

BACKGROUND ON HIV MODELS FOR MEN WHO HAVE SEX WITH MEN

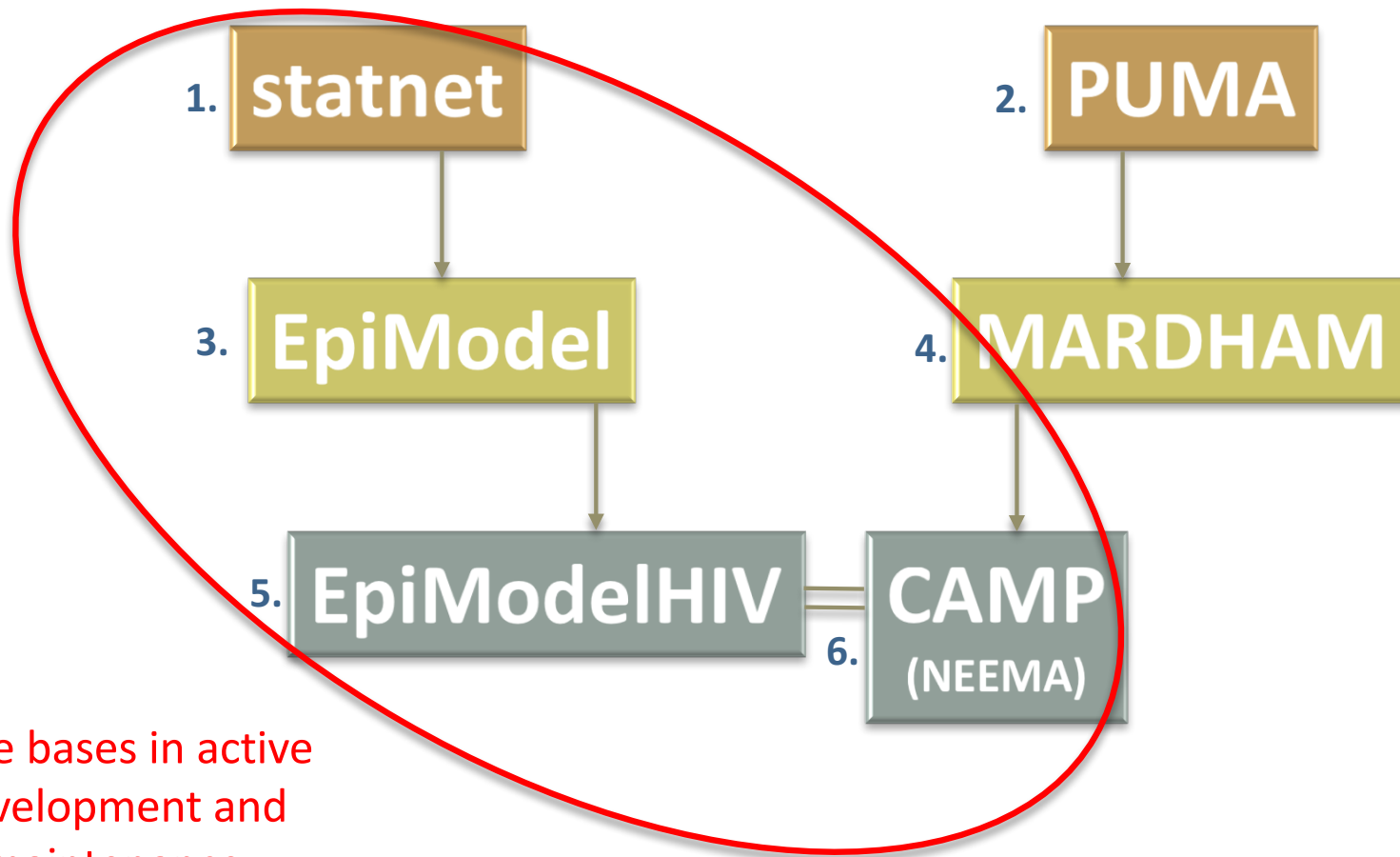
Steven M. Goodreau, Ph.D.

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Pieces overview



Code bases in active
development and
maintenance

1. statnet

statnet

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statnet wiki

Software tools for the analysis, simulation and visualization of network data.

Introduction

statnet is a suite of software packages for network analysis that implement recent advances in the statistical modeling of networks. The analytic framework is based on Exponential family Random Graph Models (ergm). **statnet** provides a comprehensive framework for ergm-based network modeling, including tools for model estimation, model evaluation, model-based network simulation, and network visualization. The statistical modeling capabilities of **statnet** include cross-sectional and temporal/dynamic modeling, latent space and latent cluster models, and models for valued/ranked/signed ties. The packages are written in a combination of (the open-source statistical language) R and (ANSI standard) C, and are called from the R command line (www.r-project.org), or from our new shiny app **statnetWeb** (more on that below in the News section).

News

- We have a new GUI for **statnet** that runs in a browser window (based on RShiny, for those who have been following that app). It's called **statnetWeb**. The point-and-click functionality is great for newbies (and thus for teachers), but even old hands will find the interface useful for simple analyses. If you are interested in this simple but powerful GUI for statnet, details and information can be found on the [statnetWeb](#) wiki page.
- The core packages were updated in March 2016 on CRAN (details on the [component packages](#) and [installation instructions](#)). The **SNA** package was updated in July 2016.

Tutorials

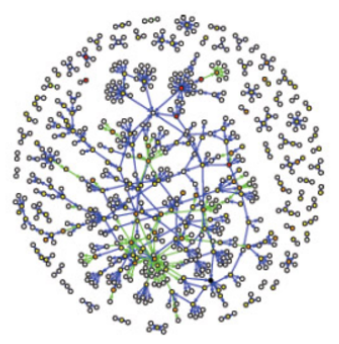
Our tutorials are updated each year, typically as we prepare to teach workshops. We are in the process of reorganizing this wiki and the tutorial archive to improve accessibility. The entry point to the tutorial sets will stay on our wiki homepage.

Tutorials from our 3 hour workshops

We teach multiple workshops on network analysis with statnet at the annual INSNA Sunbelt and European Union Social Network (EUSN) meetings. Topics include introductions to network analysis using R and statnet, cross sectional network analysis with Exponential family Random Graph Models (ERGMs), Temporal / Dynamic network analysis with Temporal ERGMs, Latent Space and Latent Class analysis for networks, Network Analysis for valued/signed/rank tie data, Using ERGMs with egocentrically sampled network data, Dynamic network visualization, and others.

- Materials from the most recent Sunbelt workshops can be found [here](#).
- Materials from the 2014 EUSN meeting can be found [here](#).

Tutorials from our longer workshops



1. statnet

- 20ish-year project
- Team came together inspired by desire to have statistical models and tools for modeling HIV dynamics
- Brought a few existing packages (network, sna) into the fold along the way
- Statnet *proper* doesn't contain anything directly related to HIV (or any other infectious disease) modeling – only relational dynamics
- Widely used in many fields (e.g. sociology, political science, biology, economics, anthropology)

1. statnet

Main constituent packages

- **network** = tools for storing and managing network data
- **sna** = routines for traditional social network analysis
- **ergm** = tools for exponential-random graph models
- **networkDynamic** = dynamic extensions of network
- **tergm** = dynamic extensions of ergms
- **statnet.common** = utilities common across statnet pkgs
- **ergm.ego** = tools to conduct egocentric network analysis (with an eye towards epidemic models)

New!!

2. PUMA

- Prevention Umbrella for MSM in the Americas (Buchbinder, PI)
- Part of NIH's MP3 program
- Focus on the US and Peru

OPEN ACCESS Freely available online



What Drives the US and Peruvian HIV Epidemics in Men Who Have Sex with Men (MSM)?

Steven M. Goodreau^{1*}, Nicole B. Carnegie², Eric Vittinghoff³, Javier R. Lama⁴, Jorge Sanchez⁵, Beatriz Grinsztejn⁶, Beryl A. Koblin⁷, Kenneth H. Mayer⁸, Susan P. Buchbinder⁹

OPEN ACCESS Freely available online



Can Male Circumcision Have an Impact on the HIV Epidemic in Men Who Have Sex with Men?

Steven M. Goodreau^{1*}, Nicole B. Carnegie², Eric Vittinghoff³, Javier R. Lama⁴, Jonathan D. Fuchs⁵, Jorge Sanchez⁴, Susan P. Buchbinder⁵

Targeting Pre-Exposure Prophylaxis Among Men Who Have Sex With Men in the United States and Peru: Partnership Types, Contact Rates, and Sexual Role

Nicole B. Carnegie, PhD,* Steven M. Goodreau, PhD,† Albert Liu, MD, MPH,‡ Eric Vittinghoff, PhD|| Jorge Sanchez, MD, MPH,|| Javier R. Lama, MD, MPH,|| and Susan Buchbinder, MD‡

HIV in men who have sex with men 1



Global epidemiology of HIV infection in men who have sex with men

Chris Beyrer, Stefan D Baral, Frits van Griensven, Steven M Goodreau, Suwat Chariyalertsak, Andrea L Wirtz, Ron Brookmeyer

Epidemics of HIV in men who have sex with men (MSM) continue to expand in most countries. We sought to understand the epidemiological drivers of the global epidemic in MSM and why it continues unabated. We did a comprehensive review of available data for HIV prevalence, incidence, risk factors, and the molecular epidemiology of HIV in MSM

Lancet 2012; 380: 367-77
Published Online
July 20, 2012



HIV in men who have sex with men 3

Successes and challenges of HIV prevention in men who have sex with men

Patrick S Sullivan, Alex Carballo-Diéguez, Thomas Coates, Steven M Goodreau, Ian McGowan, Eduard J Sanders, Adrian Smith, Prabhudhagopal Goswami, Jorge Sanchez

Lancet 2012; 380: 388-99
Published Online
July 20, 2012

Men who have sex with men (MSM) have been substantially affected by HIV epidemics worldwide. Epidemics in MSM are re-emerging in many high-income countries and gaining greater recognition in many low-income and middle-income countries. Better HIV prevention strategies are urgently needed. Our review of HIV prevention

2. PUMA

Some interesting findings:

- We estimated that about 1/3 of new infections are from main partners (in contrast to recent lit at the time)
- Capability of role versatility has large role to play in keeping HIV burden high among MSM
- PrEP has high potential to reduce HIV incidence among MSM, even with high risk compensation, but is unlikely to be a magic bullet
- PrEP works best when targeted to the highest risk men 😊
- Circumcision for MSM is a mixed bag

2. PUMA

Features of the model:

- Contains two networks: “main” partnerships and all others
- Main were modeled as duration using *tergms*
- Others were all modeled as a series of one-time contacts using *ergms*, even when they were actually durational
- Calls statnet packages for the network modeling components
- All other code is custom-made and purpose-built
- Code is modular

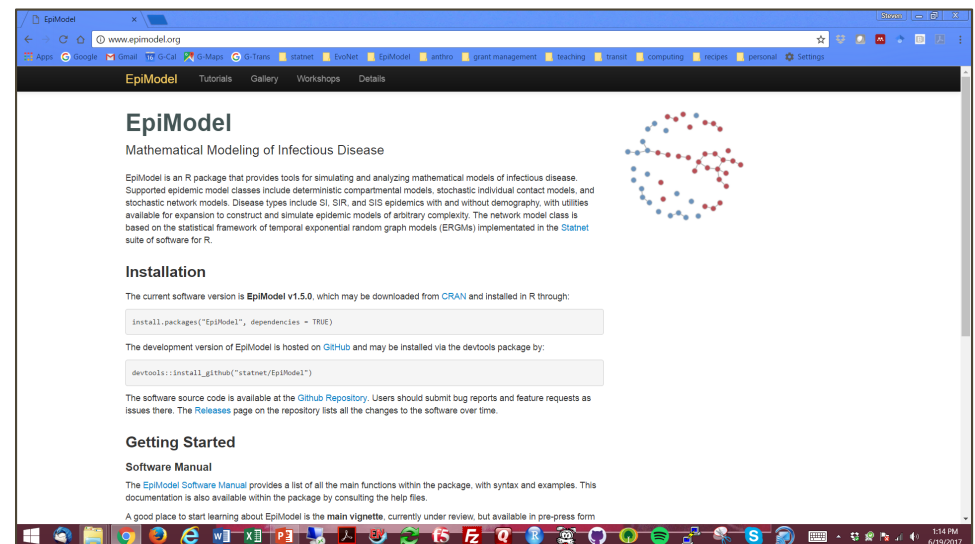
2. PUMA

Features of the model:

- Simple homogeneous **testing** module
- **Treatment** initiation module, with two adherence levels
- **Viral load** tracked – depends on time since infection and treatment
- **Network model** includes age and race mixing, degree distributions
- **UAI acts** depend on diagnosis status (acts w/o condom use not modeled)
- **Circumcision** tracked
- **PrEP use** introduced: four adherence categories, no discontinuation
- Pops represent urban MSM in the US and in Peru
- US parameters derived from NHBS, baseline Explore, and others
- Expanded to Kenya and India for Lancet series

3. EpiModel

- Development also funded by the statnet project
- Led (understatement!) by Sam Jenness while he was a grad student
- Highly integrated with statnet, but not downloaded by default with statnet
- On CRAN and github both



3. EpiModel

- Modeling tools for infectious disease
- Contains functions for running compartmental models and individual-based stochastic models, but real focus is network models
- Built-in tools handle models of class SI, SIS and SIR
- Built-in tools allow for web or command-line interface
- 49-page paper introducing the packages is about to come out in *Journal of Statistical Software*
- Highly modular
- Uses a strict API that allows for extensions while maintaining core functionality
- Base EpiModel has nothing specific to HIV or STIs in it per se

4. MARDHAM



- Modeling Approaches to Reduce Disparities in HIV among Atlanta MSM
- R21 (Goodreau PI)
- Specifically focused on Black and White MSM in Atlanta
- Specifically focused on understanding origins of racial disparities
- Parametrized from multiple studies by Eli Rosenberg and Patrick Sullivan and team at Emory

4. MARDHAM

Sources of racial disparities in HIV prevalence in men who have sex with men in Atlanta, GA, USA: a modelling study

Steven M Goodreau, Eli S Rosenberg, Samuel M Jenness, Nicole Luisi, Sarah E Stansfield, Gregorio A Millett, Patrick S Sullivan

Summary

Background In the USA, men who have sex with men (MSM) are at high risk for HIV, and black MSM have a substantially higher prevalence of infection than white MSM. We created a simulation model to assess the strength of existing hypotheses and data that account for these disparities.



Lancet HIV 2017

Published Online

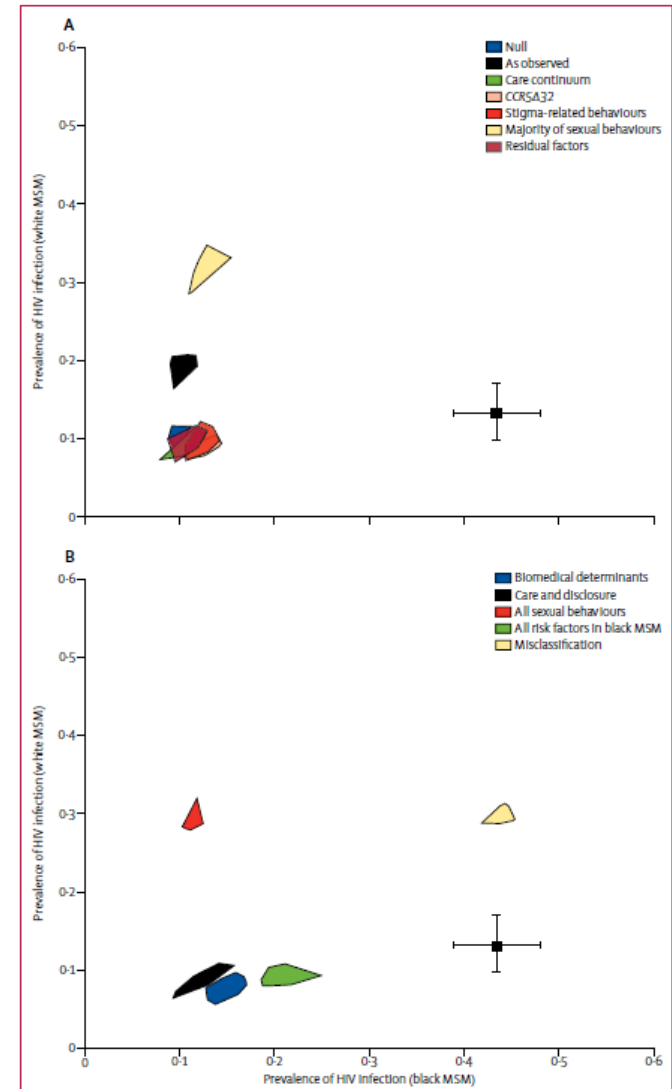
April 18, 2017

DOI:10.1016/S2468-2667(17)30001-1

	Prevalence of HIV infection in black MSM	Prevalence of HIV infection in white MSM	Ratio of prevalence of HIV infection in black MSM to prevalence of HIV infection in white MSM	% of disparity explained
Observed (Involvement cohort)	197/454 (43.4%, 38.9 to 48.0)	46/349 (13.2%, 9.9 to 17.0)	3.30 (2.47 to 4.40)	N/A
Null	544/5578 (9.8%, 9.4 to 10.0)	556/5605 (9.9%, 9.2 to 10.3)	0.99 (0.92 to 1.04)	-0.4% (-3.5 to 1.8)
As observed	558/5540 (10.1%, 9.5 to 10.3)	1078/5568 (19.4%, 19.1 to 20.0)	0.52 (0.50 to 0.54)	N/A
Factor groups in isolation				
Care continuum	609/5557 (11.0%, 10.6 to 11.7)	505/5630 (9.0%, 8.4 to 9.4)	1.23 (1.13 to 1.31)	10.0% (5.7 to 13.7)
CCRSΔ32	694/5523 (12.6%, 12.0 to 13.5)	490/5593 (8.8%, 8.2 to 9.1)	1.44 (1.35 to 1.54)	19.1% (15.4 to 23.5)
Stigma-associated behaviours	691/5552 (12.4%, 11.3 to 13.6)	542/5561 (9.7%, 9.1 to 10.3)	1.29 (1.17 to 1.41)	12.7% (7.2 to 17.8)
Majority of sexual behaviours	703/5591 (12.6%, 12.0 to 13.0)	1708/5381 (31.7%, 31.1 to 32.4)	0.40 (0.37 to 0.41)	N/A
Residual factors	612/5591 (10.9%, 10.6 to 11.4)	561/5596 (10.0%, 9.7 to 10.7)	1.10 (1.02 to 1.16)	4.3% (1.0 to 6.8)
Combined factor groups				
Biomedical determinants	844/5519 (15.3%, 14.4 to 16.2)	451/5630 (8.0%, 7.6 to 8.7)	1.93 (1.77 to 2.05)	40.5% (33.7 to 45.5)
Care and disclosure	696/5528 (12.6%, 12.1 to 13.2)	512/5601 (9.1%, 8.8 to 9.7)	1.38 (1.31 to 1.46)	16.4% (13.6 to 20.0)
All sexual behaviours	638/5609 (11.4%, 11.0 to 11.8)	1572/5387 (29.2%, 28.6 to 29.5)	0.39 (0.38 to 0.40)	N/A
All risk factors in black MSM	1113/5423 (20.5%, 19.4 to 21.3)	508/5600 (9.1%, 8.4 to 9.4)	2.28 (2.18 to 2.36)	55.5% (51.3 to 59.1)
Misclassification of risk behaviours	2255/5116 (44.1%, 43.9 to 44.0)	1635/5483 (29.8%, 29.2 to 30.7)	1.48 (1.45 to 1.53)	20.8% (19.7 to 22.9)

Data are n/N, unless otherwise specified. For observed values (ie, the first row), we report 95% CIs; all other data are reported with the IQR. For simulated prevalence numbers, values represent the mean (IQR) observed at the end of the 16 simulations, with initial population size of 10 000. Simulated prevalence ratios are calculated separately at the end of each of the 16 runs and are reported as mean (IQR). For percentage of disparity explained, we compared the mean (IQR) of the 16 simulated prevalence ratios with the observed point estimate, using the formula $(PR_{sim}-1)/(PR_{obs}-1)$, where PR_{sim} is the simulated prevalence ratio and PR_{obs} is the observed prevalence ratio. For scenarios in which all simulations yielded a larger prevalence of HIV infection for white than for black MSM, we report the percentage disparity as N/A. The percentage disparity explained for the null model should be centered on 0, with stochasticity, by design. MSM=men who have sex with men. N/A=not applicable.

Table 4: Racial disparity in prevalence of HIV infection generated by specific measured proximal factors, alone or in combination



4. MARDHAM

- Code started from scratch based on lessons learned in PUMA
 - Makes nearly all parameters a function of race (or race-combo in dyads)
 - Adds third network (casual but persistent)
 - With two persistent networks, momentary degree is a matrix
 - Adds explicit modeling of both condomless and condom-protected AI acts
 - Adds in more complex treatment dynamics (going on and off)
 - Adds in more complexity to disclosure
 - Adds in CCR5 genotype
-
- Initially not coded in EpiModel, since the two were in development in parallel
 - Converted over into EpiModel nomenclature and syntax by Sam

5. EpiModelHIV

- Set of EpiModel extensions modules and default parameters designed for modeling HIV (and now other STIs)
- Like everything in EpiModel, it is designed to be editable or extendable through the use of modules
- Contains separate code bases for MSM and heterosexuals
- MSM code began its life as the Mardham code converted over into EpiModel API
- Has now been extended considerably over the course of the CAMP project
- Different CAMP sub-projects create parallel versions of modules
- This yields a database of existing modules to choose from as starts
- Is continually in development
- Default parameters reflect the Atlanta mode, but are all replaceable
- Lives on github only

5. EpiModelHIV

EpiModelHIV

build passing

An R package for simulating HIV transmission dynamics among men who have sex with men and heterosexual populations, developed as an extension to our general network-based epidemic modeling platform, [EpiModel](#).

[EpiModel](#) and [EpiModelHIV](#) use the statistical framework of temporal exponential-family random graph models to fit and simulate models of dynamic networks. These [statistical methods](#) have been developed and implemented as open-source software, building on the extensive efforts of the [Statnet](#) research group to build software tools for the representation, analysis, and visualization of complex network data.

These packages combine these Statnet methods with an agent-based epidemic modeling engine to simulate HIV transmission over networks, allowing for complex dependencies between the network, epidemiological, and demographic changes in the simulated populations. Readers new to these methods are recommended to consult our [EpiModel](#) repository including our main [Vignette](#) describe the theory and implementation.

Installation

You can install [EpiModelHIV](#) in R using `devtools`:

```
install.packages("EpiModel", dependencies = TRUE)
devtools::install_github("statnet/tergmLite")
devtools::install_github("statnet/EpiModelHPC")
devtools::install_github("statnet/EpiModelHIV")
```

Documentation on using this software package is forthcoming, although limited function documentation is provided with the package and available with the `help(package = "EpiModelHIV")` command.

Network Models a

statnet / **EpiModelHIV** Unwatch 8 Star 1 Fork 3

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Network Models of HIV Transmission Dynamics among MSM and Heterosexuals Edit

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467 commits 8 branches 4 releases 5 contributors GPL-3.0

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smjenness Remove LICENSE.md from build Latest commit 9e47fb4 5 days ago

R	Update documentation	2 months ago
data	Update built-in data to include est and st	a year ago
inst	Continue merge	5 months ago
man	Build docs	2 months ago
src	Remove RcppExports.cpp	2 months ago
tests	Continue merge	5 months ago
.Rbuildignore	Remove LICENSE.md from build	5 days ago
.gitignore	Update gitignore	2 months ago
.travis.yml	Add Travis integration to slack	5 days ago
DESCRIPTION	Update documentation	2 months ago
LICENSE.md	Create LICENSE.md	5 days ago
NAMESPACE	Continue merge	5 months ago
README.md	Update citations	2 months ago

README.md

6. CAMP

- Coalition for Applied Modeling Projects
- Broad name for all of the Emory/UW/JHU NEEMA projects
- Some of these (i.e. any involving Sam or Steve) use EpiModelHIV

The Journal of Infectious Diseases

MAJOR ARTICLE



Impact of the Centers for Disease Control's HIV Preexposure Prophylaxis Guidelines for Men Who Have Sex With Men in the United States

Samuel M. Jenness,¹ Steven M. Goodreau,⁴ Eli Rosenberg,¹ Emily N. Beylerian,⁵ Karen W. Hoover,³ Dawn K. Smith,³ and Patrick Sullivan^{1,2}

Departments of ¹Epidemiology, and ²Global Health, Emory University, and ³Division of HIV/AIDS Prevention, Centers for Disease Control and Prevention, Atlanta, Georgia; ⁴Department of / and ⁵Center for Studies in Demography and Ecology, University of Washington, Seattle

RESEARCH ARTICLE

Individual HIV Risk versus Population Impact of Risk Compensation after HIV Preexposure Prophylaxis Initiation among Men Who Have Sex with Men

Samuel M. Jenness^{1*}, Akshay Sharma¹, Steven M. Goodreau², Eli S. Rosenberg¹, Kevin M. Weiss¹, Karen W. Hoover³, Dawn K. Smith³, Patrick Sullivan^{1,4}

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Network Models a

6. CAMP

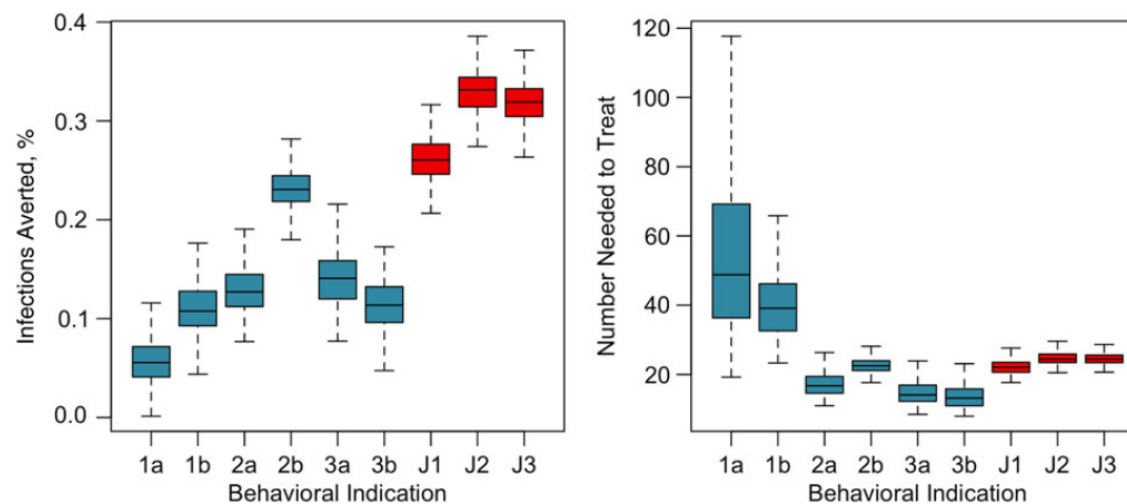


Figure 2. Box plots of the percentage of infections averted and number needed to treat to prevent 1 new infection by the individual behavioral indications (1a–3b; *blue*) and joint guideline scenarios (J1–J3; *red*) outlined in Table 1. Boxes indicate interquartile ranges; whiskers, 95% credible intervals for outcomes across all 250 simulations for each scenario.

- “Overall, taking into account the direct and indirect effects, implementing PrEP based on the indications in the CDC guidelines strikes a good balance between impact and efficiency according to our study, with 33% of infections averted and an NNT of 25.”

6. CAMP

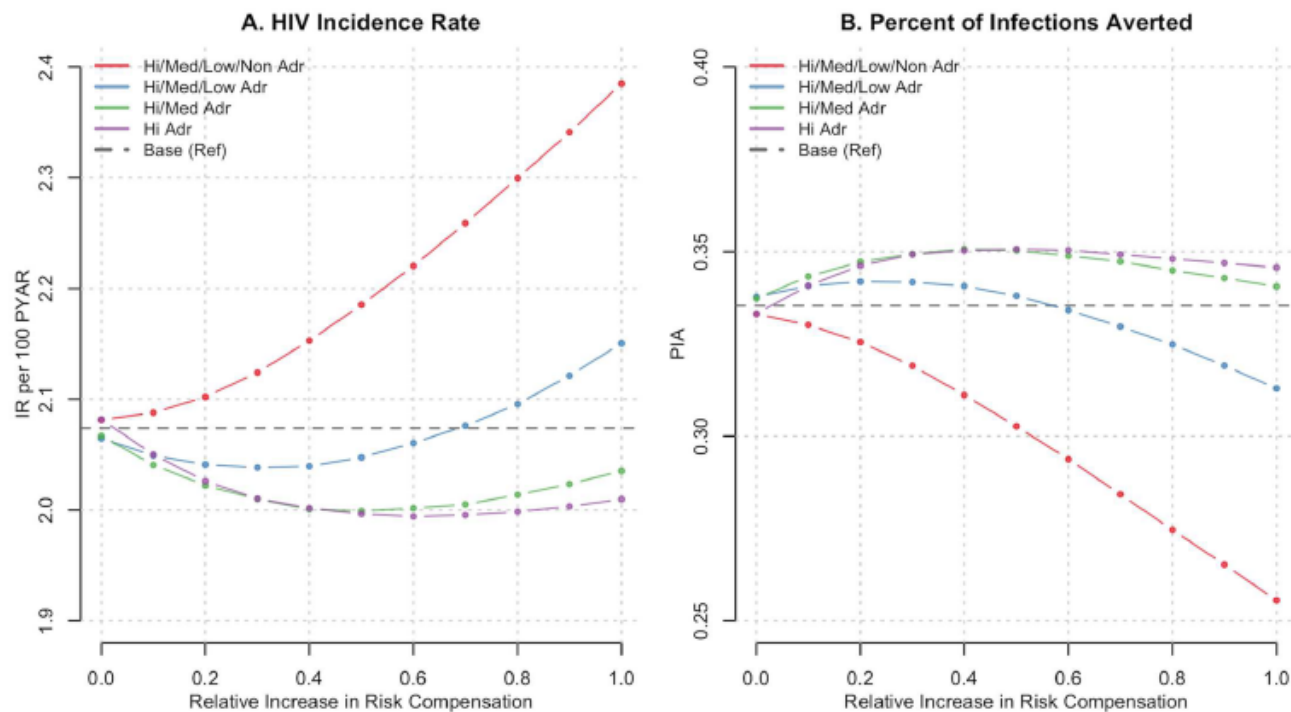


Fig 1. The HIV incidence rate per 100 person-years at risk (Panel A) and percent of infections averted relative to a scenario in which no PrEP was used (Panel B), by the interaction of relative levels of condom-related risk compensation (RC) and PrEP adherence profile in which compensation occurred. The red line depicts RC in all four PrEP medication adherence profiles (high, medium, low, and non-adherent), the blue in the top three (high, medium, low) green in the top two (high and medium) and purple in the high only. The horizontal dashed lines shows a comparison of the two outcomes (incidence and PIA) if RC were not to occur (0% RC). All points summarize the empirical distribution of 250 simulations of each scenario.

doi:10.1371/journal.pone.0169484.g001

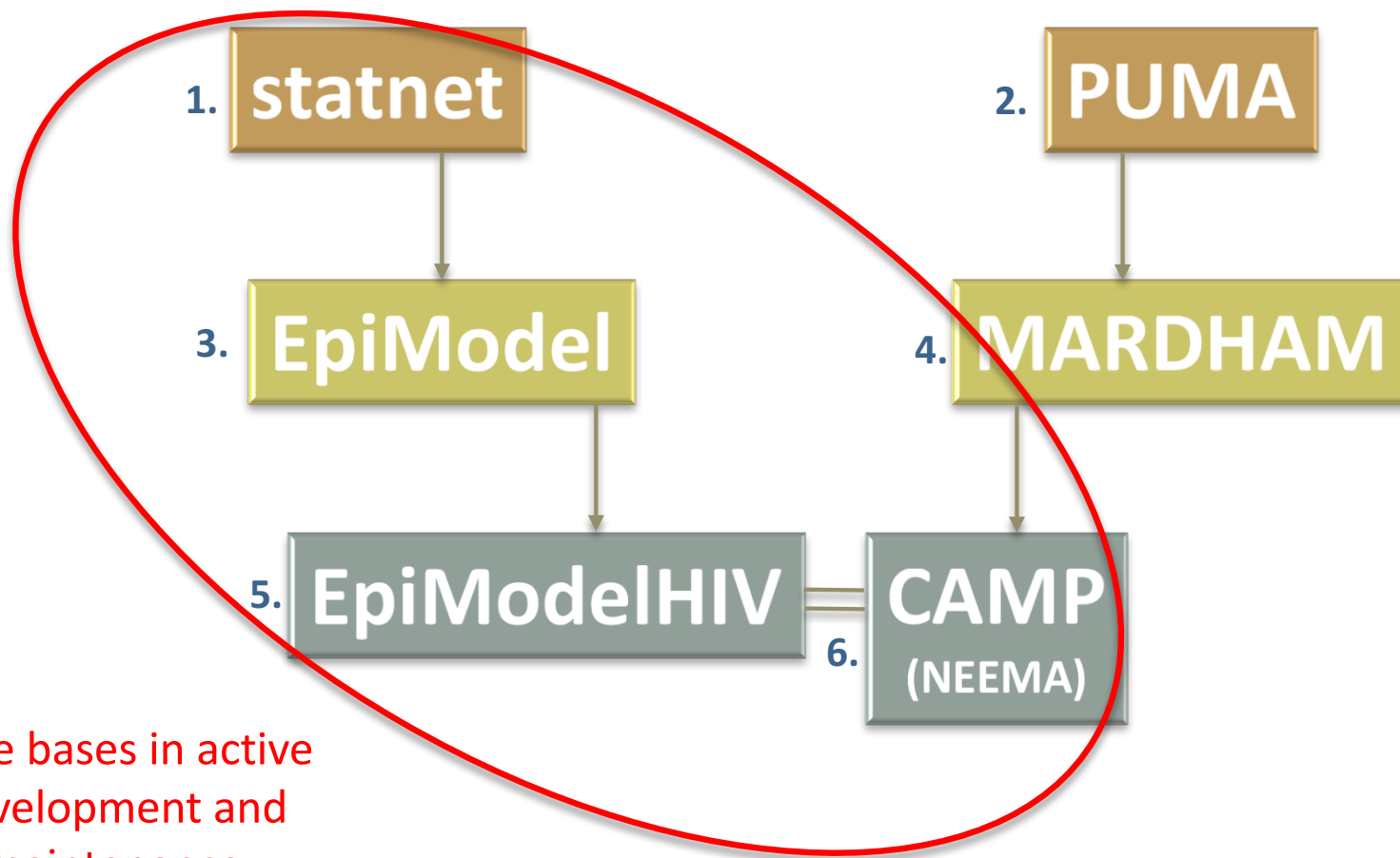
6. CAMP

- Additional CAMP papers in press or in progress using EpiModelHIV:
 - PrEP's impacts on STIs among MSM
 - Race-specific impacts of PrEP among adult MSM
 - PrEP among adolescent sexual minority males (ASMM)
 - Race-specific impacts of PrEP among ASMM

6. CAMP

- **Modules or features added to EpiModelHIV through CAMP:**
 - Much fancier PrEP modules (e.g. targeting based on discordant partnership status, recent partner counts)
 - Code to track these added metrics
 - Full suite of code for other STIs (gonorrhea, chlamydia, syphilis) and their interactions
 - Code for arrival at different ages (now set down to 13), and for sexual debut separate from arrival in population
 - Code to model infections from outside modeled population
 - Code for up to 5 race groups

Pieces overview



Code bases in active
development and
maintenance