Building a Sequencing Revolution: Enabling Research & Policy Through Diverse Tools

Emma B Hodcroft, PhD
ISPM, University of Bern
Sequencing has been key in the pandemic
Unprecedented Viral Sequencing!
How does that compare...?
Sequencing has been key to getting us where we are
Variants & Sequencing

- Previously: detected epi changes $\rightarrow$ mutational changes $\rightarrow$ impact
- Omicron: mutational changes $\rightarrow$ impact assessment & epi changes
Sequencing has been key to getting us where we are

- Vaccines
- Initial Spread
- Transmission
- Mutations
- Variants
Sequences are the raw material...

- Pandemic: beyond publications
  - Still important, but not informing real-time response!
Sequences are the raw material...

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- Revolution in analysis & information:
  - Enabling analyses is key (volume becomes an issue!)
  - Building new tools and resources is critical
  - Sharing and collaboration is essential
Tools that aid monitoring

- Dashboards breaking down variants, mutations

CoVariants.org

Outbreak.info
Tools to analyse

- Dashboards breaking down variants, mutations
- Phylogenetic analyses & QC
Tools to identify & discuss

- Dashboards breaking down variants, mutations
- Phylogenetic analyses & QC
- Real-time integration of publicly identified lineages
Resources to build on other work

- Dashboards breaking down variants, mutations
- Phylogenetic analyses & QC
- Real-time integration of publicly identified lineages
- Intermediate data, collaborative lists of bad sequences or bad sites

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github.com/nextstrain/ncov/defaults/exclude.txt

github.com/W-L/ProblematicSites_SARS-CoV2
Everyone has different analysis questions and needs

- This is a strength! 💪
  - If we can empower them
  - If we can build on different strengths & perspectives
  - If we can combine and share analyses and outcomes

In a world of diverse pathogens - need diverse tools and approaches to enable analyses!
nextstrain - Enabling Analyses

Providing open-source software to allow researchers to do custom phylogenetic analyses

- Start of pandemic: set up SARS-CoV-2-specific workflow
- Has made pandemic phylogenetic analysis accessible to large community
- Tutorials, weekly office hours
- Community interaction & feedback
- Used by hundreds of independent labs worldwide - US CDC, Africa CDC
Looking forward 🕵️

- How do we empower appropriate surveillance?

Graphic thanks to Cornelius Römer
Looking forward

- How do we empower appropriate surveillance?
  - Both for current pandemic and for endemic diseases!
    - All countries can benefit from sequencing & analysis
    - Better understanding of all viruses is best preparation
Looking forward 🪤

- Not just about sequences - but how we use them!

- How to we empower researchers to analyse their own data?
  - To answer the questions that matter to them, in their setting!

- How do we empower better & diverse tool development?
  - For true ownership of sequences & the information from them!

Thank you!

Sequence generators

Tool developers  Data analysists  Researchers