

LOCALLY GROUNDED NETWORK MODELS FOR HIV POLICY PLANNING

HIV Behavioral Research and Mathematical Modeling

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Start by acknowledging my



Modelers

UW Network Modeling Group
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 Jeanette Birnbaum

Epidemiologists

Joint UW/PHSKCSarah GlickRoxanne Kerani

Advisory Board

- PHSKC Amy Bennett, Susan Buskin, Katelyn Gardner Toren
- WA DOH Jason Carr, Tom Jaenicke
- UW Matt Golden, David Katz

Funding: NIAID R21

Outline

- Project overview: Seattle HIV Applied Modeling for Prevention (SHAMP)
 - When is a model a "local model"?
 - How do you assess this?
- Overview of model structure and data sources
 - Demography
 - Transmission system
 - Care continuum and clinical outcomes
- Data Descriptives (focusing on the network and behavioral data)
- Epidemic simulation results
 - Preliminary first set of calibrated runs
- Implications for HIV prevention

Project goals

- Build locally grounded projection model for the local heterosexual HIV epidemic
- Designed to support HIV policy decision making

Keeping in mind

- Factors specific to local HIV prevalence and dynamics
- Prevention policy options at the State/County/Local level
- Demonstrate proof of concept
 - This is a feasibility project
 - To identify locale-specific policy questions
 - Determine whether the necessary local data exist to model this
 - Assess the preliminary validity of a model-based simulation

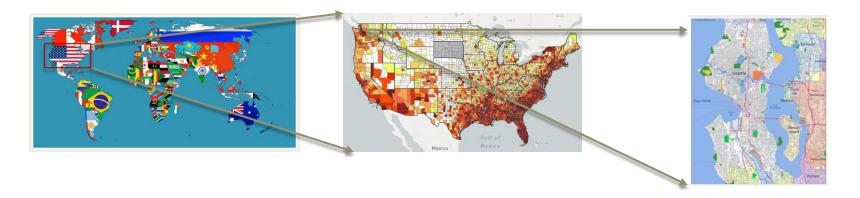
What is a "local" model?

Not a simple geographic definition ... more an integrated perspective

| Policy + | The project is motivated by specific policy questions that arise in a public health jurisdiction |
|----------|--|
| Data + | The data used to inform all aspects of the model are sourced from the population in this same jurisdiction |
| Model | The model structure is designed to answer these questions, after calibration and validation to local data |

This does have geographic implications

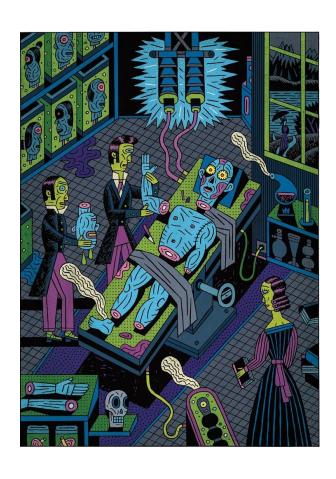
Policy levers, heterogeneity and boundary effects all vary by geographic focus



And not in a simple linear way

- Bigger units (global) may not have simple policy levers to shift, nations may or may not, smaller units like cities also often do not
- Smaller units like cities may have less heterogeneity to model, but more transmission occurring from outside their boundaries

Frankenmodels: what we're trying to avoid



- Data come from different
 - Places
 - Times
 - Samples
- What are the model projections good for then?
 - Fine as a theoretical exercise (if this, then that)
 - Not a good basis for applied local planning

Behavioral data often the most abused

- Will show an example next
 - Not to bash this particular paper or authors
 - It's very common to see this kind of Frankenmodel approach to the behavioral components of a model
 - This paper comes from 2018...

Improving the impact of HIV pre-exposure prophylaxis implementation in small urban centers among men who have sex with men: An agent-based modelling study

- You may need to drill down in a paper to find this information
 - The supplementary appendix
 - And/Or a deep dive into the references listed

Table 1. Overview of model parameters and processes.

| Processes | Provenance | Sources |
|--|--|--------------------------------|
| Demography | | |
| Population size | Rhode Island | [16,17] |
| Age (15-74) | Rhode Island | [18] |
| Background mortality | Rhode Island | [19] |
| Sexual Behavior | | |
| Condom use | External | [20] |
| Sexual role | External | [21] |
| Sexual Networks | | |
| Annual partner number | Rhode Island Selection into clinic (Rhode Island, primary data) | [22] |
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| HIV transmission risk reduction conferred by full and partial adherence | External | [5] |

Note: many different sources referenced

PLWH, people living with HIV; PrEP, pre-exposure prophylaxis; ART, antiretroviral therapy. Parameters, their values, and their sources are discussed in more detail in S1 Appendix.

https://doi.org/10.1371/journal.pone.0199915.t001

Gantenberg JR, King M, Montgomery MC, Galárraga O, Prosperi M, et al. (2018) Improving the impact of HIV pre-exposure prophylaxis implementation in small urban centers among men who have sex with men: An agent-based modelling study. PLOS ONE 13(7): e0199915. https://doi.org/10.1371/journal.pone.0199915



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National sample:

October 2010

respondents recruited online from "one the world's largest operators of Internet web sites for men who seek social or sexual interactions with other men"

Last act of anal intercourse

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EXPLORE study:

1999-2001 longitudinal

ACASI survey of MSM from 6 cities in the US

HIV- men only

UAS role last 6 mos

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City STI clinic:

2012 to 2014

Chart review of individuals presenting to a publicly-funded STD clinic in Providence, Rhode Island

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National sample:

March-April 2009

online survey recruited respondents from MySpace

"Most recent partner"

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"Assumed"

10 – another modeling study

24 - Peru & US data 2012

25 – Statistical methods (I'm a co-author, and the example was based on heterosexual data...)

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Keep this in mind as I describe our study

- We, too, will have to make some compromises
- But not all compromises are created equal
 - Some may have clear implications for bias, inconsistency and temporal obsolescence
 - Others may not
- If you are using secondary data you may not have many choices
 - But, that doesn't mean you should ignore the implications

Project goals in context

- We have several ongoing "local modeling" projects
 - Two focused on MSM (Darcy Rao dissertation and WHAMP)
 - One on heterosexuals (SHAMP)
 - Another on modeling both populations together (Kenya project)
- Why focus SHAMP on the heterosexual epidemic in King County?
 - Because the other projects are focused on MSM
 - But also:
 - Small, but potential for eradication
 - First step towards a more comprehensive model
 - It's a challenge...

Why is it a challenge? (1)

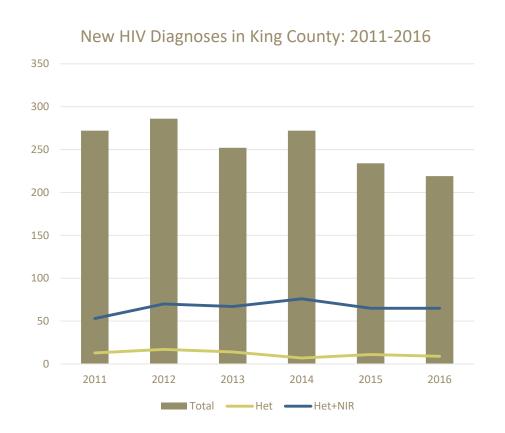
DATA

The empirical data we need are measured with substantial uncertainty

- Not just the sexual behavior data
- But also the surveillance data on HIV diagnoses
 - And we will use these as targets for model validation

Heterosexual cases of HIV

This "risk classification" is measured with uncertainty



In King County

- 6-7% of new diagnoses are attributed to known heterosexual contact with HIV+ partner
- Another 15-20% is "No Identified Risk" (NIR)
 - Many may be cases of heterosexually acquired HIV
- Possible range: 6-27%

Why is it a challenge? (2)

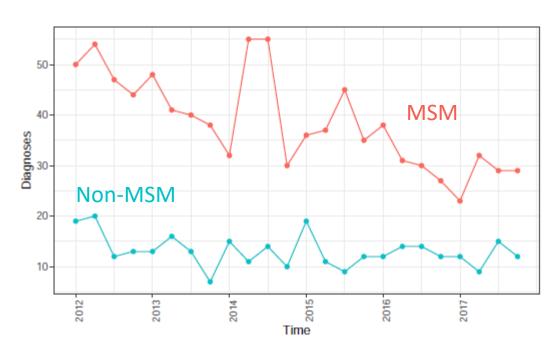
MODELS

- Modeling Heterosexual HIV transmission in isolation
 - Does not generate persistent epidemics for the US
 - Yet we do see a persistent epidemic...
- What could explain this?
 - Transmission within the Het population is below the epidemic threshold
 - Boundary dynamics with other risk groups must be represented

Key Boundary dynamics for KC (1)

Local MSM epidemic

HIV diagnoses in King County: 2011-2017



- Majority of our epidemic is MSM
- Good progress in "bending the curve"
- Uptick in 2017 may just be a blip, or not.

MSM – Heterosexual Boundary

- Several papers have shown evidence that there is substantial bridging across subpopulations
 - Based on phylogenetic clustering of HIV sequence data
- In the US: Oster et al. (2015)

"Of heterosexual women for whom we identified potential transmission partners,

- 29% were linked to MSM,
- 21% to heterosexual men
- a higher percentage of women in the West (52%) were linked to MSM"

Key boundary dynamics for KC (2)

Racial disparities, but with a specific local pattern

HIV Prevalence: 2016

| | Estimated HIV Prevalence/100K | |
|----------|-------------------------------|--|
| White | 314.2 | |
| Black | 1001.0 | |
| Hispanic | 434.6 | |

| US Born | Foreign Born |
|---------|--------------|
| 93% | 2% |
| 56% | 41% |
| 42% | 52% |

We see large racial disparities

With profound differences in country of origin by race

What this suggests

- Boundary transmissions need to be explicitly represented in our model of the local heterosexual population
- Prevention policy question:
 - Is Het HIV transmission in KC below the persistence threshold?
 - If so, would targeting the boundary(s) leverage impact?
- Model this specific, locally relevant policy question, using local data

The modeling framework

The framework is general

The structure and parameters are local

One slide background on modeling

Three basic types of modeling frameworks

- Deterministic compartmental models (DCMs)
 - The traditional approach -- most heavily used until very recently
 - Limited ability to represent partnerships
- Stochastic Individual-based or Agent-based models
 - Becoming more common
 - Limited ability to represent multiple network features
- Stochastic Network models
 - New firmly grounded in statistical estimation from data
 - Able to represent the "joint distribution" of multiple network features

Network modeling for epidemics

- The result of a long research program
 - Supported by 20+ years of NIH funding (which continues)
- Relies on statistical methods
 - For the network estimation and simulation
 - Specifically: Exponential family Random Graph Models (ERGMs)
- Designed to use very simple network data
 - "Egocentric" sampled network data
 - Implemented like a traditional cross sectional sample survey

Key components of our framework

- Transmission system
 - Dynamic partnership network
 - Multilayer: Cohab, Persistent and one-time partnerships
 - Behavior within partnerships
 - Transmission
 - Function of viral load/stage of infection
- Care continuum
 - Testing, treatment, viral suppression
- Demography
 - Aging
 - Travel
 - Entry/Exit

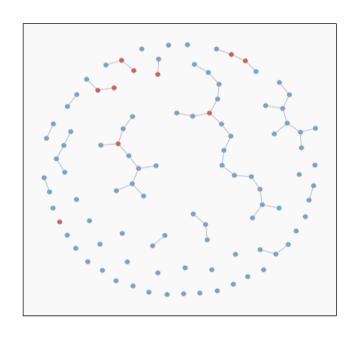
piMed 530 October 2018

statnet
software

EpiModel software

All software is open source, well documented and free

Dynamic network model(s)



Unique multi-network approach

Partnerships modeled with a separable temporal ERGM (STERGM)

- Formation model
- Dissolution model
- Estimated from egocentrically sampled data

3 different types of partnerships

- Cohabiting
- Persistent So three different STERGMs
- One-time

Transmission system components

Several processes are overlaid, and interact with the network

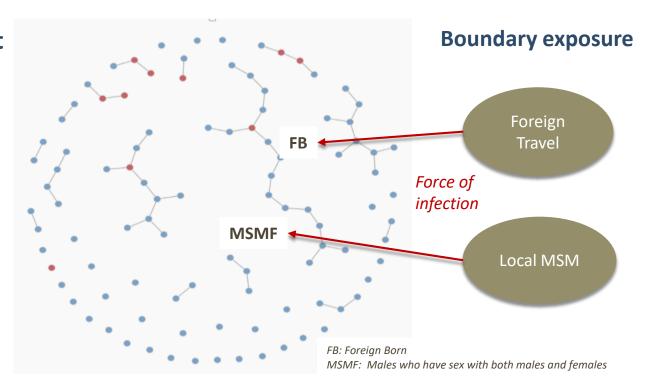
Within discordant partnerships:

Behavior

- Coital Frequency
- Condom Use

Infectivity, by

- Stage
- CC engagement
- Clinical outcome



Model implication: multiple subgroups

- Race / Immigration subgroups (5)
 - US and foreign-born Black
 - US and foreign-born Hispanic
 - Other (predominantly White and Asian)
- Sex / Sexual preference subgroups (3)
 - Female (F)
 - Males who have sex with females only (MSF)
 - Males who have sex with males and females (MSMF)
- And age...

Other model components

Engagement in Care

- HIV Testing (at sex and race-specific rates, some never test)
- Treatment with ARVs
- Adherence, with episodes of drop and return
- Viral Suppression (some fraction are not full suppressors)

Clinical progression after infection

- 4 stages (acute rise, acute fall, chronic, AIDS)
- Progression time: 6.4 wks, 3 wks, 10 yrs, 2 yrs
- Stage-specific viral load (influences infectivity)

Demography: Open population model

- Entry at 18, exit at 45
- Age and AIDS-specific mortality rates
- Travel for foreign born (pauses local sexual activity, activates boundary exposure)

Data sources

Free range, Locally sourced, ... when possible

Network data: What do we need?

- Sample: needs to be representative of KC population
 - Rules out convenience samples, clinic samples, surveillance data
- Quex items:
 - Respondents, minimally:
 - Race/imm group
 - Age
 - Sexually active (lifetime, last year)
 - Partner specific questions: minimally:
 - Partner attributes: Sex, race/imm, age
 - Cohab or not
 - Duration (dates of first and most recent sex)
 - Status (ongoing or not)
 - Sexual behavior (type and frequency of sex, condom use)
 - Ideally up to 3-5 most recent partners

Partner is not interviewed

Respondent gives the info

This is called "egocentrically sampled network data"

Model components and data

| Model Component | Governs: | Source |
|--|--|-----------------------------|
| Sexual network | Partnership formation/dissolution dynamics | Use the NSFG |
| Behavior within partnerships | Coital frequency, condom use, HIV status disclosure | USE THE NOTE |
| Natural history of within- host HIV infection | Viral load, CD4, symptoms and infectivity | Global Estimates |
| Clinical care cascade | Testing, referral, adherence, suppression | PHSKC HIV Core Surveillance |
| Demographics | Entries and Exits into the population (pop'n growth, mortality and in/out migration) | King County Census |

National Survey of Family Growth (NSFG)

- US Data on sexual behavior & networks (2006-15)
 - Representative national sample with annual surveys
 - Age 15-45
 - Egocentric data on last 3 heterosexual partners in last 12 mos
 - Partner attributes (age, race/immig, cohab, duration/once only, ongoing)
 - Behavior within partnerships
 - Sex of partners, lifetime and last year
 - HIV testing rates

Combined sample size: ~40K

- Reweighted by age, sex, race/immigration group
 - To match King County demographics

The respondents are not from KC

- So our sexual network, and our sexual behavior, will be based on data from a national sample.
 - Note: we are reweighting for demographic composition

- Does this matter?
- If so, how?

Local data on travel back to home country:

collected in public health interviews of new HIV diagnoses in KC

Yes No Unknown Refused If so, where?

IMMIGRATION HX

Were you born outside the U.S.? 99 77 Ð Ð Birthplace specify Birthplace 1 67. When did you move to the U.S.? moveus (MM/DD/YYYY) 68. Did you ever test for HIV prior to moving to the US? HEST before US (MM/DD/YYYY) D No 4 Unknown Refused Yes. Last tíme: test beforeus date 69. What was the result of that test? +est beforeus result-💠 Positive 🙎 Negative 🕱 Indeterminate 🙀 Unknown 📭 Refused 70. Have you been back to your home country/area since moving to the US? homecountryreturn Yes O No 99 Unknown 77 Refused nomecountryreturrsex 71. Did you have sex while back in your home area? 1) Yes () No 99 Unknown 37 Refused 72. Have you tested HIV negative since you last had sex in your home country? Neg Home Country Sex 1) Yes () No 99 Unknown 77 Refused 73. How many people have you had sex with since moving to the US? O Number: 99 Unknown 77 Refused sexparmersus

Added in 2010

But ... only for persons with newly diagnosed HIV

Local "Care Continuum" data

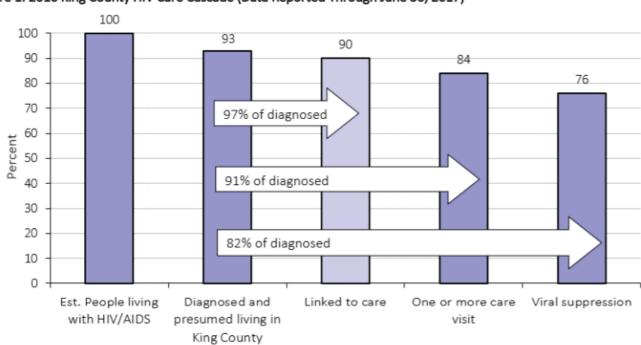


Figure 1: 2016 King County HIV Care Cascade (Data Reported Through June 30, 2017)

We use sex/race specific values

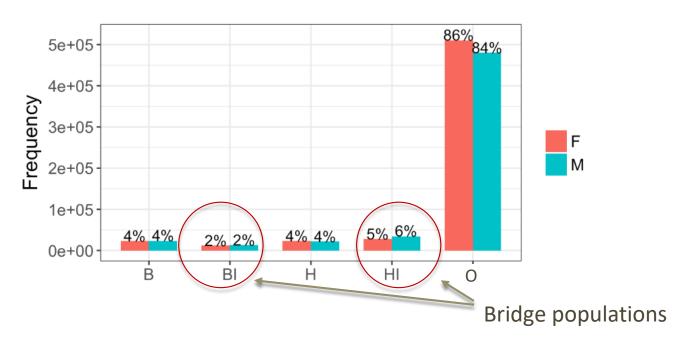
Some descriptive statistics

Population attributes

Partnership network patterns

KC Demographics by race/imm/sex

- King County is predominantly "Other": white (68%) and Asian (18%)
- About 14% of the population is Black or Hispanic
 - About half of those are foreign born



Sexual behavior and networks

All of these estimates are based on the NSFG survey

- Reweighted to KC demographics by the joint distribution of:
 - Age
 - Race
 - Sex

KC Sex Group estimates

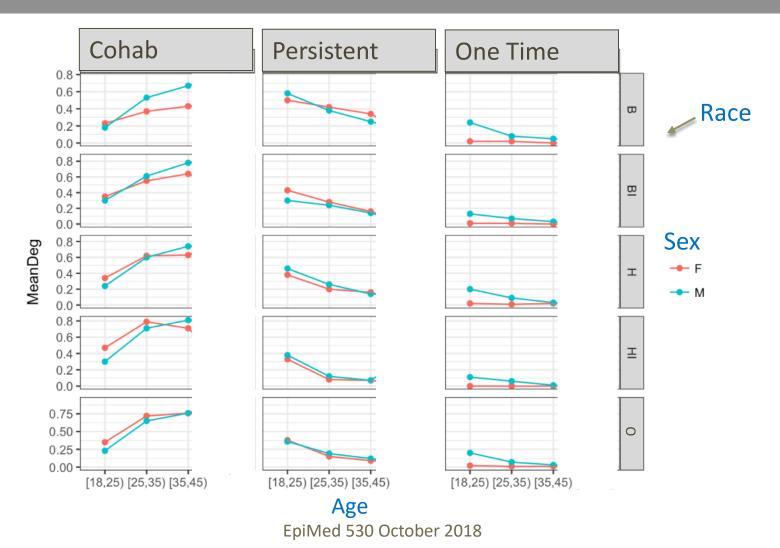
by age

About 1% of the population are MSMF

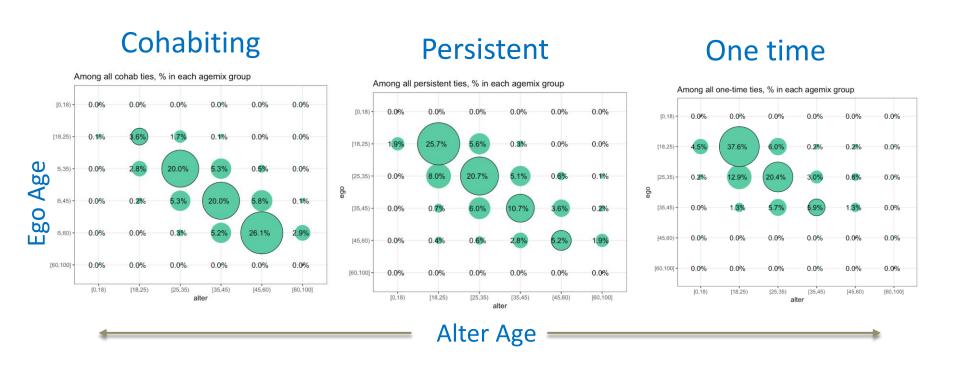


Partnership Type Prevalence

by Age, Sex, and Race



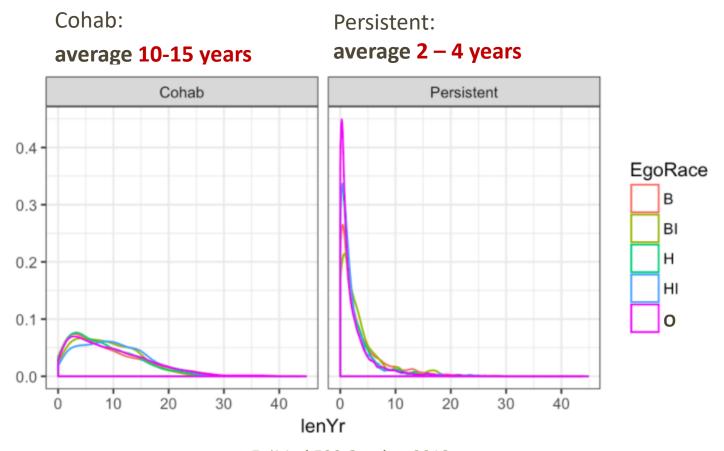
Age Mixing



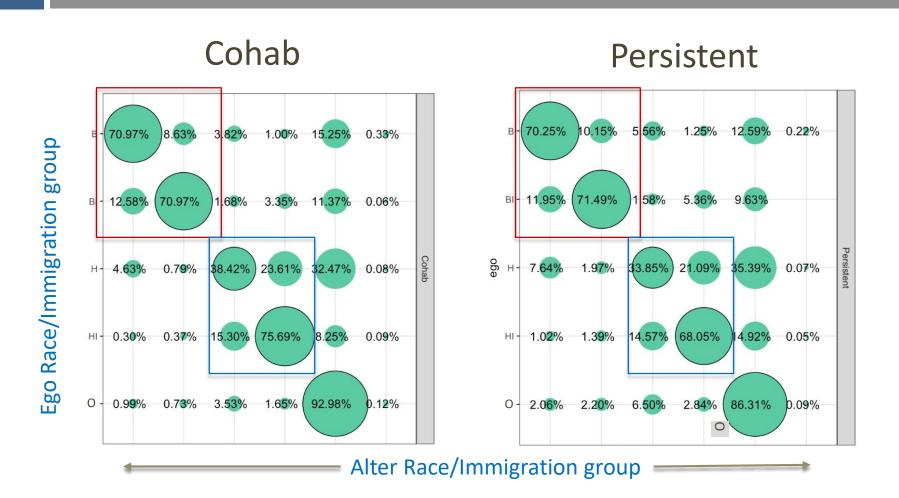
Strong age homophily for all types of partnerships

Partnership Durations: Cohab & Persistent by Race

AGE OF ACTIVE TIES



Mixing by Race/Immigration group



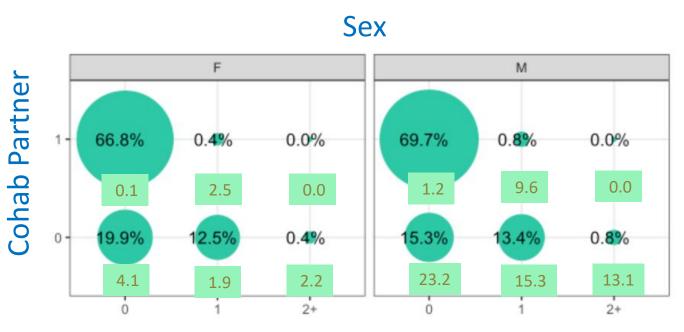
Overlapping partnerships

- Definition: When a person has more than one active sexual partnership at a time
 - Aka "concurrent partnerships"
 - Note: not the same as "multiple partners" in a specified time frame (6 mos, 12 mos, etc.)
 - And not the same as "effective concurrency," which is an incorrect term
- Has a powerful impact on network connectivity
 - Cross-sectionally: creates component sizes > 2
 - Longitudinally: increases the reachable path of infection
- And on transmission dynamics
 - Reduces the "generation interval" between transmissions
 - Allows for transmission back to partners that started earlier in time
 - Supports epidemic persistence even for less active populations

Overlapping partnership networks

On any day, a person can have none, or some of each partnership type

About 1-2% of the population has two or more concurrent partners on any day

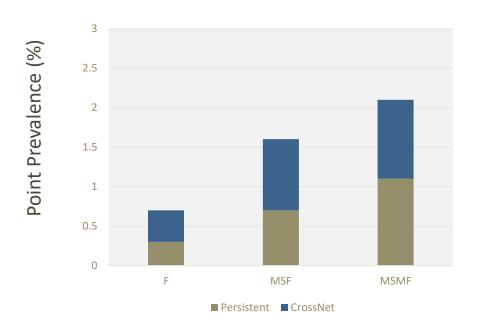


This is the "point prevalence"

> Rate of 1 time partners per 100 persons per year

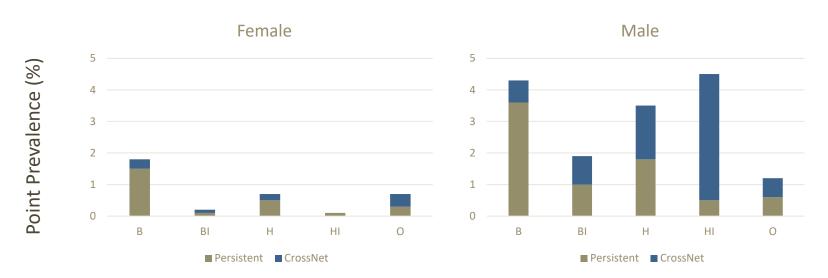
Persistent Partners

Concurrency by sex group



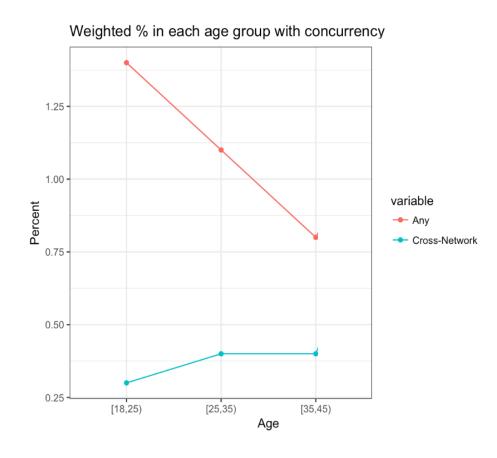
- Highest overall rates are in the bridge population: MSMF ~2%
 - About half of this is cross-network
- This is just the concurrency with opp sex partners
 - MSMF may also have a concurrent M partner (NSFG does not allow us to estimate this exactly; 65% have a male partner in the last year)
- Lowest overall rates are among women: ~0.5%

Concurrency by race/immigration group



- Highest rates are for Black, Hispanic and Hispanic immigrant men ~4%
 - Mostly multiple persistent partners for Black men
 - Mostly cross-network for Hispanic immigrants
 - Split equally for US born Hispanics
- Black women have slightly higher rates among females : ~2%

Concurrency: By age



- This is a young person's game
 - Highest rates for young men:3-7%
- The configuration changes with age too
 - The cross-network fraction rises, as rates of cohabitation rise

Boundary force of infection

Boundary Groups:

| | ВІ | HI | MSMF |
|---------------------------------|------------------------------|--------------------------|-----------------|
| Percent of population | 2.3% | 5.4% | 1.5% |
| Exposure probabilities | Depart: 0.01 Return: 0.25 | | 2.5 partners/yr |
| HIV acquisition probabilities * | F: 2.0e-04 M: 1.0e-04 | F: 2.0e-05 M: 9.9e-06 | 7.2e-06 |
| 1 | 141. 1.00 04 | 141. 5.50 00 | / |

^{*} The HIV acquisition probabilities are a function of several components, and determine the FOI at the boundary

For example for MSMF:

MSM prevalence x condom use (.304) x efficacy (cond.rr=.4) x P(transmission | contact) (((.0082*1.09)+(.0031*1.09))/2) x P(contact per week) (2.5/52)

That's a lot of numbers

Key message:

- The force of infection across these boundaries is low
 - small boundary populations
 - low sexual exposure rates
 - low probabilities of transmission
- Can such a small boundary dynamic have an impact?
 - ... we'll see

Network Model Results

Just a peek at the estimates, and assessing the validity of the simulations

These dynamic partnership network simulations are the foundation for the epidemic simulations

ERGM Formation model estimates

| | | Cohab | Pers | ОТ |
|---------------------|--------------------|--------------|--------------|---------------|
| Age | | -0.87 | -0.20 | -0.38 |
| Age ² | | 0.02 | 0.00 | 0.01 |
| sqrt(abs(Age Diff)) | | -3.22 | -2.59 | -2.40 |
| Race (main) | Black Black Imm | 1.10 1.14 | 1.14 1.61 | 0.42 -0.52 |
| | Hispanic | 3.17 | 2.00 | 0.52 |
| | Hisp Imm | 1.63 | 1.13 | -0.78 |
| Race (matching) | Black | 3.35 | 3.21 | |
| | Black Imm | 3.85 | 2.86 | |
| | Hispanic | 0.01 | 0.27 | |
| | Hisp Imm | 2.88 | 2.30 | |
| | Other | 3.14 | 2.17 | |
| Concurrency | Cross net | -5.96 | -4.36 | |
| | Within net | NA | -2.85 | |

N.S.

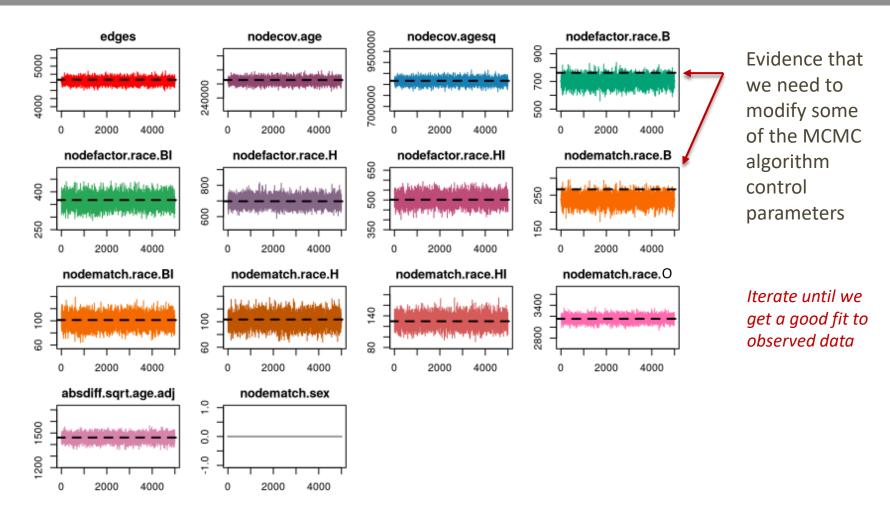
Model assessment: Network fidelity

- The dynamic simulations should reproduce the observed network statistics (on average)
 - Degree distributions (# of concurrent partners)
 - Within and between networks
 - By sex, age, race/imm
 - Mixing patterns
 - By age, race/imm
 - Partnership durations

ERGMS should be able to reproduce the joint distribution of all of the network statistics

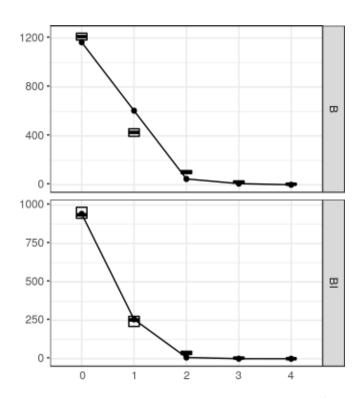
in each partnership network

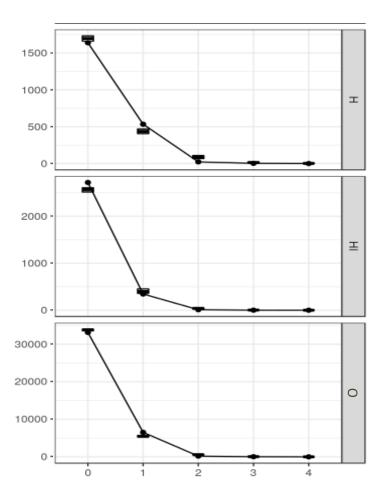
Example: Persistent network model stats



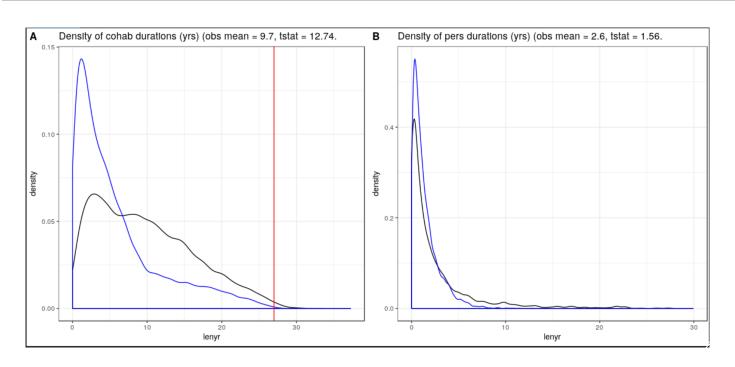
Example: Persistent degree by race

Good fit to observed, even though the degree terms are not in the model





Age of partnerships by type



Observed Simulated

Cohab duration distribution is not well fit yet

Persistent partner durations are ok, but not perfect

This is a more complex basic research issue that we are deferring to another project

Epidemic results

Now we can simulate the epidemic

On a network that we know represents the patterns in our observed network very well

... with the one exception of cohab duration

Simulation detail

- These results are from a network size of 50,000
 - Large by most standards
 - But still not big enough
 - The prevalence of HIV in KC is low -- ~0.07% overall
 - In a 50K simulation, very few prevalent cases: 50K * .07% = 36 cases
 - There is not much analysis we can do on this 😊
 - We have simulations running now on networks of size 800,000 (!)
 - Should generate about 600 prevalent cases each year
- Run for ~300 years
 - To "equilibrium"

Model calibration parameters

- All simulation models have calibration parameters
 - Parameters whose value is tweaked to obtain outputs that match observed targets
 - The choice of parameter, and observed target vary
 - Modelers often use sexual behavior parameters, with gross deviations from observed values
 - And many papers don't even report this...
- Calibration should be separated from validation
 - Using a different set of empirical targets
 - You can make a model fit almost any target with enough calibration parameters
 - That doesn't mean it is valid
 - First calibrate (to intermediate targets), then validate (to separate targets)
- Ideally: Use observed prevalence to validate, not calibrate

Our model calibration parameters

- This is a small feasibility project
 - So we will be calibrating to observed prevalence
 - To establish that this model can produce the observed KC prevalence profile
 - And will not be validating the model
- We have 3 calibration parameters
 - all related to transmission probability per act

So we didn't need to change this

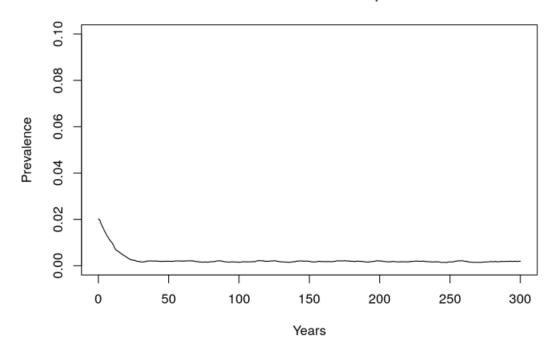
| Calibration Parameter | Controls | Target | Factor used | |
|-----------------------|-------------------------------|----------------------|----------------|---|
| Baseline infectivity | P(transmission) per act of VI | Overall prevalence | 1 | ~ |
| MSMF FOI | Weekly exposure rate | MSMF prevalence | 5 | |
| FB FOI | Weekly exposure rate | BI and HI prevalence | 10 | |

Rationale: Model calibration parameters

- Substantial uncertainty in the boundary FOI estimates
 - Both for the input parameters
 - MSMF prevalence and behavior based on national sample
 - Foreign travel data collected only on new diagnosed HIV cases
 - And the target values
 - MSMF HIV prevalence in KC is not estimated with precision
 - So calibration is justified
- There's a much longer discussion here ...
 - We have ideas for intermediate targets (phylogenetic analyses)
 - But not for this presentation

Persistence and equilibrium

Simulation Results: HIV prevalence

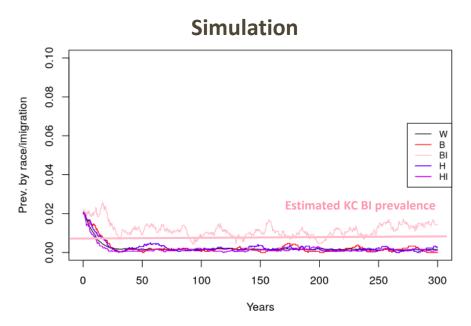


- 1. We get a persistent epidemic, overall
- 2. And equilibrium prevalence for Het+NIR is a bit above our target value:

Observed: 0.07%

• Simulated: 0.2%

Prevalence by race & immigration status

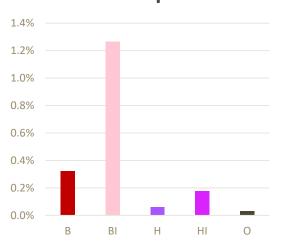


Here, the rank order is roughly correct

With the small group sizes the number of cases is very noisy

The FB prevalence is about right

Estimated KC prevalence

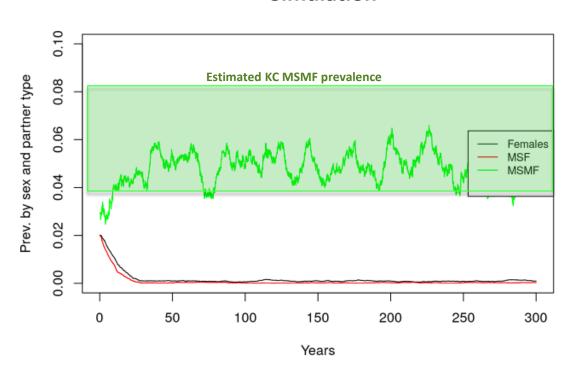


Source: Het+NIR special calculation from PHSKC

| | ВІ | HI |
|-----------|-------|-------|
| Observed | 1.3 % | 0.06% |
| Simulated | 1.5% | 0.10% |

Prevalence by sexual partner group

Simulation



Here the rank order is again correct

And the prevalence for MSMF is ... in the zone

Observed: ~4-8%

Simulated: 4.7%

There is *substantial* uncertainty in our target estimate of true MSMF prevalence in KC

Key question

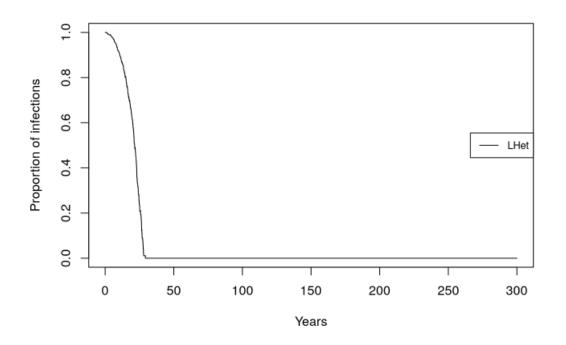
What is the impact of boundary transmissions on the Heterosexual HIV epidemic?

How we answer this:

- After the simulation run
- Break down all of the infections by source
 - Original seeds, and their downstream chain of transmissions
 - Boundary infections, and downstream chain of transmissions
 - MSMF boundary
 - Foreign boundary

Original seeds and downstream infections

Simulation Results: Fraction of PLHIV



No persistence

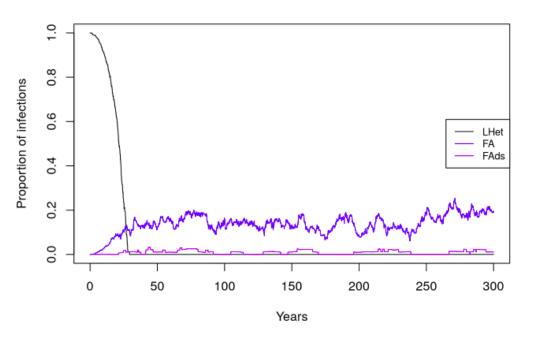
As a fraction of all infections

the number of cases in these chains decline steadily

and the epidemic goes extinct in about 30 years

Foreign boundary and downstream

Simulation Results: Fraction of PLHIV



Persistence

At equilibrium:

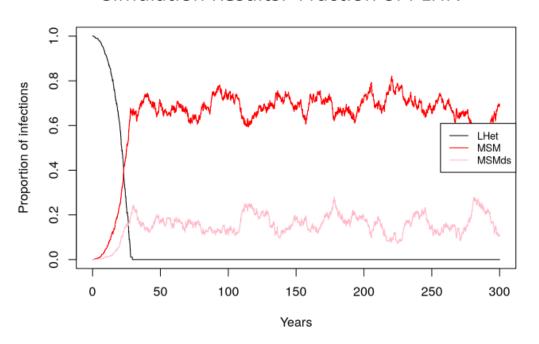
- Boundary infections: 15-20%
- Downstream infections: 1-2%

So, these chains also go extinct quickly

But new ones are always being started

MSMF boundary and downstream

Simulation Results: Fraction of PLHIV



Persistence

At equilibrium:

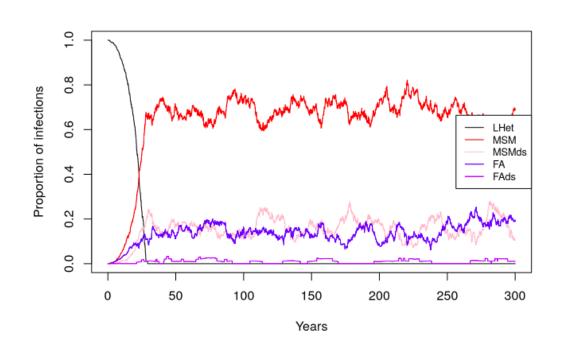
- Boundary infections: 60-70%
- Downstream infections: 10-20%

These chains also go extinct, but more slowly

And new ones are always being started

Summary

Simulation Results: Fraction of PLHIV



Persistence is due to boundary infection dynamics

The key boundary population is MSMF

No infection chains were longer than 3 generations

Implications for prevention

- HIV transmission within the local heterosexual population is below the persistence threshold in Seattle/King Co.
 - When infections cross over a bridge to this population, the chains die out pretty quickly
 - Contact tracing is important for treatment, but may have little impact on prevention
- Boundary infections are a strategic target for prevention
 - These are small, identifiable boundary risk groups
 - Effective tailored prevention here can have a large impact

Limitations

- These are preliminary results from a prototype model
 - We know they do not reproduce the observed epidemic yet
 - The model will need to be calibrated, using separate targets, in order to validate it
- The boundary with IDU is not represented
- The results should not be extrapolated to other locales
 - This is a feature, not a bug
 - The modeling framework is general
 - The empirical data inputs are local
 - So the model predictions are local

One final thought

- The political context of this type of science, and policy, must be explicitly acknowledged and articulated
- Care must be taken
 - Whenever we are talking about marginalized groups
 - The potential for harm is present when "targeting" prevention policy and resources
- To achieve any potential benefits in practice
 - The science-policy link must be approached holistically
 - The community stakeholders need to be at the table
 - And the modeling results are just a small part of that picture

Thank You

Modeling Examples

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- 3. Krivitsky PN, Morris M. Inference for social network models from egocentrically sampled data, with application to understanding persistent racial disparities in HIV prevalence in the US. *Annals of Applied Statistics*. 2017;11(1):427-55.

EpiModel software

Jenness SM, Goodreau SM, Morris M. EpiModel: An R Package for Mathematical Modeling of Infectious Disease over Networks. Journal of Statistical Software. 2018;84(8). doi: 10.18637/jss.v084.i08.

We teach a weeklong intensive workshop on Network Modeling for Epidemics every summer at the University of Washington: https://statnet.github.io/nme/

Examples of Network Modeling for HIV/STI

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- 4. Carnegie NB, Goodreau SM, Liu A, Vittinghoff E, Sanchez J, Lama JR, Buchbinder S. Targeting Pre- Exposure Prophylaxis Among Men Who Have Sex With Men in the United States and Peru: Partnership Types, Contact Rates, and Sexual Role. Jaids-Journal of Acquired Immune Deficiency Syndromes. 2015;69(1):119-25. doi: 10.1097/qai.000000000000555. PubMed PMID: WOS:000353033300023.
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Examples of Network Modeling for HIV / STI

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