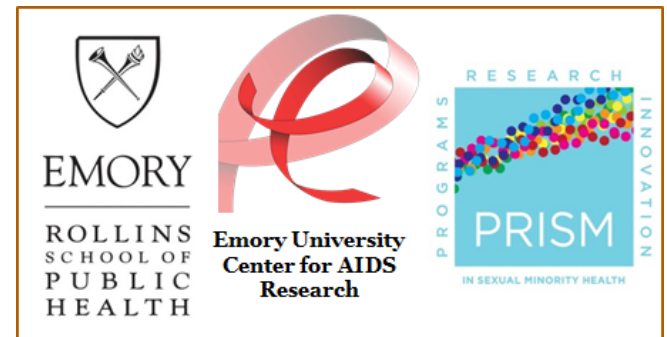


PARAMETERS II: BEHAVIORAL PARAMETERS

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Outline for this session

- Big-picture structural choices
- Behaviors within AI dyads
 - Disclosure of HIV statuses
 - Number of AI acts
 - Condom use
 - Intra-event versatility
- Few things not covered but in the appendix
- Implementating in the model

Big-picture structural choices

- Only behaviors (and HIV transmission) modeled within HIV serodiscordant dyads.
- Other relationships form/dissolve, but uninformative
- Order of evaluation in model is order of presentation
 - Disclosure of HIV statuses
 - Number of AI acts/roles
 - Condom use (conditional on above 2)
 - Intra-event versatility

Disclosure of HIV statuses

HIV status disclosure: concept

- HIV status disclosure (AKA: serodiscussion)
 - Traditionally, MSM living with HIV sharing status with sex partners
 - Also important for HIV-negative MSM to share statuses
 - Can happen at different points in relationship and by varied modalities (ie: conversation vs. online profile)
 - Many issues and stigmas reduce likelihood of disclosure
- Important pre-requisite to HIV risk reduction strategies:
 - Position
 - Condoms
 - PrEP
 - Have sex at all?

Start Talking. Stop HIV. is a campaign that seeks to reduce HIV infections among gay, bisexual, and other men who have sex with men by encouraging open discussion between sex partners and friends about a range of HIV prevention strategies.



Centers for Disease Control and Prevention
CDC 24/7: Saving Lives, Protecting People™

SEARCH



CDC A-Z INDEX ▾

Act Against AIDS



Language: English ▾



CONDOMS



Condoms are highly effective at preventing both HIV and other STDs.

PrEP



Pre-exposure prophylaxis (PrEP) can greatly reduce your risk of HIV.

HIV TESTING



Knowing your HIV status helps you choose options to stay healthy.

TREATMENT



HIV Treatment keeps you healthy and protects others.

HIV status disclosure: assessment

- We assessed at first and last sex. Used first sex:

if had sex "more than once" above:
Did you and [%%454:cur_partner_nam %%] share both of your HIV statuses before you first had sex?

if had sex "once" above:
Did you and [%%454:cur_partner_nam %%] share both of your HIV statuses before you had sex?

1 () Yes
0 () No
9 () Don't know
discussstatusfsP1 – P5

discussstatusfsP1

if yes then #222

222 *If 'yes' to discussing status:*
What was [%%454:cur_partner_nam %%]'s status at that time?

1 HIV-negative
0 HIV-positive
9 Don't know
statu: 1 – P5

statusfsP1

if pos or neg, then #223
if don't know, then #225

- In subsequent studies have made more complicated:
 - Source and recentness of HIV test results
 - ART and PrEP use of partners

HIV status disclosure: model metric

- Probability of disclosure of statuses in relationships of HIV+ egos

Probability of Disclosure of HIV+ Status	Black	White
to new main partner at outset of relationship	0.685	0.889
to new casual partner at outset of relationship	0.527	0.828
to one-time contact	0.445	0.691

- Note that this assumes self-awareness of HIV+ status (more to come on testing!)
 - Assumed that if a new diagnosis was made DURING existing relationship, then disclosure occurs at next time step with $p=1$

Number of AI acts

Number of AI acts: assessment

In the last six months, how many times have you had anal or oral sex with [%%454:cur_partner_nam %%]?

[Pull-down menu of choices:]

- 1 1
- 2 2
- 3 3
- 4 4
- 5 5
- 6 6
- 7 7
- 8 8
- 9 9
- 10 10
- 9 More than 10 (coded as 50)
- 10 *xfreqmpP1 – P5*

sexfreqmpP1

if 50, then #237

If "mc" 50 in 10 times"

237 About how often did you have anal or oral sex with [%%454:cur_partner_nam %%] in the last six months?

- 1 About once a month
- 2 2 or 3 times a month
- 3 About once a week
- 4 2 or 3 times a week
- 5 More than 3 times a week
- 5 *xfreqoftenmpP1 – P5*

sexfreqoftenp1

- For >10 acts, multiplied frequency response by relationship duration during recall period

Number of AI acts: model metric

- One-time partner = 1 😊
- Poisson rate parameter in model, estimated from Poisson regression model of dyads:
 - Y variable: number of acts
 - X variables: race combo, main/casual type
 - No interaction (equiv. to stratified analysis), given sparseness
 - Restricted to HIV+ egos with discordant (neg/unk) relationships

AI Acts/Week/Partnership	B-B Dyads	B-W Dyads	W-W Dyads
Main partnerships	1.19	1.79	1.56
Casual partnerships	0.75	1.13	0.98

Condom use

Condom use: concept

- Latex condoms have long been a pillar of HIV prevention
 - When used appropriately, highly effective (>>90%)
 - Real-world effectiveness lower
 - Errors in usage of condoms and lubricants
 - CDC estimate: 70% for MSM
- Use of condoms influenced by many things
 - Risk perceptions of unprotected sex
 - HIV/STI statuses of each partner and/or partner trust/monogamy
 - Sex positions
 - Emotions and pleasure
 - Norms
 - Substance use
 - Availability!

Condom use: assessment

- Used last-sex version of question

256 Did [%%454:cur_partner_nam %%] use a condom the last time you had receptive anal sex (when you were the bottom)?

- 1 [%%454:cur_partner_nam %%] did not use a condom 1
- 2 [%%454:cur_partner_nam %%] used a condom part of the time 2
- 3 [%%454:cur_partner_nam %%] used a condom the whole time 3
- 4 [%%454:cur_partner_nam %%] used a condom, but it broke 4
- 4 Don't know 9
- 9 *11IscondomP1 – P5*

RAIscondomP1

Condom use: analysis

- Analysis again considered only HIV+ partner in serodiscordant dyads (simplicity and accuracy of discordance)
- Logistic regression model considered predictors:
 - Race combo
 - Partnership type
 - Awareness of HIV+ status
 - Disclosure of HIV+ status
 - ~~■ Sex position (*not sig.*)~~
 - ~~■ Perceived relationship monogamy (*not sig.*)~~

Condom use: model metrics

- P(condom use) parametrized in model on logit scale
- For referent group of undiagnosed HIV+ partner (and thus no disclosure)

	B-B Dyads	B-W Dyads	W-W Dyads
Main partnership	-0.49	-2.20	-1.73
Casual partnership	-0.45	-2.09	-1.66
One-time contact	-0.04	-1.73	-1.27

- Additive factors

Condition	Coefficient
HIV+ diagnosis	0.67
HIV+ status disclosure	0.85

Intra-event versatility

Intra-event versatility: concept

- What happens when two versatile men have AI?
- Examined same earlier “last sex” act questions on overall versatility by race combo
 - BB: 42% have sex in both positions in 1 AI encounter
 - BW: 56%
 - WW: 49%
- And if they don't have IEV, who's in which position?
 - Originally was coin toss
 - “each man's probability of being the insertive partner equals his insertivity quotient divided by the sum of the two men's insertivity quotients.”

Few things not covered but in the
appendix

Not covered but in the appendix

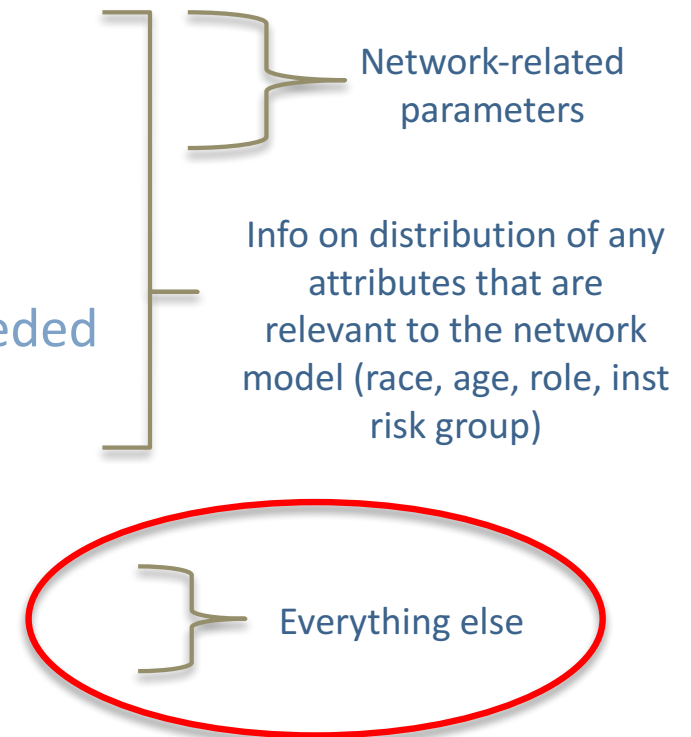
- Demography
 - Race distribution (50:50 B:W)
- Vital dynamics
 - Entry
 - All-cause mortality
 - Aging out

Implementation in the model!

Simulation

■ Steps:

- 1. Set (st)ergm formulas
- 2. Calculate target stats
- 3. Create initial network(s)
 - set of nodes and their attributes needed
 - ties *not* needed
- 4. Estimate model(s)
- 5. Do simulation



Simulation

```
help(package=  
  "EpiModelHIV")
```

Help Pages

EpiModelHIV-package	Modeling Approaches to Racial Disparities in HIV in Atlanta MSM in EpiModel
acts.mard	Sexual Acts Module
aging.mard	Aging Module
assign_degree	Assign Degree Vertex Attribute on Network Objects
base_nw.mard	Construct Base Network for Model Estimation and Simulation
births.mard	Births Module
calc_nwstats.mard	Calculate Target Statistics for Network Model Estimation
condoms.mard	Condom Use Module
control.mard	Epidemic Model Control Settings for MARDHAM Models
deaths.mard	Death Module
disclose.mard	Disclosure Module
edges_correct.mard	Adjustment for the Edges Coefficient with Changing Network Size
EpiModelHIV	Modeling Approaches to Racial Disparities in HIV in Atlanta MSM in EpiModel
est	Fitted Network Models for 200 Person Network
init.mard	Epidemic Model Initial Conditions for MARDHAM Models
InitErgmTerm.absdiffnodemix	Definition for absdiffnodemix ERGM Term
initialize.mard	Initialization Module
param.mard	Epidemic Model Parameters for MARDHAM Models
position.mard	Position Module
prep.mard	PrEP Module
prevalence.mard	Prevalence Calculations within Time Steps
progress.mard	Disease Progression Module
reinit.mard	Re-Initialization Module
simnet.mard	Network Resimulation Module
test.mard	HIV Testing Module
trans.mard	Transmission Module
tx.mard	Treatment Module
update_aiclass.mard	Update Role Class in One-Off Partnerships
update_degree	Update Degree Vertex Attribute on Network Objects
update_roleclass.mard	Update Role Class in Main and Casual Partnerships
update_vl.mard	Viral Load Module
verbose.mard	Verbose Module

Simulation

- **control.mard** indicates that all of the *.mard modules are to be used during the simulation (and in what order)
- **params.mard** includes defaults for all the model parameters that match Eli's values
- **init.mard** sets the network up with default population sizes and HIV prevalence values.

Vital dynamics

- param.mard:

```
part.suppl.down.slope = 0.25, part.suppl.up.slope = 0.25, part.suppl.down  
part.suppl.up.slope = 0.25, b.B.rate = 0.001/7, b.W.rate = 0.001/7,  
birth.age = 18, b.method = "fixed", URAI.prob = 0.0082 *  
1.09, UIAI.prob = 0.0031 * 1.09, acute.rr = 4, circ.rr = 0.4,
```

- birth.mard:

```
nBirths.B <- rpois(1, b.B.rate * numB)  
nBirths.W <- rpois(1, b.W.rate * numW)  
nBirths <- nBirths.B + nBirths.W
```

“Birth” rates

- param.mard:

```
part.suppl.down.slope = 0.25, part.suppl.up.slope = 0.25, part.suppl.down  
part.suppl.up.slope = 0.25, b.B.rate = 0.001/7, b.W.rate = 0.001/7,  
birth.age = 18, b.method = "fixed", URAI.prob = 0.0082 *  
1.09, UIAI.prob = 0.0031 * 1.09, acute.rr = 4, circ.rr = 0.4,
```

- birth.mard:

```
nBirths.B <- rpois(1, b.B.rate * numB)  
nBirths.W <- rpois(1, b.W.rate * numW)  
nBirths <- nBirths.B + nBirths.W
```

Death rates and aging out

- All the way back in the d4_calc_target_stats file:

```
3 ages <- 18:39
4 asmr.B <- c(rep(0, 17),
5             1 - (1 - c(rep(0.00159, 7),
6                       rep(0.00225, 10),
7                       rep(0.00348, 5)))) ^ (1/(365/time.unit)),
8             1)
9 |
0 asmr.W <- c(rep(0, 17),
1             1 - (1 - c(rep(0.00103, 7),
2                       rep(0.00133, 10),
3                       rep(0.00214, 5)))) ^ (1/(365/time.unit)),
4             1)
5
```

- Why?
- deaths.mard:

```
death.B.prob <- dat$param$asmr.B[age.B]
deaths.B <- alive.B[rbinom(length(death.B.prob), 1, death.B.prob) ==
1]
```

Disclosure

- param.mard:

```
condom.rr = 0.25, disc.outset.main.B.prob = 0.685, disc.outset.main.W.prob = 0
889,
disc.at.diag.main.B.prob = 1, disc.at.diag.main.W.prob = 1,
disc.post.diag.main.B.prob = 0, disc.post.diag.main.W.prob = 0,
disc.outset.pers.B.prob = 0.527, disc.outset.pers.W.prob = 0.828,
disc.at.diag.pers.B.prob = 1, disc.at.diag.pers.W.prob = 1,
disc.post.diag.pers.B.prob = 0, disc.post.diag.pers.W.prob = 0,
disc.inst.B.prob = 0.445, disc.inst.W.prob = 0.691, circ.B.prob = 0.874,
circ.W.prob = 0.918, ccr5.B.prob = c(0, 0.034), ccr5.W.prob = c(0.021,
```

- discl.mard:

```
diag.status <- dat$attr$diag.status
diag.time <- dat$attr$diag.time
race <- dat$attr$race
if (type == "main") {
  disc.outset.B.prob <- dat$param$disc.outset.main.B.prob
  disc.at.diag.B.prob <- dat$param$disc.at.diag.main.B.prob
  disc.post.diag.B.prob <- dat$param$disc.post.diag.main.B.prob
}
discl <- which(rbinom(length(d1.prob), 1, d1.prob) ==
  1)
if (length(discl) > 0) {
```

AI acts (for discordant pairs)

- param.mard:

```
base.ai.main.BB.rate = 1.19/7, base.ai.main.BW.rate = 1.79/7,  
base.ai.main.WW.rate = 1.56/7, base.ai.pers.BB.rate = 0.75/7,  
base.ai.pers.BW.rate = 1.13/7, base.ai.pers.WW.rate = 0.98/7,  
ai.full.supp.main.rr = 1, ai.part.supp.main.rr = 1, ai.diag.main.rr = 1,  
ai.disc1.main.rr = 1, ai.full.supp.pers.rr = 1, ai.part.supp.pers.rr = 1,  
ai.diag.pers.rr = 1, ai.disc1.pers.rr = 1, cond.main.BB.prob = 0.38,  
cond.main.BW.prob = 0.1, cond.main.WW.prob = 0.15, cond.pers.BB.prob = 0.20
```

- acts.mard:

AI acts (for discordant pairs)

- acts.mard:

```
disc.el <- rbind(disc.el, el[status[el[, 2]] - status[el[,
  1]] == 1, 2:1, drop = FALSE])
if (nrow(disc.el) > 0) {
  ai.rate <- rep(NA, dim(disc.el)[1])
  race.1 <- race[disc.el[, 1]]
  race.2 <- race[disc.el[, 2]]
  num.B <- (race.1 == "B") + (race.2 == "B")
  ai.rate <- (num.B == 2) * base.ai.BB.rate + (num.B ==
    1) * base.ai.BW.rate + (num.B == 0) * base.ai.WW.rate
  pos.diag <- diag.status[disc.el[, 1]]
  pos.tx <- tx.status[disc.el[, 1]]
  pos.tt.traj <- tt.traj[disc.el[, 1]]
  dlist <- dat$temp$dlist
  disclosed <- sapply(1:nrow(disc.el), function(x) {
    length(intersect(which(uid[disc.el[x, 1]] ==
      dlist$pos), which(uid[disc.el[x, 2]] == dlist$neg))) !=
    0
  })
  ai.rate[pos.diag == 1] <- ai.rate[pos.diag == 1] *
    ai.diag.rr
  ai.rate[disclosed == TRUE] <- ai.rate[disclosed ==
    TRUE] * ai.disc1.rr
  ai.rate[pos.tx == 1 & pos.tt.traj == "YF"] <- ai.rate[pos.tx ==
    1 & pos.tt.traj == "YF"] * ai.full.sup.rr
  ai.rate[pos.tx == 1 & pos.tt.traj == "YP"] <- ai.rate[pos.tx ==
    1 & pos.tt.traj == "YP"] * ai.part.sup.rr
  if (fixed == FALSE) {
    ai <- rpois(length(ai.rate), ai.rate)
  }
}
```

Condom use (for disc. pairs)

- param.mard:

```
ai.disc1.main.rr = 1, ai.full.supp.pers.rr = 1, ai.parc.supp.pers.rr = 1,  
ai.diag.pers.rr = 1, ai.disc1.pers.rr = 1, cond.main.BB.prob = 0.38,  
cond.main.BW.prob = 0.1, cond.main.WW.prob = 0.15, cond.pers.BB.prob = 0.39,  
cond.pers.BW.prob = 0.11, cond.pers.WW.prob = 0.16, cond.inst.BB.prob = 0.49,  
cond.inst.BW.prob = 0.15, cond.inst.WW.prob = 0.22, cond.fsupp.main.beta = 0,  
cond.psupp.main.beta = 0, cond.diag.main.beta = -0.67, cond.disc1.main.beta = -0.85,  
cond.fsupp.pers.beta = 0, cond.psupp.pers.beta = 0, cond.diag.pers.beta = -0.67,  
cond.disc1.pers.beta = -0.85, cond.fsupp.inst.beta = 0, cond.psupp.inst.beta = 0,  
cond.diag.inst.beta = -0.67, cond.disc1.inst.beta = -0.85,  
cond.fsupp.main.prob = 0.42, cond.psupp.main.prob = 0.56, cond.inst.main.prob = 0.48,
```

- condoms.mard:

Condom use (for disc. pairs)

- condoms.mard:

```
if (nrow(da1) > 0) {
  cond.prob <- rep(NA, dim(da1)[1])
}
race.1 <- race[da1[, 1]]
race.2 <- race[da1[, 2]]
num.B <- (race.1 == "B") + (race.2 == "B")
cond.prob <- (num.B == 2) * cond.BB.prob + (num.B ==
  1) * cond.BW.prob + (num.B == 0) * cond.WW.prob
uai.prob <- 1 - cond.prob
uai.logodds <- log(uai.prob/(1 - uai.prob))
pos.diag <- diag.status[da1[, 1]]
dlist <- dat$temp$disc1.list
disc1 <- sapply(1:nrow(da1), function(x) {
  sum(dlist$pos == uid[da1[x, 1]] & dlist$neg == uid[da1[x,
    2]]) > 0
})
pos.tx <- tx.status[da1[, 1]]
pos.tt.traj <- tt.traj[da1[, 1]]
isDx <- which(pos.diag == 1)
uai.logodds[isDx] <- uai.logodds[isDx] + diag.beta
isDisc <- which(disc1 == 1)
uai.logodds[isDisc] <- uai.logodds[isDisc] + disc1.beta
isFS <- which(pos.tx == 1 & pos.tt.traj == "YF")
uai.logodds[isFS] <- uai.logodds[isFS] + fsupp.beta
```


Role selection and intra-event versatility

- Note: role preference was assigned all the way back in the d4_calc_target_stats file. Why?
- param.mard:

```
vv.iev.BB.prob = 0.42, vv.iev.BW.prob = 0.56, vv.iev.WW.prob = 0.49,
```

- position.mard:

```
dal$ins[neg.role.class == "K"] <- "P"  
vv <- which(pos.role.class == "V" & neg.role.class == "V")  
vv.race.combo <- paste0(race[dal$pos[vv]], race[dal$neg[vv]])  
vv.race.combo[vv.race.combo == "WB"] <- "BW"  
vv.iev.prob <- (vv.race.combo == "BB") * vv.iev.BB.prob +  
  (vv.race.combo == "BW") * vv.iev.BW.prob + (vv.race.combo ==  
  "WW") * vv.iev.WW.prob  
iev <- rbinom(length(vv), 1, vv.iev.prob)  
dal$ins[vv[iev == 1]] <- "B"  
vv.remaining <- vv[iev == 0]  
inspos.prob <- ins.quot[dal$pos[vv.remaining]] / (ins.quot[dal$pos[vv.remaining]] +  
  ins.quot[dal$neg[vv.remaining]])  
inspos <- rbinom(length(vv.remaining), 1, inspos.prob)  
dal$ins[vv.remaining[inspos == 1]] <- "P"  
dal$ins[vv.remaining[inspos == 0]] <- "N"
```