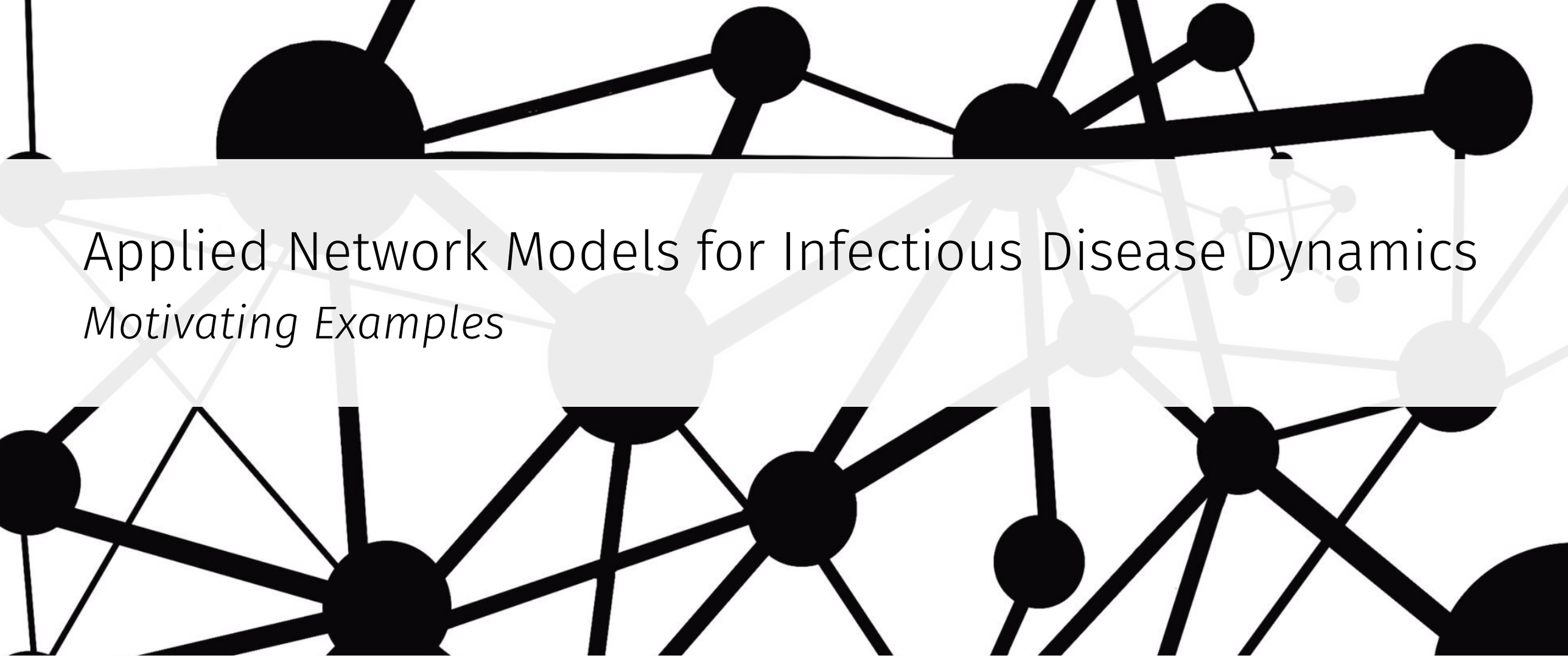
Applied Network Models for Infectious Disease Dynamics

Motivating Examples

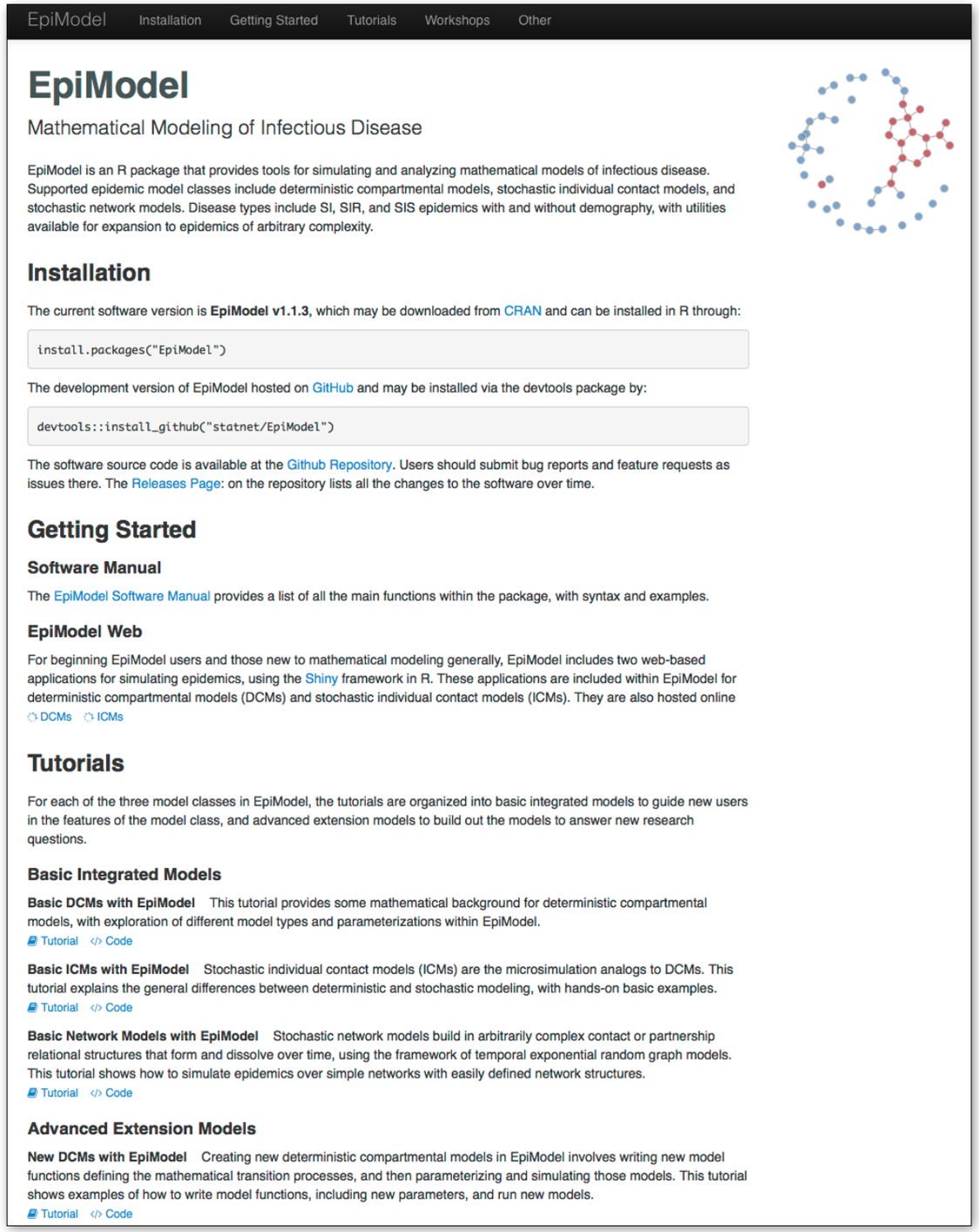


Network Modeling for Epidemics

Day 5

Models of Infectious Disease Agents Studies (MIDAS)

- NIH mechanism to understand and respond to infectious diseases
  - Started with focus on outbreaks and acute epidemics
  - Shifted towards addressing endemic diseases
- Our EpiModel 2.0 R01
  - Developing the next generation of methods and software tools for network-based modeling of infectious diseases
  - Primary focus on HIV/STI models, but methods useful broadly…



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

[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]

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]

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]

Research Applications of EpiModel Across Diseases

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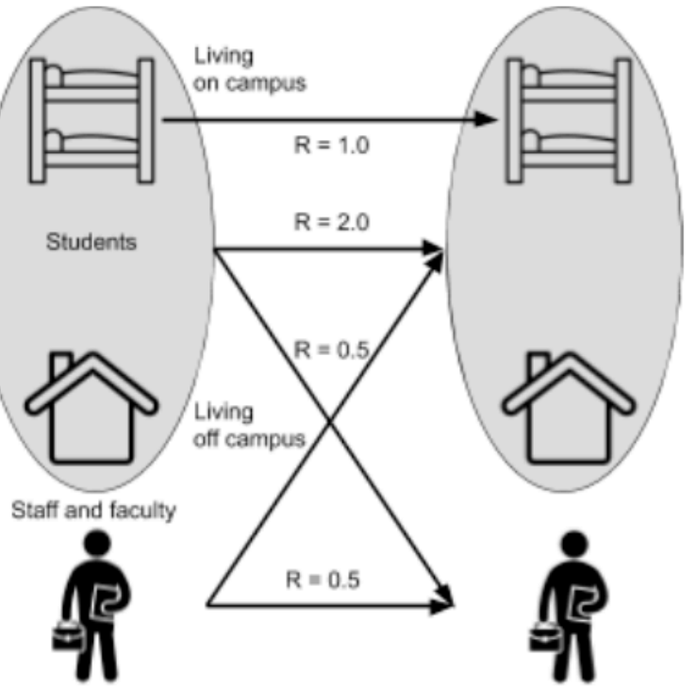
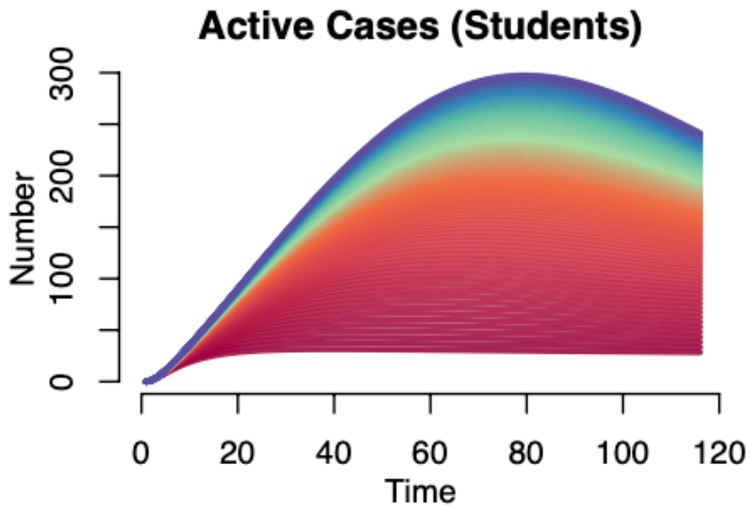
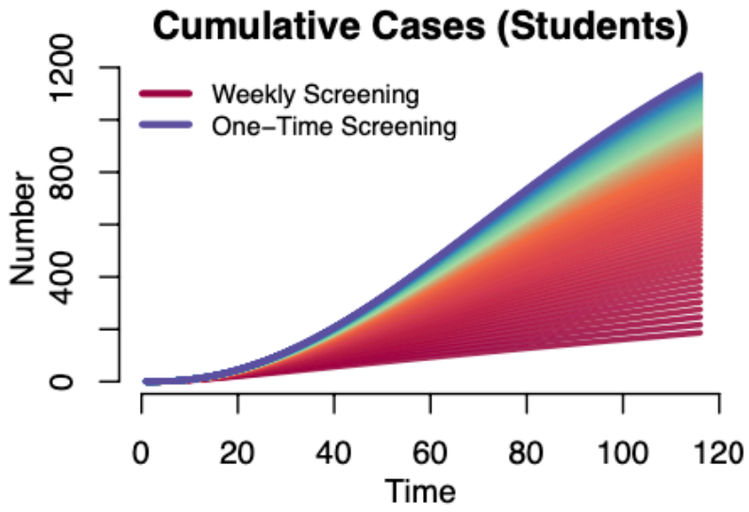
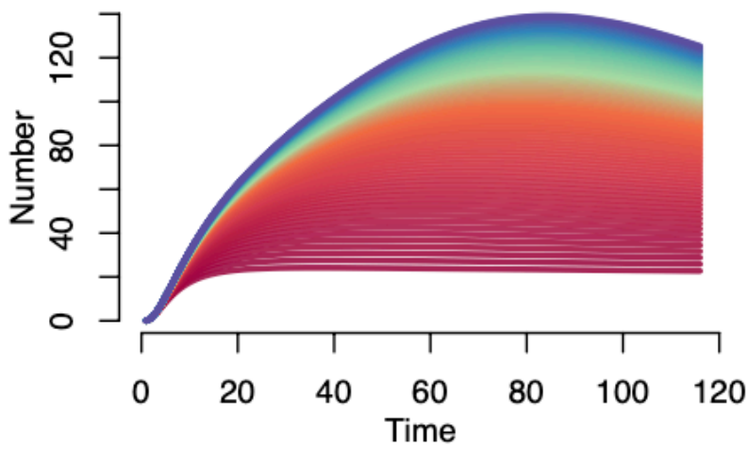
https://github.com/statnet/EpiModel/wiki

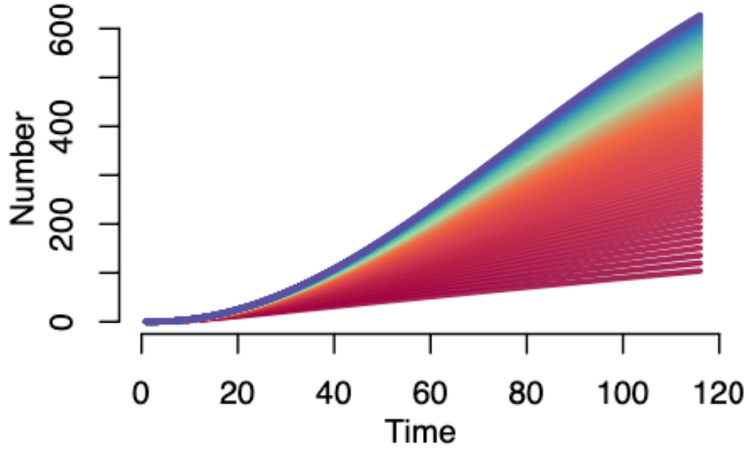
COVID University DCM with EpiModel











- 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

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?

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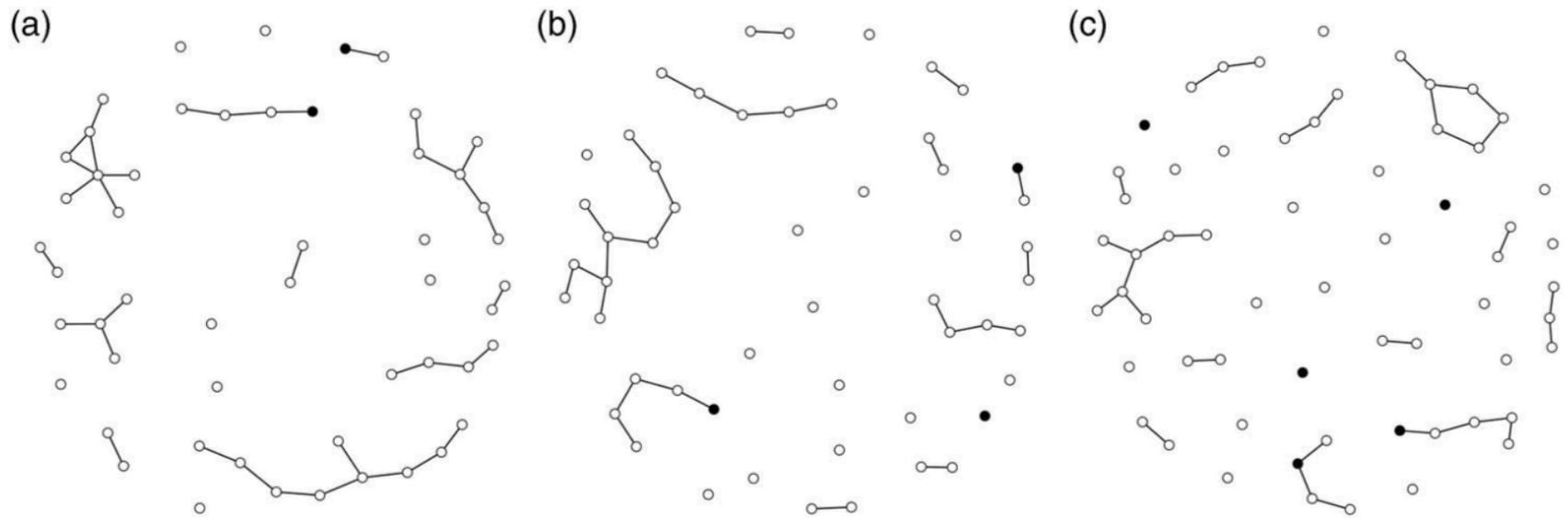

- Network model of MRSA infection within a NICU setting
- Networks defined as shared hospital worker contacts between infants

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

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Ecology

Subject Areas:
health and disease and epidemiology, ecology

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

Author for correspondence:
Stacie J. Robinson
e-mail: stacie.robinson@noaa.gov

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]

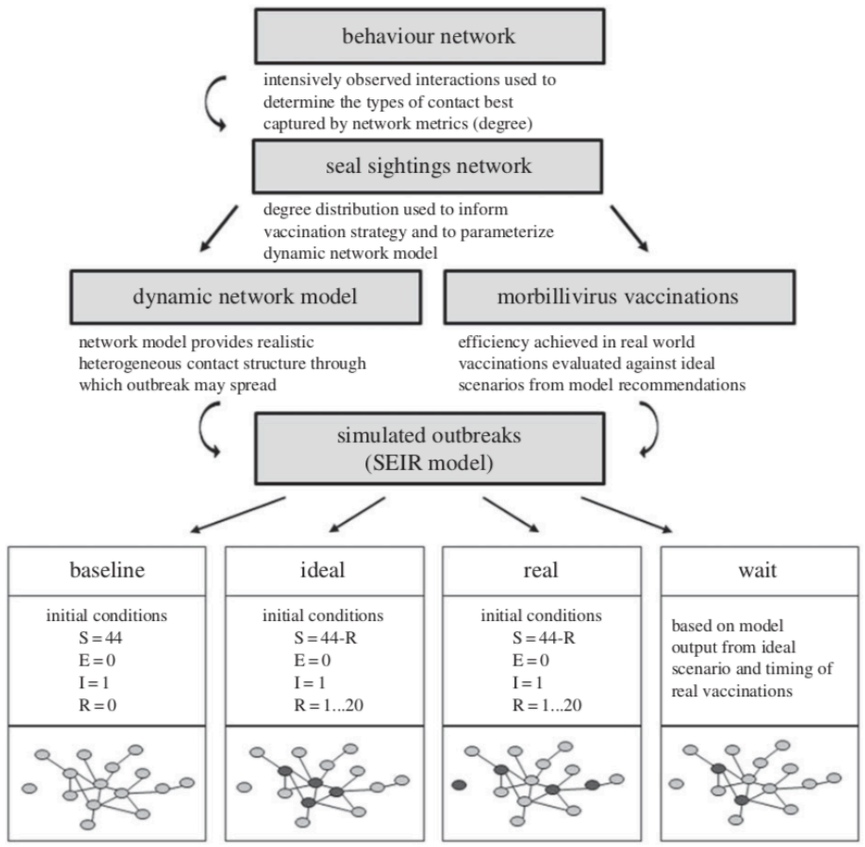
[1]NOAA National Marine Fisheries Service, Pacific Islands Fisheries Science Center, 1845 Wasp Boulevard, Honolulu, HI, USA
[2]University of Washington, Seattle, WA, USA
[3]Harting Biological Consulting, Bozeman, MT, USA
[4]College of Veterinary Medicine, University of Minnesota, St Paul, MN, USA

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

Why is PrEP 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
- 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

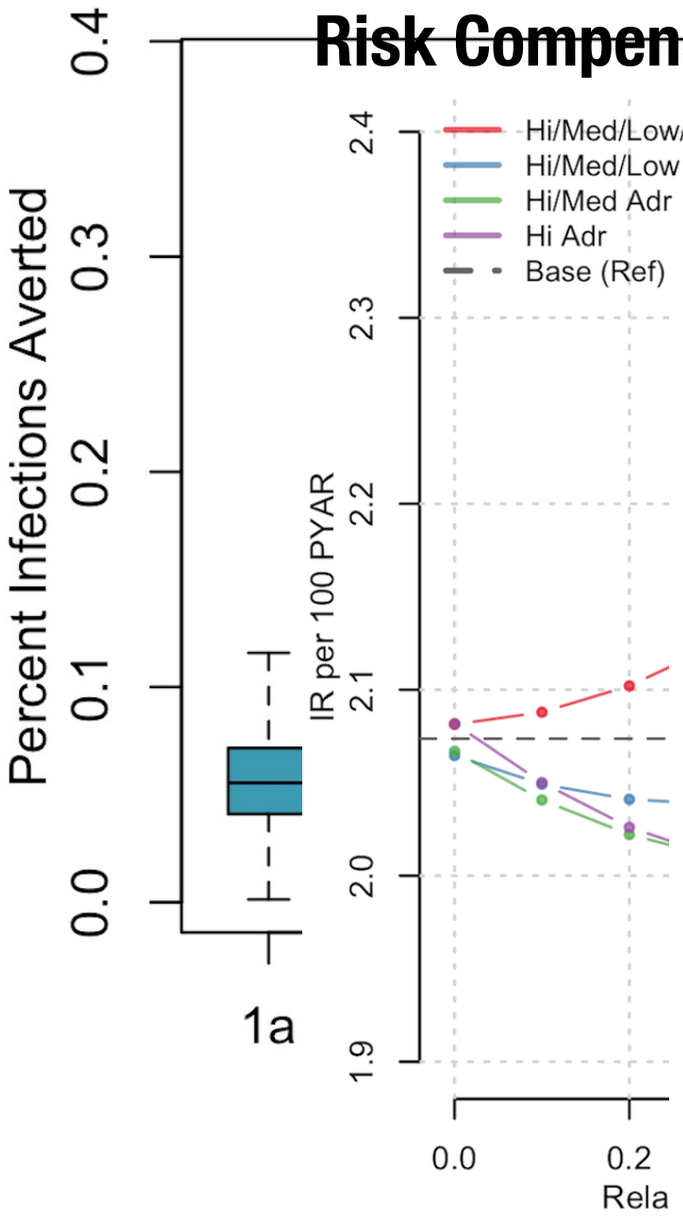
- Many math models have represented HIV PrEP
- Compartmental models typically represent simple high/low risk groups
  - Loosely related to empirical data on partnership change rates

🔥🔥 Model frameworks that do not realistically reflect underlying contact processes that drive transmission dynamics are limited in modeling primary prevention interventions 🔥🔥

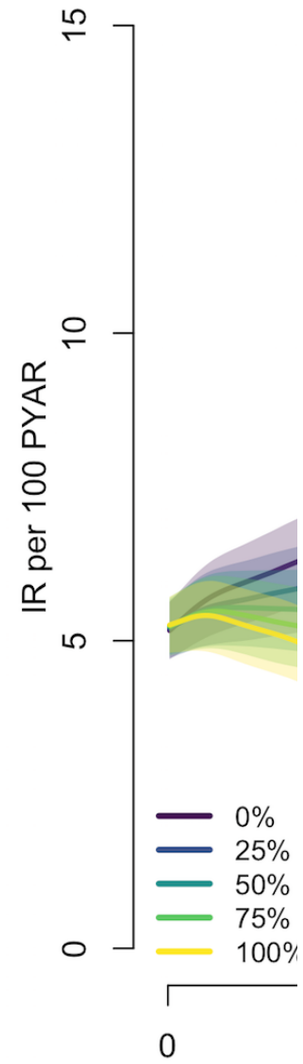
Our Models for HIV Preexposure Prophylaxis

Evaluating CDC Guidelines

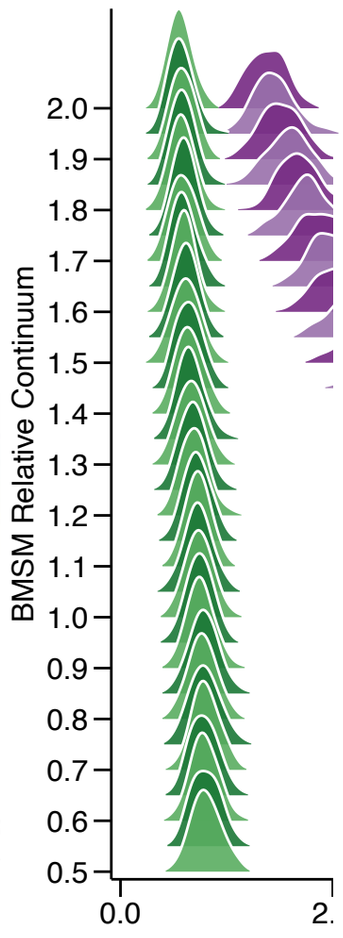
Risk Compensation & Adherence



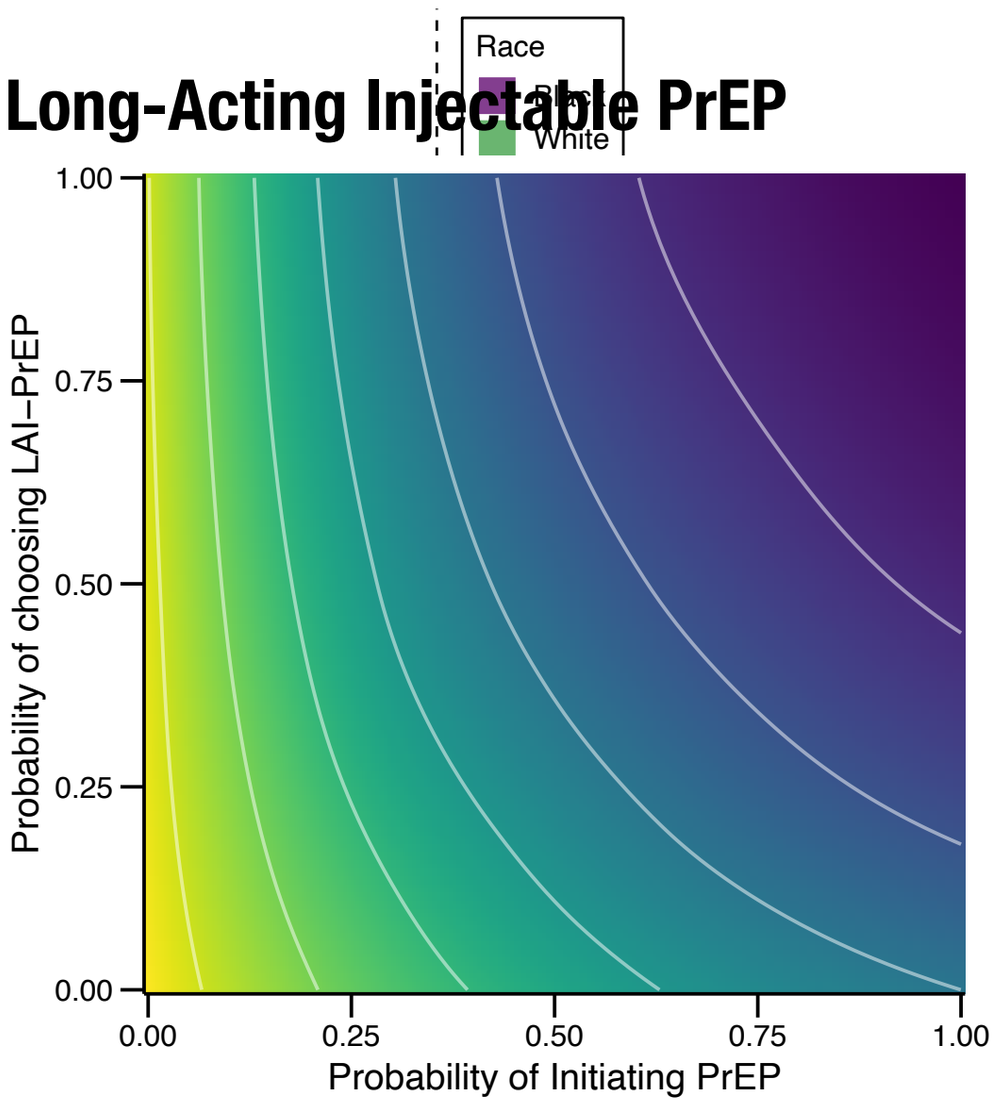
Impact on Bacterial STIs



PrEP & Racial Disparities



Long-Acting Injectable PrEP



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

Collee
Eli S.

A

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The State of Engagement in HIV Care in the United S
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Michael J. Mugaver

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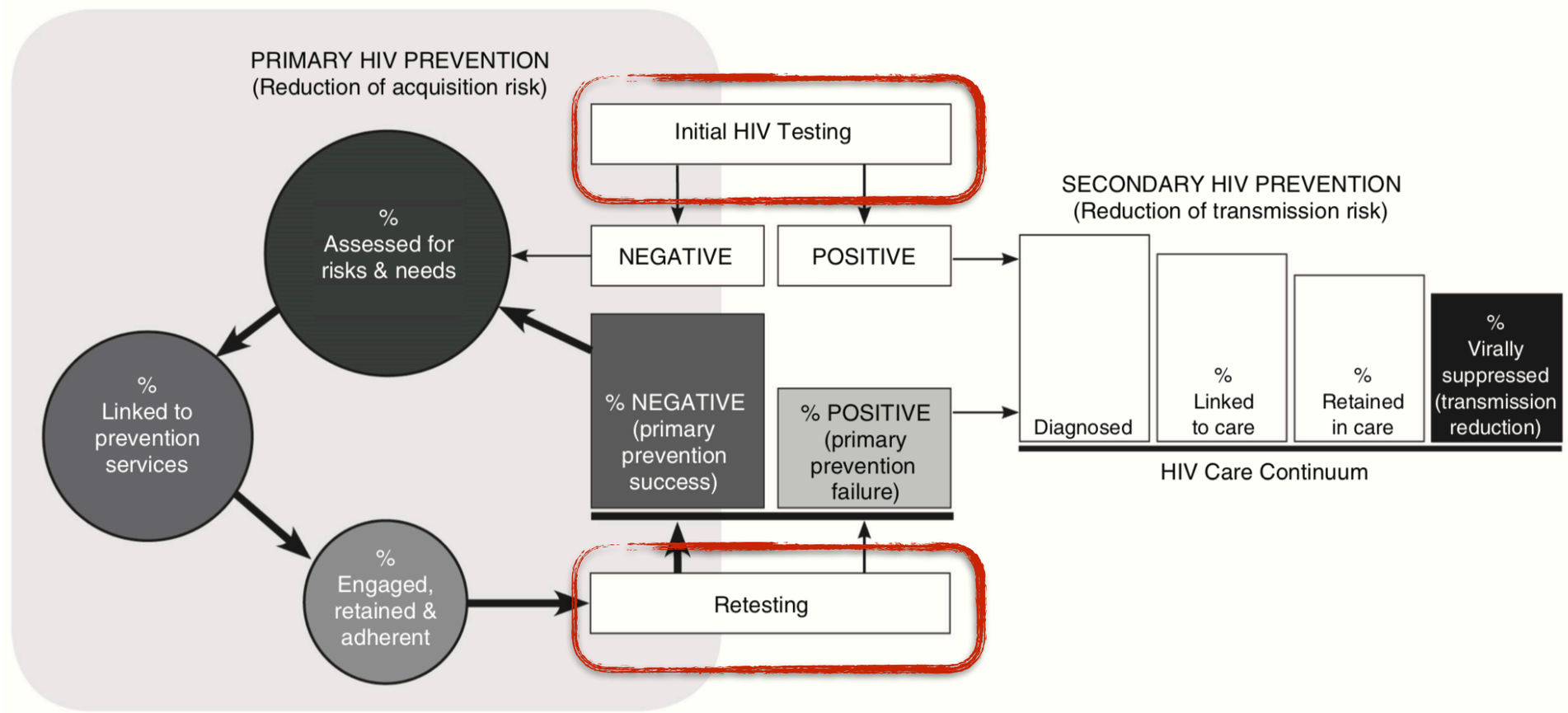
HIV Infect

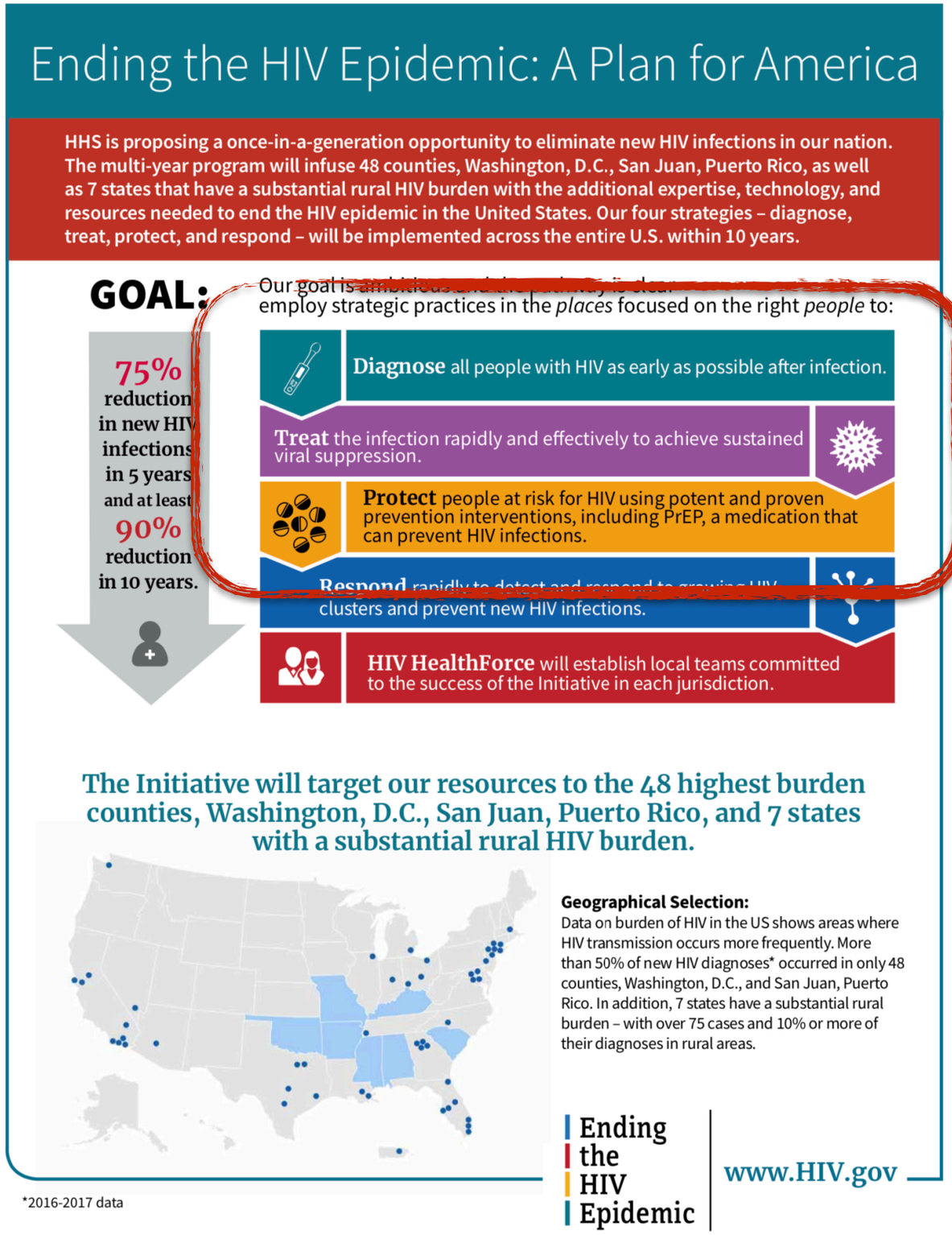
Towards an integrated primary and secondary HIV prevention continuum for the United States: a cyclical process model

Tim Horn[§,1], Jennifer Sherwood*[,2], Robert H Remien[3], Denis Nash[4] and Judith D. Auerbach*[,5], 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



Study Aims

- **Using modeling to understand an integrated HIV prevention and care continuum to achieve EHE goals**

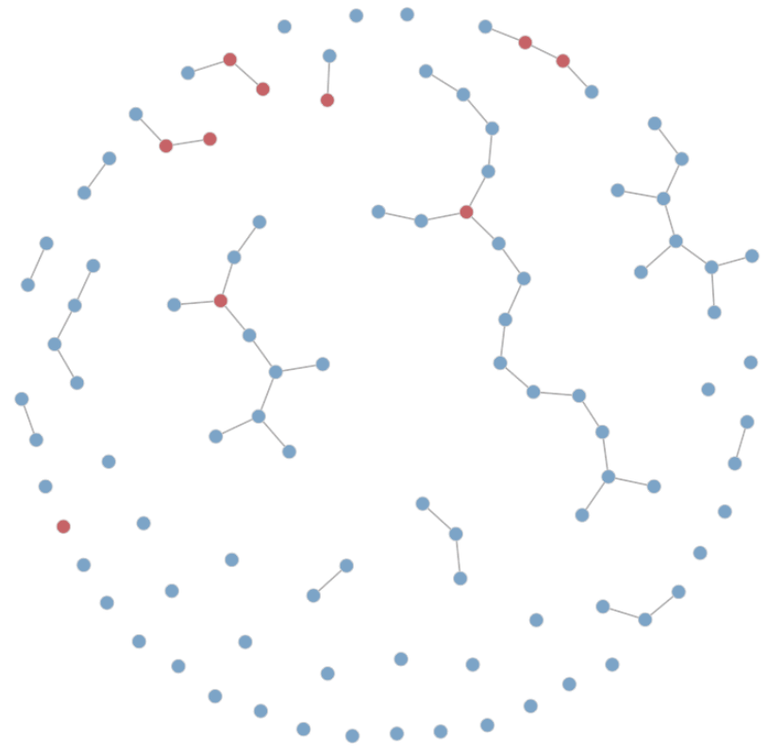
- *Primary Study Question*
  - What combinations of improvements to HIV screening (alone or as a gateway to PrEP initiation), HIV care linkage, and HIV care retention could meet the 2030 EHE goal of a 90% reduction in HIV incidence?

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 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
- Model code mechanics:
  - Estimation (netest): https://github.com/EpiModel/CombPrev/blob/master/estimation/estimation.R
  - Simulation (module for netsim): https://github.com/statnet/EpiModelHIV/blob/CombPrev/R/mod.simnet.R

Empirical Data ⇝ 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 ⇝ 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, …

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

Kevin M. Weiss[a], Steven M. Goodreau[b], Martina Morris[c], Pragati Prasad[a], Ramya Ramaraju[a], Travis Sanchez[a], Samuel M. Jenness[a,*]

[a] Department of Epidemiology, Emory University, Atlanta, Georgia, United States
[b] Department of Anthropology, University of Washington, Seattle, Washington, United States
[c] Departments of Statistics and Sociology, University of Washington, Seattle, Washington, United States

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-

* Corresponding author at: Department of Epidemiology, Emory University, 1520 Clifton Road, Atlanta, GA 30322, United States.
E-mail address: samuel.m.jenness@emory.edu (S.M. Jenness).

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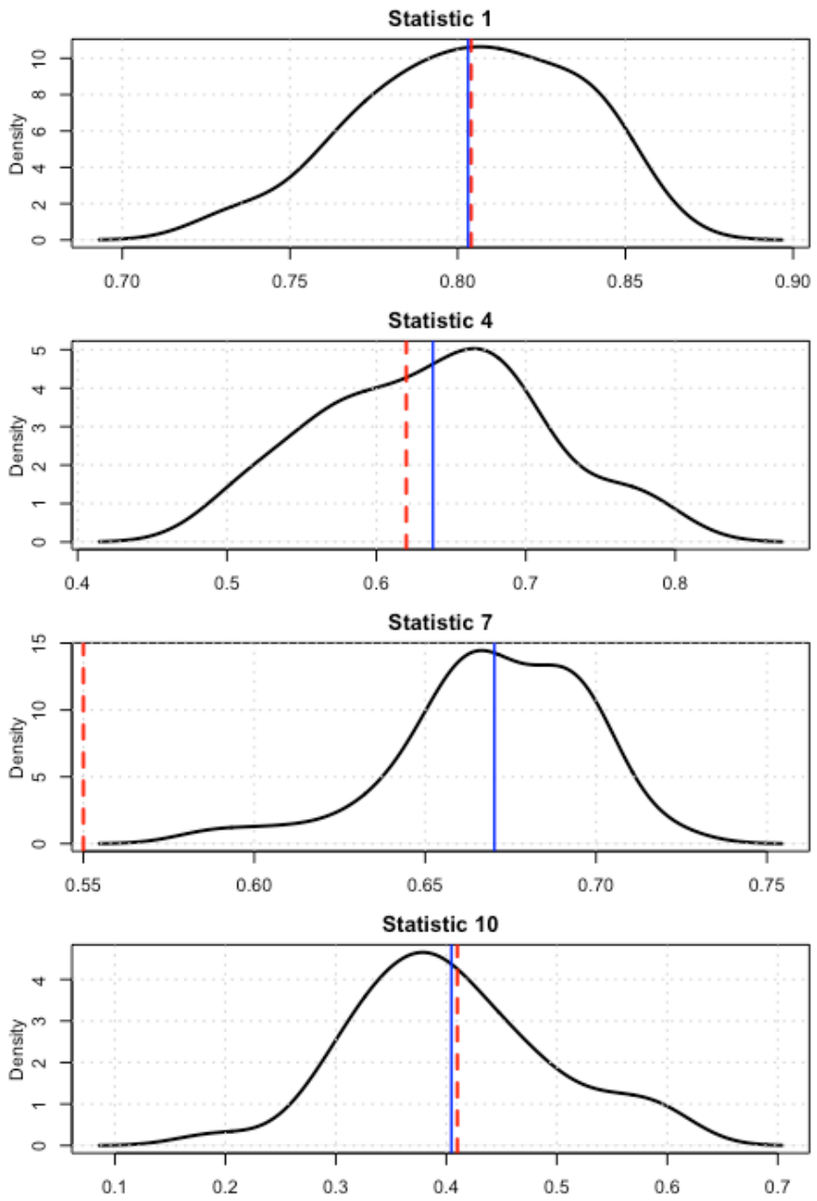
Available online 24 January 2020

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

Model Calibration for Reference Scenario

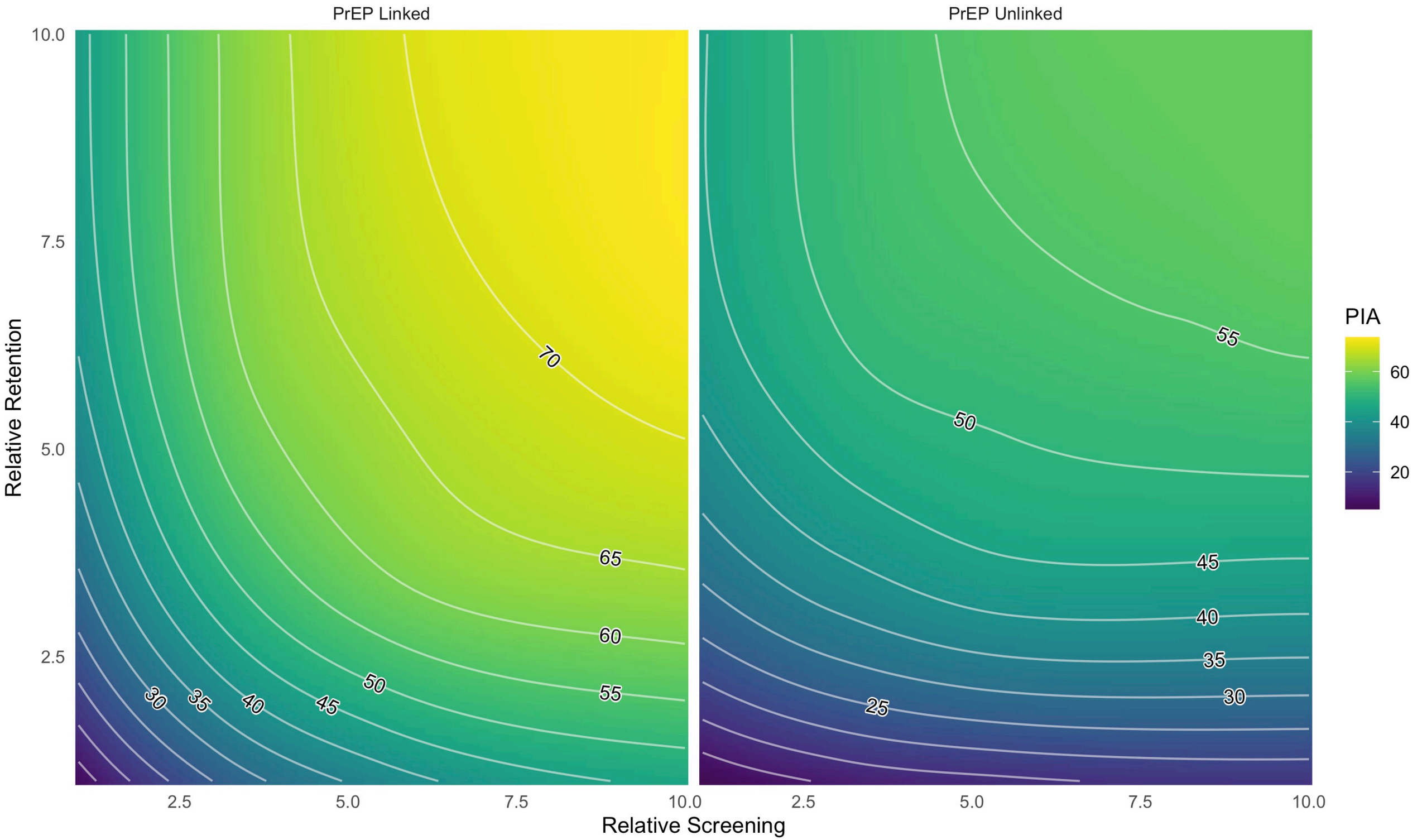
- Prevalence of diagnosed HIV Infection among MSM
  - Rosenberg, Ann Epidemiol, 2018
  - B/H/W targets: 33.3%, 12.7%, 8.4%
- Proportion of HIV+ MSM who are diagnosed
  - Singh, Ann Intern Med, 2018
  - B/H/W targets: 80.4%, 79.9%, 88.0%
- Proportion of diagnosed MSM linked to care within 1m
  - GA DPH 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%



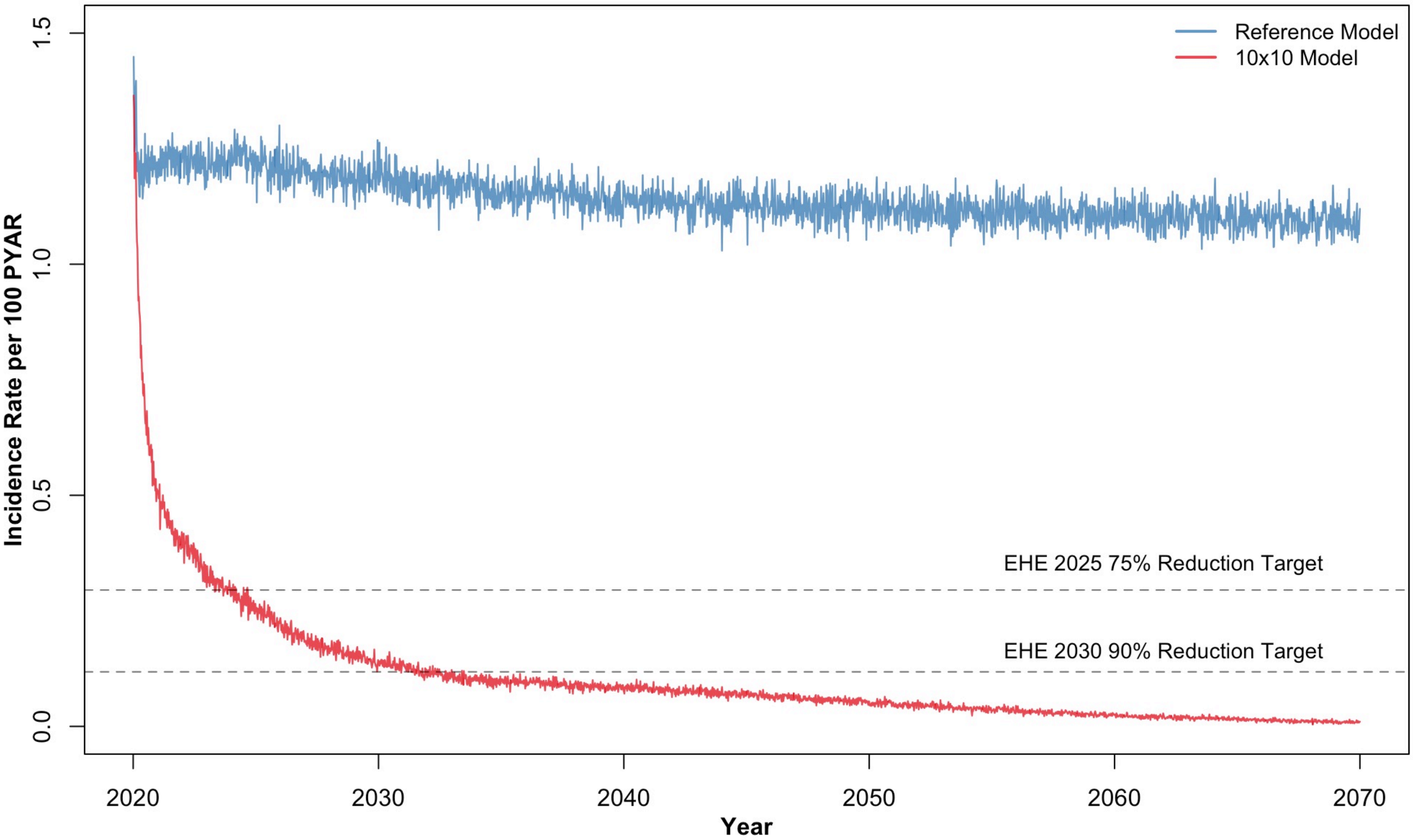
Bayesian Approaches to Model Calibration

- 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



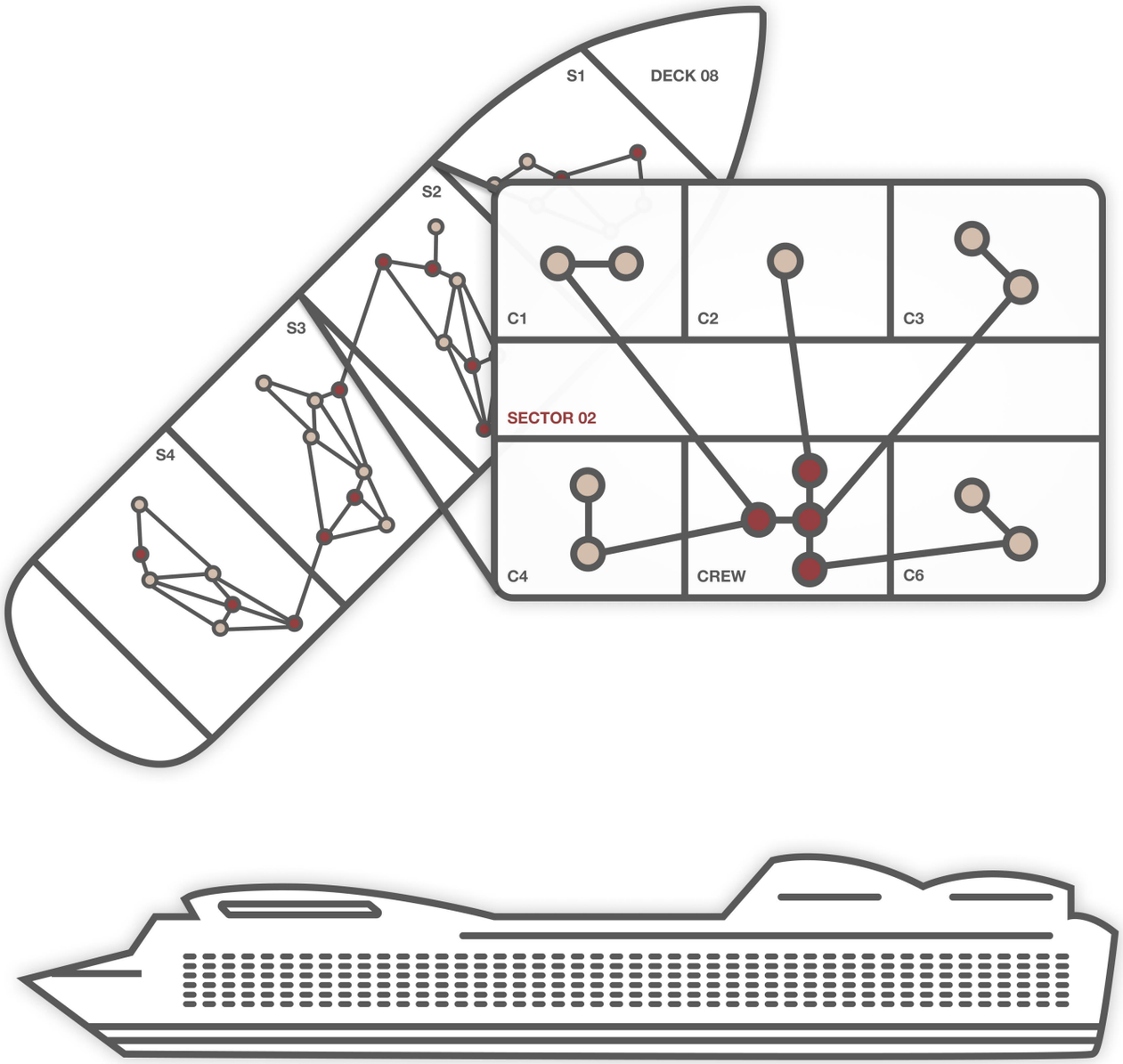
How Long Will it Take to Achieve the EHE Goals?

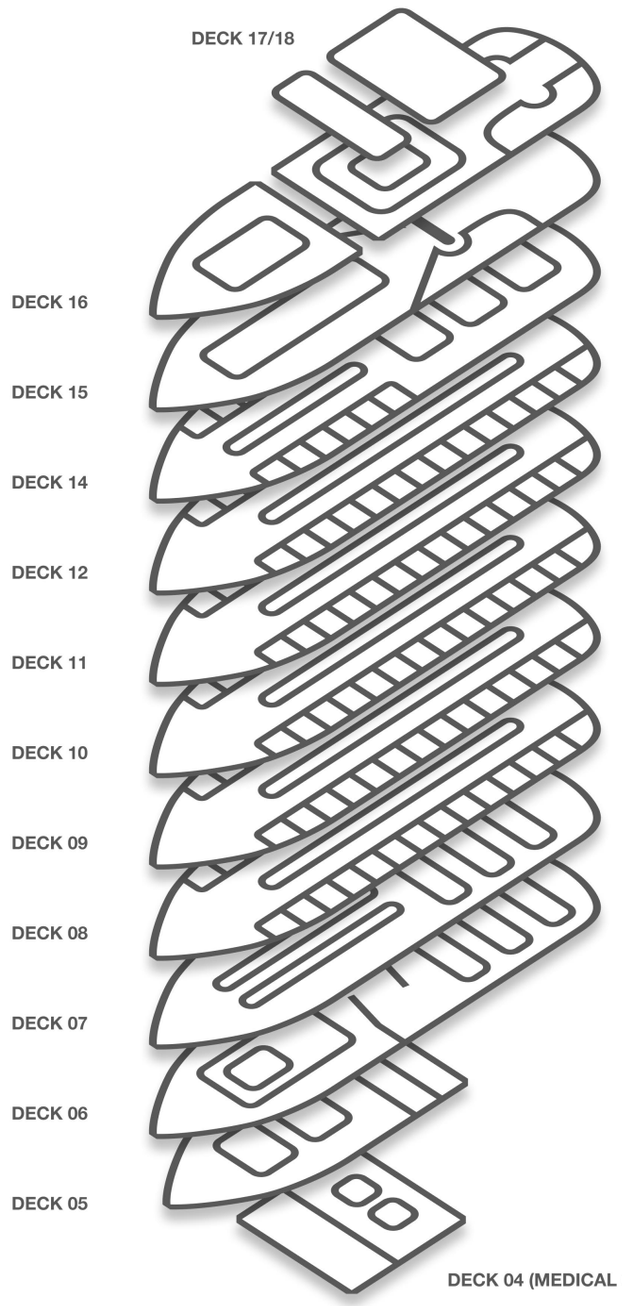


COVID Model Example

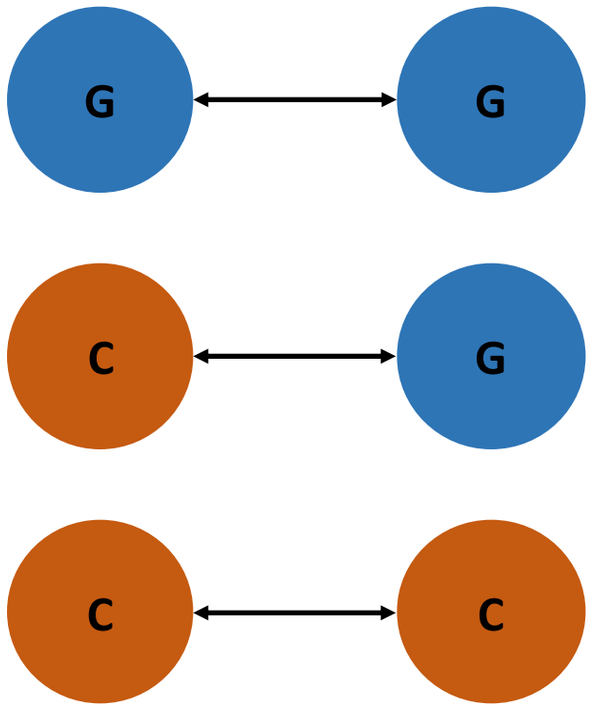
- Jenness SM, Willebrand KS, Malik AA, Lopman BA, Omer SB. Modeling Dynamic Network Strategies for SARS-CoV-2 Control on a Cruise Ship.
  - Pre-Print: https://doi.org/10.1101/2020.08.26.20182766
  - EpiModelCOVID Code: https://github.com/epimodel/epimodelcovid
  - Model scripts for paper: https://github.com/EpiModel/COVID-CruiseShip

Cruise Ship Network Model Schematic



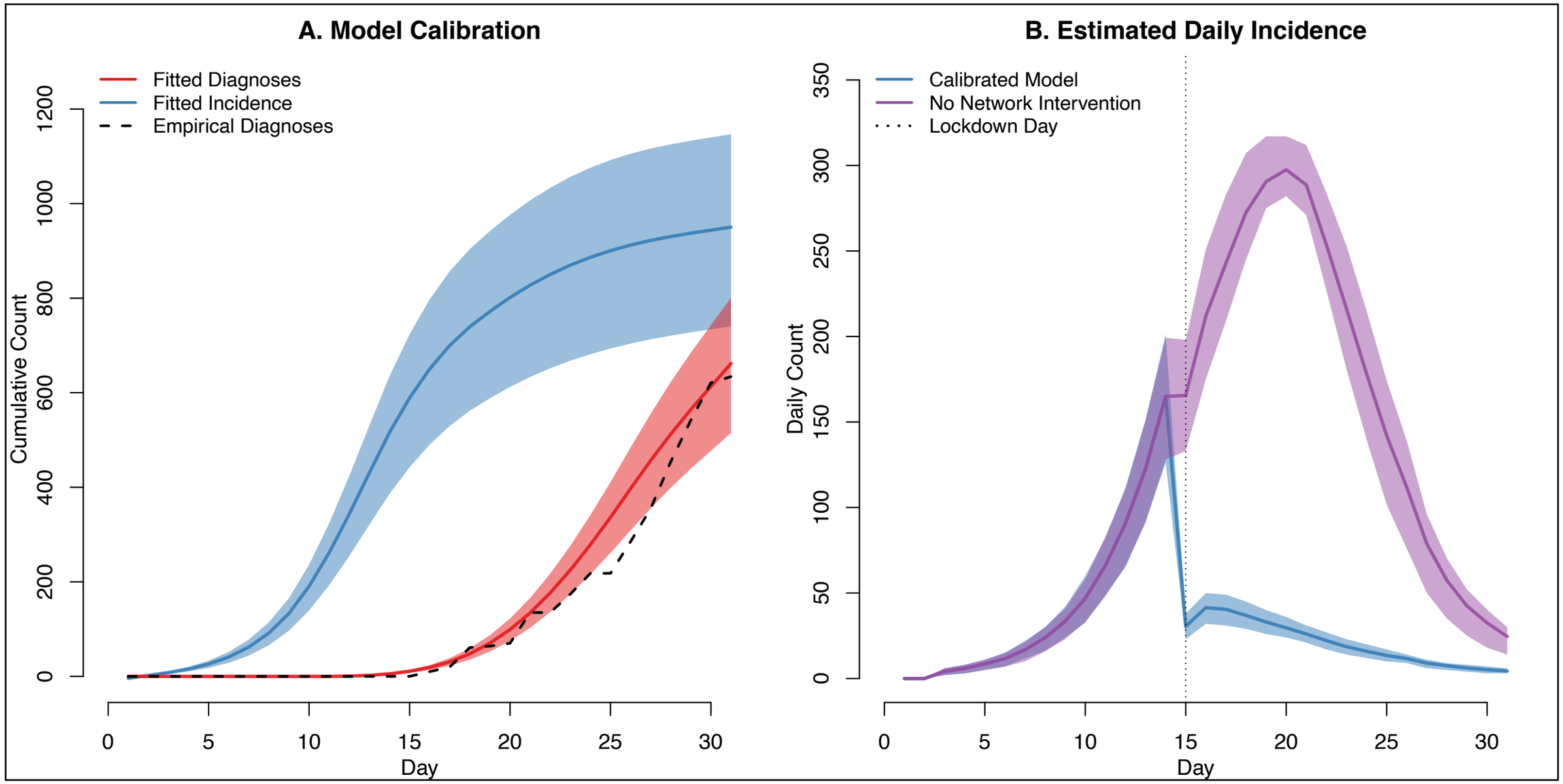


Multi-Layer Dynamic Contact Networks



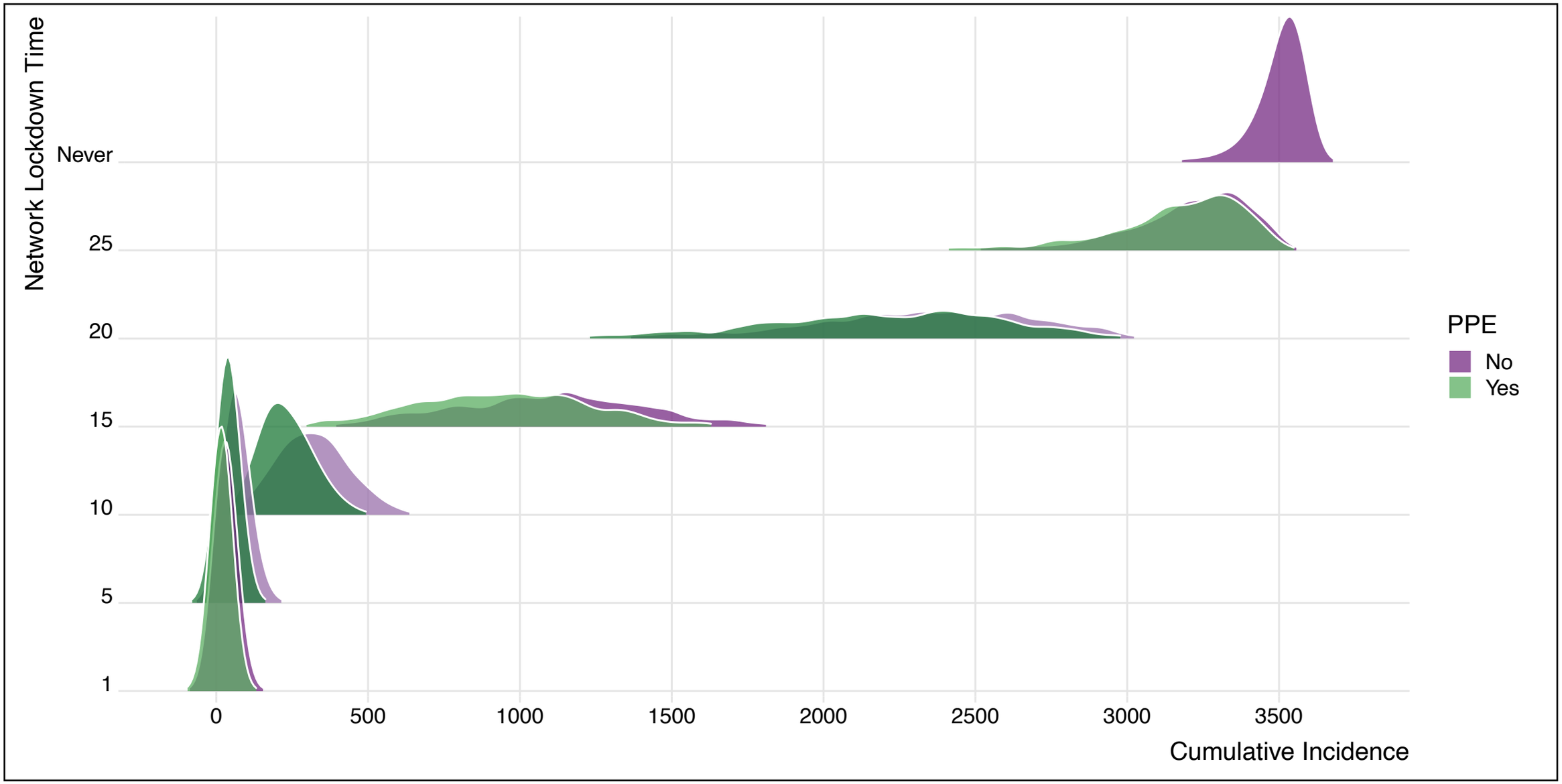
- Three overlapping ERGMs to represent guest/guest, crew/guest, and crew/crew contacts
- Multi-level structure: guests within cabins, cabins within ship sectors, crew assigned to cabins within sectors
  - x2 ERGMs, for pre-lockdown and post-lockdown network structures
- ERGMs with ship structure allow 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 Passenge	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)*
With Contact Intensity Reductions, Network Lockdown, and PPE at Day 15					
Base Scenario					
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)
Varying Passenger-Passenger Contact Intensity					
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)
Varying Passenger-Crew Contact Intensity					
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)
Varying Crew-Crew Contact Intensity					
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

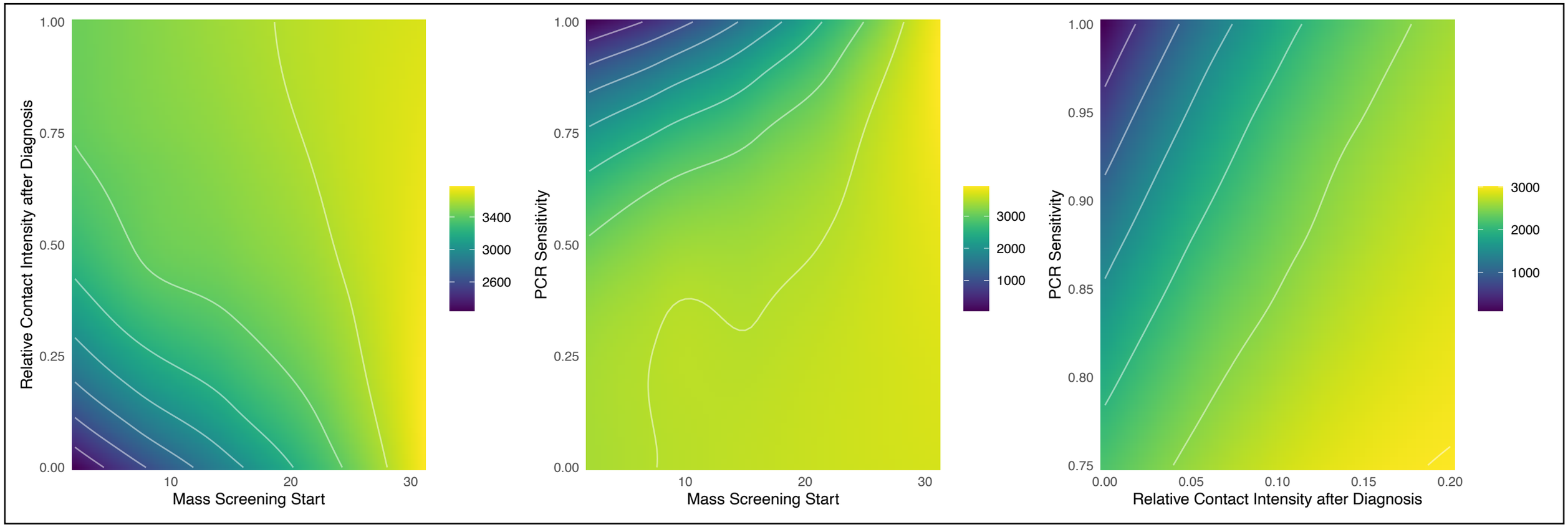
Model Results 4: Prevention with Mass Screening

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[1]	PIA[2]	Total	NDA[3]	PDA[4]
	Median (95% SI)	*Median (95% SI)*	*Median (95% SI)*	*Median (95% SI)*	*Median (95% SI)*	*Median (95% SI)*
Varying Timing of Mass Screening (Never PPE)						
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)
Varying Timing of Mass Screening (Always PPE)						
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