HIV Data in Action:

A regional approach to using molecular HIV data to prevent infections and improve health

Philip Peters, MD, CAPT (USPHS)

Medical Officer, Office of AIDS

California Department of Public Health

January 24, 2020

A Regional Response to End the HIV Epidemic in California

Overview

- HIV molecular / sequence data process

- Data sharing

- Assistance and Capacity Building

- Community concerns

- Challenges:

  - multi-jurisdictional

  - data delays

 - best practices/prioritizing

- Future directions

What is HIV molecular data and how is it used?

- Drug resistance testing recommended for all HIV-infected persons

- Testing generates HIV nucleotide sequence data of the virus (*molecular HIV data*)

- Sequences can be used to identify if there are large groups of similar sequences indicating rapid HIV transmission

- **New process**: We can use this information to focus prevention efforts
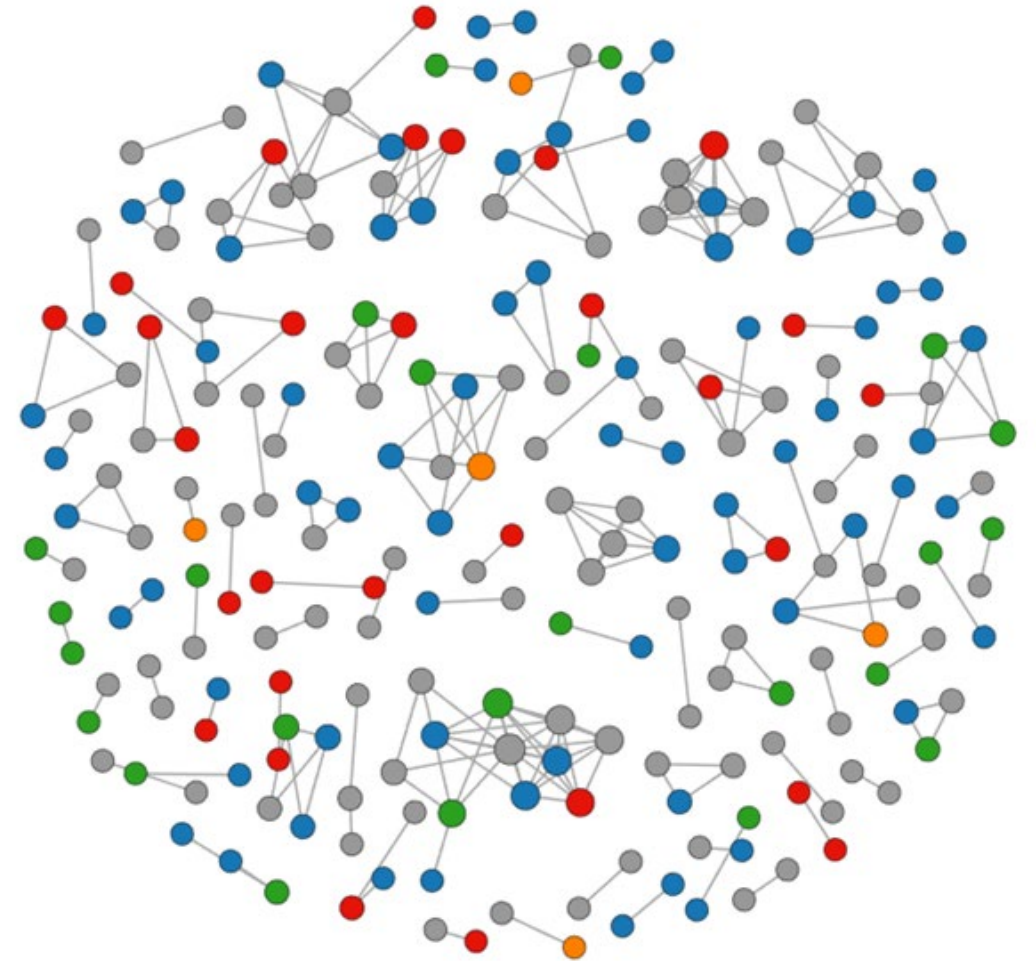
Routine molecular analysis to detect large groups that represent recent, rapid transmission

- Secure HIV Trace program analyzes HIV pol sequences
  - Analysis focused on the most recent 3 years
  - Highly related viral sequences (<0.5% different)
  - **Priority**: At least 5 persons with HIV diagnosed within the recent 12 month period
- Monthly data analysis
  - Standardized aggregate data summary and line list
  - Share data (via SAFE) with majority jurisdiction
  - Outreach to other counties (fewer people) by majority jurisdiction or state
  - Data sharing: case-by-case
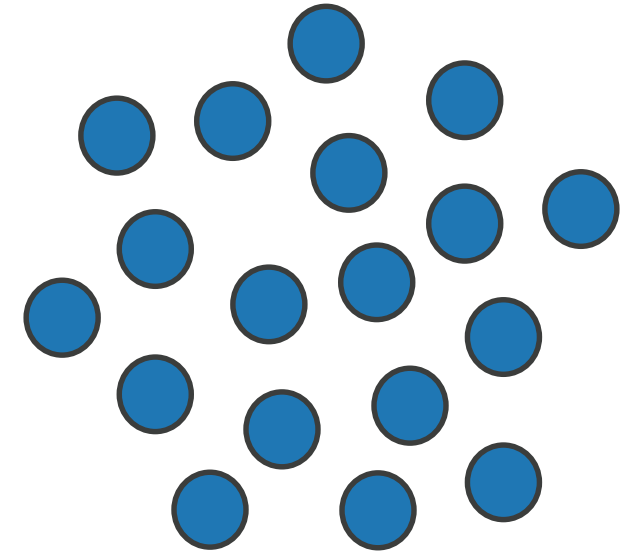
Assistance and Capacity Building for Molecular Data

- New technology – lessons learned
- Collaboration to develop protocols to:
  - Interpret molecular data – optimal formats / visuals
  - Share data as appropriate
  - Educate field investigators, medical providers, case managers, and community organizations (ongoing process)
  - Prioritize and provide services based on the data at individual and group levels
- California Prevention Training Center (PTC) – capacity building grant related to services in response to molecular data
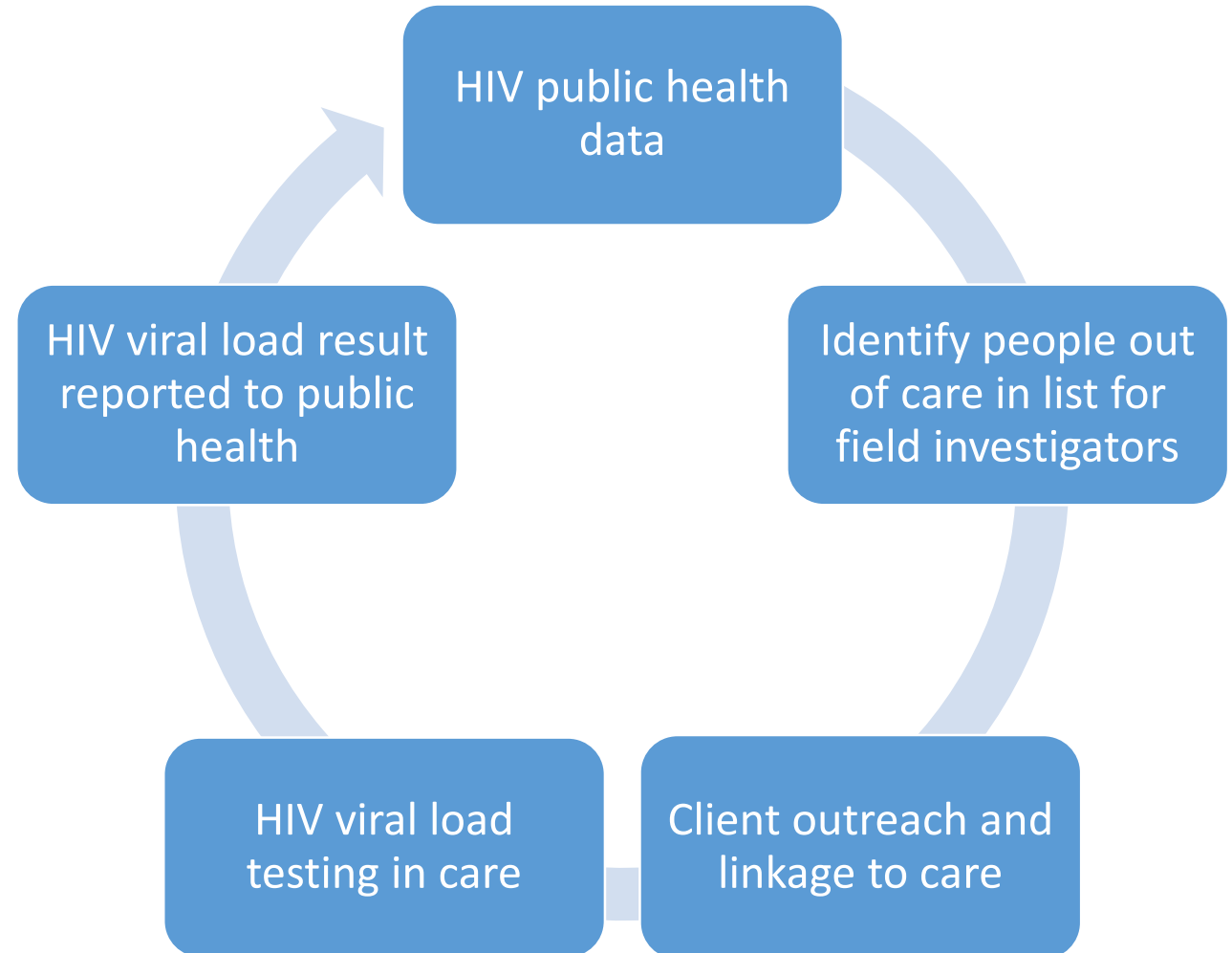
Community Questions and Concerns Raised

- Data security and privacy

- Criminalization – many states have HIV specific criminal laws

- Consent – information on notifiable conditions including certain infections is automatically reported

- Stigma – especially in small communities

HIV Data-to-Care:
Example of using identifiable public health data

- As part of HIV clinical monitoring, HIV viral load testing is performed
- HIV laboratory results are automatically reported to public health
- Benefits of viral suppression to individual health and to preventing HIV transmission (U=U)
- Risk (no individual consent) mandates additional protections and very limited access to the viral load data

HIV public health data

Identify people out of care in list for field investigators

Client outreach and linkage to care

HIV viral load testing in care

HIV viral load result reported to public health

Molecular analysis:

- ***Does NOT*** test a person's genetics – only the virus is sequenced
- ***Does NOT*** identify a person
  - Multiple people can have an identical sequence
  - The sequence within a person changes over time
- ***Does NOT*** determine direct links between people
- ***Does NOT*** determine directionality of transmission
- ***Does NOT*** replace partner services or community outreach

HIV Transmission not Limited by County Boundaries

- ~90% priority clusters include people from multiple counties

- Partner networks span similar geographic areas

- Local field investigators most likely to recognize a pattern but limited to data access

- Discussion: Regional data sharing for cluster response

- ⬤ Southern CA1
- ⬤ Southern CA2
- ⬤ Southern CA3
- ⬤ Southern CA4
- ⬤ Northern CA1
- ⬤ Northern CA2
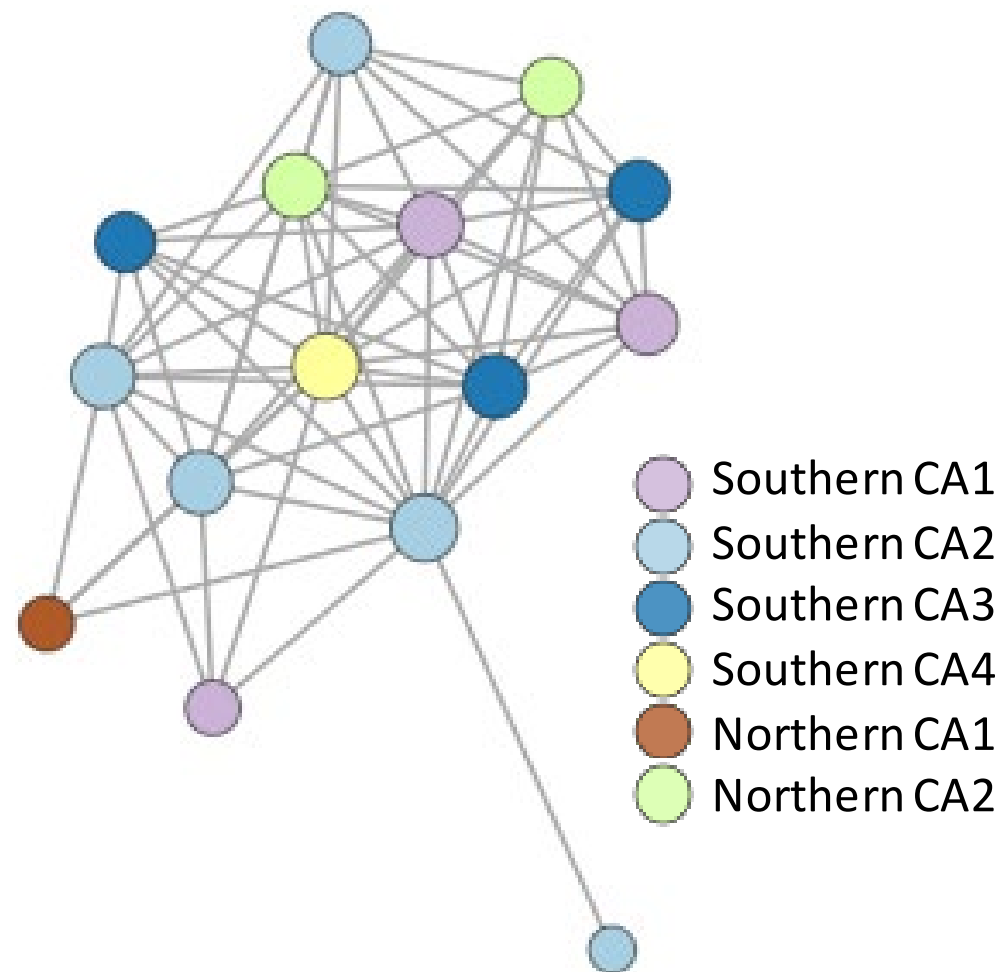
Understanding Data Delays and Underreporting

■ Sequence obtained after linkage to HIV care

■ Missing sequence if not diagnosed, not linked to care, sequence not obtained, lab not reporting, poor sequence quality

■ Recently detected clusters do not always include people with a recent diagnosis
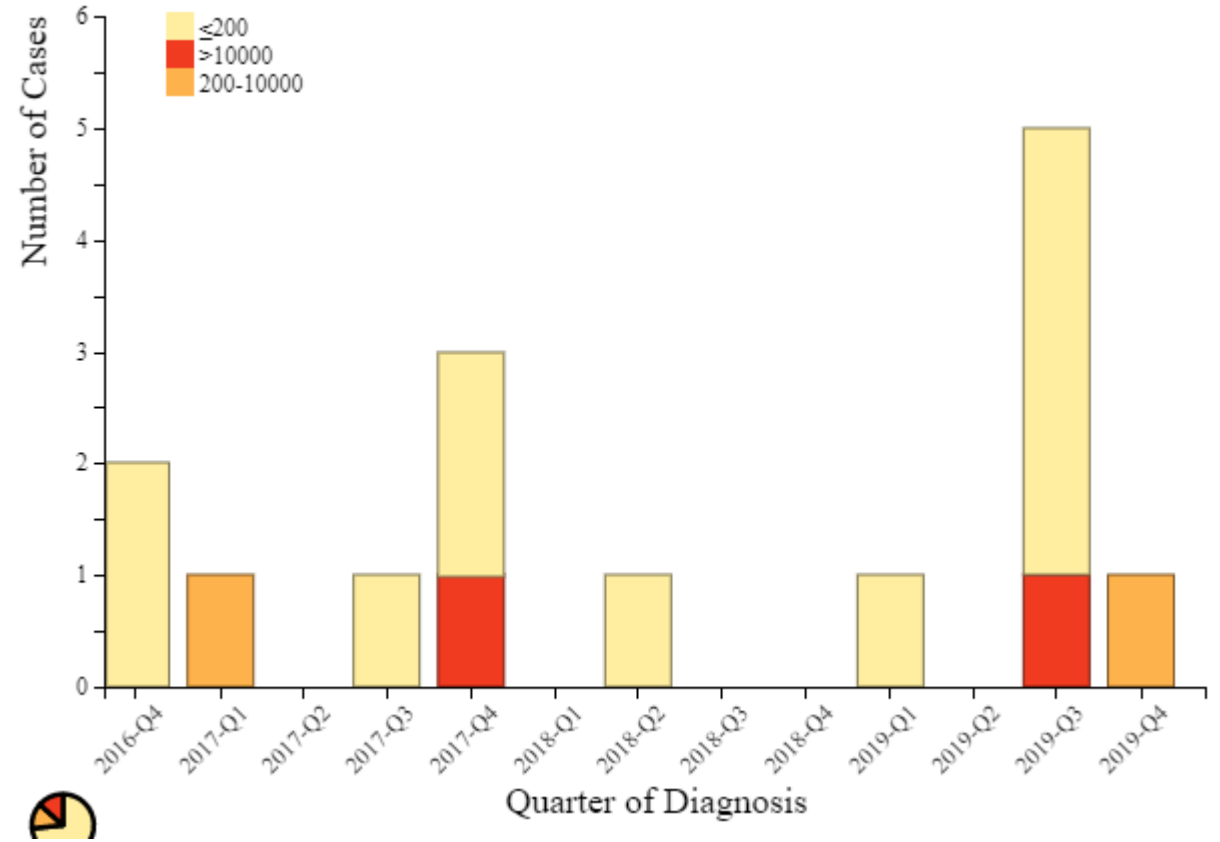
Best Practices and Prioritization

- Best practices and prioritization being developed

- Differences with injection drug use and sexual transmission

- Partner services and three year interval emphasized

- Linkage to care and viral suppression **highest priority**

- Consider social network or snowball sampling approaches
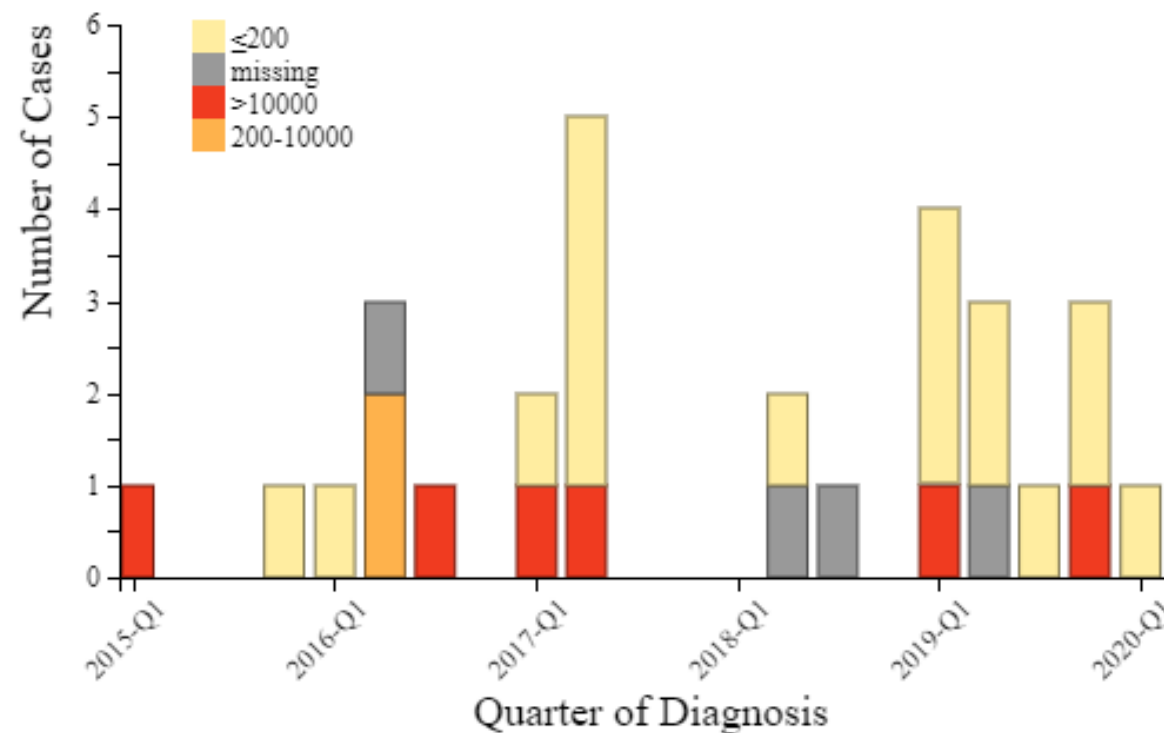
Future directions for Molecular Data

- New technology – lessons learned

- Collaboration to develop protocols

- Implementation of statewide data systems for HIV and partner services data

- Regional approach to secure, protected, and confidential molecular data sharing

- Evaluation of novel approaches to HIV prevention utilizing molecular data

Acknowledgements

CDPH

- Marisa Ramos
- Deanna Sykes
- Diem Tran
- Nannie Song
- Jing Feng
- Andy Pham
- Will Wheeler
- Hannah Johnson

- Abel Martinez
- Betsie Cialino
- Romni Neiman
- Ryan Murphy
- Anna Branzuela
- Tambi Shaw

CDC

- Alexa Oster