Using Surveillance Data to Inform Prevention
Molecular Epidemiology and HIV

- HIV mutates over time
- People living with HIV whose viral strains are genetically similar may be more closely related in transmission

- Analysis: compare nucleotide sequences to determine relatedness

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ACCGGATAACGGTTATCCG
ACTGGATAACGGTTATCCG
ACCGGATAACGGTTATCCG
AATCACGGAAATCCG
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Identifying Transmission Clusters

Link drawn between 2 sequences with close genetic distance

Compare all pairs of sequences to calculate genetic distance between them

Identify pairs of sequences that are very closely related

Connect all closely related pairs to identify clusters

Image courtesy of Joel Wertheim
Molecular Epidemiology and HIV

• Analysis: compares nucleotide sequences to determine relatedness

We can infer a direct OR indirect epidemiologic link; we cannot infer directionality
Interpreting Transmission Cluster Data

- Includes only those cases that have been diagnosed and have a sequence.

- This represents a subset of the underlying sexual/risk network, which can also include:
  - People who are diagnosed but do not have a sequence included in analysis
    - Diagnosed, but never linked to care
    - Linked to care, but haven’t received a genetic resistance test
    - Sequence hasn’t been reported to health department
  - People with undiagnosed infection
  - HIV-negative contacts who may be at risk of acquiring HIV
Transmission Cluster and Risk Network

- HIV-infected, diagnosed, linked to care
- HIV-infected, diagnosed but no sequence available
- HIV-infected, not diagnosed
- HIV-uninfected, at risk of acquiring HIV
Current Residence of all Cluster cases:

Confirmed, Probable, Possible and Negative High-Risk