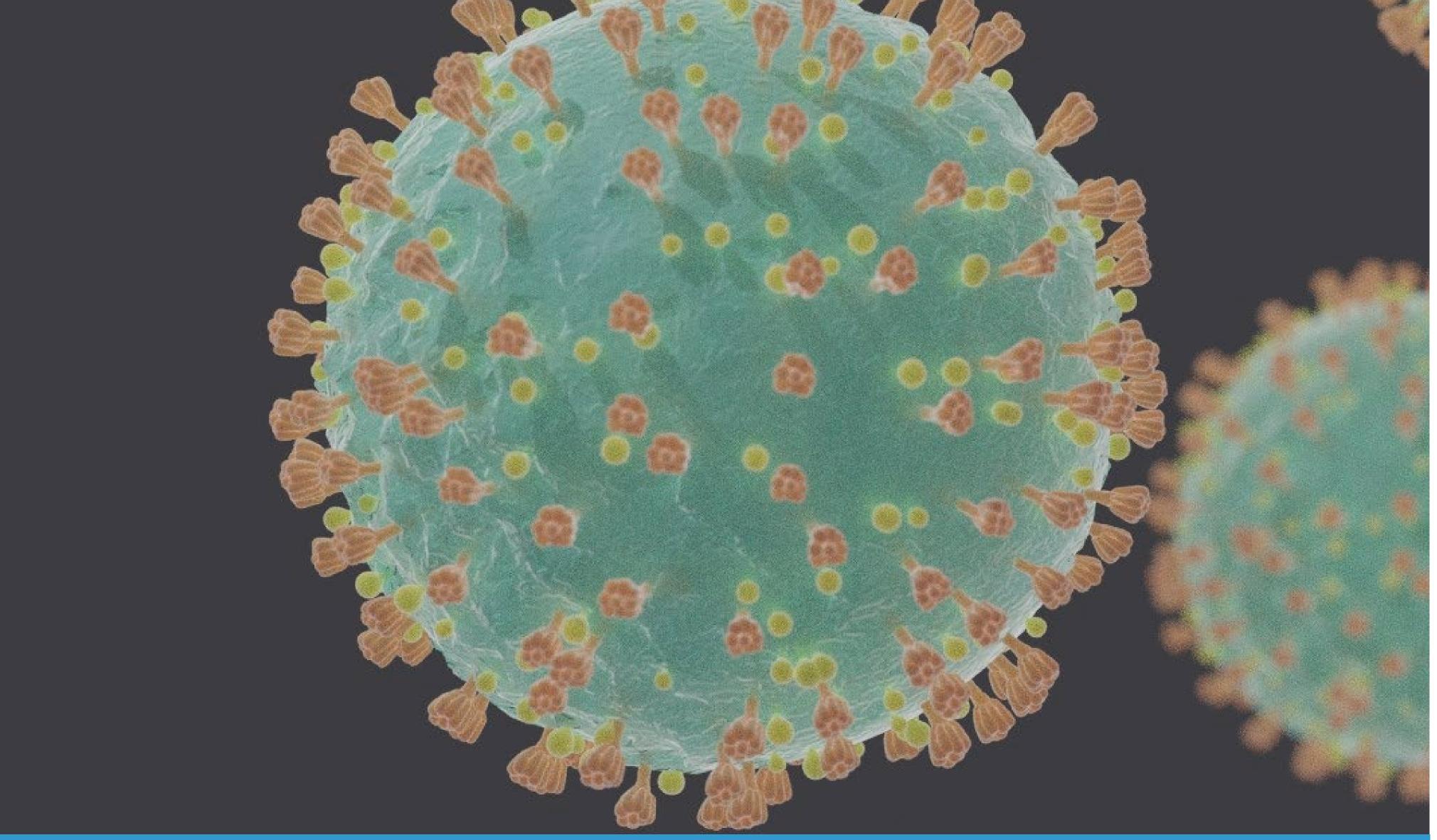
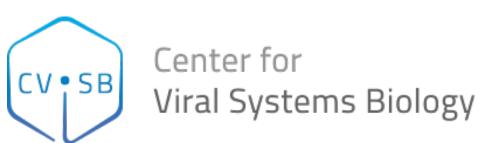
Outbreaky'omics



















Surveilance Emergence Detection

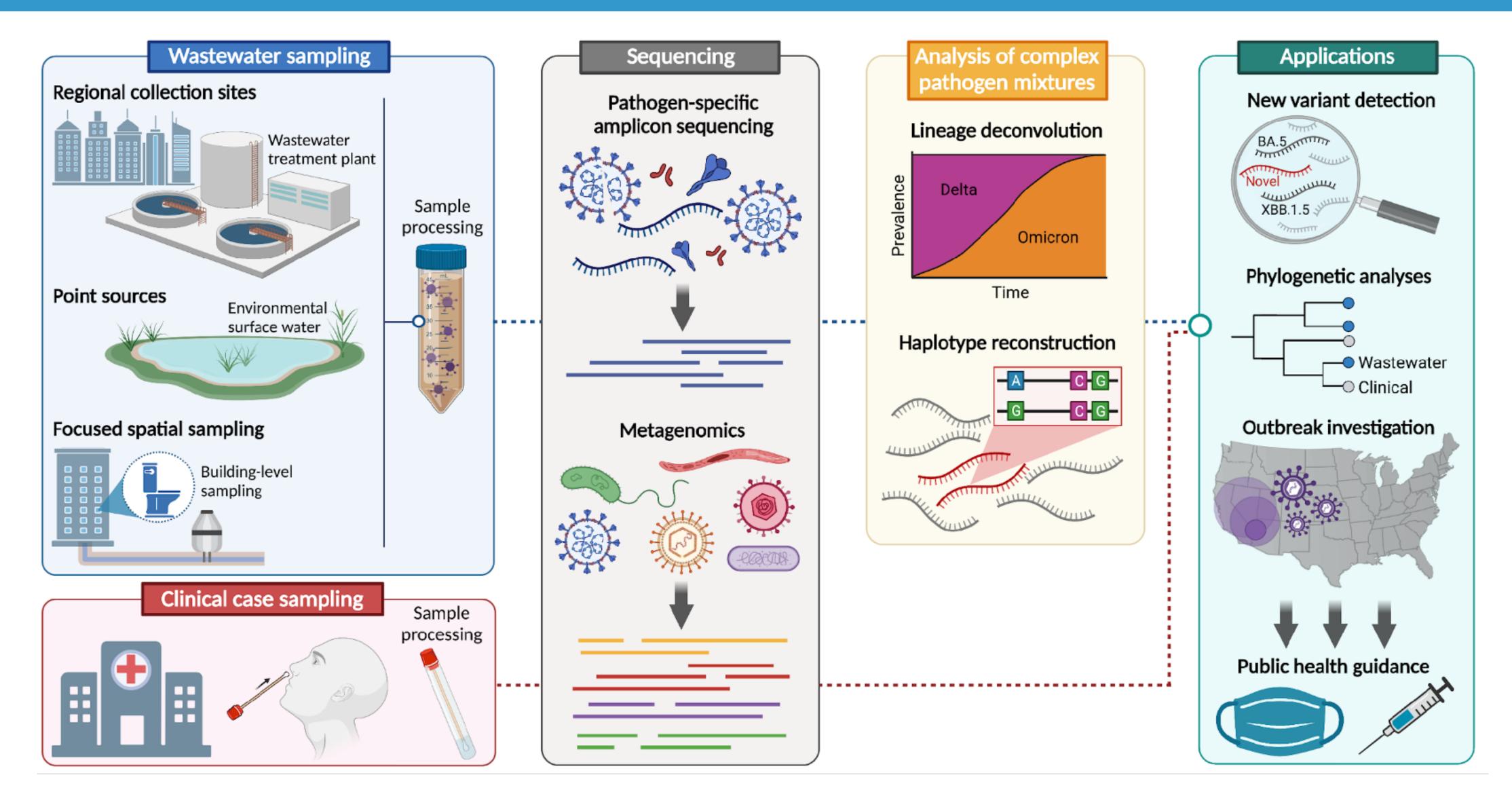
Epidemic > Endemic

What is out there?

ACTIVE Bassive Surveillance

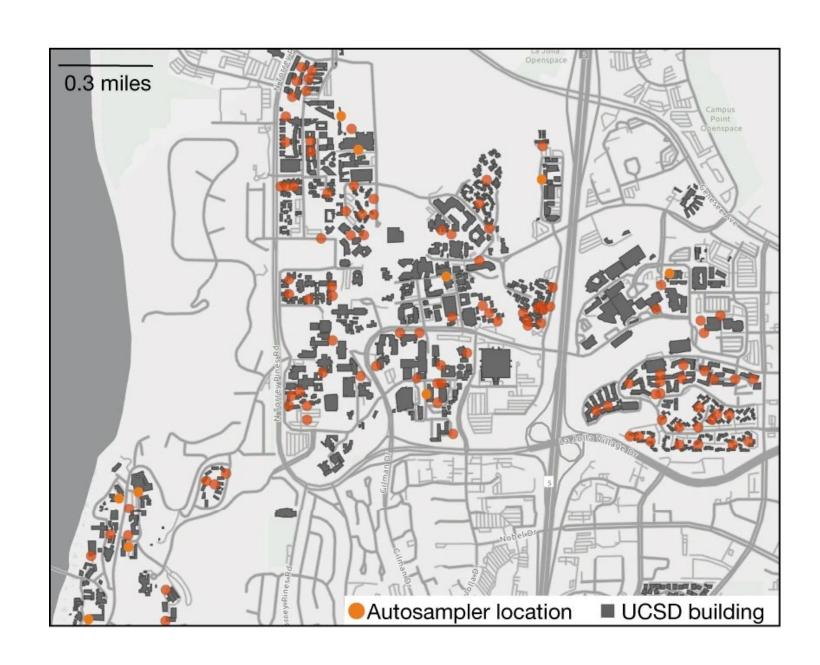
EXPECTEC Onexpected

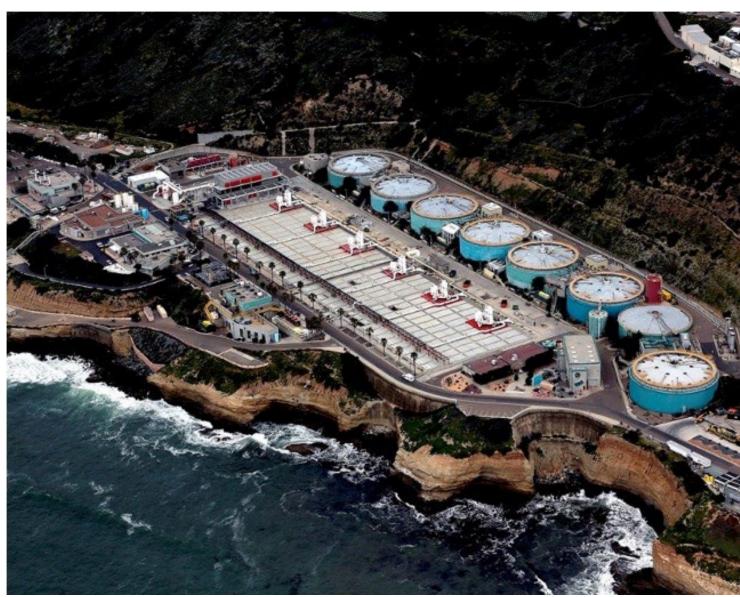
the future!

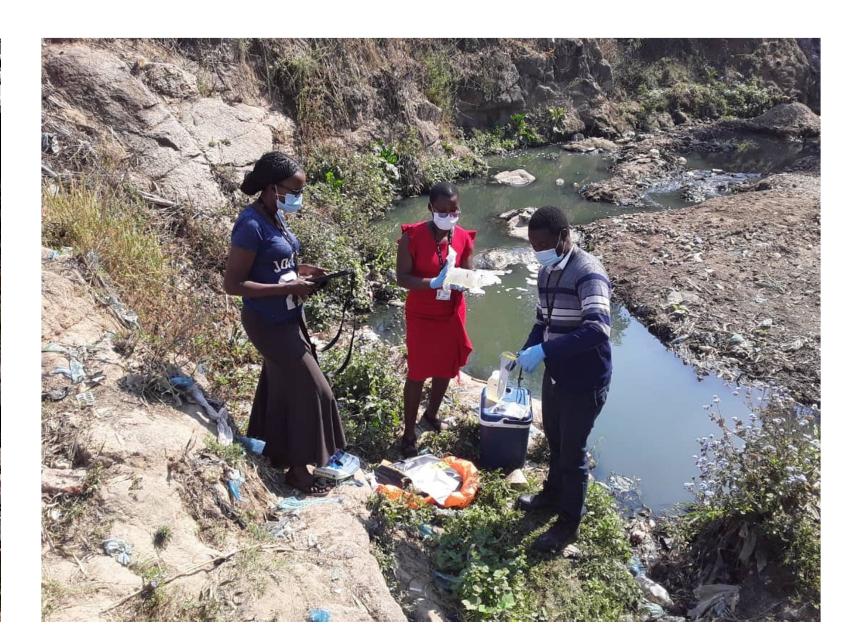


Passive surveillance Active

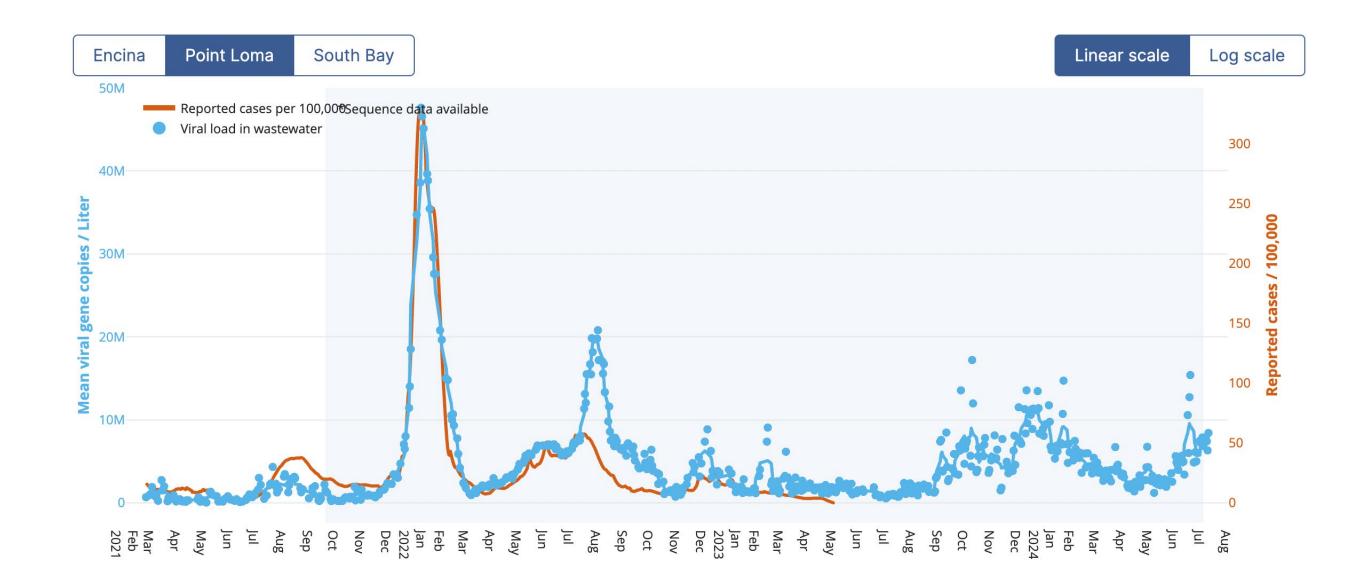
What is possible in San Diego should also be possible anywhere else







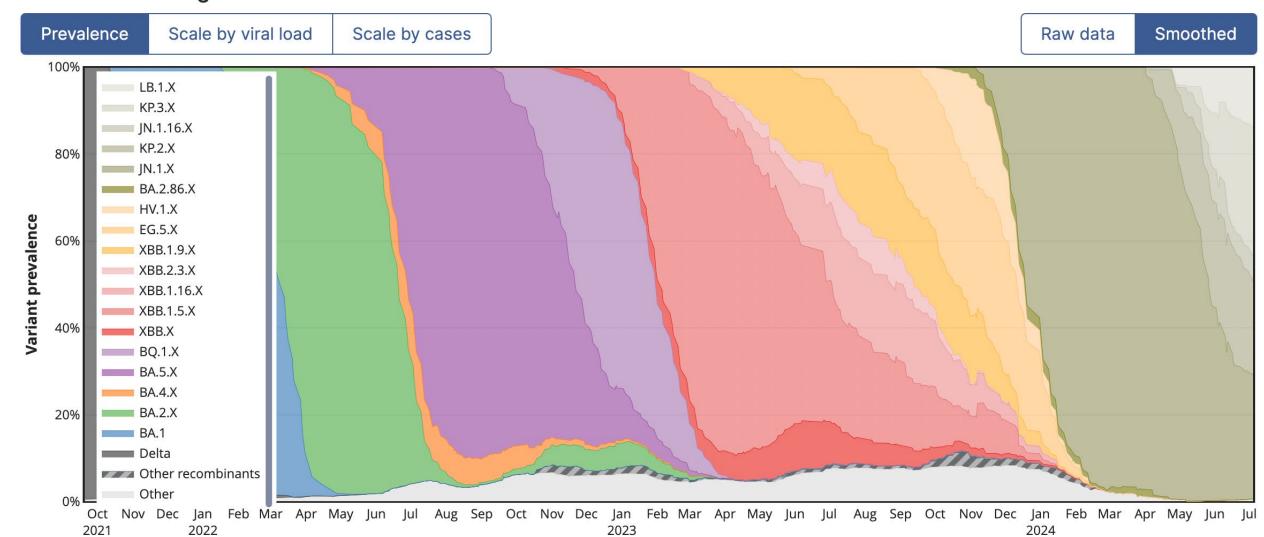
Real-time monitoring of viral dynamics | San Diego



Lineage	Growth Advantage	Bootstrap 95% CI
KP.3.X	11.7%	[6.07% , 19.90%]
KP.2.X	2.8%	[-3.69%, 9.61%]
LB.1.X	1.9%	[-26.94%, 26.40%]
JN.1.11.X	-3.0%	[-14.35%, 5.76%]
JN.1.16.X	-4.8%	[-17.57% , 11.75%]
KQ.1.X	-12.4%	[-249.77%, -6.18%]
JN.1.7.X	-26.0%	[-164.21% , -16.11%]
JN.1.X	-129.2%	[-215.28%, 34.53%]

Updated at July 15 @ 06:33 PM PDT

Wastewater lineages















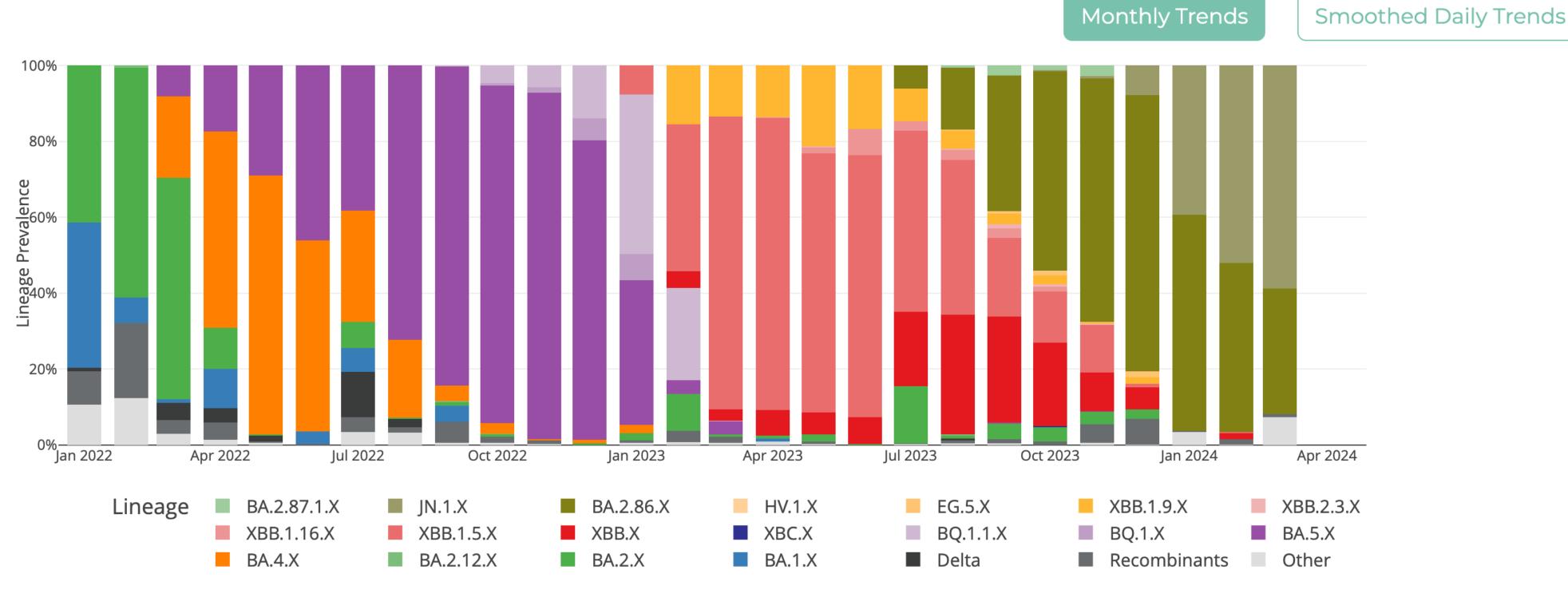
Real-time monitoring of viral dynamics | South Africa







Lineage Prevalence Observed via Wastewater



Participating Institutions



Division of the National Health Laboratory Service



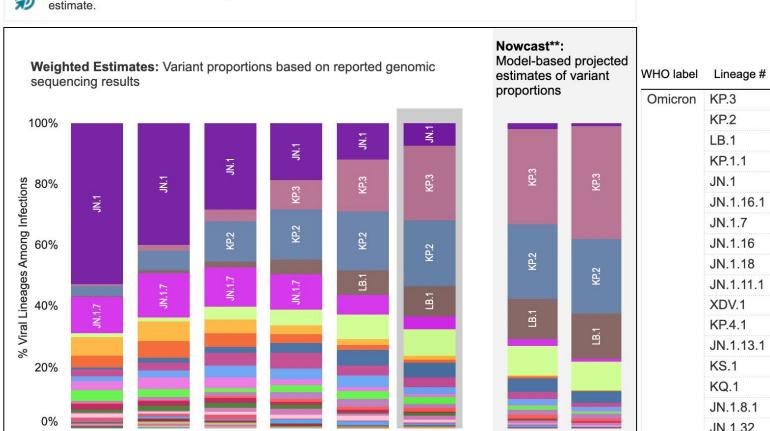


Real-time monitoring of viral dynamics | United States



Weighted Estimates in United States for 2-Week Periods in 3/17/2024 – 7/6/2024

Weighted Estimates in United States for 5/26/2024 – 6/8/2024

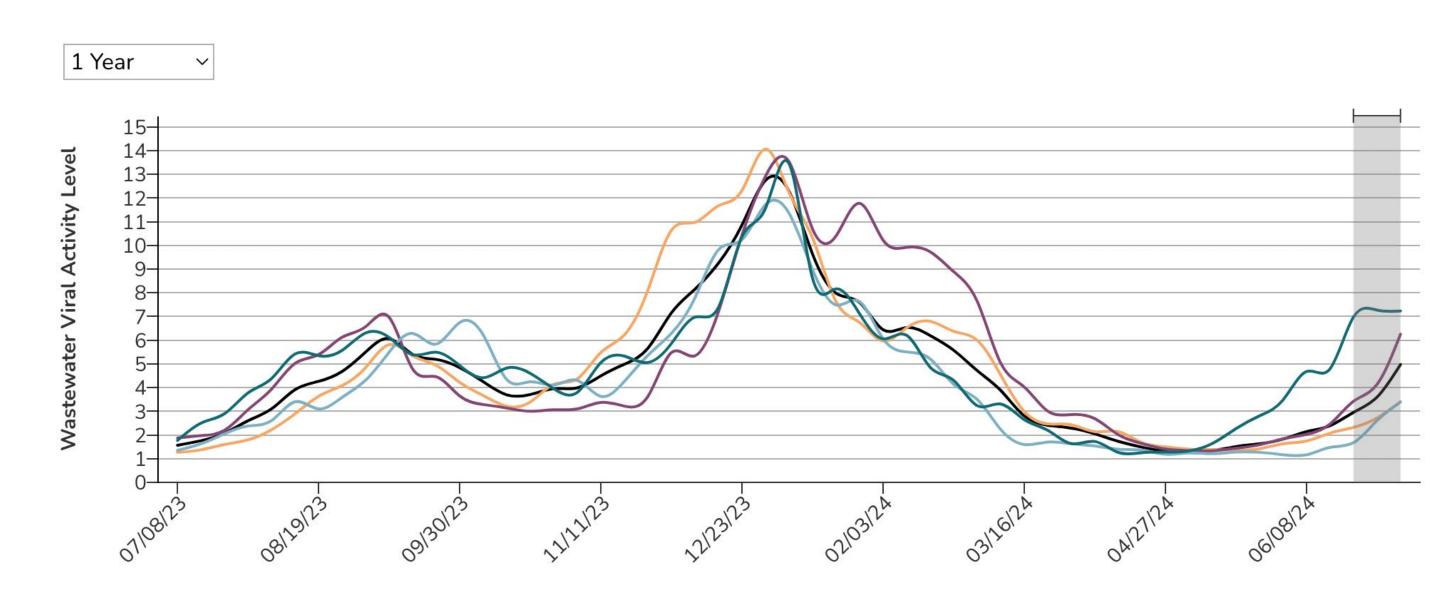


Collection date, two-week period ending

VHO label	Lineage #	%Total		95%CI
Omicron	KP.3		24.5%	18.4-31.6%
	KP.2		21.5%	17.5-25.9%
	LB.1		10.0%	5.2-17.0%
	KP.1.1		8.9%	4.6-15.2%
	JN.1		7.4%	4.8-10.9%
	JN.1.16.1		4.8%	2.5-8.2%
	JN.1.7	†	4.0%	1.7-7.9%
	JN.1.16		3.1%	1.6-5.4%
	JN.1.18		2.2%	1.2-3.7%
	JN.1.11.1		2.1%	1.1-3.7%
	XDV.1	†	1.4%	0.2-5.0%
	KP.4.1	†	1.3%	0.4-3.4%
	JN.1.13.1	†	1.2%	0.3-3.0%
	KS.1	†	1.1%	0.4-2.6%
	KQ.1	†	1.1%	0.1-3.7%
	JN.1.8.1	†	1.0%	0.3-2.4%
	JN.1.32	†	0.8%	0.0-4.4%
	KW.1.1	†	0.8%	0.2-2.2%
	XDP	†	0.6%	0.1-1.8%
	KV.2	†	0.3%	0.0-1.2%
	JN.1.4.3	†	0.3%	0.0-1.5%
	BA.2	†	0.0%	0.0-0.4%

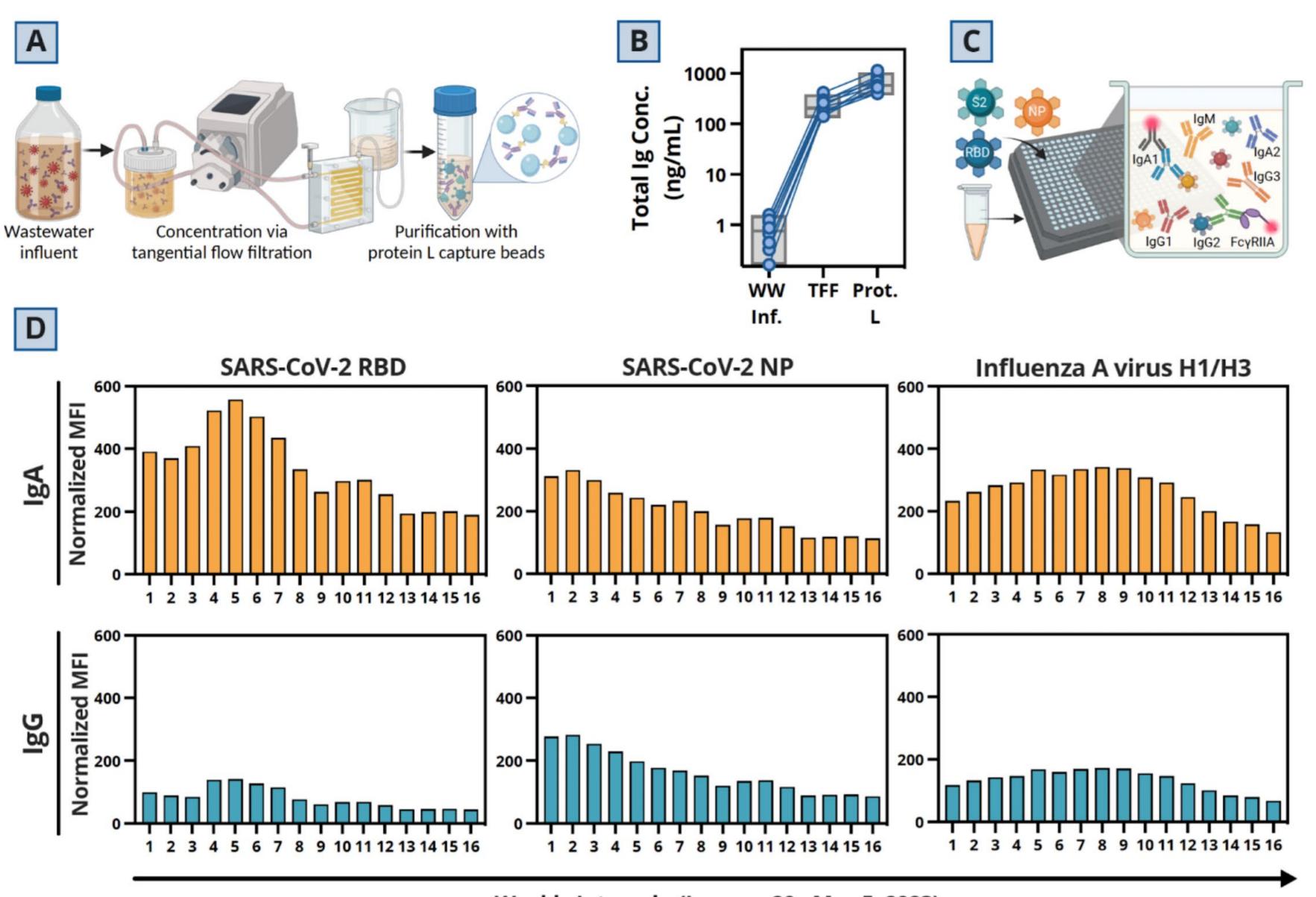


National Wastewater Surveillance System (NWSS)



Profiling population-wide immunity using





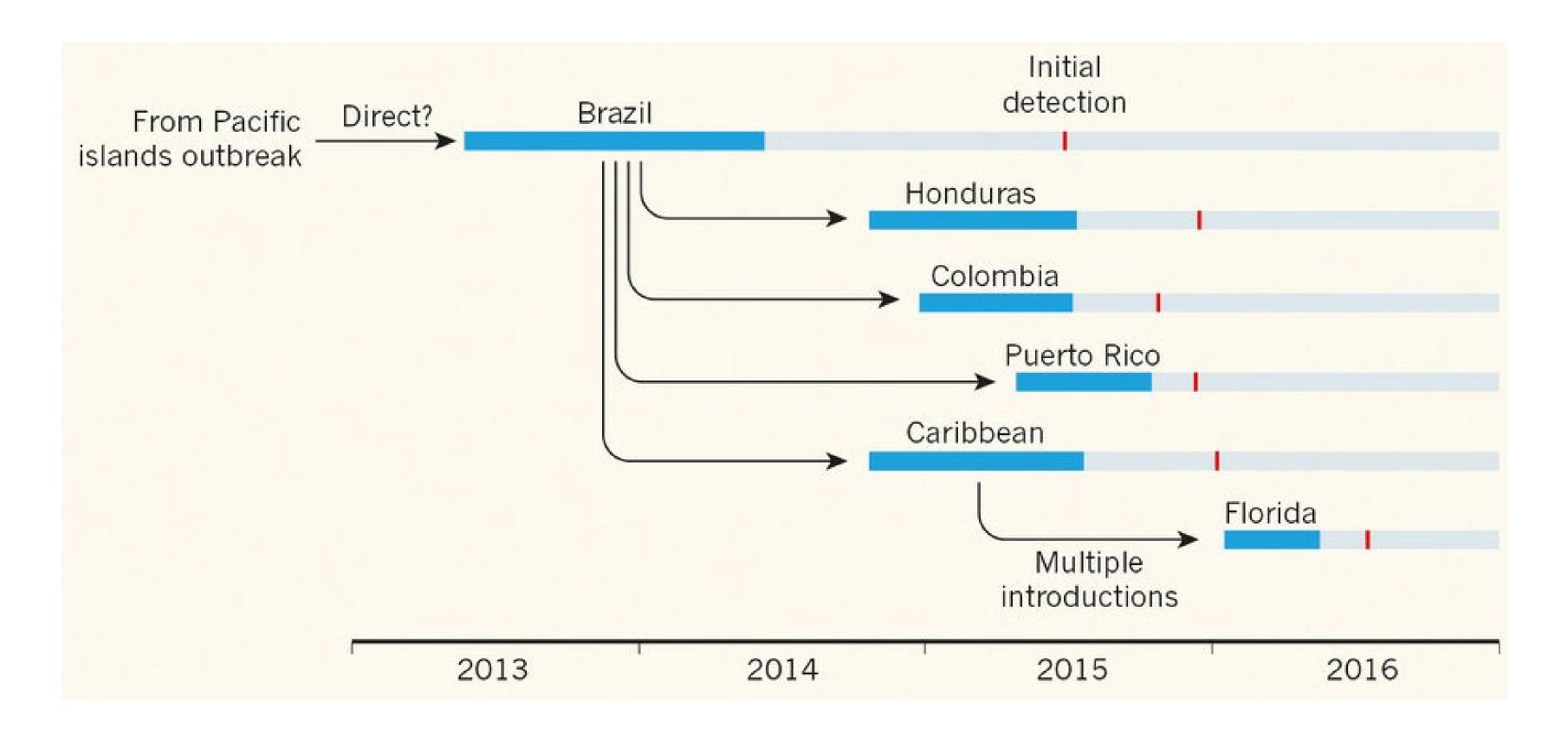






Shortening surveillance gaps

Surveillance Gaps are widespread | Zika example



Genomic epidemiology reveals multiple introductions of Zika virus into the United States

Nathan D. Grubaugh, Jason T. Ladner, Moritz U. G. Kraemer, Gytis Dudas, Amanda L. Tan,
Karthik Gangavarapu, Michael R. Wiley, Stephen White, Julien Thézé, Diogo M. Magnani, Karla
Prieto, Daniel Reyes, Andrea M. Bingham, Lauren M. Paul, Refugio Robles-Sikisaka, Glenn
Oliveira, Darryl Pronty, Carolyn M. Barcellona, Hayden C. Metsky, Mary Lynn Baniecki, Kayla G.
Barnes, Bridget Chak, Catherine A. Freije, Adrianne Gladden-Young, ... Kristian G. Andersen

Nature **546**, 401–405 (2017) Cite this article

Zika virus evolution and spread in the Americas

Hayden C. Metsky, Christian B. Matranga, Shirlee Wohl, Stephen F. Schaffner, Catherine A.

Freije, Sarah M. Winnicki, Kendra West, James Qu, Mary Lynn Baniecki, Adrianne GladdenYoung, Aaron E. Lin, Christopher H. Tomkins-Tinch, Simon H. Ye, Daniel J. Park, Cynthia Y.
Luo, Kayla G. Barnes, Rickey R. Shah, Bridget Chak, Giselle Barbosa-Lima, Edson Delatorre,
Yasmine R. Vieira, Lauren M. Paul, Amanda L. Tan, Carolyn M. Barcellona, ... Pardis C.

Sabeti + Show authors

Nature **546**, 411–415 (2017) Cite this article

Establishment and cryptic transmission of Zika virus in Brazil and the Americas

N. R. Faria, J. Quick, I.M. Claro, J. Thézé, J. G. de Jesus, M. Giovanetti, M. U. G. Kraemer, S. C. Hill, A. Black, A. C. da Costa, L. C. Franco, S. P. Silva, C.-H. Wu, J. Raghwani, S. Cauchemez, L. du Plessis, M. P. Verotti, W. K. de Oliveira, E. H. Carmo, G. E. Coelho, A. C. F. S. Santelli, L. C. Vinhal, C. M. Henriques, J. T. Simpson, ... O. G. Pybus

Nature **546**, 406–410 (2017) Cite this article

From: Worobey, Nature 2017

Surveillance Gaps lead to cryptic transmissions

Ebola, West Africa: ~3 months (unexpected, new region)

Zika, Brazil: ~1.5 years (unexpected, new region)

Zika, United States: ~3 months (expected)

Mpox, Nigeria: ~2 years (unexpected, human-to-human transmission)

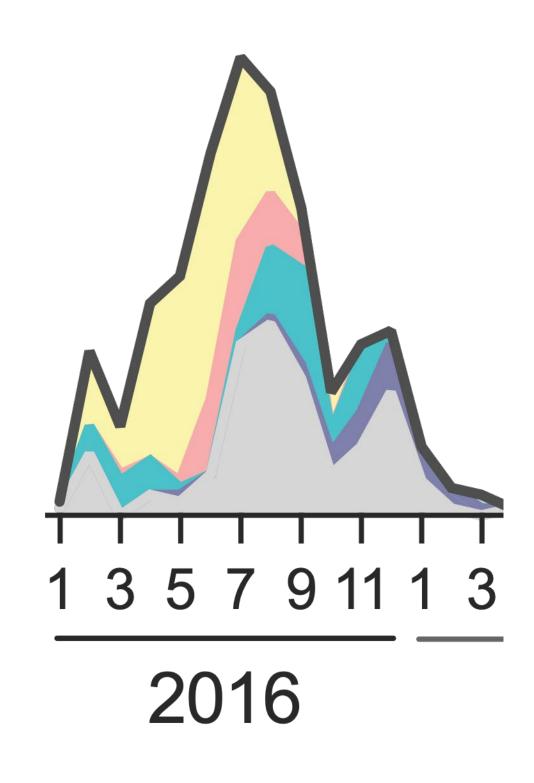
H5N1, United States: ~3 months (should have been expected)

SARS-CoV-2, China: ~1 month (novel)

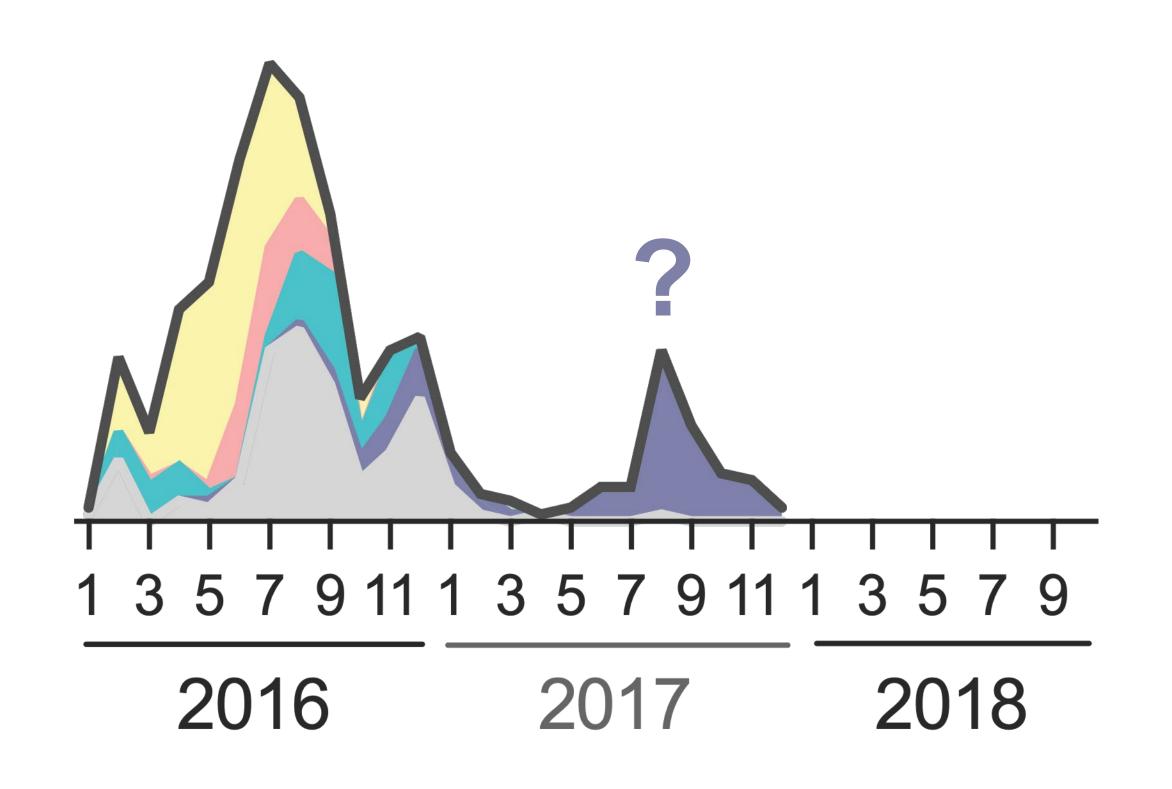
SARS-CoV-2, United States: ~1 month (expected)

SARS-CoV-2 variants, South Africa: ~a few weeks (semi-novel)

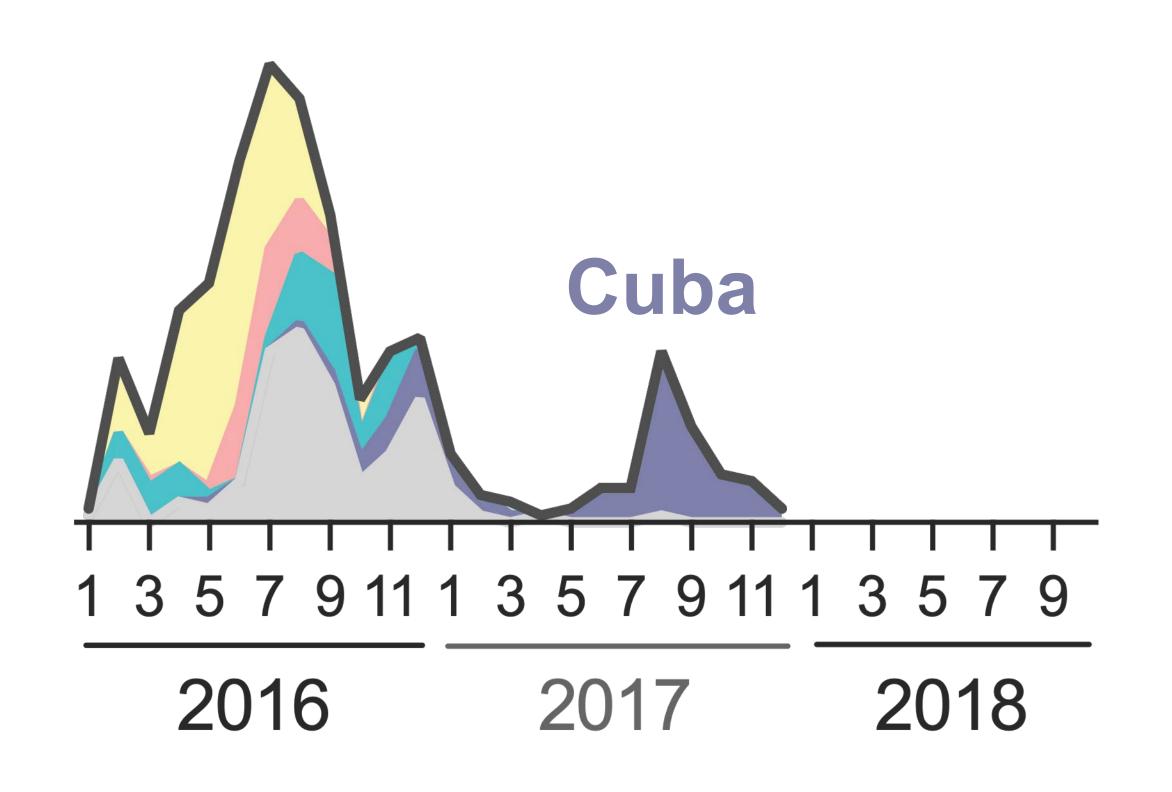
Detecting outbreaks that we don't know about (travel surveillance)



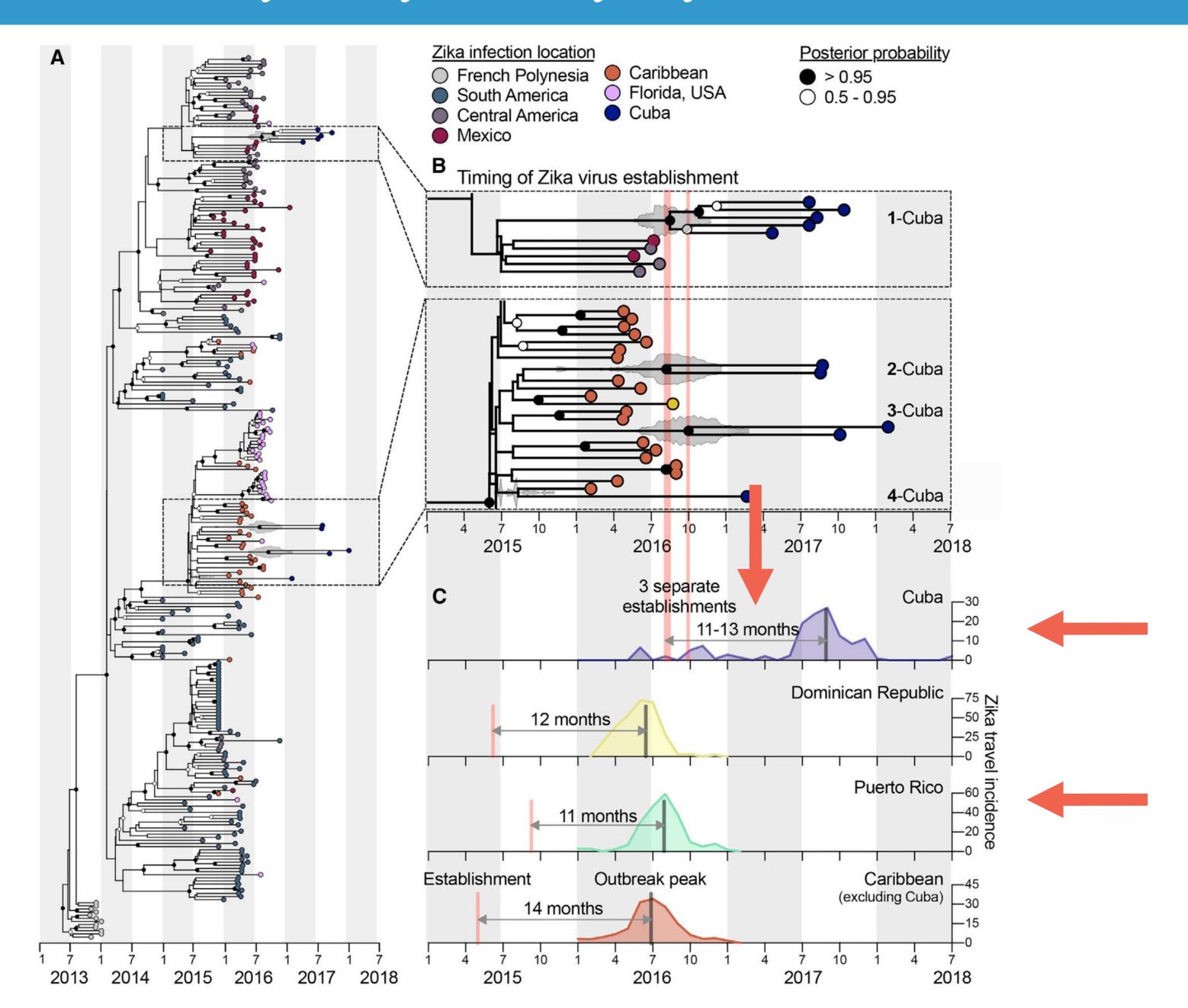
Detecting outbreaks that we don't know about (travel surveillance)



Detecting outbreaks that we don't know about (travel surveillance)



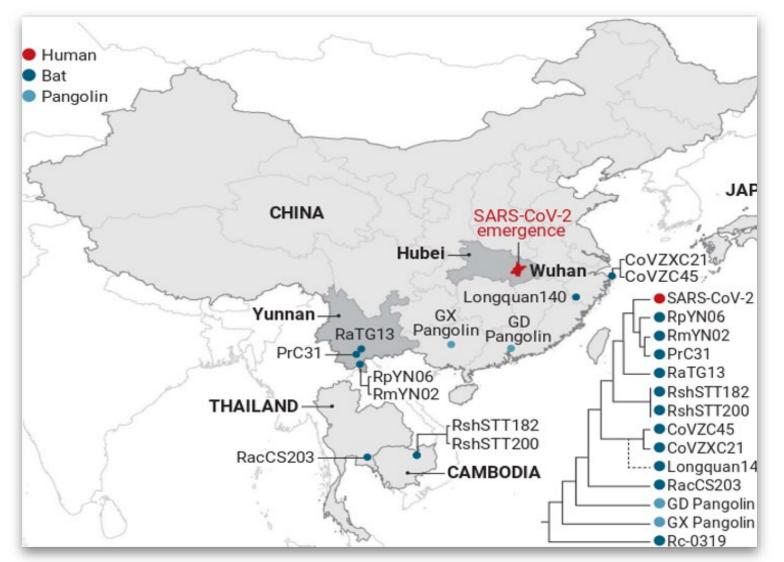
Outbreak in Cuba was delayed by exactly a year



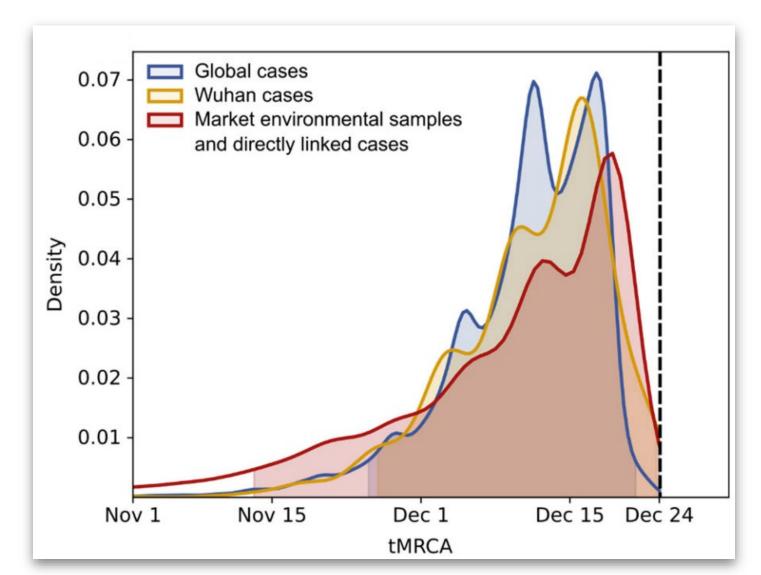
Understanding emergence



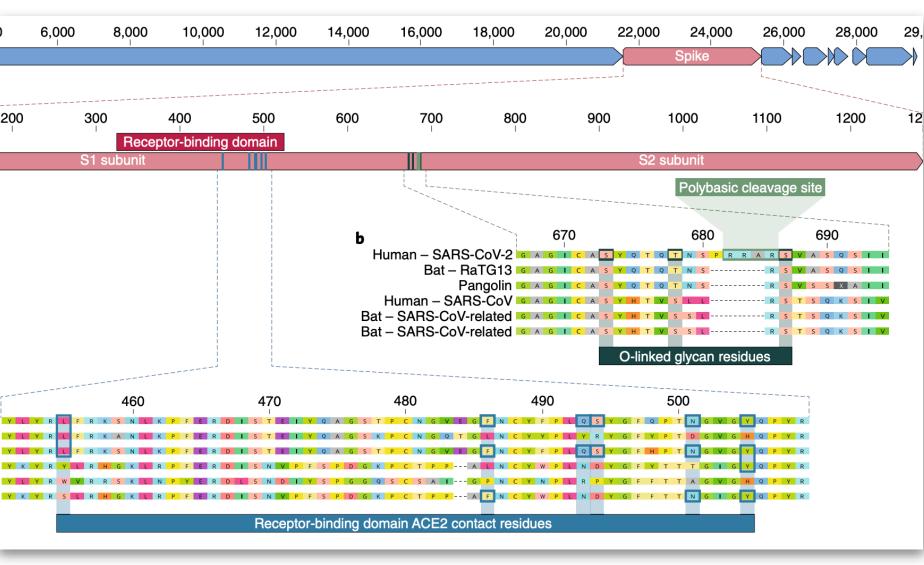
The origin of SARS-CoV-2 links to a single market in the middle of Wuhan



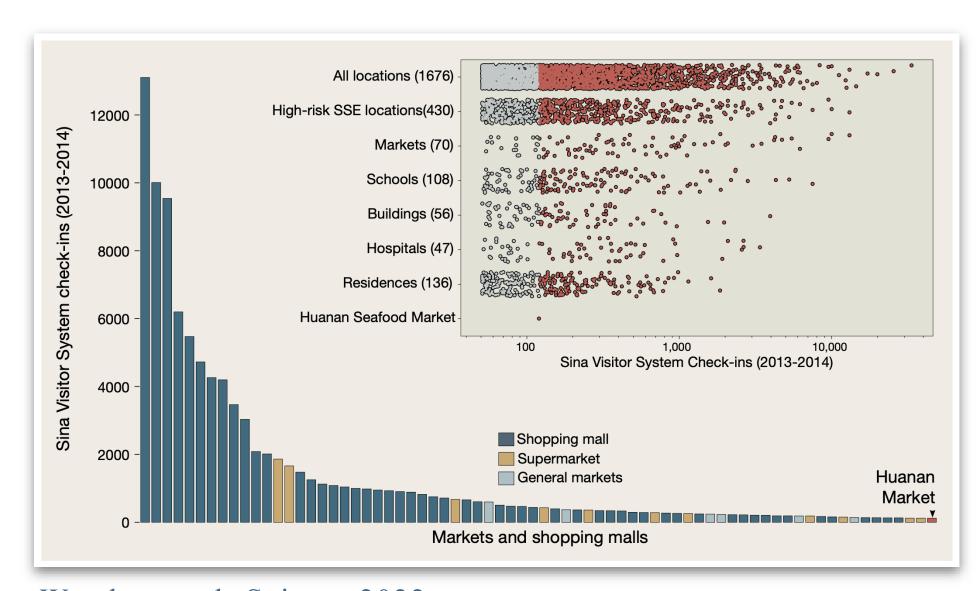
From: Lytras et al., Science 2021



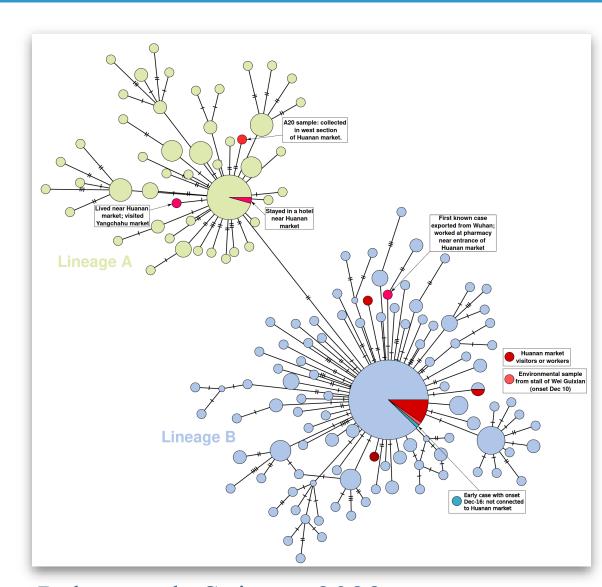
Crits-Christoph et al., Cell (accepted)



Andersen et al., Nature Medicine 2020

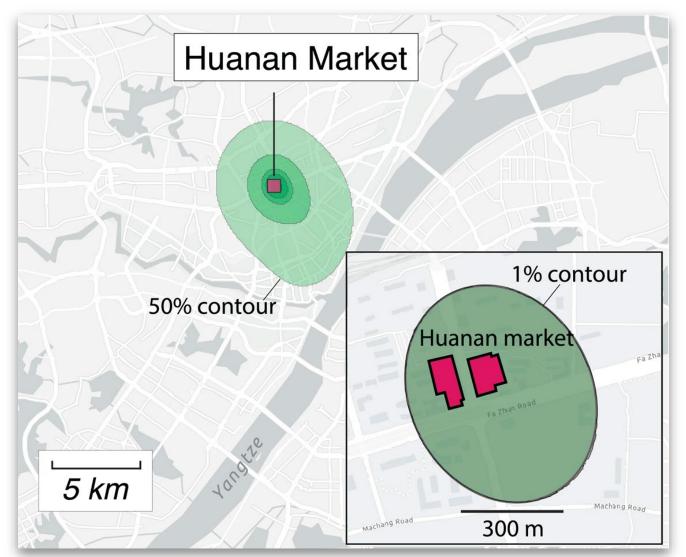


Worobey et al., Science 2022



Pekar et al., Science 2022

The origin of SARS-CoV-2 links to a single market in the middle of Wuhan



Worobey et al., Science 2022

Hannan 0.5% 4/662

Jiangxia 0.4% 6/935

Seropositivity (%)

No data

1.00 - 5.00

<0.1 0.01 - 0.99 County

Not available

0.01 - 0.99

1.00 - 4.99 5.00-11.20

From: Li et al., Lancet Reg Health West Pac 2021

Region/province

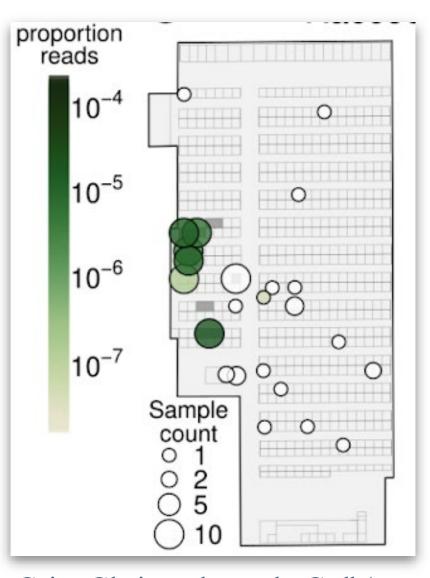


Excess Deaths

Holmes et al., Cell 2021



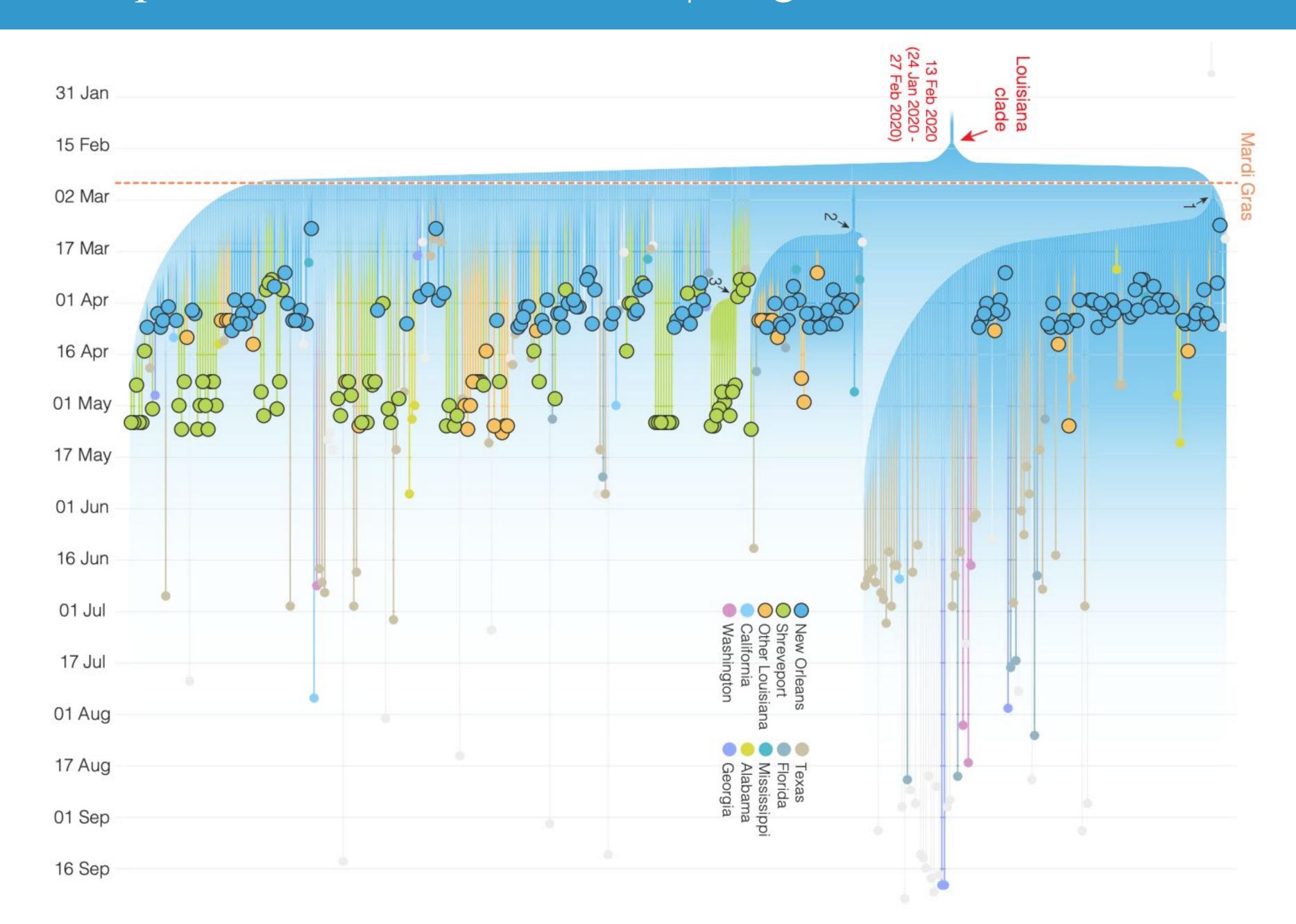




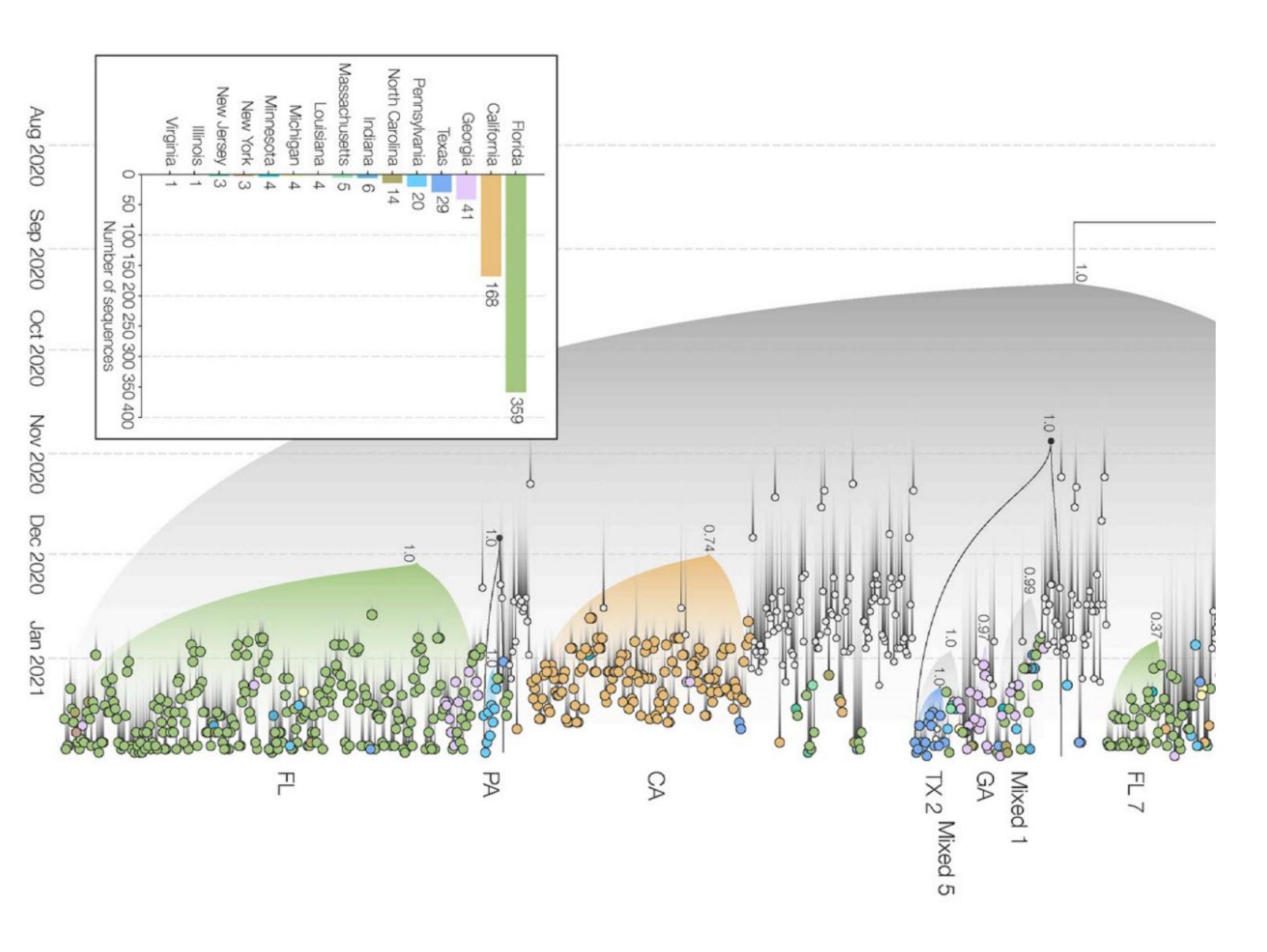
Crits-Christoph et al., Cell (accepted)

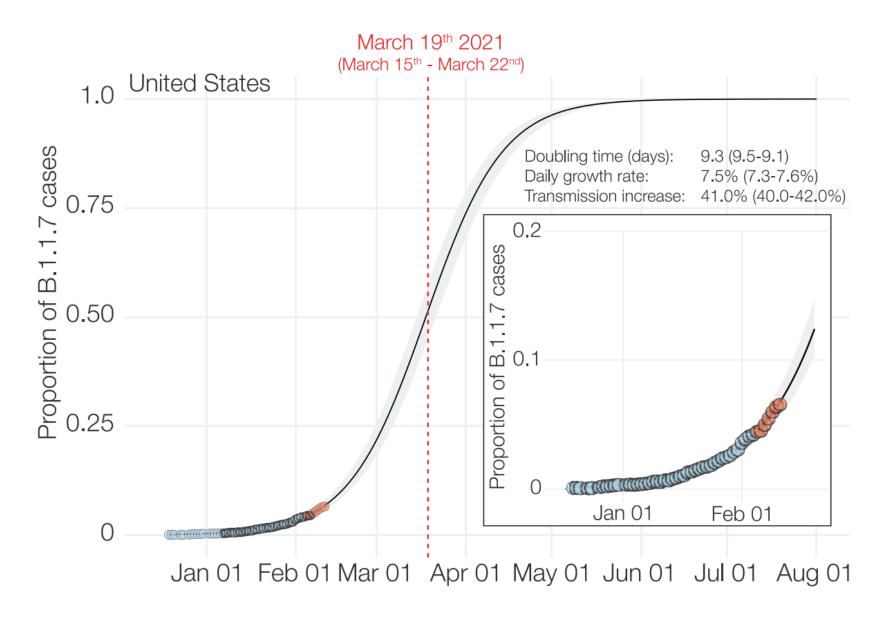
Epidemic > Endemic

Early explosive spread in the United States | Single introduction into New Orleans

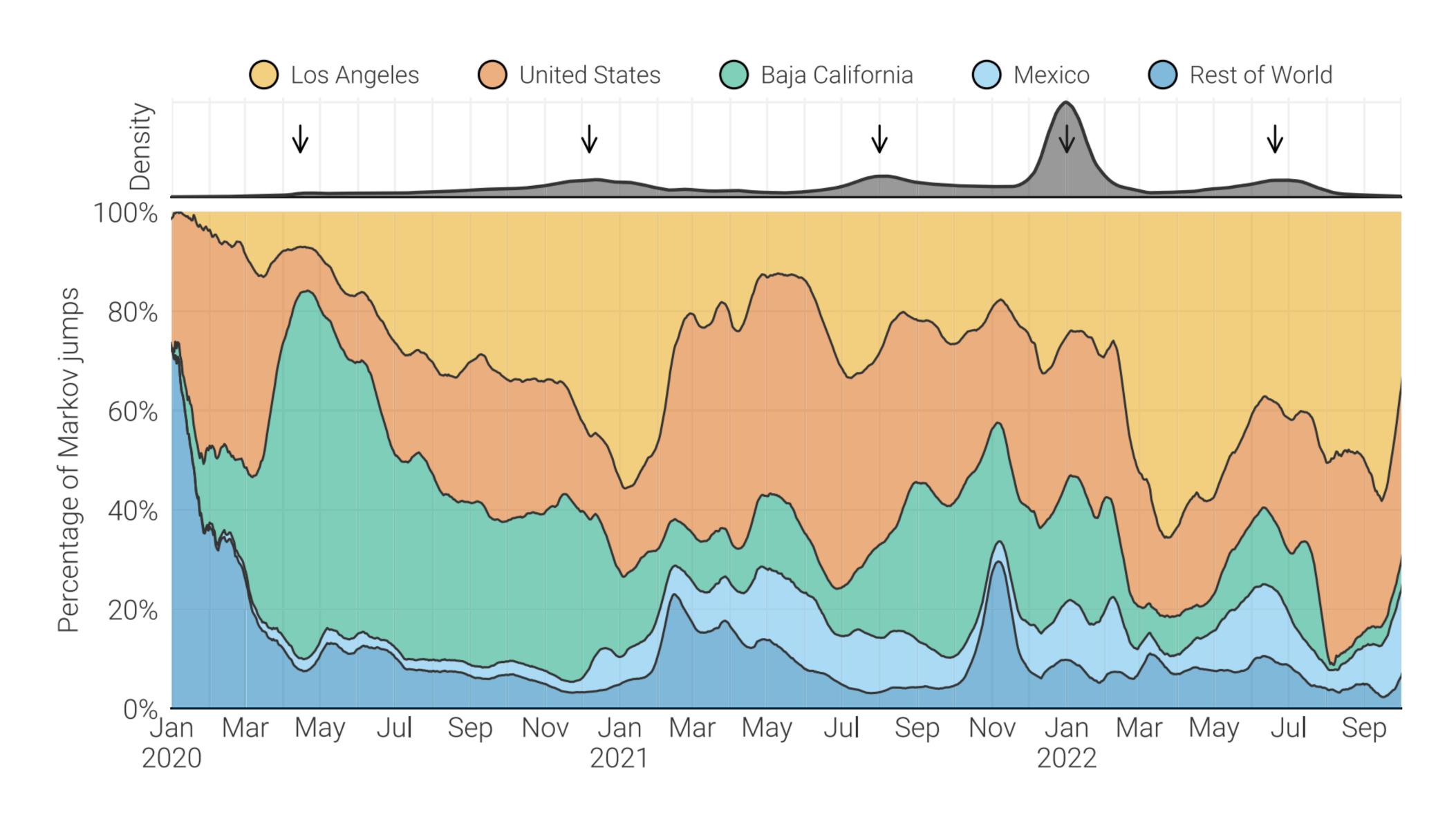


Then came the variants





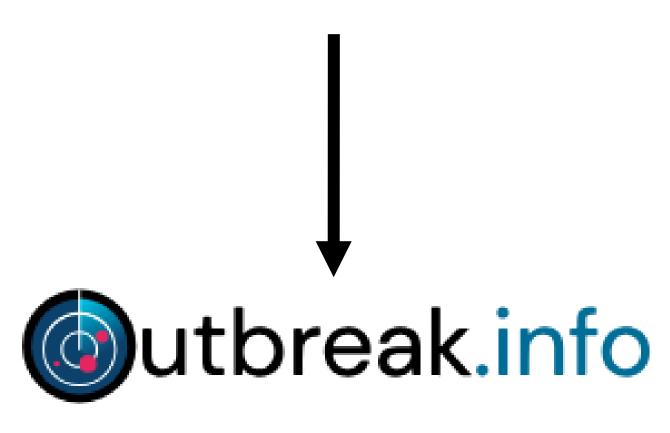
Connectedness was dynamic and changed as we moved from pandemic to endemic



Endemic | Functional surveillance

Software





Gangavarapu et al., Nature Methods 2023 Tsueng et al., Nature Methods 2023



De facto standard
FDA
CDC
Biobot
Internationally

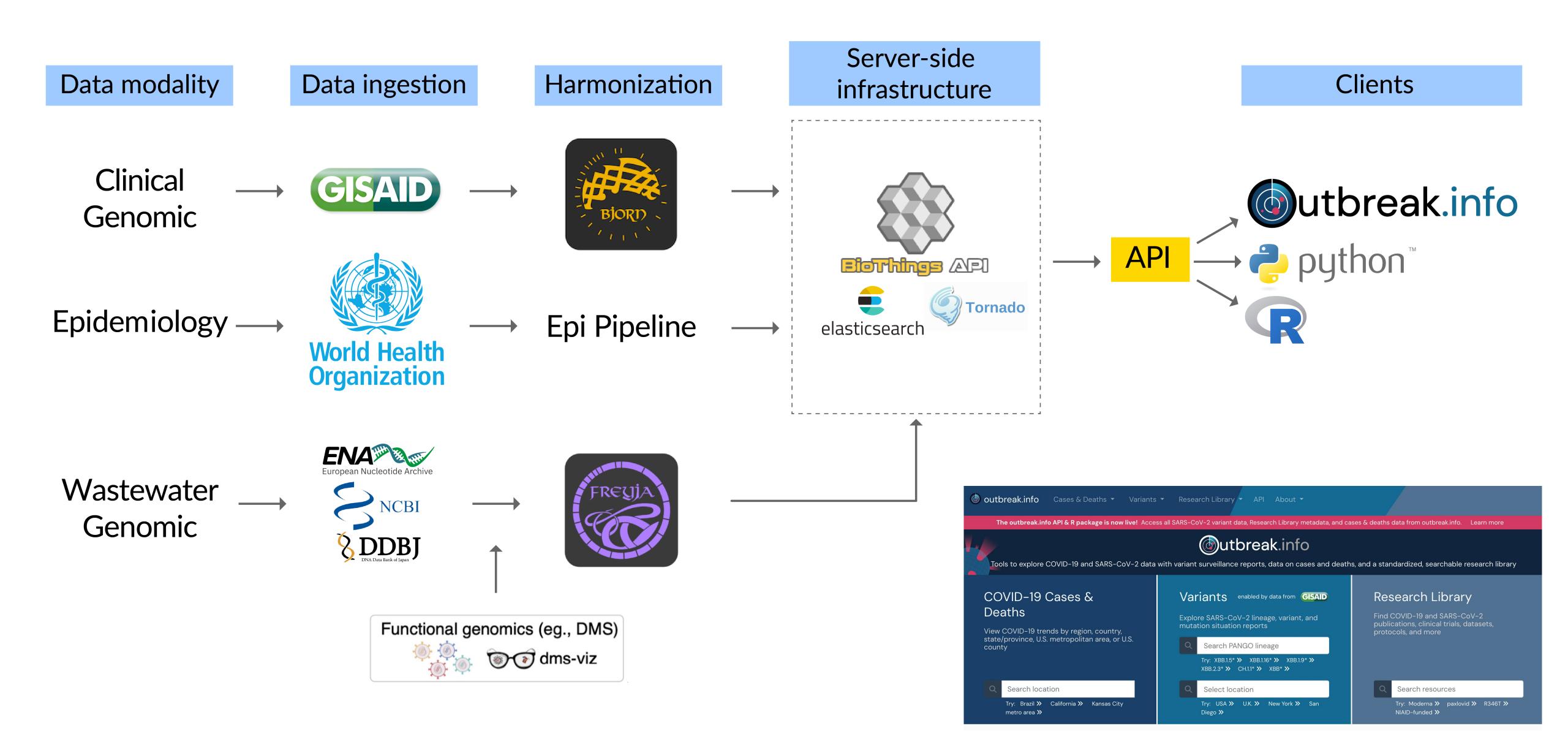


De facto standard Millions of download

Karthikeyan et al., Nature 2022

Grubaugh et al., Genome Biology 2019

Integrated programs | H5N1, SARS-CoV-2, others



Acknowledgements















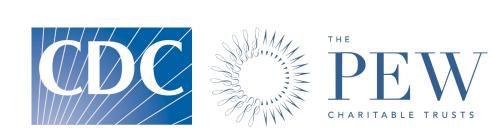
















US DK MX IN NL FR ZA LT SL

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