



## The Added Role of Phylogenetics in the HIV Prevention Toolbox

Guest Editor:

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Deadline for manuscript  
submissions:

**closed (15 December 2021)**

### Message from the Guest Editor

Inferences from phylogenetics can delineate the structure of transmission networks at an unprecedented detail, providing novel insights into regional epidemic drivers. In 2019, the US Centers for Disease Control and Prevention advanced phylogenetics as an essential ingredient in the design of prevention strategies towards epidemic control by 2030.

With this Special Issue, we wish to explore precisely what phylogenetics adds to the HIV prevention toolbox. We welcome articles that describe phylogenetic insights into specific issues, including

- (1) The influence of route transmission and disease stage in divergent patterns of spread.
- (2) The influence of migration and globalization in patterns of viral spread.
- (3) The mixing of epidemics in key vulnerable populations.
- (4) The evolution of viral epidemics in the era of highly potent therapy (e.g., integrase inhibitors and preexposure prophylaxis).
- (5) Variations in the calling of clusters based on selected methodologies and topological cutoffs.
- (6) Scientific validity and the ethics of recent publications that predict partners and directionality of transmission.





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## Editor-in-Chief

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## Message from the Editor-in-Chief

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Electronic files or software regarding the full details of the calculation and experimental procedure, if unable to be published in a normal way, can be deposited as supplementary material.

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