

Stemming the spread of HIV by accurately predicting its spread

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by Thomas Leitner

One of the challenges with stemming the spread of HIV lies in understanding how it is spread. Because HIV mutates so rapidly, it has historically been difficult—if not impossible—to trace exactly who transmitted the virus to whom. Without that understanding, it's easy for the disease to run unfettered through a population—with devastating results. Each year, HIV infects approximately 1.8 million people worldwide. All told, nearly 37 million people are currently estimated to be living with HIV/AIDS. But that might be changing.

In a study published this week in the journal [*Nature Microbiology*](#), my colleagues and I demonstrate that computer simulations can accurately predict the transmission of HIV across populations, which could aid in preventing the disease.

The simulations were consistent with actual DNA data obtained from a [global public HIV database](#), developed and maintained by Los Alamos National Laboratory. The archive has more than 840,000 published HIV sequences for scientific research.

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