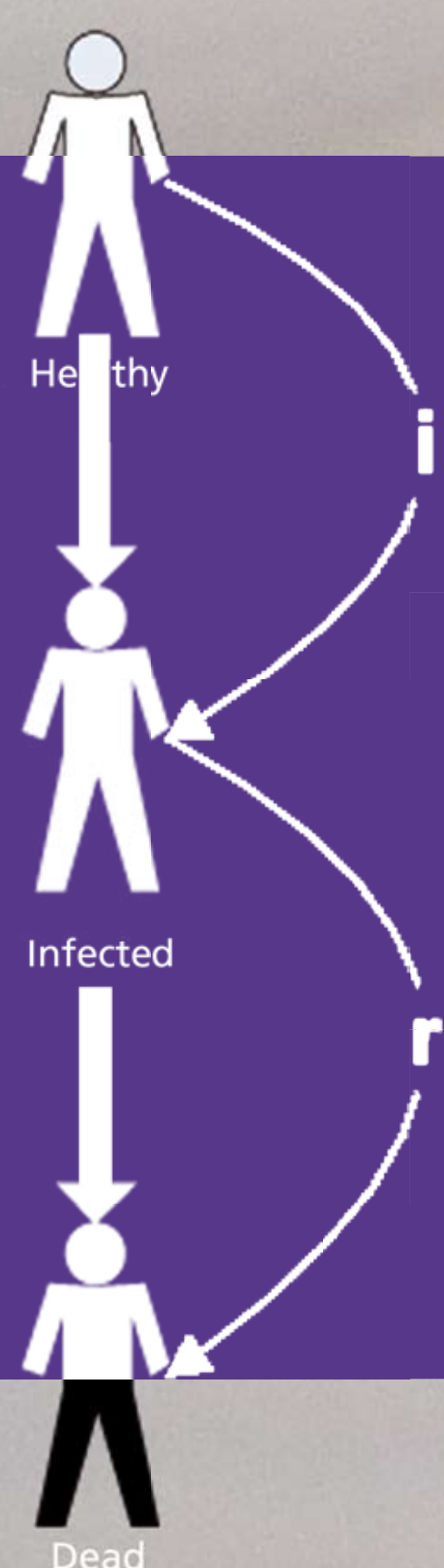


Stochastic Simulation of HIV Population Dynamics through Complex Network Modeling

Introduction

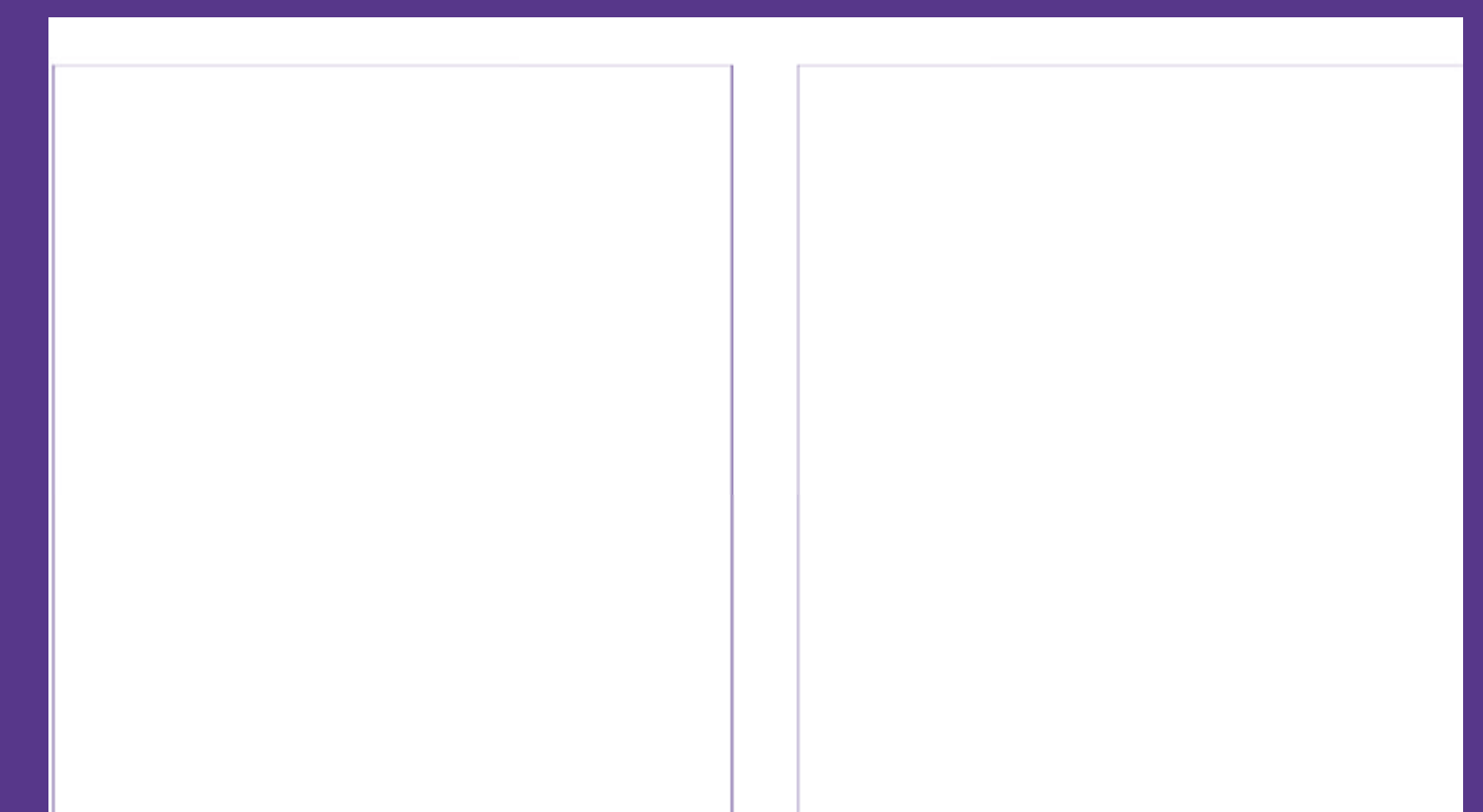
Despite the availability of a large number of mathematical models describing the spreading of HIV, a good understanding of the spreading dynamics through numerical analyses is still a major challenge. The true incidence of the HIV/AIDS-epidemic is quite uncertain since many people may be unaware of their infection; moreover HIV has a very long asymptomatic incubation period which makes study of the actual infection spreading a very complicated task. In this work we combine epidemiological processes with sociological models and network sciences.



Traditionally SIR models provide useful tools for simulating 'heterogeneous' epidemics

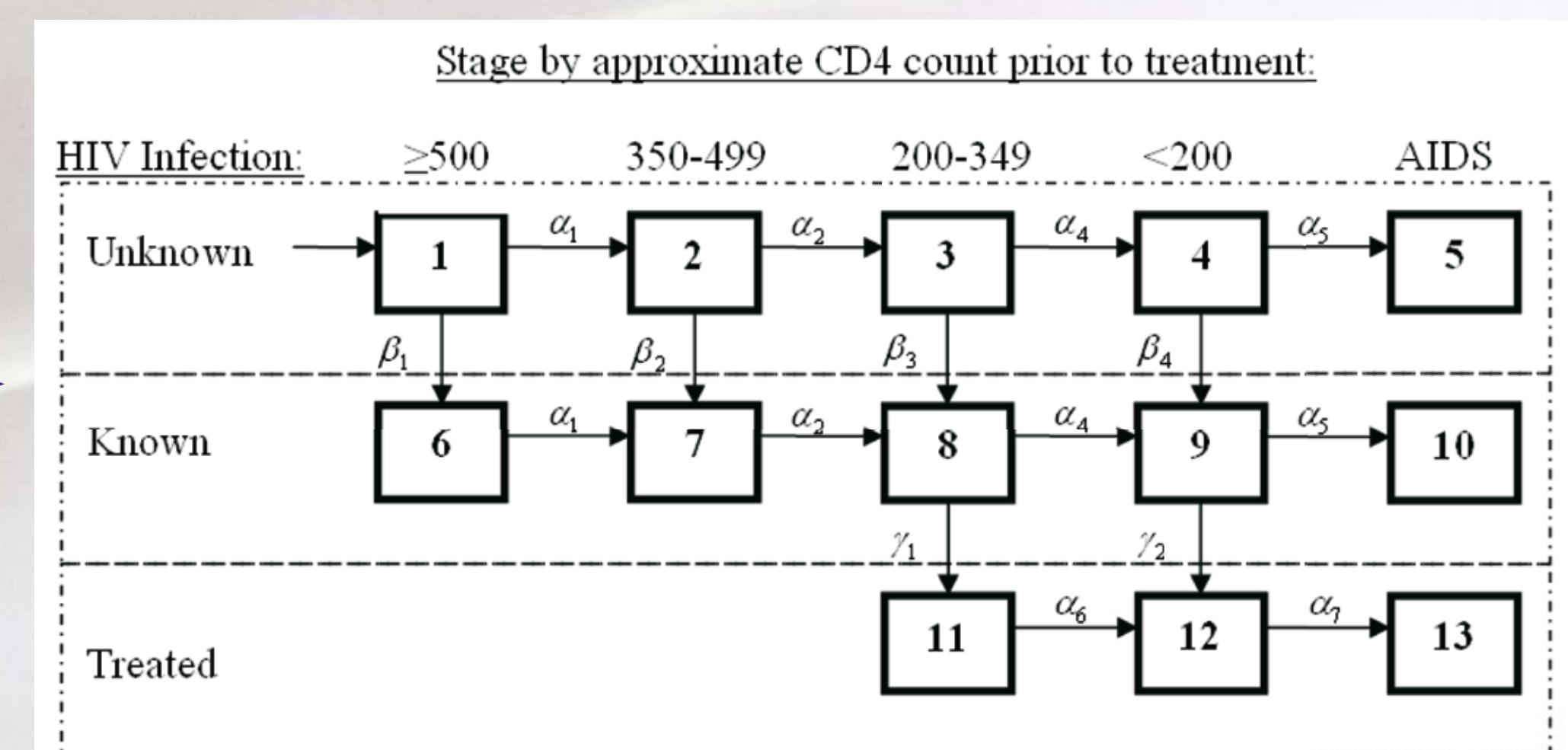
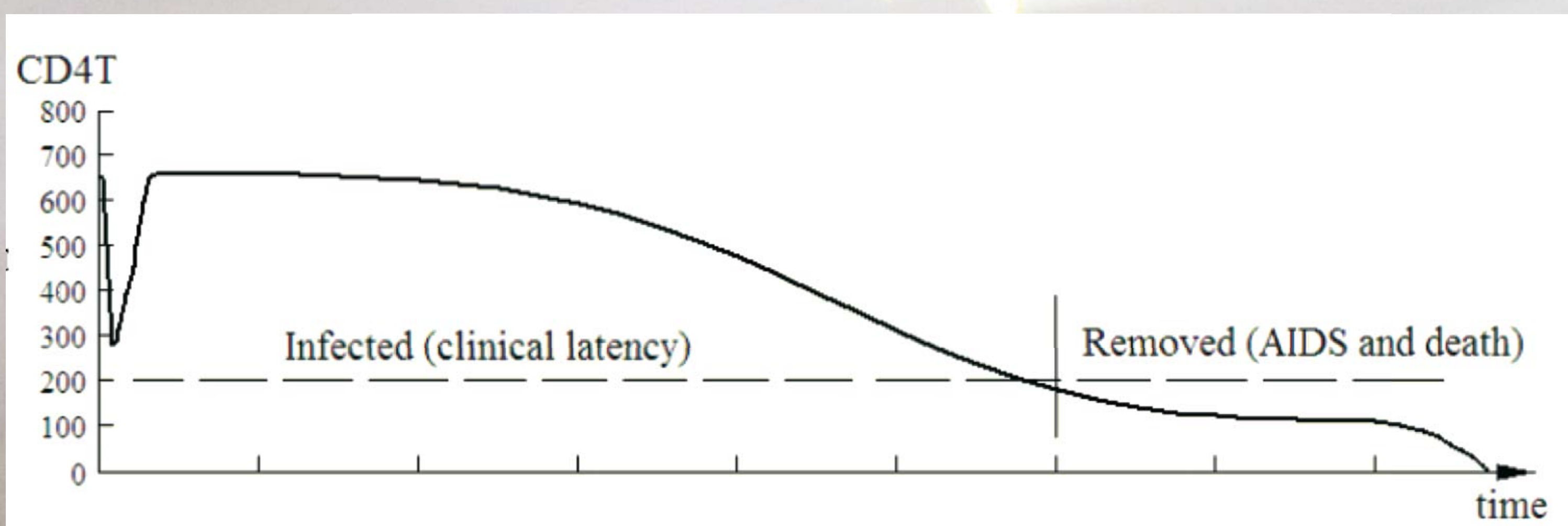
SIR models are based on the dynamics of three groups:
 S - susceptible (healthy individuals who are capable of contracting the disease)
 I - infected (individuals who are capable of transmitting the disease)
 R - removed (dead individuals because of disease)

Addition of Sexual Contact Networks to SIR



Sexual contact networks over a one year period. (left) - heterosexual network; right - MSM (men having sex with men) network. The network structure is scale free, with $P(k) \sim k^{-\gamma}$ and $2 < \gamma < 3$ and κ the number of outgoing links per node.

Modeling of Nodes Evolution (progression of HIV/AIDS)



A multi-state Markov model represents stages of the HIV infection and the diagnosis and treatment. The pre-AIDS stages of HIV infection are defined in terms of the level of CD4+ T lymphocytes (CD4 counts). Four states are specified corresponding to CD4 counts of 500 or higher ($\times 10^6$ cells/l), 350-499, 200-349 and below 200. The mean occupancy times for states 1,2,3 and 4 are 5.5, 2, 2, and 1 year, respectively. It reflects a median incubation time of 8.6 years and a mean of 10.5 years.

Conclusion

We developed a parameterized Complex Network (CN) model describing the dynamics of HIV spreading "on top of it". The model has some distinctive features: It takes into consideration all the existing kinds of HIV spreading. Homosexual and heterosexual spreading is described by a scale-free network, drug users spreading is described with the assumption of homogeneous mixing inside the exposure group. All the network parameters have been taken from medicine literature and did not change during numerical in the USA. (left) MSM exposure groups; (right) heterosexual exposure groups, Circles are the annual officially registered number of AIDS cases (CDC Data). The solid lines indicate simulation results.

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www.virolab.org

