

NETWORK-BASED MODELING FOR HCV IN US DRUG INJECTORS: TREATMENT AS PREVENTION

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Introduction: Hepatitis C virus (HCV) and HIV infection are the two most prevalent chronic viral infections globally (170 and 34 million, respectively) and in the U.S. (5.2 and 1.2 million), respectively, with HCV prevalence estimated as high as 80.8% among HIV+ people who inject drugs (PWID). Few analyses using social network analysis have modeled an injection network of PWID in order to understand HCV and HIV transmission and evaluate the effectiveness of various HCV treatment as prevention (TasP) in US PWIDs.

Methods: A network model was first developed and calibrated using ‘empirical’ data collected from 3102 PWID and their injection partners in Hartford, Connecticut; 1357 were excluded because they had no reported injection ties within the network. Graph models were fit to real injection network data, and synthetic networks were generated that were statistically similar to the observed original injection partnerships. A dynamic HCV transmission model using a combination of the selected network model and agent-based micro-interactions was simulated in order to analyze the effect of network structures on time to primary HCV infection and evaluate the effectiveness of four potential TasP strategies on chronic HCV prevalence and incidence over a 10 year period.

Results: Exponential Random Graph Models were found to fit the collected data reasonably relative to Preferential Attachment and Small World models. Among the different TasP strategies, policies that target network degree will not be effective unless TasP coverage exceeds 15% annually, which would result in HCV prevalence to decrease by 10% over 10 years.

Conclusion: Mathematical modeling using injection network data provides important information about how to intervene most effectively for TasP strategies in PWIDs, and is likely to differ markedly based on settings where injection networks differ.

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