COVIDTracker

Routine genomic epidemiology for local public health

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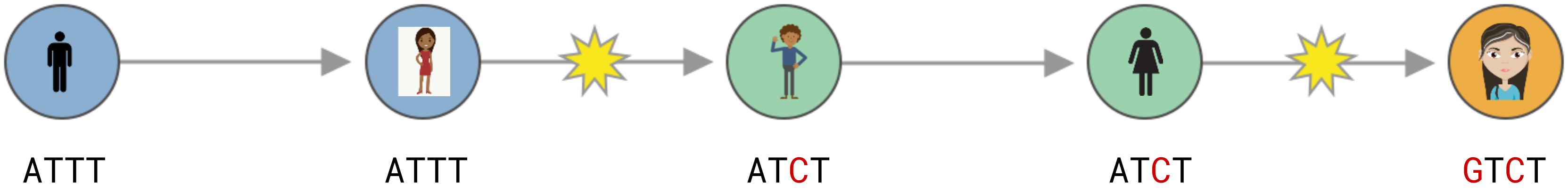
What is COVID Tracker?

An end-to-end program to empower **local** public health to **use genomic data** in their COVID19 response.

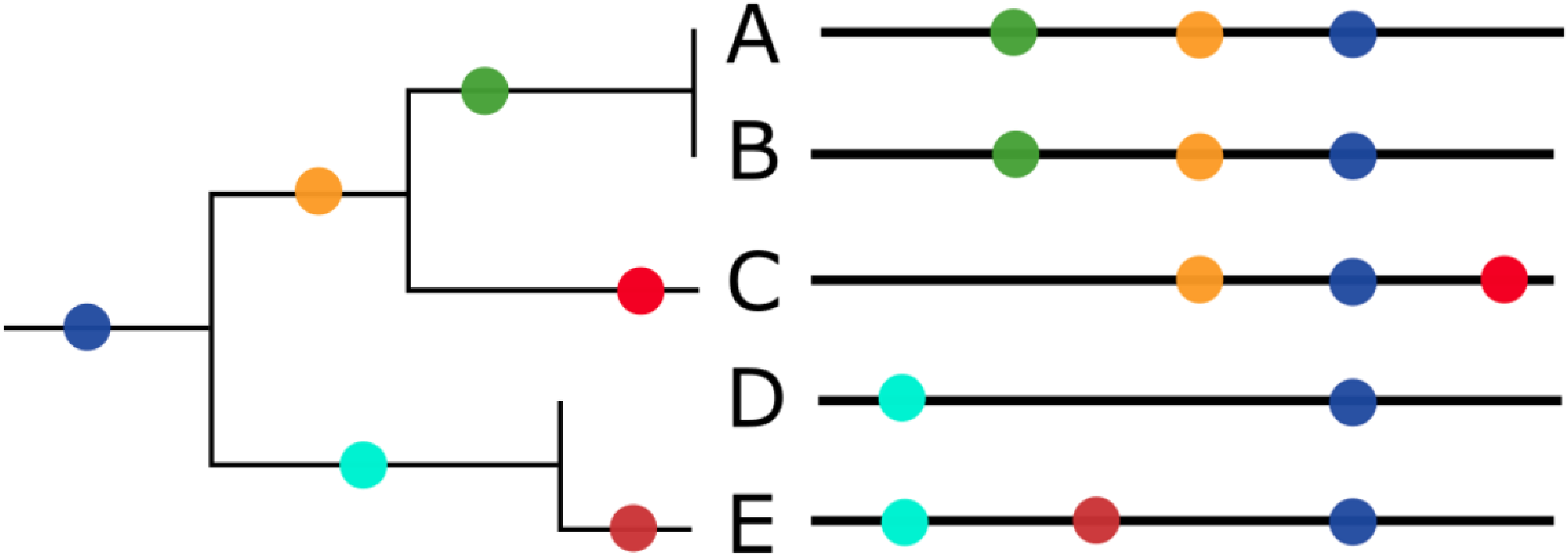
What is genomic data?

Viruses accumulate mutations as they spread

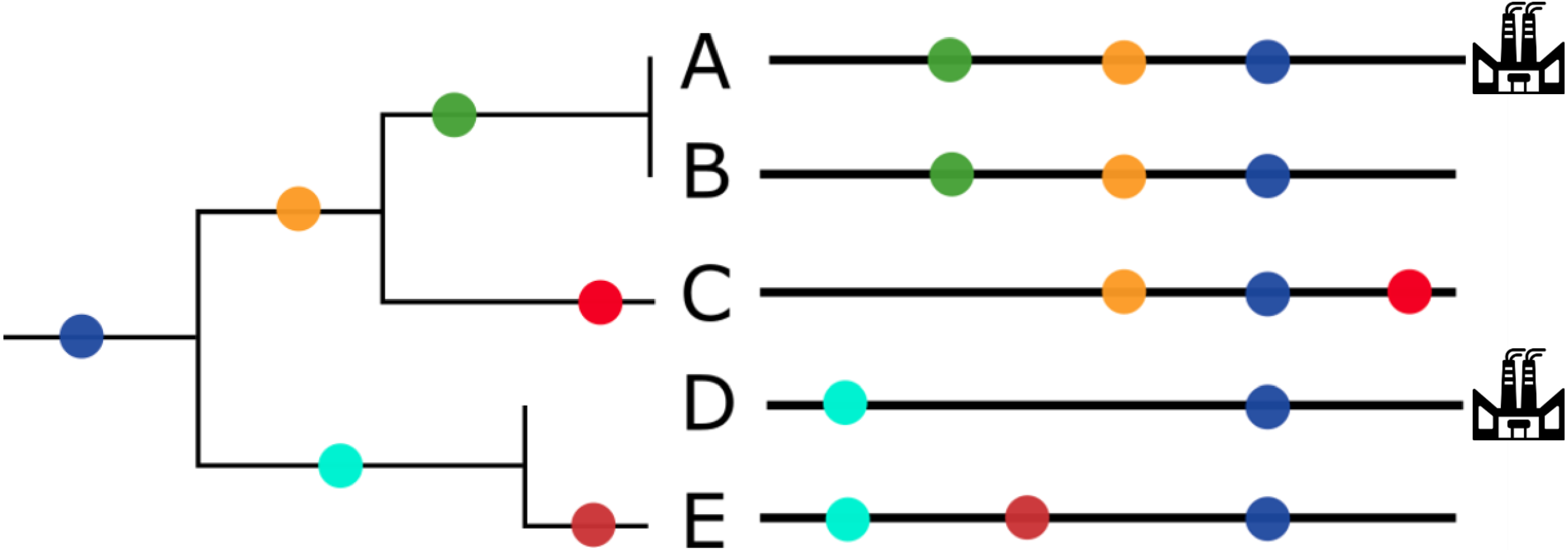


These mutations allows us to <u>fingerprint</u> and <u>trace</u> a particular virus

Shared mutations indicate cases with shared transmission history

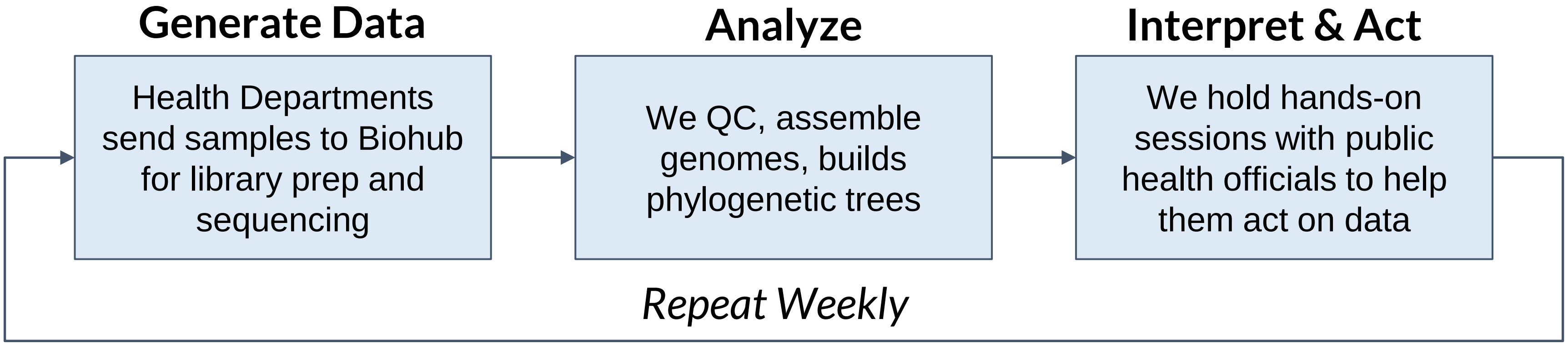


Genetic Links Focus Response



Cases unlinked → Focus interventions outside work setting

COVIDTracker Workflow



Generate Data

Health Departments send samples to Biohub for library prep and sequencing

Analyze

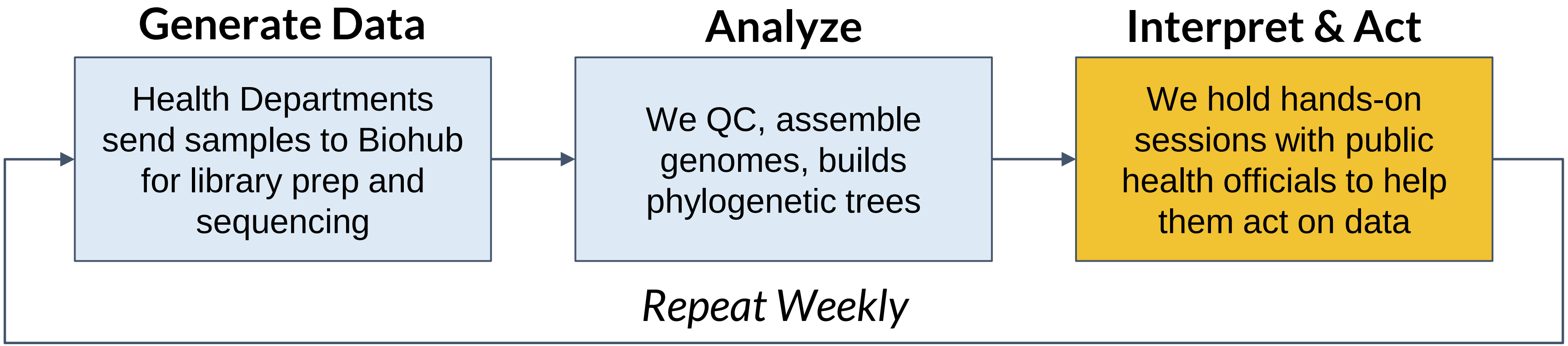
We QC, assemble genomes, builds phylogenetic trees

Interpret & Act

We hold hands-on sessions with public health officials to help them act on data

Repeat Weekly

COVIDTracker Workflow



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This is the last mile - crucial for impact, as this is new tech

What does “using” genomic data mean?

1. Rule out a suspected cluster
    a. Save Public Health $$
2. Confirm suspected cluster based on other data
    a. Inform infection control
3. Establish transmission links between facilities
    a. Hard data for 3rd parties to change practice

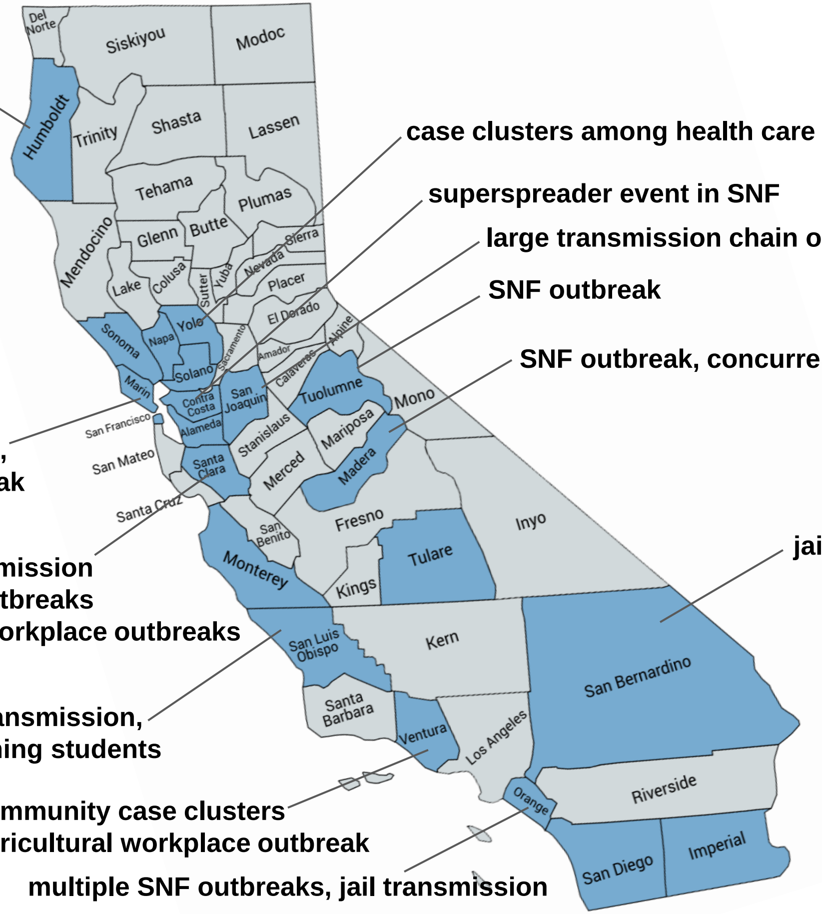
Our impact has largely been retrospective - our data is being used to assess and change policy.

Real-time impact is also possible (e.g., intervening to interrupt transmission chains based on genetic links) but requires faster end to end turn-around-time.

COVID Tracker Status

- Partnerships with **25 DPHs** in California, and produced **almost 2,000 assembled genomes**
- **Spent hundreds of hours** leading hands-on weekly training sessions with county DPHs to help interpret their data and make it actionable
- Began **capacity building** for the future: building a state-wide network of NGS facilities for public health with **CDPH** and initiated a webinar series, attended by **70 county public health officials**, on how to bring NGS & routine genomic epidemiology in-house.
- Our data & outreach has informed local public health response in **dozens of county COVID-19 investigations**, including fish packing plants, avocado processing facilities, nursing homes, prisons and more.
- We contributed **over half of all California SARS-CoV-2 sequences** in public databases, enabling academic and public health groups world-wide to improve COVID-19 modeling and tracking efforts.

Hundreds of hours training county epidemiologists on genomic data



Importations
Missing links

case clusters among health care workers

superspreader event in SNF

large transmission chain of cases

SNF outbreak

SNF outbreak, concurrent community clusters

community clusters,
San Quentin outbreak

jail transmission

jail transmission
3 SNF outbreaks
2 large workplace outbreaks

jail transmission,
returning students

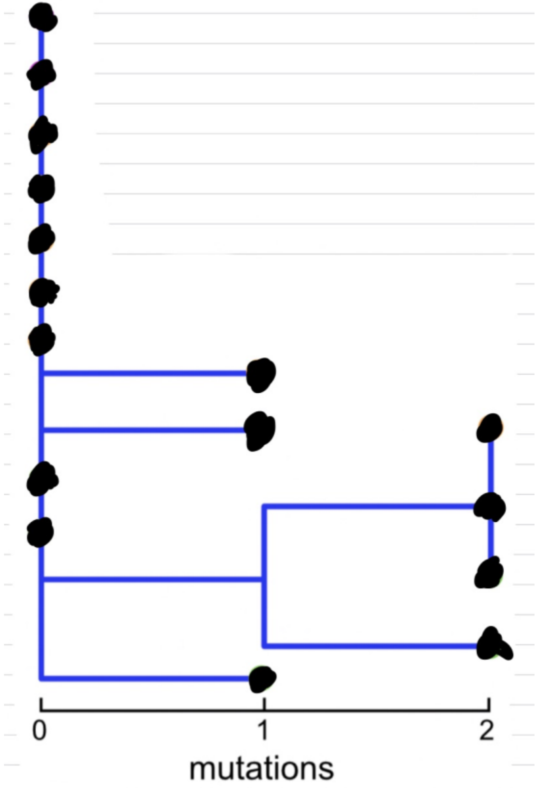
community case clusters
agricultural workplace outbreak

multiple SNF outbreaks, jail transmission

We hold hands-on sessions with public health officials to help them act on data

Vignette #1: The Facilities That Share Staff

A county flagged multiple outbreaks occurring at several nursing homes.



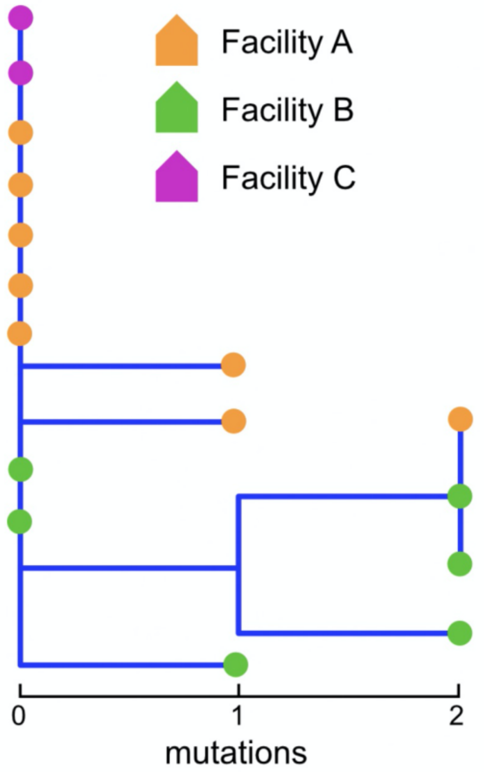
Vignette #1: The Facilities That Share Staff

A county flagged multiple outbreaks occurring at several nursing homes.

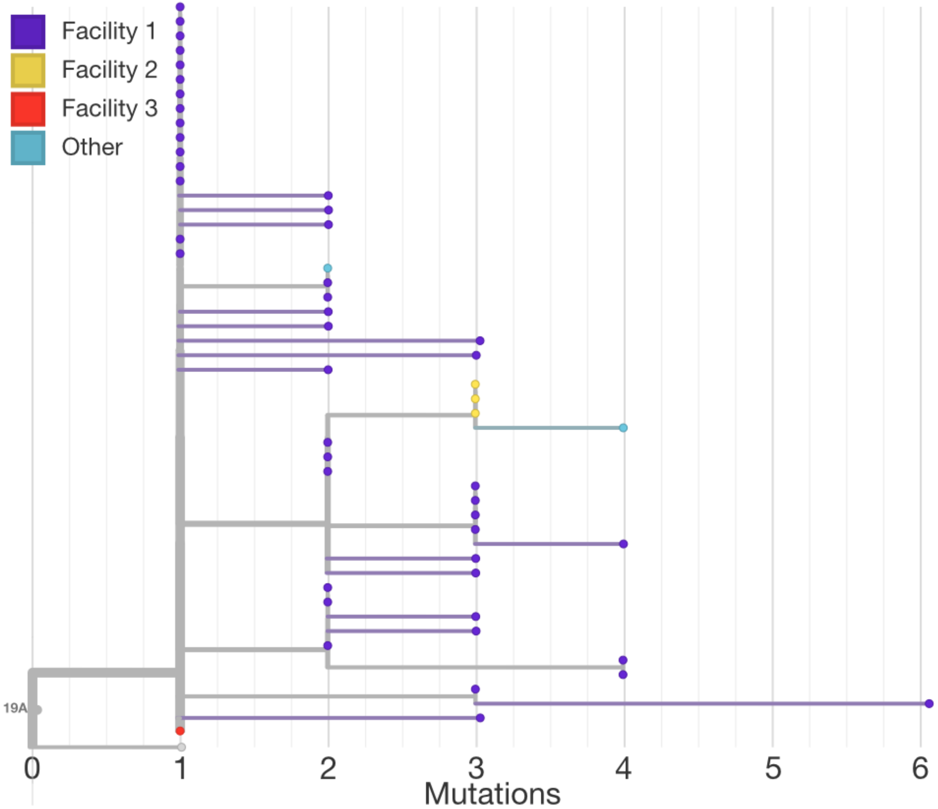
Their epidemiologists add facility metadata to the tree.

Conclusion: Transmission is occurring between these facilities

Action: Hard evidence for these private facilities to change practice



Vignette #2: Onward Transmission



Large outbreak at Facility 1

Onward transmission to Facility 2

Potential source: Facility 3

Workers deeper in tree → likely infected on the job

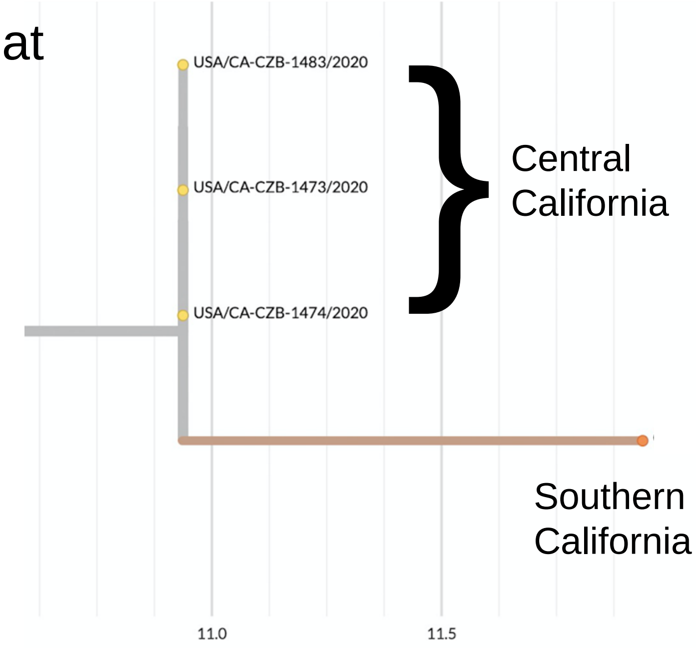
Vignette #3: Transmission Between Counties

A county in Southern California sent samples that clustered closely with samples from a Central California county we had processed.

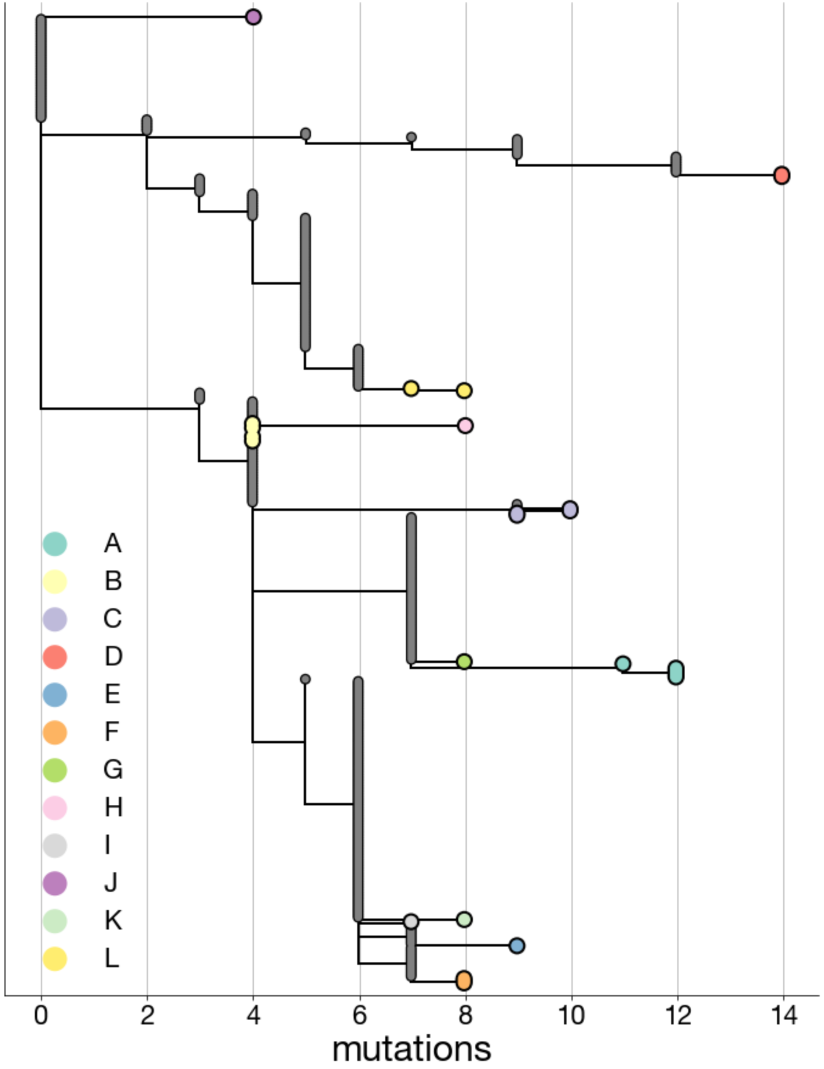
The Southern California sample was from a county jail.

We knew from our outreach with the Central California county that the linked samples were from a prison.

Action: Review testing policy for transfers.



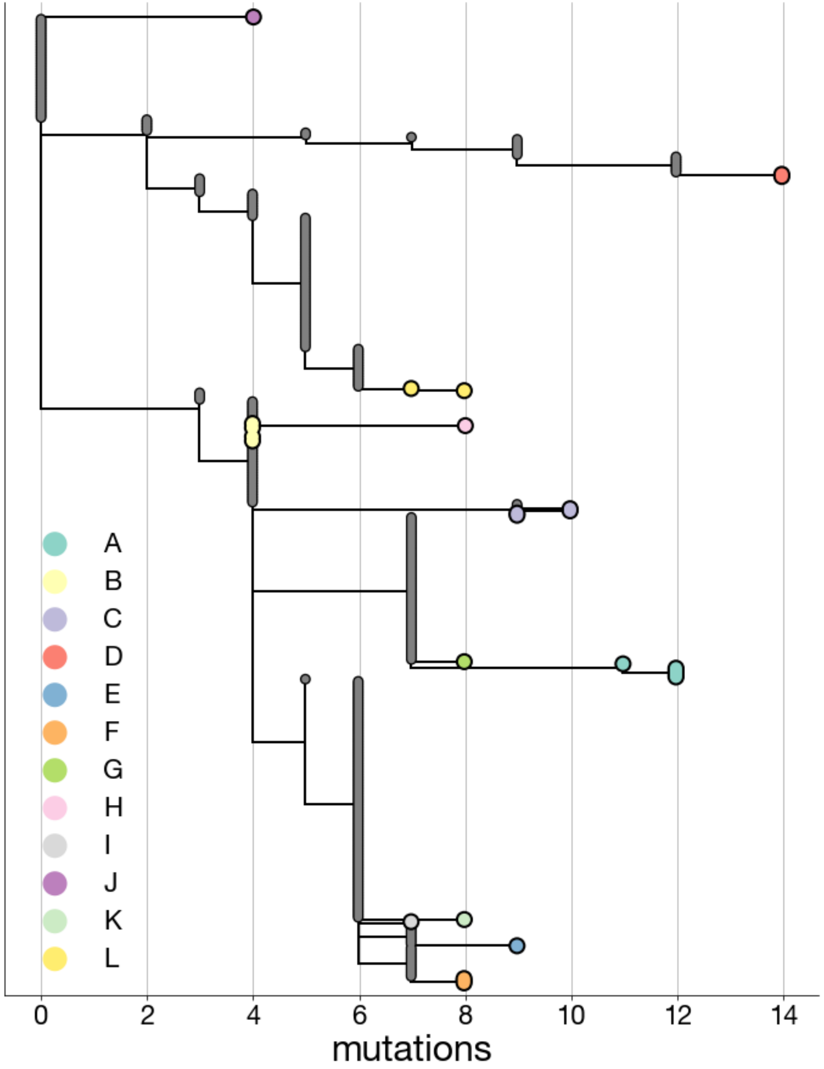
Vignette #4: Importations drive cases in rural county



Vignette #4: Importations drive cases in rural county

Each case cluster is genetically distinct.

Action: Focus interventions on travelers.

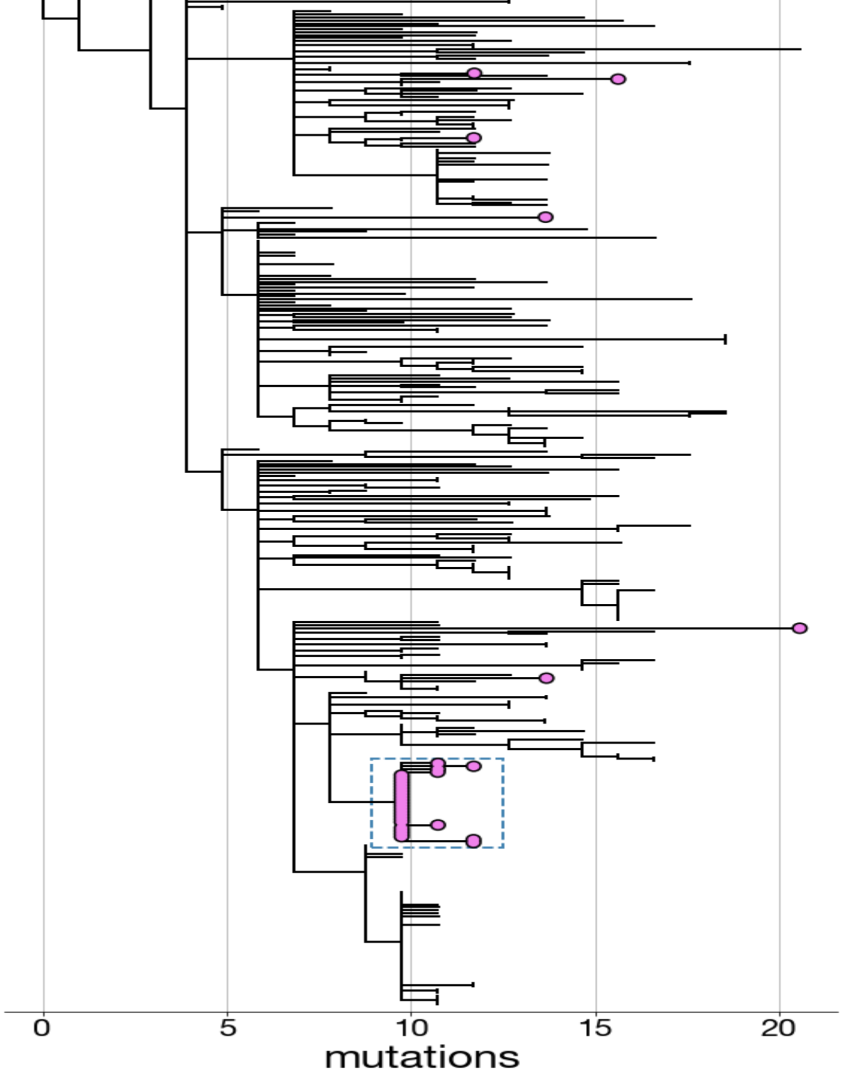


Vignette #5: Successful screening in county jail

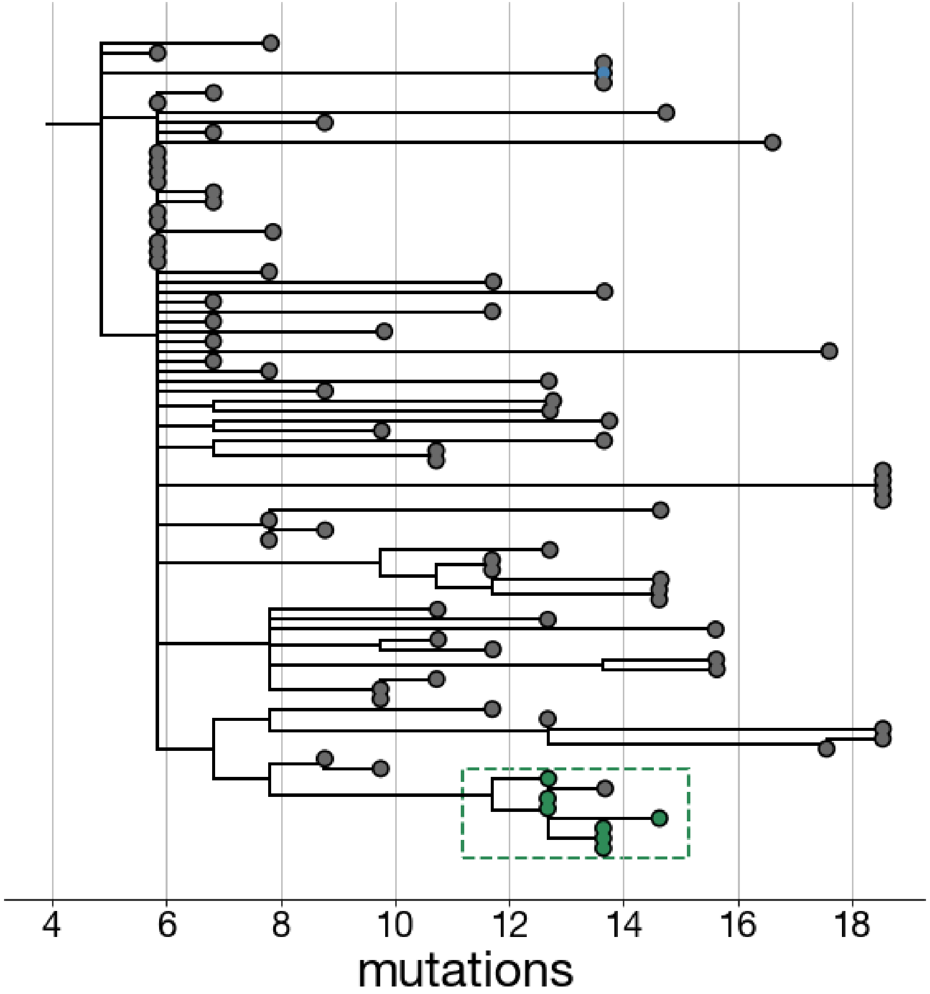
Ongoing outbreak

Inmate screening

Action: Continue screening/monitoring



Vignette #6: Confirm Outbreak at Fish Packing Plant

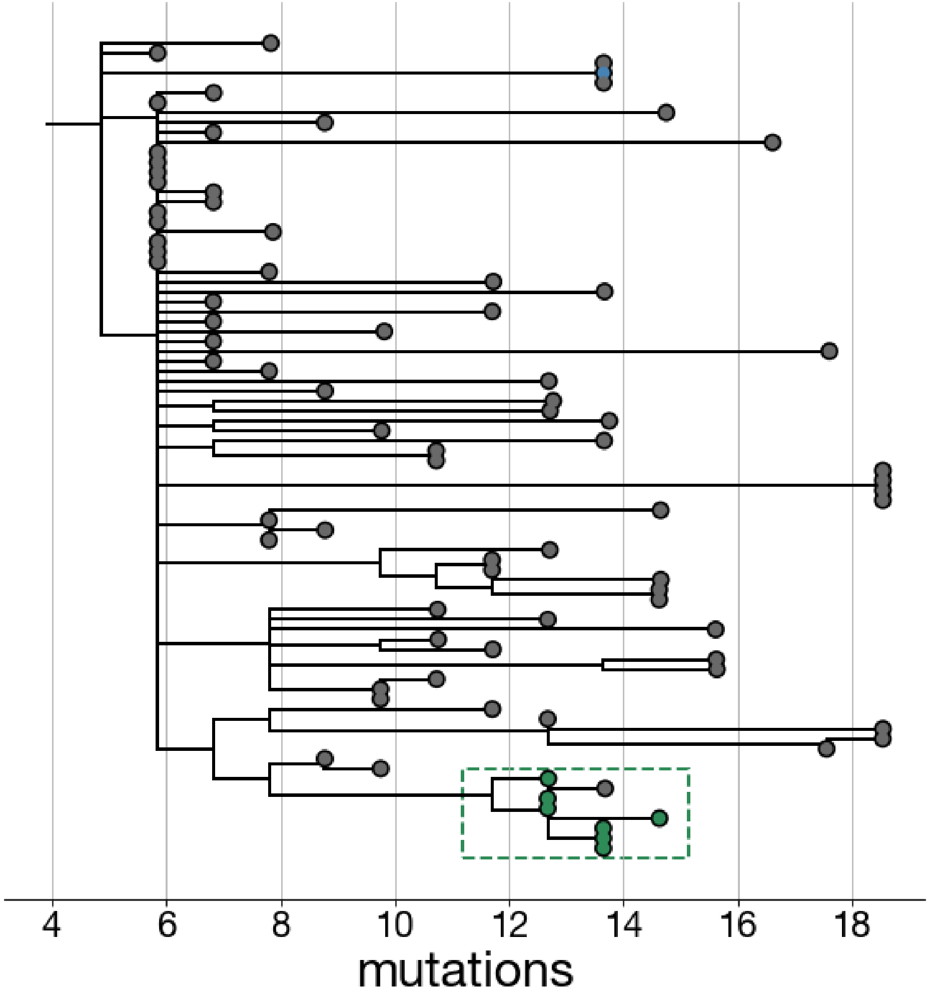


Vignette #6: Confirm Outbreak at Fish Packing Plant

Single cluster

Action: Certify outbreak to owners

Action: Increase infection control



Work Buckets

Wetlab

RNA extraction

Sequencing library preparation

Sample QC

Analysis & Visualization

From raw sequence data to actionable reports

Action

Ensure local epis can interpret data and act on it

Bench Science

Bioinformatics/ Engineering

Public Health

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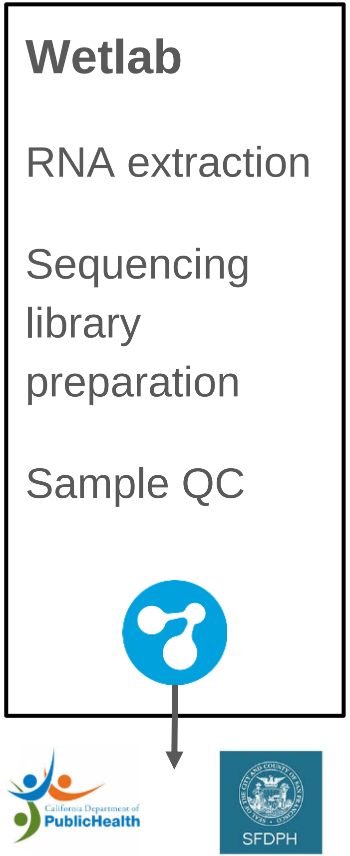
Public Health

Increasing Adoption



Wetlab

RNA extraction

Sequencing library preparation

Sample QC

Biohub committed to end-to-end program through Q1 2021 w/Q2 extension.

How can we catalyze more sequencing data generation?

1. Counties do their own sequencing
   a. 2021 capacity building plans w/trainers
2. Sequencing-as-service for counties
   a. CDPH COVIDNet, data integration is an issue
   b. How to fund?
3. Sequencing-as-service state wide
   a. E.g., sequencing @ the Valencia CDPH Branch Lab mass testing facility

Increasing Adoption

Analysis & Visualization

From raw sequence data to actionable reports

From sequence data to reports for your epis

We’ve built the COVIDTracker pilot for counties. Where should this product live for maximum adoption?

1. Do we host the data platform?
2. Does CDPH host the data platform?
3. Do counties do their own analysis? *
4. Something else?

Increasing Adoption

How can we transfer capability to county health departments to build sustainable capacity for data-driven pandemic response?

Action

Ensure local epis can interpret data and act on it

We plan a mix of wetlab, bioinformatics, and genomic epi trainings to build capacity based on counties' needs, supported by statewide tools for data management and bioinformatics analysis.

Buy-in from epis, disease controllers, PHNs, etc is crucial

+

COUNTY OF SAN LUIS OBISPO

Santa Clara County PUBLIC HEALTH

California Department of PublicHealth

SFDPH

VENTURA COUNTY PUBLIC HEALTH

SACRAMENTO COUNTY PUBLIC HEALTH
Promote • Prevent • Protect

The Importance Of Centralizing Data

Should counties sequence and analyze their own data for their own epis? *

Genomic epidemiology is most effective when a large volume of genomic data from across the entire state is jointly analyzed, compared and made available to both state and local public health officials.

Local health jurisdictions should share and compare their genomic data **across jurisdictions** to understand where locally occurring lineages came from, to quickly contact relevant jurisdictions to investigate inter-county transmission chains and more.

Sequence data and analyses should be rapidly and automatically shared state-wide, regardless of who sequenced or analyzed it.

- Ca state DPH
- Ca county DPHs
- CDCR
- & other epi specialists

Outreach


Patrick Ayscue


Josh Batson


Emily Crawford


David Dynerman


Lucy Li

- MOUs
- MTAs

Legal


Garima Syal

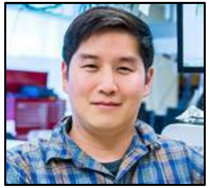

Annette Parent


Maureen Sheehy

Logistics


Maira Phelps


John Haliburton


Eric Chow


Lienna Chan

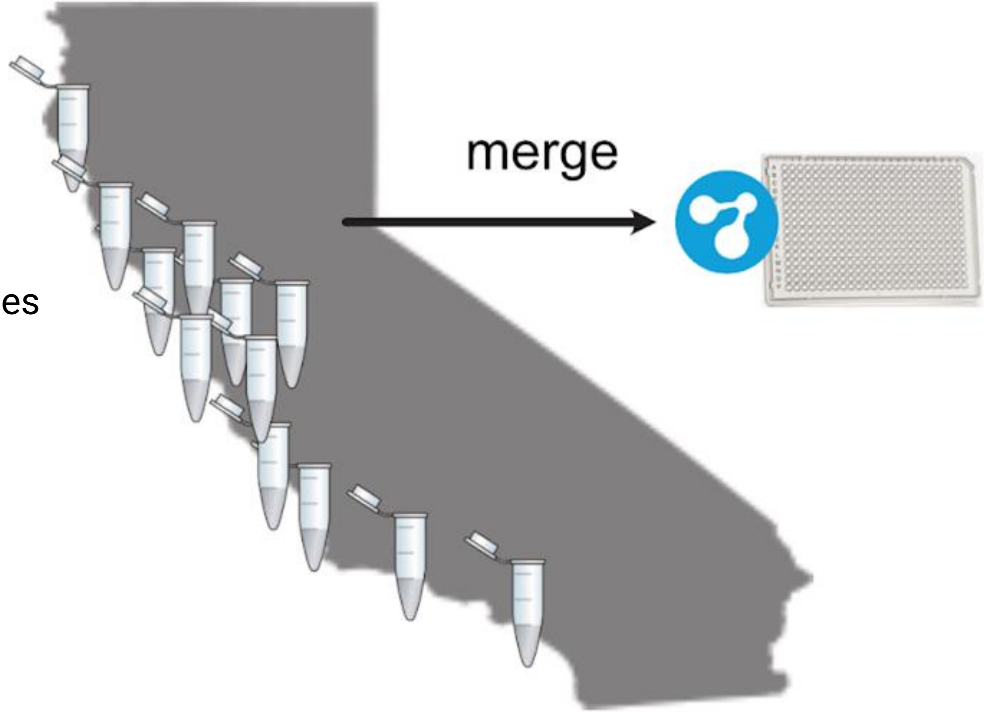

Angela Pisco


Shannon Axelrod

- Sample intake: internal & external
- Automation/robotics
- Sample merging workflows
- Tracking both internal & external sources


Gorica Margulis


Esther Ho



Sequencing


Lienna Chan


Karan Bhatt


Ashley Byrne


Anna Sellas


Kalani Ratnasiri


Angela Detweiler


Vida Ahyong


Saj Mwakibete


Sabrina Mann


Gloria Castaneda


Rene Sit


Renu Kumar


Michelle Tan


Norma Neff

ARTICnetwork
http://artic.network | @NetworkArtic

ARTIC amplicon sequencing - capture **only** SARS-CoV-2


SARS-CoV-2 genome

primer pool 1 amplicons
primer pool 2 amplicons

400bp long
(~75bp overlap)

Bioinformatics

&

Interpretation


Patrick Ayscue


Josh Batson


Karan Bhatt


Sidney Bell


David Dynerman

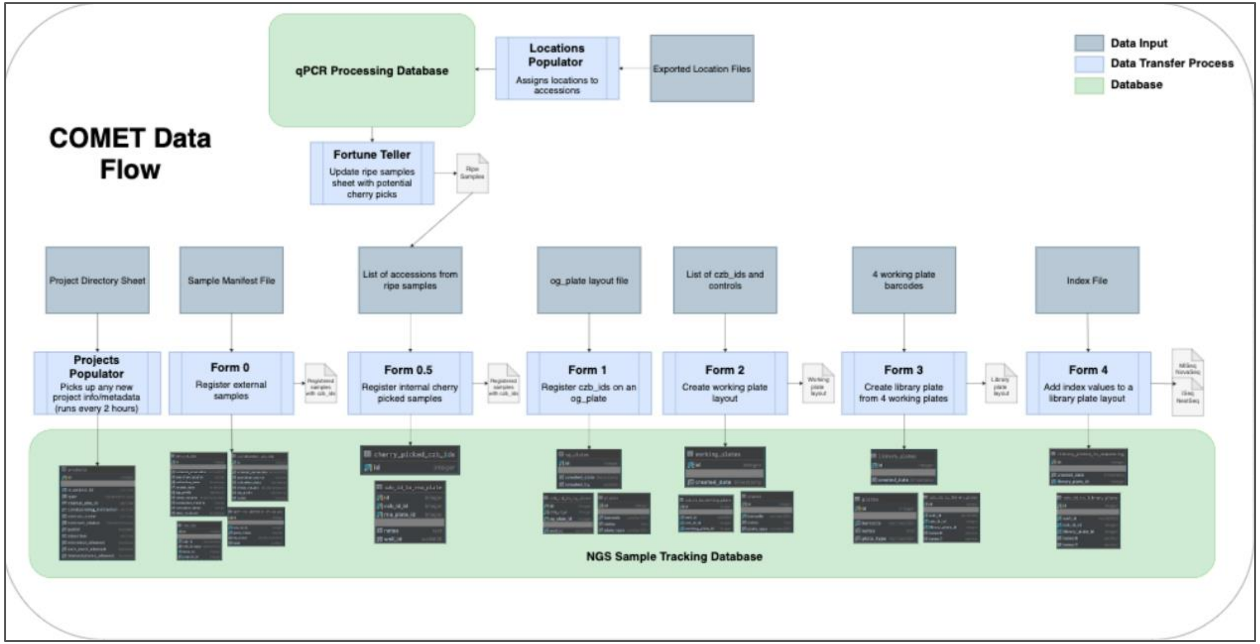

Sam Hao


Jack Kamm


Lucy Li


Aaron McGeever

Data management



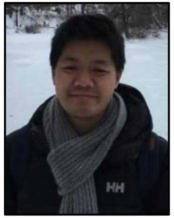
Shannon Axelrod

Phoenix Logan

Josh Batson

Angela Pisco

TJ Chen



Tony Tung

David Dynerman

James Webber

Thank you!

To do this in your county contact covidtracker@czbiohub.org