

**BIOGRAPHICAL SKETCH**

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NAME: Steven Michael Goodreau

eRA COMMONS USER NAME (credential, e.g., agency login): SMGOODREAU

POSITION TITLE: Professor of Biological Anthropology, Adjunct Professor of Epidemiology

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

| INSTITUTION AND LOCATION                            | DEGREE<br>(if applicable) | Completion Date<br>MM/YYYY | FIELD OF STUDY          |
|---|---------------------------|----------------------------|-------------------------|
| University of Washington – Seattle                  | PostDoc                   | 09/2004                    | Epidemic Modeling       |
| The Pennsylvania State University – University Park | Ph.D.                     | 12/2001                    | Biological Anthropology |
| The Pennsylvania State University – University Park | M.A.                      | 06/1998                    | Biological Anthropology |
| Harvard University                                  | A.B.                      | 06/1994                    | Biological Anthropology |

**A. Personal Statement**

**My training and research lie at the junction of HIV/STI modeling; data analysis for empirical network and population structure; and development of statistical methods and tools for network analysis and its integration both with demography and evolutionary modeling.** On the methods side, I have been a member of the Statnet Development Team for the last 20 years, which has developed the statnet suite of software packages for statistical analysis and simulation of network data and models. I have published on the statistical theory behind these models, published multiple peer-reviewed tutorials, and given dozens of workshops on the methods and tools at conferences, universities and public health agencies around the world. One key role I have long played is conducting translation of these methods into HIV/STI modeling work, identifying when the methods are or are not tractable for answering questions of practical interest, and proposing broad solutions when not. This methodological development has been essential to conducting all of the applied HIV/STI modeling work described below. The integration of these two streams of my research trajectory can be found in the more recent development of the *EpiModel* and *EpiModelHIV* packages, of which I am a co-developer.

My modeling work, which, in addition to serving as a laboratory for these new methods and tools, has the broad goal of understanding the sources of disparities in infectious disease burden among populations, the potential impact of interventions, and the evolution of virulence. In the first area, I have published work on behavioral aspects of the HIV epidemic, including sexual role versatility; commercial sex venues; serosorting; and concurrent partnerships, as well as work integrating many causal factors for racial disparities in HIV. In the latter, I have addressed the impact of interventions around sexual behavior, circumcision, PrEP, testing and treatment, primarily among populations of men who have sex with men in multiple domestic and international settings. My evolutionary modeling work focuses on the network determinants of viral load variation among individuals and populations.

Ongoing and recently completed projects that I would like to highlight include:

CDC TBD Bradley (PI) 09/30/24 – 09/29/29  
Modeling HIV, Viral Hepatitis, STI, and TB to Improve Public Health - CAMP 3.0: The Coalition for Applied Modeling for Prevention  
Role: Co-Investigator

NIH P2C HD042828s6604 Goodreau (PI) 05/01/22 – 04/30/27  
Demography Center (Center for Studies in Demography and Ecology) Development Core



1. **Origins of disparities in HIV among communities of men who have sex with men (MSM).** Men who have sex with men are among the most affected communities for HIV in most countries around the world. Yet, HIV burden varies widely among MSM populations, for reasons that are not fully understood in each case. In this line of work, I have used a combination of sexual network data and innovative modeling methods to identify the drivers of HIV transmission and disparities in and between MSM communities. Findings include the large proportion of the variation in burden among communities that can be explained by differences in sexual role segregation, the significant role of long-term main partnerships in HIV transmission for MSM in multiple countries with disparate behavioral patterns (e.g. the US and Peru) and the high proportion of transmissions still occurring from men who are undiagnosed or diagnosed but off treatment in the US and elsewhere.
  - a. **Goodreau SM**; Rosenberg ES, Jenness SM, Luisi N, Stansfield SE, Millett GA, Sullivan PS. 2017. Sources of racial disparities in HIV prevalence in men who have sex with men in Atlanta, GA, USA: a modelling study. *The Lancet HIV* 4(7):e311-e320. doi: 10.1016/S2352-3018(17)30067-X. PMC5706457.
  - b. **Goodreau SM**, Carnegie NB, Vittinghoff E, Lama JR, Sanchez J, Grinsztejn B, Koblin BA, Mayer KH, Buchbinder SP. 2012. What drives the US and Peruvian HIV epidemics in men who have sex with men (MSM)? *PLoS One*, 7(11): e50522. PMC3510067.
  - c. Beyrer C, Baral SD, van Griensven F, **Goodreau SM**, Chariyalertsak S, Wirtz AL, Brookmeyer RD. 2012. The Global Epidemiology of HIV Infection among Men who have Sex with Men. *The Lancet*. 380(9839): 367-377. PMC3805037.
  - d. **Goodreau SM** and Golden MR. 2007. Biological and demographic causes of high HIV and STD prevalence in men who have sex with men. *Sexually Transmitted Infections*. 83(6):458-62. PMC2031833.
  
2. **Modeling the impact of HIV prevention interventions among adult MSM, especially pre-exposure prophylaxis (PrEP).** The HIV prevention landscape has been shifting rapidly in recent years. Identifying the likely effectiveness of these interventions, alone or in combination, requires both data on the unique behavioral landscape among different MSM communities, and complex modeling methods that can incorporate both this behavioral heterogeneity and the numerous interventions now available. In this line of work, I have collaborated with field researchers to design and implement detailed sexual network surveys in multiple MSM populations, and integrated these with secondary data analysis of multiple large-scale and local studies, to generate rich sets of sexual network parameters for different MSM populations. I have then developed network modeling tools to integrate these data to predict intervention impacts and refine our understanding of intervention targeting. Examples include PrEP prioritization by partnership types throughout the US and Peru; impact of the CDC PrEP guidelines; individualized testing strategies in California; male circumcision for MSM; and treatment as prevention in four countries representing highly divergent cultural, legal and behavioral settings for MSM: the US, Peru, India and Kenya.
  - a. Hamilton DT, Rosenberg ES, Sullivan PS, Wang LY, Dunville RL, Barrios LC, Aslam MV, Mustanski B, **Goodreau SM**. 2021. Modeling the impact of PrEP programs for adolescent sexual minority males based on empirical estimates for the PrEP continuum of care. *Journal of Adolescent Health* 68(3): 488–496. PMC7876162.
  - b. Jenness SM, Weiss KM, **Goodreau SM**, Gift T, Chesson H, Hoover KW, Smith DK, Liu AY, Sullivan PS, Rosenberg ES. Incidence of Gonorrhea and Chlamydia Following HIV Preexposure Prophylaxis among Men Who Have Sex with Men: A Modeling Study. *Clinical Infectious Diseases*. Published online May 2017. DOI: 10.1093/cid/cix439. PMC5848234.
  - c. Jenness SM, **Goodreau SM**, Rosenberg, ES, Beylerian EN, Hoover KW, Smith DK, Sullivan PS. 2016. Impact of the Centers for Disease Control's HIV Pre-Exposure Prophylaxis Guidelines for Men Who Have Sex with Men in the United States. *The Journal of Infectious Diseases*. Published online first, July 14, 2016. doi:10.1093/infdis/jiw224. PMC5142082.
  - d. **Goodreau SM**, Carnegie NB, Vittinghoff E, Lama JR, Fuchs JD, Sanchez J, Buchbinder SP. 2014. Can male circumcision have an impact on the HIV epidemic in men who have sex with men? *PLoS One*, 9(7): e102960. DOI:10.1371/journal.pone.0102960. PMC4116164.

3. **Development and dissemination of statistical network methodology for HIV/STI epidemiology.** Over the last decade and a half, my colleagues and I have adapted the family of exponential random graph models to the domain of social network analysis, resolving numerous statistical and practical issues in order to make this approach into a tractable method for estimating, assessing, conducting inference on, interpreting, and simulating from arbitrarily complex network models. These methods face additional technical and practical challenges when applied to the specific domain of infectious disease modeling, where actors include a particularly complex set of dynamic characteristics, e.g. disease status and stage, diagnosis and treatment status, all of which interact and which can depend on demographic characteristics such as age, race and sex. In this branch of work, I have identified and resolved numerous of these statistical issues, collaborated in the development of user-friendly open-source software for the application of the resulting methods to general network modeling of infectious disease, and aimed to explain the power of such methods relative to more traditional compartmental modeling techniques for answering questions of vital public health relevance.
  - a. Jenness S, **Goodreau SM**, Wang L, Morris M. 2015. EpiModel: mathematical modeling of infectious disease. Open-source software package.
  - b. Carnegie NB, Krivitsky PN, Hunter DR, **Goodreau SM**. 2015. An approximation method for improving dynamic network model fitting. *Journal of Computational and Graphical Statistics*. 24(2): 502-519. DOI:10.1080/10618600.2014.903087. PMC4548897.
  - c. Handcock MS, Hunter DR, Butts CT, **Goodreau SM**, and Morris M. ergm: a package to fit, simulate and diagnose exponential-family models for networks.
  - d. **Goodreau SM**, Handcock MS, Hunter DR, Butts CT and Morris M. 2008. A statnet tutorial. *Journal of Statistical Software*, 24(9): 1-26. PMC2443947.
4. **Integration of sexual networks into research on HIV evolution.** The structure of the sexual networks on which HIV spreads affects not only its distribution among populations, but also the evolution of the virus itself. My early work demonstrated various ways in which phylogenetic reconstructions of HIV's early population dynamics were sensitive to assumptions about sexual network structure. More recently, I have published on the impact of sexual role, levels of relational concurrency, relational duration, and coital frequency on the evolution of HIV set point viral load, a measure of overall virulence. I have also contributed to work predicting how the magnitude of viral resistance to partially effective vaccines will likely differ based on sexual networks and risk community.
  - a. **Goodreau SM**, Stansfield SE, Murphy JT, Peebles KC, Gottlieb GS, Abernethy NF, Herbeck JT, Mittler JE. Sexual network structure, HIV prevalence, and the evolution of set point viral load. *Virus Evolution*, 2018, 4(2): vey032. doi: 10.1093/ve/vey032. PMC6249390.
  - b. Stansfield SE, Mittler JE, Gottlieb GS, Murphy JT, Hamilton DT, Detels R, Wolinsky SM, Jacobson LP, Margolick JB, Rinaldo CR, Herbeck JT, **Goodreau SM**. 2018. Sexual role and HIV-1 set point viral load among men who have sex with men. *Epidemics*. 2018. PMC Journal - In Process.
  - c. Herbeck JT, K Peebles, Edlefsen PT, Rolland M, Murphy JT, Gottlieb GS, Abernethy N, Mullins JI, Mittler JE, **Goodreau SM**. 2018. HIV population-level adaptation can rapidly diminish the impact of a partially effective vaccine. *Vaccine* 36: 514:520. PMID: PMC6701864.
  - d. **Goodreau SM**. 2006. Assessing the effects of human mixing patterns on HIV-1 interhost phylogenetics through social network simulation. *Genetics*. 142(4):2033-2045. PMC1456410.
5. **Elucidating and clarifying the role of concurrency in generalized heterosexual HIV epidemics.** The HIV burden among the general population is uniquely high in Eastern and Southern Africa. Understanding the proximate causes of that disparity is crucial for designing and implementing effective interventions. One hotly debated theory is that a key driver of these epidemics is the relatively high level of relational concurrency present, which can allow for a generalized heterosexual epidemic even in settings like these where reported lifetime partner numbers are not particularly high. In this line of work, I refined existing models to demonstrate how concurrency and acute infection can interact to make heterosexual epidemics possible given reported relational networks, but not with lower levels typically seen in other settings. As the debate around concurrency unfolded, I also sought to clarify, through my own modeling work and through synthesis and review, a variety of misconceptions that have arisen repeatedly in the literature with regard to the concurrency hypothesis.

- a. **Goodreau SM**, Stansfield SE, Murphy JT, Peebles KC, Gottlieb GS, Abernethy NF, Herbeck JT, Mittler JE. 2018. Relational concurrency, HIV prevalence, and the evolution of set point viral load. *Virus Evolution* 4(2): vey032. doi: 10.1093/ve/vey032. PMC6249390.
- b. **Goodreau SM**. 2013. Is two a 'high number of partners'? Modeling, data, and the power of concurrency, *Sexually Transmitted Diseases*, 40(1): 61. PMC3673695.
- c. **Goodreau SM**, Cassels S, Kasprzyk D, Montañó DE, Greek A and Morris M. 2012. Concurrent partnerships, Acute Infection and Epidemic Dynamics among Young Adults in Zimbabwe. *AIDS and Behavior* 16(2): 312-322. PMC3394592. [Most cited article in AIDS and Behavior in 2013].
- d. **Goodreau SM**. 2011. A decade of modelling research yields considerable evidence for the importance of concurrency: a response to Sawers and Stillwaggon. *Journal of the International AIDS Society*. 14(12). Published online 2011 March 15. DOI: 10.1186/1758-2652-14-12. PMC3065394

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