

A background graphic consisting of a network graph with black and white nodes and edges. The nodes are circles of varying sizes, and the edges are lines of varying thicknesses connecting them. The graph is dense and complex, with many connections between nodes.

# Applied of Network Models for Epidemics

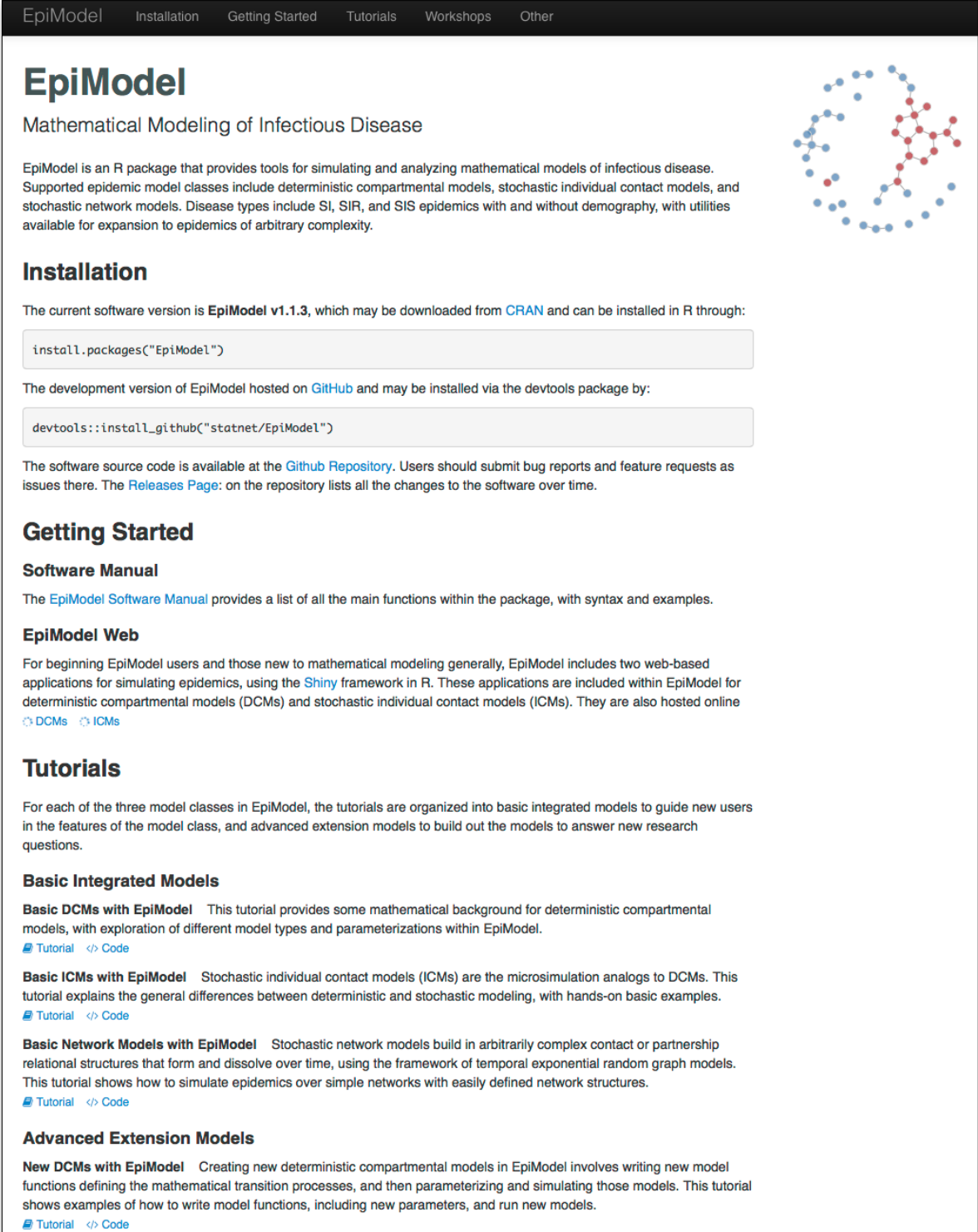
*Motivating Examples in HIV and COVID*

**Network Modeling for Epidemics @ SISMID 2024**

Module 10

- 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.*



The screenshot shows the EpiModel website with a navigation bar containing links for EpiModel, Installation, Getting Started, Tutorials, Workshops, and Other. The main content area features the EpiModel logo (a network graph with blue and red nodes) and the following sections:

- EpiModel**: Mathematical Modeling of Infectious Disease. Description: EpiModel is an R package that provides tools for simulating and analyzing mathematical models of infectious disease. Supported epidemic model classes include deterministic compartmental models, stochastic individual contact models, and stochastic network models. Disease types include SI, SIR, and SIS epidemics with and without demography, with utilities available for expansion to epidemics of arbitrary complexity.
- Installation**: The current software version is EpiModel v1.1.3, which may be downloaded from CRAN and can be installed in R through:

```
install.packages("EpiModel")
```

The development version of EpiModel hosted on GitHub and may be installed via the devtools package by:

```
devtools::install_github("statnet/EpiModel")
```

The software source code is available at the GitHub Repository. Users should submit bug reports and feature requests as issues there. The Releases Page: on the repository lists all the changes to the software over time.
- Getting Started**
- Software Manual**: The EpiModel Software Manual provides a list of all the main functions within the package, with syntax and examples.
- EpiModel Web**: For beginning EpiModel users and those new to mathematical modeling generally, EpiModel includes two web-based applications for simulating epidemics, using the Shiny framework in R. These applications are included within EpiModel for deterministic compartmental models (DCMs) and stochastic individual contact models (ICMs). They are also hosted online: [DCMs](#) [ICMs](#)
- Tutorials**: For each of the three model classes in EpiModel, the tutorials are organized into basic integrated models to guide new users in the features of the model class, and advanced extension models to build out the models to answer new research questions.
- Basic Integrated Models**
  - Basic DCMs with EpiModel**: This tutorial provides some mathematical background for deterministic compartmental models, with exploration of different model types and parameterizations within EpiModel. [Tutorial](#) [Code](#)
  - Basic ICMs with EpiModel**: Stochastic individual contact models (ICMs) are the microsimulation analogs to DCMs. This tutorial explains the general differences between deterministic and stochastic modeling, with hands-on basic examples. [Tutorial](#) [Code](#)
  - Basic Network Models with EpiModel**: Stochastic network models build in arbitrarily complex contact or partnership relational structures that form and dissolve over time, using the framework of temporal exponential random graph models. This tutorial shows how to simulate epidemics over simple networks with easily defined network structures. [Tutorial](#) [Code](#)
- Advanced Extension Models**
  - New DCMs with EpiModel**: Creating new deterministic compartmental models in EpiModel involves writing new model functions defining the mathematical transition processes, and then parameterizing and simulating those models. This tutorial shows examples of how to write model functions, including new parameters, and run new models. [Tutorial](#) [Code](#)

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<sup>1</sup>, Michelle M. Barbieri<sup>1</sup>, Samantha Murphy<sup>2</sup>, Jason D. Baker<sup>1</sup>, Albert L. Harting<sup>3</sup>, Meggan E. Craft<sup>4</sup> and Charles L. Littnan<sup>1</sup>

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

James D. Forester and Meggan E. Craft

Stochastic Bayesian Markov model for health economic evaluations of interventions against infectious diseases

Katrin Haeussler, Ardo van den Hout, Gianluca Baio

September 5, 2018

A stochastic network-based model to simulate pathogen dynamics (PD) in the Norwegian salmon industry considering movements and seaway distance between

Sara Amirpour Haredasht<sup>a</sup>, Saraya Tavoranpanich<sup>b</sup>, Trude Marie Lyngstad<sup>b</sup>, Tadaishi Yatabe<sup>a</sup>, Edgar B. Bratland<sup>a</sup>, Debra L. Martin<sup>a</sup>

<sup>a</sup> Center for Animal Disease Modeling and Surveillance (CADMS), Department of Medicine & Epidemiology, School Veterinary Medicine, University of California, Davis, CA, USA

<sup>b</sup> 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;<sup>1,2</sup> Stephen C. Eppes, MD;<sup>1</sup> Amy Mackley, MSN;<sup>1</sup> Deborah Tuttle, MD;<sup>1</sup> David A. Paul, MD<sup>1,2</sup>

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

Alain Vandormael,<sup>1,2\*</sup> Adrian Dobra,<sup>3</sup> Till Bärnighausen,<sup>1,4,5,6</sup> Tulio de Oliveira<sup>2,7</sup> and Frank Tanser<sup>1,6,7,8</sup>

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

Elizabeth A. Archie<sup>1</sup>, Elizabeth A. Archie<sup>2</sup>, Meggan E. Craft<sup>3</sup>, Dana M. Hawley<sup>5</sup>, David B. Clark<sup>6</sup>, Janice Moore<sup>7</sup> and Lauren White<sup>4</sup>



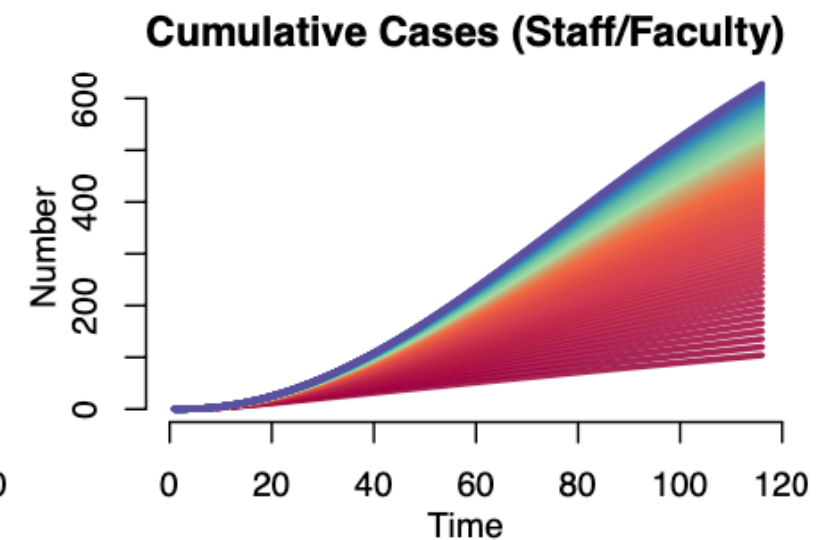
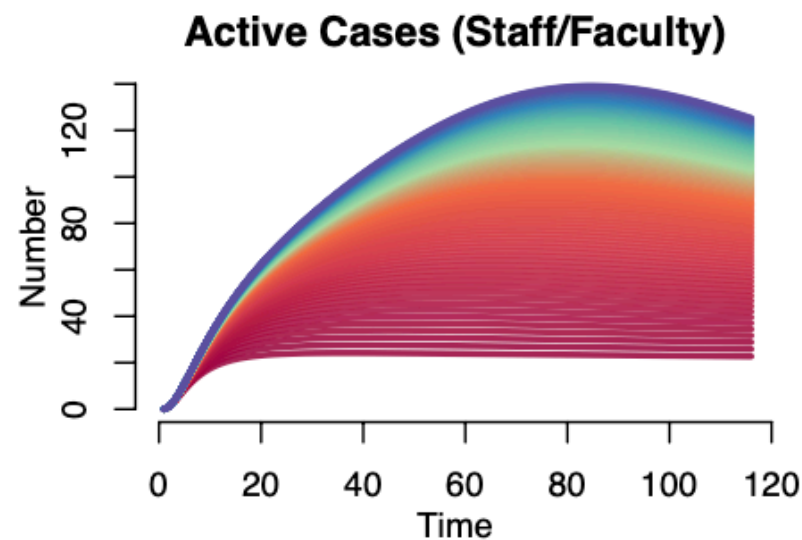
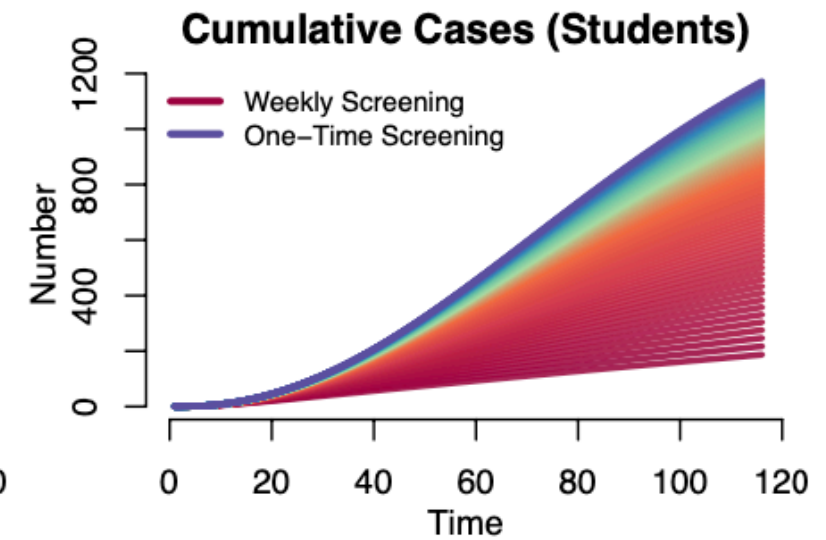
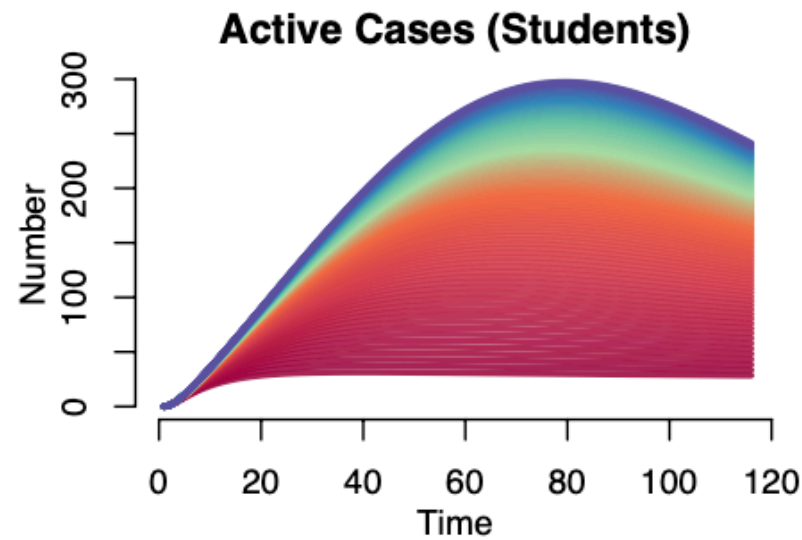
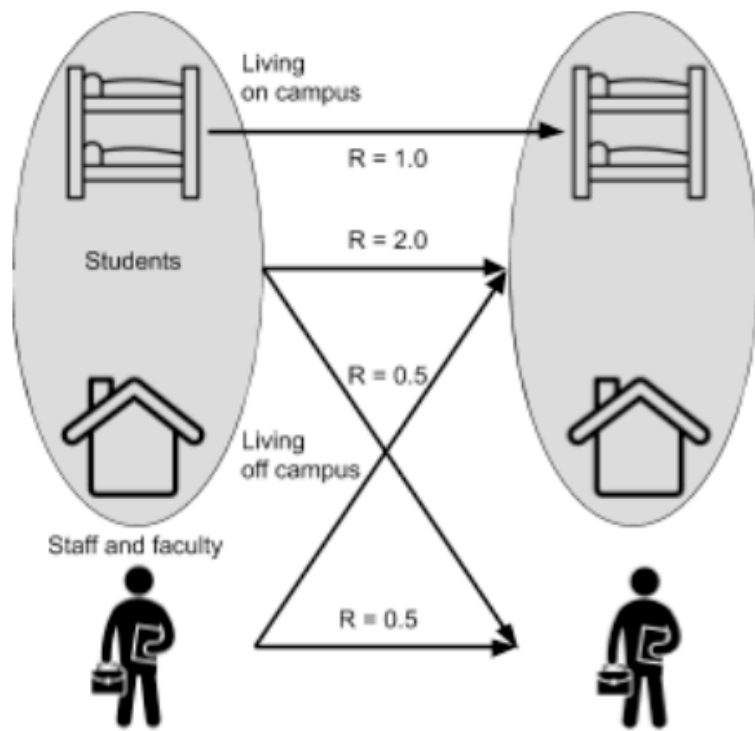
# Research Applications of EpiModel Across Diseases

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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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45. Al-Khani AM, Khalifa MA, AlMazrou A, Saquib N. The SARS-CoV-2 pandemic course in Saudi Arabia: A dynamic epidemiological model. *medRxiv*. 2020; DOI: 10.1101/2020.06.01.20119800. [\[LINK\]](#)
46. Bhavani DSD, Rani DTS, Rapolu T, Nutakki B. A Time-Dependent SEIRD Model for Forecasting the COVID-19 Transmission Dynamics. *medRxiv*. 2020; DOI: 10.1101/2020.05.29.20113571. [\[LINK\]](#)
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>



# 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

## COVID University

- Introduction
- Main Scenarios
- Sensitivity Analyses
- Raw Model Parameters

### Run Sensitivity Analysis

**Run New Simulations**      **Number of Samples**

This section computes sensitivity analysis using probability sampling. Use the sliders below to choose the range of the parameters, then press the **Run** button. *Note:* Running analyses with greater number of samples will increase the total computing time.

### Model Plots

**Populations**

- On Campus Students
- Off Campus Students
- All Students
- Staff and Faculty Members
- Everyone

**Compartments**

- Susceptible
- Latent
- Infectious
- Symptomatic
- Isolated
- Recovered
- Infectious (Cumulative)
- Isolated (Cumulative)
- Quarantined
- Quarantined (Cumulative)
- Hospitalized (Cumulative)
- Deaths (Cumulative)
- Tests Performed (Cumulative)

### Model Summary

	Base Model: No Intervention	Intervention Model
<b>Students</b>		
Total at Last Time Step	14,993 (14,990 - 14,997)	14,999 (14,998 - 15,000)
Cummulative Cases	7,723 (6,109 - 9,363)	1,052 (452 - 1,651)

### Model Options - Intervention Parameters

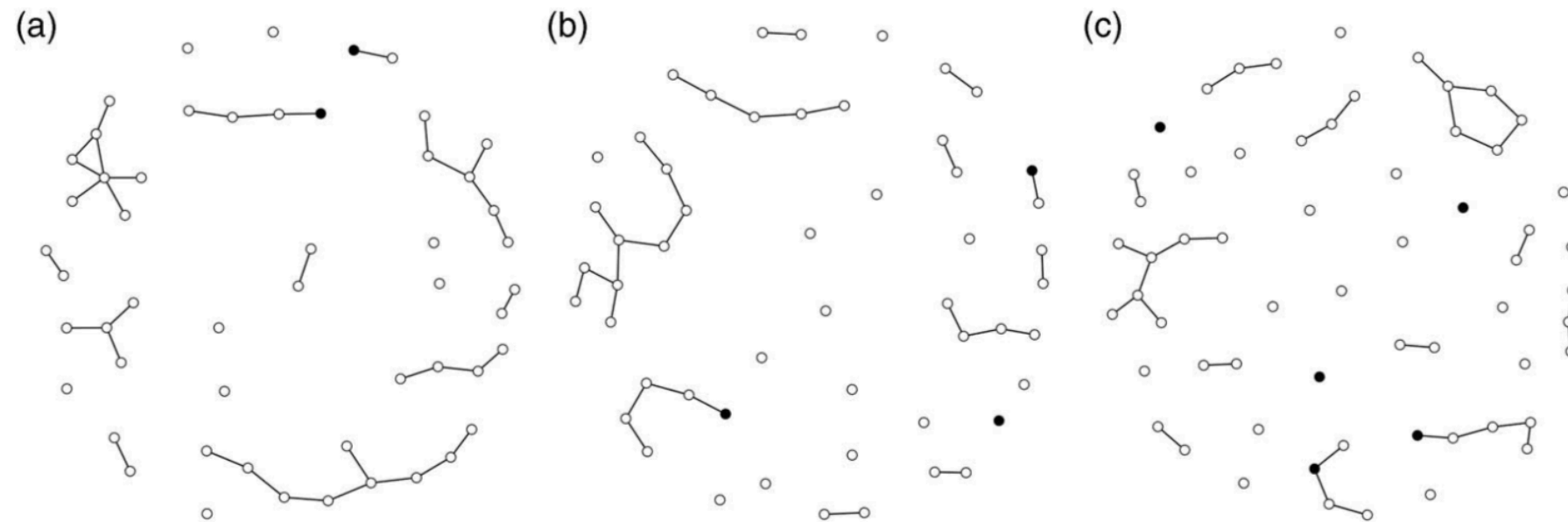
**Test Delay in Days (0 = no Testing)**

**Screening Interval in Days (0 = no Screening)**

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

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

Neal D. Goldstein, PhD, MBI;<sup>1,2</sup> Stephen C. Eppes, MD;<sup>1</sup> Amy Mackley, MSN;<sup>1</sup> Deborah Tuttle, MD;<sup>1</sup> David A. Paul, MD<sup>1,2</sup>



- 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](http://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>

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

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

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

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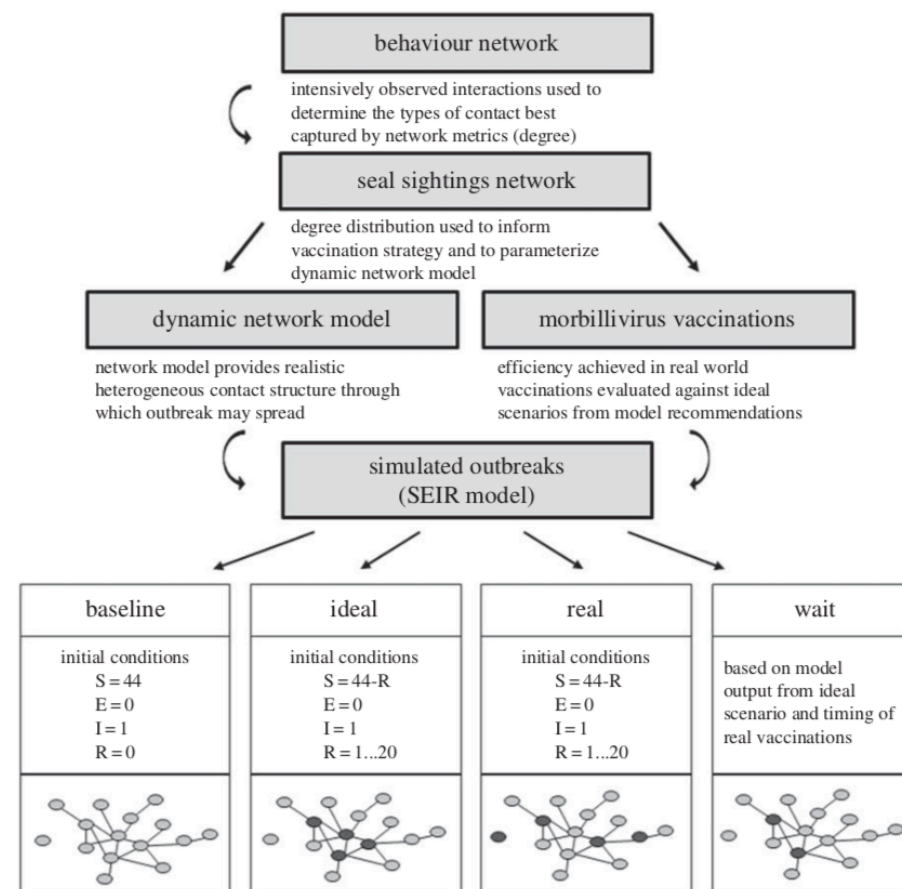
SJR, 0000-0002-0539-0306

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

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# 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



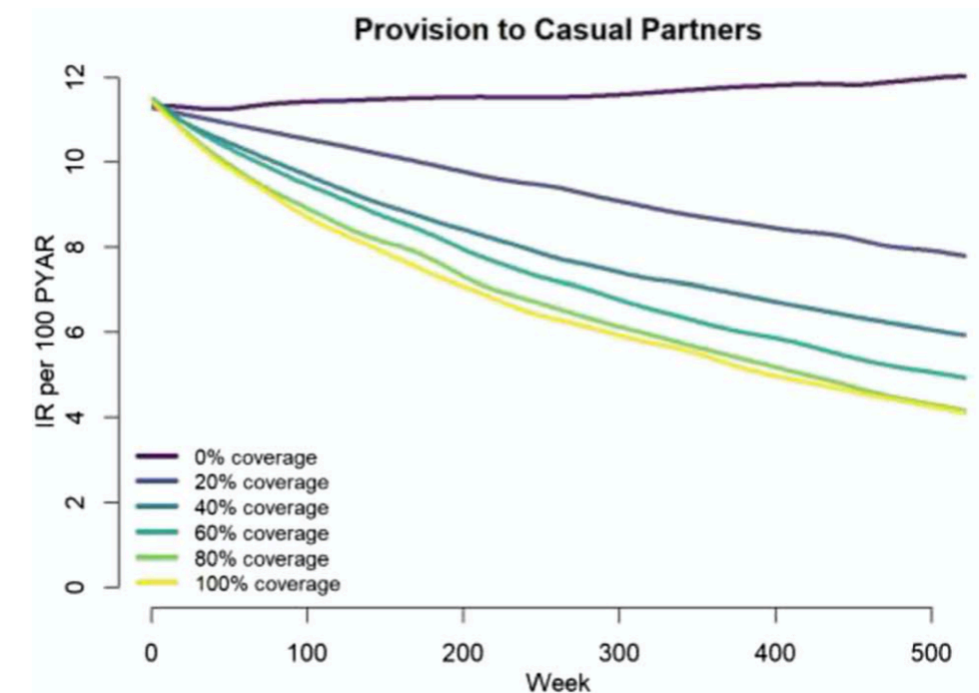
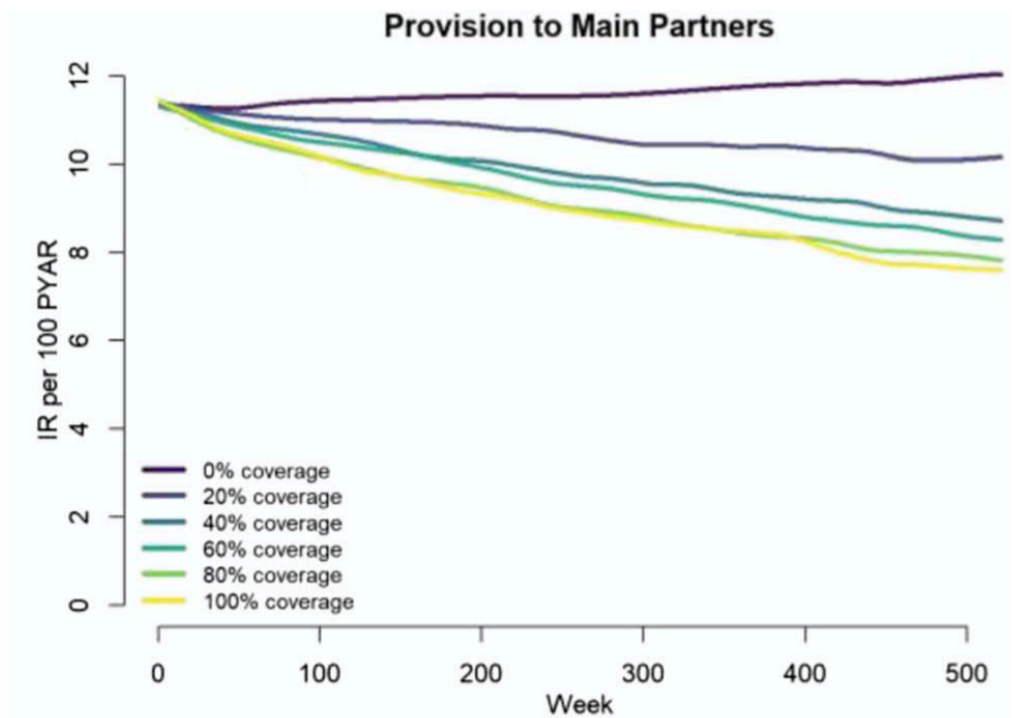


# Partner Notification Interventions Across Networks

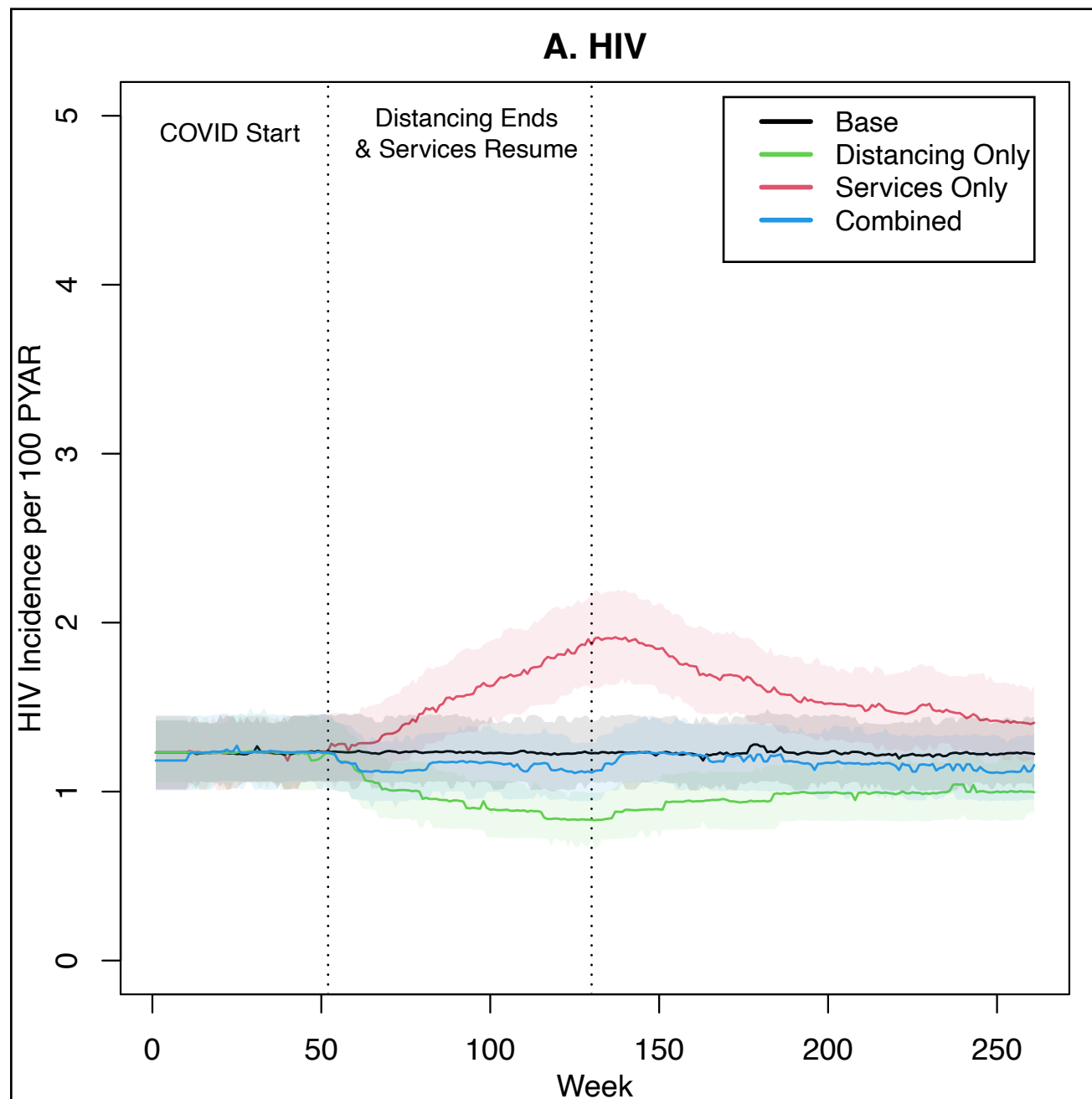
## Epidemiological Impact of Expedited Partner Therapy for Men Who Have Sex With Men: A Modeling Study

*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

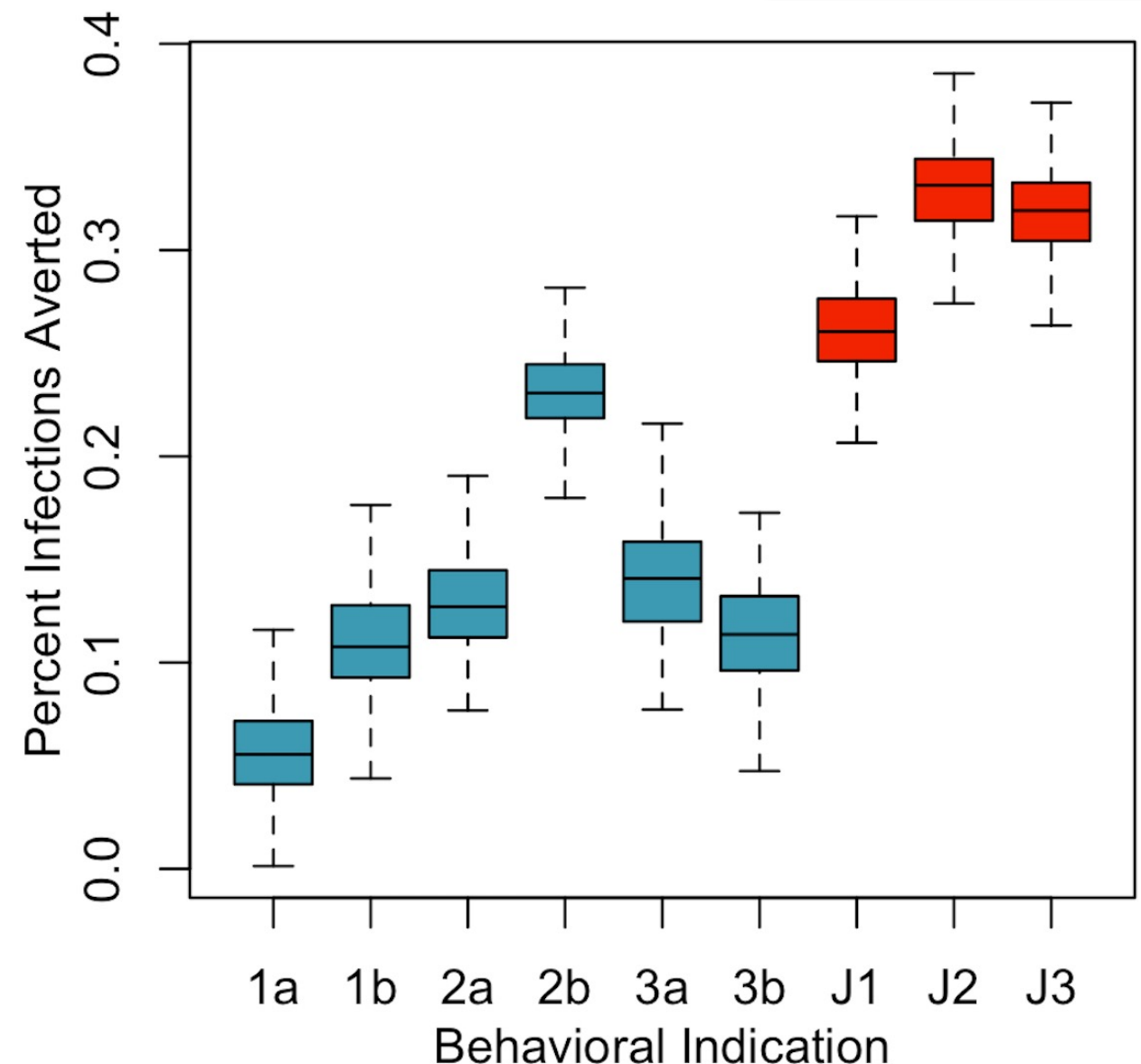
Jenness SM, Le Guillou A, Chandra C, Mann L, Sanchez T, Westreich D, Marcus JL. Projected HIV and Bacterial STI Incidence Following COVID-Related Sexual Distancing and Clinical Service Interruption. *Journal of Infectious Diseases*. 2021; 223(6): 1019–28.

# 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.

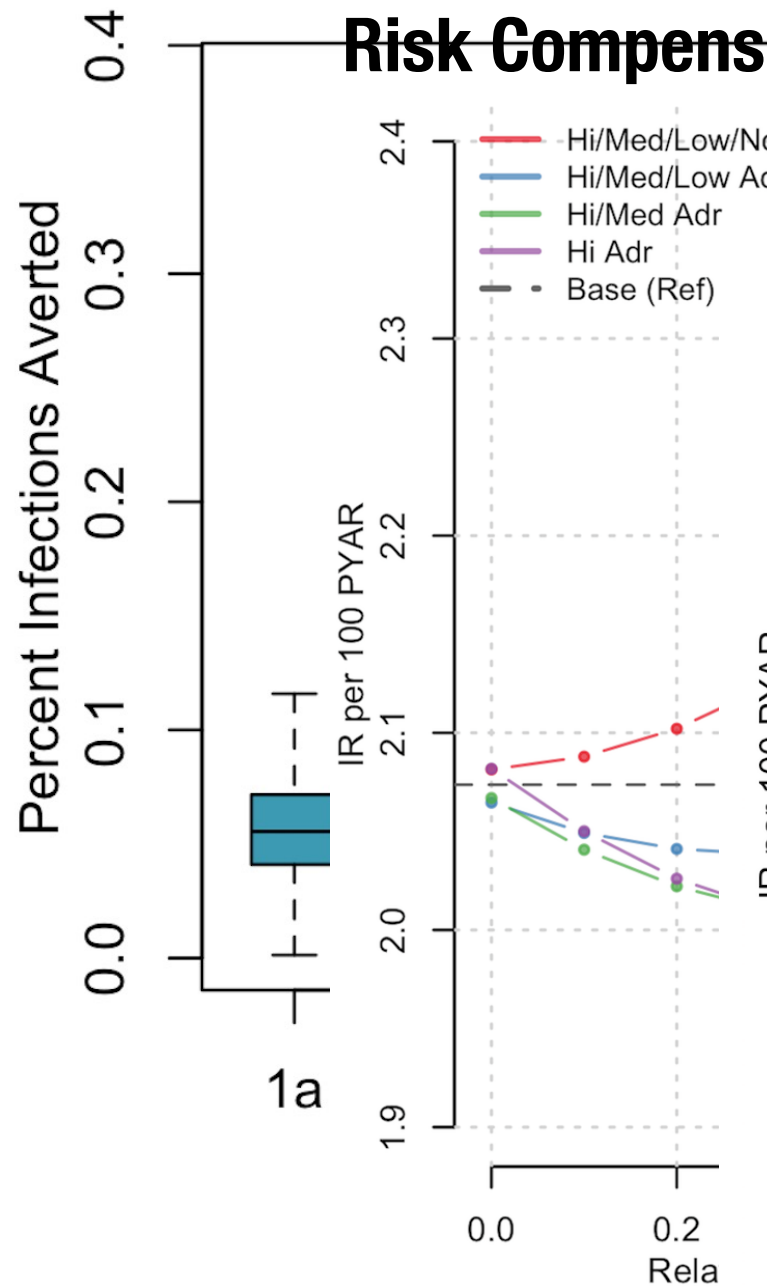




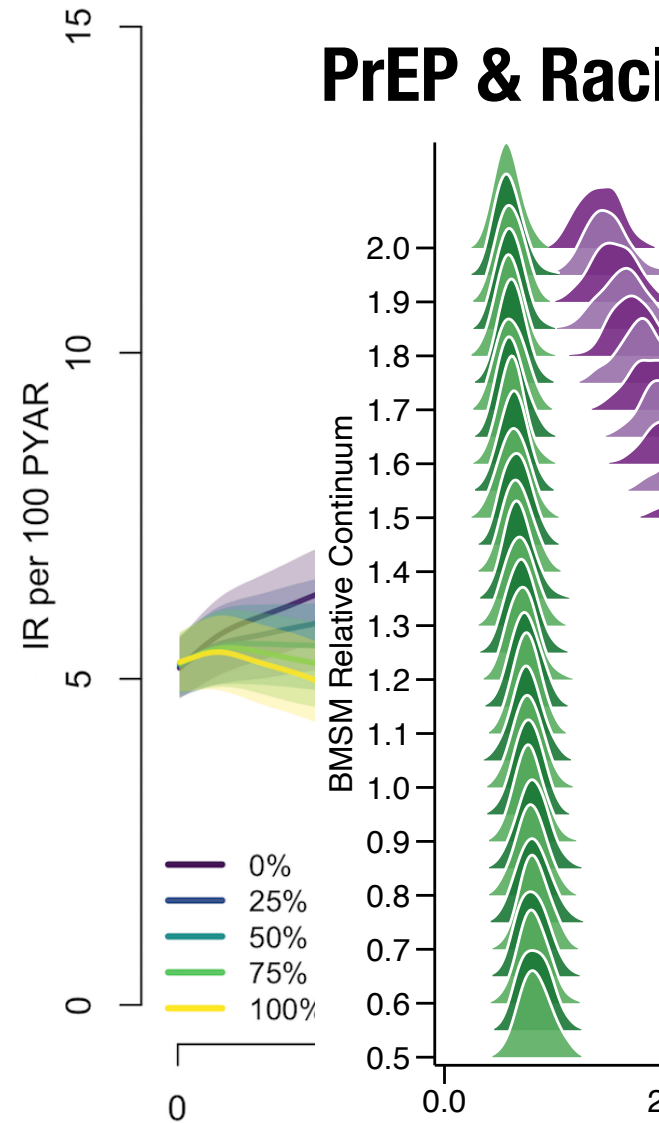
# Our Models for HIV Preexposure Prophylaxis

## Evaluating CDC Guidelines

### Risk Compensation & Adherence

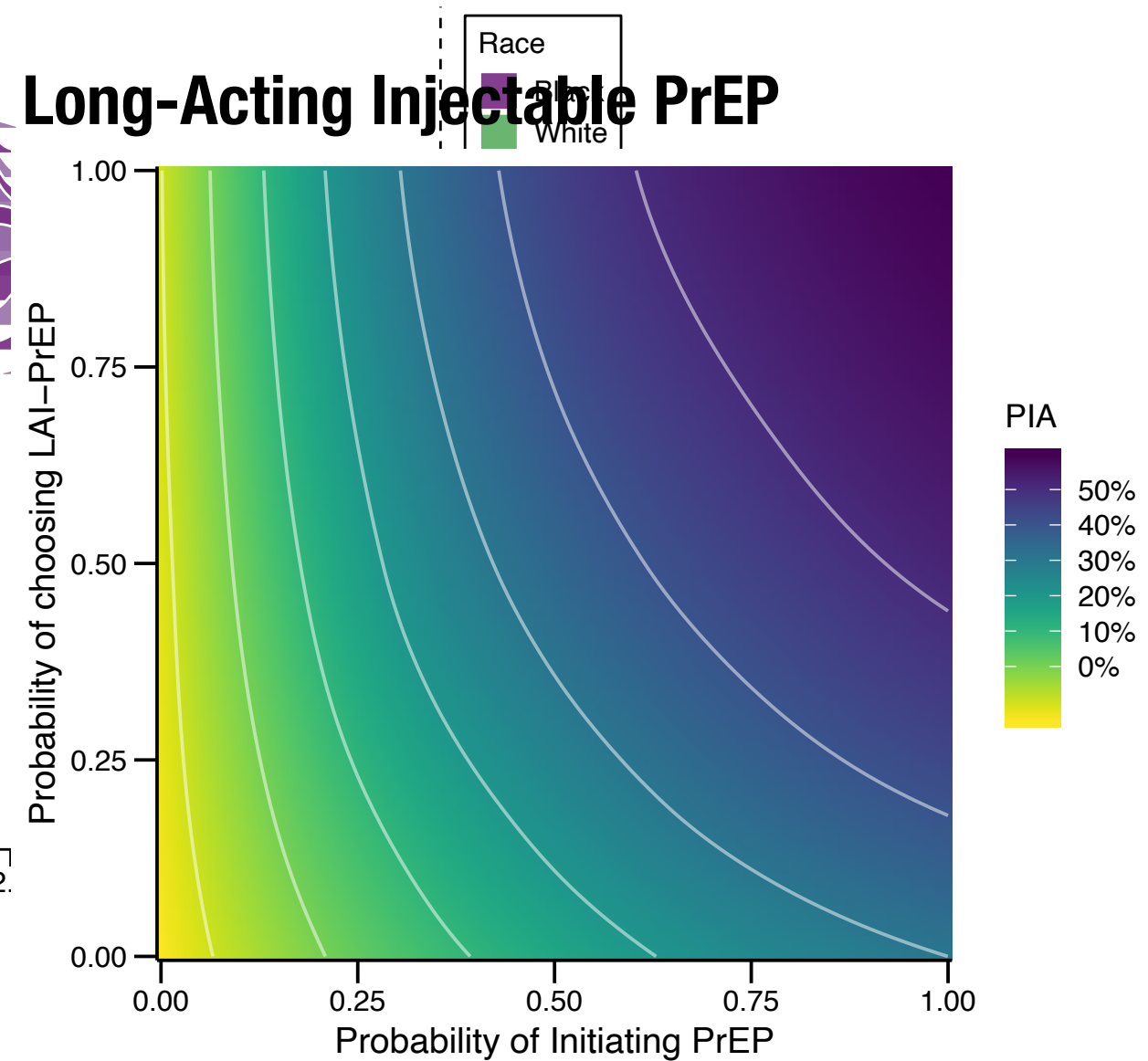


### Impact on Bacterial STIs



### PrEP & Racial Disparities

### Long-Acting Injectable PrEP



# Our Network Needs for HIV 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 HIV transmission models on top

# HIV Model Example

- Jenness SM, Johnson JA, Hoover KW, Smith DK, Delaney K. Modeling an Integrated HIV Prevention and Care Continuum to Achieve the Ending the HIV Epidemic Goals. *AIDS*. 2020; 34(14): 2103–2113.
  - PDF of paper: <http://samueljenness.org/pdf/Jenness-2020-AIDS.pdf>
  - EpiModelHIV Code: <https://github.com/statnet/EpiModelHIV>
  - Model scripts for paper: <https://github.com/epimodel/combprev>



# An Integrated Prevention & Care Continuum

Applying a PrEP Continuum of Care for Men Who Have Sex With Men in Atlanta, Georgia

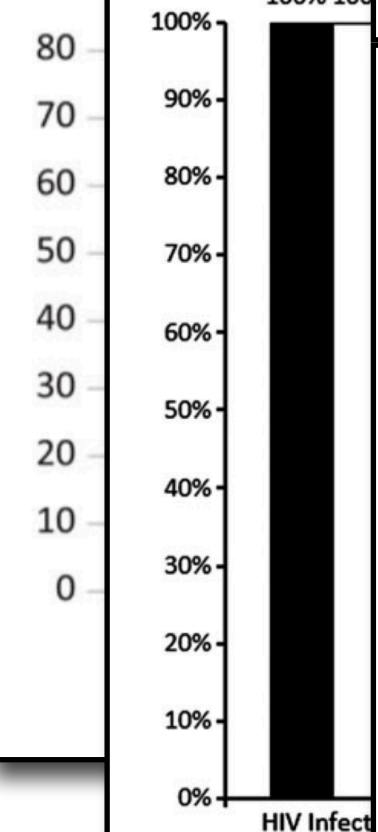
The State of Engagement in HIV Care in the

United States to Control

A

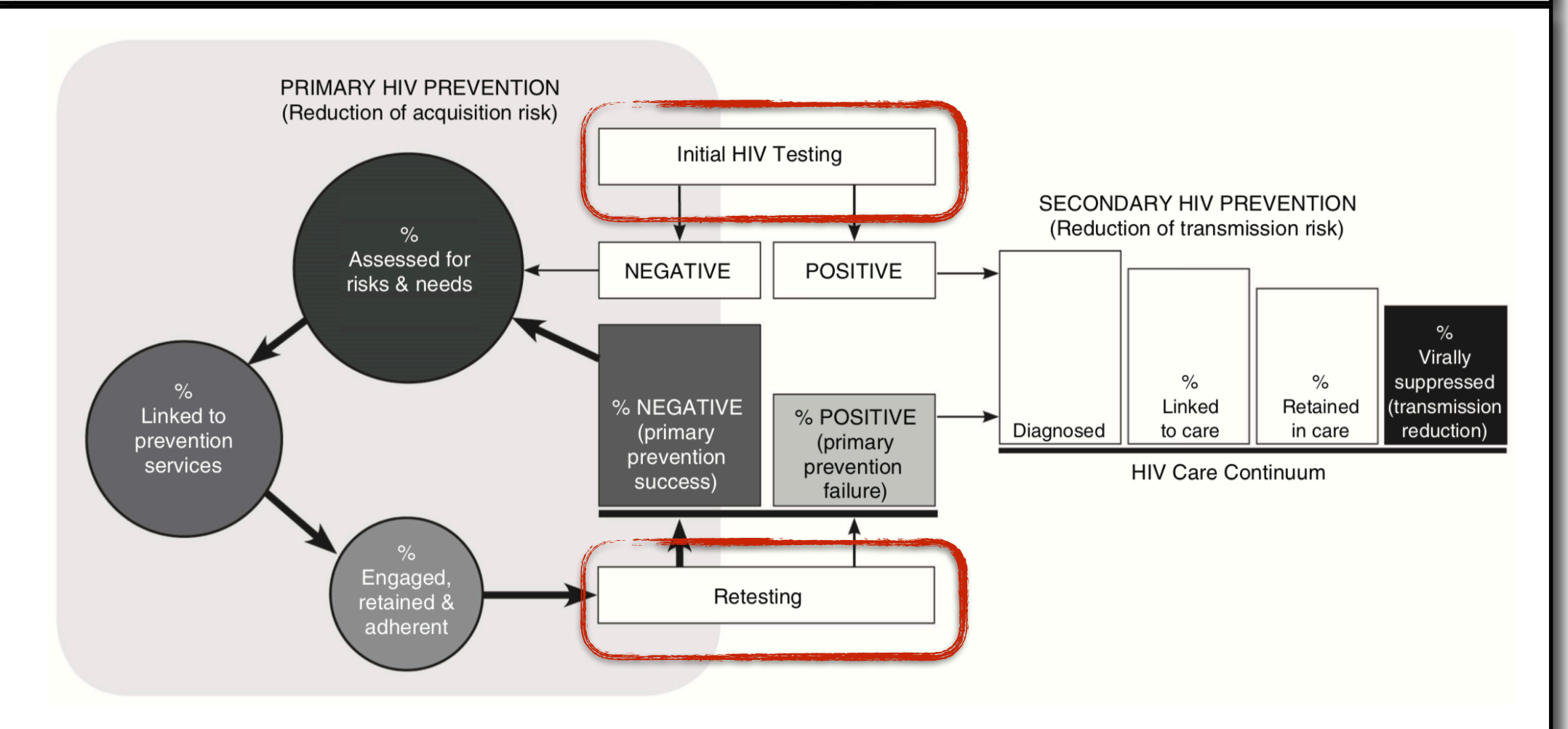
Michael J. Mugavero

100% 100%



## Towards an integrated primary and secondary HIV prevention continuum for the United States: a cyclical process model

Tim Horn<sup>S,1</sup>, Jennifer Sherwood<sup>\*,2</sup>, Robert H Remien<sup>3</sup>, Denis Nash<sup>4</sup> and Judith D. Auerbach<sup>\*,5</sup>, for the Treatment Action Group and Foundation for Aids Research HIV Prevention Continuum Working Group



# Ending the Epidemic Plan

- Ending the HIV Epidemic plan introduced in Feb 2019
  - ▶ 75% incidence reduction by 2025
  - ▶ 90% reduction by 2030
  - ▶ Resources directed at high-burden counties and states
- Will it be enough for HIV?
  - ▶ Lowest levels of HIV viral suppression in the Southern states where Medicaid not expanded through ACA

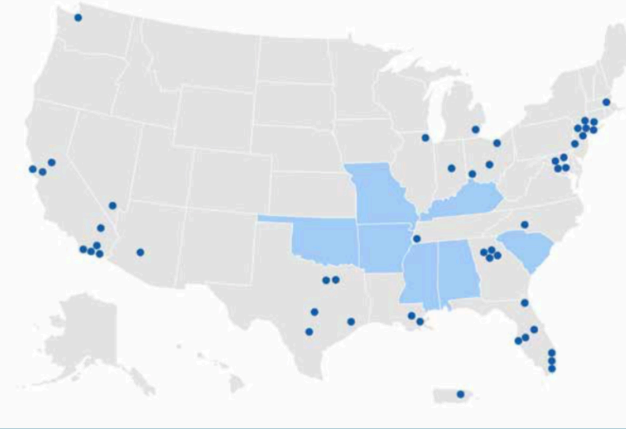
## Ending the HIV Epidemic: A Plan for America

HHS is proposing a once-in-a-generation opportunity to eliminate new HIV infections in our nation. The multi-year program will infuse 48 counties, Washington, D.C., San Juan, Puerto Rico, as well as 7 states that have a substantial rural HIV burden with the additional expertise, technology, and resources needed to end the HIV epidemic in the United States. Our four strategies – diagnose, treat, protect, and respond – will be implemented across the entire U.S. within 10 years.

**GOAL:** Our goal is ambitious and ambitious goals require us to employ strategic practices in the *places* focused on the right *people* to:



The Initiative will target our resources to the 48 highest burden counties, Washington, D.C., San Juan, Puerto Rico, and 7 states with a substantial rural HIV burden.



### Geographical Selection:

Data on burden of HIV in the US shows areas where HIV transmission occurs more frequently. More than 50% of new HIV diagnoses\* occurred in only 48 counties, Washington, D.C., and San Juan, Puerto Rico. In addition, 7 states have a substantial rural burden – with over 75 cases and 10% or more of their diagnoses in rural areas.

\*2016-2017 data

Ending  
the  
HIV  
Epidemic

[www.HIV.gov](http://www.HIV.gov)

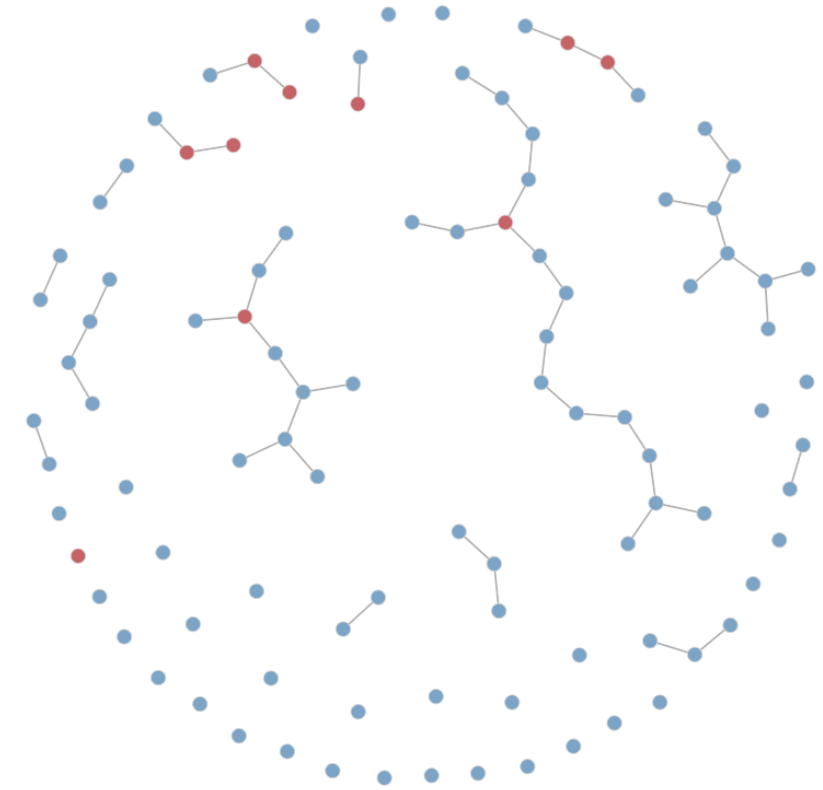
- **Using modeling to understand an integrated HIV prevention and care continuum to achieve EHE goals**
- *Primary Study Question*
  - What combinations of improvements to HIV screening (alone or as a gateway to PrEP initiation), HIV care linkage, and HIV care retention could meet the 2030 EHE goal of a 90% reduction in HIV incidence?

# Methods Overview

- Stochastic network model for HIV transmission dynamics
- Target study population:
  - Men who have sex with men (MSM) in Atlanta metropolitan area
  - Aged 15 to 65, stratified by Black, Hispanic, White/Other race/ethnicity
- Model calibrated to recent estimates of HIV care continuum steps and PrEP utilization in population
- Intervention scenarios for improvements to:
  - HIV screening
    - With and without PrEP initiation linked to HIV screening events
  - HIV care linkage
  - HIV retention in care

# Network Modeling Methods

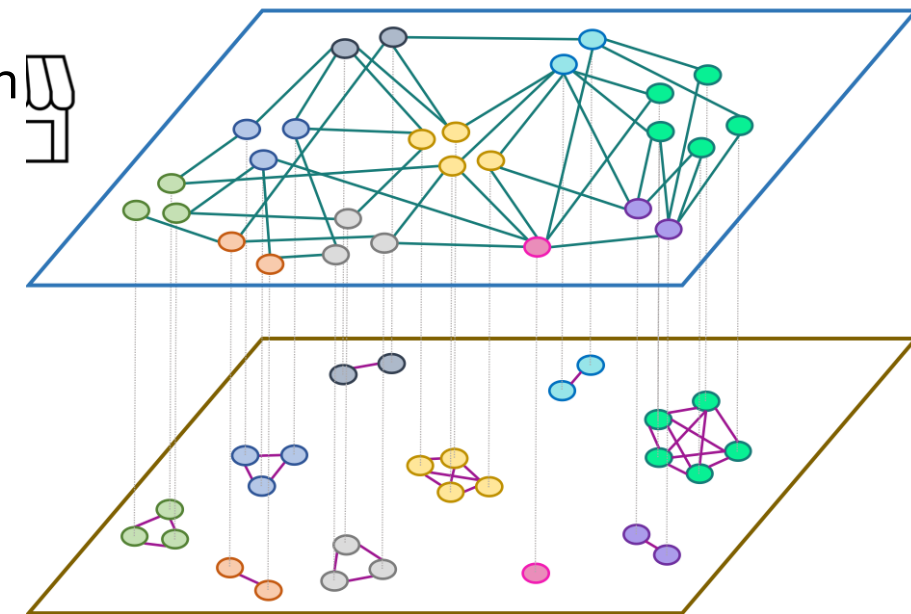
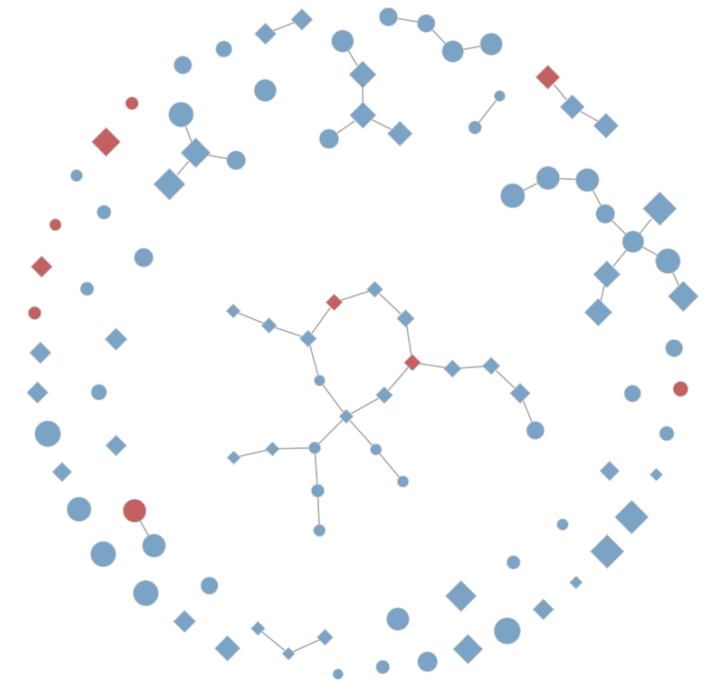
- Temporal exponential random graph models (TERGMs) define partnership formation and dissolution
  - Sexual network types: main, casual, one-off
  - Men form partnerships according to model terms based on numbers of each partner type, differential activity and mixing on race and age, sexual role segregation
- HIV epidemiology
  - Natural history (disease stages, continuous VL, HIV-related mortality)
  - ART initiation and adherence
  - HIV transmission dynamics within serodiscordant partnerships
- Demographic processes





# Multi-Layer Networks for MSM Sexual Partnerships

- Three partnership networks: main, casual, one-time
  - Same node set, different edge set
- Distinguished in both their formation and dissolution model components
  - Formation formula for main network differs from other two
  - Dissolution model varies (substantially) by average duration of partnerships
- Formation model for partnerships
  - Heterogeneity and assortative mixing by demographics, degree in other networks, sexual positioning; non-parametric degree distribution terms
- Dissolution model for partnerships
  - Mean duration of partnerships by type and age-group-specific durations (young-young partnerships shorter than old-old partnerships)



# Empirical Data $\rightsquigarrow$ Network Model Parameters

- Recently completed **ARTnet Study** of MSM in the US (R21 MH112449)
  - 4904 MSM reporting on 16198 sexual partnerships
- **Primary innovation:** data-driven statistical models embedded within ID transmission models where primary data available
  - TERGMs for network structure  $\rightsquigarrow$  simulate
  - Poisson models for coital frequency  $\rightsquigarrow$  predict
  - Logit models for condom use  $\rightsquigarrow$  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, ...

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

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**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 heterogeneous 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-

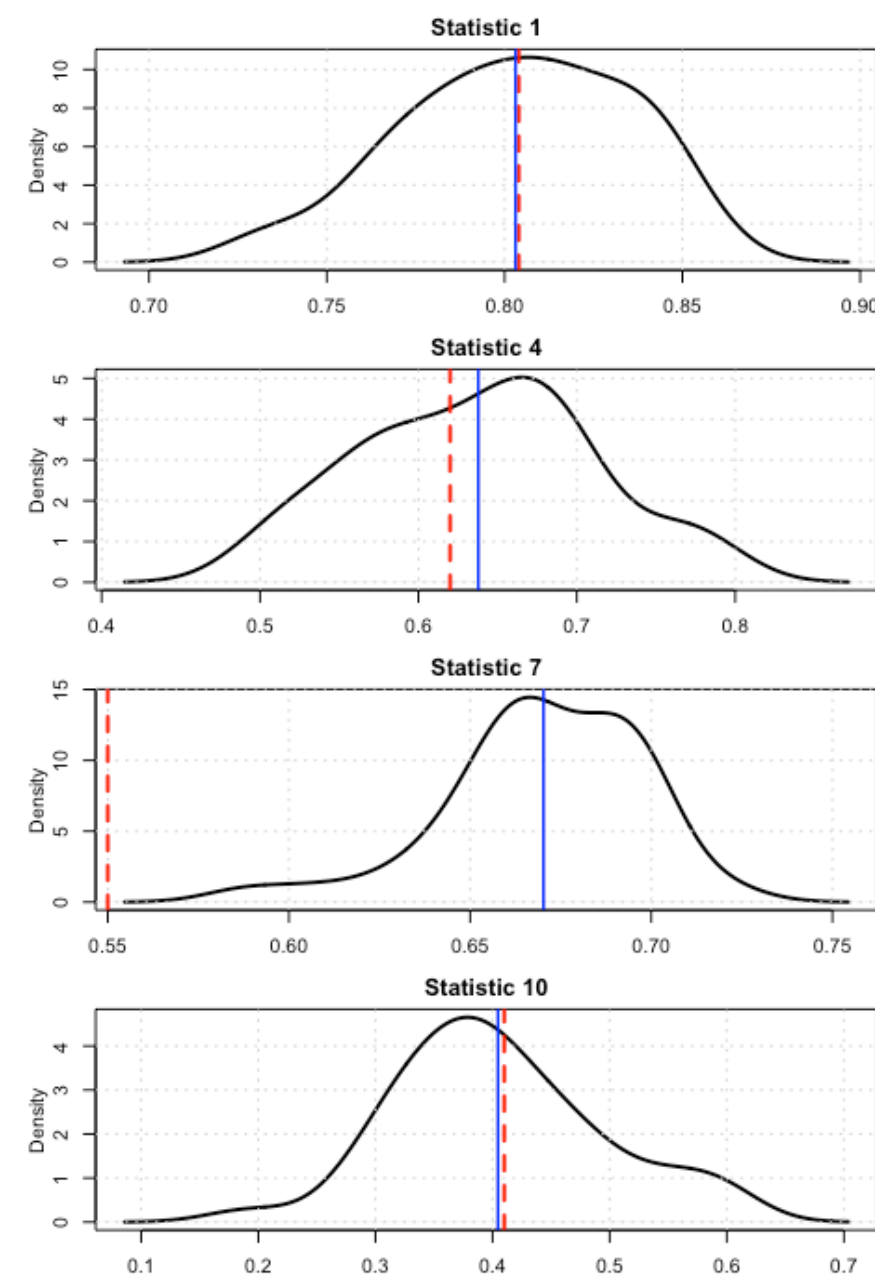
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1755-4365/ © 2020 The Authors. Published by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

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

# Model Calibration for Reference Scenario

- Prevalence of diagnosed HIV Infection among MSM
  - Rosenberg, Ann Epidemiol, 2018
  - B/H/W targets: 33.3%, 12.7%, 8.4%
- Proportion of HIV+ MSM who are diagnosed
  - Singh, Ann Intern Med, 2018
  - B/H/W targets: 80.4%, 79.9%, 88.0%
- Proportion of diagnosed MSM linked to care within 1m
  - GA DPH surveillance
  - B/H/W targets: 62%, 65%, 76%
- Proportion of diagnosed MSM with HIV VL suppression
  - GA DPH surveillance
  - B/H/W targets: 55%, 60%, 72%
- Proportion of Indicated MSM Using PrEP
  - Triangulation of ARTnet and other local estimates
  - Estimates for MSM in the Atlanta area: 15%

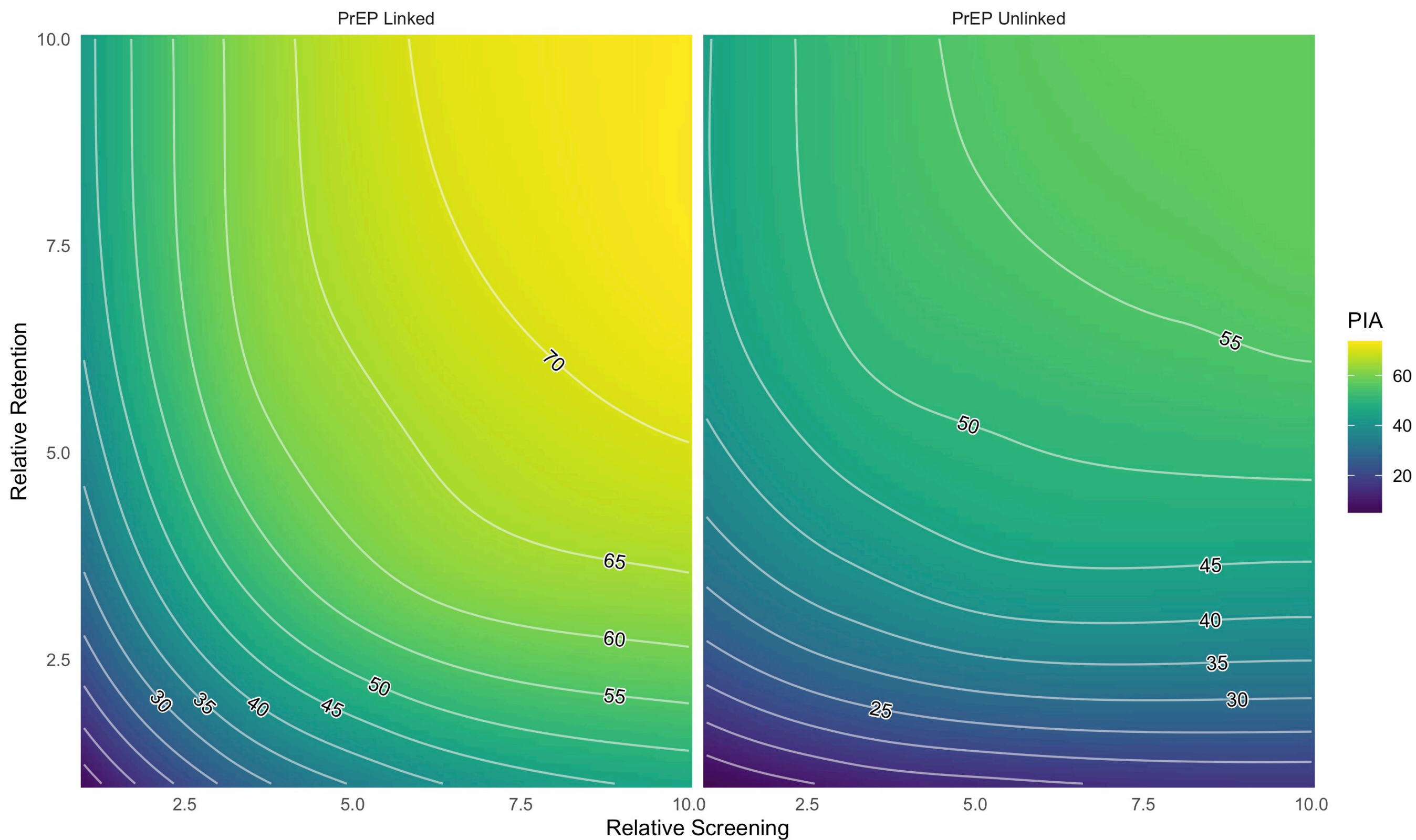


# Bayesian Approaches to Model Calibration

- When the model form becomes complicated (e.g, collinearity), or there are many parameters to estimate, Bayesian approaches are favorable
- General setup:
  - Define prior distributions for uncertain input parameters
  - Draw samples from those distributions
  - Simulate the model with that parameter sample
  - Compare outcome statistics (prevalence/incidence) to external target data points
  - Some method for iteratively selecting which parameters to keep
- Approximate Bayesian Computation
  - Toni et al: <https://royalsocietypublishing.org/doi/10.1098/rsif.2008.0172>

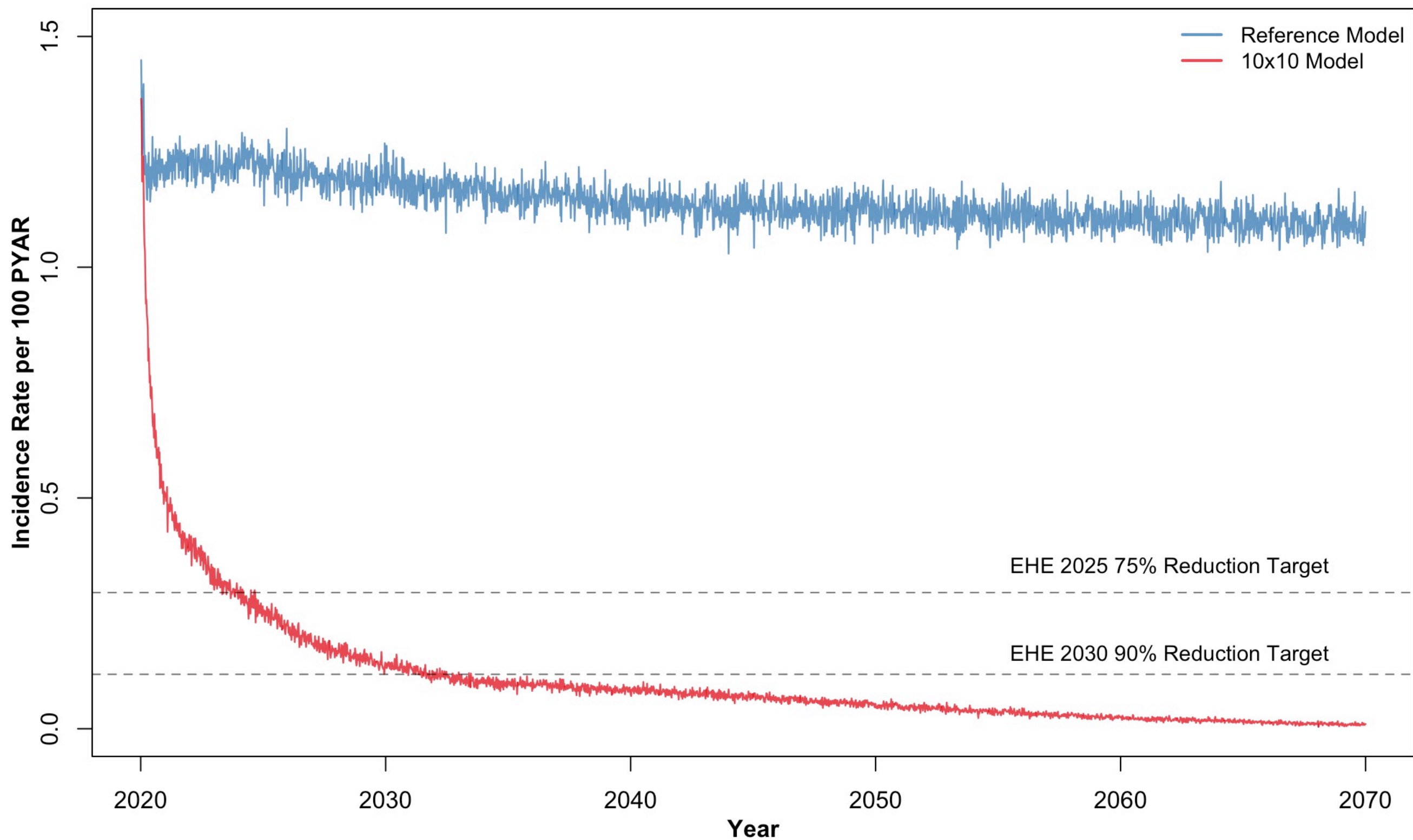


# Infections Averted Under Different Prevention Scenarios





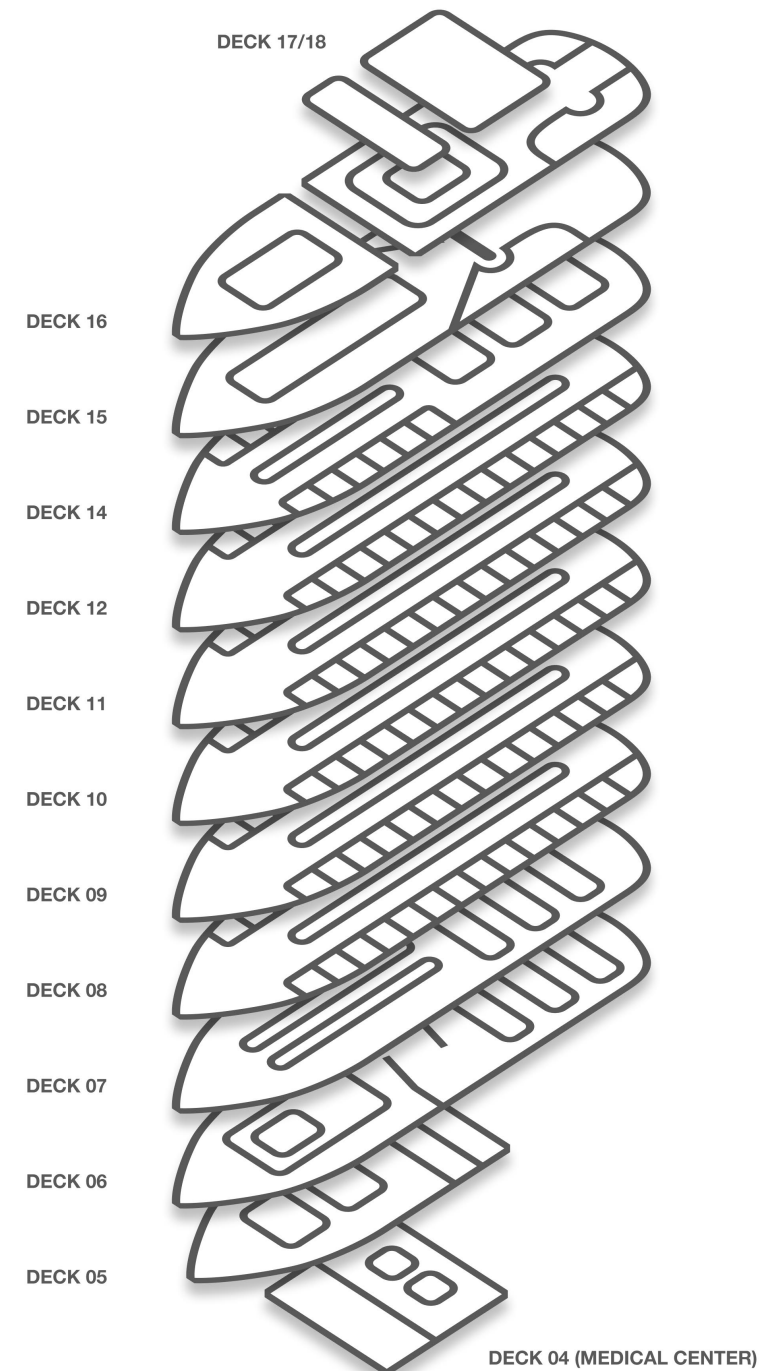
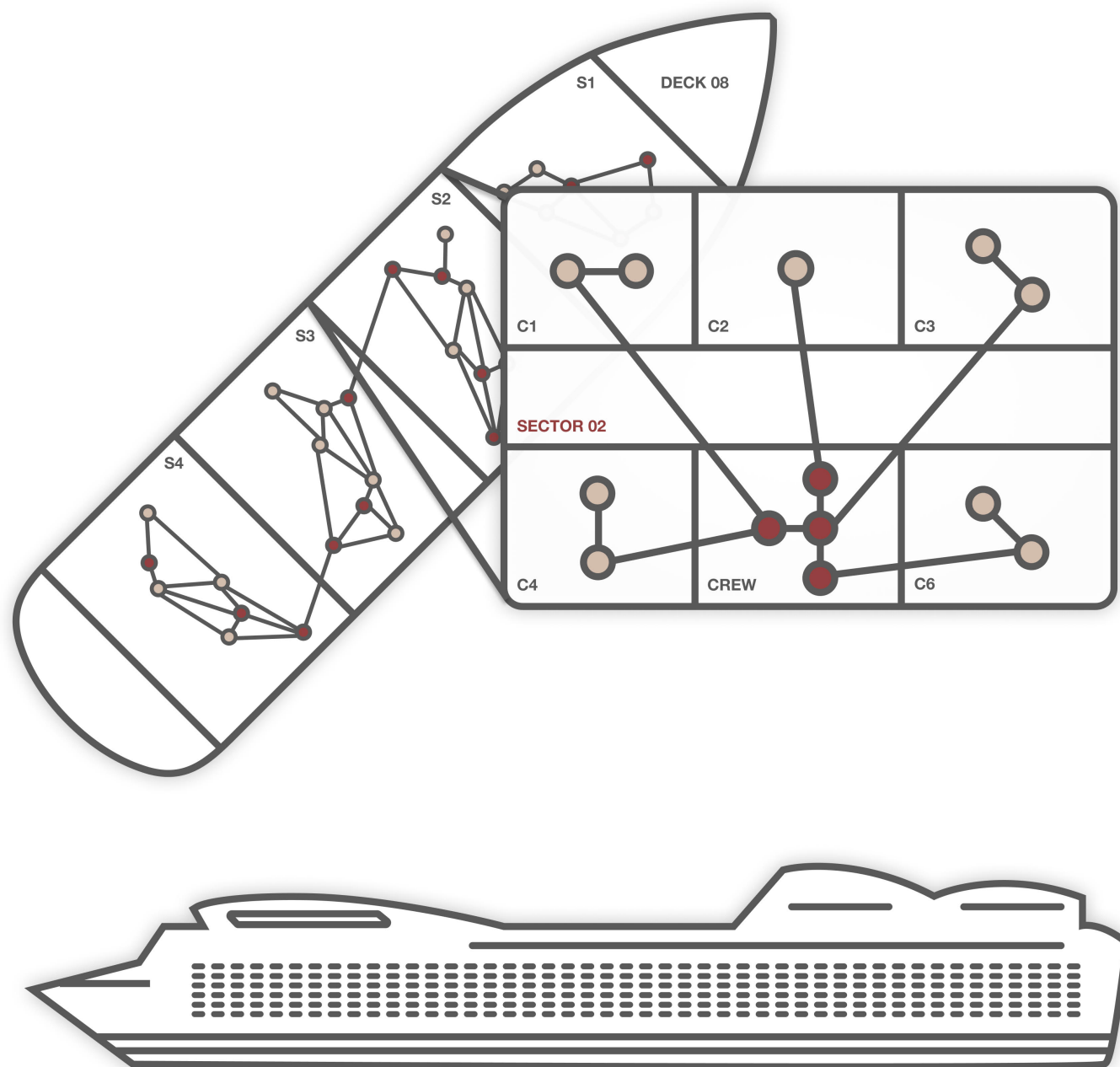
# How Long Will it Take to Achieve the EHE Goals?



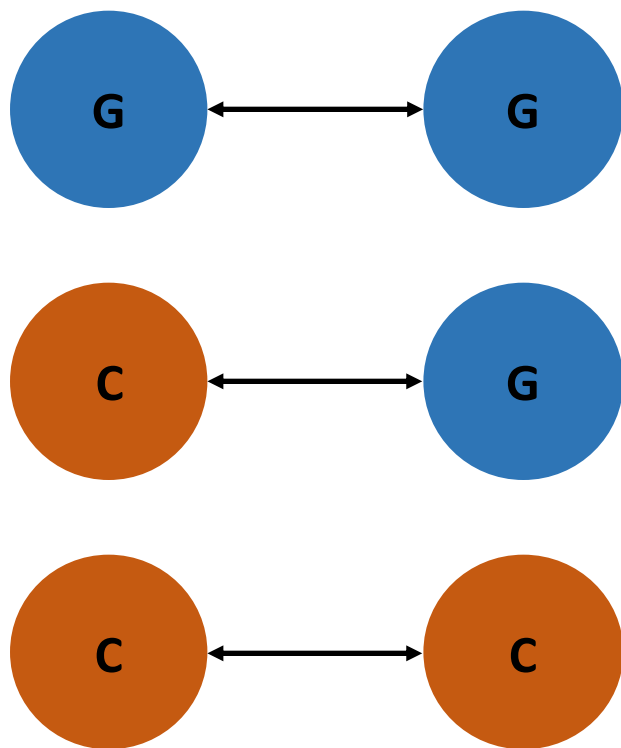
# COVID Model Example

- Jenness SM, Willebrand KS, Malik AA, Lopman BA, Omer SB. Modeling Dynamic Network Strategies for SARS-CoV-2 Control on a Cruise Ship.
  - Paper: [https://epimodel.github.io/sismid/0\\_nme\\_prep/pdf/Jenness-Epidemics-COVIDCruise.pdf](https://epimodel.github.io/sismid/0_nme_prep/pdf/Jenness-Epidemics-COVIDCruise.pdf)
  - EpiModelCOVID Code: <https://github.com/epimodel/epimodelcovid>
  - Model scripts for paper: <https://github.com/EpiModel/COVID-CruiseShip>

# Cruise Ship Network Model Schematic



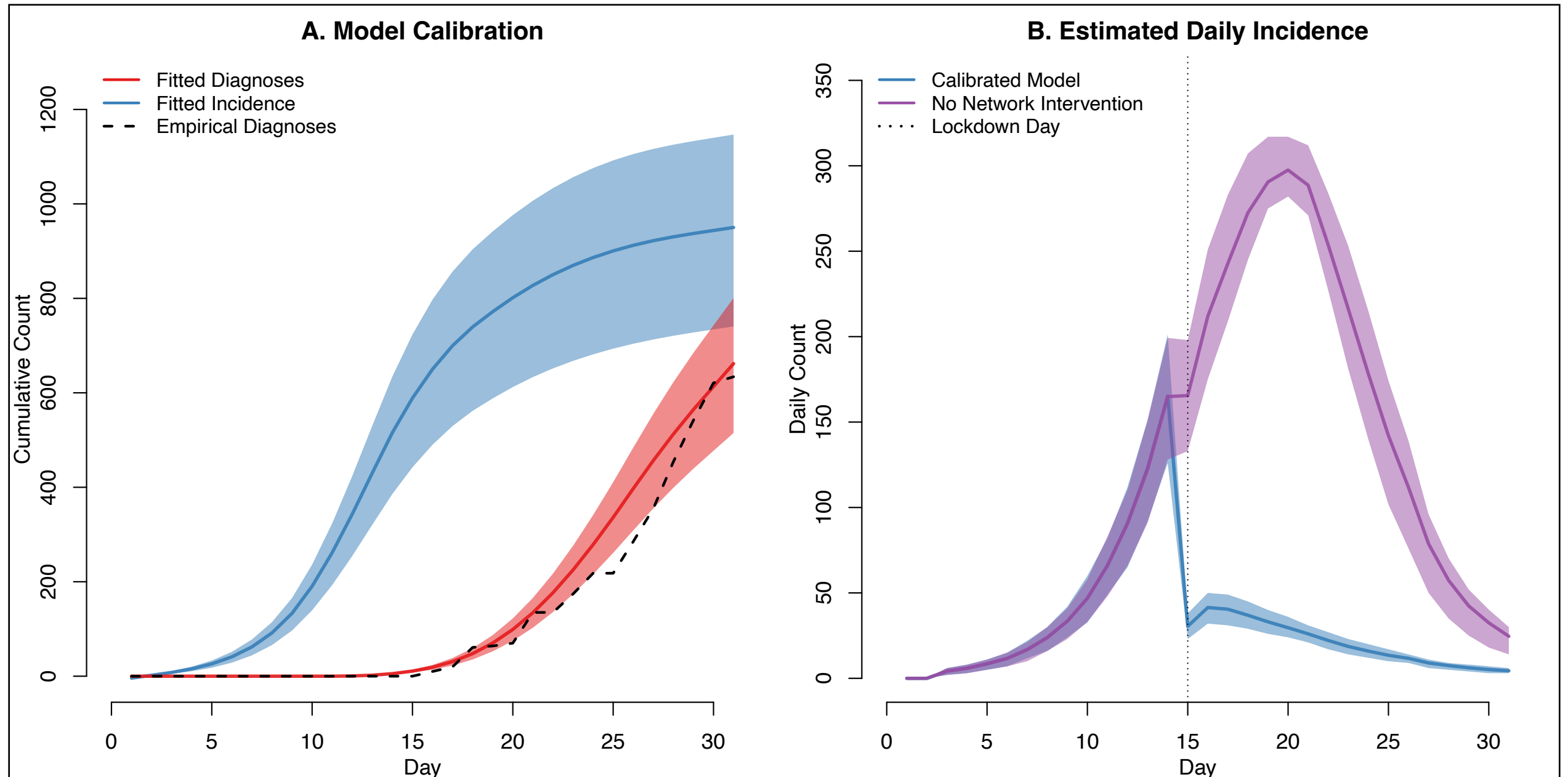
# Multi-Layer Dynamic Contact Networks



- Three overlapping ERGMs to represent guest/guest, crew/guest, and crew/crew contacts
- Multi-level structure: guests within cabins, cabins within ship sectors, crew assigned to cabins within sectors
  - x2 ERGMs, for pre-lockdown and post-lockdown network structures
- ERGMs with ship structure allow for repeated contacts with deterministic dissolution
- Scenarios focused on timing of lockdown, design of sectorization, and degree and within-cabin and within-sector mixing constraints given lockdown
  - Control-based strategies: after outbreak has started
  - Prevention-based strategies: informing future ship design

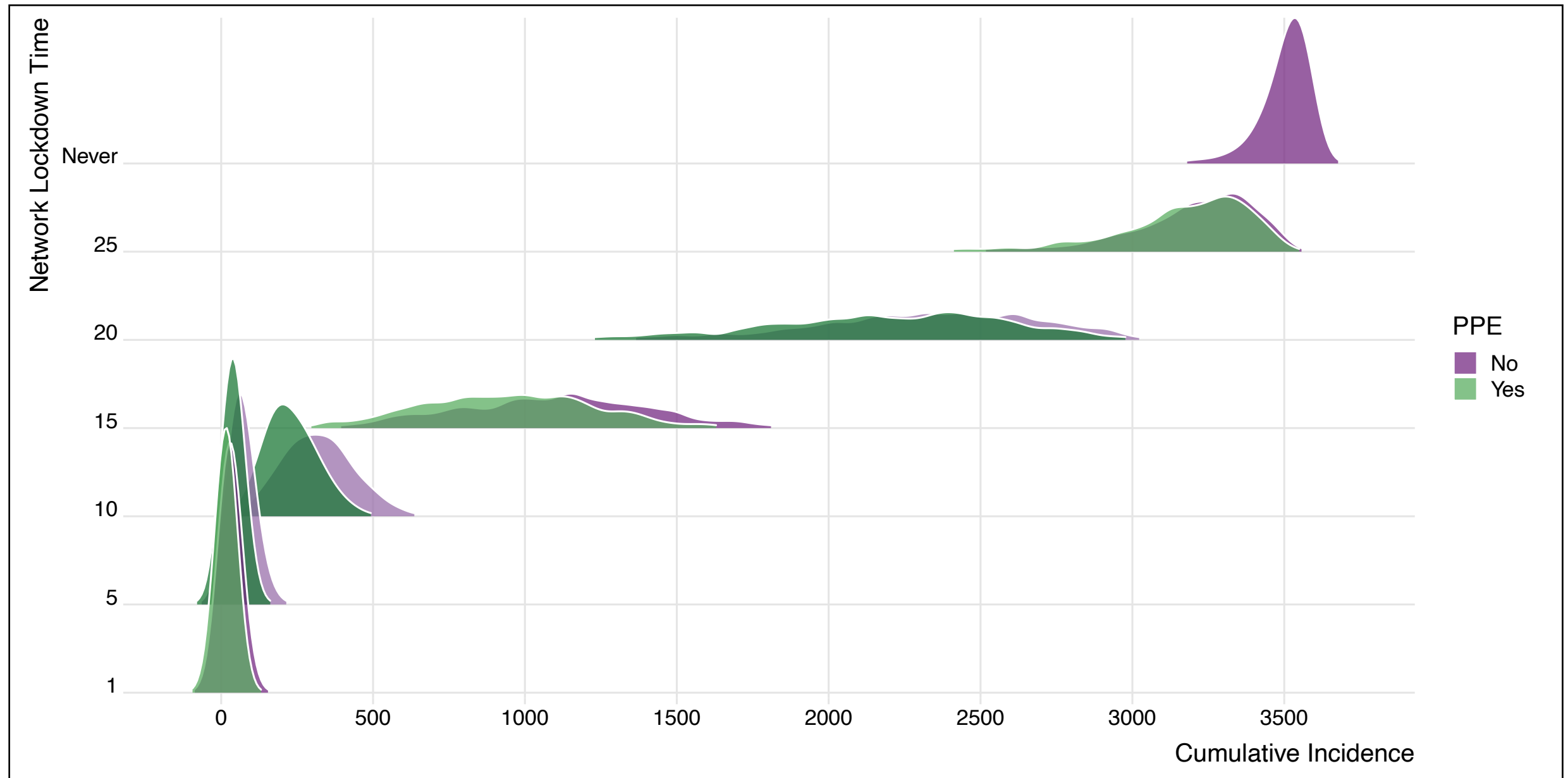


# Model Results 1: Calibration



- Fit the model transmission parameters to daily screening rates and diagnoses on ship
  - True incidence > diagnosed incidence
- Empirical lockdown occurred Day 15 of the cruise

# Model Results 2: Timing of Network Lockdown



- Distribution of cumulative incidence across 1000 simulations in each scenario
- Earlier (counterfactual) lockdown associated with major reduction in cumulative incidence compared to empirical (actual) lockdown on Day
  - Little impact of PPE in these settings: high-intensity contact and directionality of transmission...

# Model Results 3: Directionality of Transmission

**Table 2.** Directionality of Transmission and Contact Intensity Reductions, with Day 15 Network Lockdown and PPE, on COVID Incidence at 1 Month

Scenario	Total	Passenger to Passenger	Passenger to Crew	Crew to Passenger	Crew to Crew
	Cuml. Incid.	Cuml. Incid.	Cuml. Incid.	Cuml. Incid.	Cuml. Incid.
	Median (95% SI)	Median (95% SI)	Median (95% SI)	Median (95% SI)	Median (95% SI)
<b>With Contact Intensity Reductions, Network Lockdown, and PPE at Day 15</b>					
<i>Base Scenario</i>					
No Intensity Reduction	933.5 (366.0, 1556.2)	551.0 (213.9, 941.0)	163.0 (66.0, 265.0)	124.0 (46.0, 211.0)	93.0 (33.0, 175.0)
<i>Varying Passenger-Passenger Contact Intensity</i>					
50% Reduction	862.5 (353.9, 1454.0)	488.0 (203.9, 843.0)	155.0 (67.0, 257.0)	124.5 (47.0, 216.0)	93.5 (29.0, 174.0)
90% Reduction	765.5 (316.9, 1348.0)	401.0 (164.9, 727.0)	145.5 (63.0, 248.0)	122.0 (44.0, 214.0)	90.0 (31.0, 173.0)
100% Reduction	749.0 (297.9, 1255.1)	381.0 (155.9, 677.0)	147.5 (61.0, 241.0)	126.0 (44.0, 208.0)	93.0 (32.0, 168.0)
<i>Varying Passenger-Crew Contact Intensity</i>					
50% Reduction	849.0 (352.9, 1379.1)	545.0 (230.0, 868.0)	125.5 (54.0, 203.0)	87.0 (31.0, 158.1)	90.0 (31.0, 168.0)
90% Reduction	787.0 (332.9, 1346.1)	535.5 (227.0, 899.0)	96.0 (41.0, 173.0)	62.0 (17.0, 130.0)	87.0 (30.0, 170.0)
100% Reduction	744.0 (325.0, 1274.1)	519.5 (225.9, 865.0)	86.0 (37.0, 152.0)	55.0 (17.0, 117.0)	84.0 (29.0, 167.0)
<i>Varying Crew-Crew Contact Intensity</i>					
50% Reduction	897.0 (379.9, 1471.2)	542.0 (220.8, 904.0)	161.0 (70.0, 254.0)	120.0 (48.0, 203.1)	74.0 (23.0, 142.0)
90% Reduction	899.0 (404.0, 1529.2)	558.0 (255.0, 943.2)	165.0 (78.0, 274.0)	118.0 (47.0, 206.0)	61.0 (17.0, 132.0)
100% Reduction	895.5 (362.9, 1459.1)	558.0 (218.0, 909.1)	162.0 (68.0, 263.0)	115.0 (44.0, 200.0)	55.0 (15.0, 119.0)

- In base model, most transmissions were passenger to passenger
  - No/limited PPE was used within cabins
- Reducing the contact intensity could avert hundreds of infections

# Model Results 4: Prevention with Mass Screening

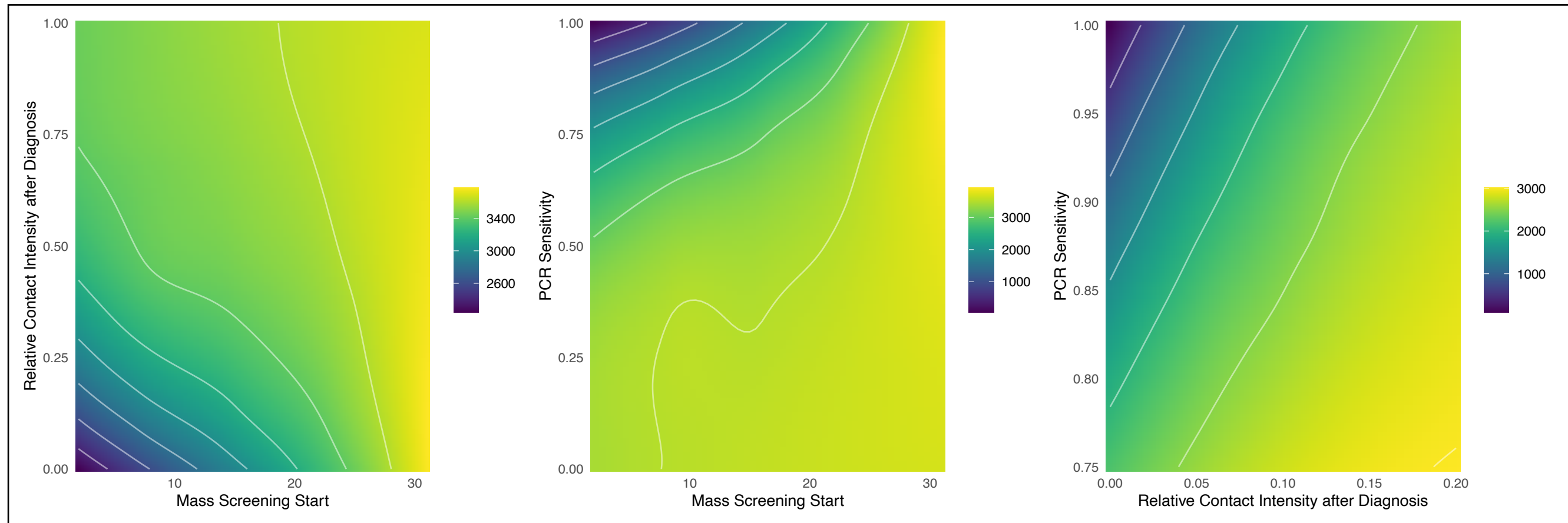
**Table 4.** Impact of Timing of Mass Asymptomatic Screening and Diagnosis-Based Case Isolation, with No Network Lockdown and Stratified by PPE Use, on COVID Incidence and Mortality at 1 Month

Scenario	Cumulative Incidence			Cumulative Mortality		
	Total	NIA <sup>1</sup>	PIA <sup>2</sup>	Total	NDA <sup>3</sup>	PDA <sup>4</sup>
	Median (95% SI)	Median (95% SI)	Median (95% SI)	Median (95% SI)	Median (95% SI)	Median (95% SI)
<i>Varying Timing of Mass Screening (Never PPE)</i>						
Day 1	2286.0 (0.0, 3421.0)	1403.5 (1396.0, 1409.0)	38.0 (37.9, 38.1)	7.0 (0.0, 24.0)	29.0 (28.0, 29.0)	81.2 (80.6, 81.8)
Day 5	2621.5 (16.0, 3353.1)	1070.5 (1067.0, 1074.0)	29.0 (28.9, 29.1)	9.0 (0.0, 23.0)	27.0 (27.0, 27.0)	75.6 (75.0, 76.0)
Day 10	2917.0 (1787.8, 3310.1)	775.0 (772.5, 777.5)	21.0 (20.9, 21.1)	13.0 (4.0, 25.0)	23.0 (22.0, 23.0)	63.6 (62.9, 64.1)
Day 15	2944.5 (2256.8, 3176.1)	746.0 (744.0, 748.0)	20.2 (20.2, 20.3)	18.0 (8.0, 32.0)	18.0 (17.0, 18.0)	50.0 (48.6, 50.0)
Day 20	3102.5 (2588.8, 3360.1)	590.0 (588.0, 591.5)	16.0 (15.9, 16.0)	30.0 (16.0, 45.0)	6.0 (6.0, 7.0)	17.1 (16.1, 18.4)
Day 25	3607.0 (3360.9, 3668.0)	85.0 (84.0, 86.0)	2.3 (2.3, 2.3)	36.0 (24.0, 50.0)	0.0 (-1.0, 0.0)	0.0 (-2.5, 0.0)
Never (Reference)	3692.0 (3679.0, 3699.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)	36.0 (25.0, 49.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)
<i>Varying Timing of Mass Screening (Always PPE)</i>						
Day 1	1629.5 (0.0, 3013.0)	2012.0 (1998.0, 2023.0)	55.3 (55.0, 55.4)	5.0 (0.0, 20.0)	27.0 (27.0, 28.0)	85.2 (84.5, 85.7)
Day 5	1856.5 (12.0, 2837.4)	1776.0 (1766.0, 1784.5)	48.8 (48.6, 49.0)	6.0 (0.0, 19.0)	26.0 (26.0, 27.0)	81.0 (80.5, 81.5)
Day 10	2240.5 (1058.0, 2815.1)	1395.0 (1387.0, 1402.0)	38.3 (38.2, 38.5)	10.0 (2.0, 20.0)	23.0 (23.0, 23.0)	70.6 (70.0, 71.1)
Day 15	2372.0 (1585.6, 2755.0)	1267.5 (1262.0, 1273.0)	34.8 (34.7, 34.9)	15.0 (5.0, 27.0)	18.0 (17.0, 18.0)	54.3 (53.5, 55.0)
Day 20	2656.0 (1980.9, 3033.0)	983.5 (977.5, 988.5)	27.0 (26.9, 27.2)	26.0 (12.0, 40.0)	7.0 (7.0, 8.0)	22.2 (20.9, 23.3)
Day 25	3354.0 (2831.8, 3537.1)	285.5 (282.0, 290.0)	7.8 (7.8, 7.9)	33.0 (20.0, 47.0)	0.0 (0.0, 1.0)	0.0 (0.0, 2.5)
Never (Reference)	3643.0 (3563.0, 3669.0)	0.0 (-1.0, 1.0)	0.0 (-0.0, 0.0)	33.0 (20.0, 45.0)	0.0 (0.0, 0.0)	0.0 (0.0, 0.0)

- In absence of behavioral change, screening and diagnosis-based case isolation could avert a substantial number of infections but not 100%
  - Here, PPE has an impact!
  - Why does Day 1 screening not prevent an outbreak?



# Model Results 5: Sensitivity Analysis for Screening Interventions



- Base model assumed 100% reduction in contacts after case isolation, 80% PCR test sensitivity, and a Day 1 screening strategy
- Only when PCR sensitivity reaches 100% is an outbreak averted in the absence of behavioral change