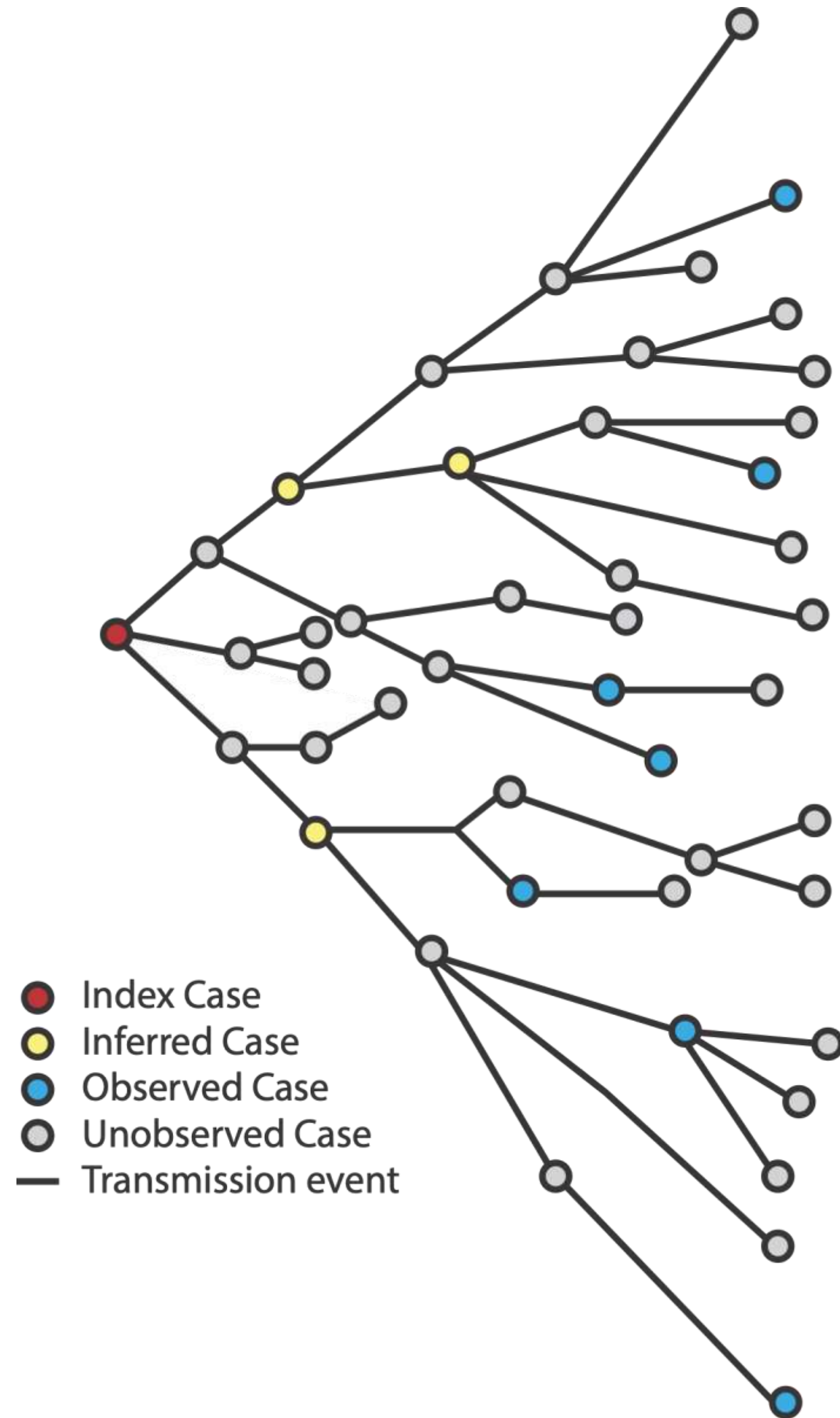


A wastewater-integrated, global virus genomic surveillance framework

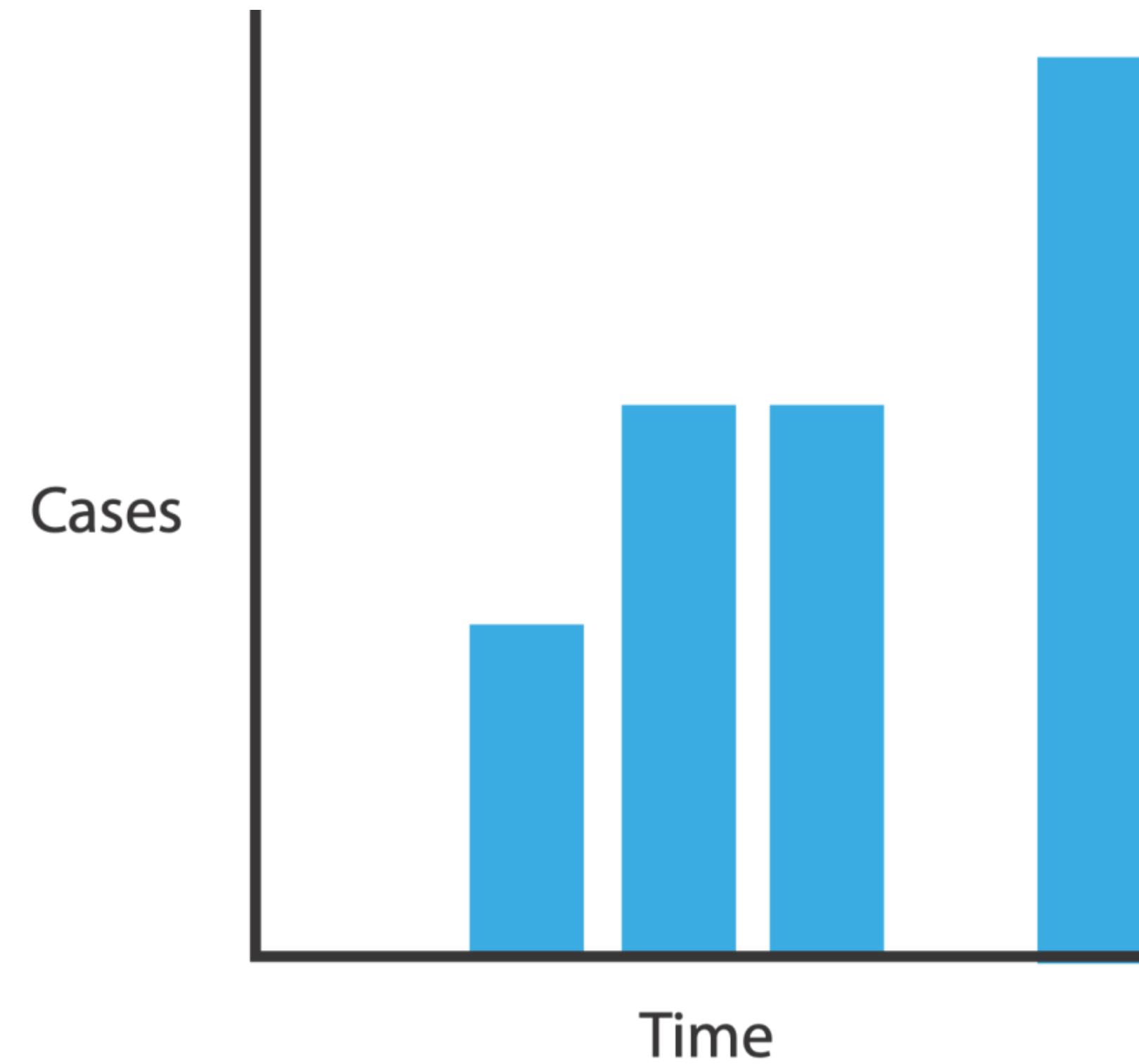
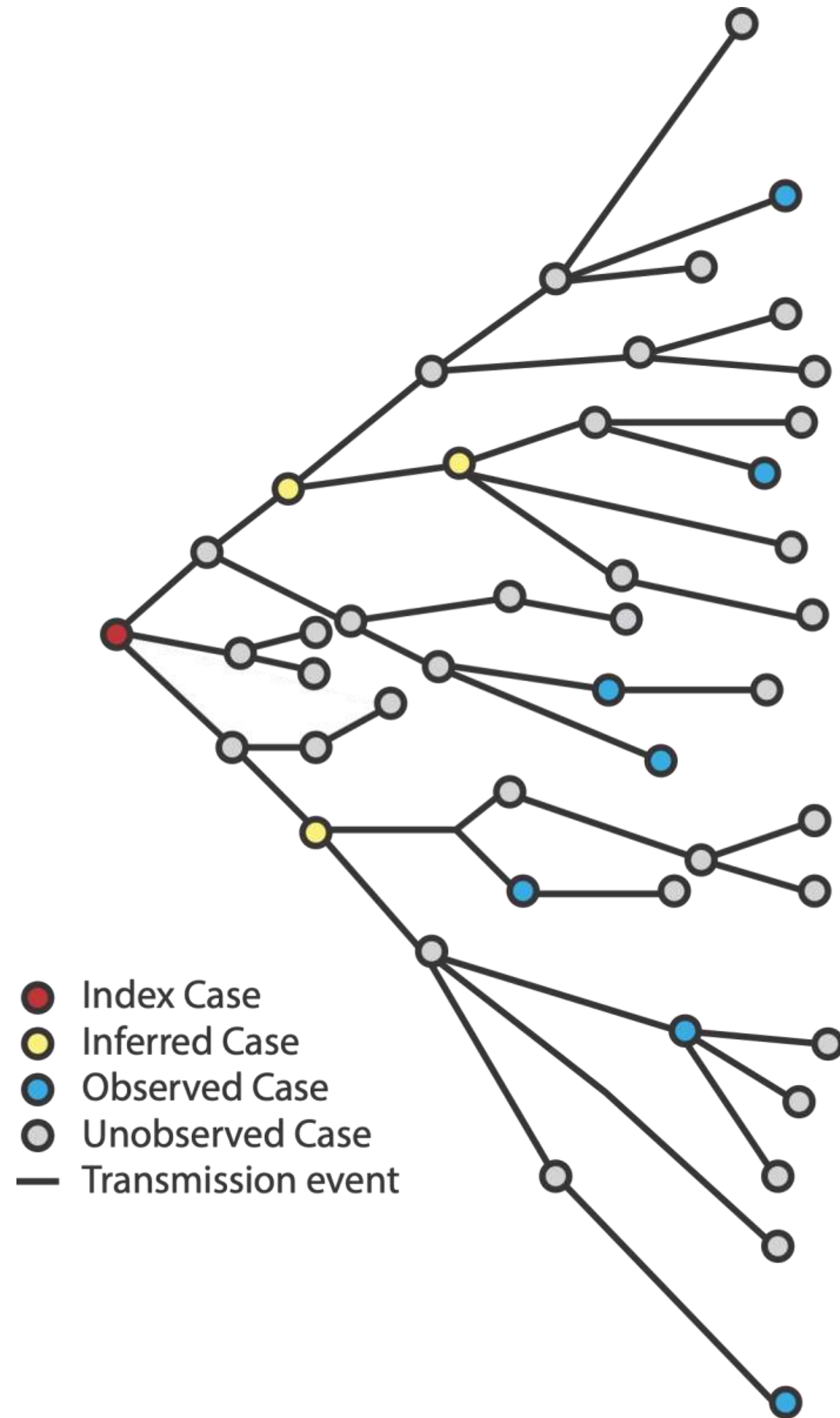
IDM Annual Meeting



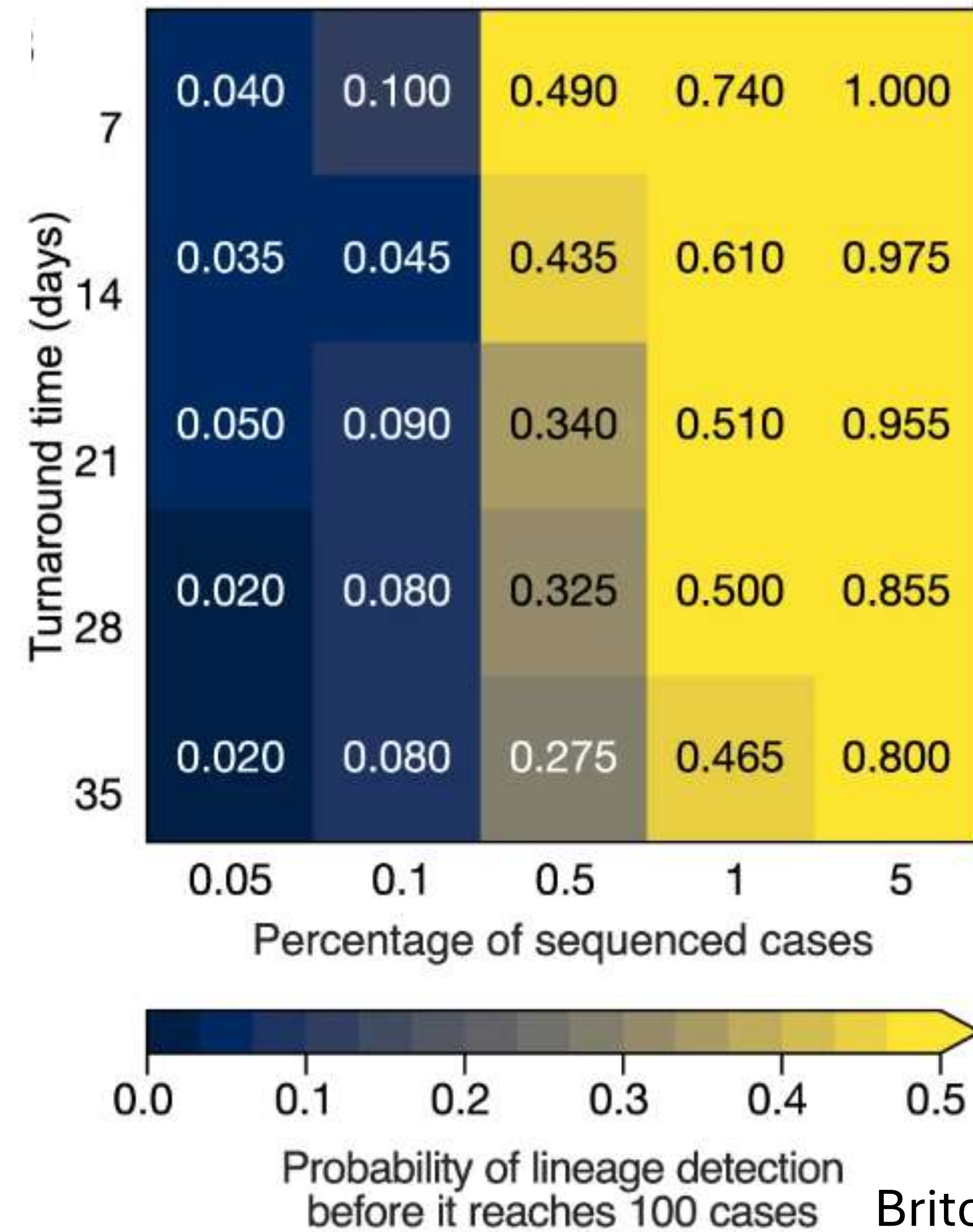
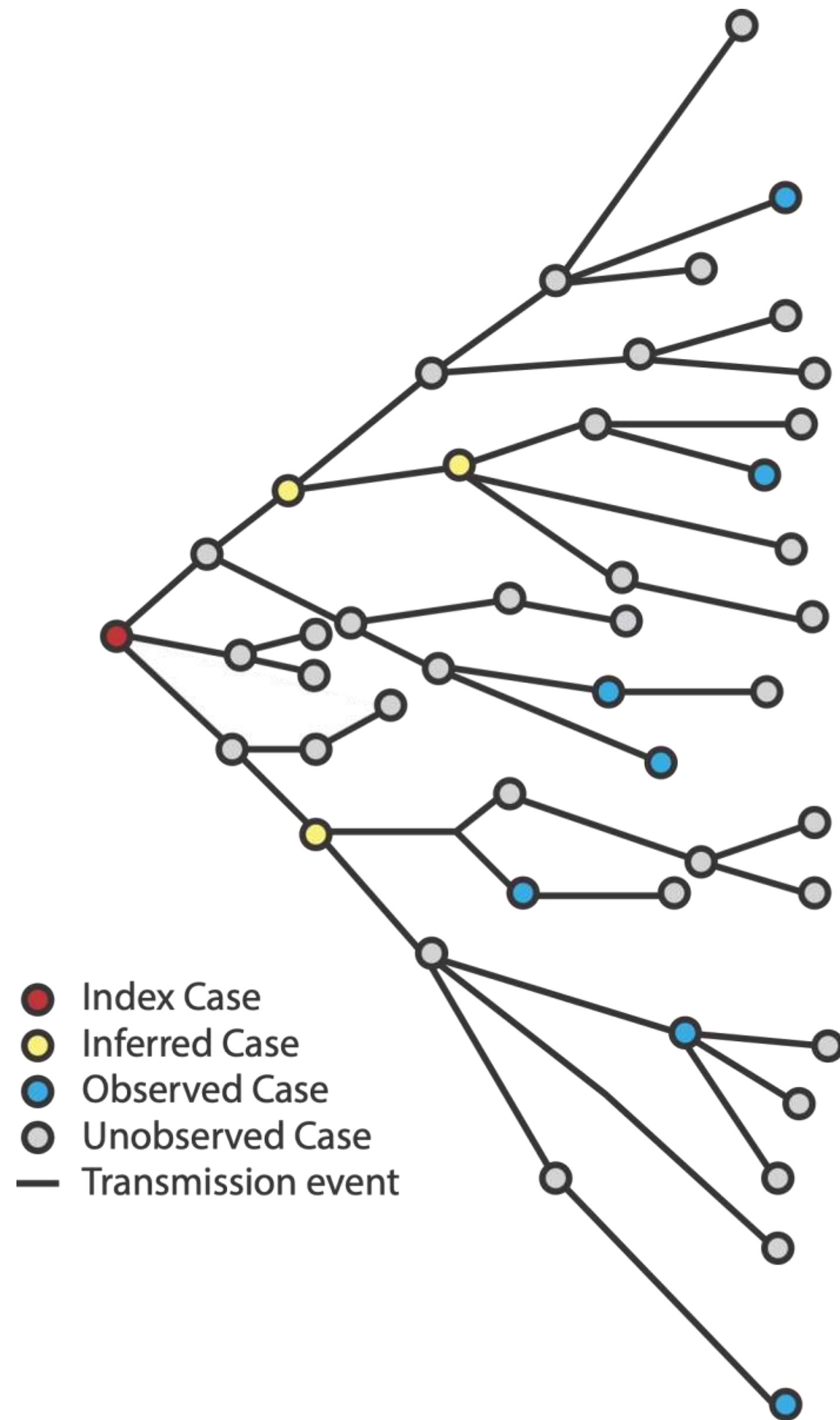
How we track viruses: case-based, clinical surveillance



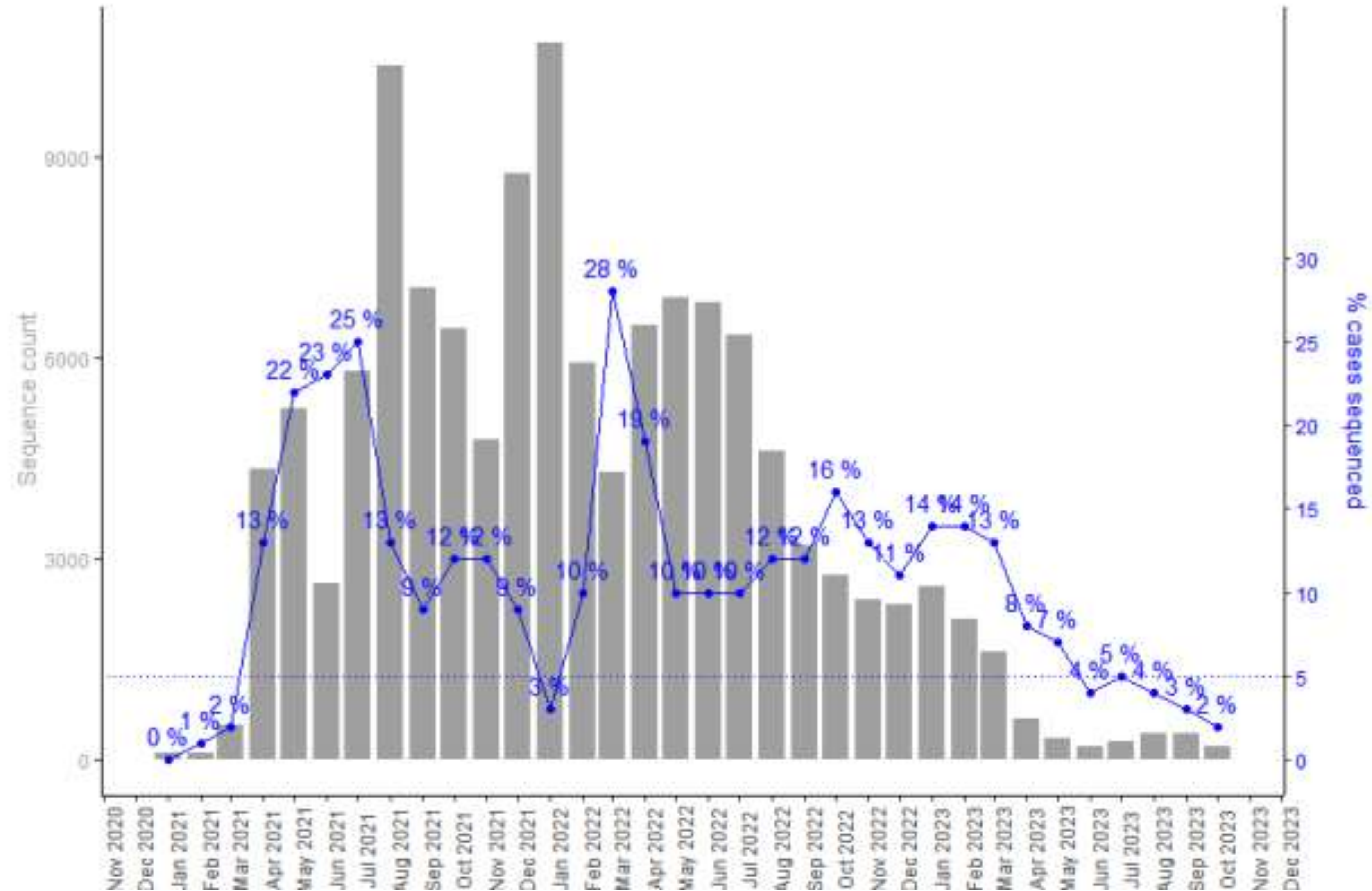
How we track viruses: case-based, clinical surveillance



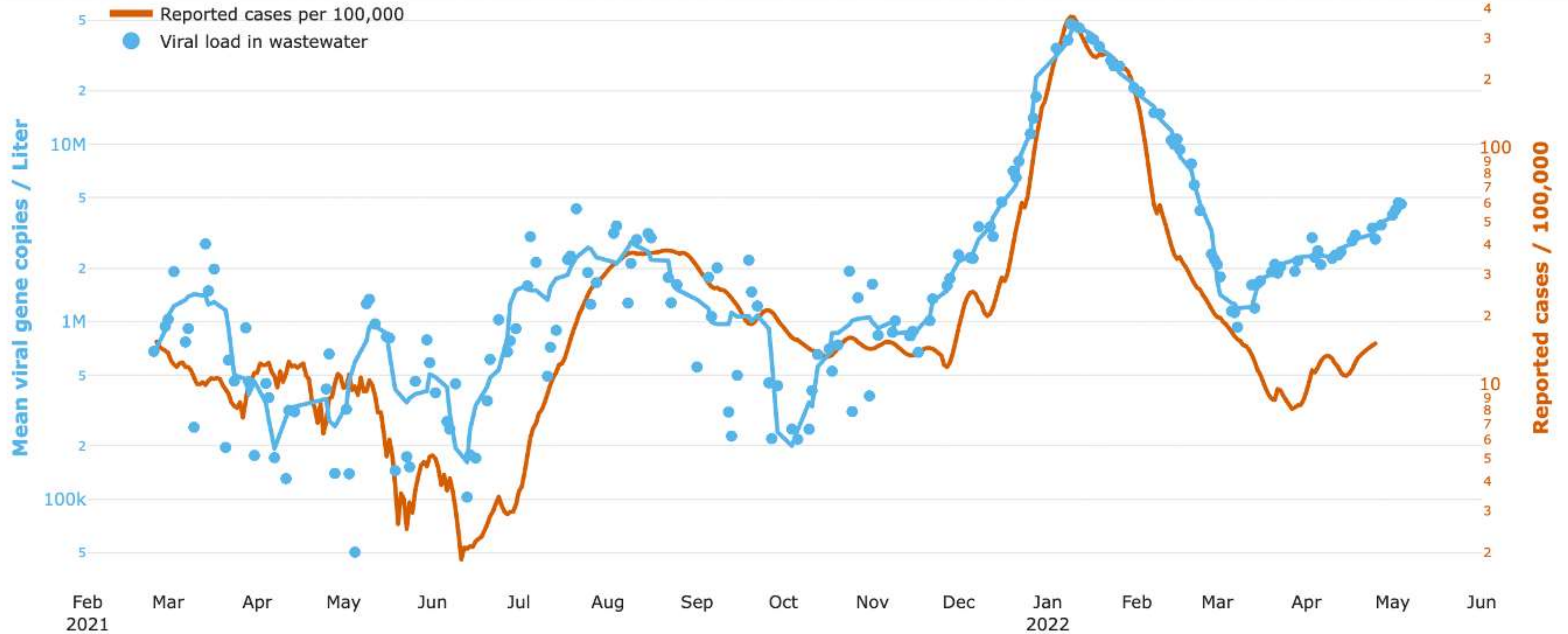
How we track viruses: case-based, clinical surveillance



Under baseline conditions, few samples are sequenced



Wastewater provides an alternative data source



Wastewater presents an alternative data source



Efficient

- Cost-effective
- Low-effort sample collection
- Only small changes to lab workflows

Comprehensive

- Community-wide representation
- Limits sampling bias
- Potential to track pathogen lineage dynamics through sequencing

Wastewater presents an alternative data source



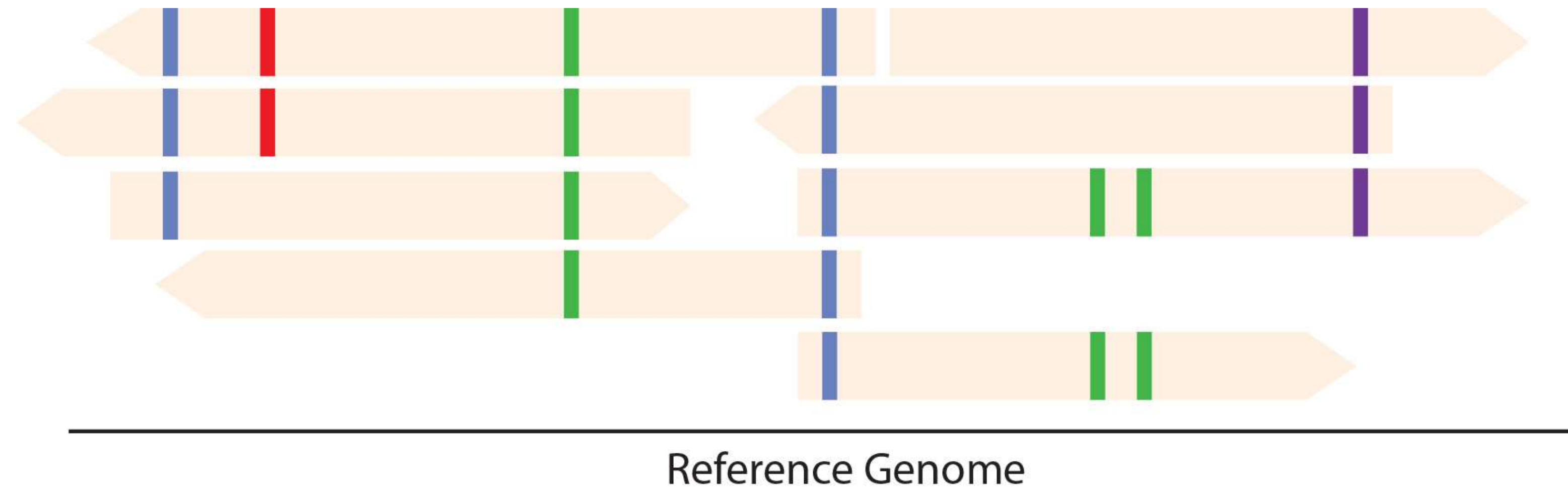
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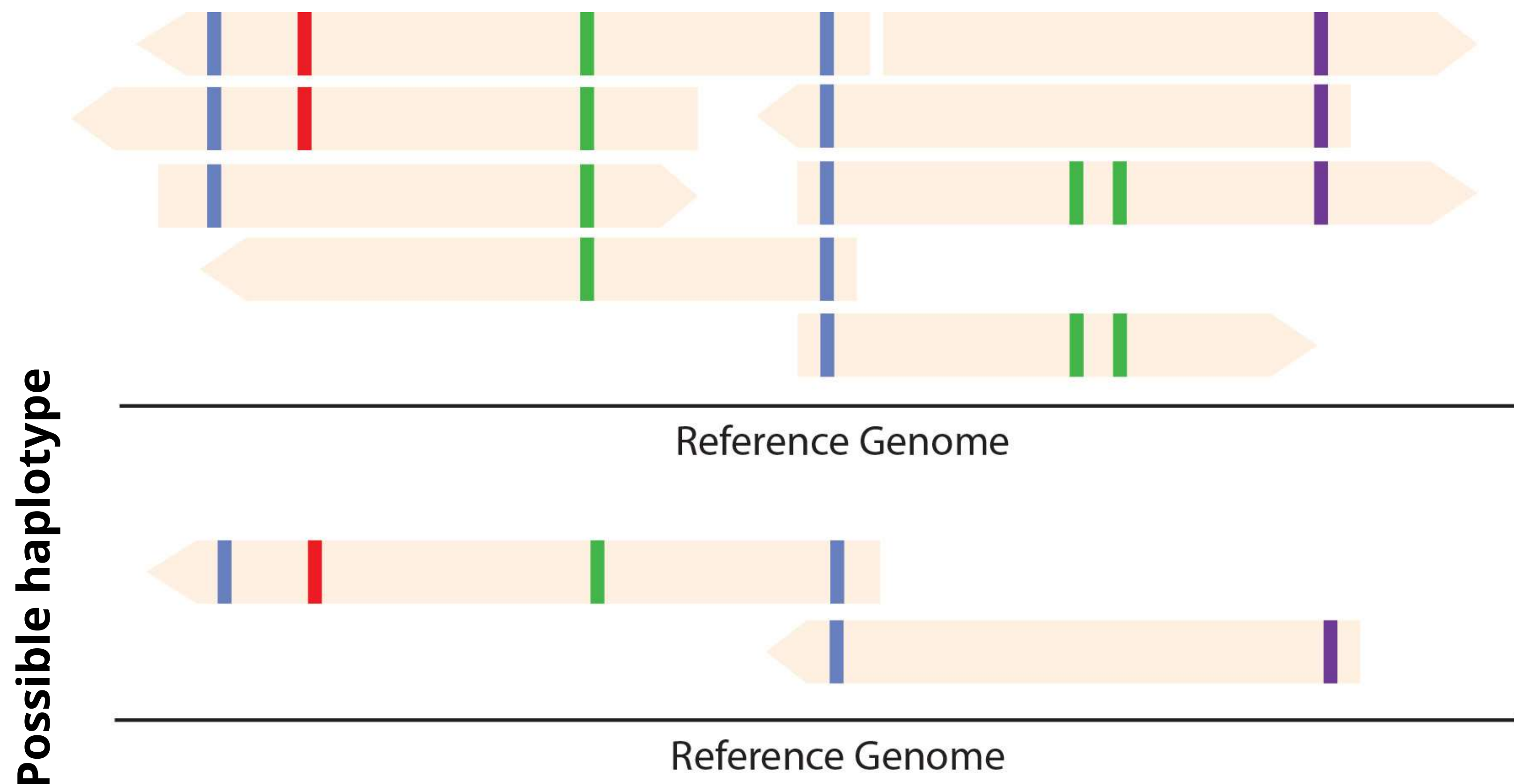
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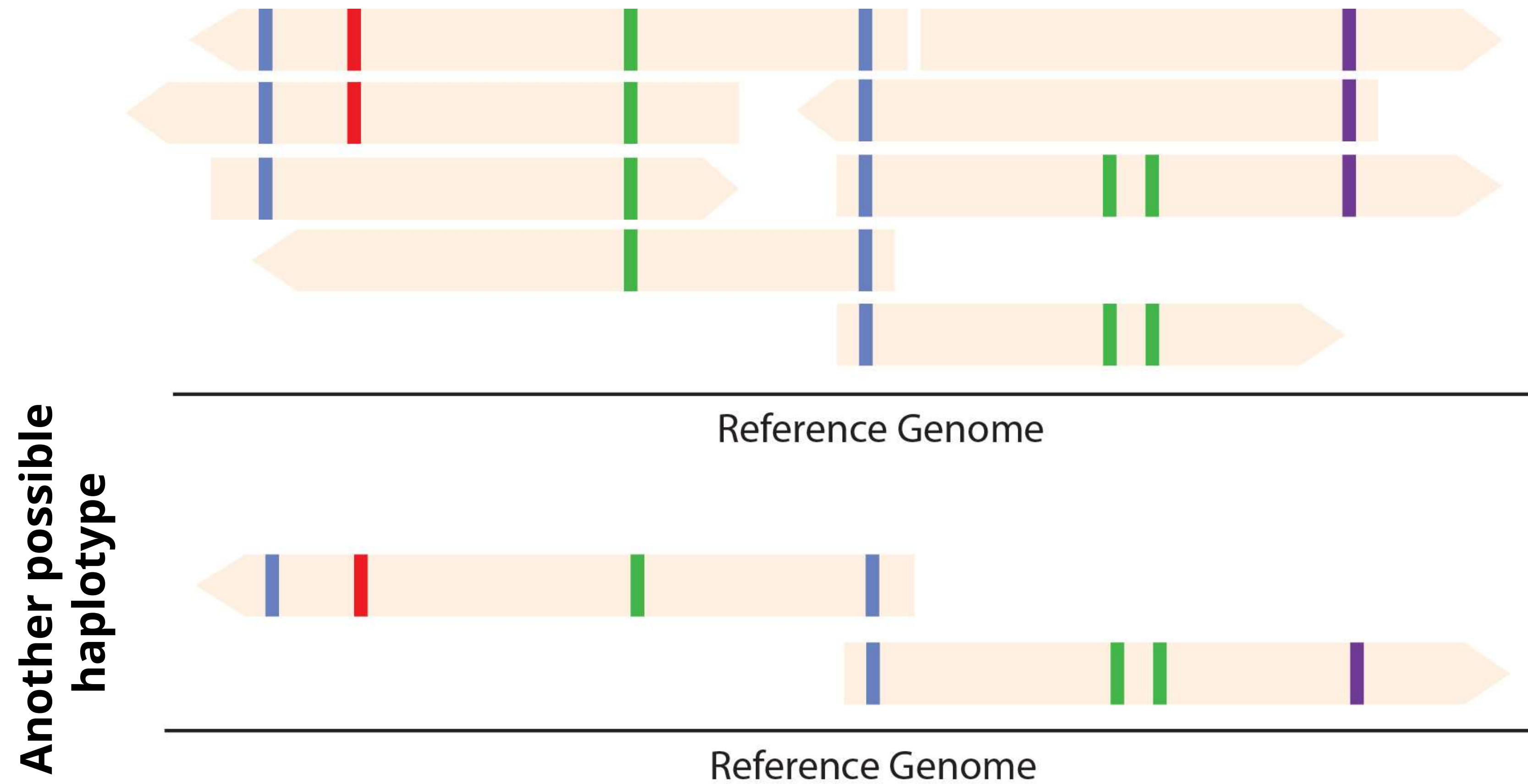
Problem: genome assembly fails for mixed virus samples



Problem: genome assembly fails for mixed virus samples

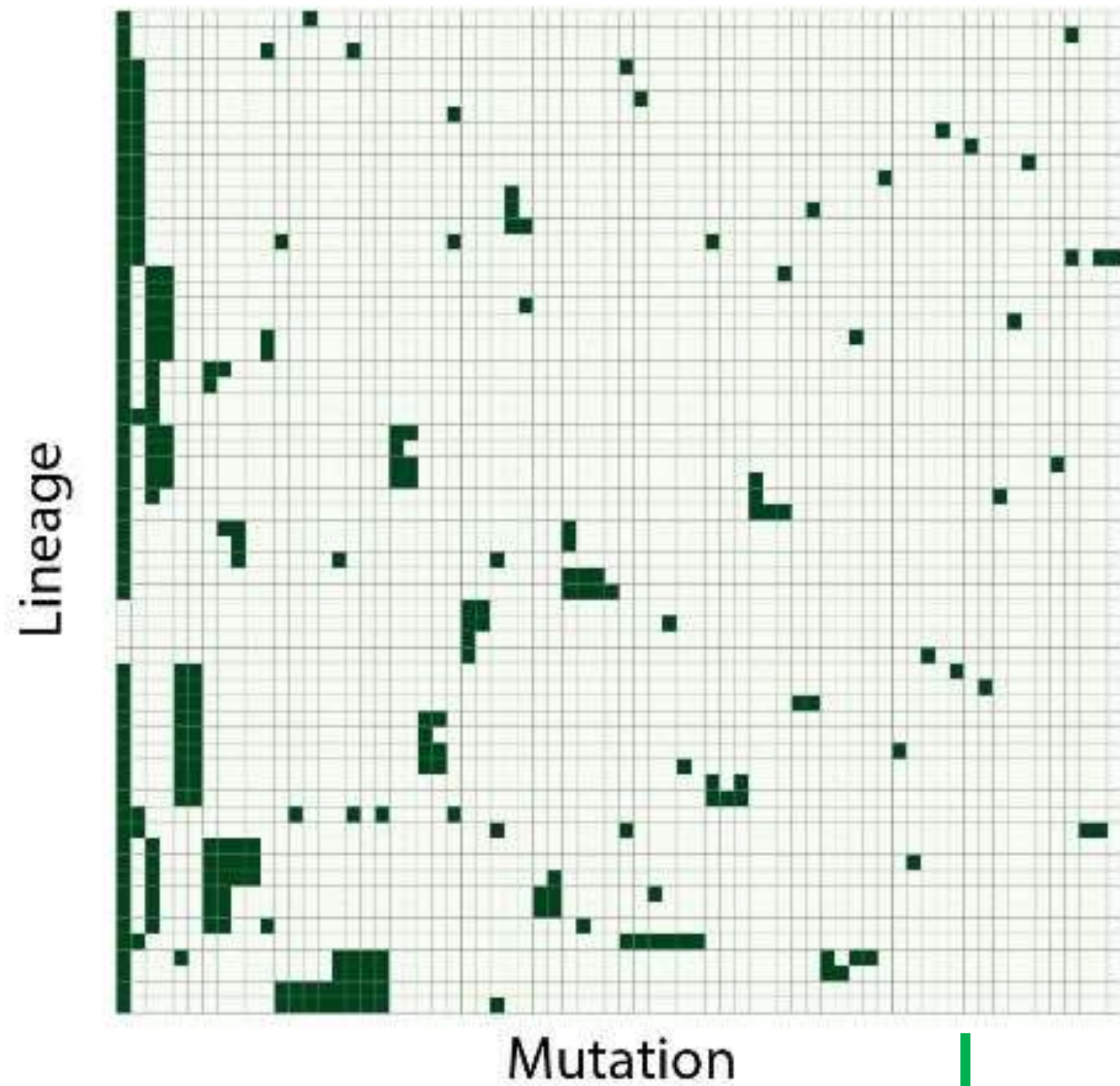


Problem: genome assembly fails for mixed virus samples



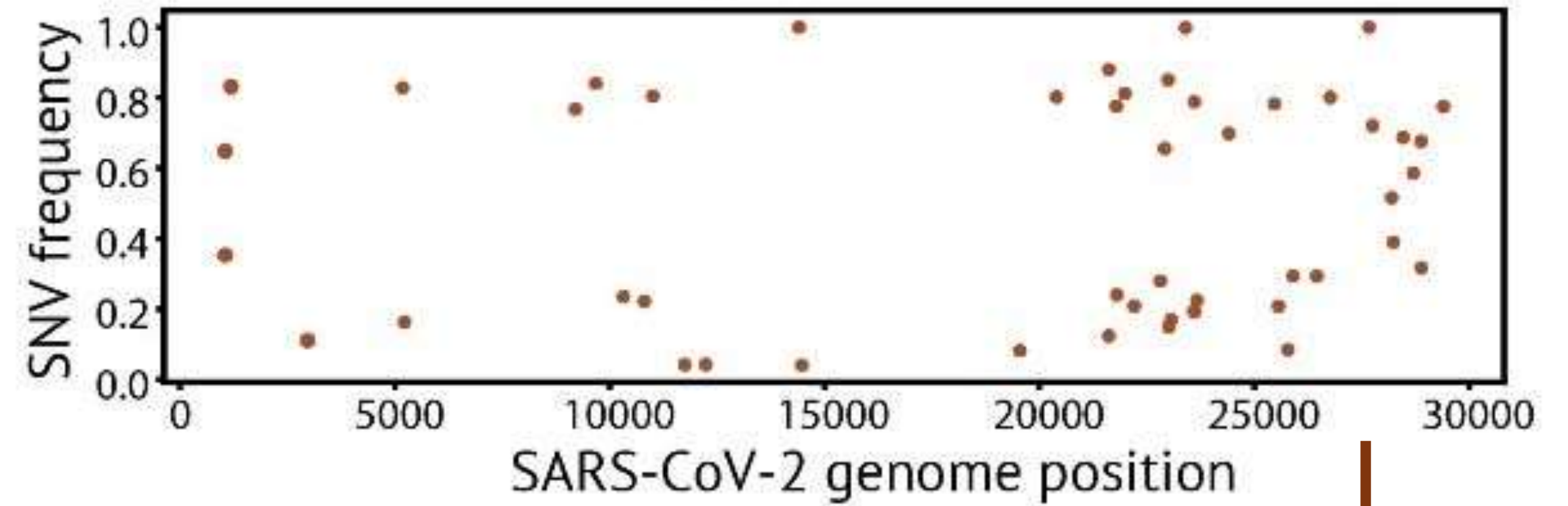
Need another approach to recover evolutionary dynamics from mixtures

Lineage Barcoding



> 4000 SARS-CoV-2 lineages

Detection of Single Nucleotide Variants

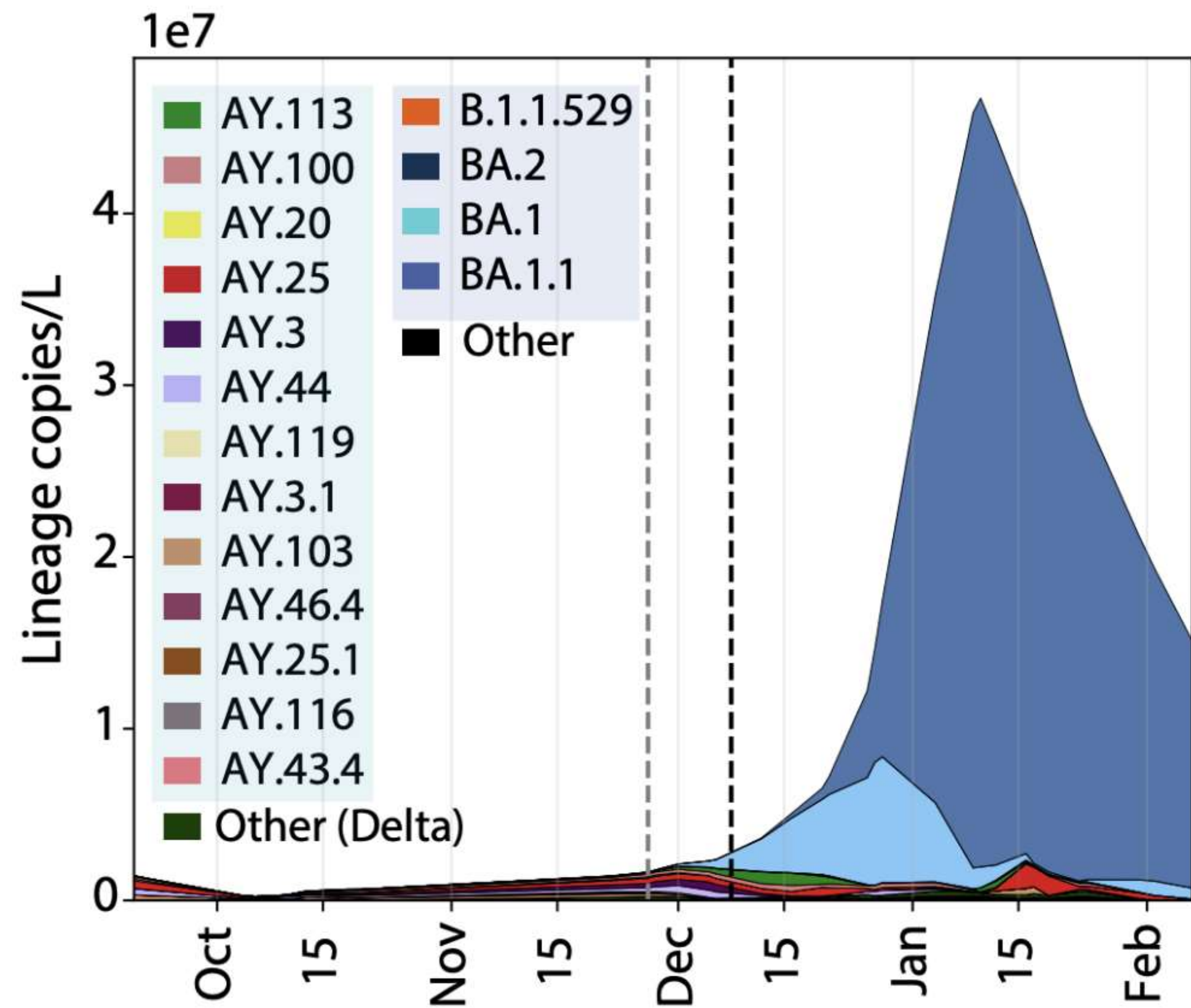
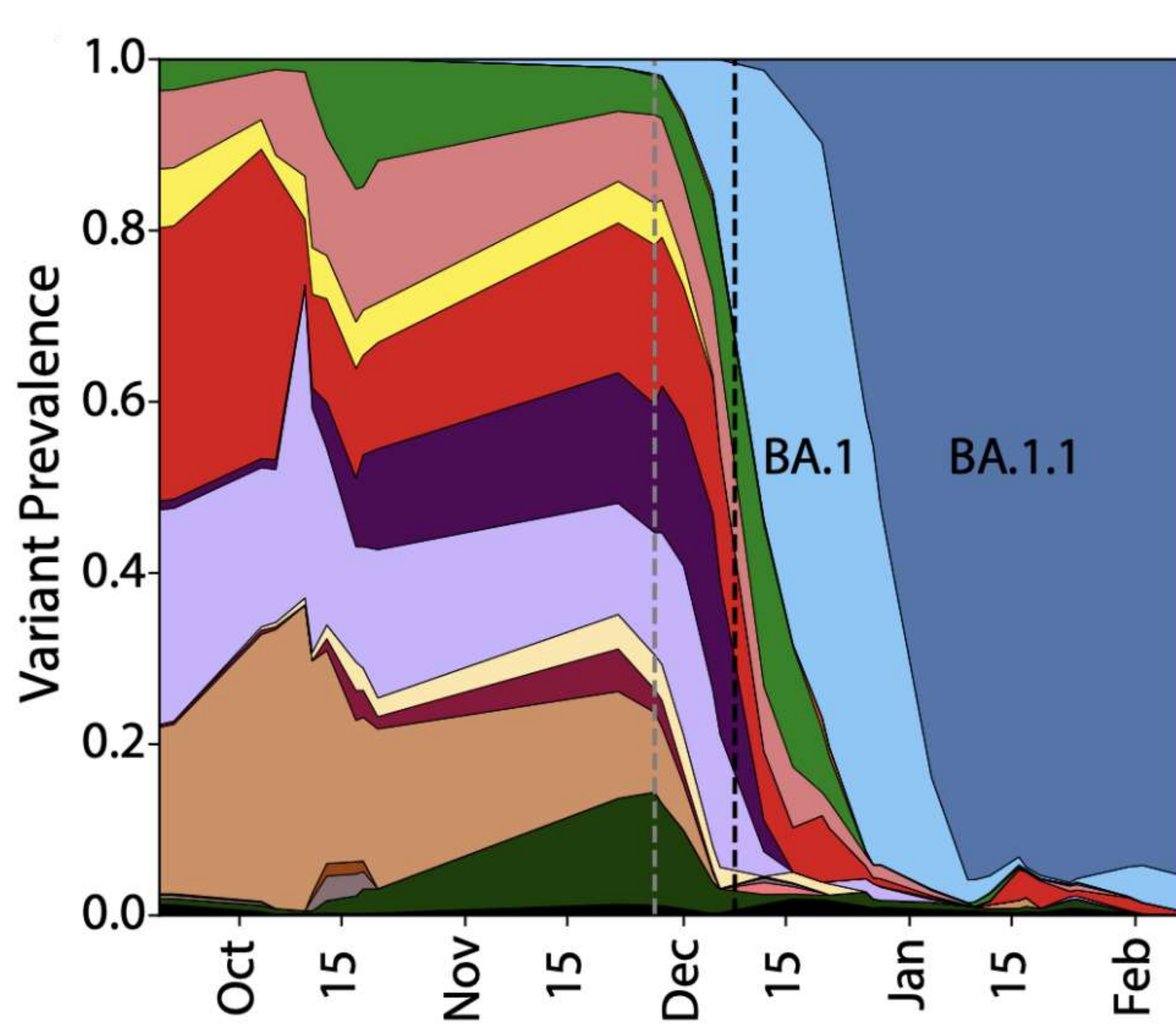


Depth-weighted de-mixing

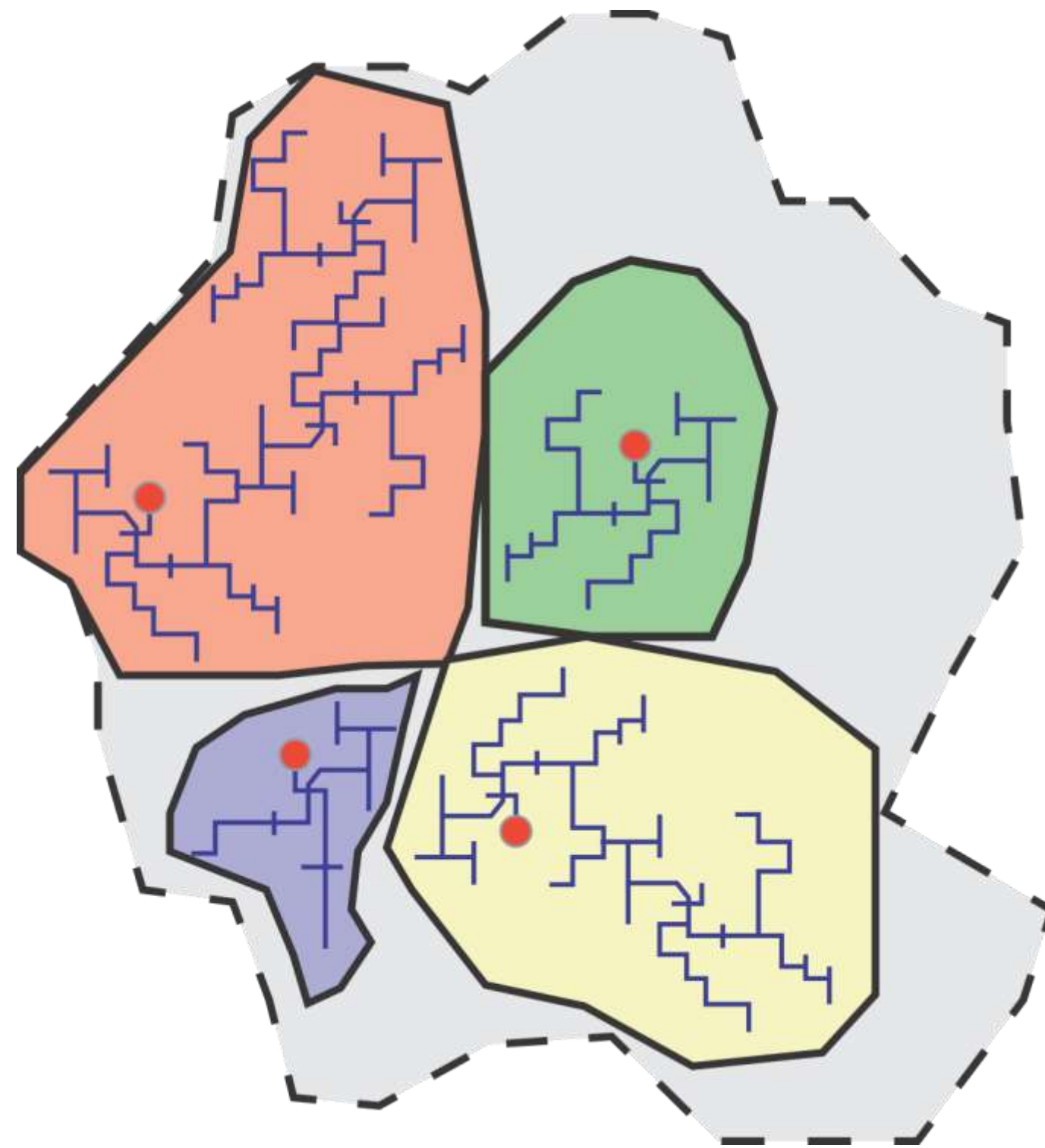
$$\hat{x} = \underset{\substack{x \geq 0 \\ \sum_{x=1}}}{\text{argmin}} ||A^T x - b||_{1W}$$



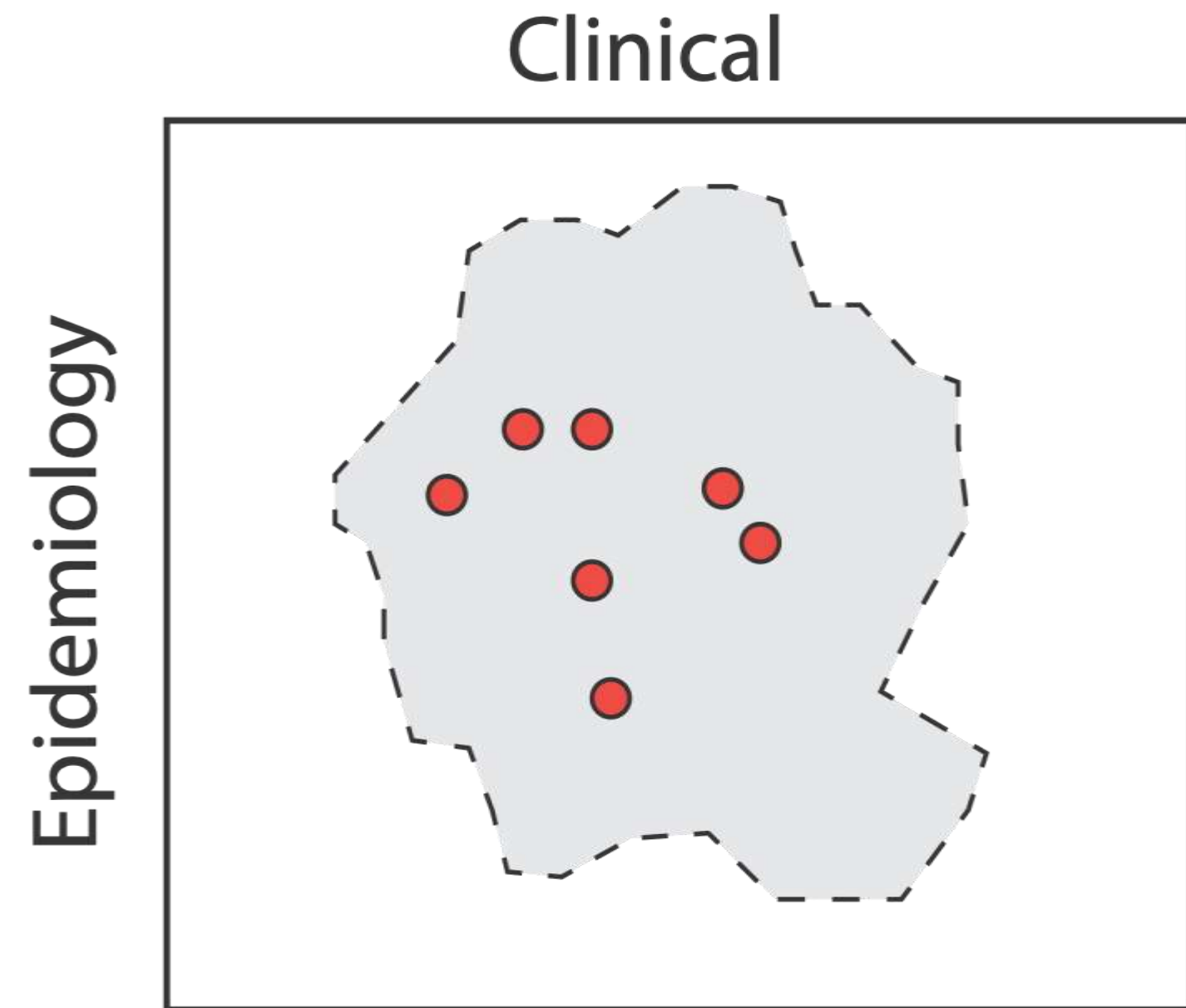
Freyja-enabled surveillance: Omicron in San Diego



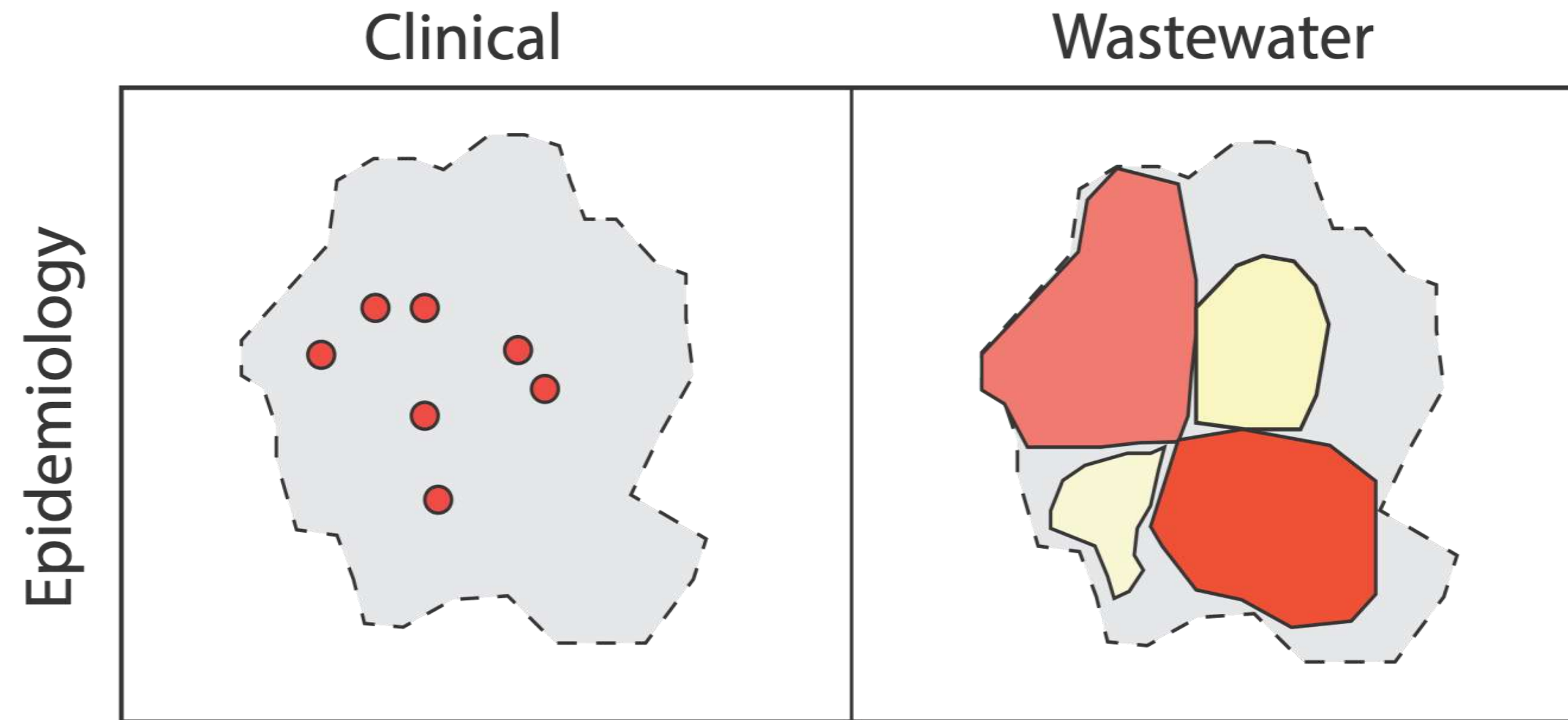
Integrated surveillance: An example region



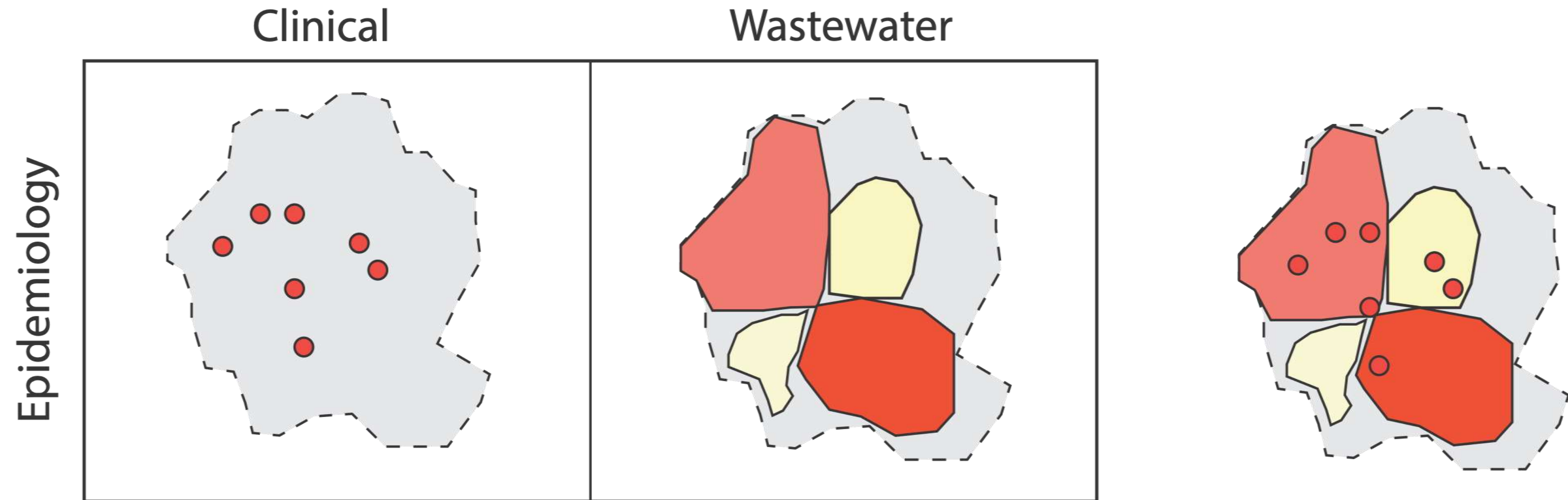
Wastewater enables comprehensive, robust



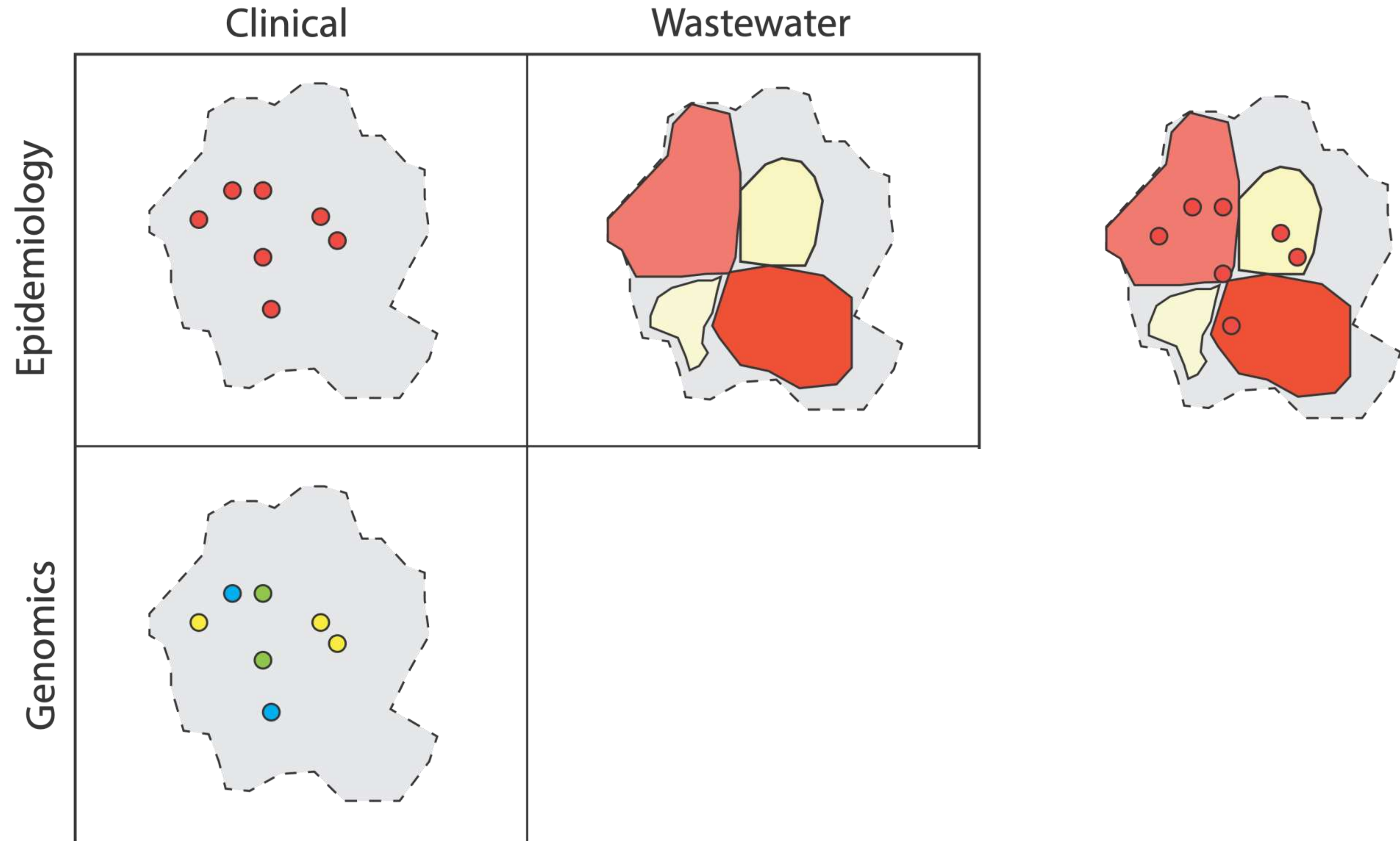
Wastewater enables comprehensive, robust



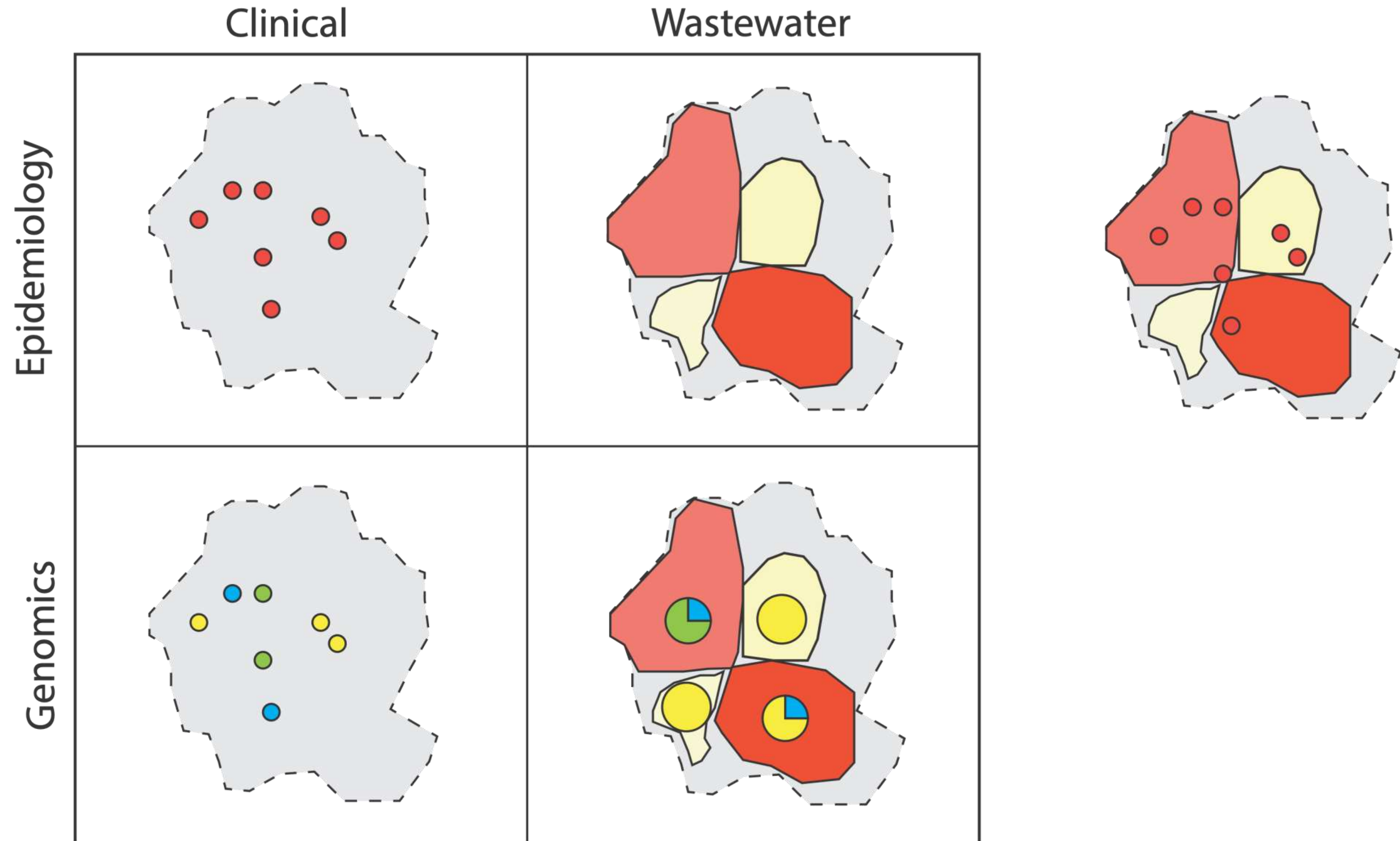
Wastewater enables comprehensive, robust



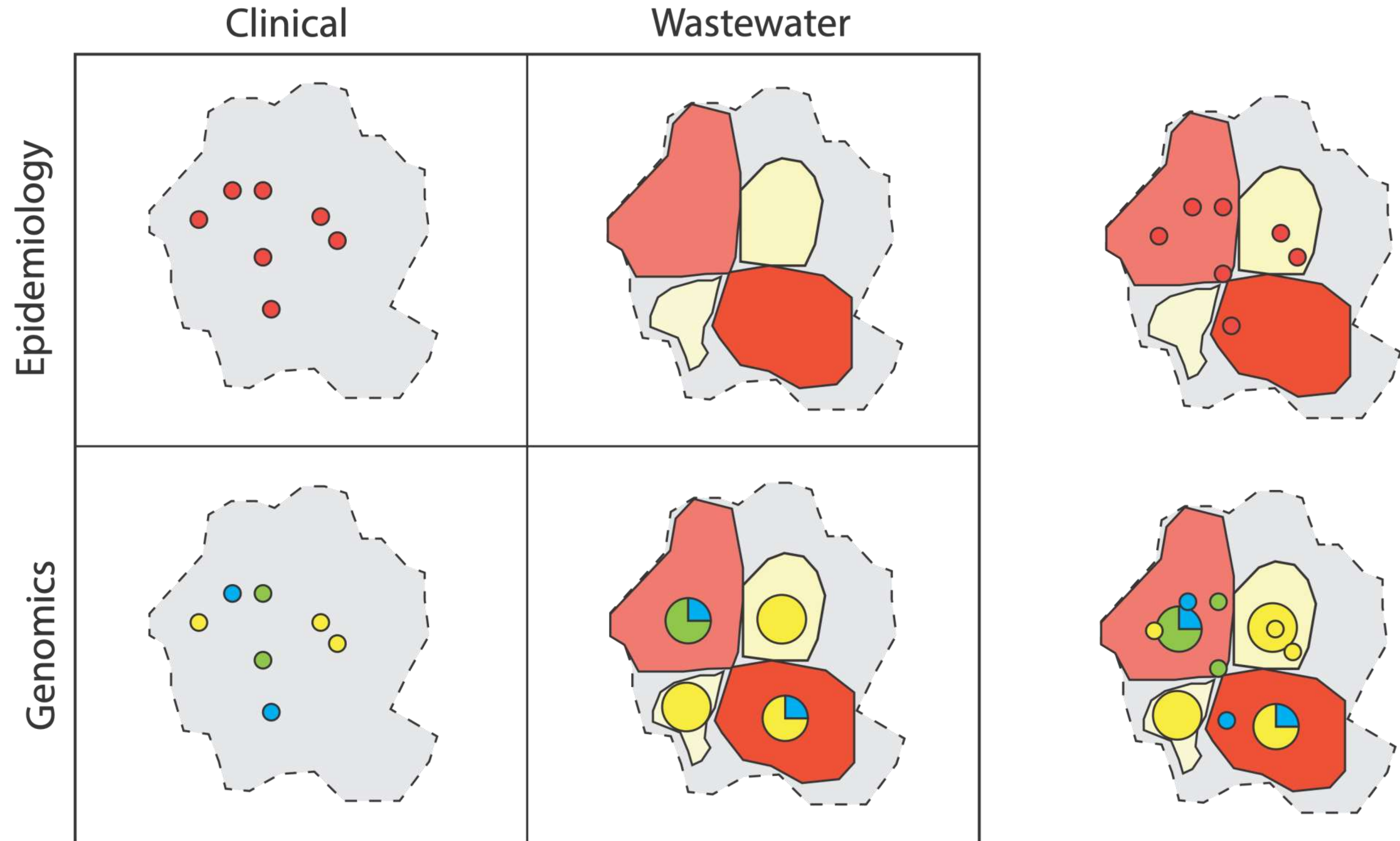
Wastewater enables comprehensive, robust



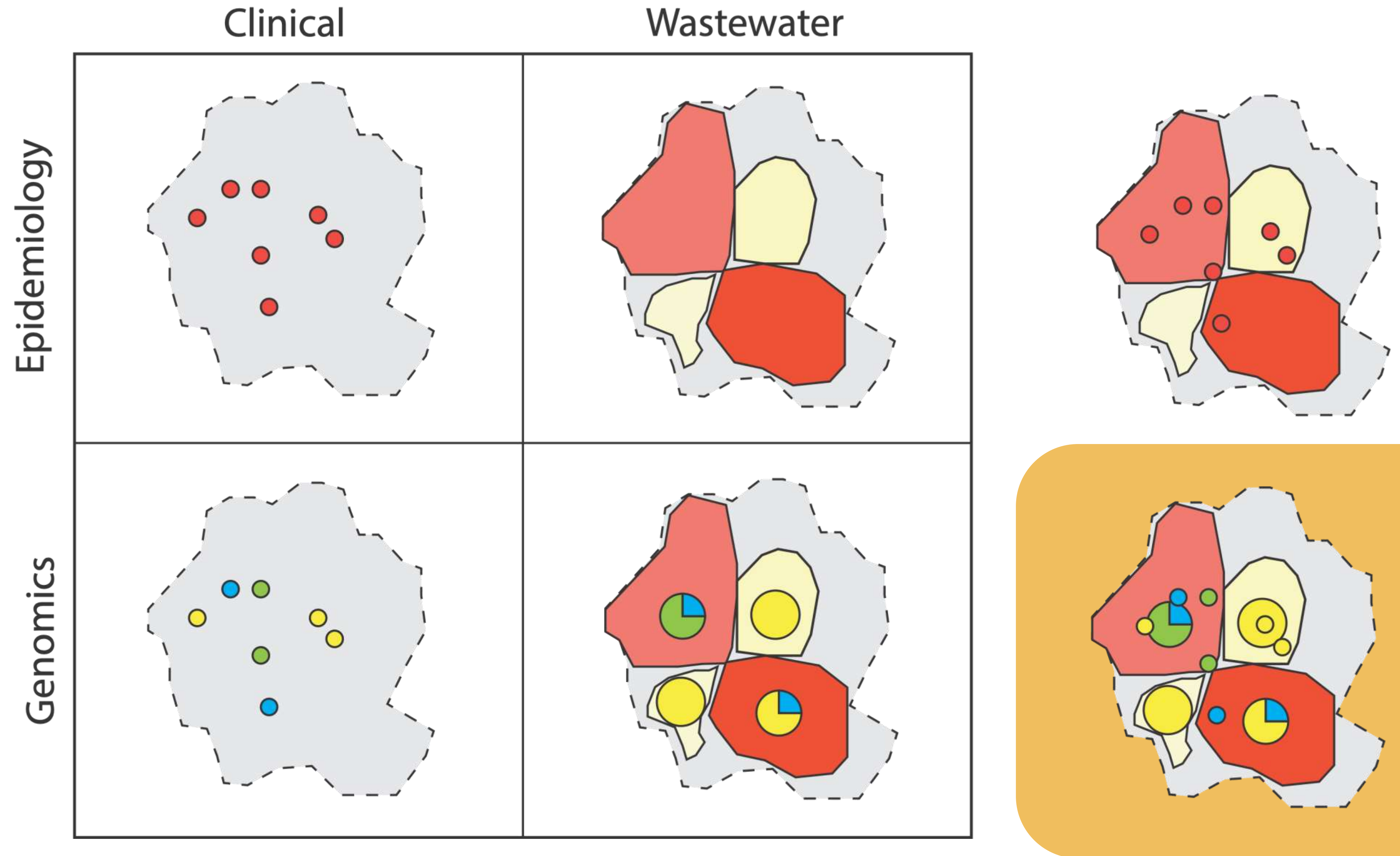
Wastewater enables comprehensive, robust



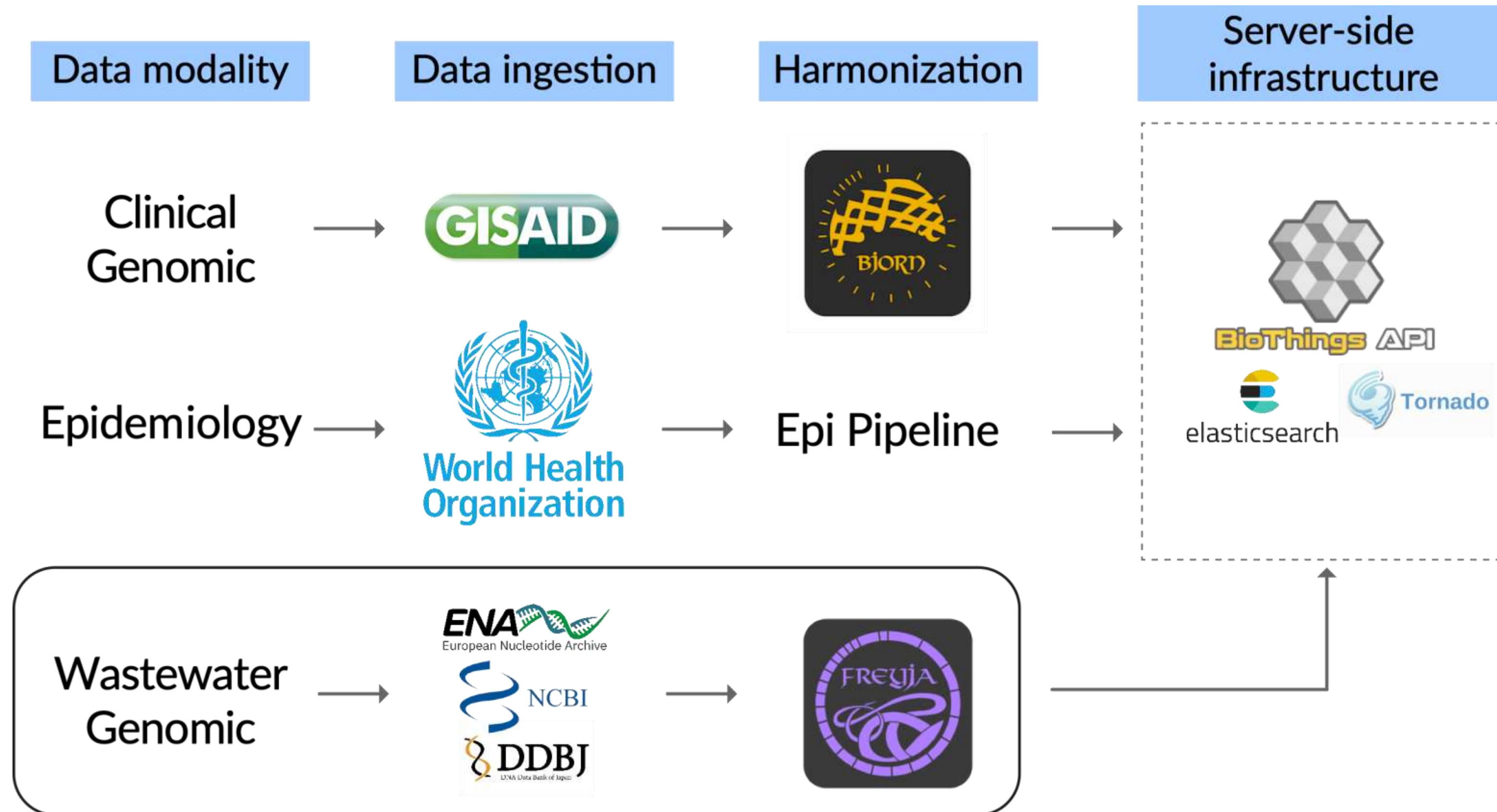
Wastewater enables comprehensive, robust



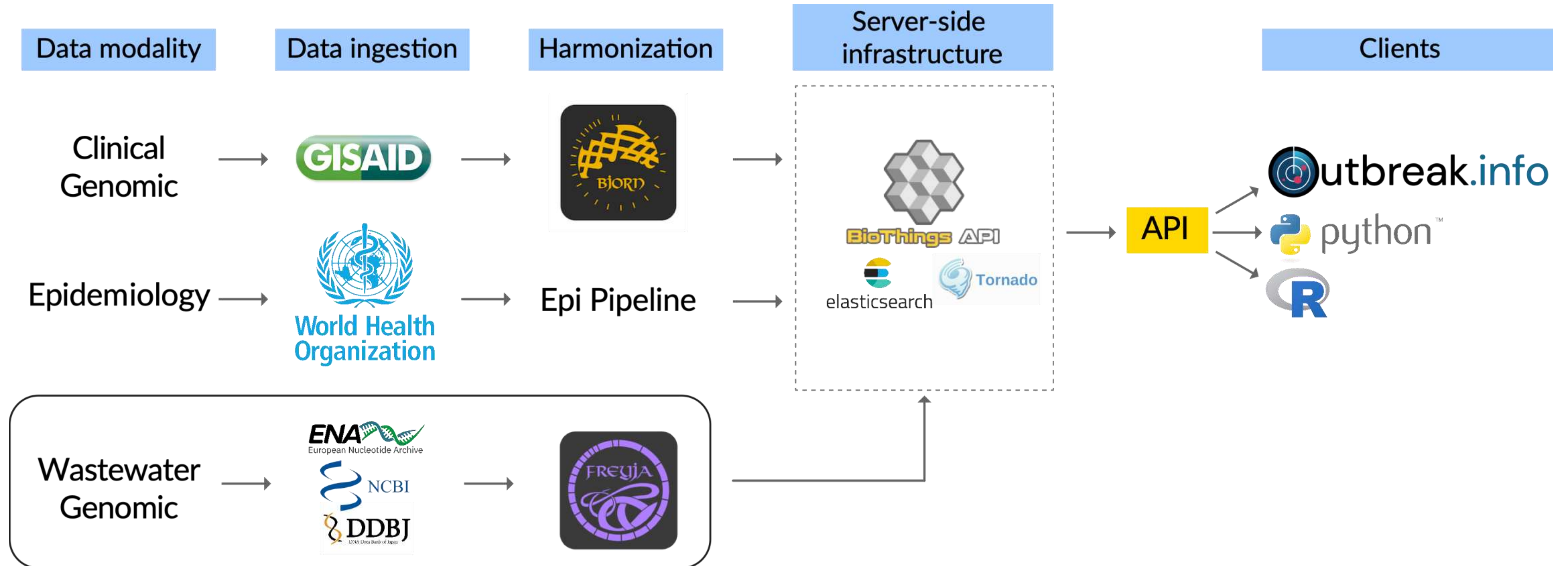
Wastewater enables comprehensive, robust



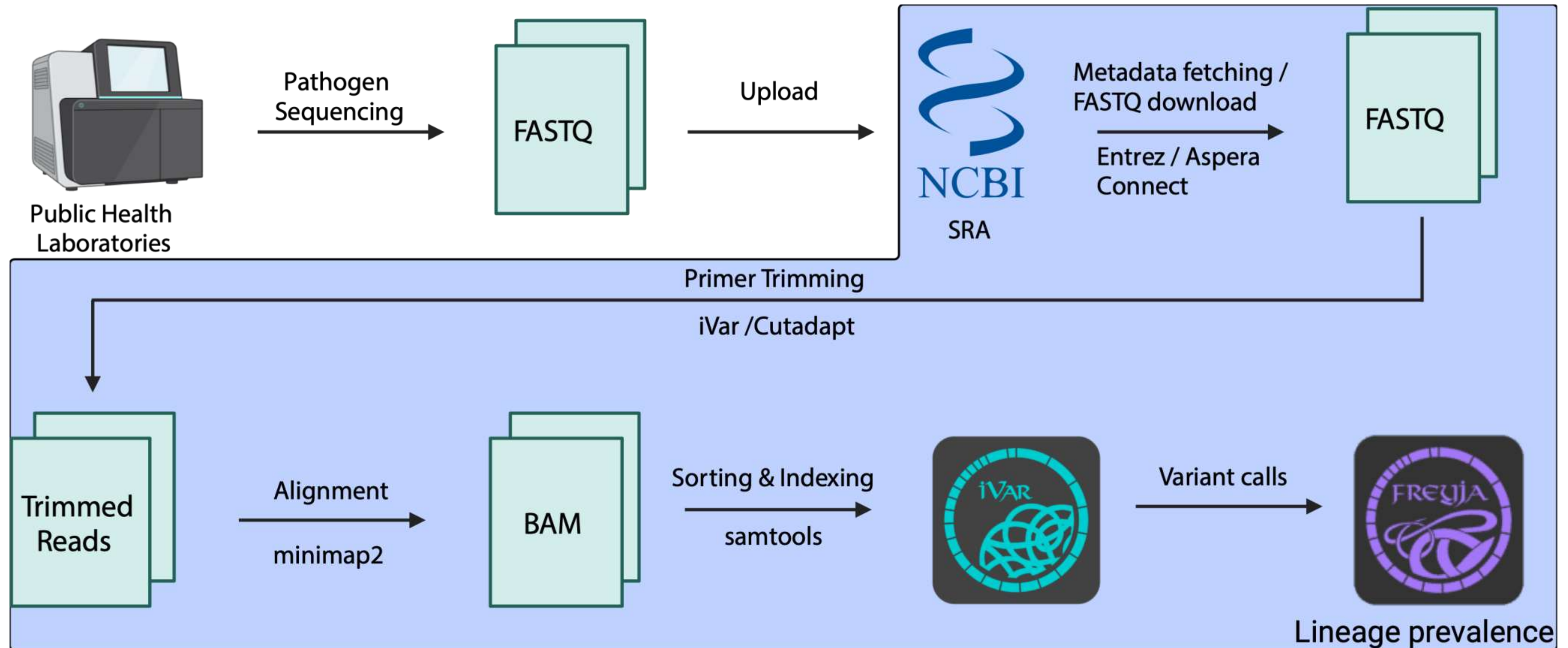
Multi-modal, pandemic scale data platform



Multi-modal, pandemic scale data platform

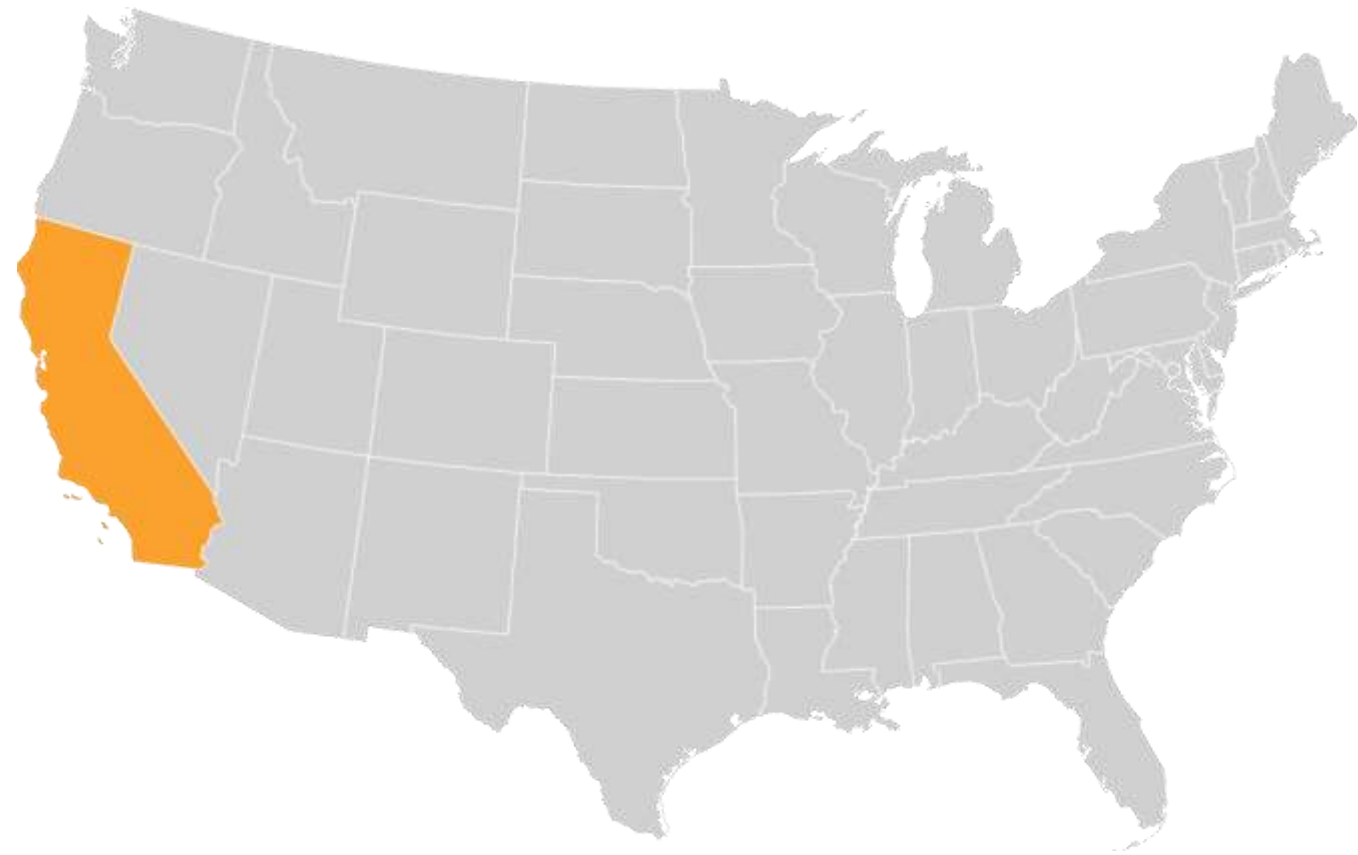


Scalable wastewater bioinformatic pipeline



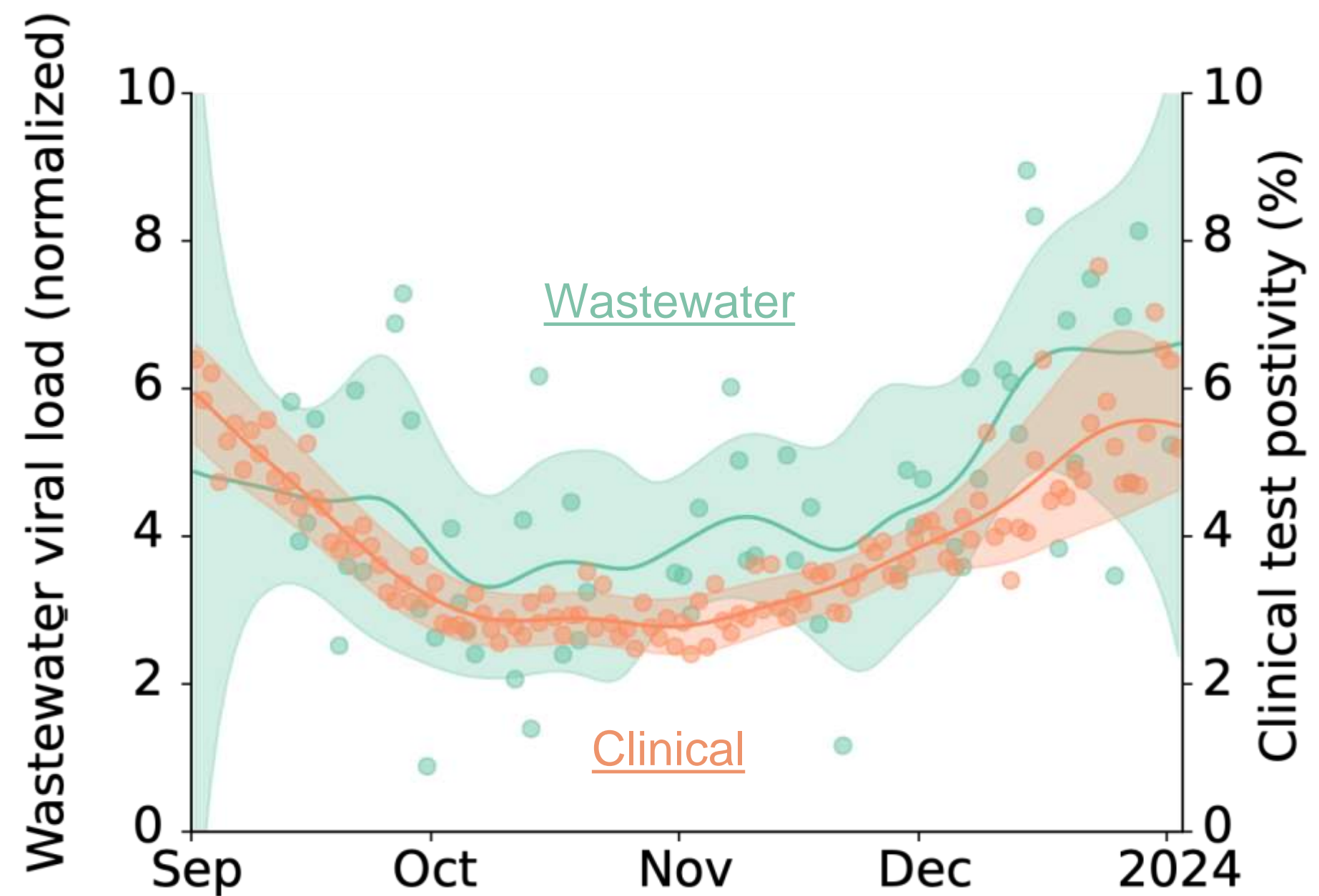
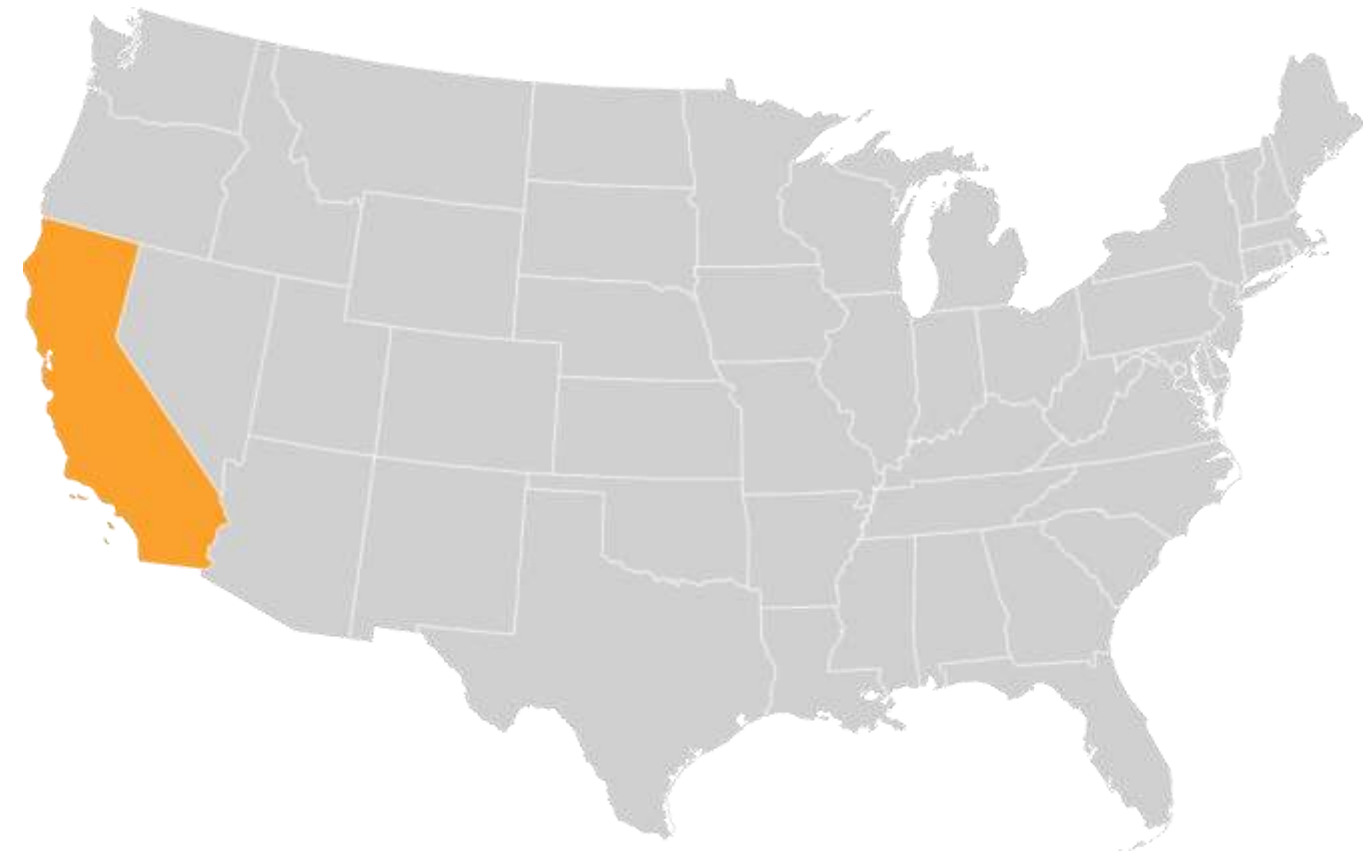
Scalable, multimodal surveillance data streams

Tracking SARS-CoV-2 burden in CA



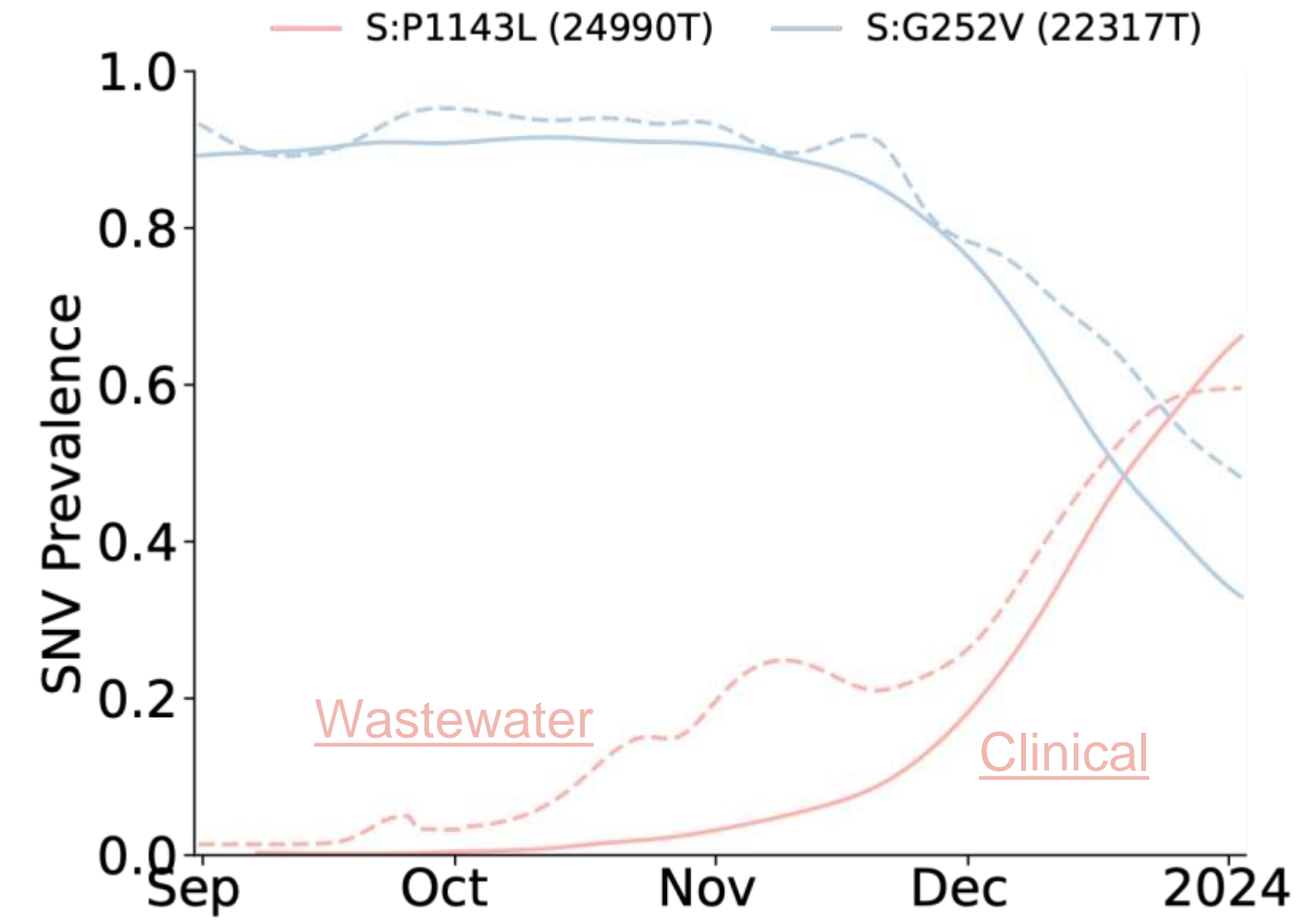
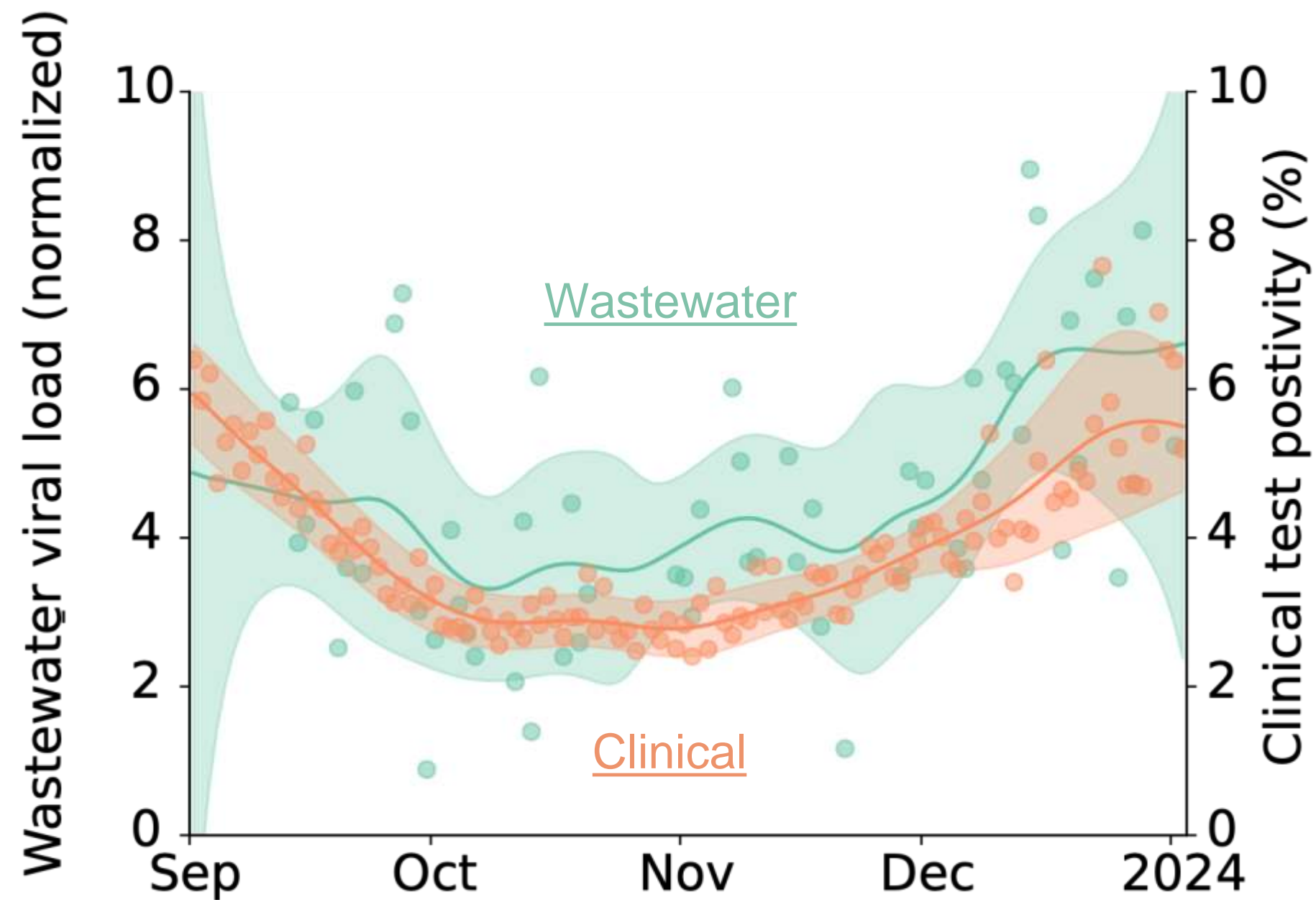
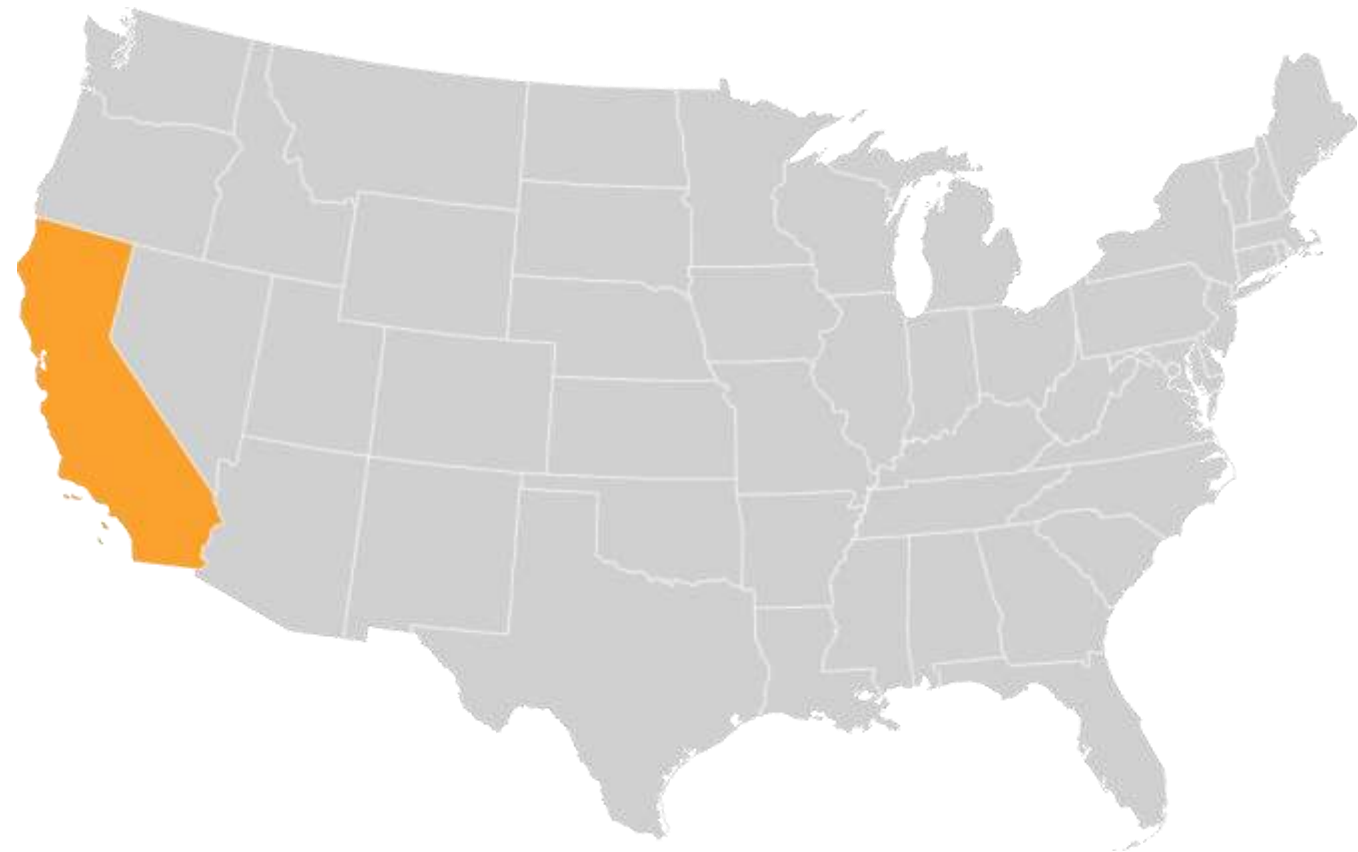
Scalable, multimodal surveillance data streams

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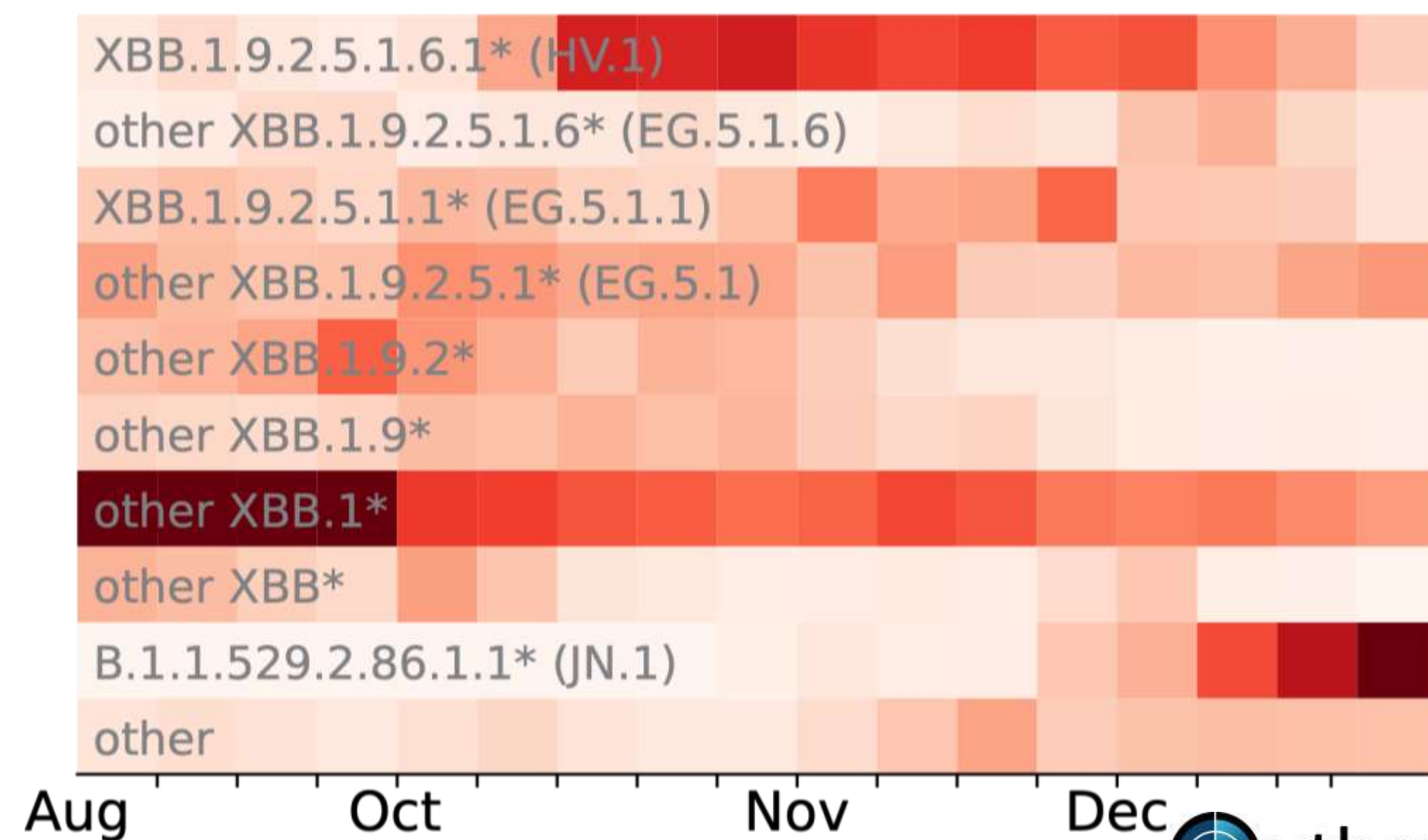
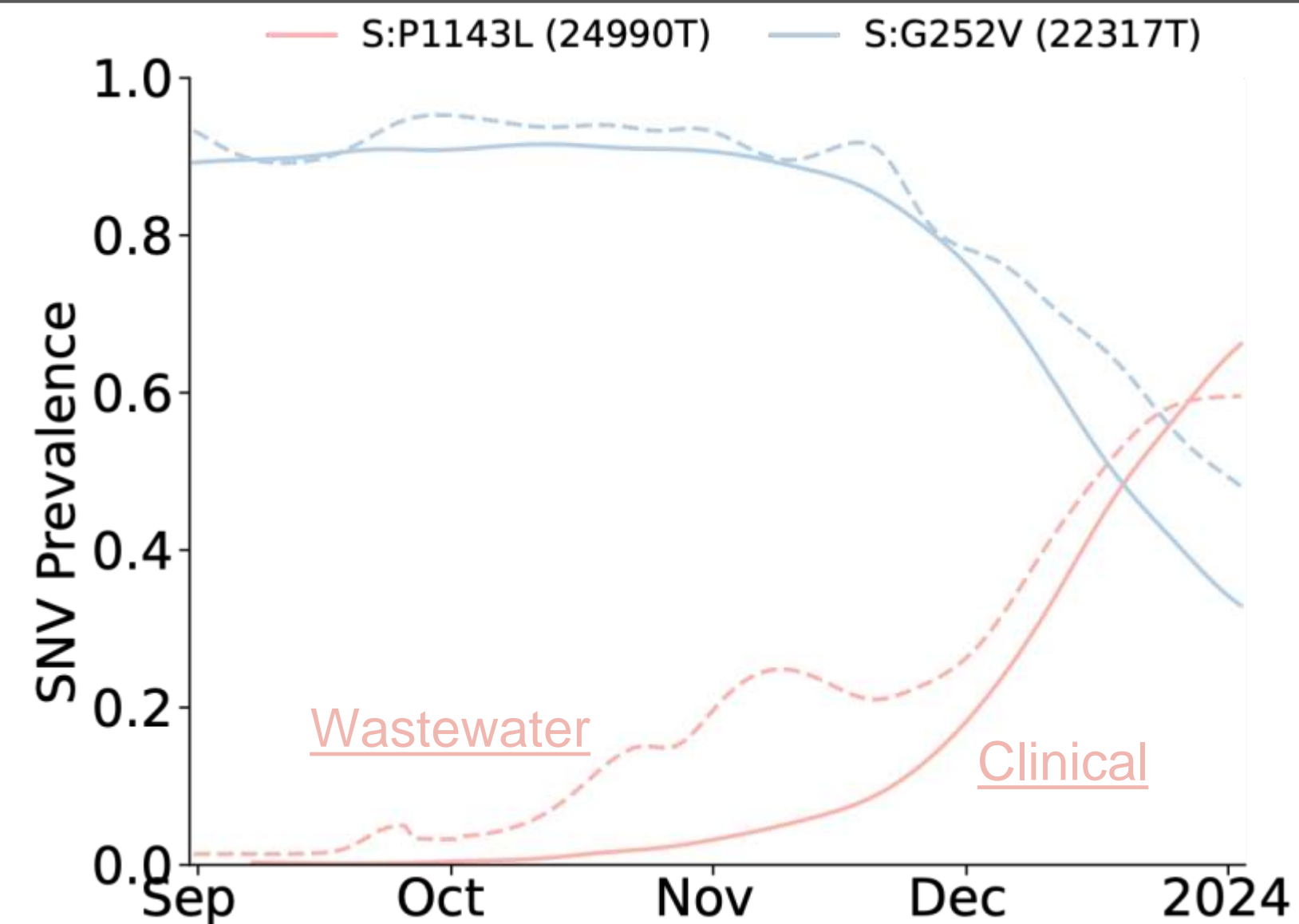
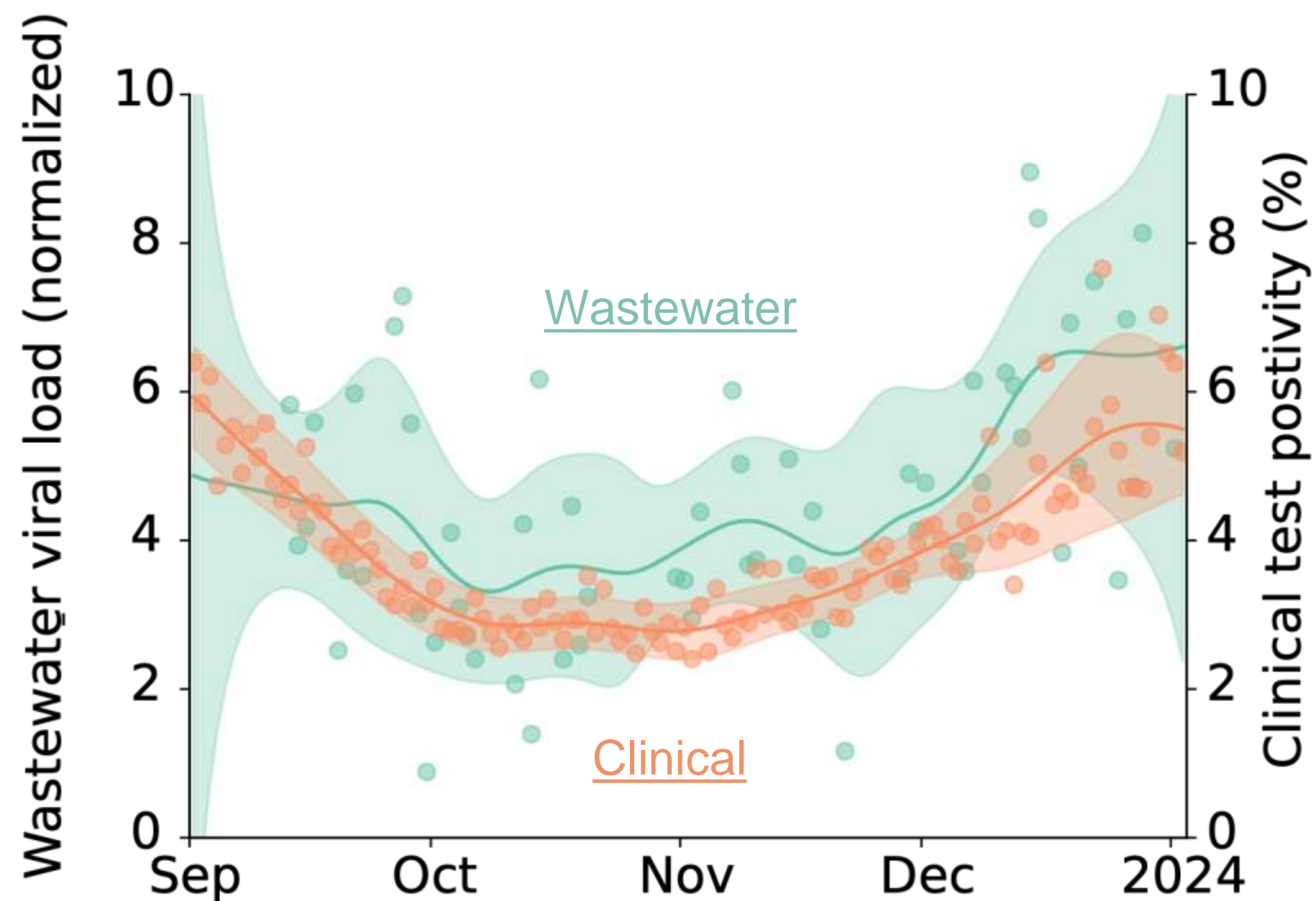
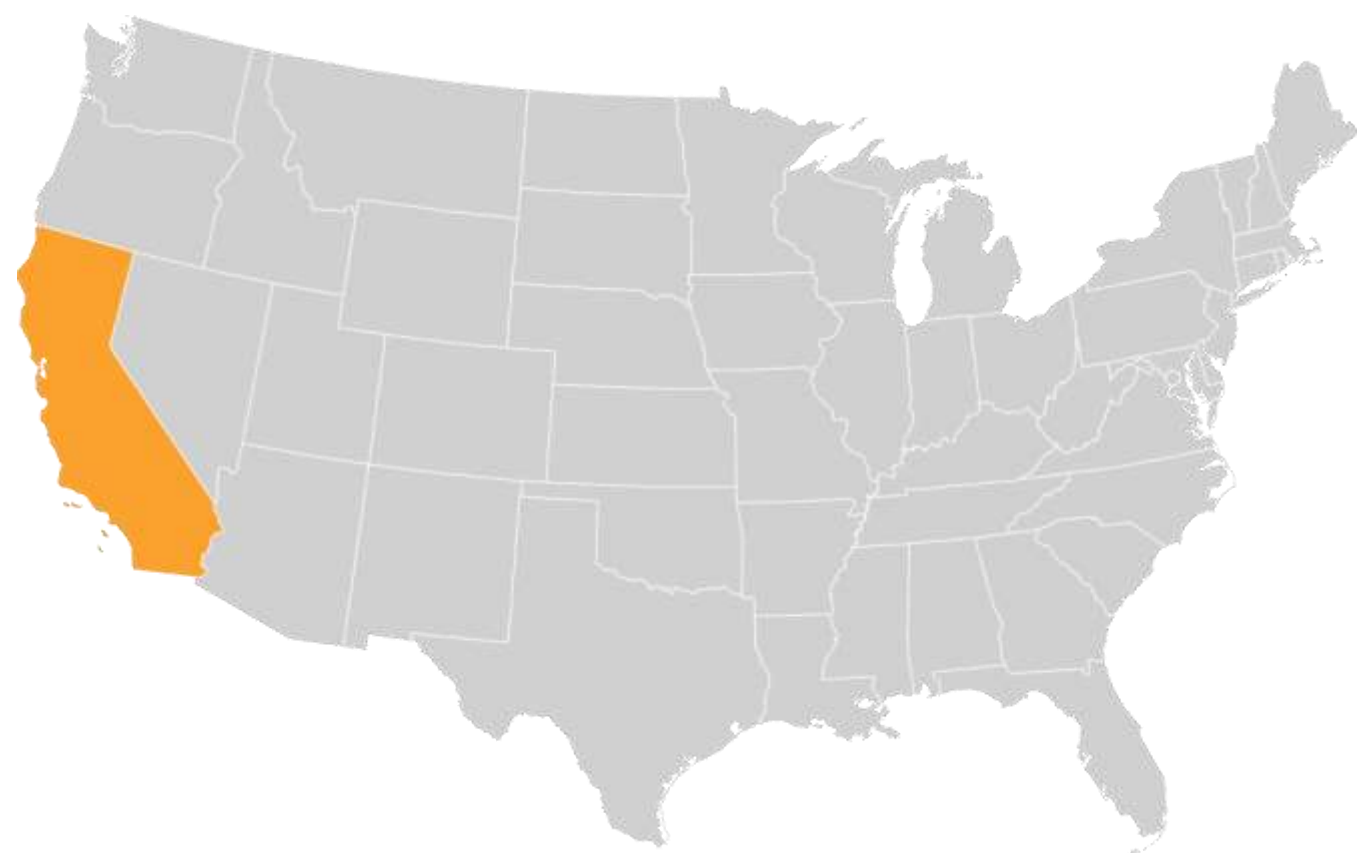
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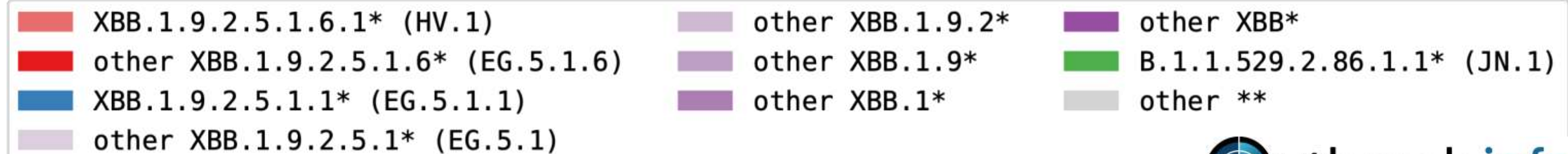
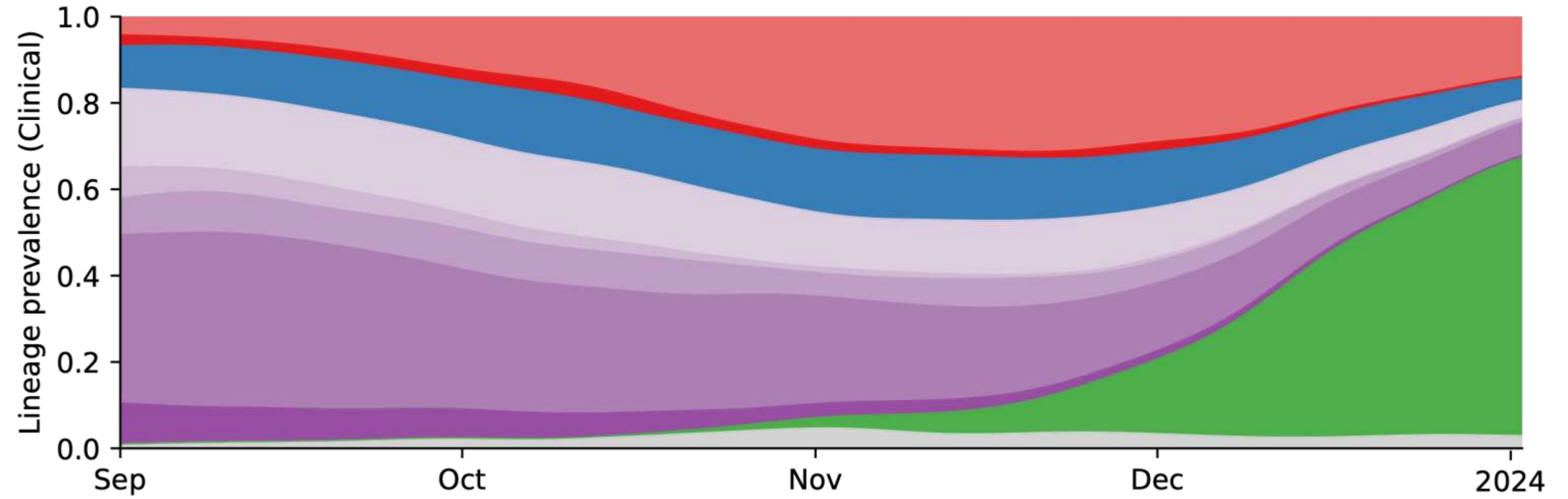
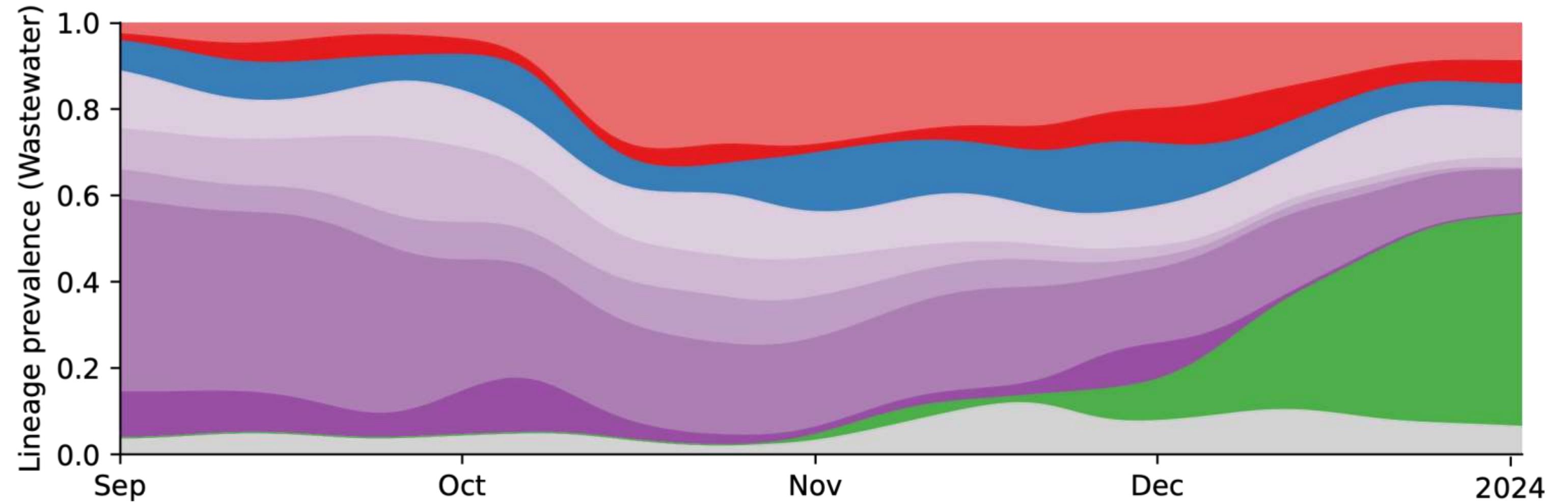
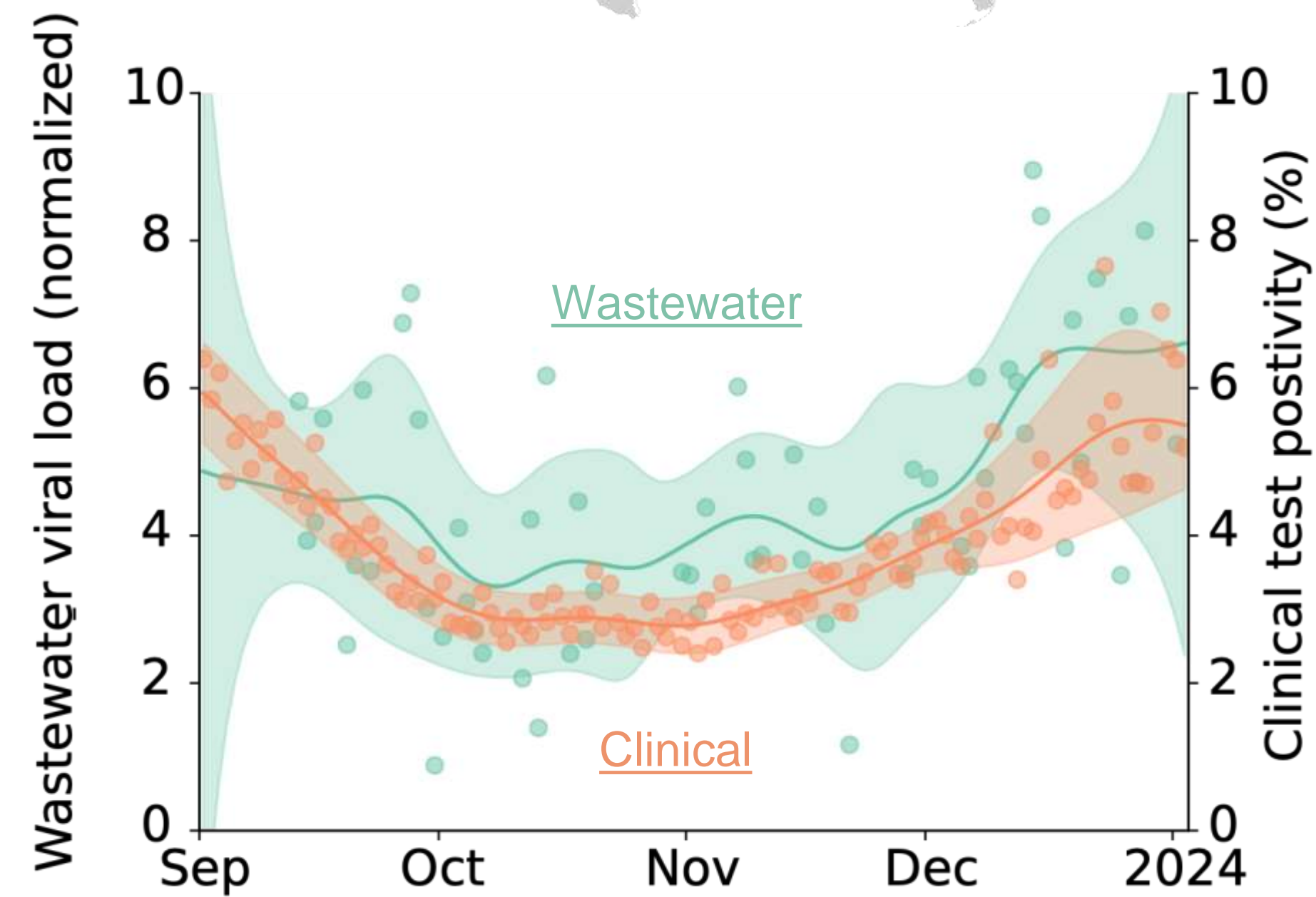
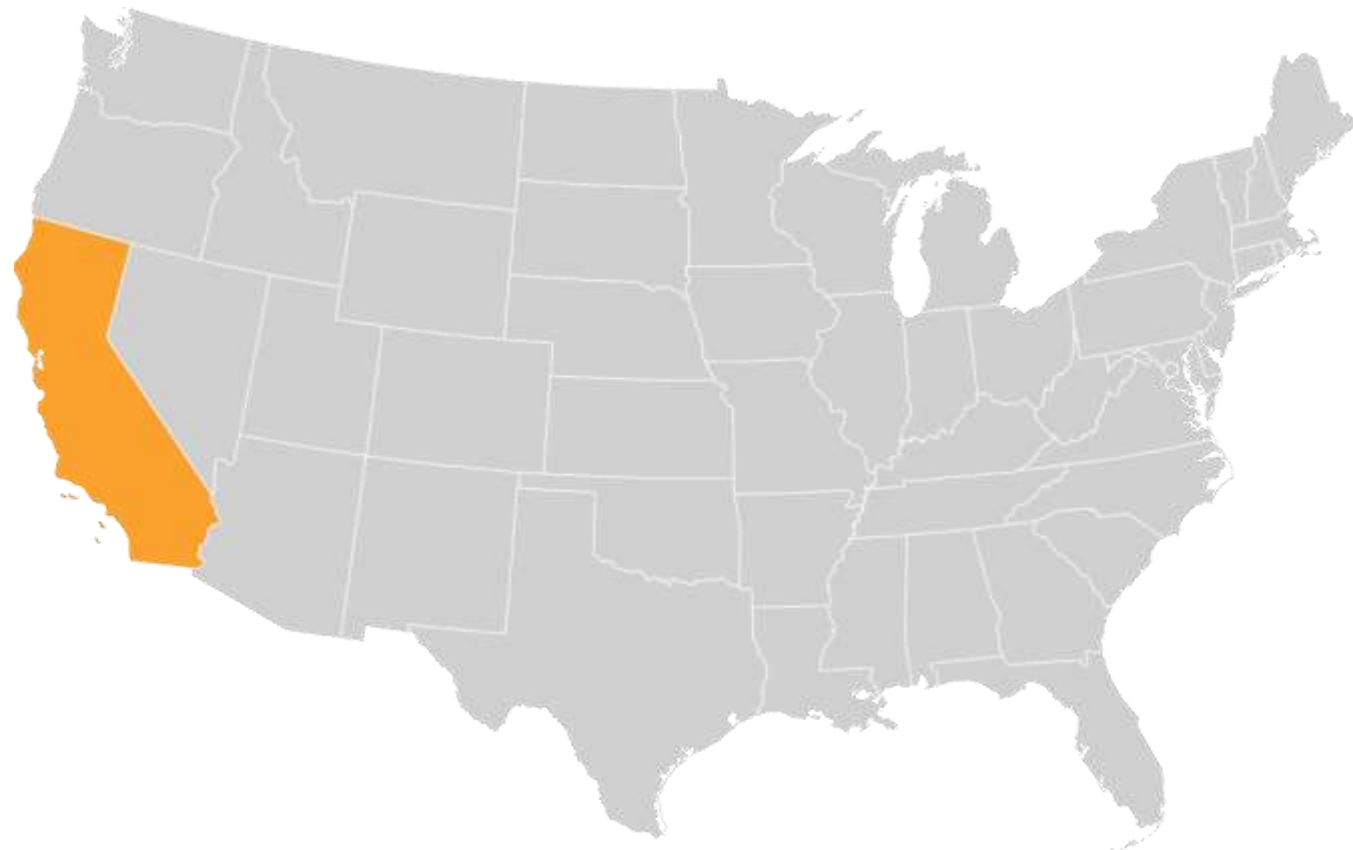
Scalable, multimodal surveillance data streams

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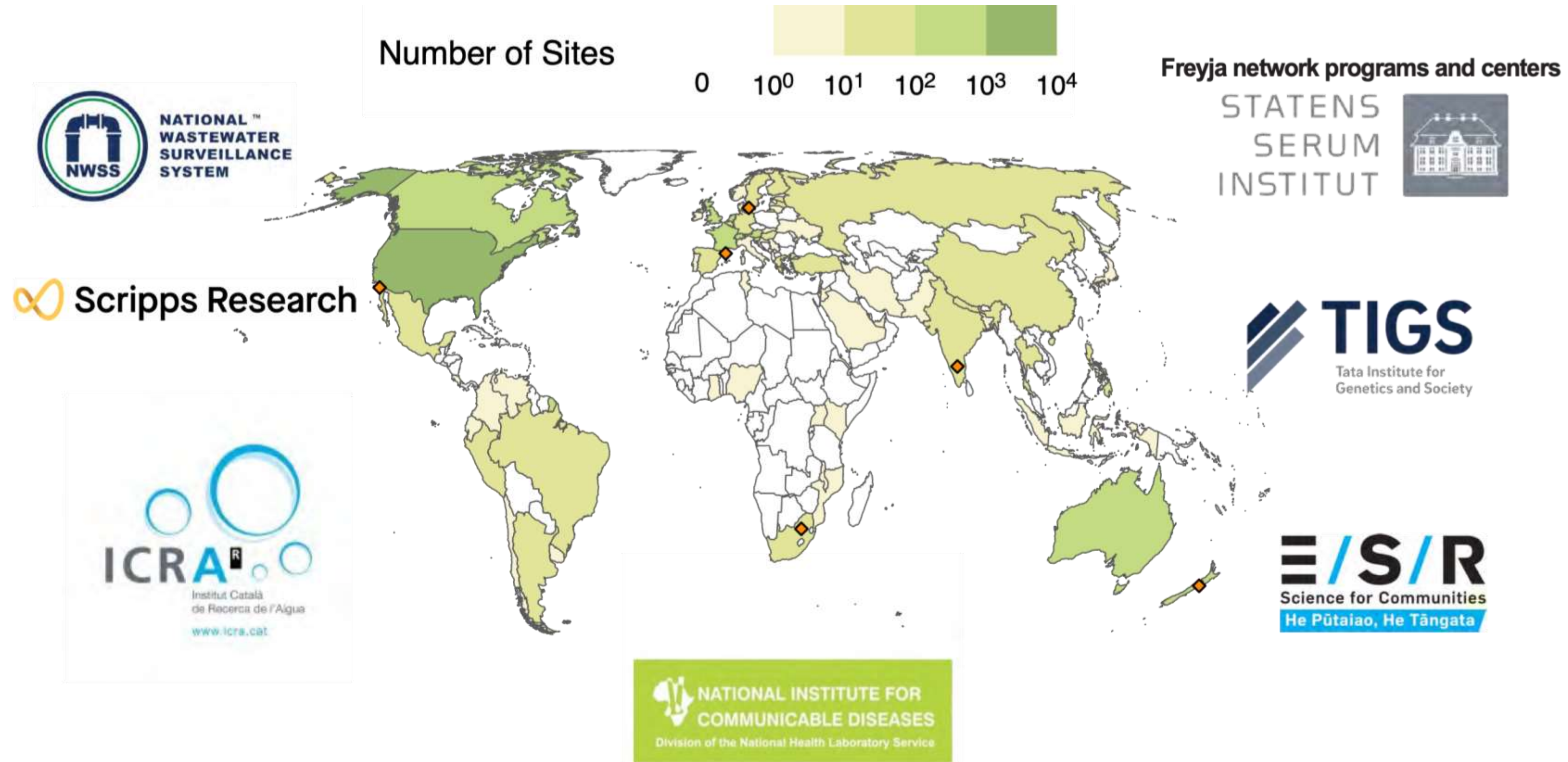


Scalable, multimodal surveillance data streams

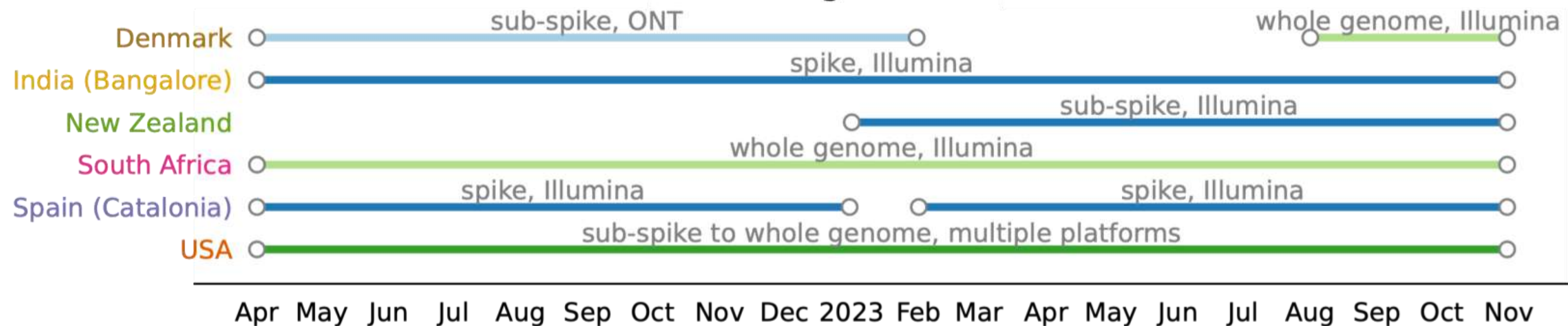
Tracking SARS-CoV-2 burden in CA



Deployment via our collaborative network

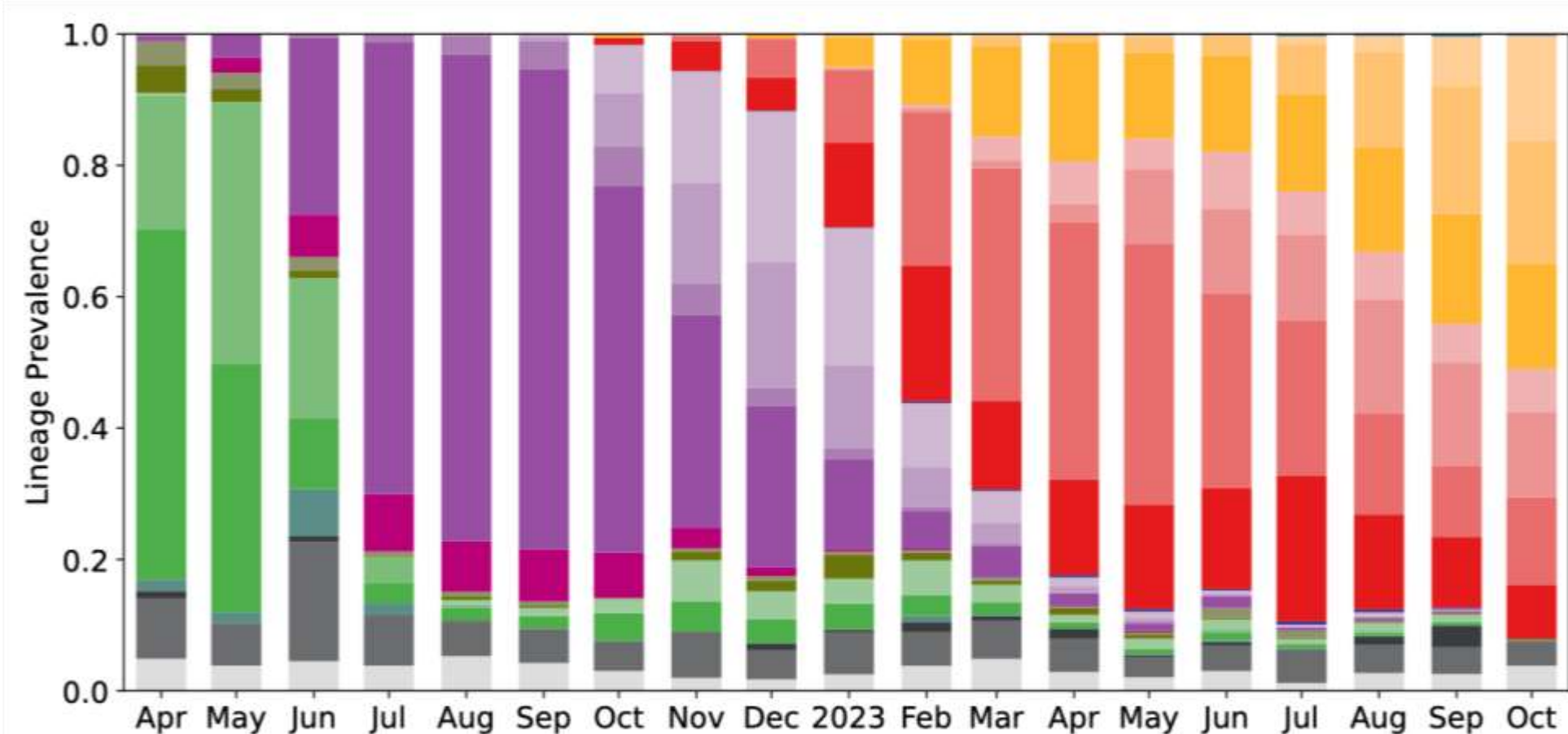


Timeline of wastewater genomic surveillance activities

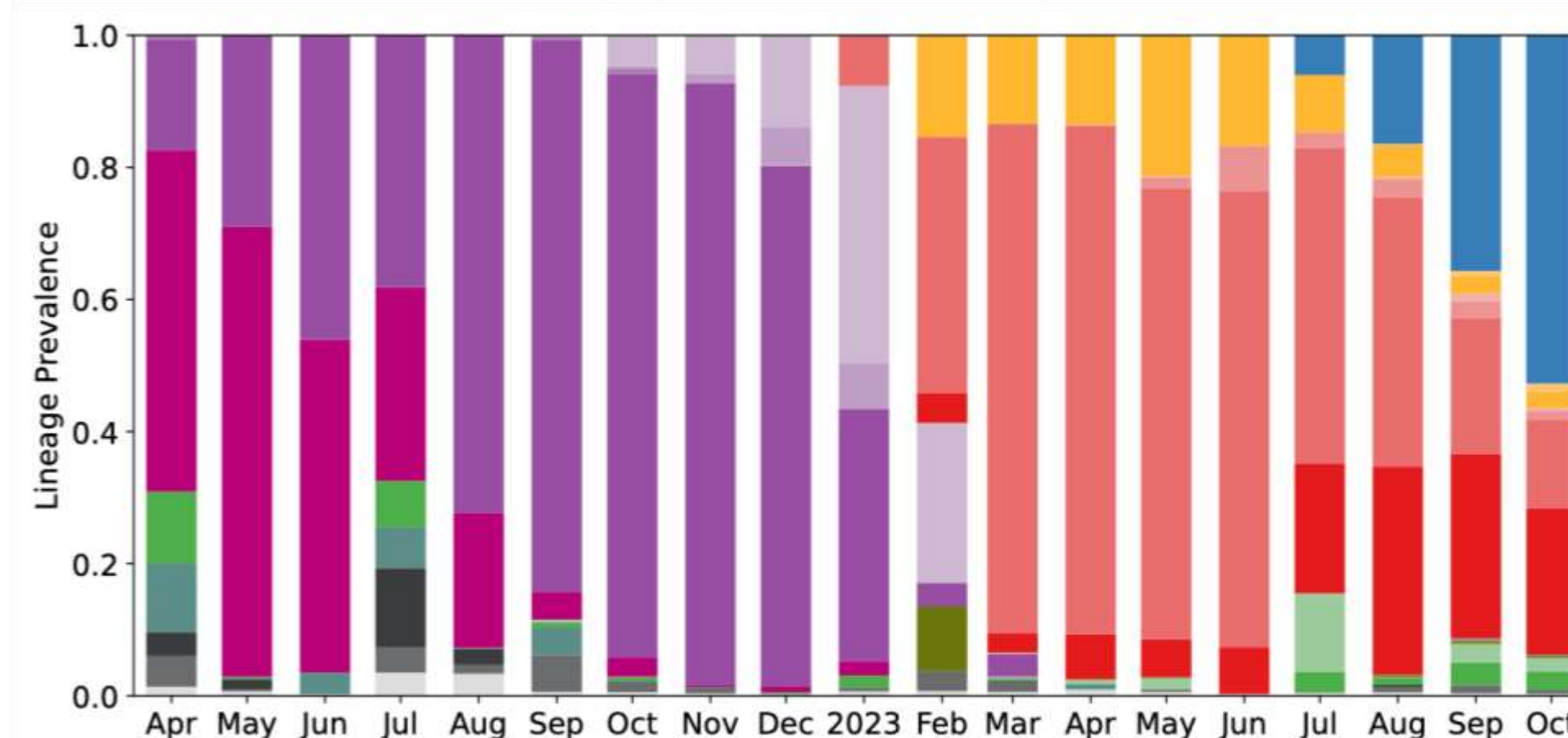


Regional and national wastewater sentinel programs

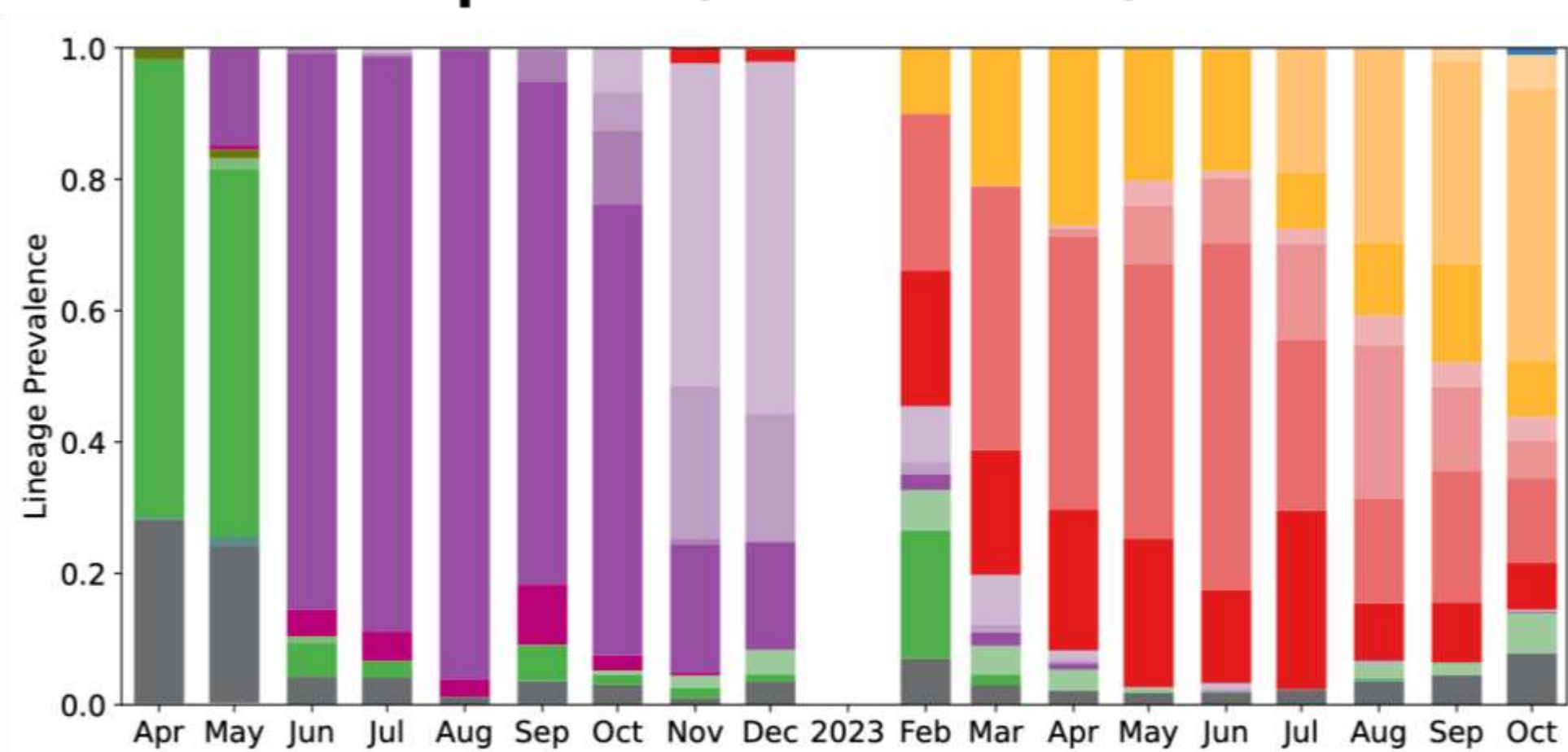
USA



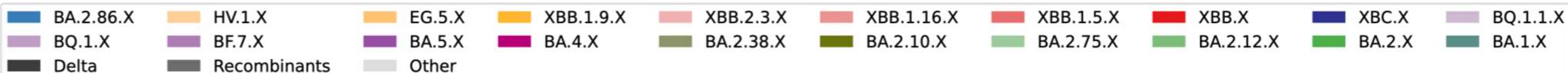
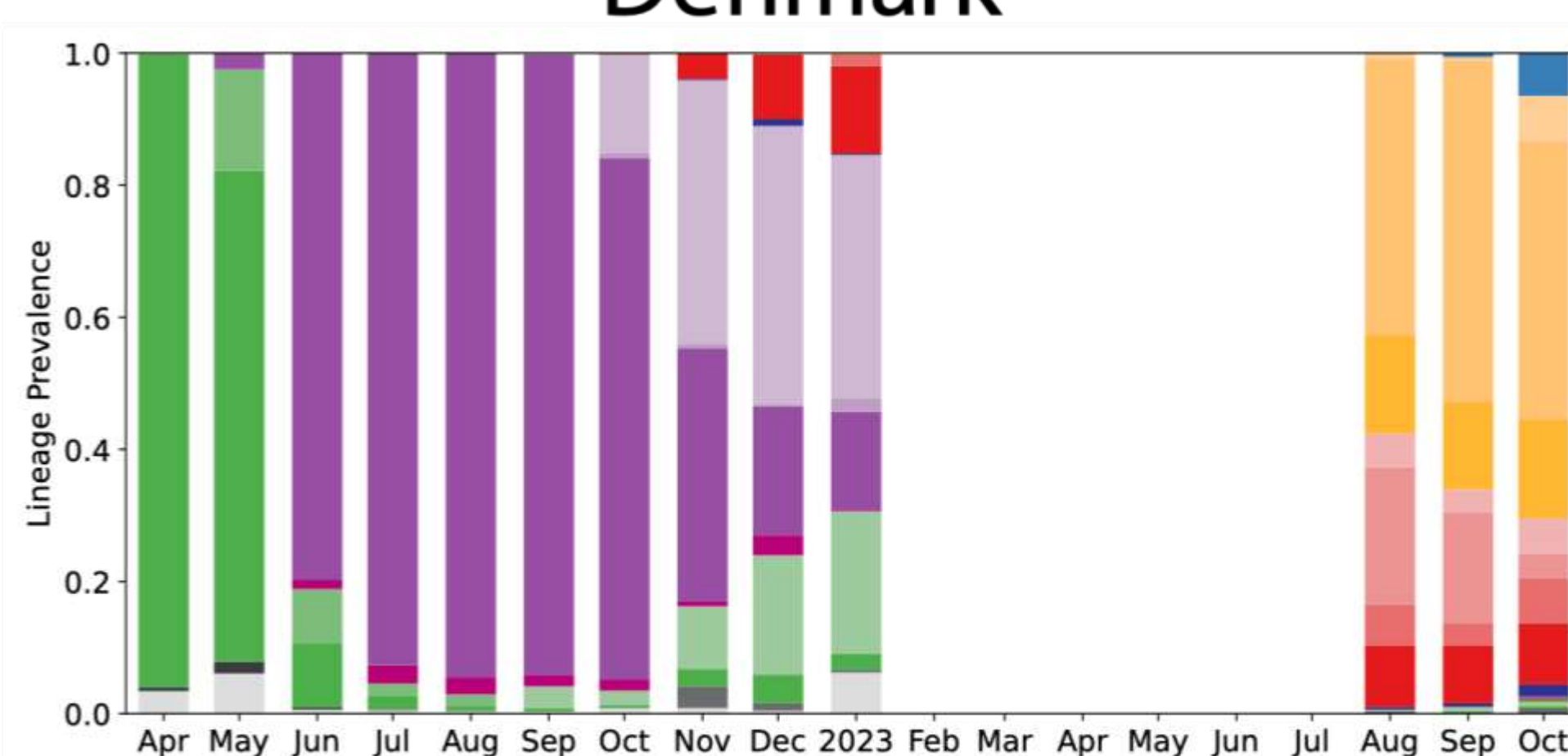
South Africa



Spain (Catalonia)

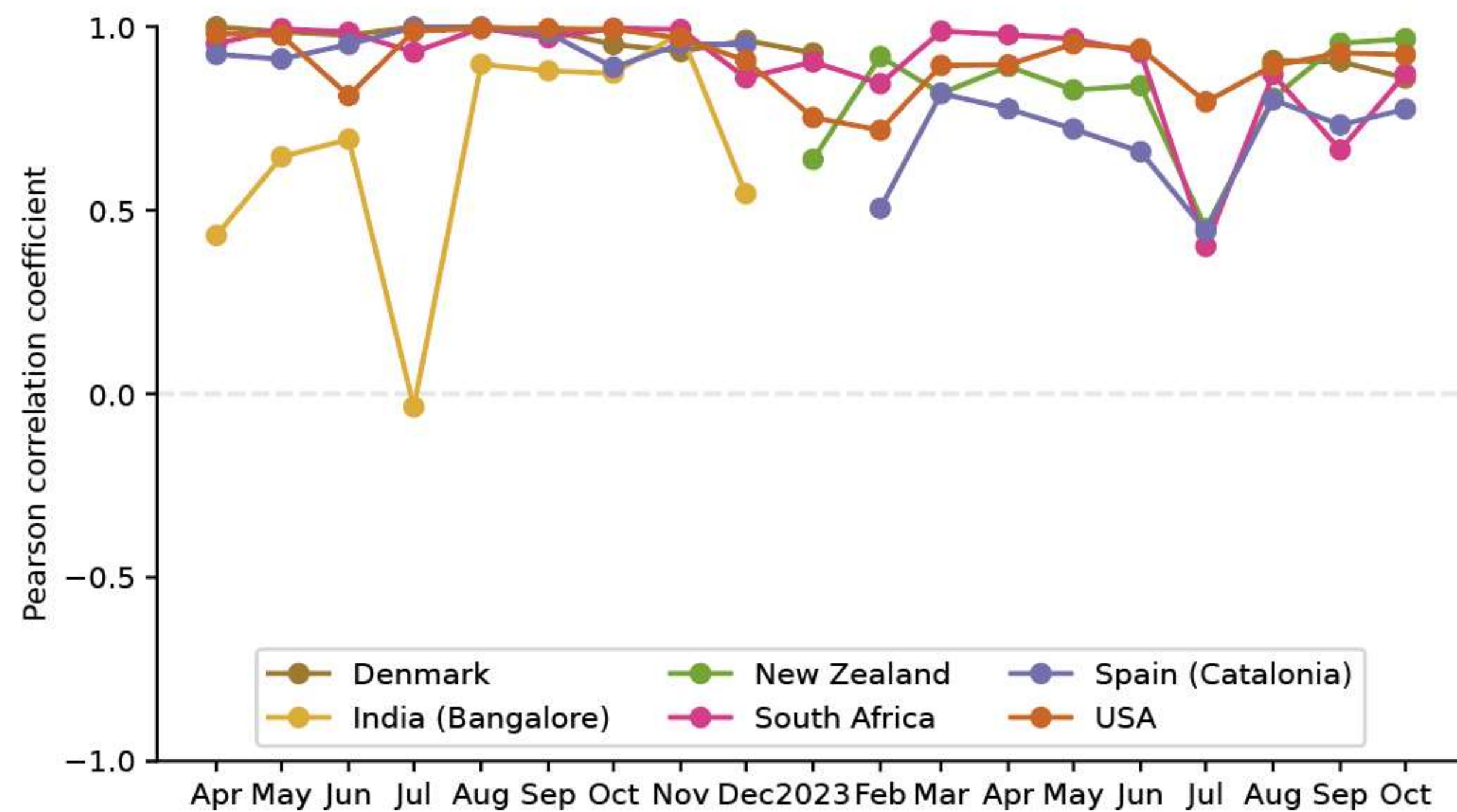


Denmark

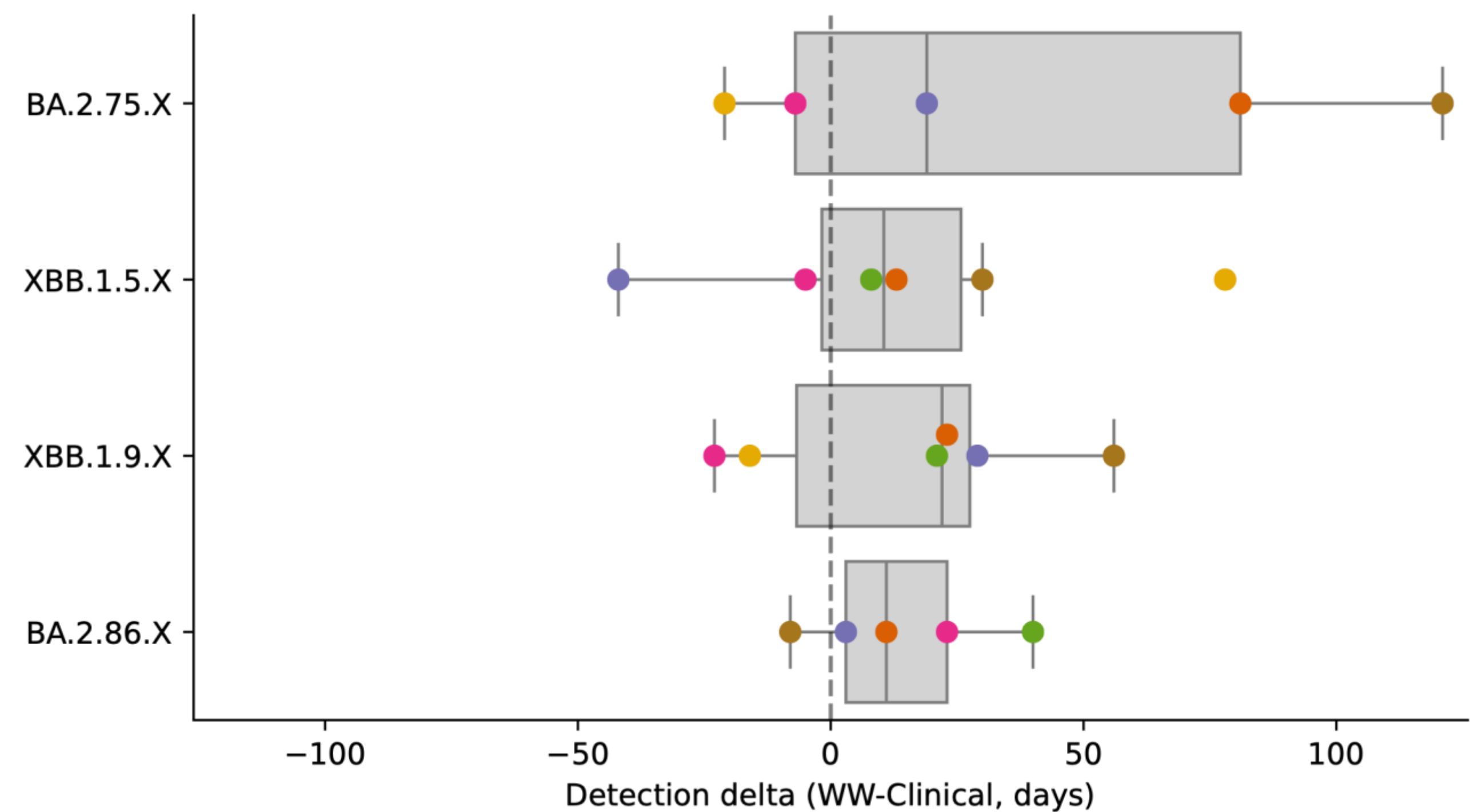


Wastewater consistently acts as a leading indicator

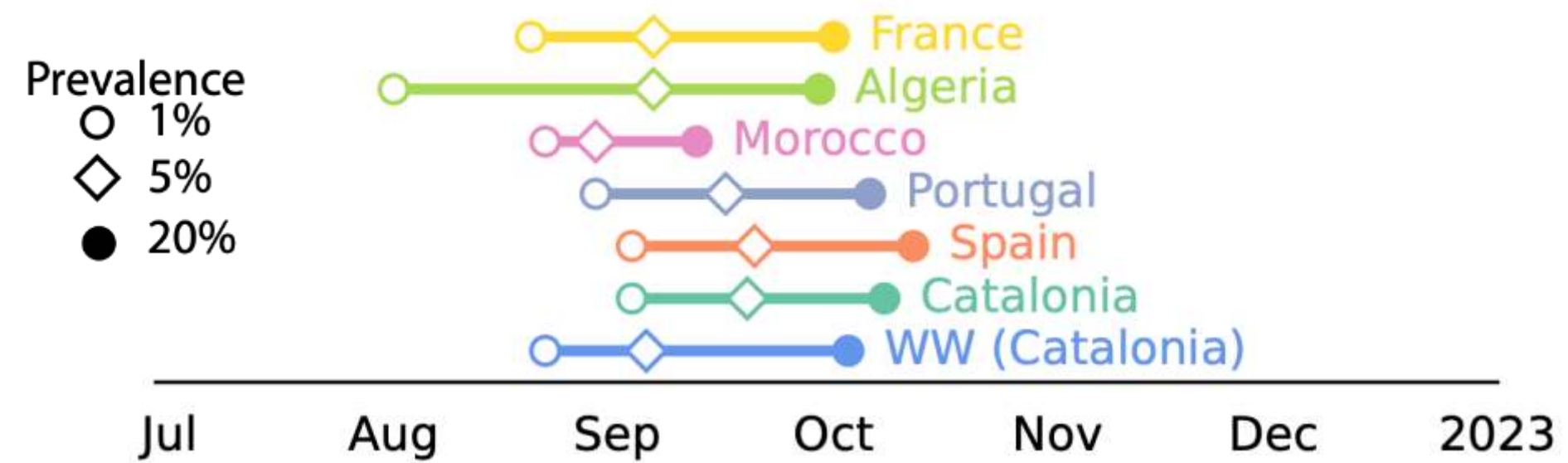
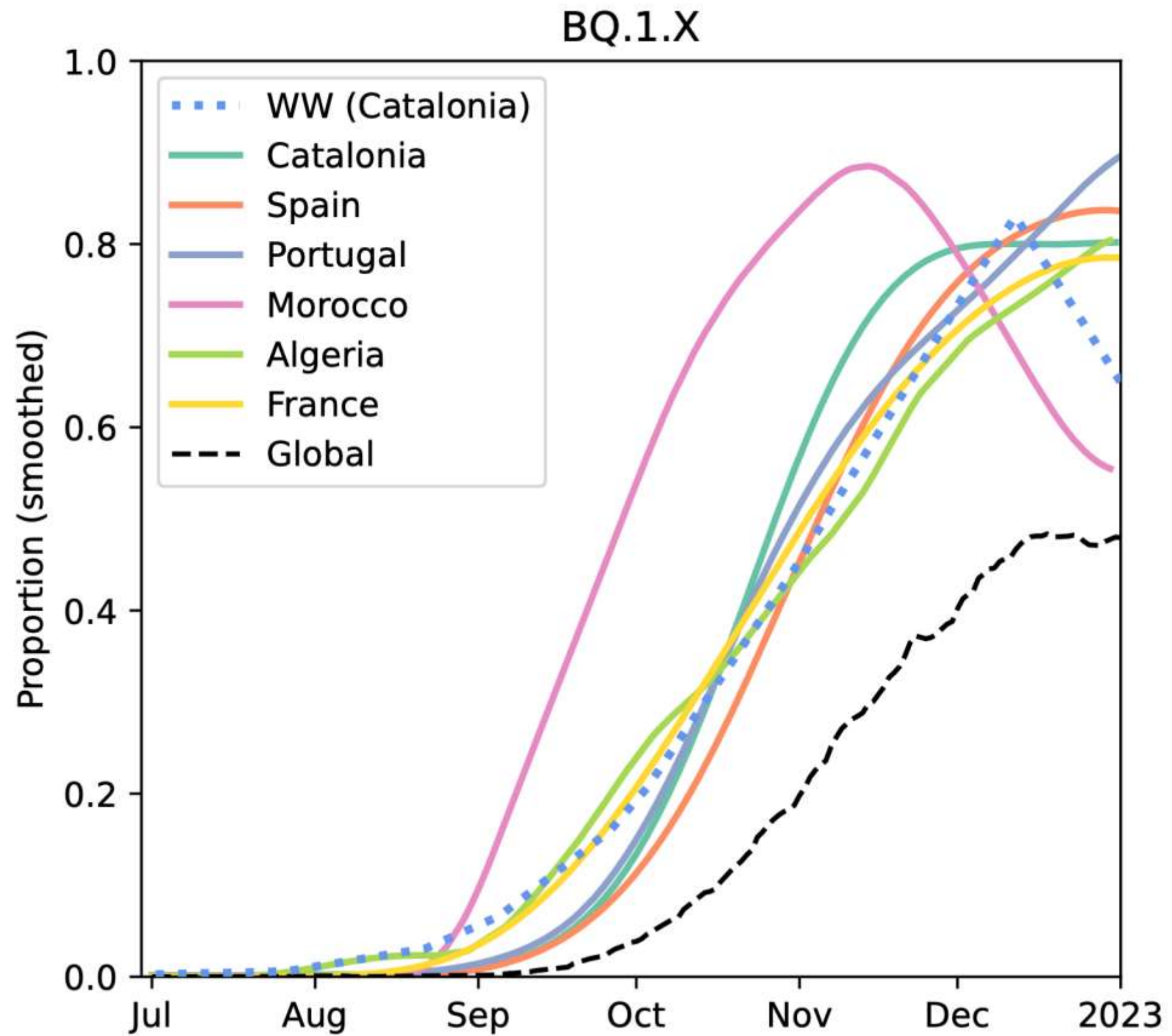
Highly correlated to clinical genomics



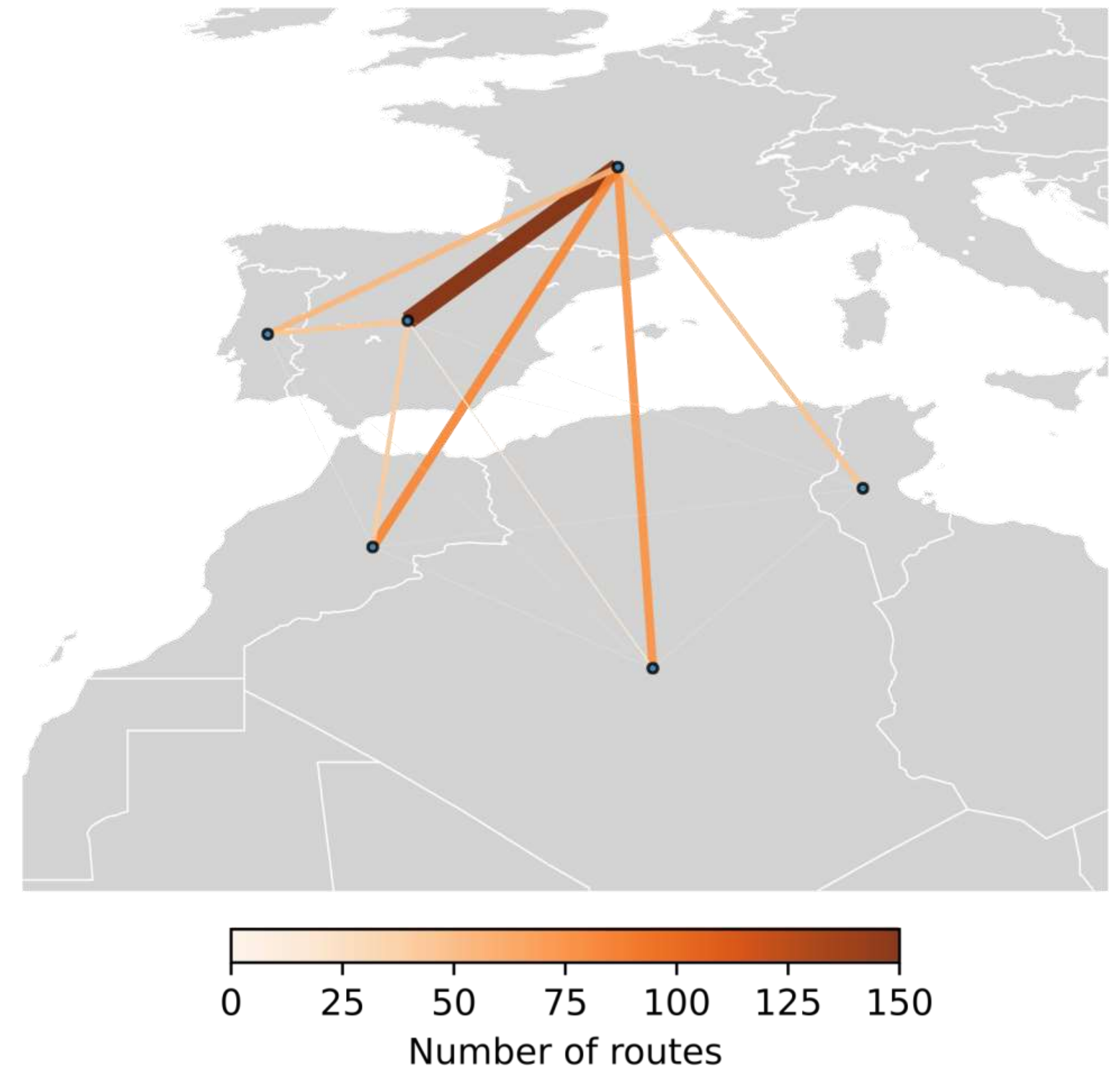
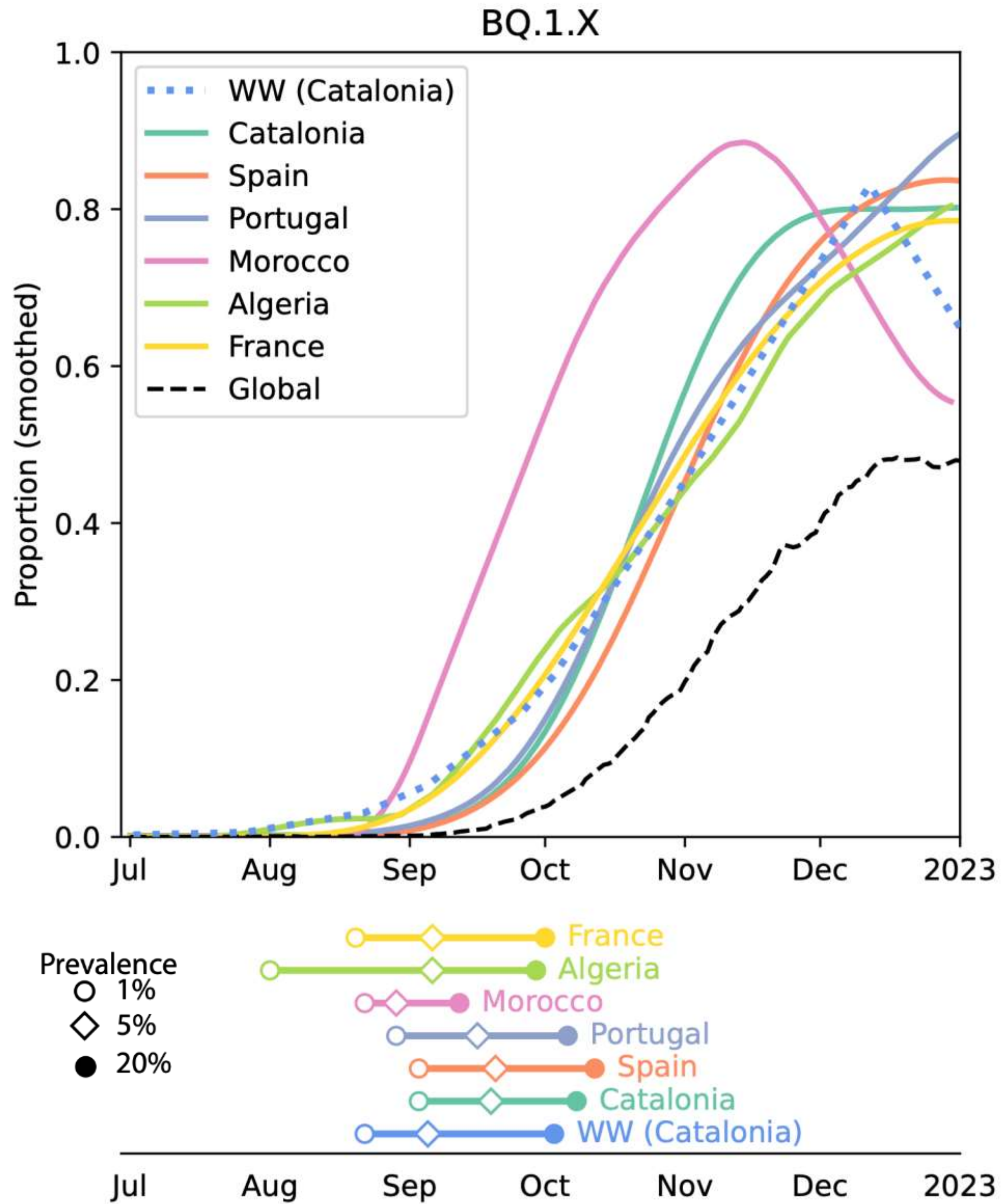
Earlier lineage detection via wastewater



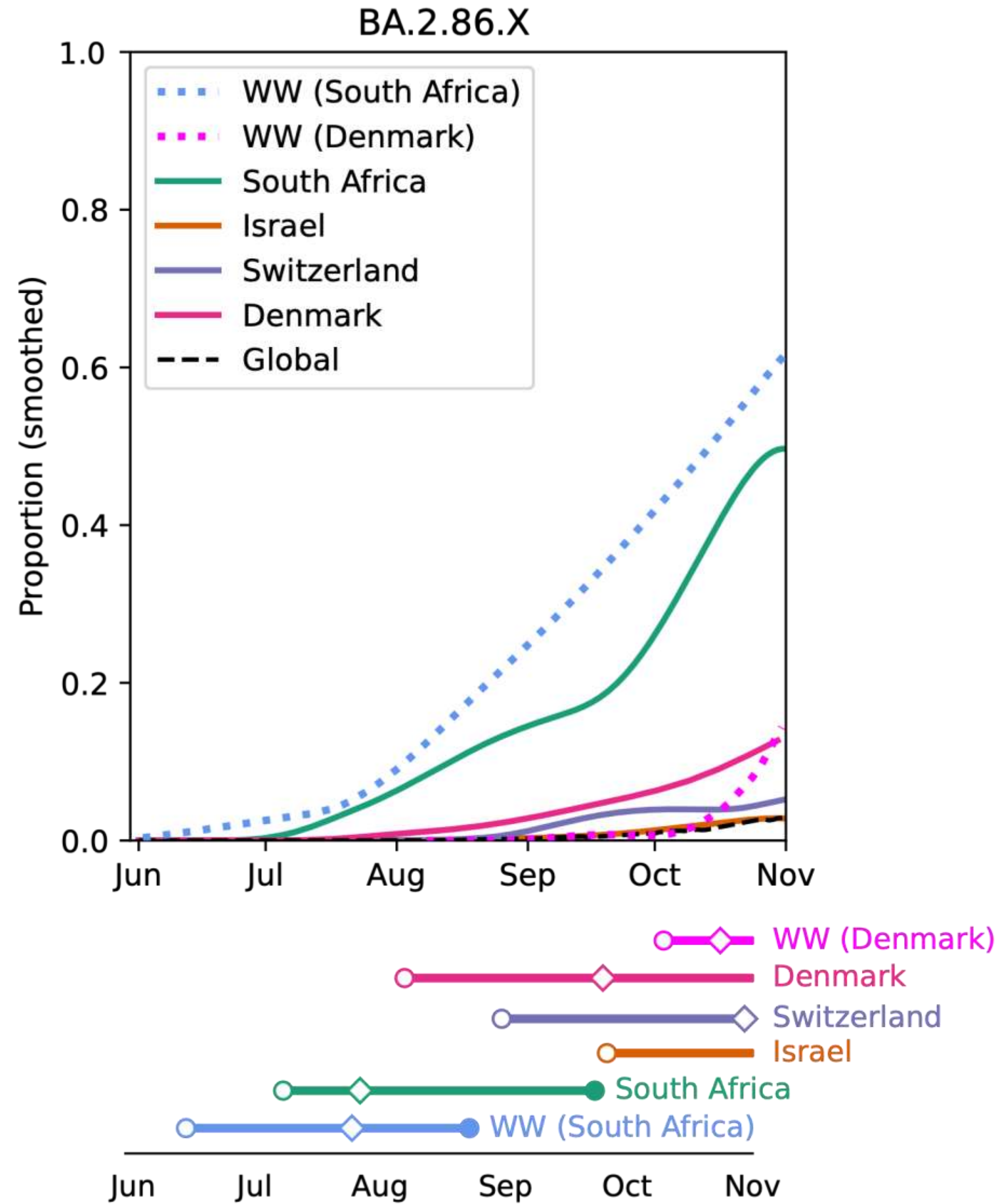
Enhanced regional outbreak tracking and prediction



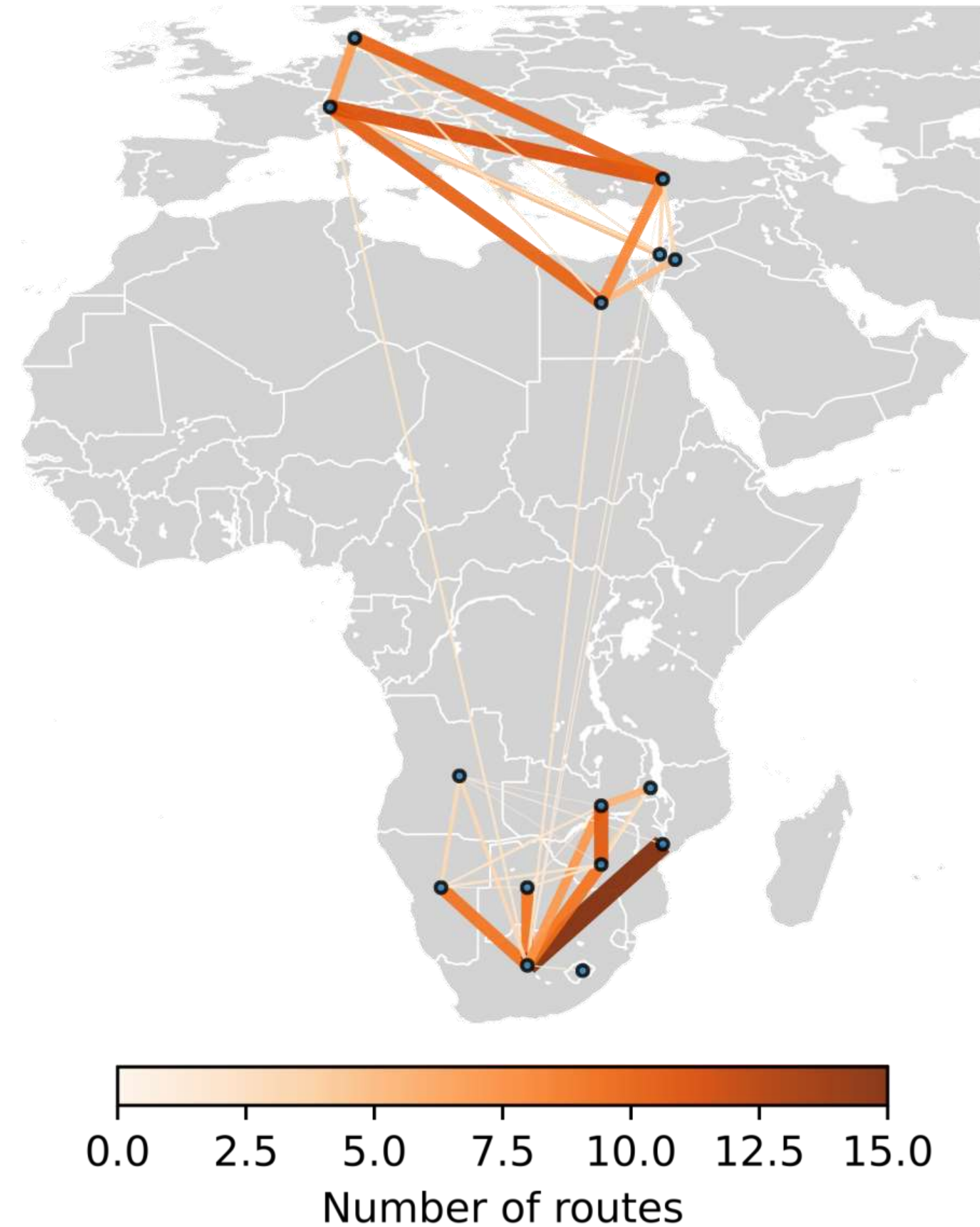
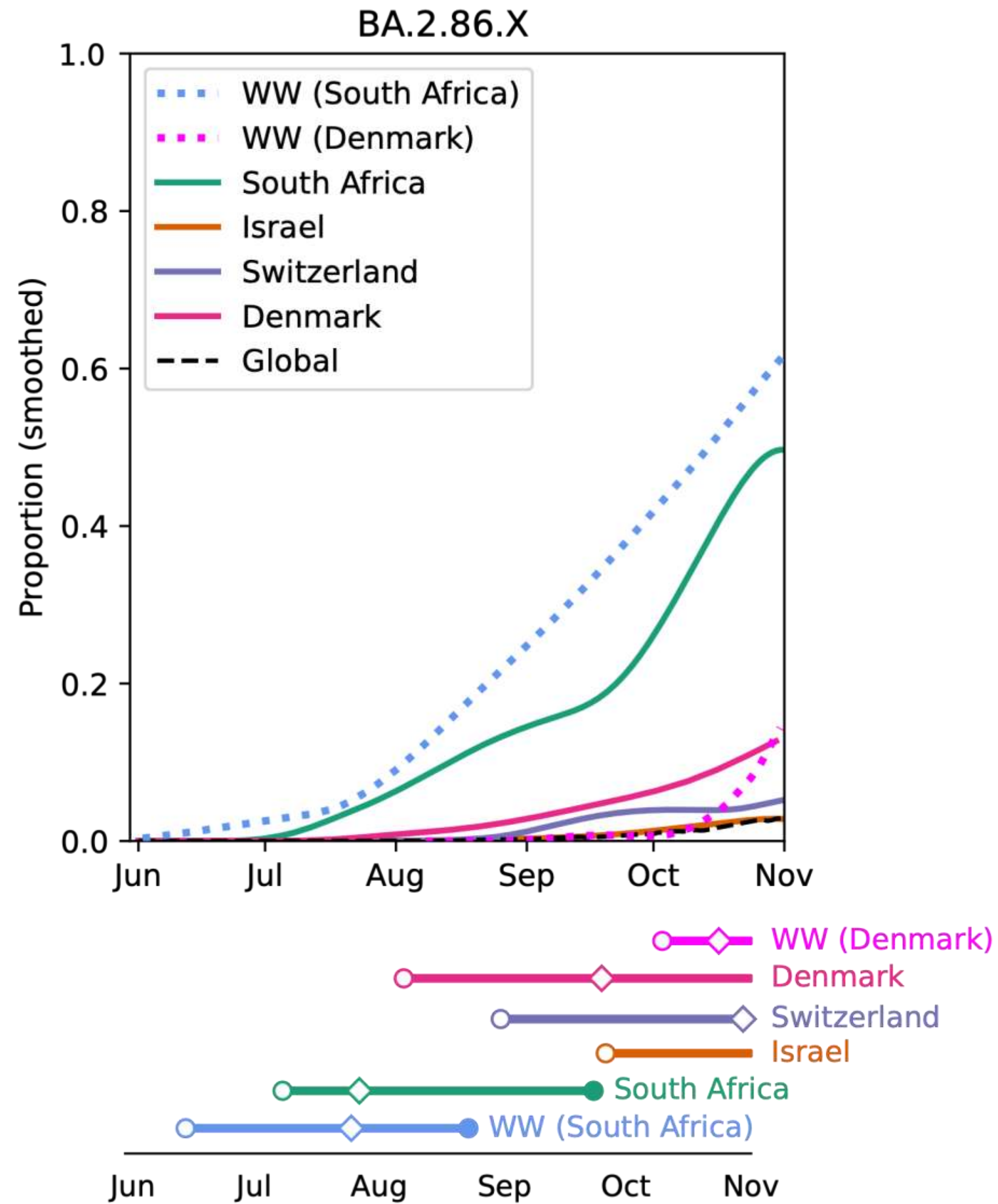
Enhanced regional outbreak tracking and prediction



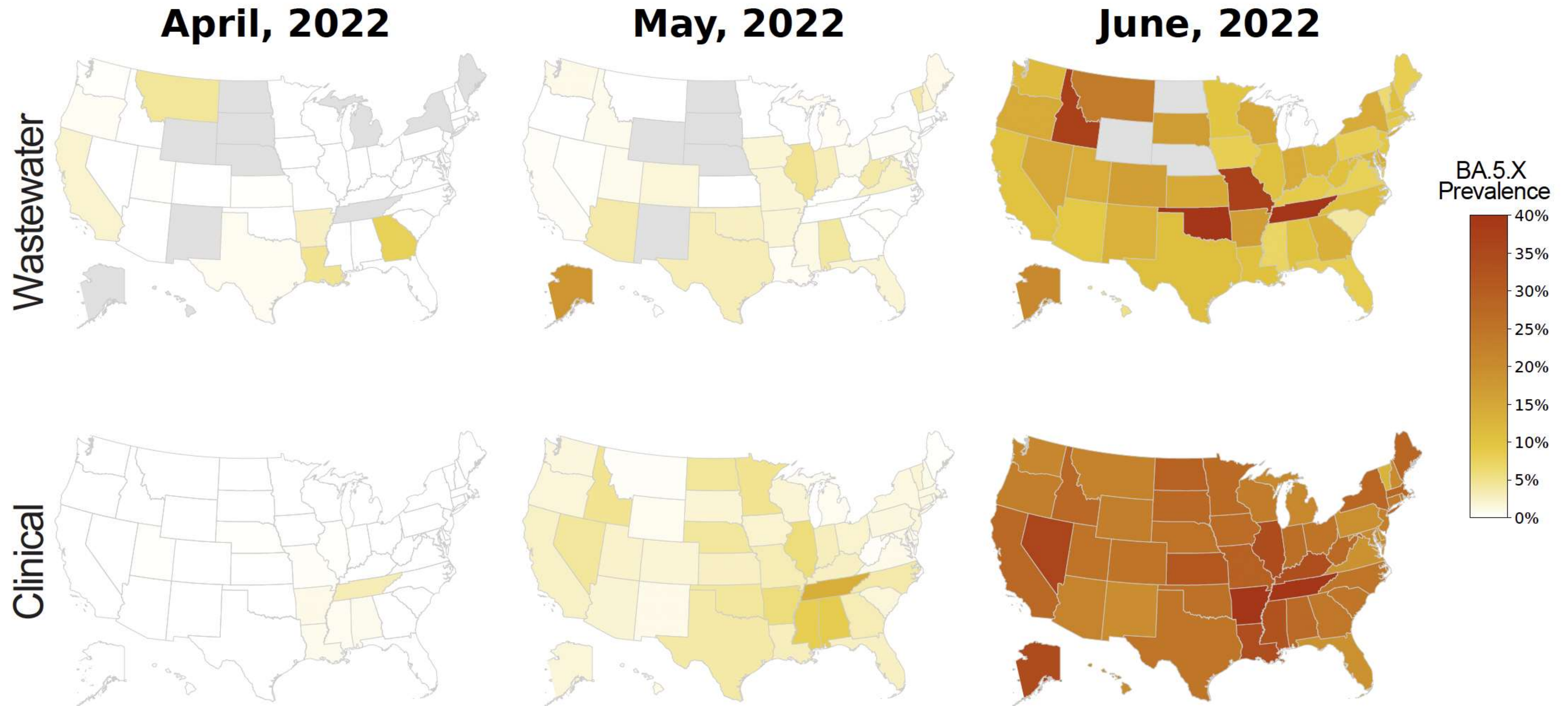
Wastewater provided first BA.2.86 detections



Wastewater provided first BA.2.86 detections

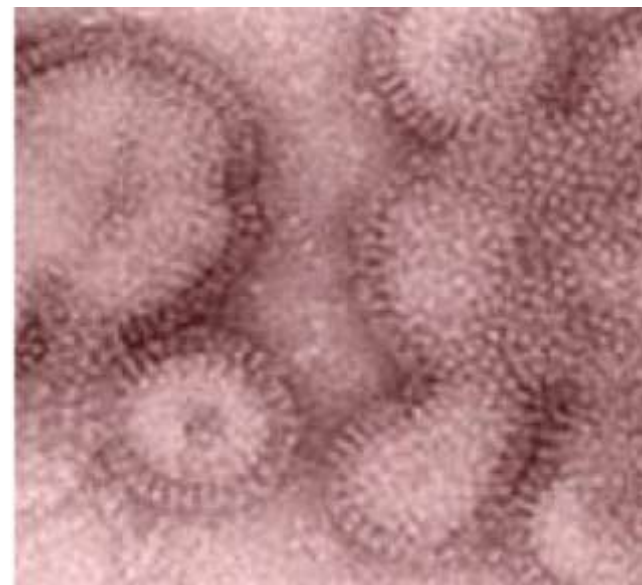


Intra-national monitoring with tunable spatial resolution

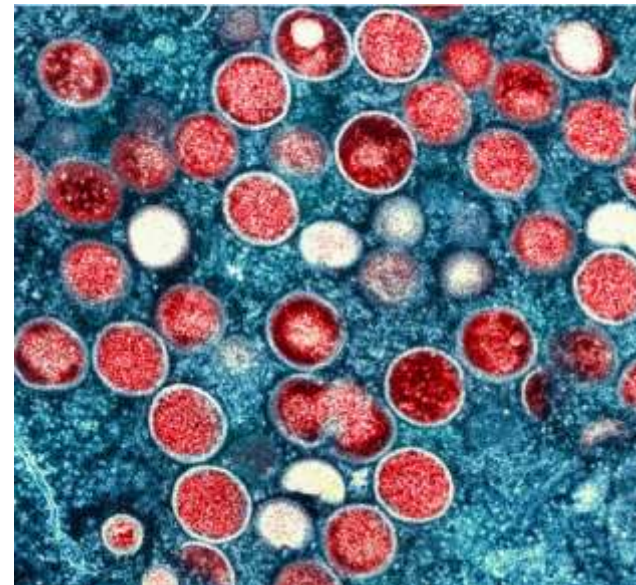


With less clinical data, wastewater is increasingly important

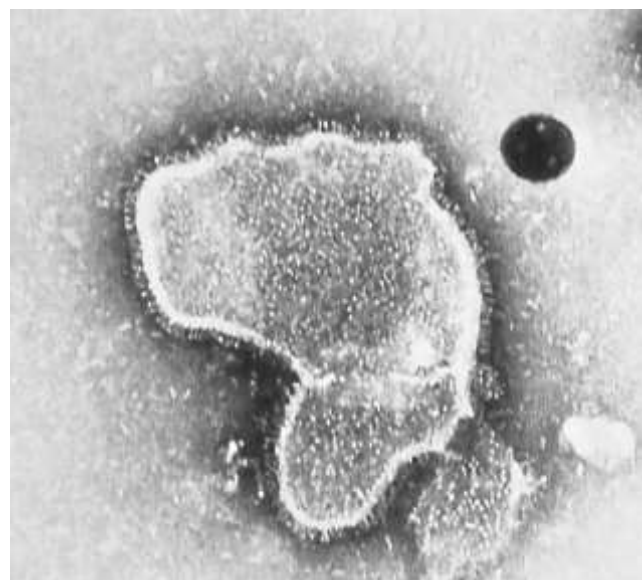
Influenza



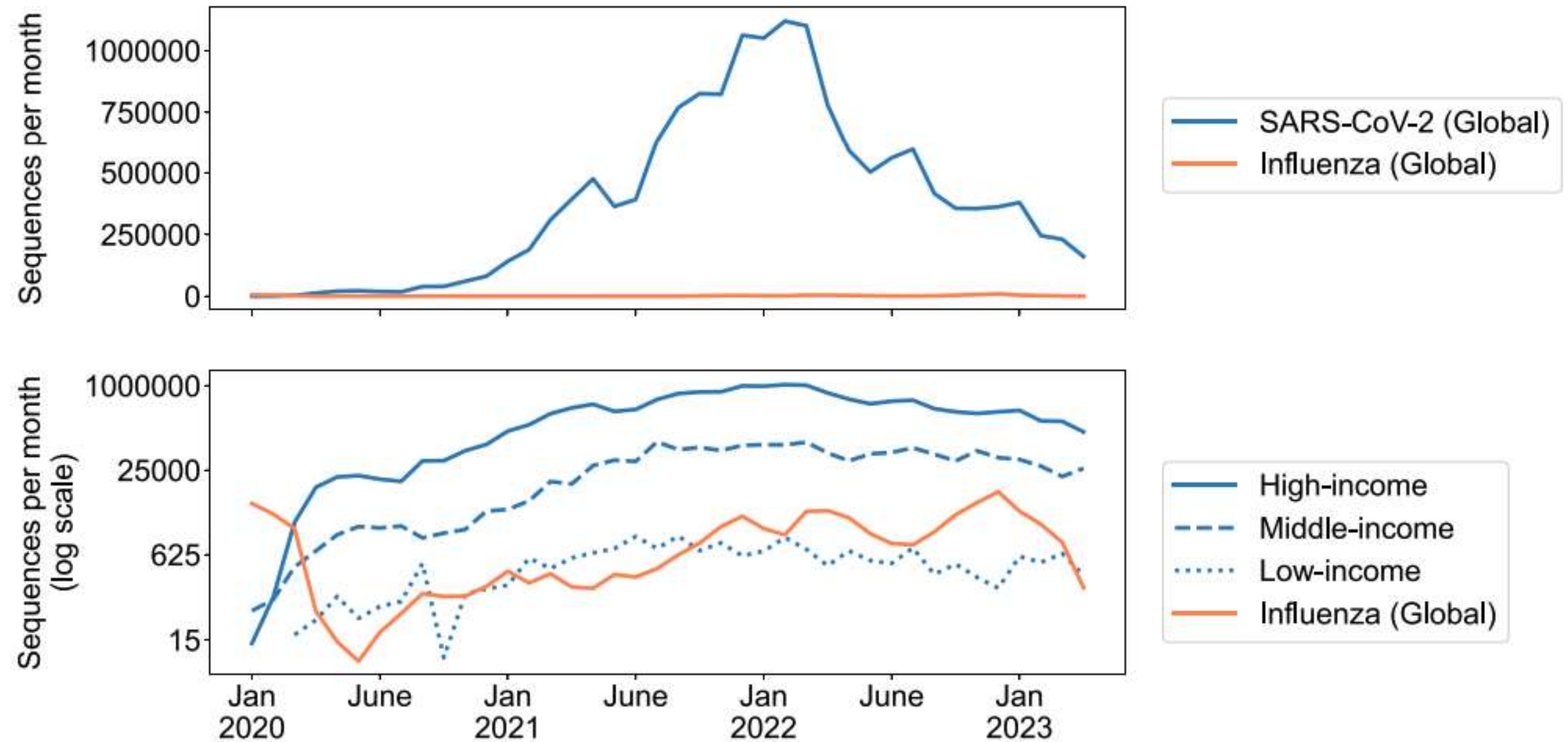
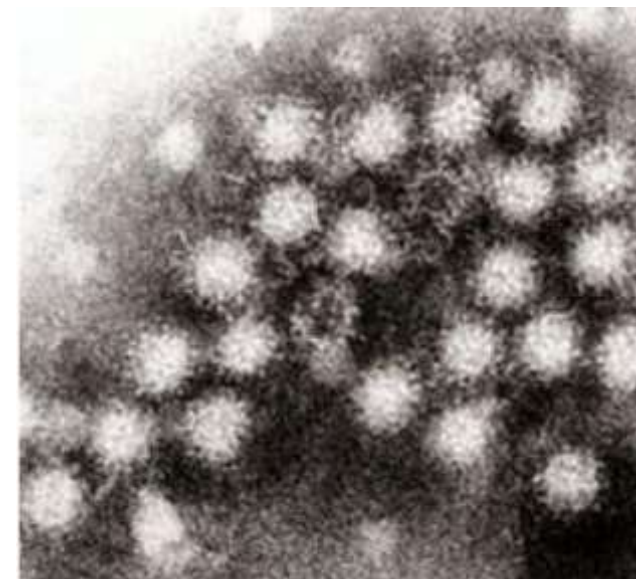
Mpox



RSV



Norovirus



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Josep F. Abril



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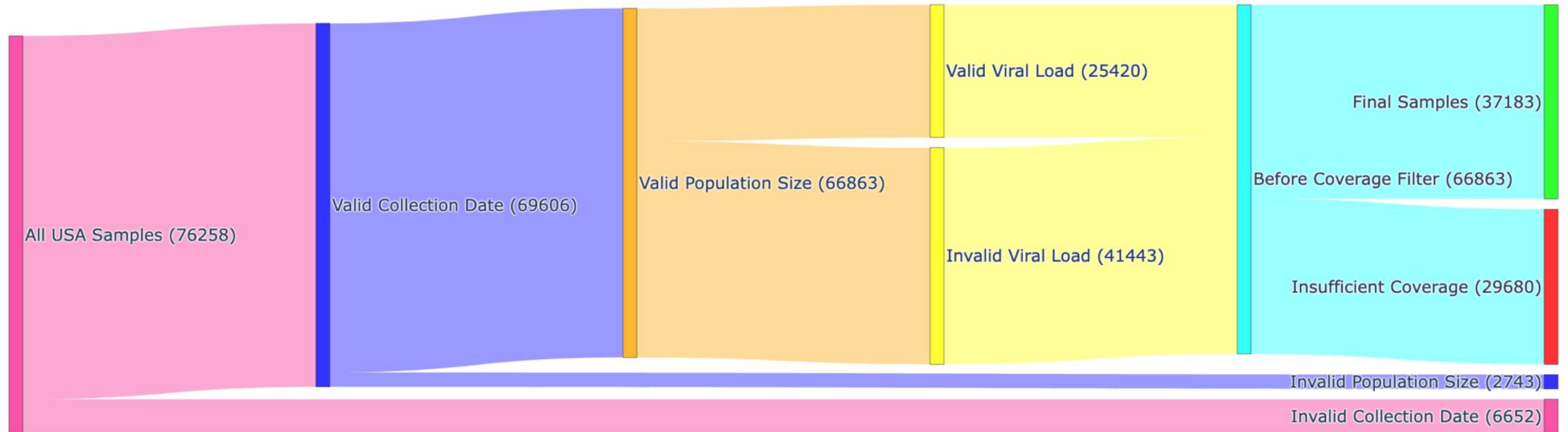


Natasha Quill
Daniel Rexin
David Winter
Joanne Hewitt



Quality assessment across the US

USA Sample Selection



Wastewater integrated genomic surveillance across diverse contexts

