A wastewater-integrated, global virus genomic surveillance framework **IDM Annual Meeting**





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Scripps Research



How we track viruses: case-based, clinical surveillance



How we track viruses: case-based, clinical surveillance







How we track viruses: case-based, clinical surveillance



55		-			10		
7	0.040	0.100	0.490	0.740	1.000		
(ska) 14	0.035	0.045	0.435	0.610	0.975		
und time	0.050	0.090	0.340	0.510	0.955		
Turnarol 85	0.020	0.080	0.325	0.500	0.855		
35	0.020	0.080	0.275	0.465	0.800		
1.3	0.05	0.1	0.5	1	5		
Percentage of sequenced cases							
0.	0 0.	1 0.2	2 0.3	0.4	0.5		
Probability of lineage detection before it reaches 100 cases Brito							



Under baseline conditions, few samples are sequenced



Washington State Department of Health



Wastewater provides an alternative data source



San Diego Epidemiology and Research for COVID Health

Wastewater presents an alternative data source





- 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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Problem: genome assembly fails for mixed virus samples



Reference Genome

Problem: genome assembly fails for mixed virus samples











Problem: genome assembly fails for mixed virus samples

<u>Need another approach to recover evolutionary dynamics from mixtures</u>



> 4000 SARS-CoV-2 lineages



Freyja-enabled surveillance: Omicron in San Diego





Karthikeyan and Levy et al., 2022

Integrated surveillance: An example region































Multi-modal, pandemic scale data platform





Multi-modal, pandemic scale data platform





Scalable wastewater bioinformatic pipeline



Tracking SARS-CoV-2 burden in CA







Tracking SARS-CoV-2 burden in CA







Tracking SARS-CoV-2 burden in CA









Tracking SARS-CoV-2 burden in CA



er viral load (normalized) Wastewat







Deployment via our collaborative network

Apr May Jun Jul Aug Sep Oct Nov Dec 2023 Feb Mar Apr May Jun Jul Aug Sep Oct Nov

Freyja network programs and centers

Regional and national wastewater sentinel programs

Spain (Catalonia)

Wastewater consistently acts as a leading indicator

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

40% -35% - 30% -25% -20% -15% -10% - 5%

Combining for more robust, comprehensive monitoring

With less clinical data, wastewater is increasingly important

Influenza

RSV

Norovirus

per month

Sequences

1000000 Sequences per month (log scale) 25000 625-15

Ladner and Sahl, 2023

Acknowledgments

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Wastewater Genomics WASTEWATER GENOMICS SYNDICATE

OUTBREAK TRACKING AT SCALE

NATIONAL INSTITUTE FOR COMMUNICABLE DISEASE

Nosihle Msomi Lindo Ndlovu Phindile Ntuli Setshaba Taukobong Victor Mabasa Kerrigan McCarthy Mukhlid Yousif

NATIONAL ** WASTEWATER SURVEILLANCE SYSTEM

STATENS SERUM INSTITUT

UNIVERSITAT DE BARCELONA

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Namrta Daroch Farah Ishtiaq

Natasha Quill Daniel Rexin **David Winter** Joanne Hewitt

National Institute of Allergy and Infectious Diseases

Quality assessment across the US

USA Sample Selection

	Valid Viral Load (25420)	Final Samples (37183	
ation Size (66863)		Before Coverage Filter (66863)	
	Invalid Viral Load (41443)	Insufficient Coverage (29680	
		Invalid Population Size (2743	
		Invalid Collection Date (6652	

Wastewater integrated genomic surveillance across diverse

aantavta

Karthikeyan, Levy et al., Nature 2022 Levy et al., Science 2023