

PARAMETERS I: MSM NETWORK STATISTICS

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Outline for this session

- Big-picture structural choices
- Network parameters
 - Mean degree
 - Relational duration
 - Expected 1x AI contacts
 - Heterogeneity in 1x AI contacts
 - Race mixing
 - Age mixing
 - Role mixing
- Putting this all together: Network implementation in EpiModelHIV

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

Guiding network structural issues

- Two-racial groups
 - Most parameters separately specified by race
 - Dyadic attributes by “race combination”: BB, BW, WW
- Three-network model
 - Main
 - Casual, but with duration
 - One-time casual
- Anal intercourse contacts only
 - Most relevant for HIV, many STI
 - Pharyngeal STI requires reparameterization, model changes

Definition of partner types

Please tell us a little about you and [%%454:cur_partner_nam %%]

Did you have sex with [%%454:cur_partner_nam %%] once, or more than once during the last 6 months?

0 () Once
1 () More than once
REQUIRED

if once=#216
if more than once=#214

morethanonceP1

If 'more than once', then ask: (one-time partners automatically casual)

214 Is/was [%%454:cur_partner_nam %%] someone that you feel or felt committed to above all others (someone you might call your boyfriend, significant other, life partner, or husband)?

0 () Yes
1 () No
9 () Don't know
REQUIRED

if #95,#97,#99,#101=yes, then #215
if #95,#97,#99,#101=no or 9, then #216

mainP1

- If morethanonce = 0 → one-time
- Else
 - If main = 1 → main
 - If main = (0, 9) → casual

General formula for this presentation

1. What concept is / how conceptualized in model
2. How measured in questionnaire
3. How analyzed for model parameterization
4. How incorporated into model code

Mean degree

Mean degree

- Momentary degree determined from dyadic question:

Do you think you will have sex with [%%454:cur_partner_nam %%] again?

1 Yes
0 No
9 Not sure

ongoingP1 – P5

ongoingp1

Mean degree

- Matrix of ego frequencies of being in relationships with #'s of main and persistent casual partners
- Originally considered more levels of partner count

	Black				White		
	0 Casual	1 Casual	2+ Casual		0 Casual	1 Casual	2+ Casual
0 Main	50.6%	15.1%	5.3%		43.5%	18.4%	9.5%
1 Main	20.7%	6.1%	2.2%		23.3%	3.3%	2.0%

Relational duration

Relational duration concepts

- Mind-blowing principle
 - Expected uncensored duration of relationship = age of relationship at any moment in time
 - Due to balancing effects of right-censoring and length bias for exponential distribution.
- So we need to measure the ages of ongoing relationships:
 - (Last sex date – first sex date)
 - These are often really messy and full of logical errors, necessitating good surveys and analysis decisions

Relational duration: First sex

*[If had sex "more than once", then the participant next completes the sections pertaining to dates of first and last sex].
[If had sex "once", then the participant is skipped to the "Ongoing relationship" section"]*

=====
Date of first sex: #1
=====

76. When did you first have sex with [%%454:cur_partner_nam %%]?

You may enter just the month and year, but if you know the exact date, please enter that instead.

If you are unsure of when you first had sex, try to select a time that you think is close.

It is OK if you first had sex with [%%454:cur_partner_nam %%] longer than 6 months ago; we still would like to know when you first had sex.

firstsexmoP1

225

(drop-down box with months. "don't know the month" is provided as option) **firstsexmoP1**

226

(drop-down box with years) "don't know the year" is provided as option) **firstsexyrP1** **firstsexyrp1**

OR

227

MM/DD/YYYY (calendar button) **firstsexdtP1**

firstsexdtP1

[ERROR: The time you first had sex with [%%454:cur_partner_nam %%] cannot be in the future. Please correct the date.]

[ERROR: Please select either the month and year OR the date you first had sex with [%%454:cur_partner_nam %%]]

if don't know then #228,#229

Relational duration: First sex

Completed only for non-one-time partners

=====

Date of first sex – unknown month or year: #1

=====

228 *if year is selected as "don't know the year"*

firstsexyearsP1

It's OK if you can't remember the exact year.

Can you remember about how many years ago you first had sex with [%%454:cur_partner_nam %%]?

- 1 Less than 1 year ago
- 2 1 – 2 years ago
- 3 2 – 5 years ago
- 4 5 – 10 years ago
- 5 more than 10 years ago

firstsexyearsP1 – P5
(REQ)

229 *if month is selected as "don't know the month" (but year is known)*

It's OK if you can't remember the exact month.

Think back to the time in [Year of first sex] when you first had sex with [%%454:cur_partner_nam %%].

Perhaps you had sex around a special time of the year such as your birthday, or a holiday like July 4th or Halloween. Maybe you can remember that it was warm outside or it was after a trip you took.

Based on what you can recall, try to select what time during [Year of first sex] you first had sex with [%%454:cur_partner_nam %%]:

- 1 January - March
- 2 April - June
- 3 July - September
- 4 October - December
- 9 (don't know when during the year)

firstsexmonthsP1

[ERROR: The time during the year you indicated for when you first had sex with [%%454:cur_partner_nam %%] is in the future. Please correct this.]

firstsexmonthsP1 – P5
(REQ)

Relational duration: Last sex

Completed only for non-one-time partners

=====

Date of last sex: #1

=====

Month of last sex is captured from partnership calendar in a hidden variable.

0 Earlier, you indicated that you last had sex with [%%454:cur_partner_nam %] in the month of [month of last sex from calendar]. Is this correct?

1 Yes

0 No

lastsexmocorrectP1

if no then #234

lastsexmocorrectP1 – P5
(REQ)

231 If 'Yes'

Do you know the exact date on which you last had sex with [%%454:cur_partner_nam %]?

1 Yes

0 No

if yes then #232

if no then #233

lastsexknowdtP1

lastsexknowdtP1 – P5
(REQ)

232

If 'Yes'

Please enter the date:

MM/DD/YYYY (calendar button)

lastsexdtP1 – P5
(REQ)

lastsexdtP1

If 'No'

That's OK. The information that you have provided us with is still extremely helpful.

End of page. Participant clicks 'Next'

One-time AI contacts

Expected Number of One-Time AI Contacts, by Main/Casual Degree

- Conceptualized as weekly probability of AI contact
- Likelihood of 1x AI contacts varies by other, ongoing relationships
- Analysis
 - $(\text{Proportion of dyads that are one-time}) * (\text{total partners in 6 months}) / 25.7$
 - Accounts for capped number of dyads queried (5 or 10) and discrepancies between dyadic and NHBS total partner responses

Expected Number of One-Time AI Contacts, by Main/Casual Degree

- Per-week one-time AI contact rates:

	Black				White		
	0 Casual	1 Casual	2+ Casual		0 Casual	1 Casual	2+ Casual
0 Main	0.073	0.091	0.080		0.057	0.084	0.091
1 Main	0.055	0.052	0.052		0.057	0.058	0.058

Heterogeneity in the One-Time Contact Rate

- Given momentary degree, still did not want one-time contact rate to be uniform.
- Wanted underlying high/low risk phenotypes to facilitate meaningful intervention questions
- Solution (based on PUMA) = quintiles of “risk” that are fixed ego attributes
- Analysis:
 - For each race, examine the overall distribution in AI contact rate

Heterogeneity in the One-Time Contact Rate

■ Analysis:

- For each race, examine the overall distribution in AI contact rate

Quintile	Black	White
Lowest quintile	0.000	0.000
Second quintile	0.010	0.003
Third quintile	0.039	0.036
Fourth quintile	0.074	0.068
Highest quintile	0.212	0.231

- Note! DF warning! Mean degree matrix crossed with mean one-time matrix above yields mean of this “quintile” matrix

Race mixing

Race mixing: concept

- Racial homophily (AKA: assortativity)
 - Tendency to select partners of same race
 - Determinant of “flow” of infection between communities
 - Key issue for models of HIV/STI disparities
- Also forms basis for narratives regarding source/continuation of racial HIV disparities
 - Higher incidence in BMSM community driven by homophilous relationships in high-prevalence community

Race mixing: assessment

- Dyadic question about participant's perception of partner race/ethnicity
- Mixing matrix is common way to summarize the proportion of one group “mixing” with another

	Black	White	Hispanic	Other
Black	X%	X%	X%	X%
White	X%	X%	X%	X%
Hispanic	X%	X%	X%	X%
Other	X%	X%	X%	X%

- Because 2-race model, restricted calculations among just B/W and separately calculated for 3 partner types

Race mixing: parameter estimates

- Proportion of “same-race” partnerships among:

	Black	White	Reconciled
Main partnerships	94.8%	91.5%	93%
Casual partnerships	90.2%	85.1%	88%
One-time contacts	90.9%	89.4%	90%

- Need same B&W assortativity estimates, given 2 groups
- Reconciled estimates ensured number of cross-race (BW) dyads are balanced given degree/durations for each race

Age mixing

Age mixing: concept

- Age homophily/assortativity also important for understanding flow of infection (from typically older partners to younger)
- Also forms basis for narratives regarding source/continuation of racial HIV disparities
 - Higher incidence in BMSM community driven by tendency for greater age disparities in relationships with older partners more likely to be HIV+.
 - See Grey et al PLOS One 2015 for strong refutation of this using empirical study data

Age mixing: assessment

202 What is [%%454:cur_partner_nam %]'s current age?

(if you are unsure of the exact age, choose an age that you think is close)

agep1

if #202=don't know then #203

If "don't know"

203 Which of the following statements about [%%454:cur_partner_nam %]'s age is most true?

- 1 He or she is more than 10 years <u>younger</u> than I am
- 2 He or she is 2-10 years <u>younger</u> than I am
- 3 He or she is within a year of my age
- 4 He or she is 2-10 years <u>older</u> than I am
- 5 He or she is more than 10 years <u>older</u> than I am
- 9 Don't know

agestatementp1

- If we were unsure of exact partner age, use the smallest value of the range responses

Age mixing: metrics for model

- Simple, single parameter representation within partner type * race combo
- Mean of absolute difference in square root of each dyad members' race
- Example: relationship between a 23-year-old and a 28-year-old would represent $|\sqrt{23} - \sqrt{28}| = 0.96$.

	B-B Dyads	B-W Dyads	W-W Dyads
Main partnerships	0.417	0.454	0.520
Casual partnerships	0.498	0.629	0.632
One-time contacts	0.456	0.585	0.590

Role mixing

Sex role mixing: concept

- Men have preferences of AI sex role (position):
 - Exclusively insertive (top)
 - Exclusively receptive (bottom) [2.6x HIV acquisition in model]
 - Versatile may be either. And maybe within sex event... stay tuned)
- Model perspective:
 - Men exclusively of same role cannot partner
 - Assumed immutable ego attribute
- Role versatility shown to be important co-factor for increased HIV/STI transmission among MSM, relative to exclusively two-mode sexual networks (hetero M/F)
 - Increases network density
 - Infection less likely to be “stuck” within person infected receptively²⁹

Sex role mixing: assessment

- What I wished we had asked:
 - A cumulative assessment of sex roles during the recall periods
 - Self-described label: “I’m always a top”
- What we did ask: sex role at last sex

255	The last time you had sex with [%%454:cur_partner_nam %%], did you have receptive anal sex? (This means that you were the bottom)
1 Yes	RAIIIsP1
0 No	
9 Don't know	
IIsP1 – P5	
258	The last time you had sex with [%%454:cur_partner_nam %%], did you have insertive anal sex? (This means that you were the top).
1 Yes	IAIIsP1
0 No	
9 Don't know	
IIsP1 – P5	

Sex role mixing: metric for model

- Classified person's role based on sex acts at last sex with each of their partners

	Black	White
Exclusively insertive	24.2%	22.8%
Versatile	43.7%	54.4%
Exclusively receptive	32.1%	22.8%

**Putting this all together: Network
implementation in EpiModelHIV**

EpiModelHIV branches

GitHub - statnet/EpiModelHIV

statnet / EpiModelHIV

467 commits 8 branches 4 releases 5 contributors GPL-3.0

Branch: master New pull request Find file Clone or download

Switch branches/tags

MSM-race-disparities

PrEPsens

cfarc

hivTP

master

prep-sti

syph_ept

commit	message	time
9e47fb4	Latest commit	6 days ago
	documentation	2 months ago
	built-in data to include est and st	a year ago
	e merge	5 months ago
	cs	2 months ago
	RcppExports.cpp	2 months ago
	e merge	5 months ago
	LICENSE.md from build	6 days ago
	gitignore	2 months ago
	vis integration to slack	6 days ago
	documentation	2 months ago
	Create LICENSE.md	6 days ago

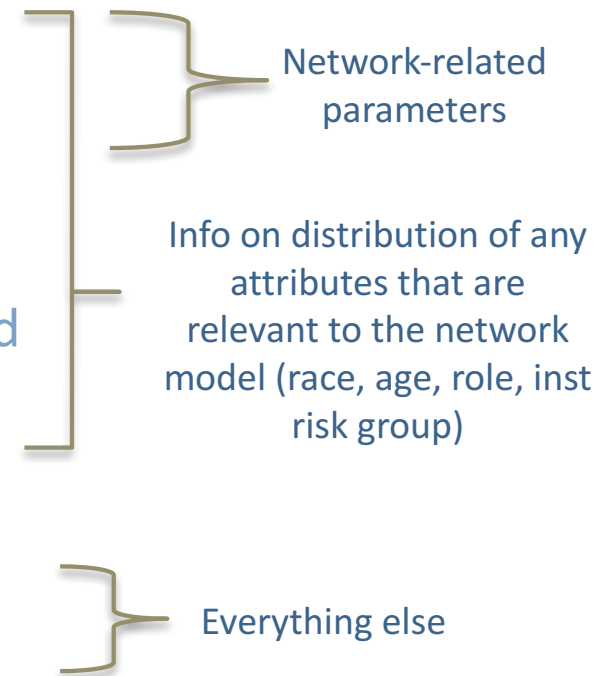
Getting the branch et al.

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

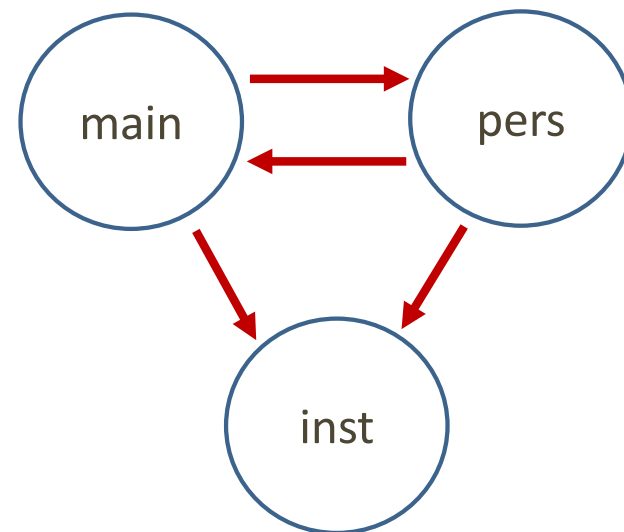
library(EpiModelHIV)
```

■ 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



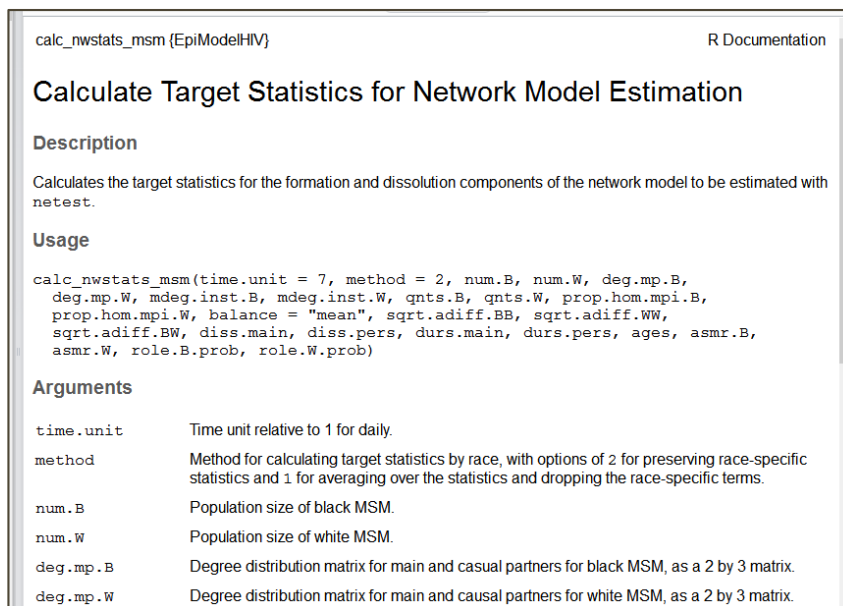
- Networks speak to each other:



- To do this:
 - Nodes possess a dynamic attribute indicating their race and current # of main partners (e.g. “B1”)
 - Nodes possess a dynamic attribute indicating their race and current # of pers. partners (e.g. “W0”)

Network estimation

- need to go from Eli's analysis to target stats for the specified ERGM models
- `calc_nwstats_msm` does this for us

A screenshot of the R Documentation page for the function `calc_nwstats_msm` from the `EpiModelHIV` package. The page is titled "Calculate Target Statistics for Network Model Estimation". It includes a "Description" section stating that it calculates target statistics for network model estimation using `netest`. The "Usage" section shows the function signature: `calc_nwstats_msm(time.unit = 7, method = 2, num.B, num.W, deg.mp.B, deg.mp.W, mdeg.inst.B, mdeg.inst.W, qnts.B, qnts.W, prop.hom.mpi.B, prop.hom.mpi.W, balance = "mean", sqrt.adiff.BB, sqrt.adiff.WW, sqrt.adiff.BW, diss.main, diss.pers, durs.main, durs.pers, ages, asmr.B, asmr.W, role.B.prob, role.W.prob)`. The "Arguments" section lists the parameters: `time.unit` (Time unit relative to 1 for daily), `method` (Method for calculating target statistics by race, with options of 2 for preserving race-specific statistics and 1 for averaging over the statistics and dropping the race-specific terms), `num.B` (Population size of black MSM), `num.W` (Population size of white MSM), `deg.mp.B` (Degree distribution matrix for main and casual partners for black MSM, as a 2 by 3 matrix), and `deg.mp.W` (Degree distribution matrix for main and casual partners for white MSM, as a 2 by 3 matrix).

- `d4-calc_target_stats.R` has code to call `calc_nwstats_msm` with params
- here we will walk through logic

- d4-calc_target_stats.R:

```
# Population size by race
num.B <- 5000
num.W <- 5000

# mean/pers degree distributions matrices.
deg.mp.B <- matrix(c(0.506, 0.151, 0.053, 0.207, 0.061, 0.022), byrow=2, nrow=2)
deg.mp.W <- matrix(c(0.435, 0.184, 0.095, 0.233, 0.033, 0.020), byrow=2, nrow=2)

# Revised rates
mddeg.inst.B <- matrix(c(0.010402, 0.012954, 0.011485, 0.007912, 0.007424, 0.007424), by
mddeg.inst.W <- matrix(c(0.008186, 0.012017, 0.013024, 0.008151, 0.008341, 0.008341), by

# Quintile distribution of overall AI rates
qnts.B <- c(0, 0.001457, 0.005536, 0.010516, 0.030226)
qnts.W <- c(0, 0.000450, 0.005102, 0.009680, 0.032970)

# Proportion in same-race partnerships (main, casl, inst)
prop.hom.mpi.B <- c(0.9484, 0.9019, 0.9085)
prop.hom.mpi.W <- c(0.9154, 0.8509, 0.8944)

# Mean age diffs (main, casl, inst)
sqrt.adiff.BB <- c(0.417, 0.498, 0.456)
sqrt.adiff.BW <- c(0.454, 0.629, 0.585)
sqrt.adiff.WW <- c(0.520, 0.632, 0.590)
```

- Note: in Eli's slides, and published appendix, and final model, metrics are all per time step (week).
- In EpiModelHIV, rates are generally expressed as per day, with a time.unit argument (7 by default) that converts all rates

Main model

- Formation model:

```
~edges +  
  nodemix("race", base = 1) +  
  nodefactor("deg.pers", base = c(1, 4)) +  
  absdiffnodemix("sqrt.age", "race") +  
  offset(nodematch("role.class", diff = TRUE, keep = 1:2))  
  
constraints: ~bd(maxout = 1)
```

- Dissolution model:

```
~offset(edges) + offset(nodemix("race", base = 1))
```

Main formation

~edges

	Black				White		
	0 Casual	1 Casual	2+ Casual		0 Casual	1 Casual	2+ Casual
0 Main	50.6%	15.1%	5.3%		43.5%	18.4%	9.5%
1 Main	20.7%	6.1%	2.2%		23.3%	3.3%	2.0%

- Total degree for B = $(20.7\% + 6.1\% + 2.2\%) * 5000 = 1450$
- Total degree for W = $(23.3\% + 3.3\% + 2.0\%) * 5000 = 1430$
- Total degree = $1450 + 1430 = 2880$
- Total edges = $2880 / 2 = 1440$

Main formation

```
nodemix("race", base = 1)
```

r

- B reports on % main partners who are B: 94.8%
- W reports on % main partners who are W: 91.5%
- Calculate expected BB ties and BW ties from B reports
- Calculate expected WW ties and BW ties from W reports
- Note that the two estimates of BW ties aren't identical
- Decide how to reconcile them (mean?)
- Fill in the two remaining values from there
- **Result:**
 - 676.05 BB ties
 - 97.90 BW ties
 - 666.05 WW ties

} Reference category
} Add to target stats

Main formation

```
nodefactor("deg.pers", base = c(1, 4))
```

	Black				White		
	0 Casual	1 Casual	2 Casual		0 Casual	1 Casual	2 Casual
0 Main	50.6%	15.1%	5.3%		43.5%	18.4%	9.5%
1 Main	20.7%	6.1%	2.2%		23.3%	3.3%	2.0%

deg.pers value	B0	B1	B2		W0	W1	W2
# men	3565	1060	375		3340	1085	575
# main ties for men in this group	1035	305	110		1165	165	100
	⌋	⌋			⌋	⌋	
	Reference category	Add to target stats			Reference category	Add to target stats	

Main formation

```
absdiffnodemix("sqrt.age", "race")
```

- ERGM term I coded up for this project
- `absdiffnodemix(x, y)` returns one statistic for each combo of `y` attributes, representing the differences in absolute value of `x` for the two actors in a tie, summed across all ties for that `y` combo

Race combo	BB	BW	WW
# ties	676.05	97.90	666.05
Mean in abs. value of the diff. in sqrt age	0.417	0.454	0.520
Total	281.91	44.45	346.35

Main formation

```
offset(nodematch("role.class", diff = TRUE, keep = 1:2))
```


- ?
- diff=TRUE means a separate term for each type of homophilous tie
- II, RR, VV (in that order b/c alphabetical)
- Keep = 1:2 -> II, RR
- offset means their coefficient is set for us
- What do you think it is set at?
 - $\ln(0) = -\ln f$
- constraints: `~bd(maxout = 1)`
akin to the deegree term you saw on Tuesday

Main dissolution

```
~offset(edges) + offset(nodemix("race", base = 1))
```

- Each race combo gets its own diss rate
- Drawn from mean durations:

• type	BB	BW	W
• mean dur	49.7	53.1	79.3
• $\ln(D-1)$	3.886	3.954	4.360


Reference category Enter as additive effects

```
~offset(edges) + offset(nodemix("race", base = 1))
```

3.886 **3.954-3.886 = 0.068** **4.360-3.886 = 0.474**

Pers. model

■ Formation model:

```
~edges + nodemix("race", base = 1) + nodefactor("deg.main",  
base = c(1, 3)) + concurrent(by = "race") +  
absdiffnodemix("sqrt.age", "race") +  
offset(nodematch("role.class", diff = TRUE, keep = 1:2))
```

```
constraints: ~bd(maxout = 2)
```

■ Dissolution model:

```
~offset(edges) + offset(nodemix("race", base = 1))
```

Pers. model

- All the same as main, with addition of:

```
concurrent (by = "race")
```

- Why?

	Black				White		
	0 Casual	1 Casual	2 Casual		0 Casual	1 Casual	2 Casual
0 Main	50.6%	15.1%	5.3%		43.5%	18.4%	9.5%
1 Main	20.7%	6.1%	2.2%		23.3%	3.3%	2.0%

- Because people can only have 0 or 1 main, but 0, 1, or 2 pers
- constraints: `~bd(maxout = 2)`

Inst. model

- Formation model:

New bits

```
~edges + nodefactor(c("deg.main", "deg.pers")) +  
nodefactor(c("race", "riskg"), base = c(3, 8)) +  
nodematch("race") + absdiffnodemix("sqrt.age", "race") +  
offset(nodematch("role.class", diff = TRUE, keep = 1:2))
```

- Dissolution model:

```
~offset(edges) [with known expected duration of 1]
```


Inst. model

```
nodefactor(c("deg.main", "deg.pers"))
```

- overall rate of inst partners based on both deg.main and deg.pers values

- B0B0
- B0B1
- B0B2
- B1B0
- B1B1
- B1B2
- W0W0
- W0W1
- W0W2
- W1W0
- W1W1
- W1W2

Inst. model

```
nodefactor(c("deg.main", "deg.pers"))
```

- Multiply # inst partners per time step per person

	Black				White		
	0 Casual	1 Casual	2 Casual		0 Casual	1 Casual	2 Casual
0 Main	0.073	0.091	0.080		0.057	0.084	0.091
1 Main	0.055	0.052	0.052		0.057	0.058	0.058

By # of men in that category

5000 x

	Black				White		
	0 Casual	1 Casual	2 Casual		0 Casual	1 Casual	2 Casual
0 Main	50.6%	15.1%	5.3%		43.5%	18.4%	9.5%
1 Main	20.7%	6.1%	2.2%		23.3%	3.3%	2.0%

Inst. model

```
nodefactor(c("deg.main", "deg.pers"))
```

184.7 57.3 68.5 15.9 21.3 5.7 124.6 66.5 77.4 9.6 43.3 5.8



Reference
category



Add to target stats

Inst. model

```
nodefactor(c("race", "riskg"), base = c(3, 8))
```

B1, B2, B3, B4, B5, W1, W2, W3, W4, W5


Multiply

Quintile	Black	White
Lowest quintile	0.000	0.000
Second quintile	0.010	0.003
Third quintile	0.039	0.036
Fourth quintile	0.074	0.068
Highest quintile	0.212	0.231

by quintile pop sizes (all 5000×0.2)

0.0	10.2	38.8	73.6	211.6	0.0	3.2	35.7	67.8	230.8
Add to target stats		Ref. Cat.	Add to target stats			Ref. Cat.	Add to target stats		

■ 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
- 
- `d4-fit_model.R`