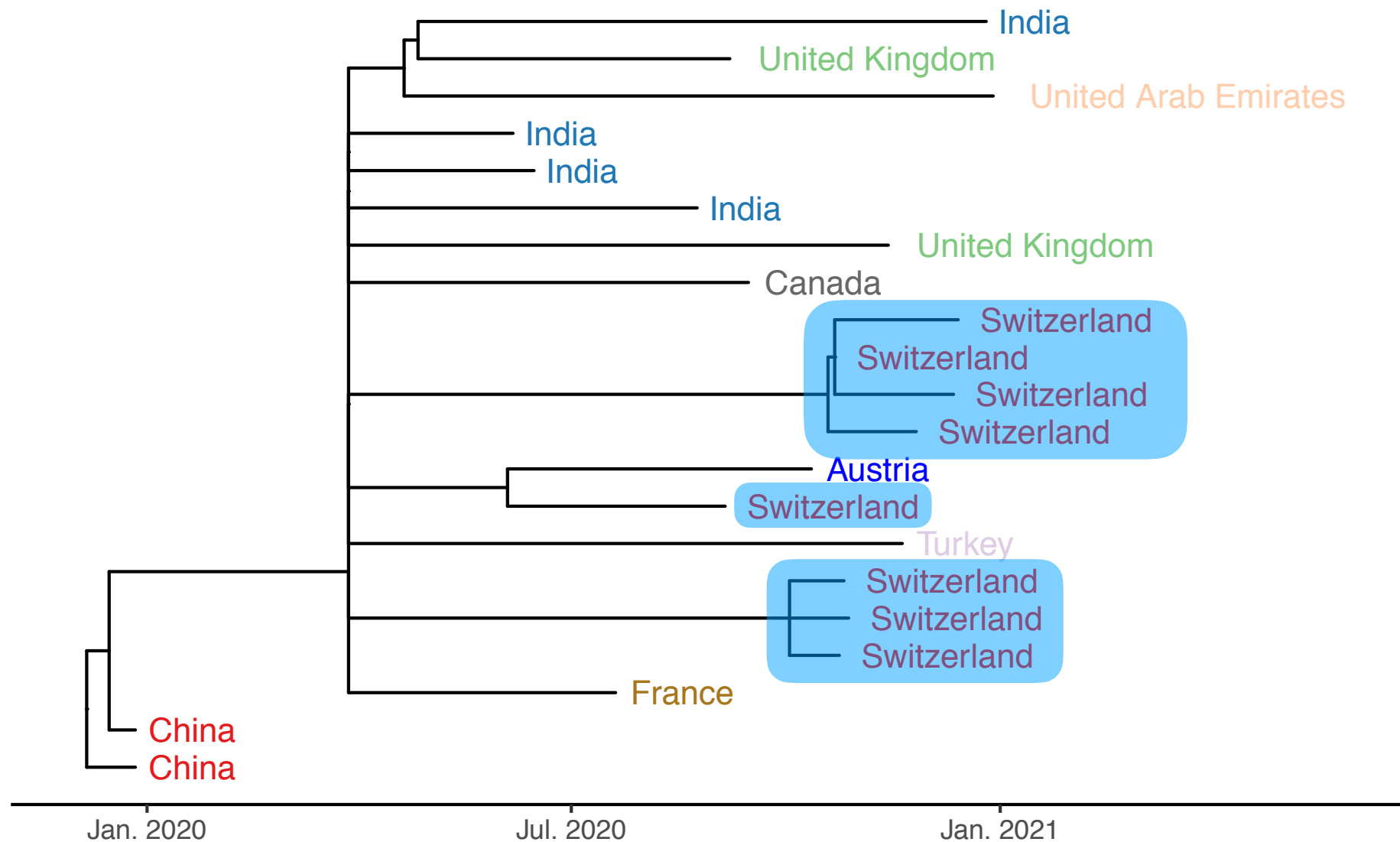
- Molecular clock: assuming a constant mutation rate, we can estimate time since lineages diverged



December 2020

Image credit: Chemical & Engineering News, adapted from Nextstrain.org

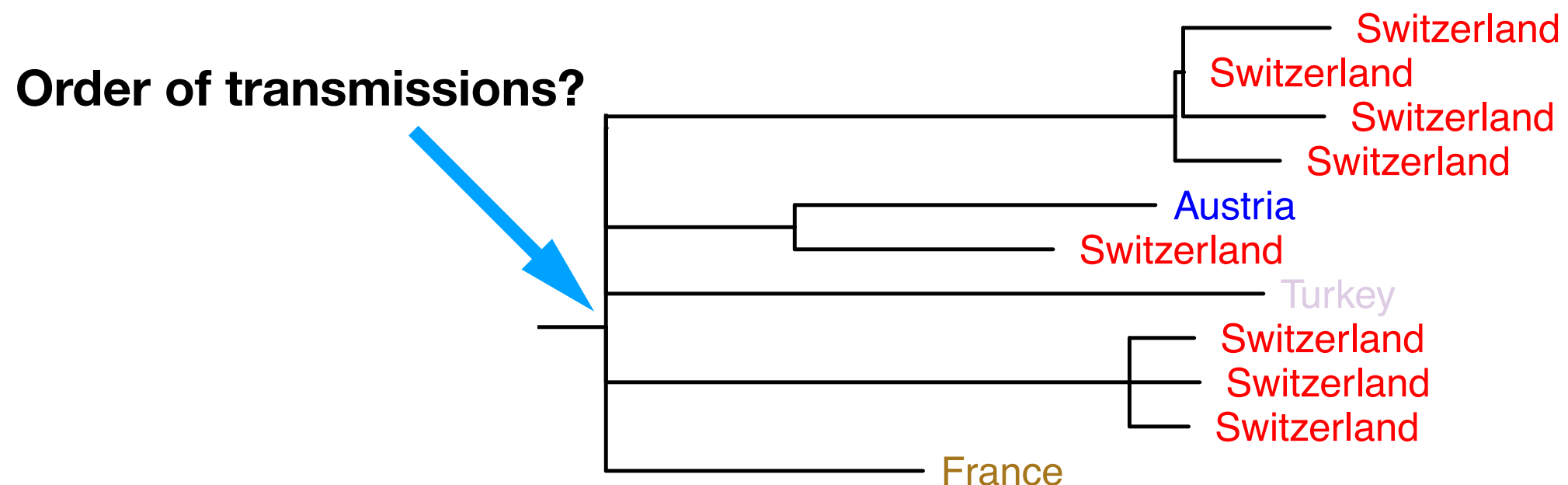
Very similar viruses from Switzerland likely part of the same transmission chain



We estimate transmission chains

*with uncertainty

- Sometimes it is unclear if a single introduction caused one big chain or several introductions caused several smaller chains



We estimate transmission chains

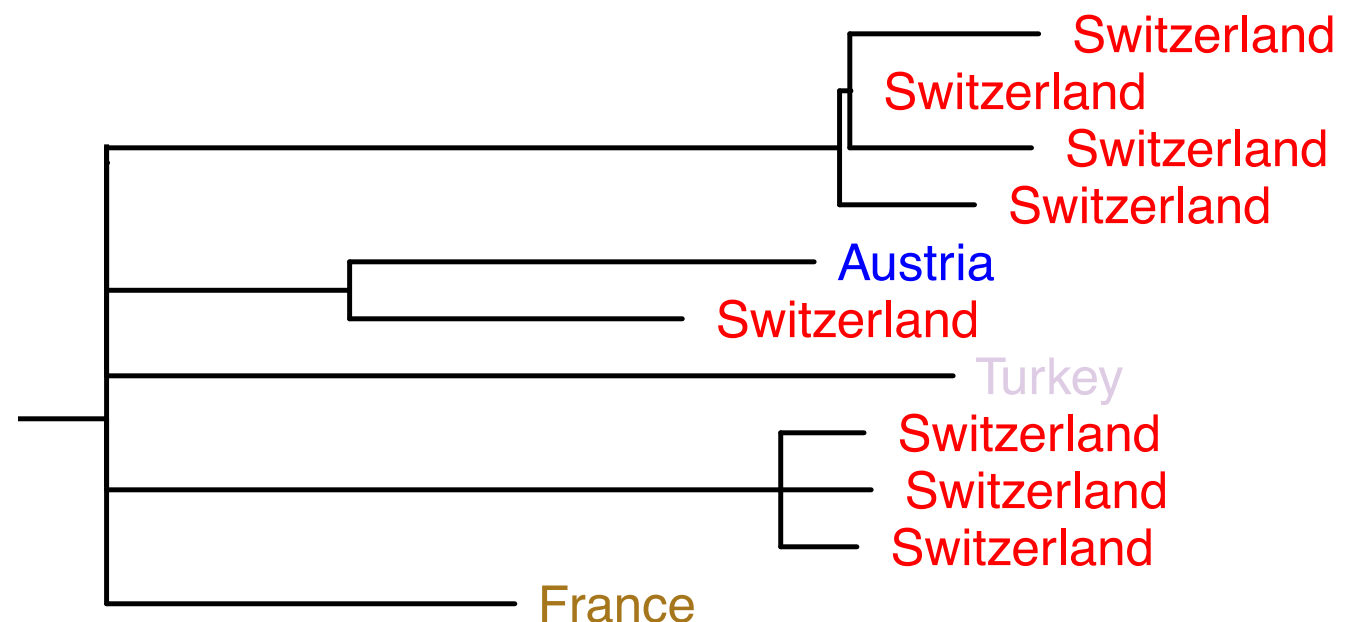
*with uncertainty

- We report under both extremes and compare/contrast

1 large chain

OR

3 smaller chains



Agenda

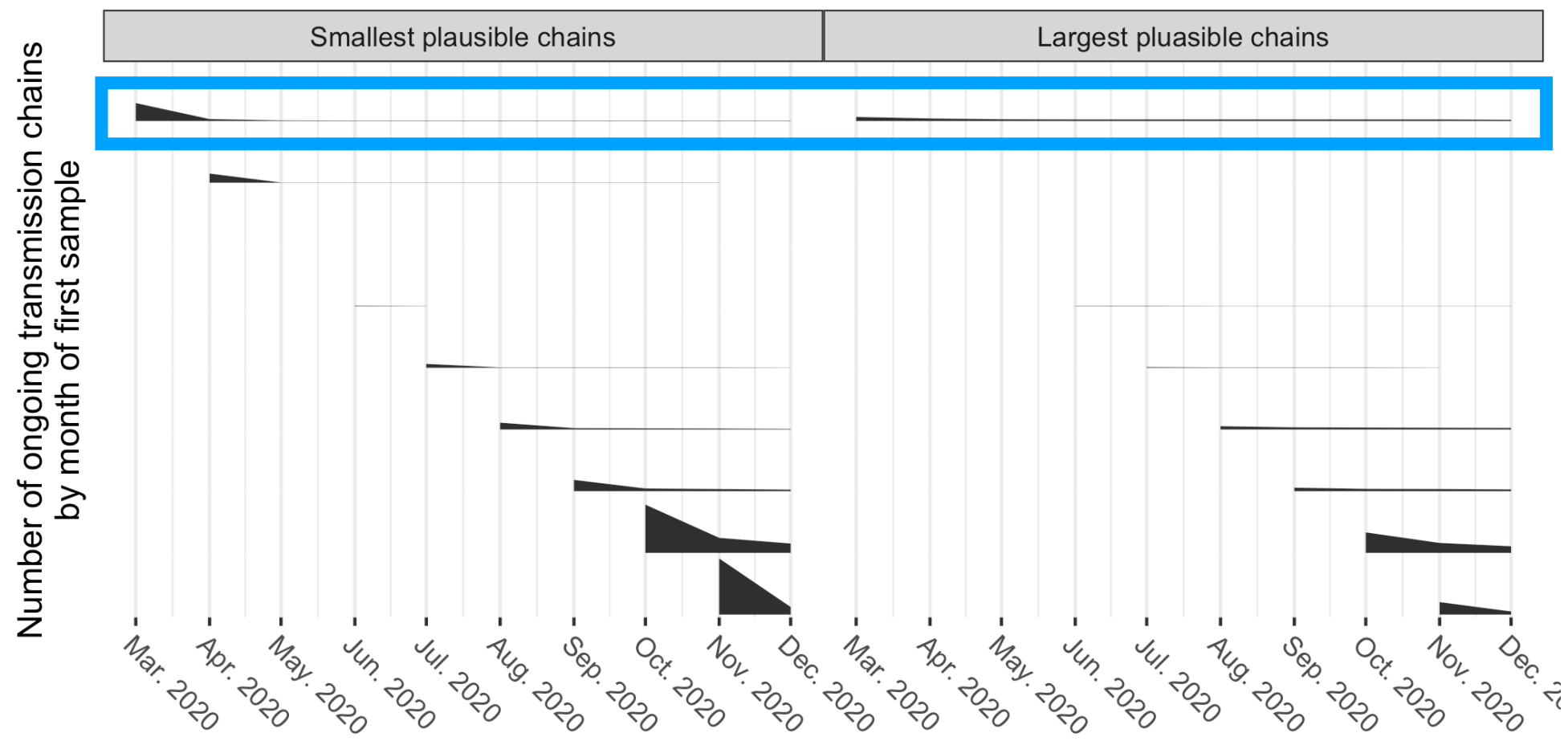
- Genomic epidemiology: definition and motivation
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- **Results:**
 - **Swiss transmission chains**
 - Estimating R_e from transmission chains

Swiss transmission chains

- 262 - 720 transmission chains until 31. December 2020
- 10 largest chains account for 33 - 50% of genome samples

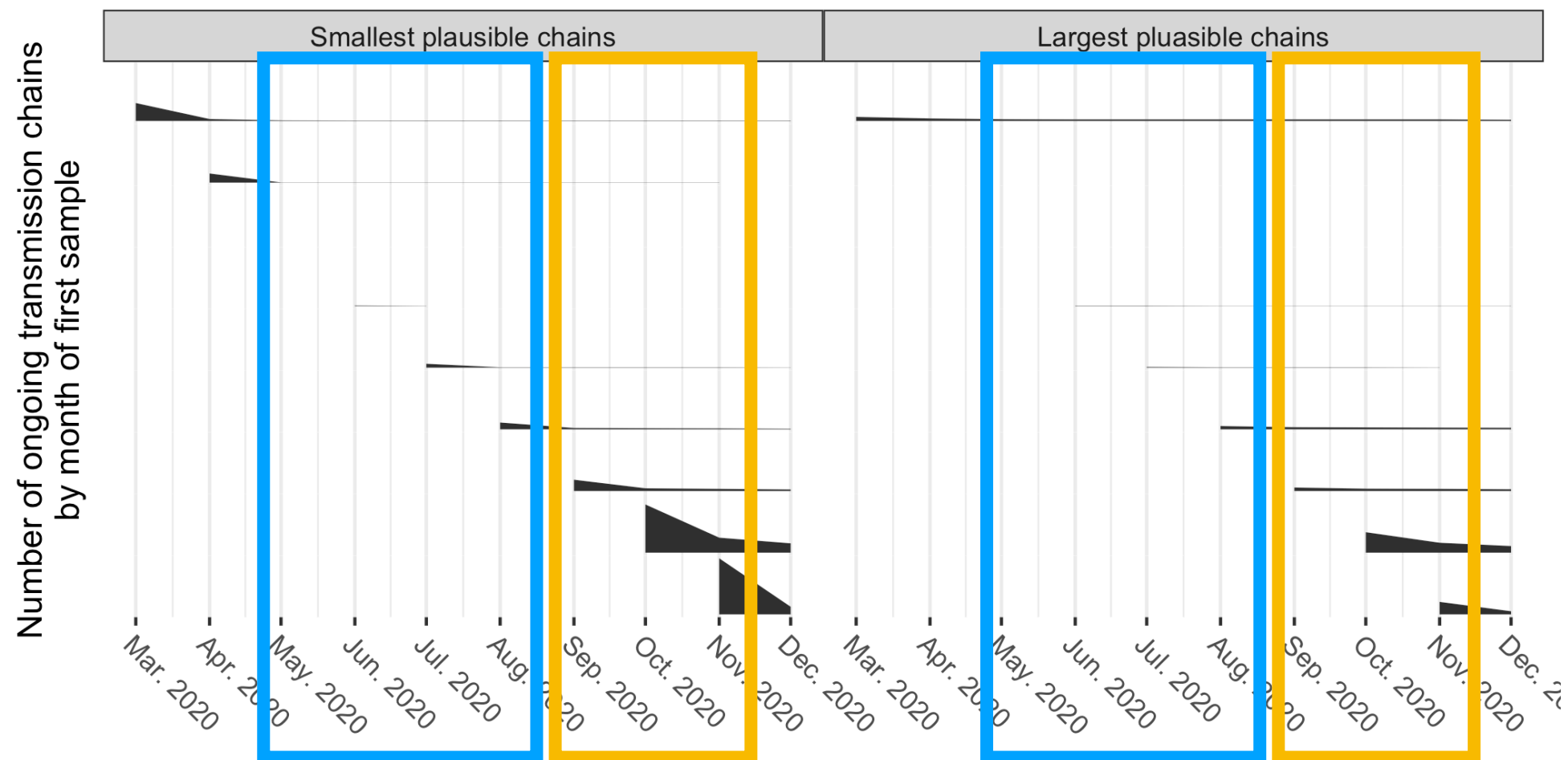
Swiss transmission chains

- 2 - 6 of the 21 - 92 transmission chains introduced in March continued spreading through December



Swiss transmission chains

- The spring border closures reduced the number of new introductions
- But new transmission chains were again sampled after the summer

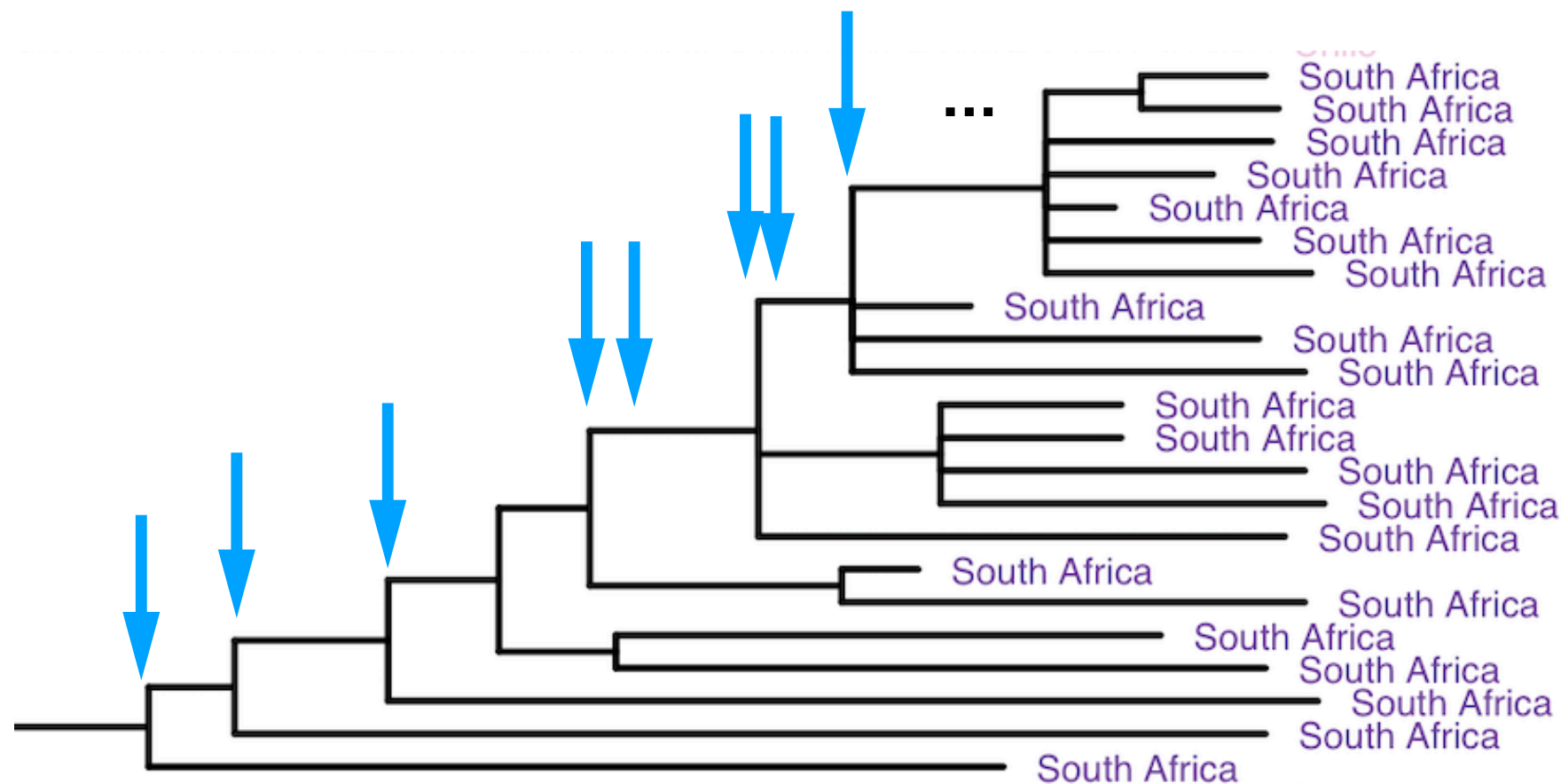


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- **Results:**
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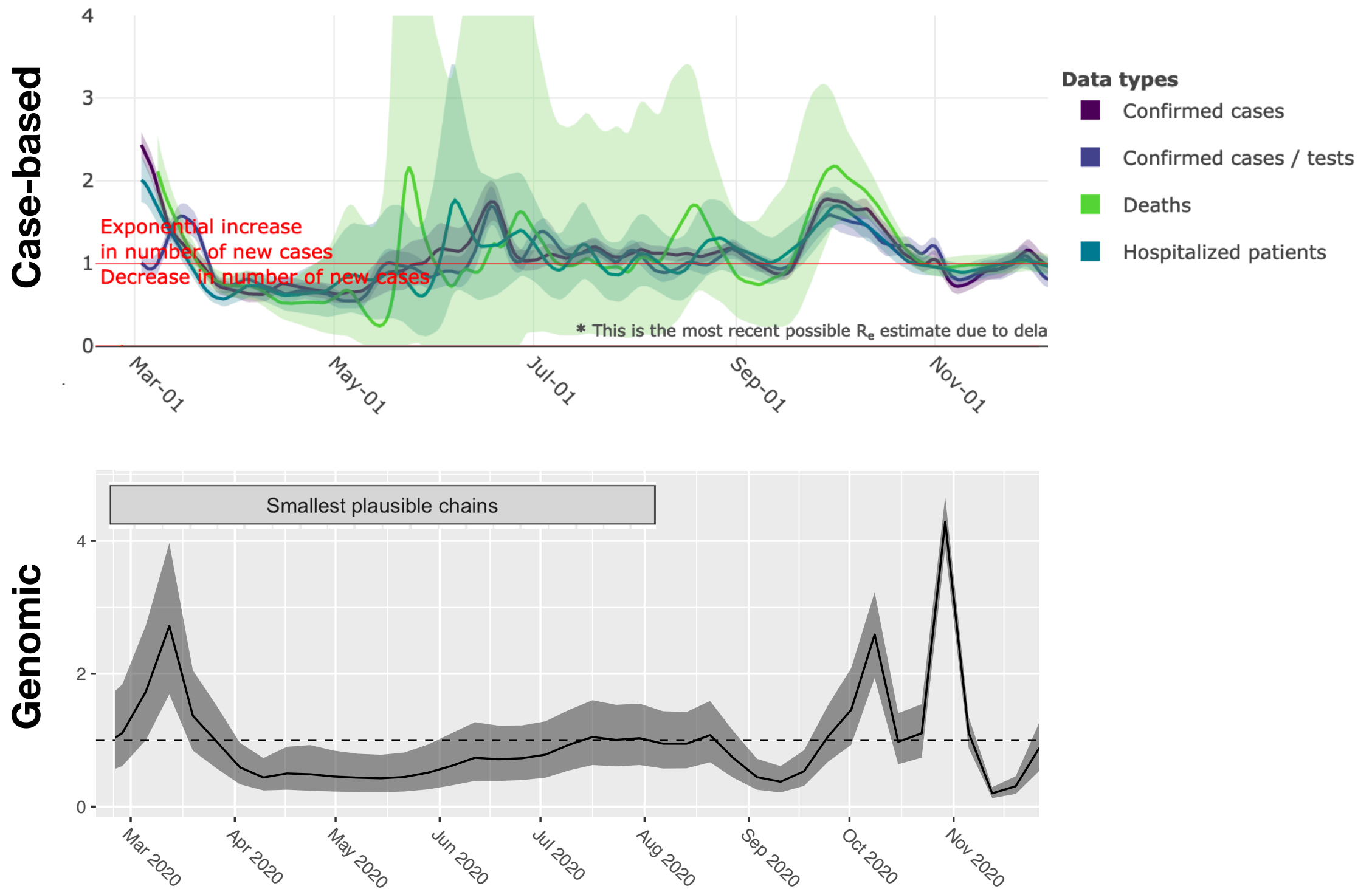
Estimating R_e from transmission chains

- Branching events correspond to sampled transmissions
- The distribution of branching times gives information on the transmission rate (and on the reproductive number)



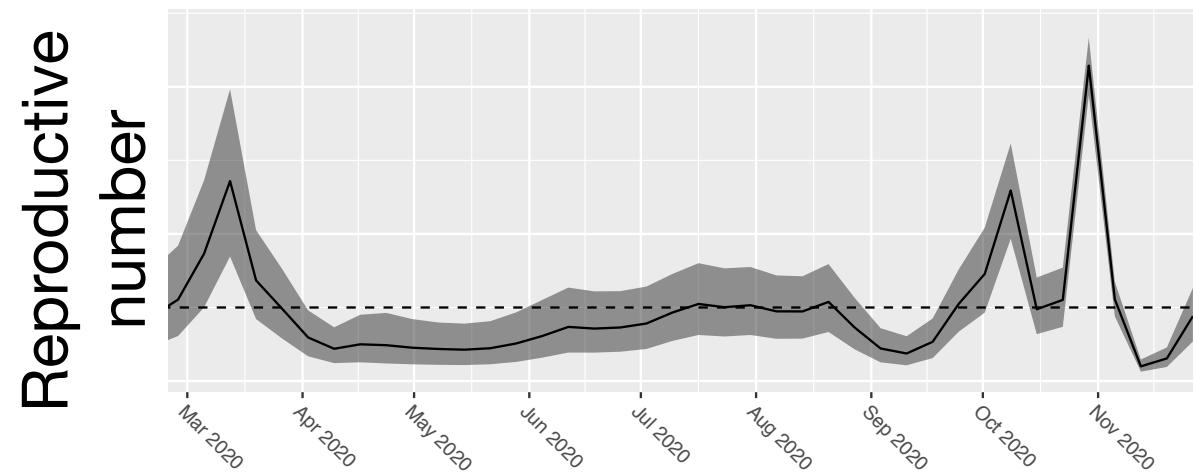
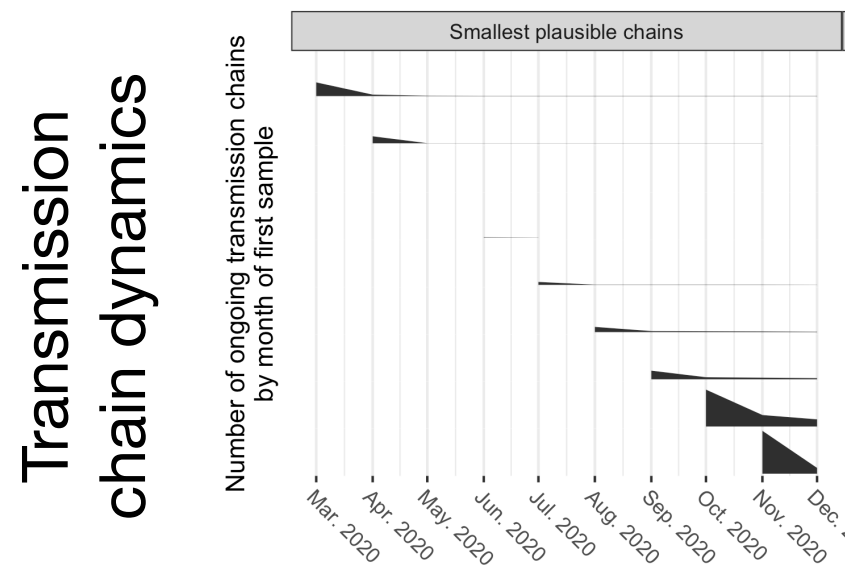
Genomic Re estimates roughly match case-based estimates

Reproductive number



Conclusion

- Genomic surveillance useful for:
 - Tracking variants of concern
 - Additional insights on epidemiological dynamics



Thank you

ETH*zürich*



Covid-19
National Research Programme

Swiss SARS-CoV-2 Sequencing
Consortium (S3C)

Particular thanks to:

- Chaoran Chen
- Timothy Vaughan
- Tanja Stadler

for analyses & input