Applied of Network Models for Epidemics

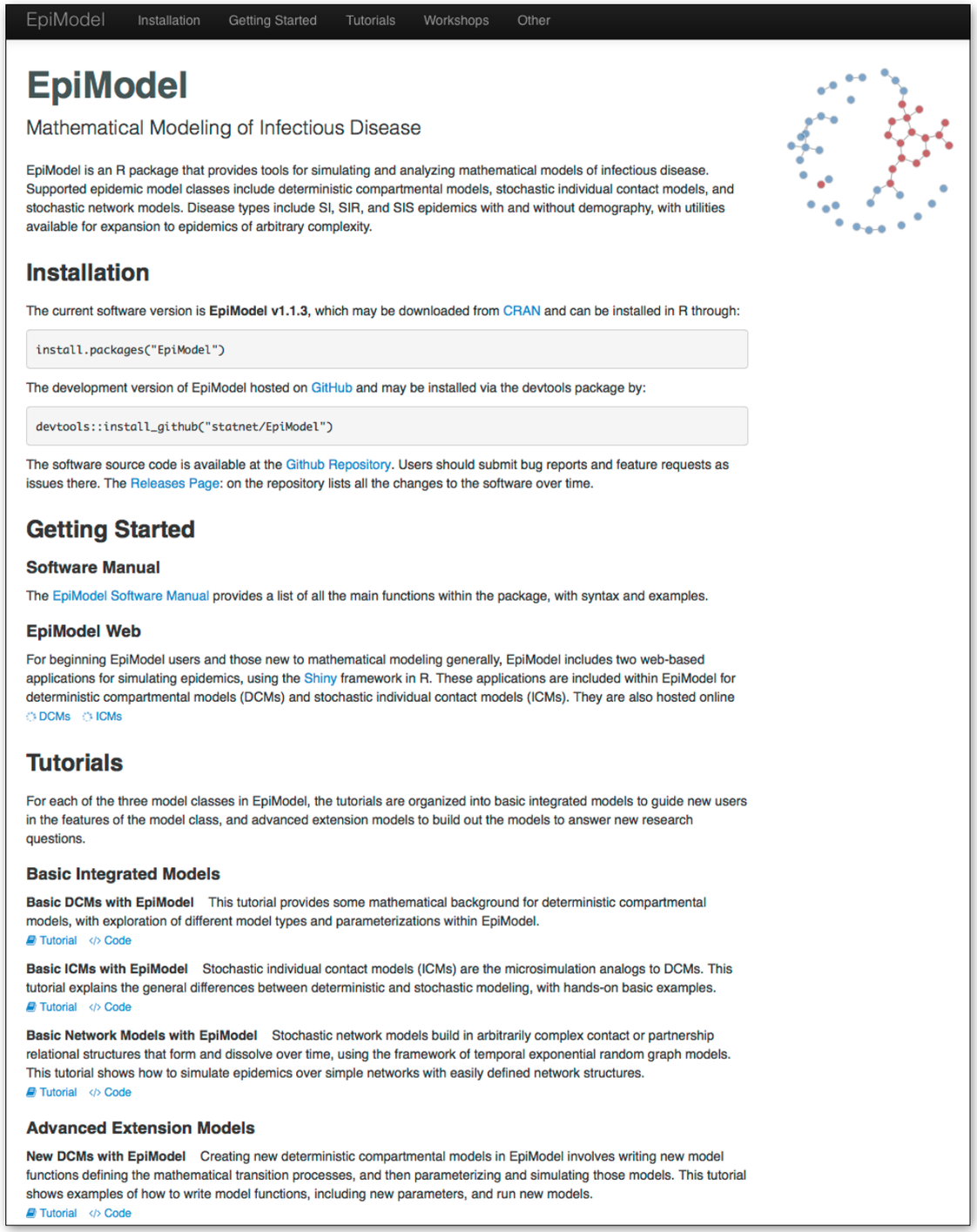
Motivating Examples for Model Building

Network Modeling for Epidemics 2025

EpiModel

- Open-source software platform for epidemic modeling in R
- Epidemics on top of TERGM statistical framework
- Built-in SI/SIS/SIR models for exploration and teaching
- Extendable API for research-level modeling
- See http://epimodel.org/

Jenness SM, Goodreau SM and Morris M. EpiModel: An R Package for Mathematical Modeling of Infectious Disease over Networks. Journal of Statistical Software. 2018; 84(8): 1-47.



NIH R01AI138783: EpiModel 2.0: Integrated Network Models for HIV/STI Prevention Science (PI: Jenness)

Research Applications of EpiModel Across Diseases

Model recommendations meet management reality: implementation and evaluation of a network-informed vaccination effort for endangered Hawaiian monk seals

Stacie J. Robinson[1], Michelle M. Barbieri[1], Samantha Murphy[2], Jason D. Baker[1], Albert L. Harting[3], Meggan E. Craft[4] and Charles L. Littnan[1]

between the physiological and behavioral s of pathogen transmission: host heterogeneity epidemic outcomes

James D. Forester and Meggan E. Craft

mic Bayesian Markov model for health economic tions of interventions against infectious diseases

Katrin Haeussler, Ardo van den Hout, Gianluca Baio

September 5, 2018

A stochastic network-based model to sim (PD) in the Norwegian salmon industry movements and seaway distance betwe

Sara Amirpour Haredasht[a], Saraya Tavornpanich[b], Trude Marie Lyngstad[b], Tadaishi Yatabe[a], Edgar B[illegible]

[a] *Center for Animal Disease Modeling and Surveillance (CADMS), Department of Medicine & Epidemiology, School Veterinary Medicin CA, USA*
[b] *Norwegian Veterinary Institute, Oslo, Norway*

A Network Model of Hand Hygiene: How Good Is Good Enough to Stop the Spread of MRSA?

Neal D. Goldstein, PhD, MBI;[1,2] Stephen C. Eppes, MD;[1] Amy Mackley, MSN;[1] Deborah Tuttle, MD;[1] David A. Paul, MD[1,2]

Incidence rate estimation, periodic testing and the limitations of the mid-point imputation approach

Alain Vandormael,[1,2]* Adrian Dobra,[3] Till Bärnighausen,[1,4,5,6] Tulio de Oliveira[2,7] and Frank Tanser[1,6,7,8]

Host behaviour–parasite feedback: an essential link between animal behaviour sease ecology

Ezenwa[1], Elizabeth A. Archie[2], Meggan E. Craft[3], Dana M. Hawley[5], rtin[6], Janice Moore[7] and Lauren White[4]

Research Applications of EpiModel Across Diseases

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39. Yap WA, Raja DB. Time-variant strategies for optimizing the performance of non-pharmaceutical interventions (NPIs) in protecting lives and livelihoods during the COVID-19 pandemic. *medRxiv.* 2020; DOI: 10.1101/2020.04.13.20063248. [LINK]

40. Yu X. Modeling Return of the Epidemic: Impact of Population Structure, Asymptomatic Infection, Case Importation and Personal Contacts. *medRxiv.* 2020; DOI: 10.1101/2020.04.26.20081109. [LINK]

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42. Earnest R, Rönn MM, Bellerose M, et al. Population-Level Benefits of Extragenital Gonorrhea Screening among Men Who Have Sex with Men: An Exploratory Modeling Analysis. *Sexually Transmitted Diseases.* 2020; Published Ahead of Print. DOI: 10.1097/OLQ.0000000000001189. [LINK]

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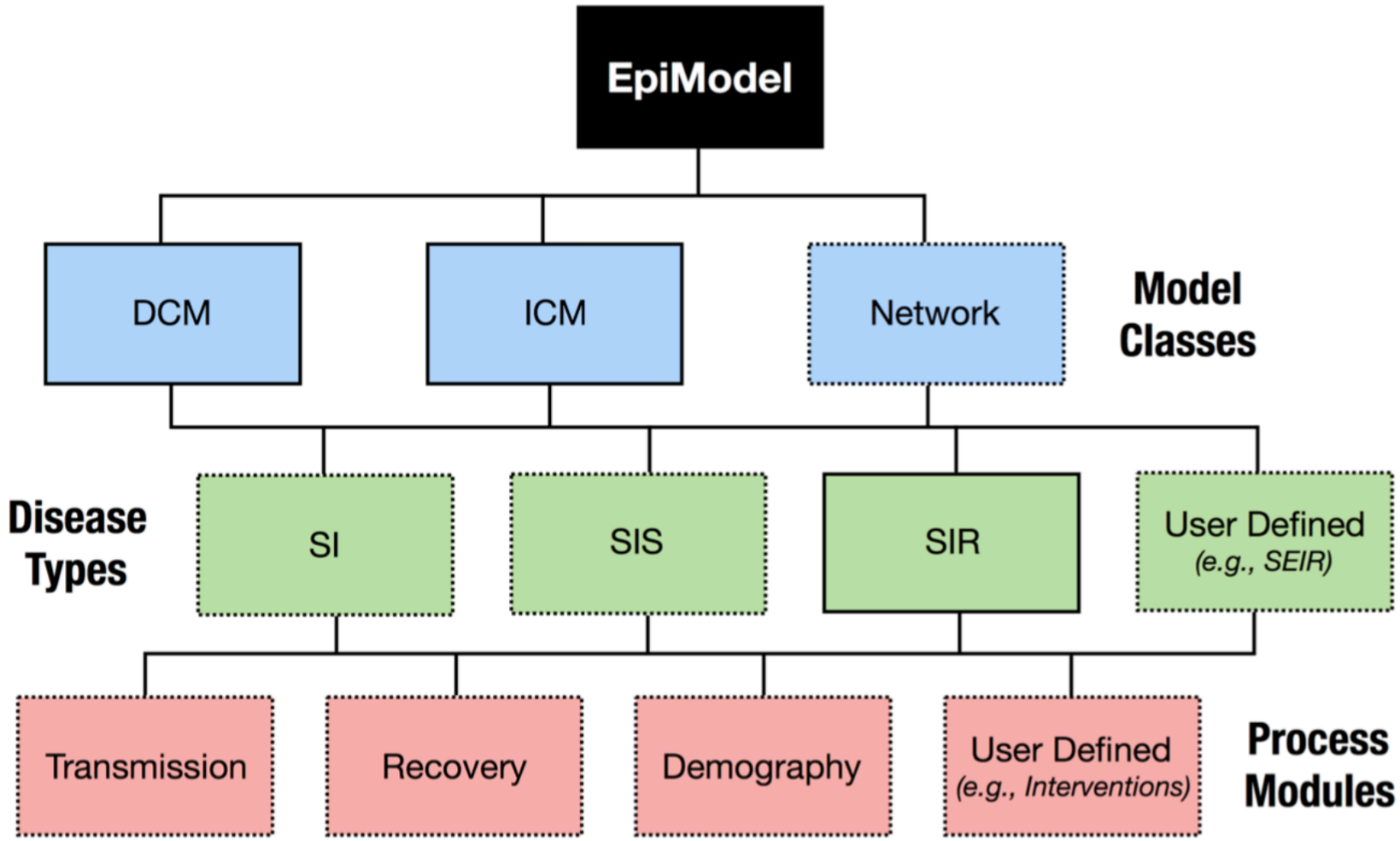
47. Churches T, Jorm L. "COVOID": A flexible, freely available stochastic individual contact model for exploring COVID-19 intervention and control strategies. *JMIR Public Health Surveill.* 2020; Published Ahead of Print. DOI:10.2196/18965. [LINK]

48. Lopman B, Liu C, Guillou AL, Lash TL, Isakov A, Jenness S. A model of COVID-19 transmission and control on university campuses. *medRxiv.* 2020; DOI: 10.1101/2020.06.23.20138677. [LINK]

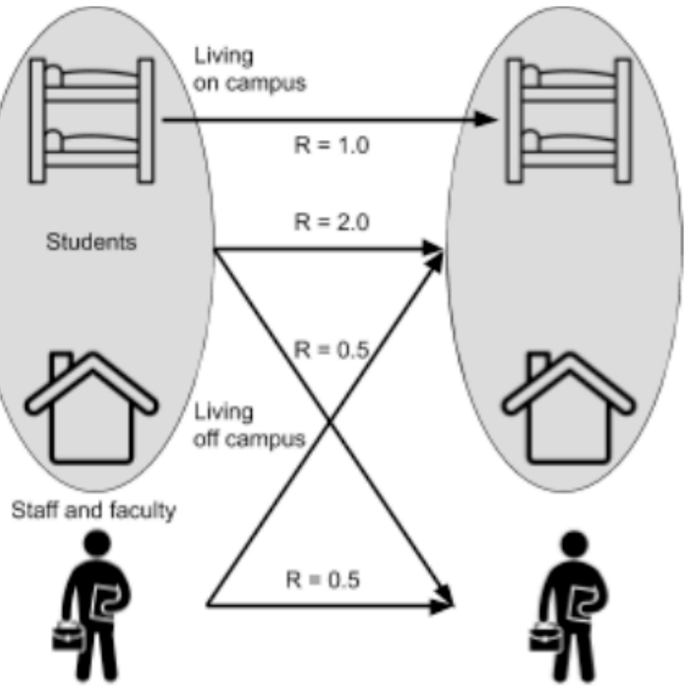
https://github.com/statnet/EpiModel/wiki

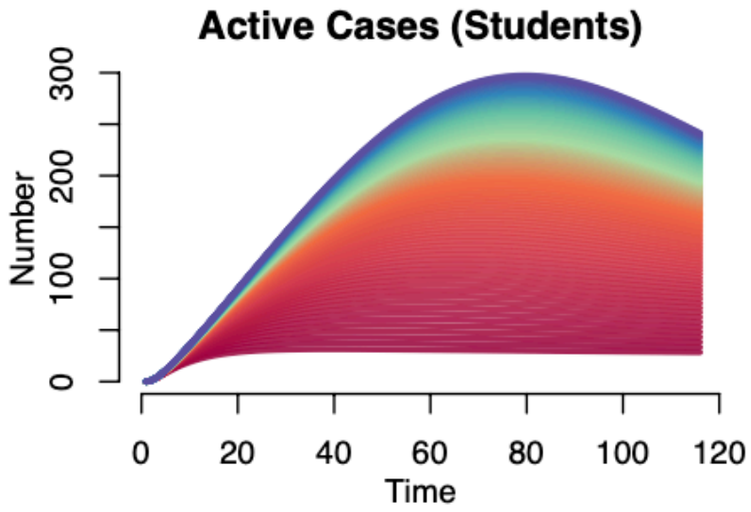
EpiModel

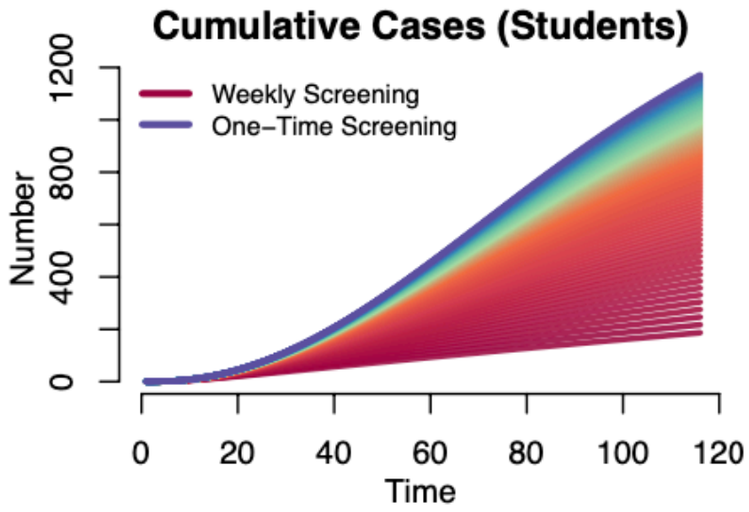


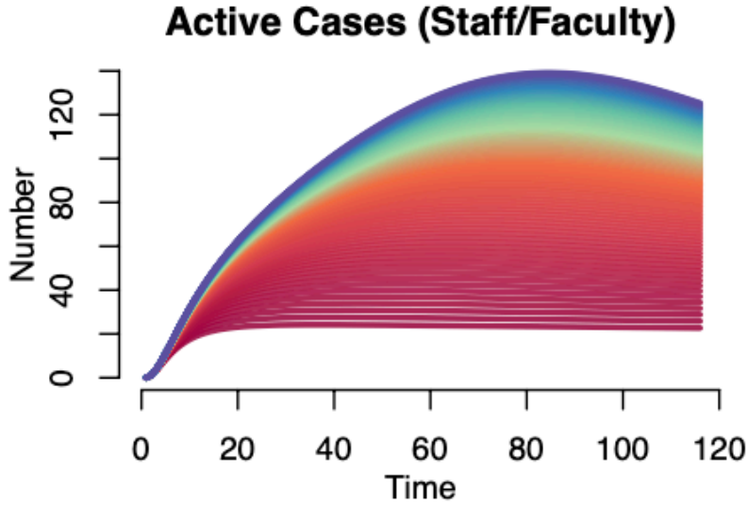
- EpiModel designed specifically to allow for both built-in ("toy models") and user-defined extensions ("research models")
- Material in this course is focus on built-in network models. Extensions are more complicated, and are the focus of NME-II

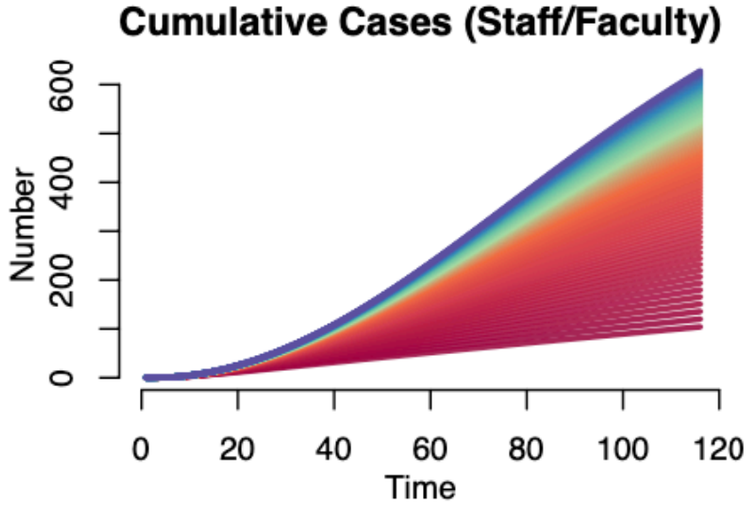
COVID University DCM with EpiModel











- Compartmental model for COVID on university campus led by Ben Lopman and Carol Liu, supported by Adrien Le Guillou and me
- Projects impact of testing & quarantine and screening & isolation strategies
- Model programmed and simulated in EpiModel

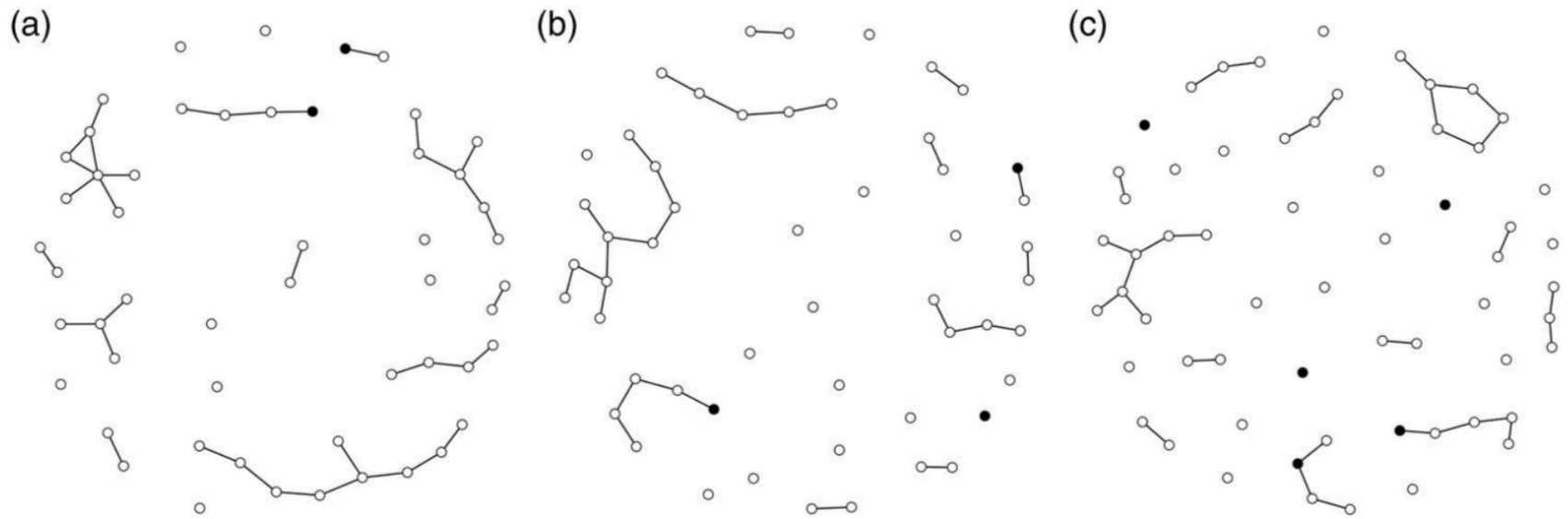
COVID University DCM with EpiModel

https://epimodel.shinyapps.io/covid-university/

Network Model for MRSA

A Network Model of Hand Hygiene: How Good Is Good Enough to Stop the Spread of MRSA?

Neal D. Goldstein, PhD, MBI;[1,2] Stephen C. Eppes, MD;[1] Amy Mackley, MSN;[1] Deborah Tuttle, MD;[1] David A. Paul, MD[1,2]



- Network model of MRSA infection within a NICU setting
- Networks defined as shared hospital worker contacts between infants

Network Model for Seal Influenza

PROCEEDINGS B

rspb.royalsocietypublishing.org

Research

Cite this article: Robinson SJ, Barbieri MM, Murphy S, Baker JD, Harting AL, Craft ME, Littnan CL. 2018 Model recommendations meet management reality: implementation and evaluation of a network-informed vaccination effort for endangered Hawaiian monk seals. *Proc. R. Soc. B* **285**: 20171899. http://dx.doi.org/10.1098/rspb.2017.1899

Received: 22 August 2017
Accepted: 4 December 2017

Subject Category:
Ecology

Subject Areas:
health and disease and epidemiology, ecology

Keywords:
Hawaiian monk seal, wildlife disease, vaccination, network model, morbillivirus

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Electronic supplementary material is available online at https://dx.doi.org/10.6084/m9.figshare.c.3957718.

THE ROYAL SOCIETY PUBLISHING

Model recommendations meet management reality: implementation and evaluation of a network-informed vaccination effort for endangered Hawaiian monk seals

Stacie J. Robinson[1], Michelle M. Barbieri[1], Samantha Murphy[2], Jason D. Baker[1], Albert L. Harting[3], Meggan E. Craft[4] and Charles L. Littnan[1]

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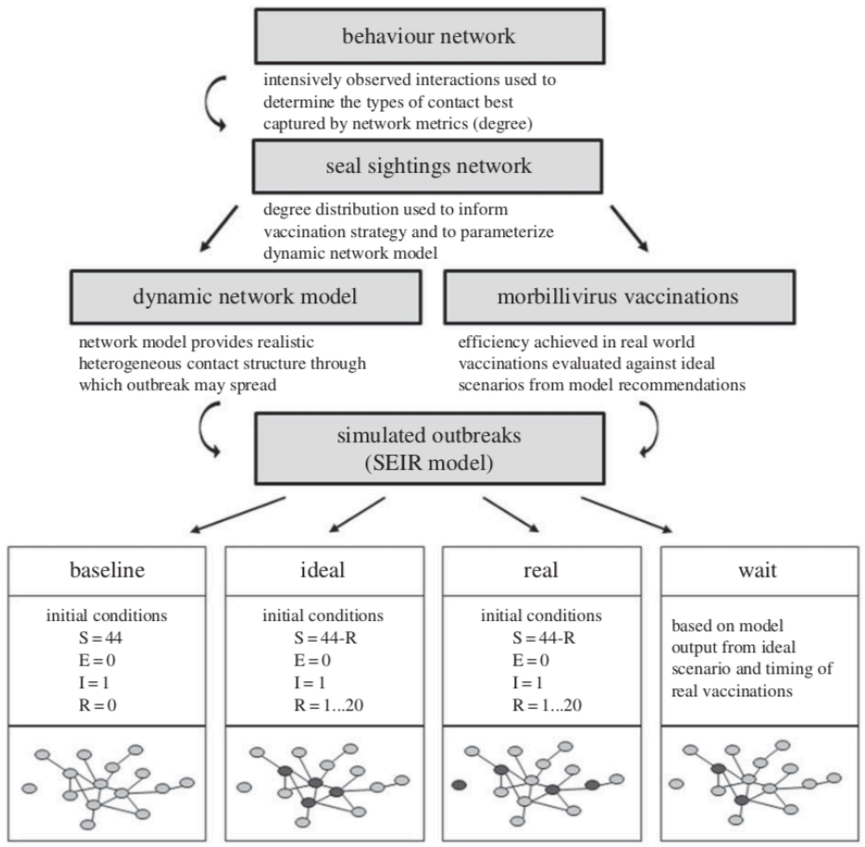
SJR, 0000-0002-0539-0306

Where disease threatens endangered wildlife populations, substantial resources are required for management actions such as vaccination. While network models provide a promising tool for identifying key spreaders and prioritizing efforts to maximize efficiency, population-scale vaccination remains rare, providing few opportunities to evaluate performance of model-informed strategies under realistic scenarios. Because the endangered Hawaiian monk seal could be heavily impacted by disease threats such as morbillivirus, we implemented a prophylactic vaccination programme. We used contact networks to prioritize vaccinating animals with high contact rates. We used dynamic network models to simulate morbillivirus outbreaks under real and idealized vaccination scenarios. We then evaluated the efficacy of model recommendations in this real-world vaccination project. We found that deviating from the model recommendations decreased the efficiency; requiring 44% more vaccinations to achieve a given decrease in outbreak size. However, we gained protection more quickly by vaccinating available animals rather than waiting to encounter priority seals. This work demonstrates the value of network models, but also makes trade-offs clear. If vaccines were limited but time was ample, vaccinating only priority animals would maximize herd protection. However, where time is the limiting factor, vaccinating additional lower-priority animals could more quickly protect the population.

1. Introduction

Infectious agents can negatively impact the demographics and fitness of wildlife populations, and disease outbreaks have the potential to threaten the persistence of small populations or endangered species [1,2]. Vaccination has become an important tool for managing disease to protect threatened populations [3]. Network models can help to characterize heterogeneous contact patterns, and are often suggested as useful means of optimizing disease control strategies [4,5]. Network models have demonstrated the potential to maximize vaccination efficiency by targeting those individuals or locations most connected in the network [6,7]. However, we do not know of instances where such model recommendations have been put into practice or evaluated under realistic field conditions encountered during wildlife vaccination efforts. This study provides



EpiModel's Modular Framework

- Allows you to easily add in any processes of interest into the ID system, and use the base EpiModel tools (estimation, simulation, analysis, plotting)
  - These are tools that we are invested in helping you master!
- It enforces you (the user) to *think* modularly: building a complex system in small, interconnected building blocks
- This facilitates efficient expansion once you have a starting codebase

HIV Preexposure Prophylaxis (PrEP)

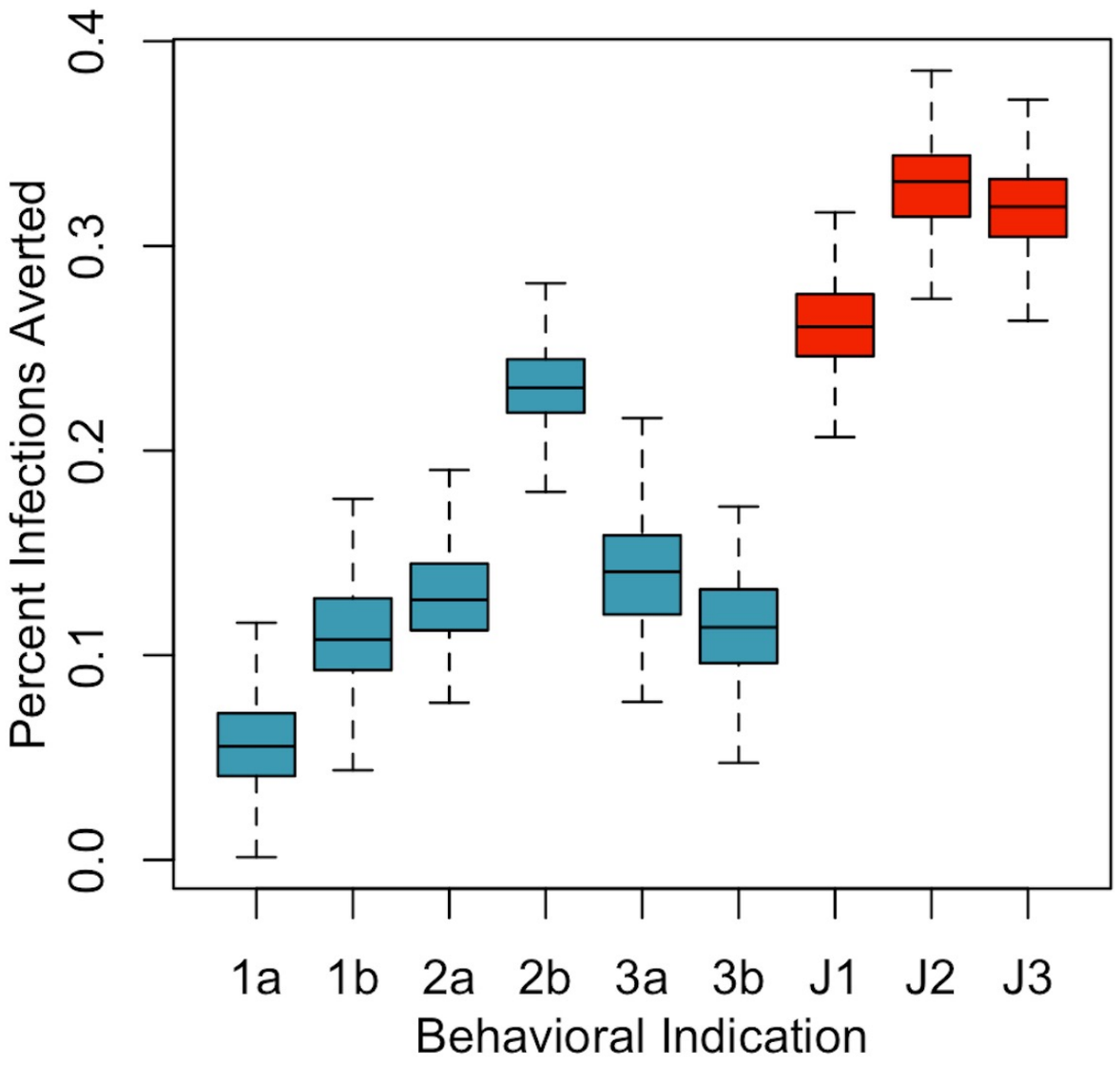
- Anti-retroviral treatment provided to HIV-uninfected persons
- Decreases biological risk of infection when HIV-infected partner has uncontrolled viral replication
- Men who have sex with men (MSM) in the US are a high-priority population for PrEP
- 5% to 50% of MSM with indications with indications currently using it

HIV PrEP Indications as a Network Problem

US CDC PrEP Indications

- US PHS/CDC released clinical practice guidelines indicating PrEP for those at "substantial risk" in 2014, revised in 2017, and again in 2021
- For MSM, prescription indications were:
  - Unprotected anal intercourse (UAI) in monogamous partnership with person not recently tested for HIV
  - UAI outside of a monogamous partnership
  - AI (including with condoms) in a known serodiscordant partnership
  - Any non-HIV STI diagnosis
- Clinicians recommended to screen for conditions in past 6 months, reevaluate risk every 12 months

Jenness SM, Goodreau SM, Rosenberg E, Beylerian EN, Hoover KW, Smith DK, Sullivan PS. Impact of CDC's HIV Pre-Exposure Prophylaxis Guidelines among MSM in the United States. *Journal of Infectious Diseases*. 2016; 214(12): 1800–1807.

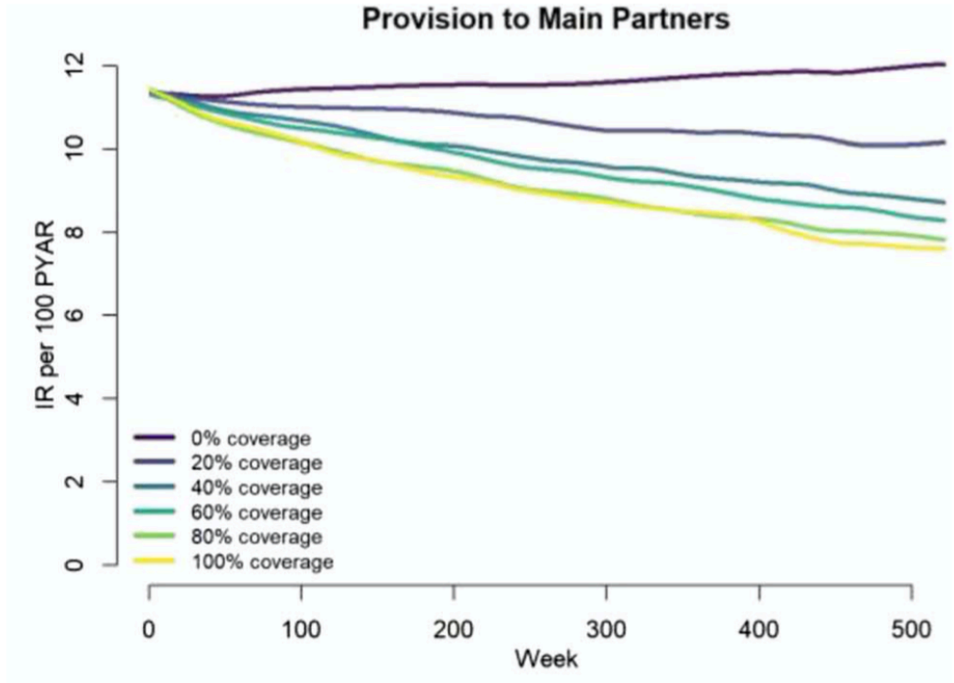


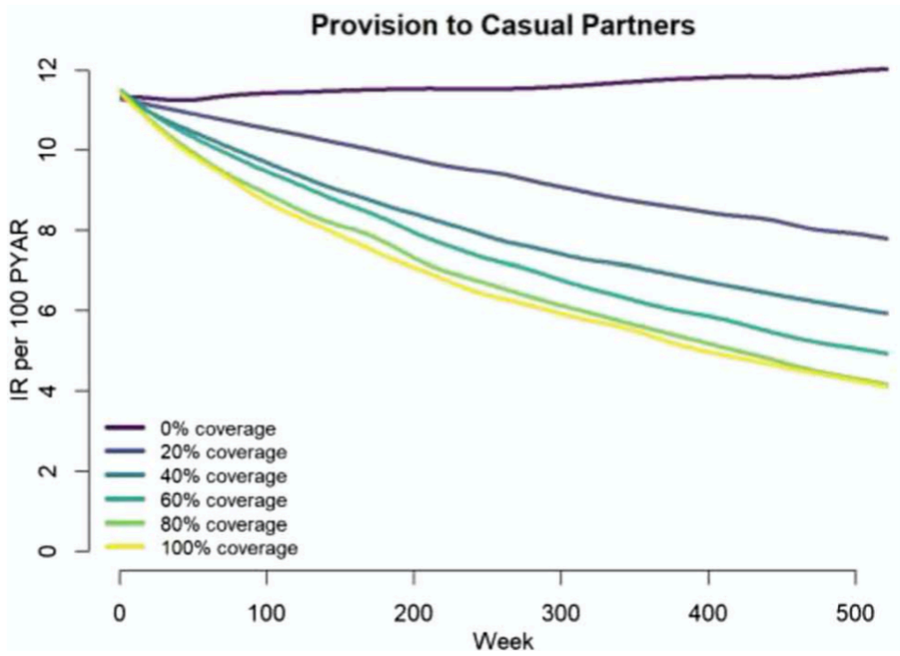
Partner Notification Interventions Across Networks

Epidemiological Impact of Expedited Partner Therapy for Men Who Have Sex With Men: A Modeling Study

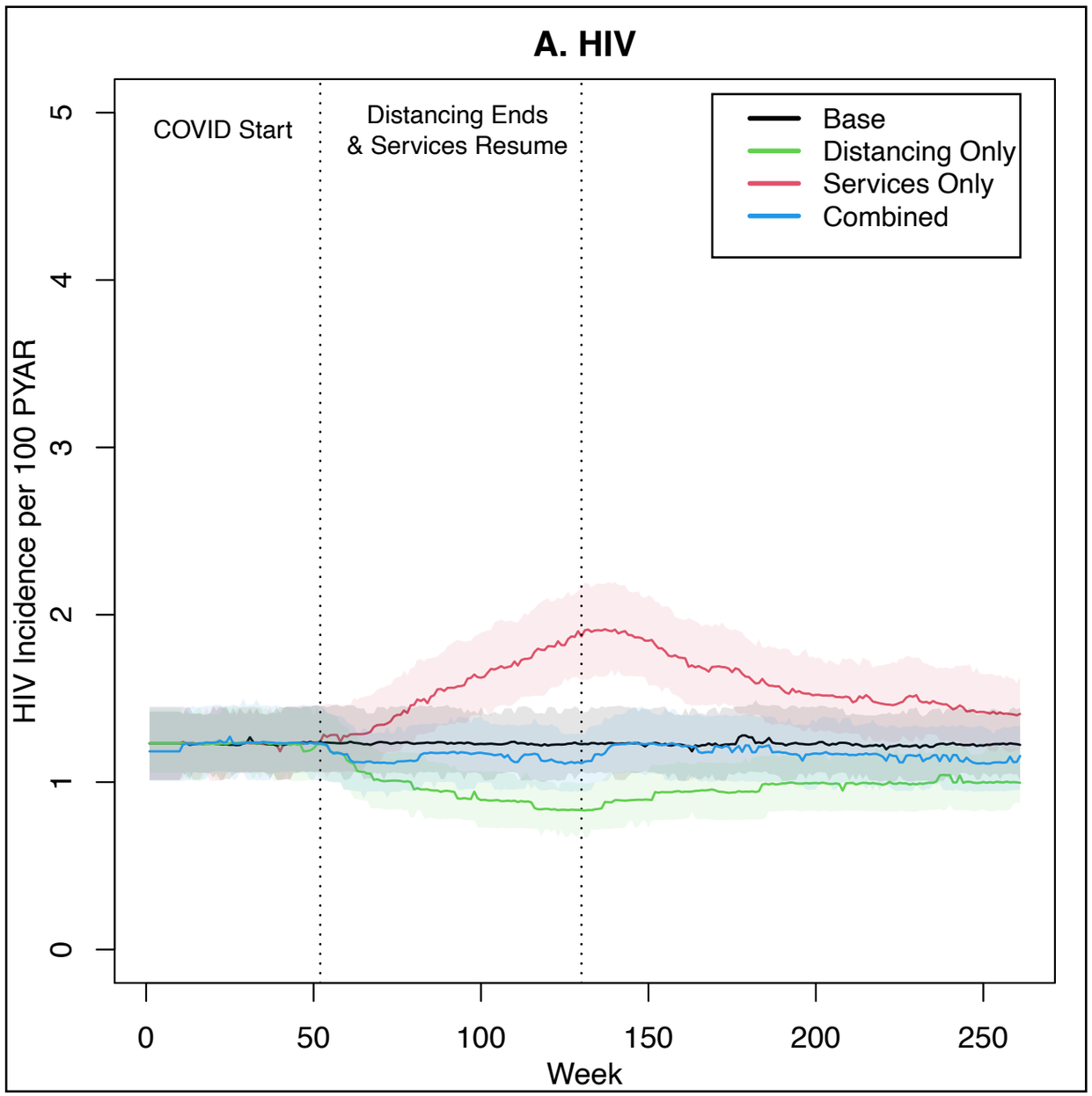
Kevin M. Weiss, MPH, Jeb S. Jones, PhD,* David A. Katz, PhD,†‡ Thomas L. Gift, PhD,§ Kyle Bernstein, PhD,§ Kimberly Workowski, MD,§¶ Eli S. Rosenberg, PhD,*|| and Samuel M. Jenness, PhD**

- Direct patient delivery of antibiotic meds to sexual partners of diagnosed "index patients"
- Example of contact-driven prevention related to partner notification (contact tracing)
- Required historical network data on partnerships in different networks to represent “look back” period for identifying recent partners
- Epi model of HIV + NG + CT co-infection
- Counterfactual models explored different deployments of EPT by partnership type





COVID's Shock to the Sexual Network



The New York Times

People Are Still Having Sex. So Why Are S.T.D. Rates Dropping?

Public health officials believe many cases are going undetected as clinics close during the pandemic and testing supplies are diverted to coronavirus screening.

- Modeling "shock" to network due to COVID-related sexual distancing, differential by partner type
- Gradual resumption of sexual activity over 2020
- Balancing decreased transmission with distancing against increased transmission with service disruption

Jenness SM, Le Guillou A, Chandra C, Mann L, Sanchez T, Westreich D, Marcus JL. Projected HIV and Bacterial STI Incidence Following COVID-Related Sexual Distancing and Clinical Service Interruption. Journal of Infectious Diseases. 2021; 223(6): 1019–28.

Our Models for HIV Preexposure Prophylaxis

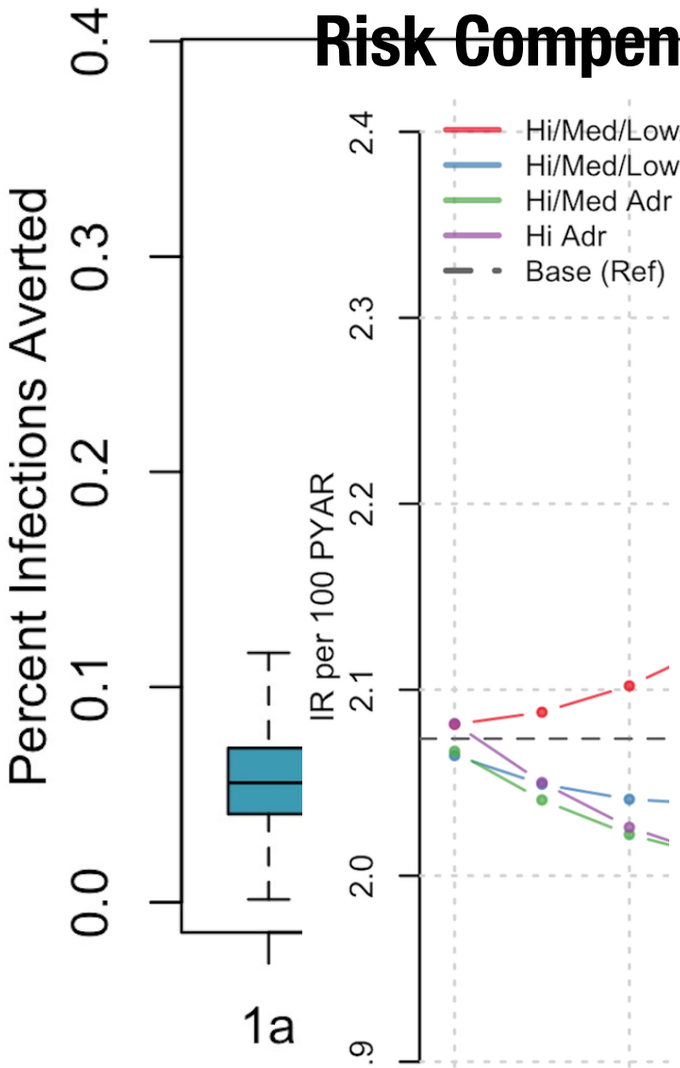
Evaluating CDC Guidelines

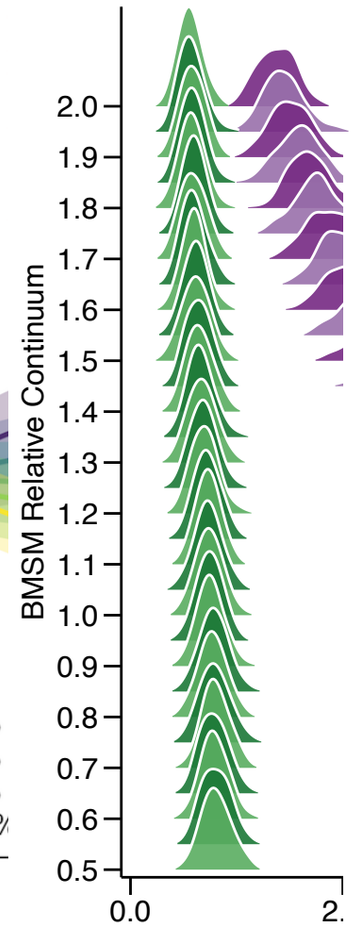
Risk Compensation & Adherence

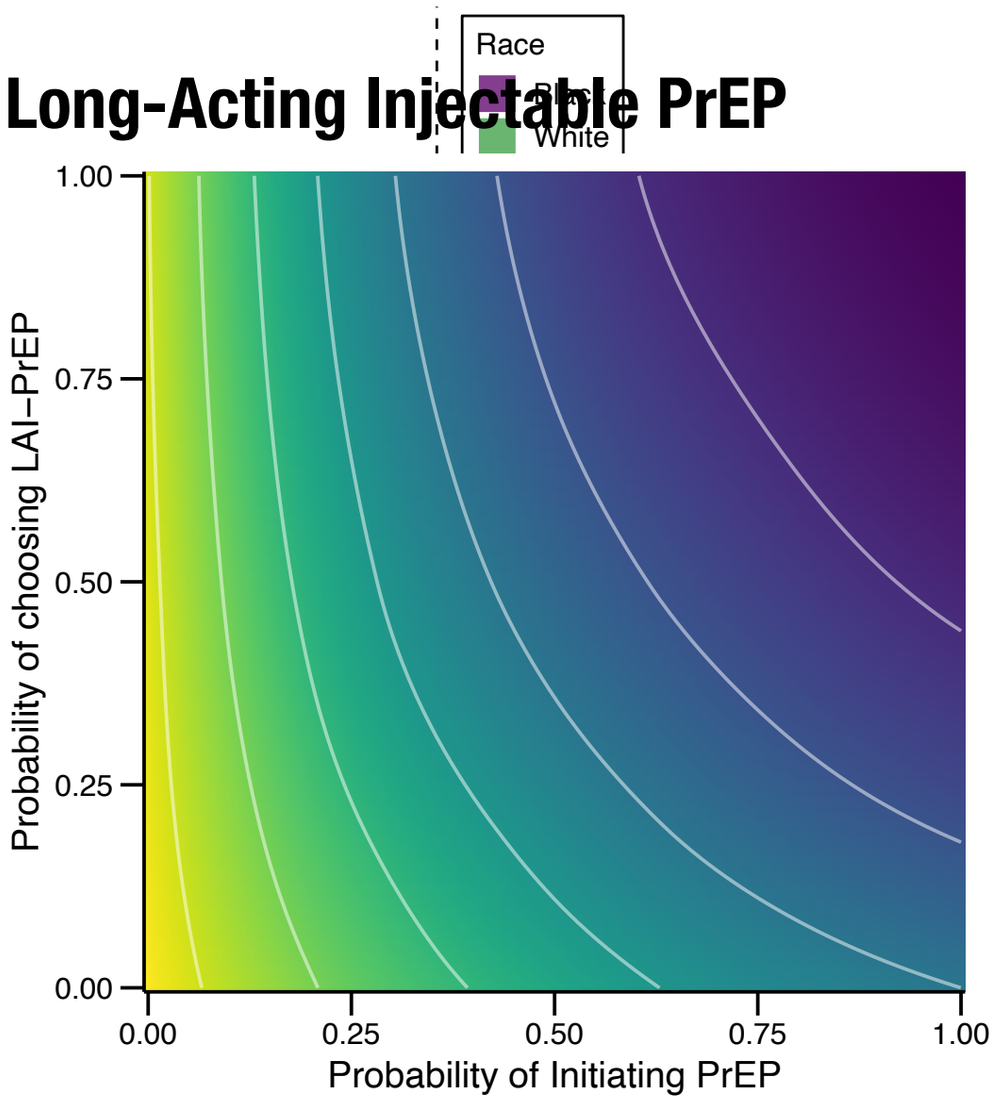
Impact on Bacterial STIs

PrEP & Racial Disparities

Long-Acting Injectable PrEP







Empirical Data ⟿ Network Model Parameters

- Recently completed **ARTnet Study** of MSM in the US (R21 MH112449)
  - 4904 MSM reporting on 16198 sexual partnerships
- Data-driven statistical models embedded within ID transmission models where primary data available
  - TERGMs for network structure ⟿ simulate
  - Poisson models for coital frequency ⟿ predict
  - Logit models for condom use ⟿ predict
- Allows for confounding adjustment and addressing parameter covariance, statistical interactions when necessary
- Secondary data for (more) universal parameters
  - PrEP/ART effectiveness, probability of HIV transmission per act, …

Epidemics 30 (2020) 100386

Contents lists available at ScienceDirect

Epidemics

journal homepage: www.elsevier.com/locate/epidemics

Egocentric sexual networks of men who have sex with men in the United States: Results from the ARTnet study

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ARTICLE INFO

Keywords:
Men who have sex with men
Sexual networks
Mathematical modeling
Network modeling
Network science

ABSTRACT

In this paper, we present an overview and descriptive results from one of the first egocentric network studies of men who have sex with men (MSM) from across the United States: the ARTnet study. ARTnet was designed to support prevention research for human immunodeficiency virus (HIV) and other sexually transmitted infections (STIs) that are transmitted across partnership networks. ARTnet implemented a population-based egocentric network study design that sampled egos from the target population and asked them to report on the number, attributes, and timing of their sexual partnerships. Such data provide the foundation needed for parameterizing stochastic network models that are used for disease projection and intervention planning. ARTnet collected data online from 2017 to 2019, with a final sample of 4904 participants who reported on 16198 sexual partnerships. The aims of this paper were to characterize the joint distribution of three network parameters needed for modeling: degree distributions, assortative mixing, and partnership age, with heterogeneity by partnership type (main, casual and one-time), demography, and geography. Participants had an average of 1.19 currently active partnerships ("mean degree"), which was higher for casual partnerships (0.74) than main partnerships (0.45). The mean rate of one-time partnership acquisition was 0.16 per week (8.5 partners per year). Main partnerships lasted 272.5 weeks on average, while casual partnerships lasted 133.0 weeks. There was strong but heterogenous assortative mixing by race/ethnicity for all groups. The mean absolute age difference for all partnership types was 9.5 years, with main partners differing by 6.3 years compared to 10.8 years for casual partners. Our analysis suggests that MSM may be at sustained risk for HIV/STI acquisition and transmission through high network degree of sexual partnerships. The ARTnet network study provides a robust and reproducible foundation for understanding the dynamics of HIV/STI epidemiology among U.S. MSM and supporting the implementation science that seeks to address persistent challenges in HIV/STI prevention.

1. Introduction

Human immunodeficiency virus (HIV) and other sexually transmitted infections (STIs) continue to present significant public health challenges. In the United States, HIV and STI incidence disparities are linked to demographics (Singh et al., 2014), risk behavior (Goldstein et al., 2017), clinical care access (Beer et al., 2017), and geography (Oster et al., 2015). Of the estimated 40,000 new HIV infections occurring in 2017, two-thirds were among men who have sex with men (MSM) (Centers for Disease Control and Prevention, 2019b). The large disparities in HIV/STI cases by race and age have worsened, with incidence increasing among younger non-white MSM while decreasing in other MSM groups (Rosenberg et al., 2018). Syphilis has also concentrated among MSM (de Voux et al., 2015), following similar demographic and geographic patterns as HIV (Grey et al., 2017; Sullivan et al., 2018). Understanding the persistent and emerging drivers of HIV/STI transmission dynamics among MSM is critical to prevention.

Sexual partnership networks are the mechanism through which all STI and most HIV transmissions circulate. The pathogens are transmitted by sexual acts embedded within partnerships, and circulation through the population depends on how those partnerships form and dissolve — a highly structured and population-specific dynamic process (Morris et al., 2009; Goodreau et al., 2012; Jenness et al., 2016a). While sexual network structure can be measured and analyzed either cross-

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https://doi.org/10.1016/j.epidem.2020.100386
Received 30 October 2019; Received in revised form 15 January 2020; Accepted 17 January 2020
Available online 24 January 2020

https://pubmed.ncbi.nlm.nih.gov/32004795/

Our Network Needs for ID Modeling

- Modeling dynamic (temporally evolving) contact networks with temporal exponential random graph models (TERGMS)…
  - … with flexible network configurations allowing for variability in aspects of social contact processes with intuitive counterfactuals on network structure
  - … data-driven parameterization, with robust sampled egocentric network data that minimizes missing data biases
  - … in multiple layers (multi-layer networks) representing different types of contacts, with each layer having different formation and dissolution components
  - … in open populations with demographic churn
  - … with ongoing temporal feedback between exogenous processes and network structure, with predictable and intuitive network response to those processes
  - … using a sparse network object representation (networkLite) that significantly speeds up simulations
- And then… adding disease transmission models on top