



## **Growth of HIV-1 Transmission Clusters in LA County**

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The rapid evolution that allows HIV to escape the immune system and acquire resistance to anti-retroviral drugs can also be used to help track its transmission. HIV evolves so rapidly that the viral genetic sequence within an infected person is almost always unique to that person. However, when two people are infected with extremely similar viral sequences (less than 1.5% divergent), it is likely that these two people are connected in a recent transmission cluster. The faster a transmission cluster has grown, the more likely it is to produce future infections. Using genetic sequence information from over 10,000 HIV-infected persons in Los Angeles County, California, (who sequences were acquired by the Department of Public Health for drug resistance surveillance) we will construct a genetic network to represent that recent transmission of HIV. Using this network, we will find HIV transmission clusters that have grown disproportionately rapidly. Next, we will determine which type of computational approach is best able to detect rapidly growing clusters. Then we will perform simulations over the transmission network to see if a targeted intervention would have been able to disrupt these growing clusters. These findings will be of particular use for city, county, and state public health departments aiming to curb the spread of HIV.