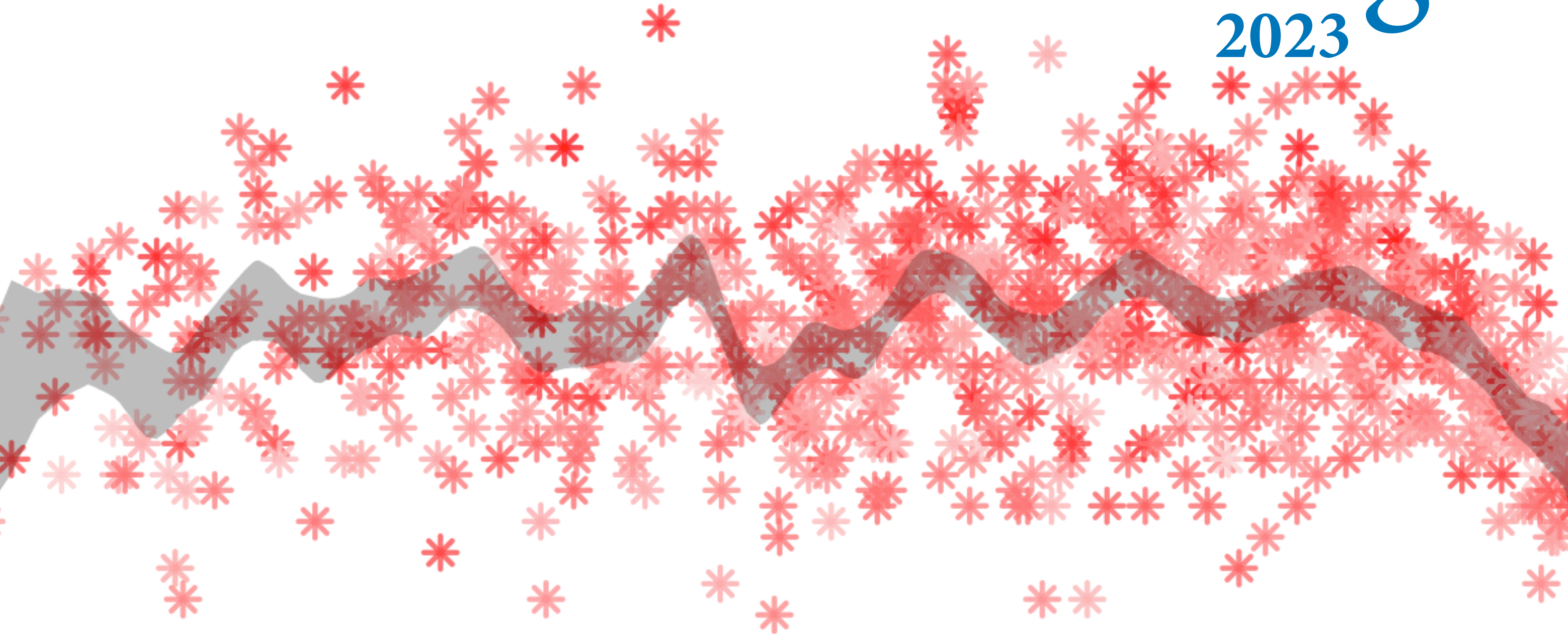


Statistical Rethinking

2023



15. Social Networks

What Motivates Sharing?

“Up in our country we are human!
And since we are human we help each
other. We don't like to hear anybody
say thanks for that. What I get today
you may get tomorrow. Up here we
say that **by gifts one makes slaves and
by whips one makes dogs.**”

Quoted in Peter Freuchen's 1961 book about the Inuit



Ingrid Vang Nyman

What Motivates Sharing?

data(KosterLeckie)

Year of food transfers among 25 households
in Arang Dak

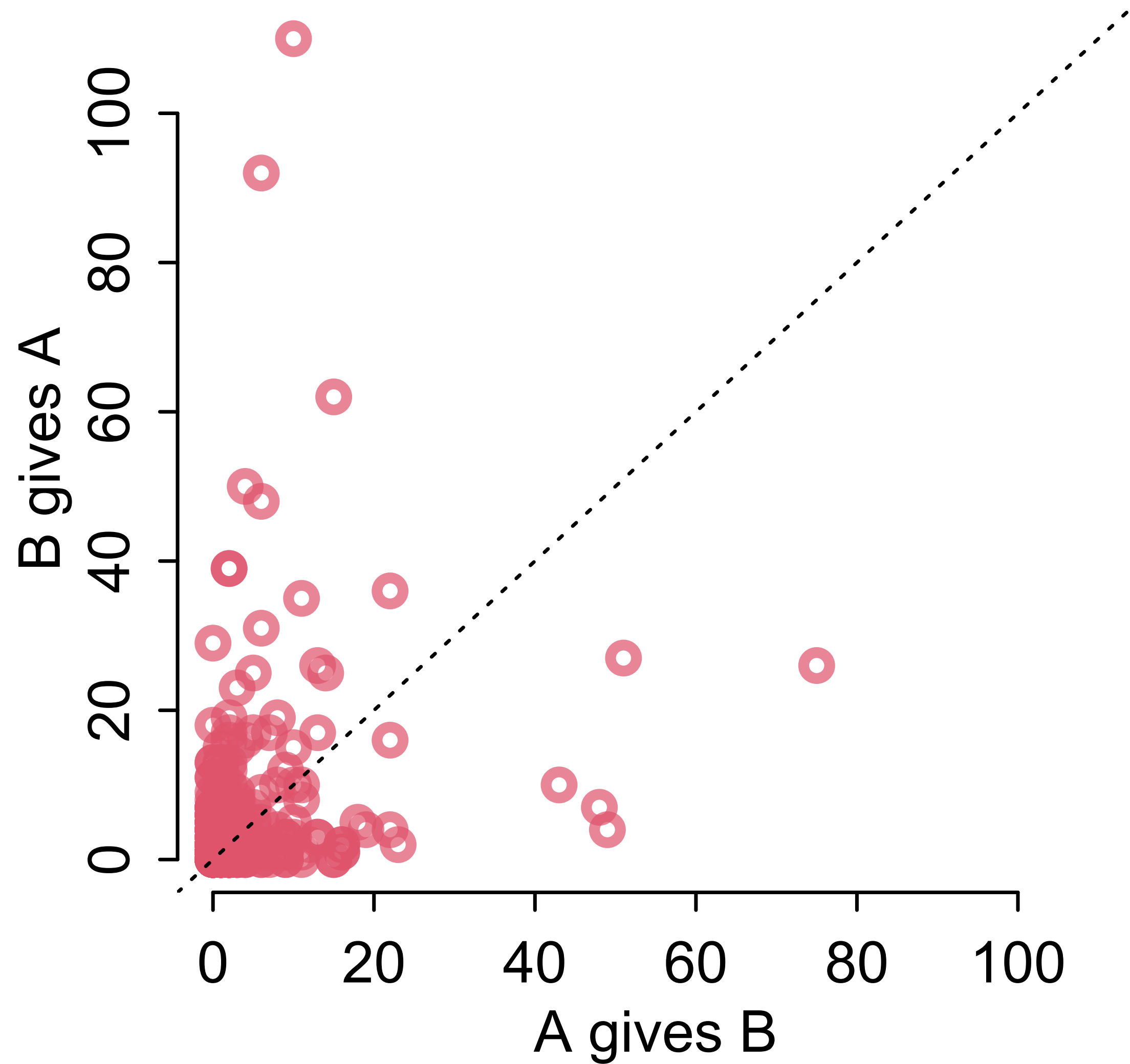
$25! / (2!(25-2)!) = 300$ dyads

2871 observed transfers between households

How much sharing explained by reciprocity?
How much by generalized giving?



What Motivates Sharing?

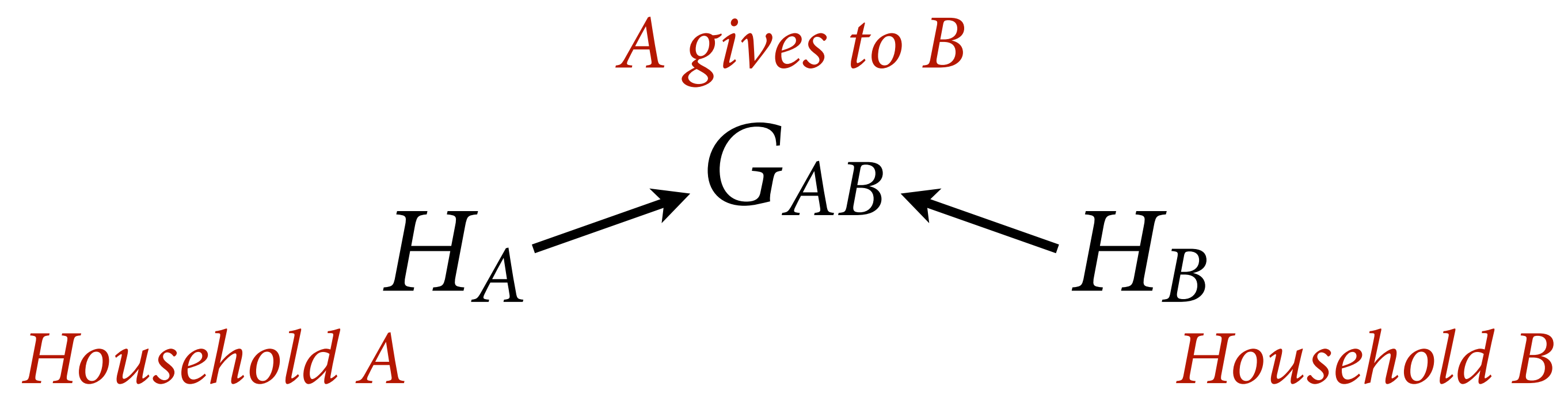


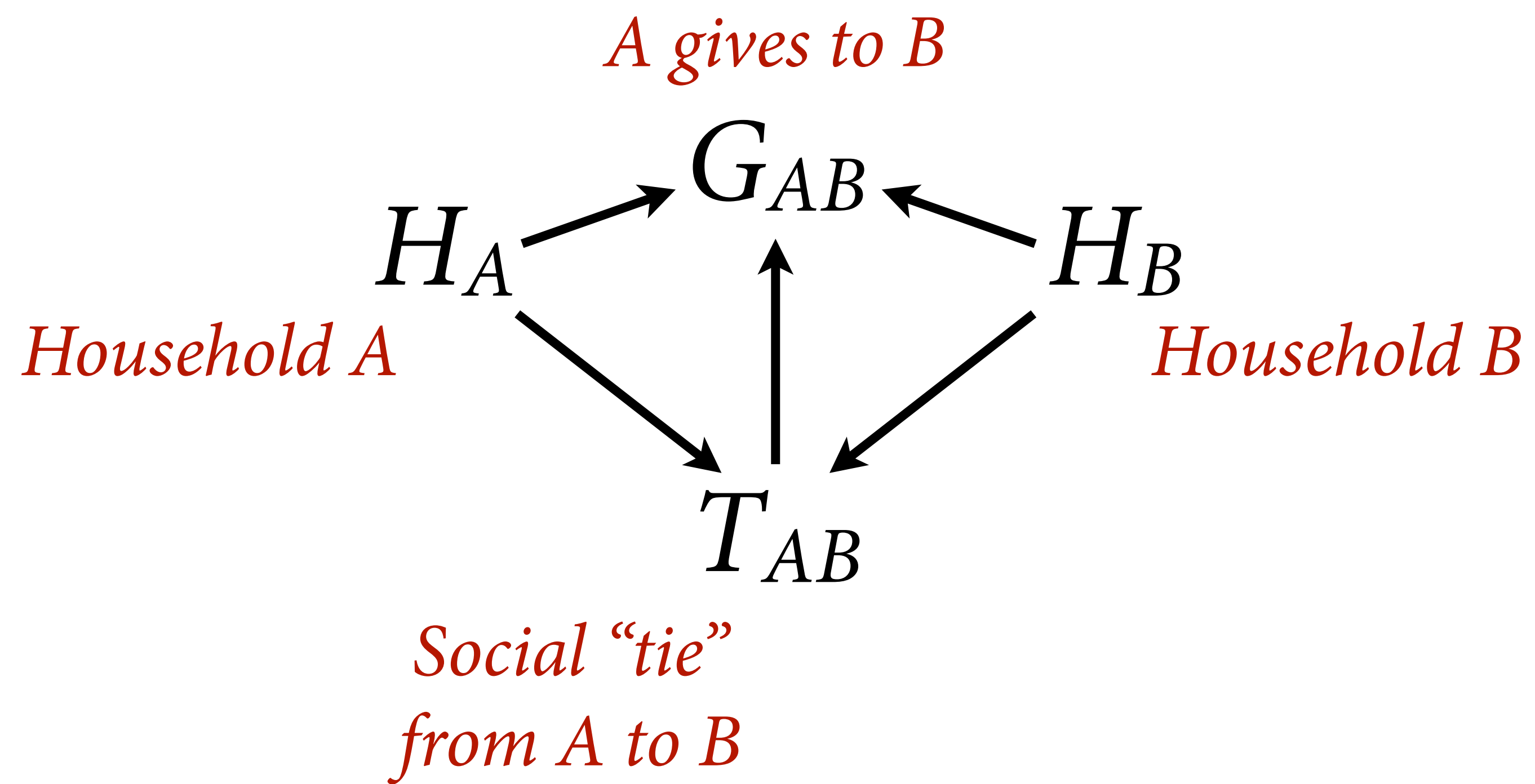
How to draw an owl

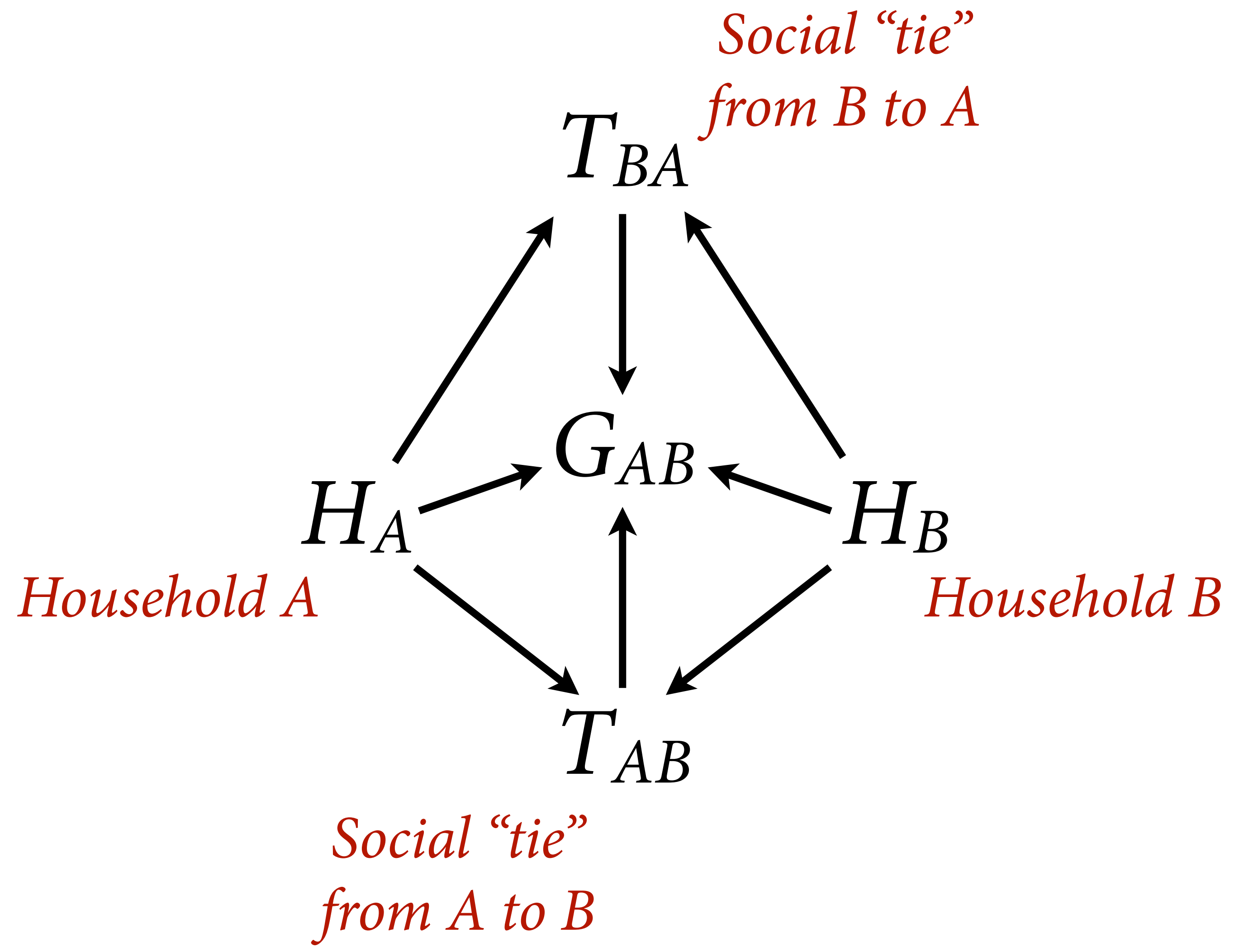
1.

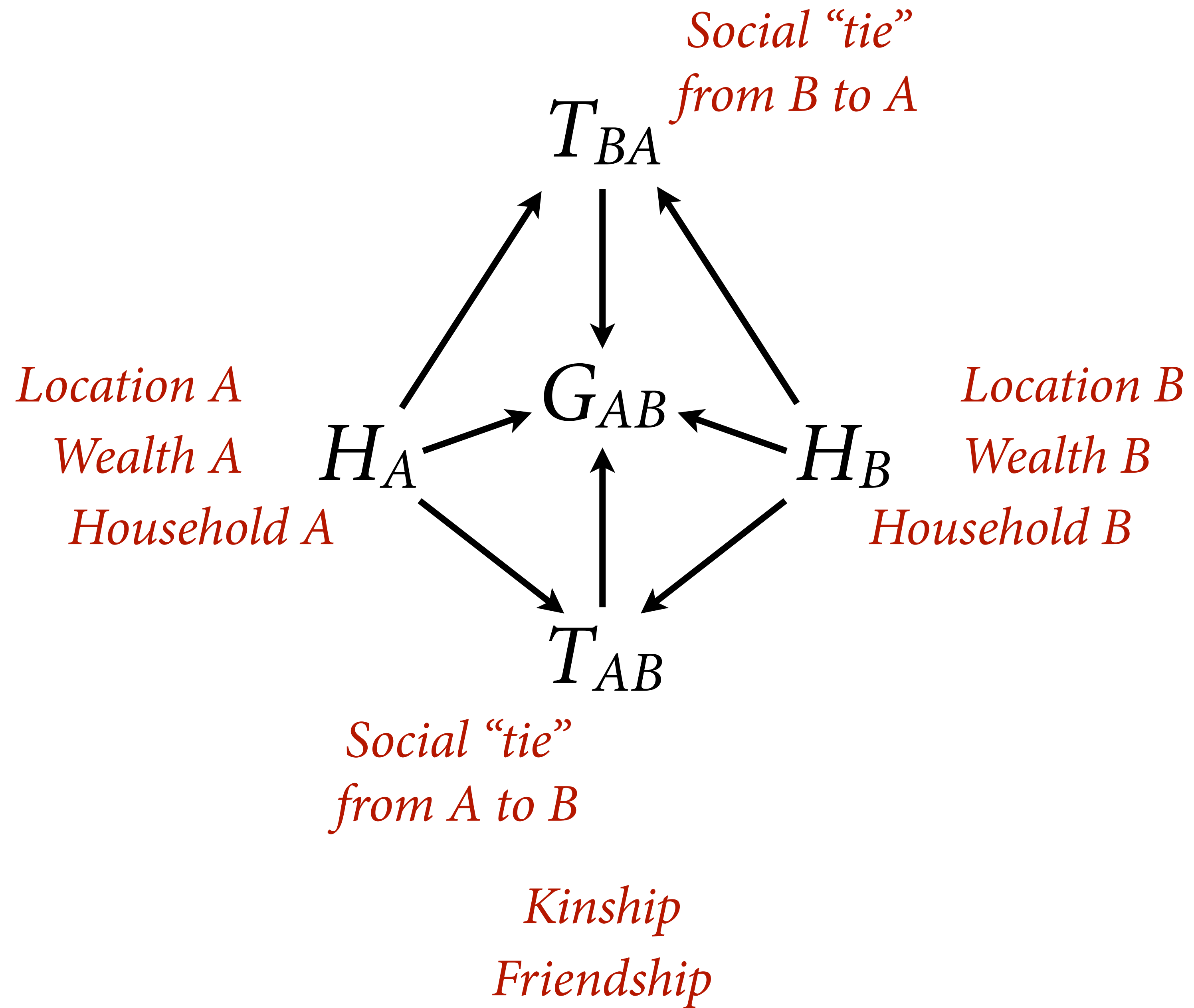


1. Draw some circles









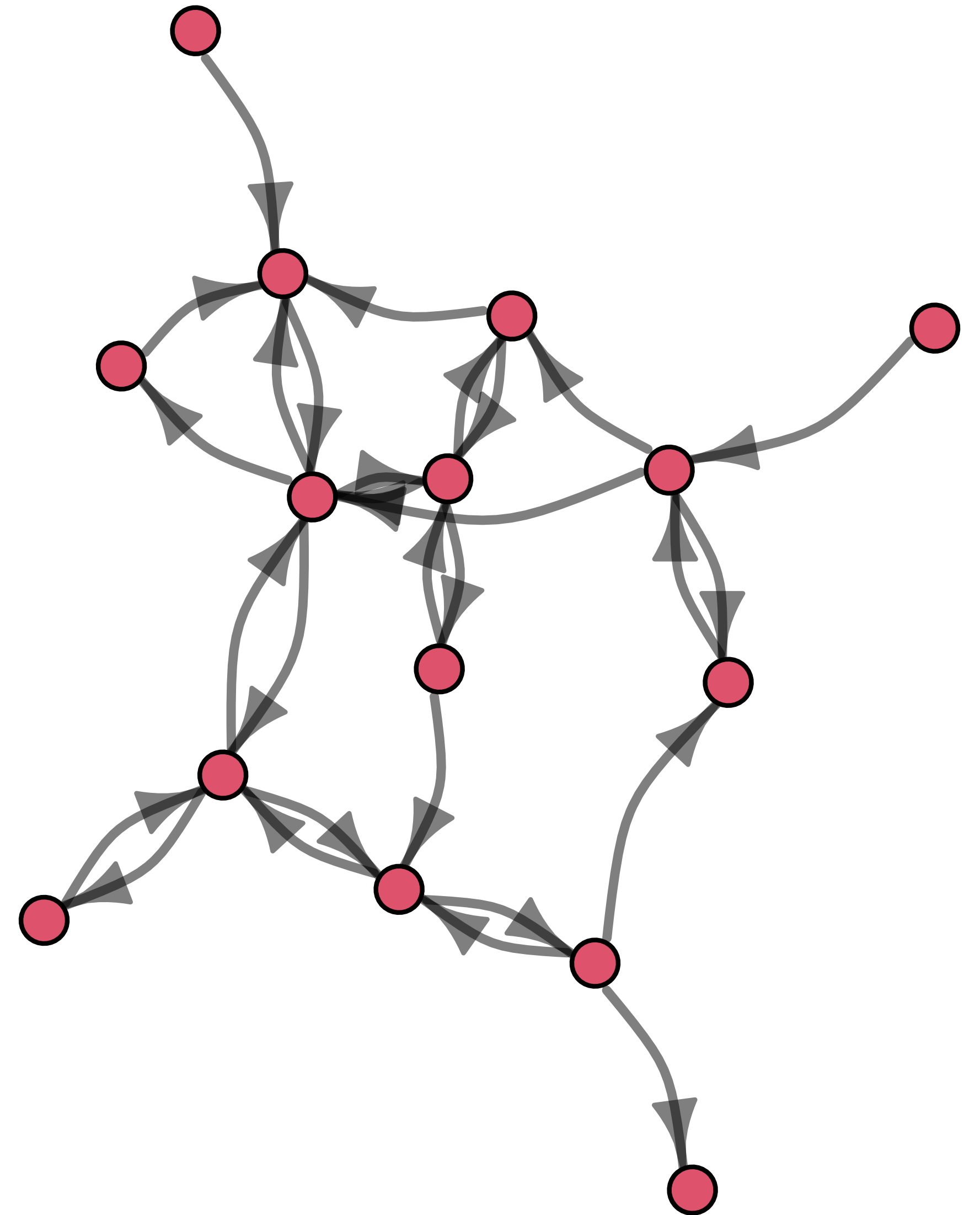
What Motivates Sharing?

T_{AB} and T_{BA} are not observable

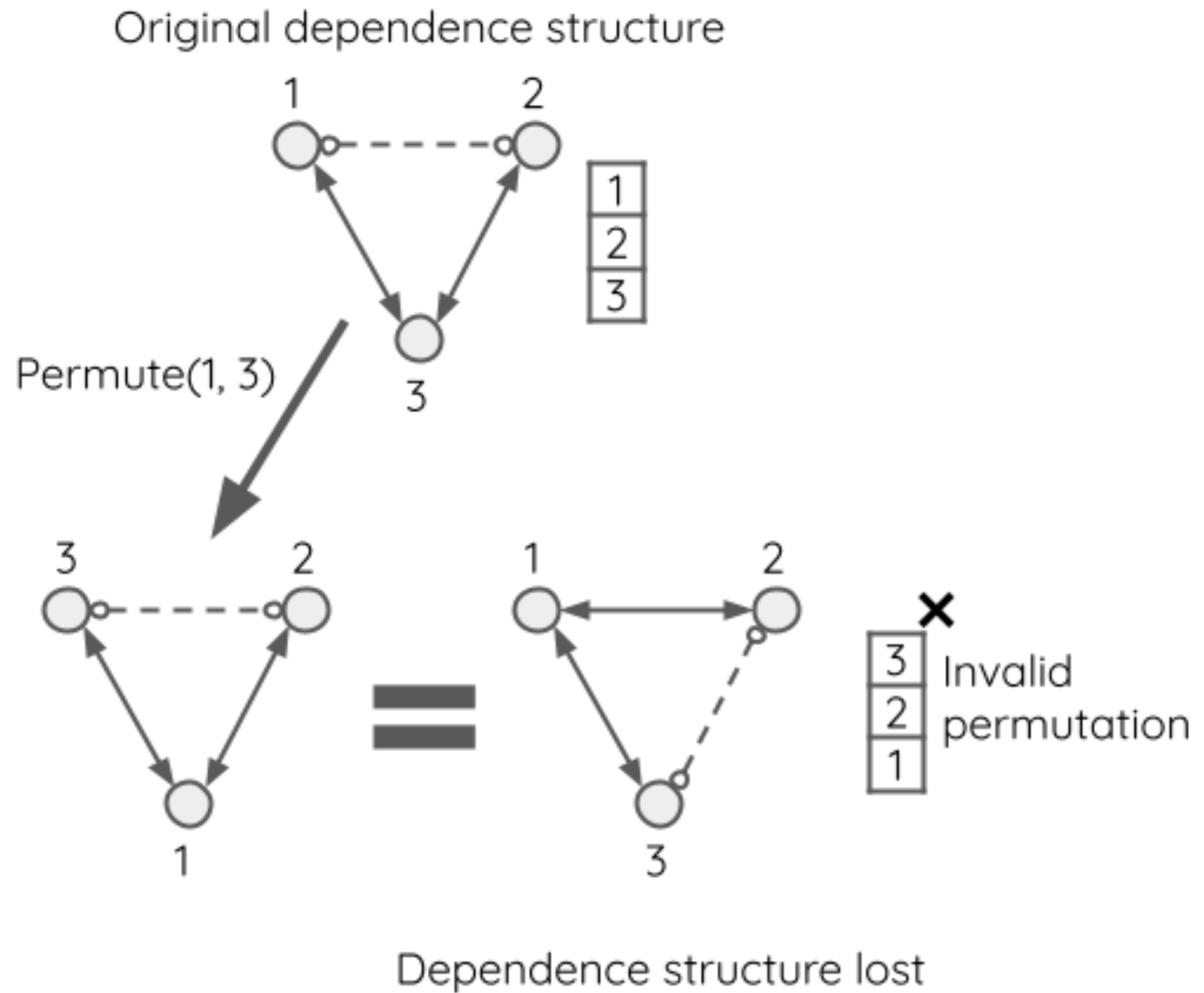
Social network: Pattern of directed exchange

Social networks are **abstractions**,
are **not data**

What is a principled approach?

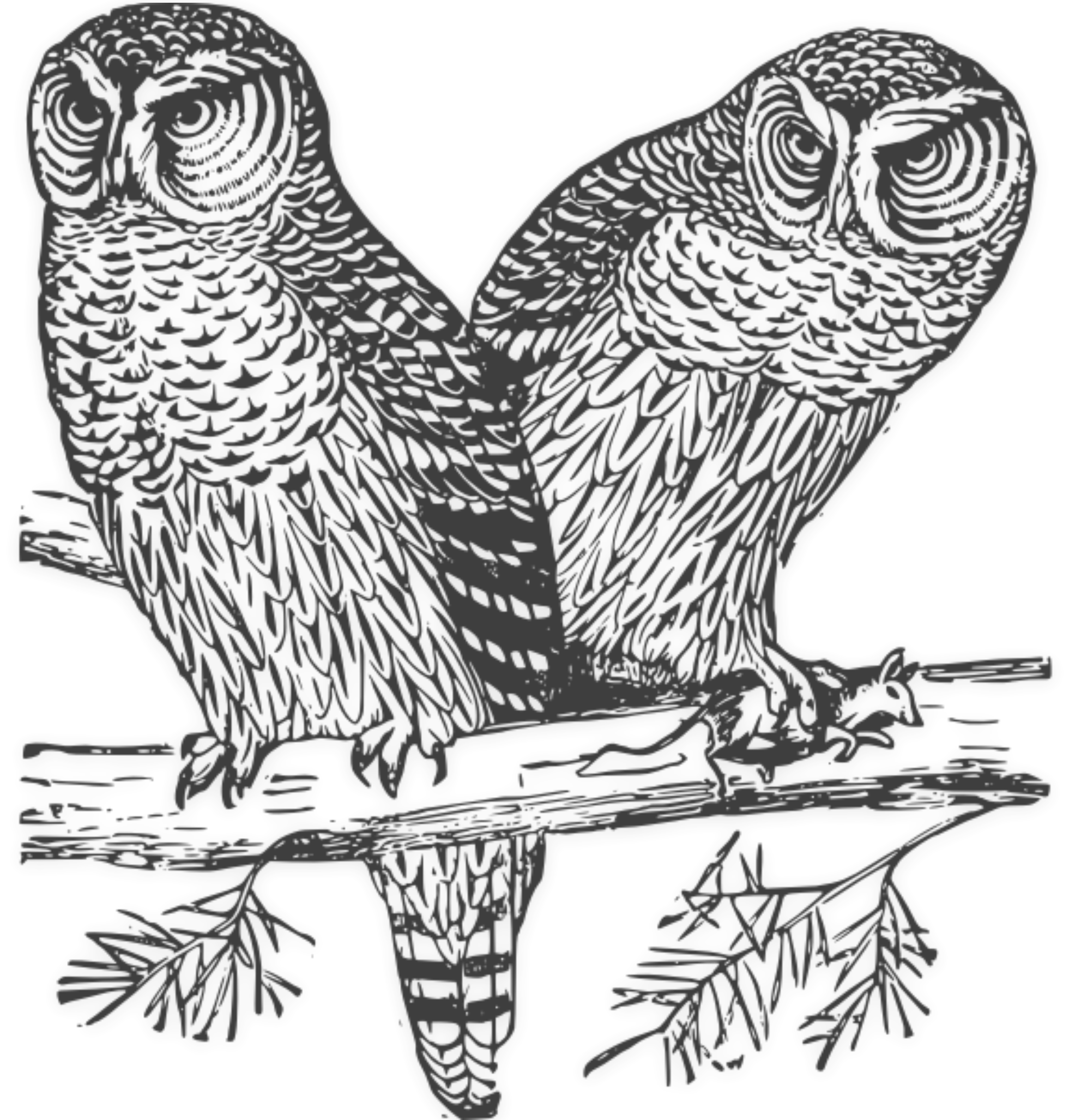


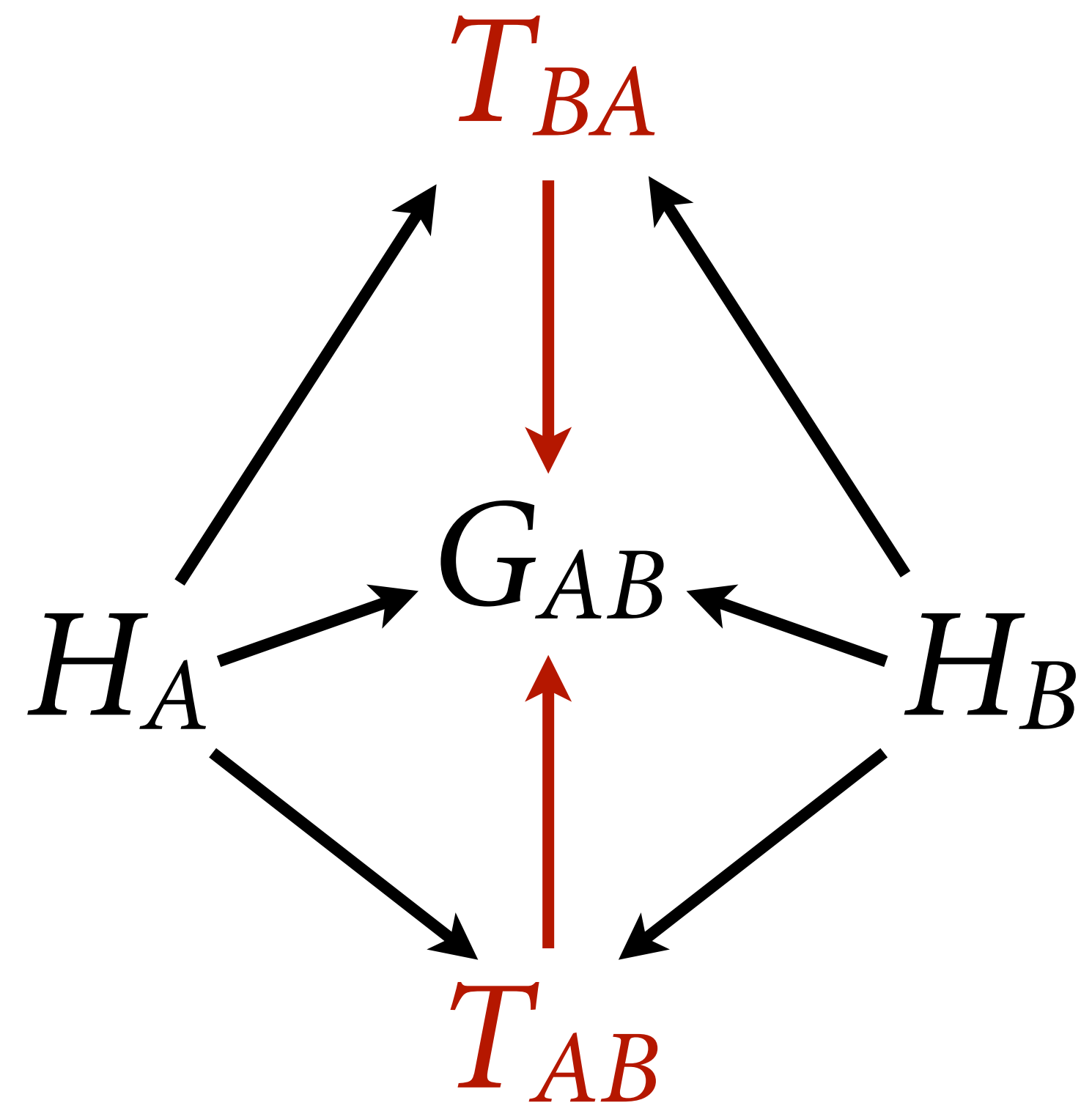
Resist Adhockery

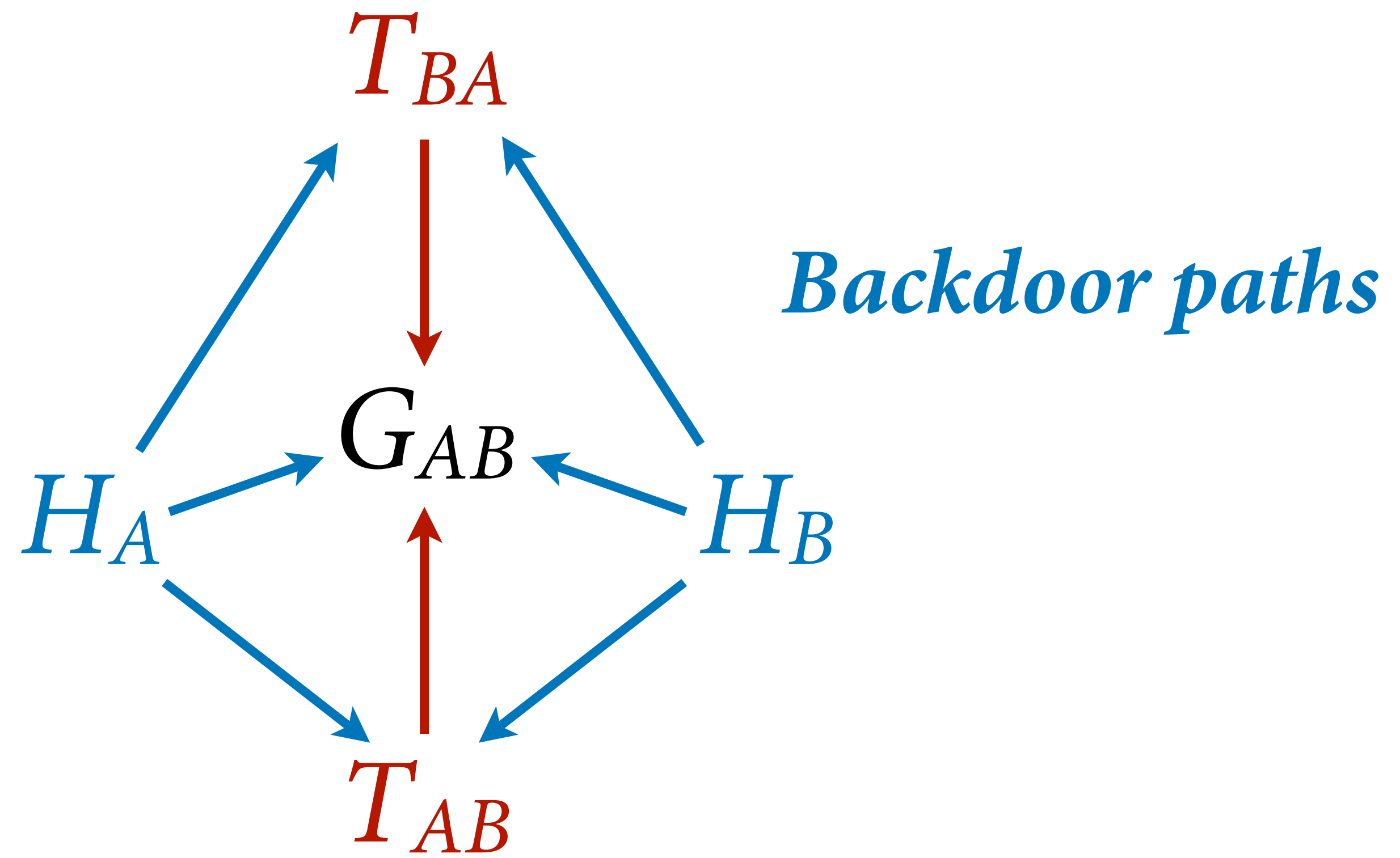


Drawing the Social Owl

- (1) Estimand: Reciprocity & what explains it
- (2) Generative model
- (3) Statistical model
- (4) Analyze sample







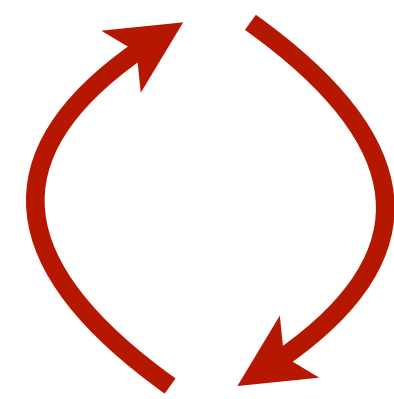
Drawing the Social Owl

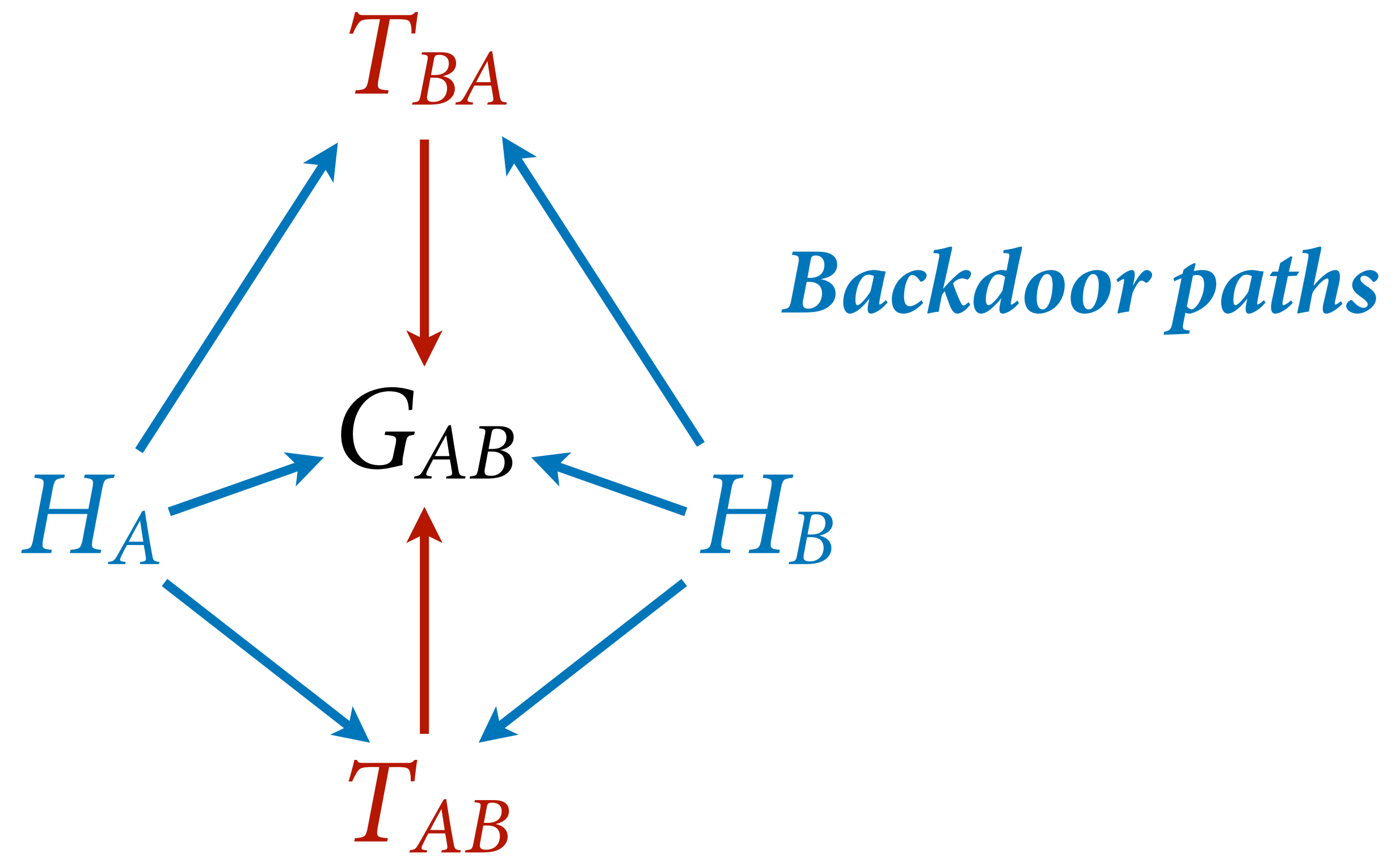
(1) Estimand: Reciprocity & what explains it

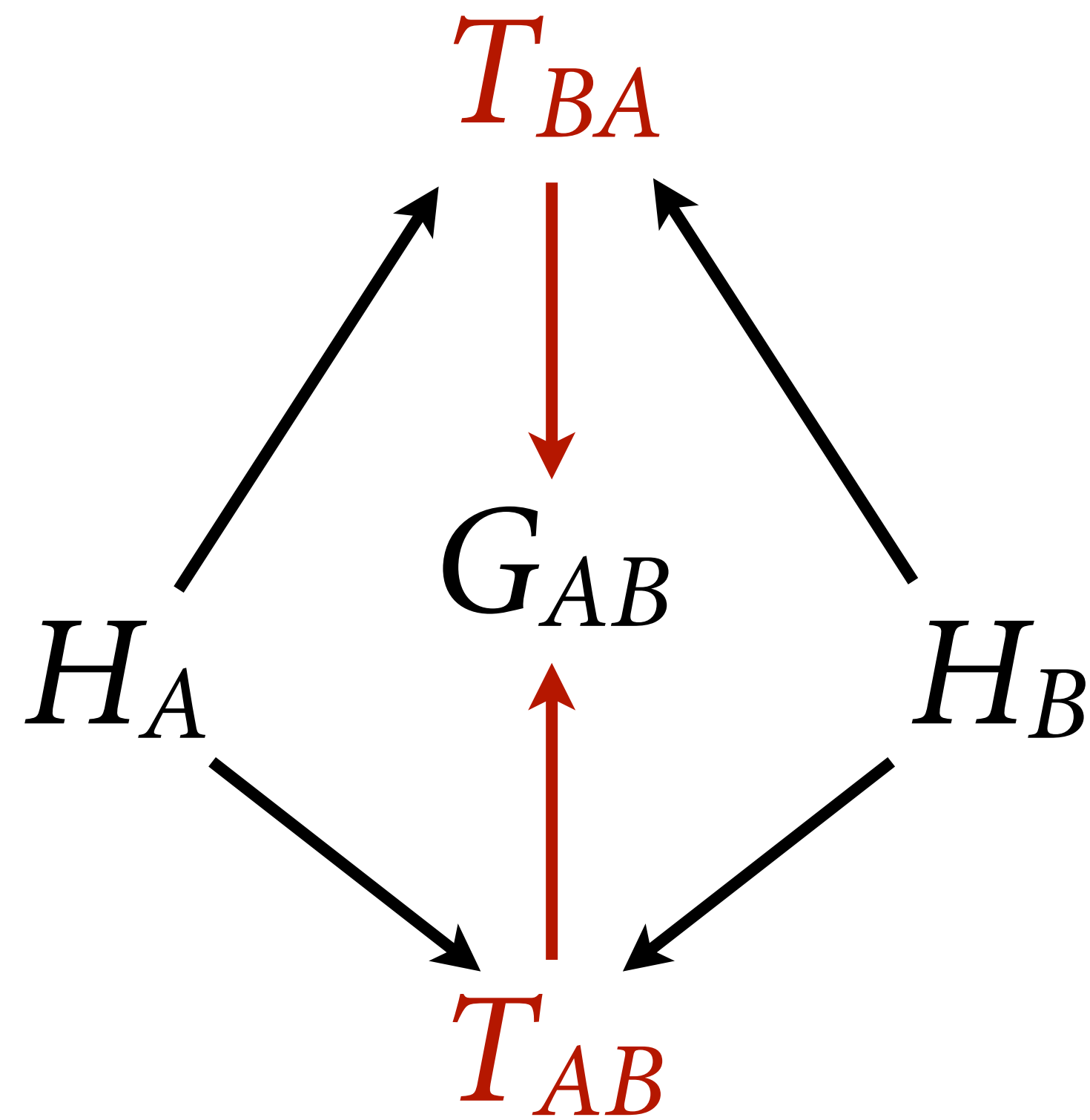
(2) Generative model

(3) Statistical model

(4) Analyze sample







Begin simple, model tie formation


```
# N households  
N <- 25  
dyads <- t(combn(N,2))  
N_dyads <- nrow(dyads)
```

```
# N households
N <- 25
dyads <- t(combn(N,2))
N_dyads <- nrow(dyads)
```

```
> dyads
      [,1] [,2]
 [1,]    1    2
 [2,]    1    3
 [3,]    1    4
 [4,]    1    5
 [5,]    1    6
 [6,]    1    7
 [7,]    1    8
 [8,]    1    9
 [9,]    1   10
[10,]    1   11
[11,]    1   12
[12,]    1   13
[13,]    1   14
[14,]    1   15
[15,]    1   16
[16,]    1   17
[17,]    1   18
[18,]    1   19
[19,]    1   20
[20,]    1   21
[21,]    1   22
[22,]    1   23
[23,]    1   24
[24,]    1   25
[25,]    2    3
[26,]    2    4
[27,]    2    5
[28,]    2    6
[29,]    2    7
[30,]    2    8
[31,]    2    9
[32,]    2   10
[33,]    2   11
[34,]    2   12
[35,]    2   13
[36,]    2   14
[37,]    2   15
[38,]    2   16
[39,]    2   17
[40,]    2   18
[41,]    2   19
[42,]    2   20
[43,]    2   21
[44,]    2   22
[45,]    2   23
[46,]    2   24
[47,]    2   25
[48,]    3    4
[49,]    3    5
[50,]    3    6
[51,]    3    7
[52,]    3    8
[53,]    3    9
[54,]    3   10
[55,]    3   11
[56,]    3   12
[57,]    3   13
[58,]    3   14
[59,]    3   15
[60,]    3   16
[61,]    3   17
[62,]    3   18
[63,]    3   19
[64,]    3   20
[65,]    3   21
[66,]    3   22
[67,]    3   23
[68,]    3   24
[69,]    3   25
[70,]    4    5
[71,]    4    6
[72,]    4    7
[73,]    4    8
[74,]    4    9
[75,]    4   10
[76,]    4   11
[77,]    4   12
[78,]    4   13
[79,]    4   14
[80,]    4   15
[81,]    4   16
[82,]    4   17
[83,]    4   18
[84,]    4   19
[85,]    4   20
[86,]    4   21
[87,]    4   22
[88,]    4   23
[89,]    4   24
[90,]    4   25
[91,]    5    6
```

```
# N households
N <- 25
dyads <- t(combn(N,2))
N_dyads <- nrow(dyads)

# simulate "friendships" in which ties are shared
f <- rbern(N_dyads,0.1) # 10% of dyads are friends
```

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# now simulate directed ties for all individuals
# there can be ties that are not reciprocal
alpha <- (-3) # base rate of ties; -3 ≈ 0.05
y <- matrix(NA,N,N) # matrix of ties
```

```

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N <- 25
dyads <- t(combn(N,2))
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# now simulate directed ties for all individuals
# there can be ties that are not reciprocal
alpha <- (-3) # base rate of ties; -3 ≈ 0.05
y <- matrix(NA,N,N) # matrix of ties
for ( i in 1:N ) for ( j in 1:N ) {
  if ( i != j ) {
    # directed tie from i to j
    ids <- sort( c(i,j) )
    the_dyad <- which( dyads[,1]==ids[1] & dyads[,2]==ids[2] )
    p_tie <- f[the_dyad] + (1-f[the_dyad])*inv_logit( alpha )
    y[i,j] <- rbern( 1 , p_tie )
  }
}#ij

```

```

# N households
N <- 25
dyads <- t(combn(N,2))
N_dyads <- nrow(dyads)

# simulate "friendships" in which ties are shared
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    y[i,j] <- rbern( 1 , p_tie )
  }
}#ij

```

*friends
share ties*

```
# now simulate gifts
giftsAB <- rep(NA,N_dyads)
giftsBA <- rep(NA,N_dyads)
lambda <- log(c(0.5,2)) # rates of giving for y=0,y=1
for ( i in 1:N_dyads ) {
  A <- dyads[i,1]
  B <- dyads[i,2]
  giftsAB[i] <- rpois( 1 , exp( lambda[1+y[A,B]] ) )
  giftsBA[i] <- rpois( 1 , exp( lambda[1+y[B,A]] ) )
}
```

```

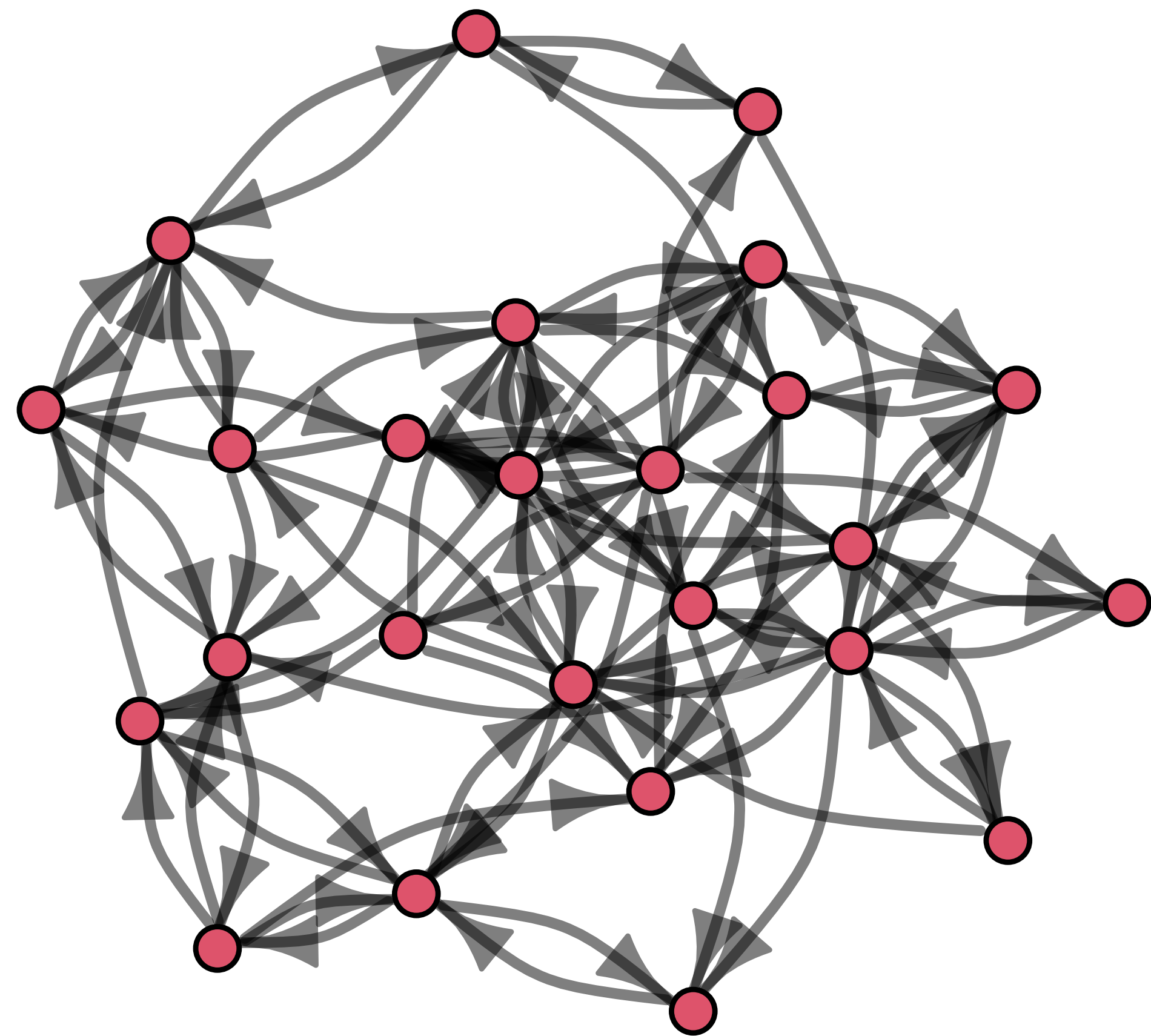
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lambda <- log(c(0.5,2)) # rates of giving for y=0,y=1
for ( i in 1:N_dyads ) {
  A <- dyads[i,1]
  B <- dyads[i,2]
  giftsAB[i] <- rpois( 1 , exp( lambda[1+y[A,B]] ) )
  giftsBA[i] <- rpois( 1 , exp( lambda[1+y[B,A]] ) )
}

```

```

# draw network
library(igraph)
sng <- graph_from_adjacency_matrix(y)
lx <- layout_nicely(sng)
vcol <- "#DE536B"
plot(sng , layout=lx , vertex.size=8 ,
edge.arrow.size=0.75 , edge.width=2 ,
edge.curved=0.35 , vertex.color=vcol ,
edge.color=grau() , asp=0.9 , margin = -0.05 ,
vertex.label=NA )

```



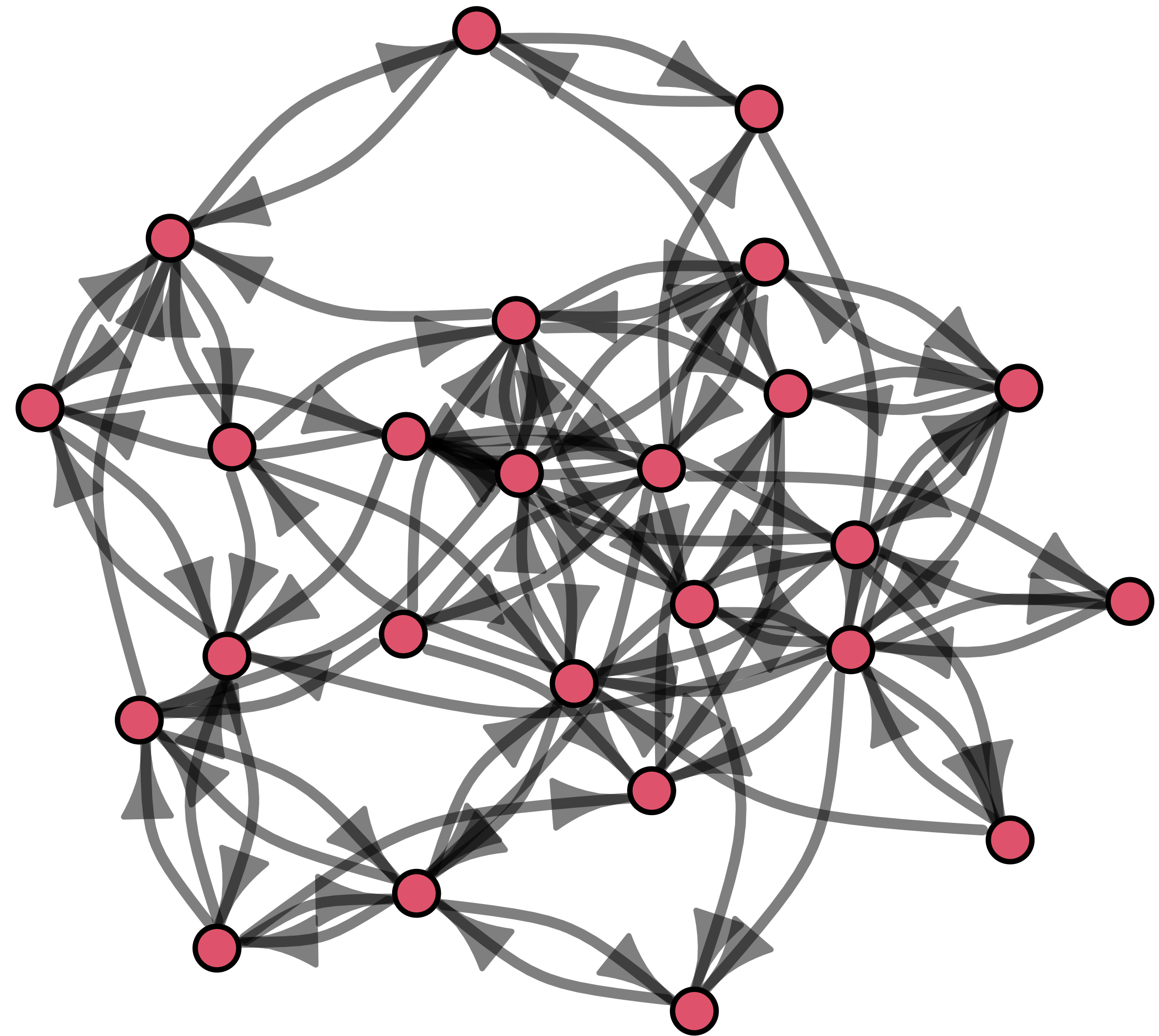
Drawing the Social Owl

(1) Estimand: Reciprocity & what explains it

(2) Generative model

(3) **Statistical model**

(4) Analyze sample



Gifts A to B

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB}$$

average

Tie A to B

Gifts A to B

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB}$$

average

Tie A to B

Gifts B to A

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA}$$

Tie B to A

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB}$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA}$$

The AB dyad $\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$

*covariance
within dyads*

*variance
among ties*

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB}$$

$$\log(\lambda_{BA}) = \alpha + T_{BA}$$

partial pooling for network ties

$$\begin{cases} \begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right) \\ \rho \sim \text{LKJCorr}(2) \\ \sigma \sim \text{Exponential}(1) \\ \alpha \sim \text{Normal}(0,1) \end{cases}$$

```

# dyad model
f_dyad <- alist(
  GAB ~ poisson( lambdaAB ),
  GBA ~ poisson( lambdaBA ),
  log(lambdaAB) <- a + T[D,1] ,
  log(lambdaBA) <- a + T[D,2] ,
  a ~ normal(0,1),

  ## dyad effects
  transpars> matrix[N_dyads,2]:T <-
    compose_noncentered( rep_vector(sigma_T,2) , L_Rho_T , Z ),
  matrix[2,N_dyads]:Z ~ normal( 0 , 1 ),
  cholesky_factor_corr[2]:L_Rho_T ~ lkj_corr_cholesky( 2 ),
  sigma_T ~ exponential(1),

  ## compute correlation matrix for dyads
  gq> matrix[2,2]:Rho_T <<- Chol_to_Corr( L_Rho_T )
)

mGD <- ulam( f_dyad , data=sim_data , chains=4 , cores=4 , iter=2000 )

```

```
# dyad model
```

```
f_dyad <- alist(  
  GAB ~ poisson( lambdaAB ),  
  GBA ~ poisson( lambdaBA ),  
  log(lambdaAB) <- a + T[D,1] ,  
  log(lambdaBA) <- a + T[D,2] ,  
  a ~ normal(0,1),
```

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

```
## dyad effects
```

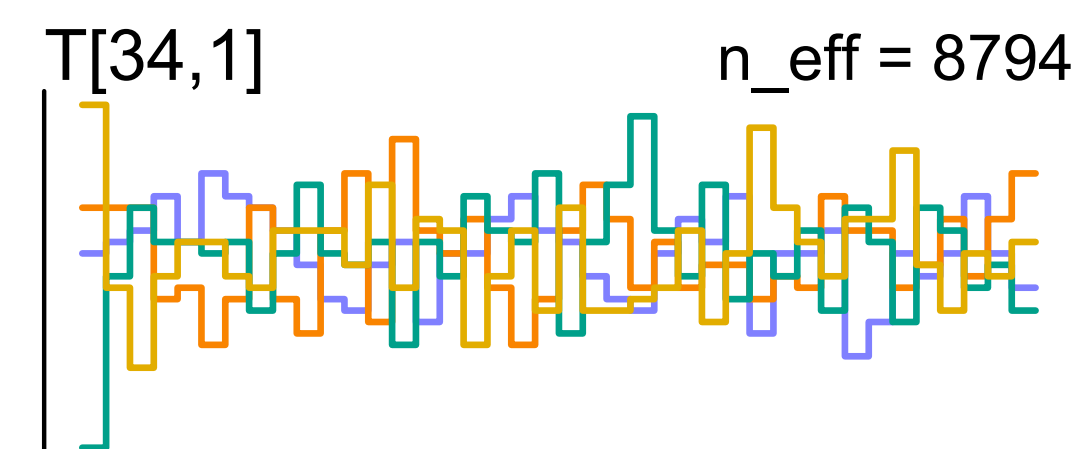
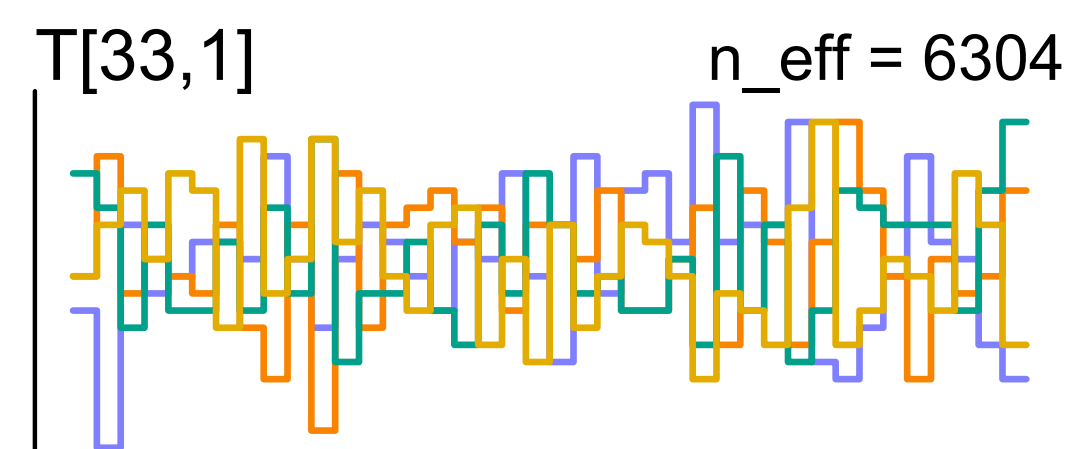
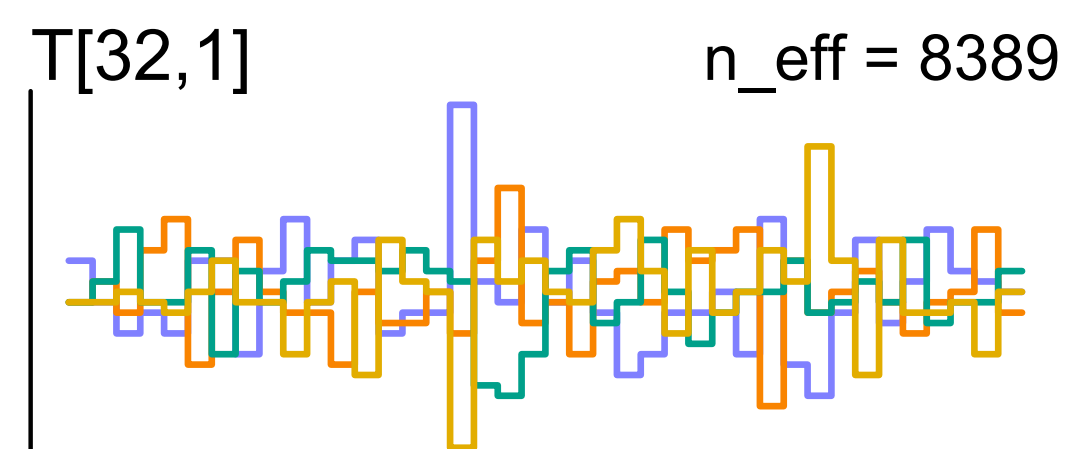
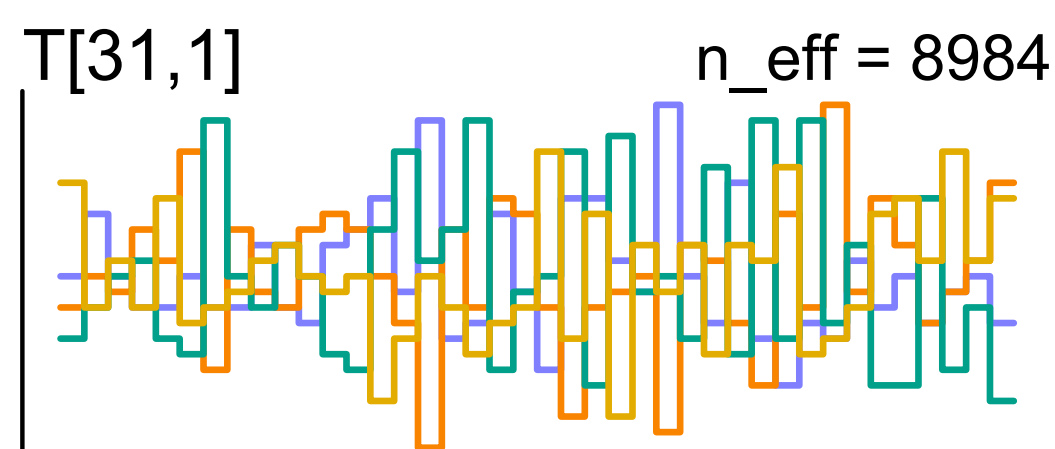
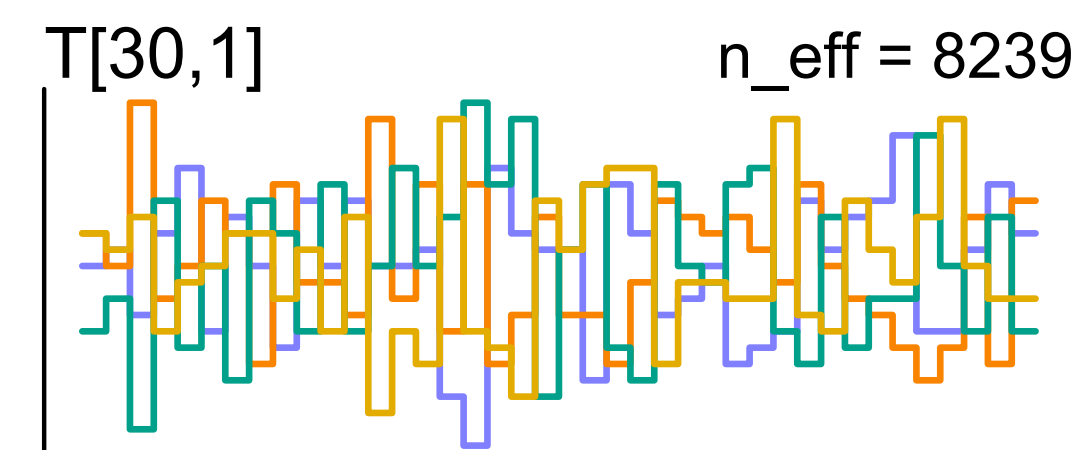
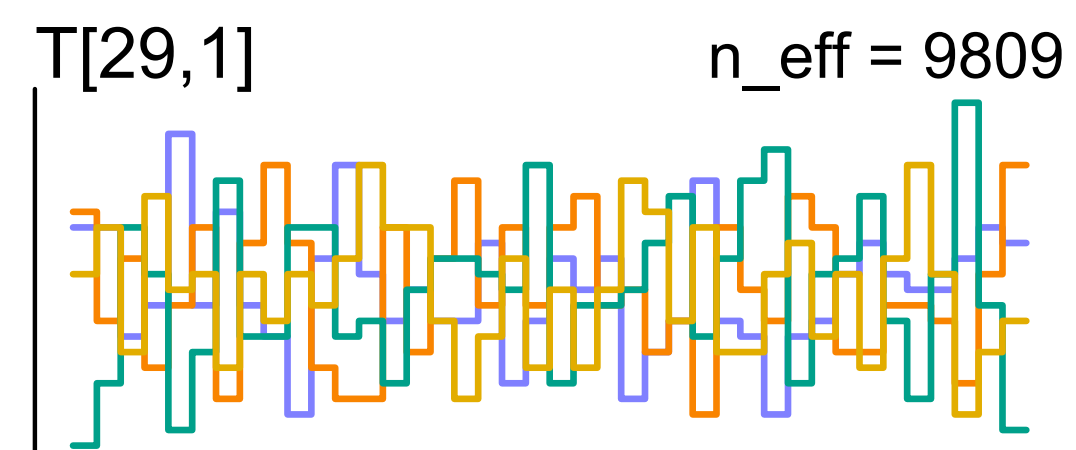
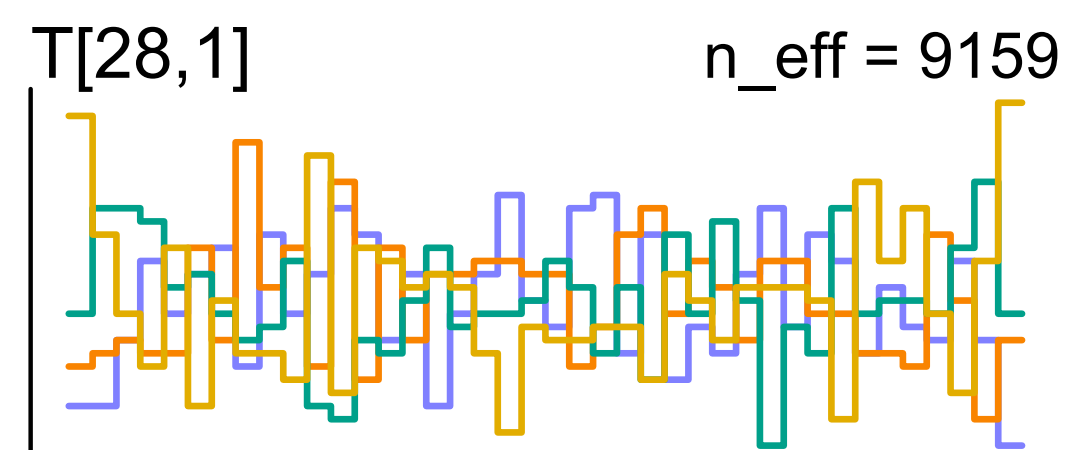
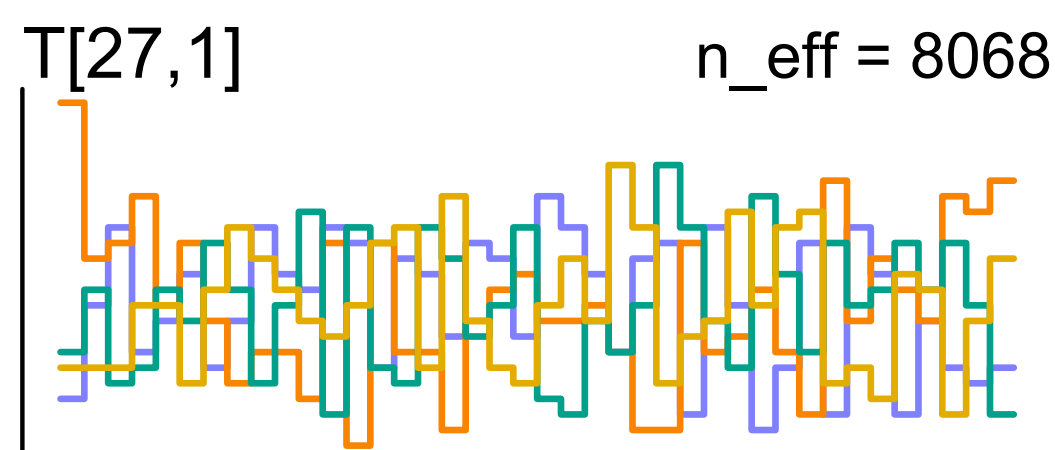
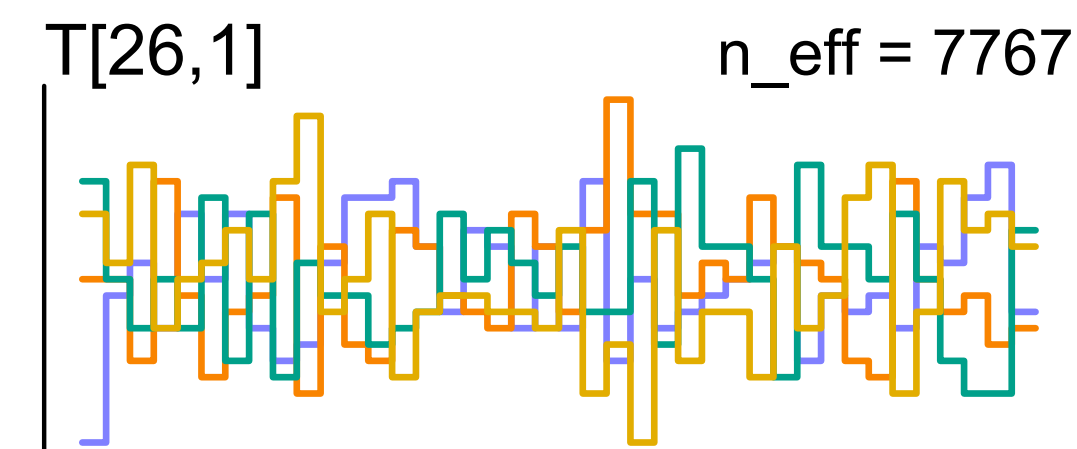
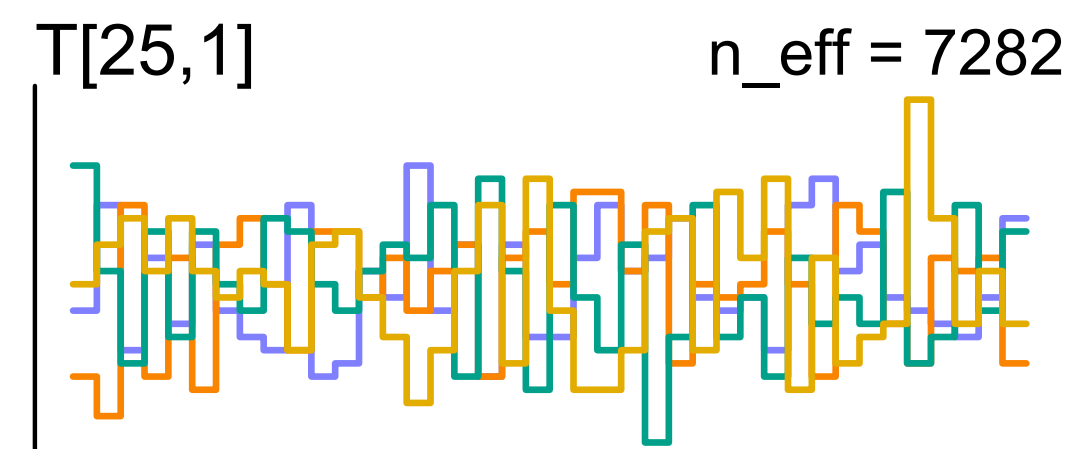
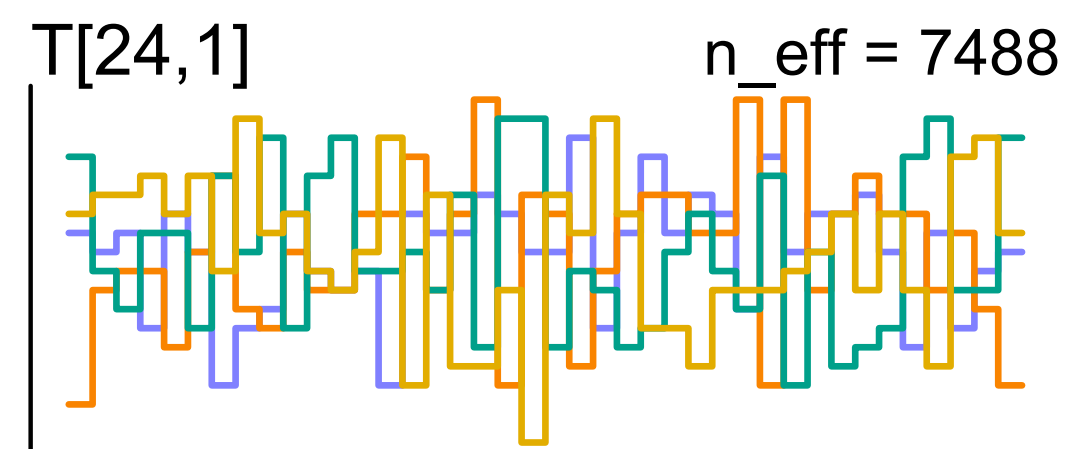
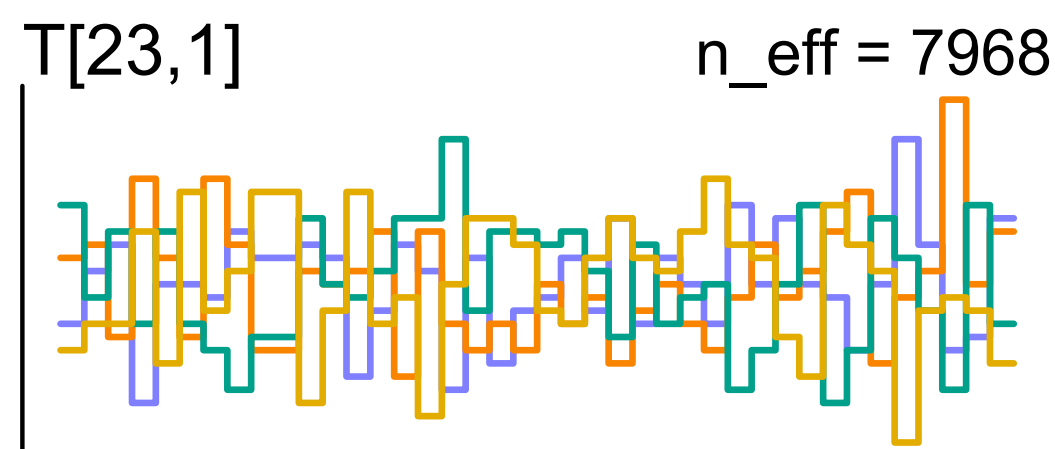
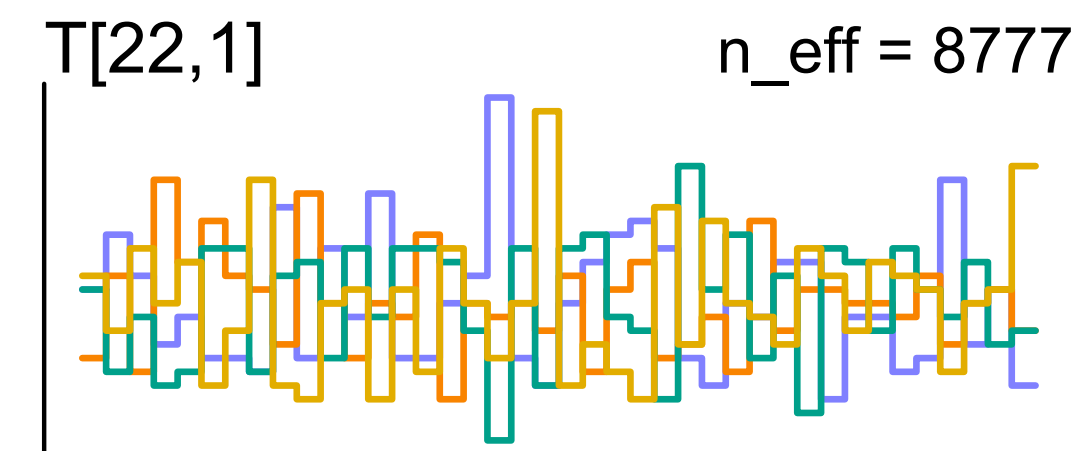
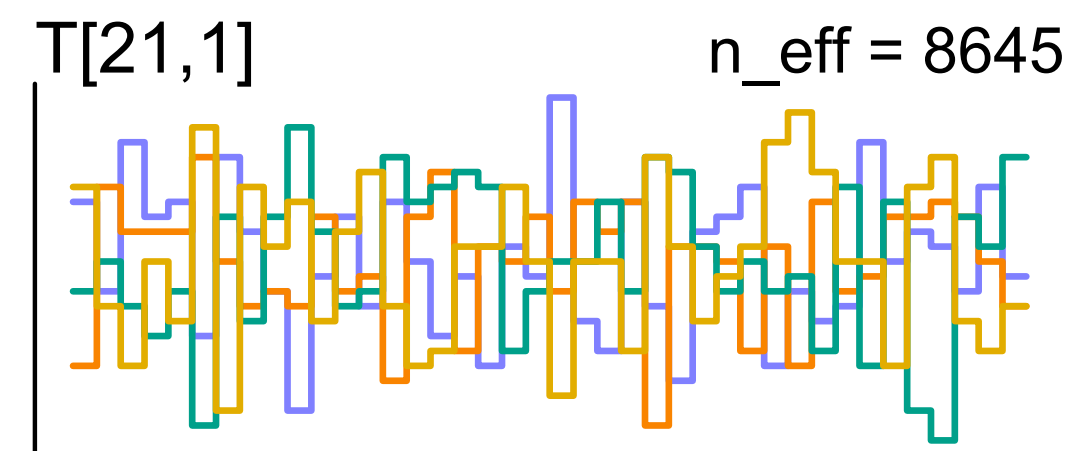
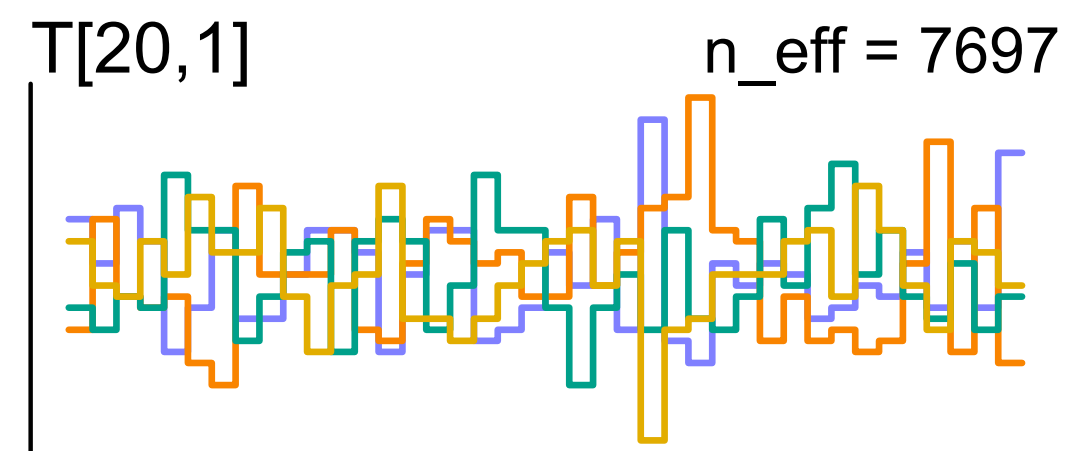
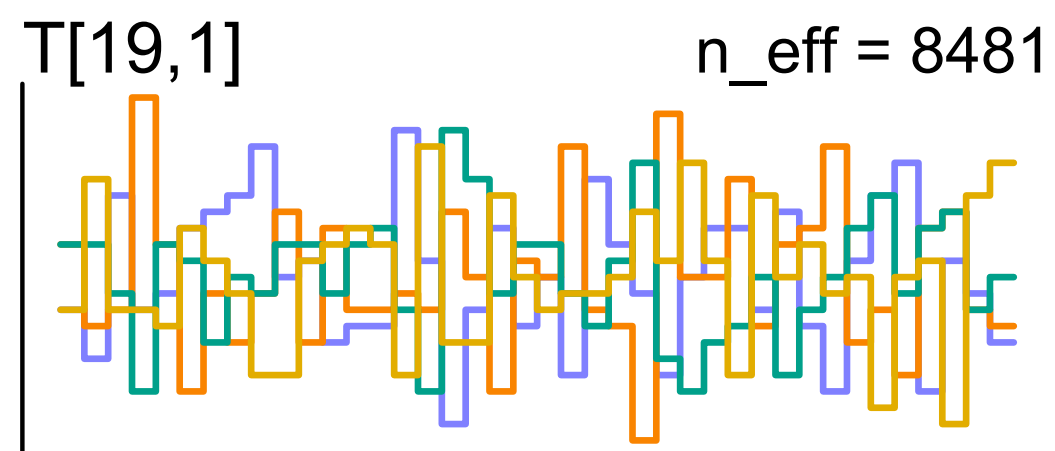
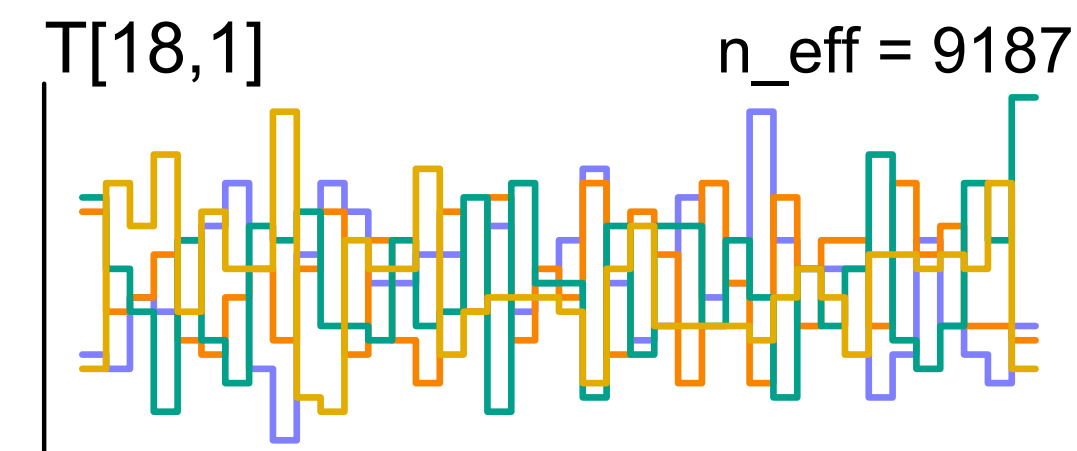
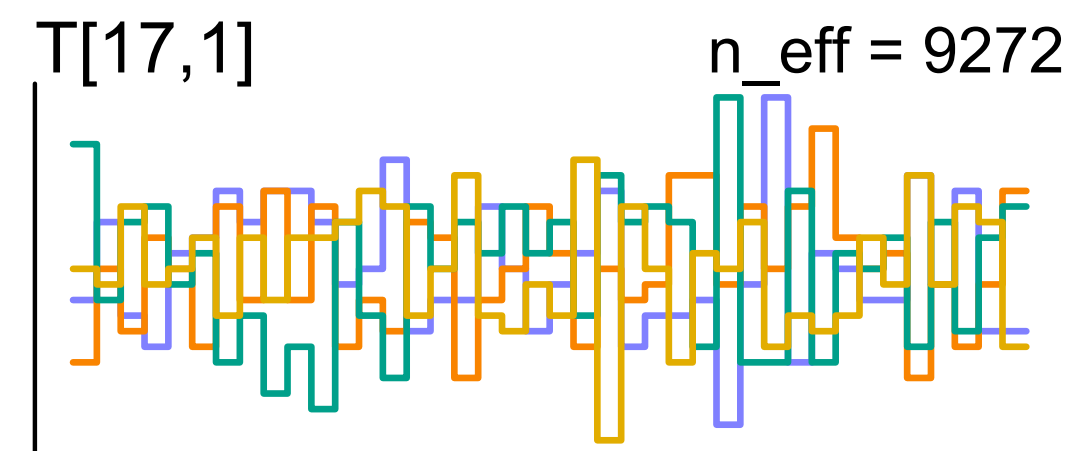
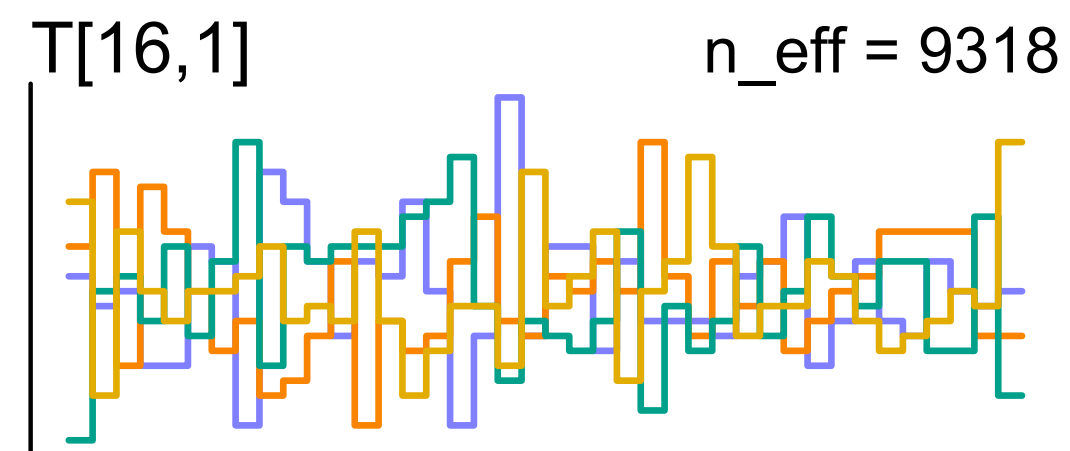
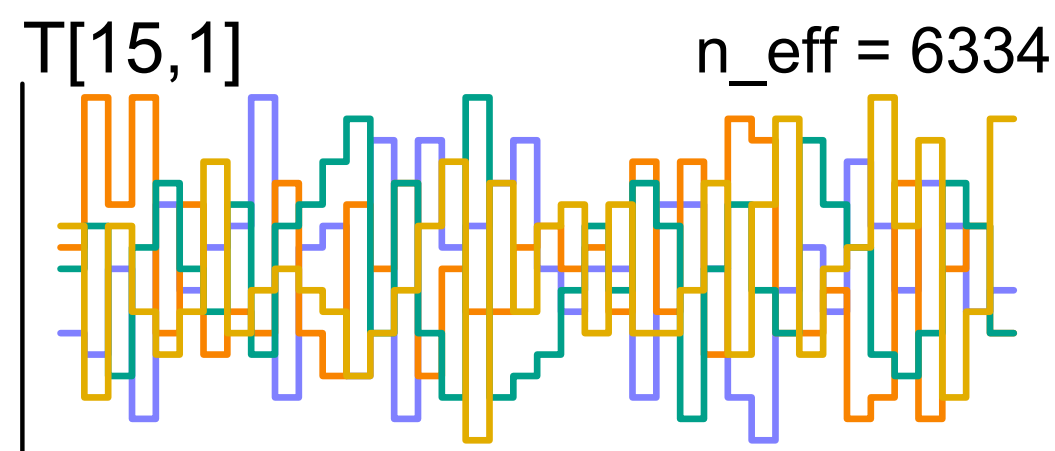
```
transpars> matrix[N_dyads,2]:T <-  
  compose_noncentered( rep_vector(sigma_T,2) , L_Rho_T , Z ),  
matrix[2,N_dyads]:Z ~ normal( 0 , 1 ),  
cholesky_factor_corr[2]:L_Rho_T ~ lkj_corr_cholesky( 2 ),  
sigma_T ~ exponential(1),
```

```
## compute correlation matrix for dyads
```

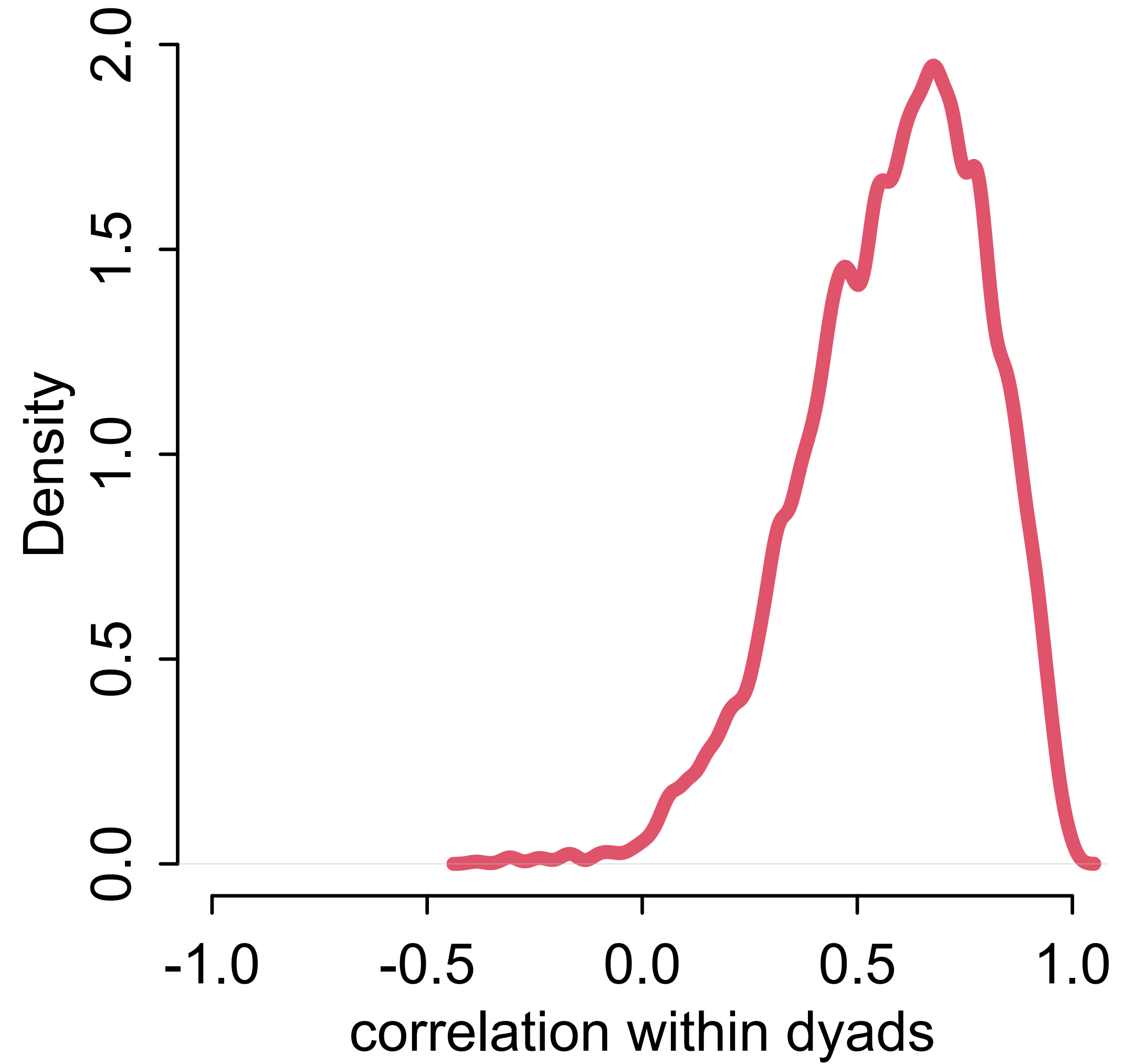
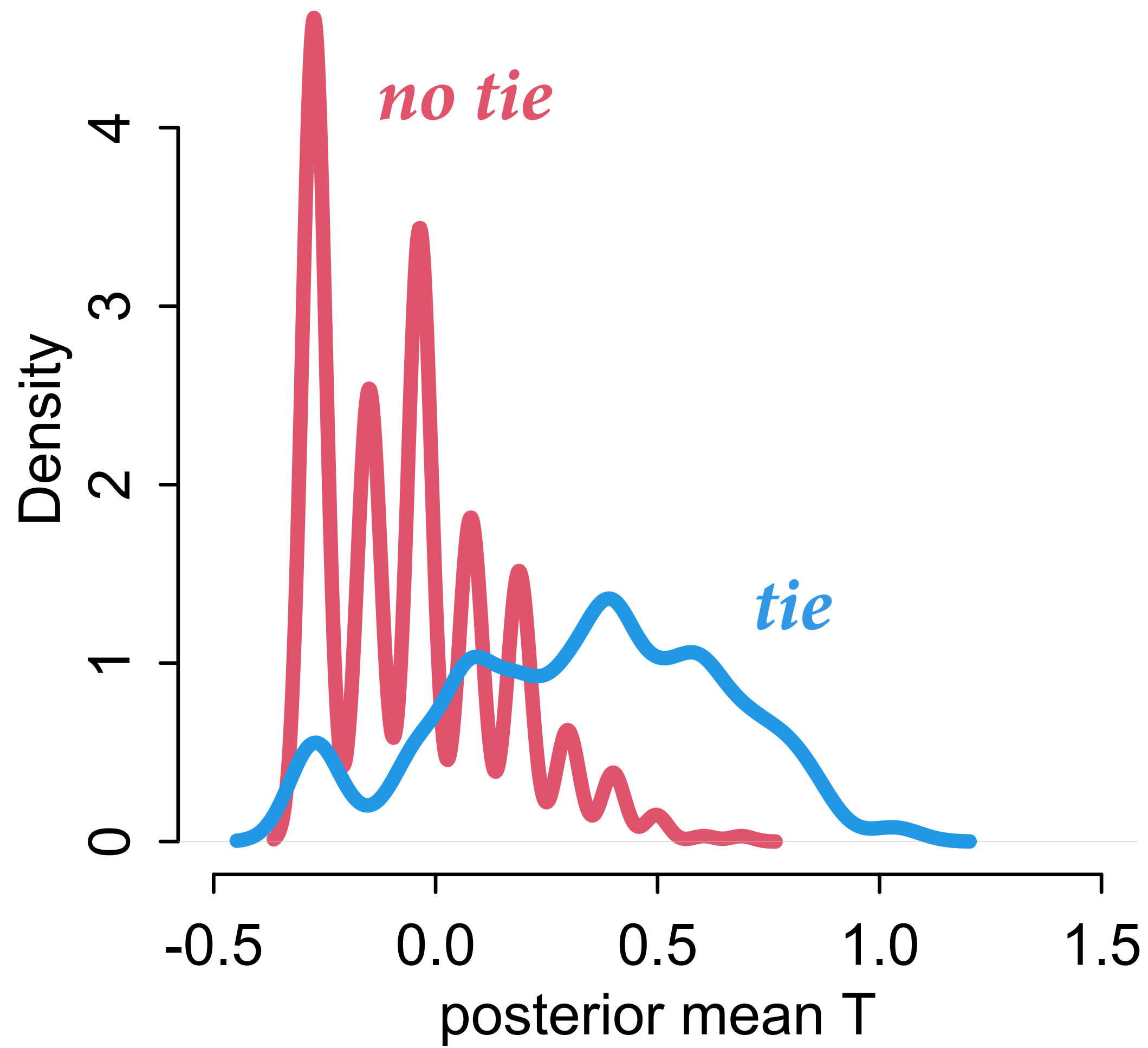
```
gq> matrix[2,2]:Rho_T <<- Chol_to_Corr( L_Rho_T )
```

```
)
```

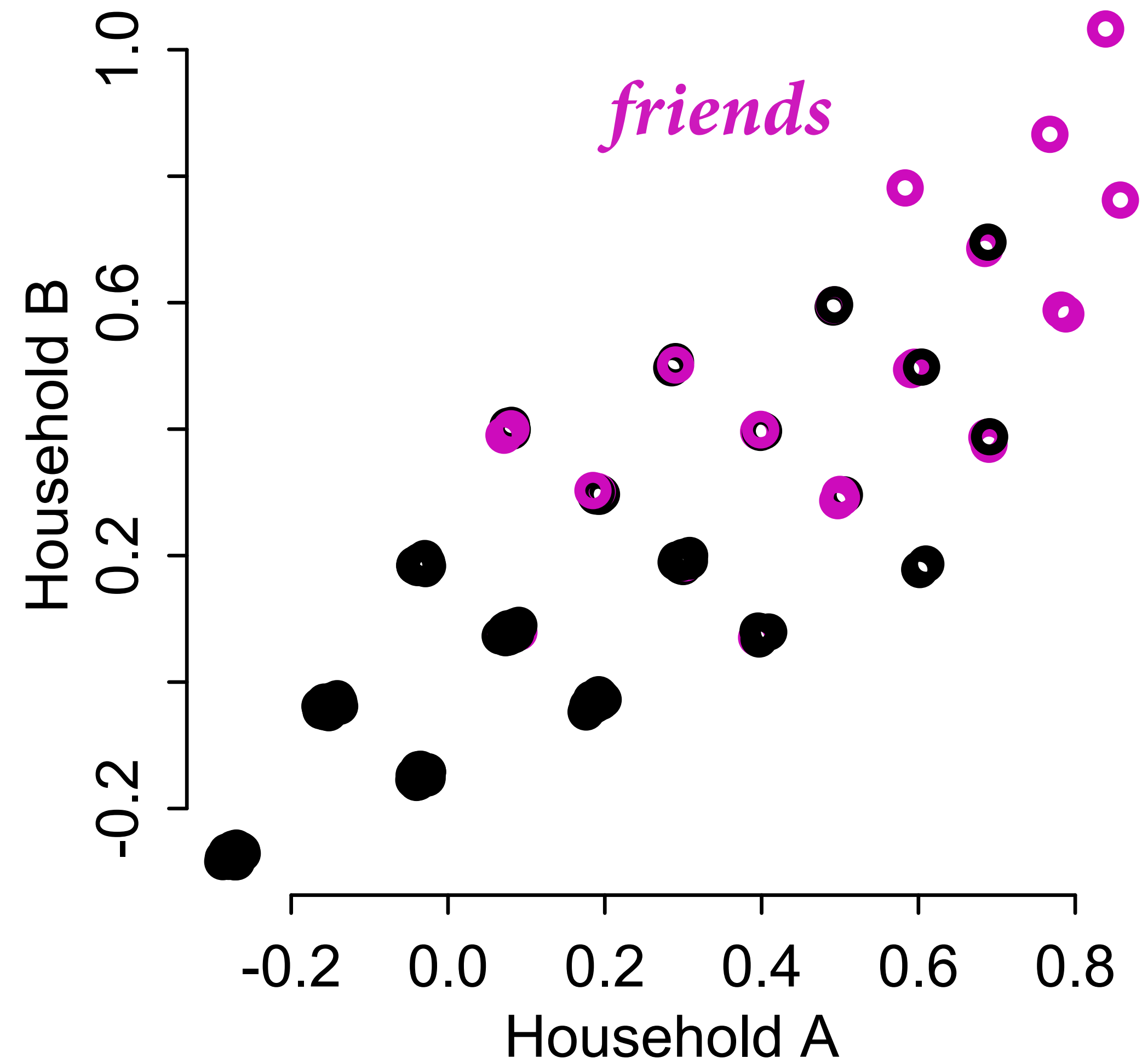
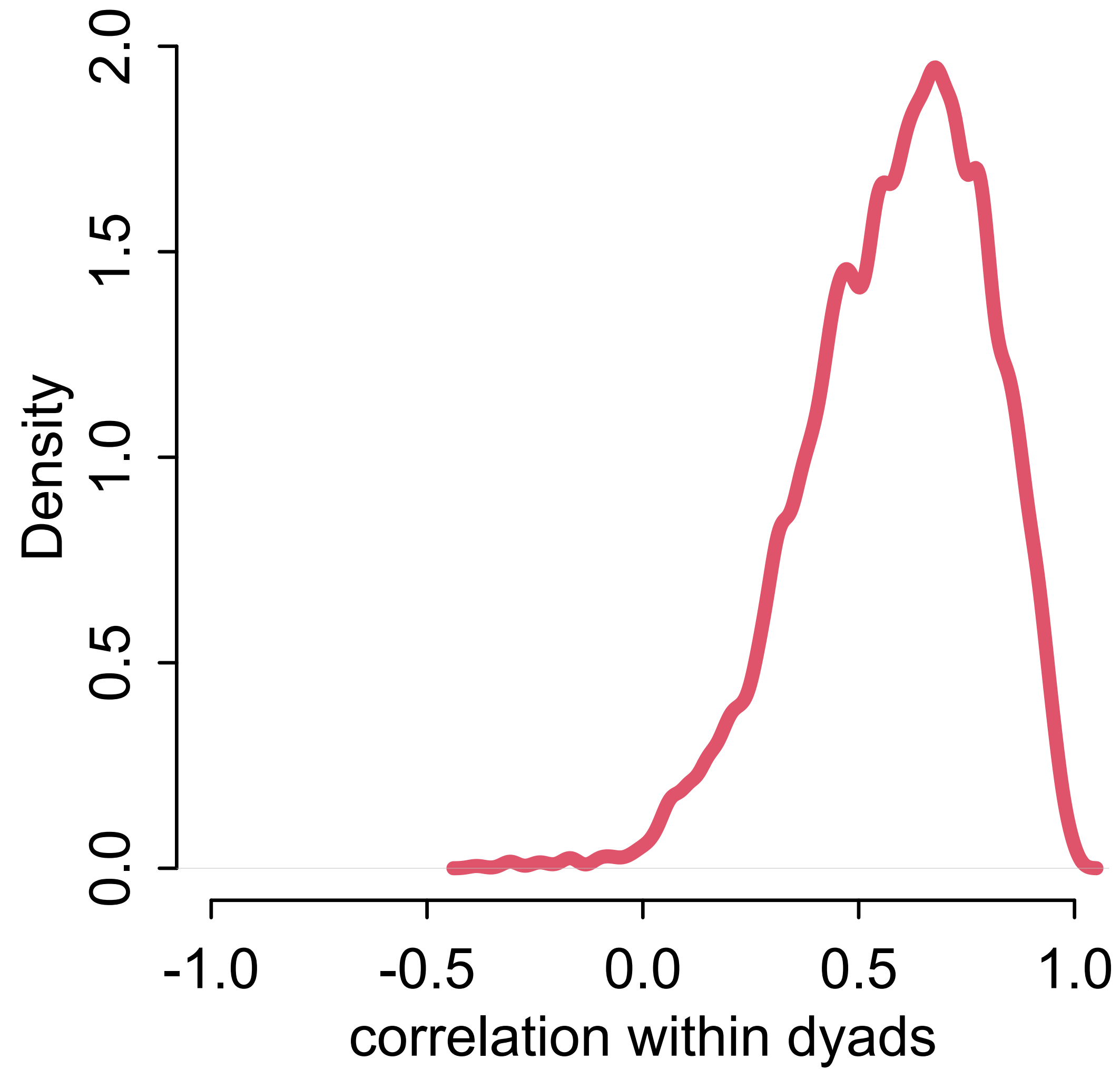
```
mGD <- ulam( f_dyad , data=sim_data , chains=4 , cores=4 , iter=2000 )
```



Posterior ties



Posterior ties



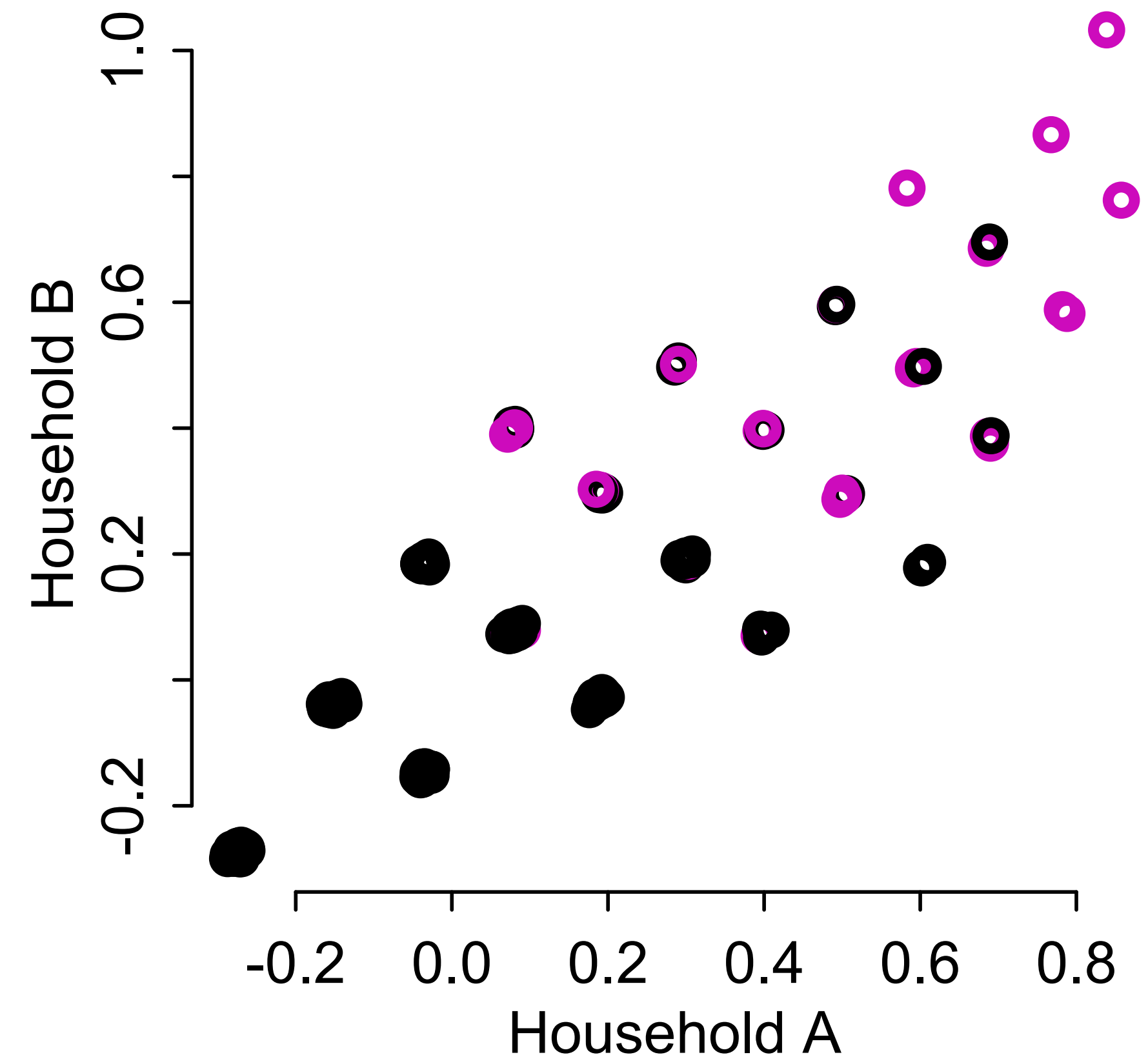
Drawing the Social Owl

(1) Estimand: Reciprocity & what explains it

(2) Generative model

(3) Statistical model

(4) Analyze sample



```
# analyze sample
kl_data <- list(
  N_dyads = nrow(kl_dyads),
  N_households = max(kl_dyads$hidB),
  D = 1:nrow(kl_dyads),
  HA = kl_dyads$hidA,
  HB = kl_dyads$hidB,
  GAB = kl_dyads$giftsAB,
  GBA = kl_dyads$giftsBA )

mGDkl <- ulam( f_dyad , data=kl_data , chains=4 , cores=4 , iter=2000 )

precis( mGDkl , depth=3 , pars=c("a","Rho_T","sigma_T") )
```

```

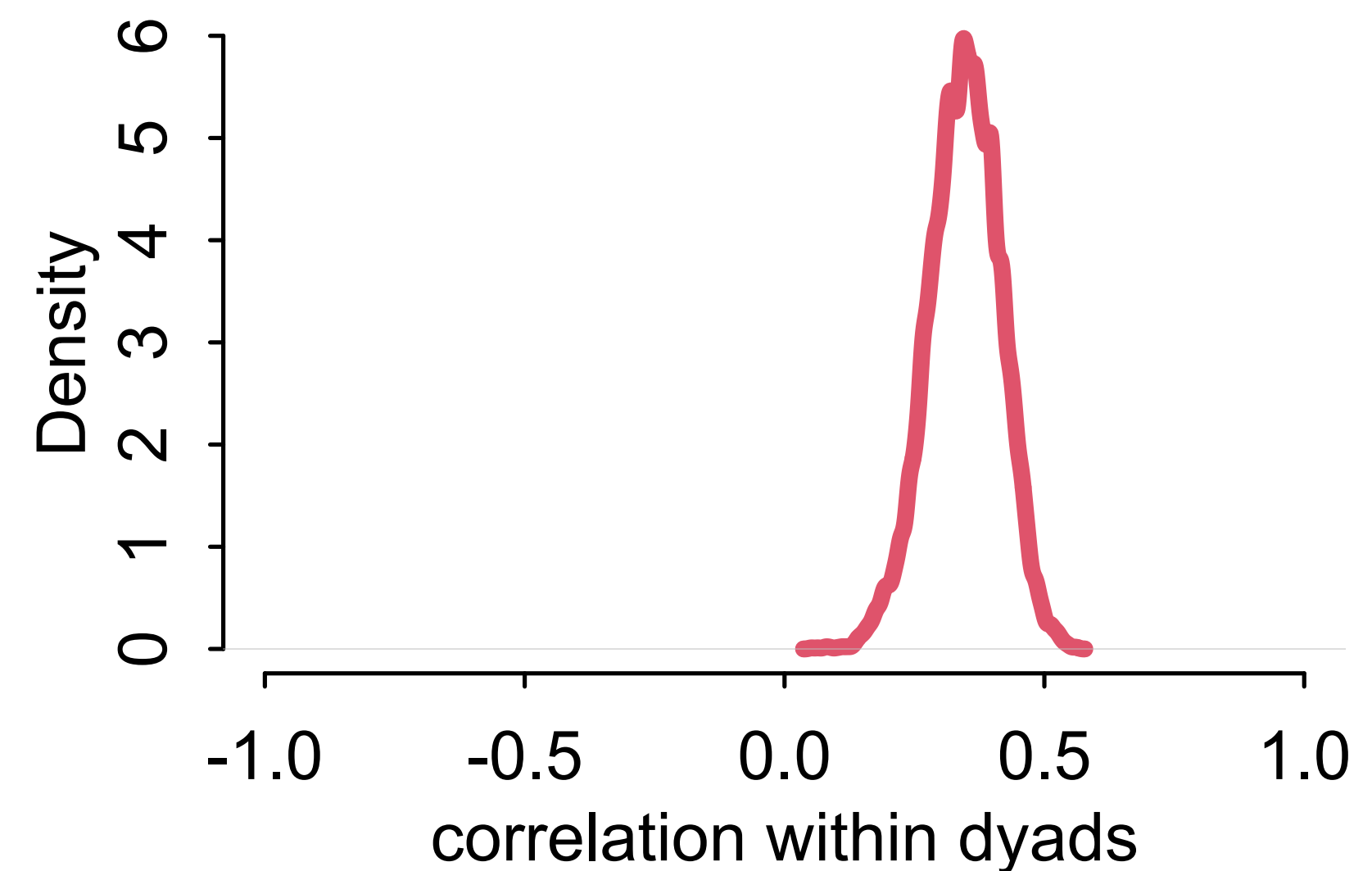
# analyze sample
kl_data <- list(
  N_dyads = nrow(kl_dyads),
  N_households = max(kl_dyads$hidB),
  D = 1:nrow(kl_dyads),
  HA = kl_dyads$hidA,
  HB = kl_dyads$hidB,
  GAB = kl_dyads$giftsAB,
  GBA = kl_dyads$giftsBA )

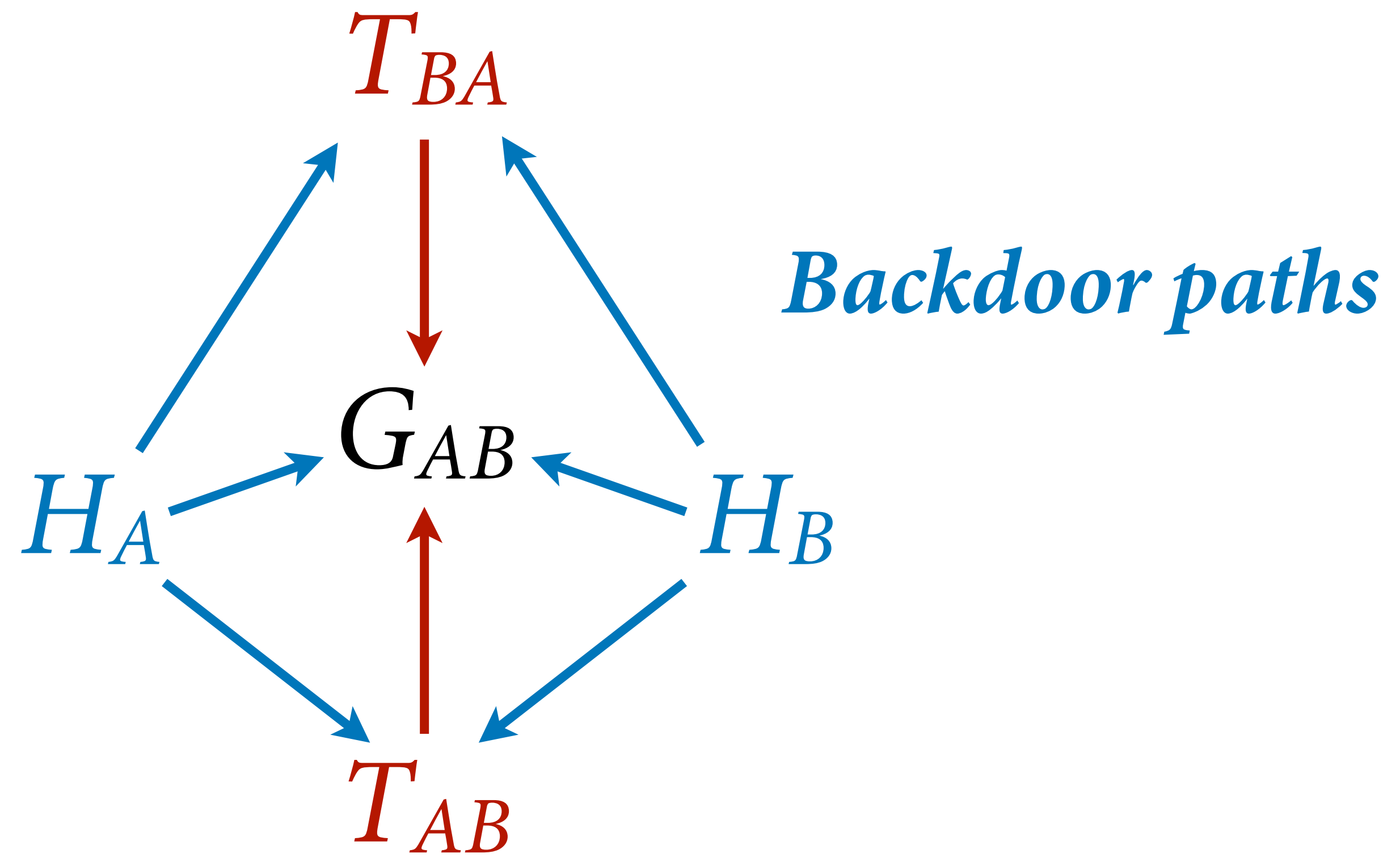
mGDkl <- ulam( f_dyad , data=kl_data , chains=4 , cores=4 , iter=2000 )

precis( mGDkl , depth=3 , pars=c("a","Rho_T","sigma_T") )

```

| | mean | sd | 5.5% | 94.5% | n_eff | Rhat4 |
|------------|------|------|------|-------|-------|-------|
| a | 0.55 | 0.08 | 0.42 | 0.68 | 2246 | 1.00 |
| Rho_T[1,1] | 1.00 | 0.00 | 1.00 | 1.00 | NaN | NaN |
| Rho_T[1,2] | 0.35 | 0.07 | 0.24 | 0.45 | 1351 | 1.00 |
| Rho_T[2,1] | 0.35 | 0.07 | 0.24 | 0.45 | 1351 | 1.00 |
| Rho_T[2,2] | 1.00 | 0.00 | 1.00 | 1.00 | NaN | NaN |
| sigma_T | 1.44 | 0.06 | 1.35 | 1.55 | 1249 | 1.01 |





PAUSE

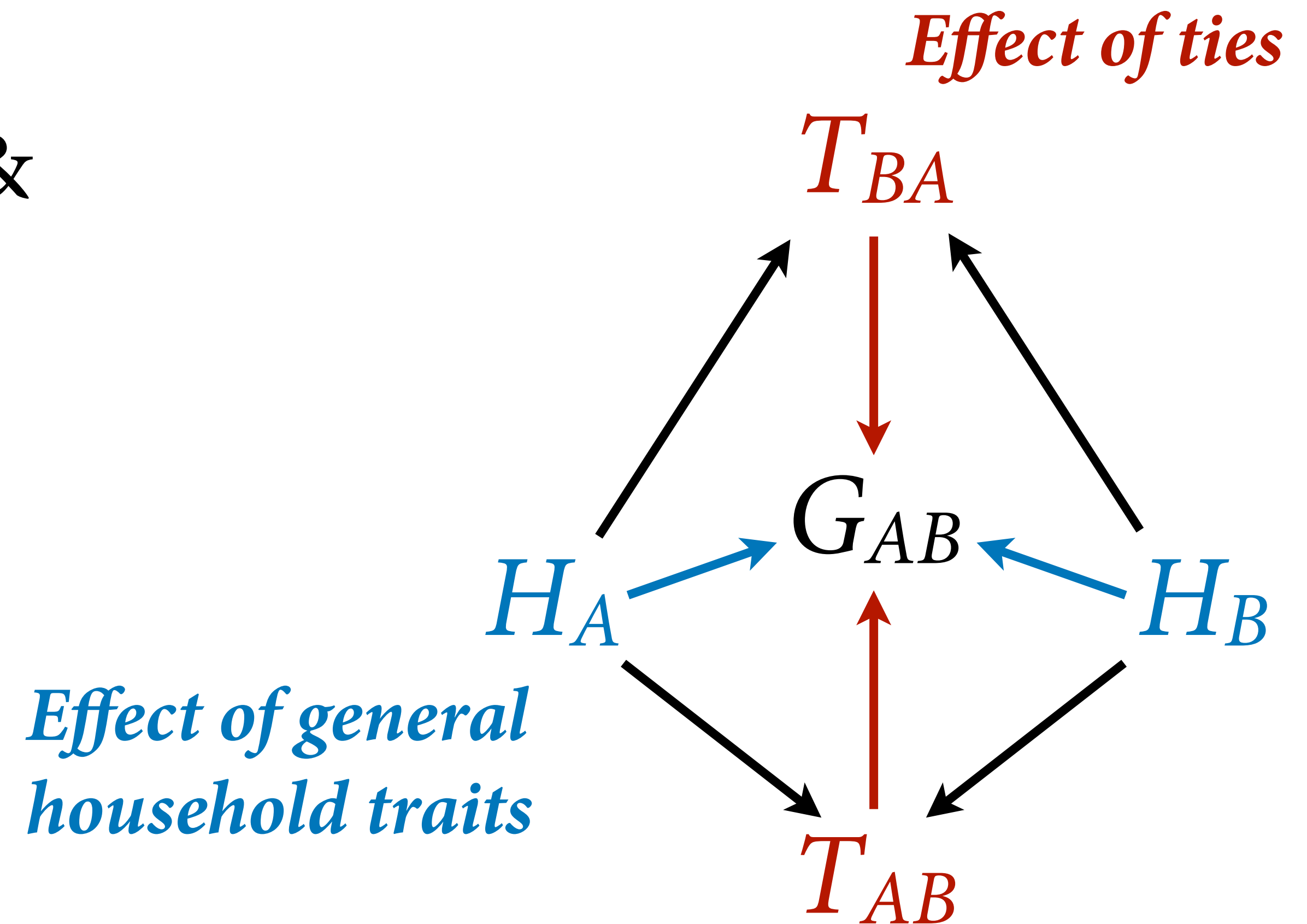
Drawing the Social Owl

(1) Estimand: Reciprocity & what explains it

(2) Generative model

(3) Statistical model

(4) Analyze sample




```

# N households
N <- 25
dyads <- t(combn(N,2))
N_dyads <- nrow(dyads)

# simulate "friendships" in which ties are shared
f <- rbern(N_dyads,0.1) # 10% of dyads are friends

# now simulate directed ties for all individuals
# there can be ties that are not reciprocal
alpha <- (-3) # base rate of ties; -3 ≈ 0.05
y <- matrix(NA,N,N) # edge list
for ( i in 1:N ) for ( j in 1:N ) {
  if ( i != j ) {
    # directed tie from i to j
    ids <- sort( c(i,j) )
    the_dyad <- which( dyads[,1]==ids[1] & dyads[,2]==ids[2] )
    p_tie <- f[the_dyad] + (1-f[the_dyad])*inv_logit( alpha )
    y[i,j] <- rbern( 1 , p_tie )
  }
}#ij

```

```

# simulate wealth
W <- rnorm(N) # standardized relative wealth in community
bWG <- 0.5 # effect of wealth on giving - rich give more
bWR <- (-1) # effect of wealth on receiving - rich get less / poor get more

# now simulate gifts
giftsAB <- rep(NA,N_dyads)
giftsBA <- rep(NA,N_dyads)
lambda <- log(c(0.5,2)) # rates of giving for y=0,y=1
for ( i in 1:N_dyads ) {
  A <- dyads[i,1]
  B <- dyads[i,2]
  giftsAB[i] <- rpois( 1 , exp( lambda[1+y[A,B]] + bWG*W[A] + bWR*W[B] ) )
  giftsBA[i] <- rpois( 1 , exp( lambda[1+y[B,A]] + bWG*W[B] + bWR*W[A] ) )
}

```

```
# simulate wealth
```

```
W <- rnorm(N) # standardized relative wealth in community
```

```
bWG <- 0.5 # effect of wealth on giving - rich give more
```

```
bWR <- (-1) # effect of wealth on receiving - rich get less / poor get more
```

```
# now simulate gifts
```

```
giftsAB <- rep(NA, N_dyads)
```

```
giftsBA <- rep(NA, N_dyads)
```

```
lambda <- log(c(0.5, 2)) # rates of giving for y=0, y=1
```

```
for ( i in 1:N_dyads ) {
```

```
  A <- dyads[i,1]
```

```
  B <- dyads[i,2]
```

```
  giftsAB[i] <- rpois( 1 , exp( lambda[1+y[A,B]] + bWG*W[A] + bWR*W[B] ) )
```

```
  giftsBA[i] <- rpois( 1 , exp( lambda[1+y[B,A]] + bWG*W[B] + bWR*W[A] ) )
```

```
}
```

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB}$$

$$\log(\lambda_{BA}) = \alpha + T_{BA}$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

$$\rho \sim \text{LKJCorr}(2)$$

$$\sigma \sim \text{Exponential}(1)$$

$$\alpha \sim \text{Normal}(0,1)$$

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

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$$\rho \sim \text{LKJCorr}(2)$$

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$$\alpha \sim \text{Normal}(0,1)$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

A's generalized giving

B's generalized receiving

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

$$\rho \sim \text{LKJCorr}(2)$$

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$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} G_A \\ R_A \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma_G^2 & r\sigma_G\sigma_R \\ r\sigma_G\sigma_R & \sigma_R^2 \end{bmatrix} \right)$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

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A's giving & receiving

Covariance matrix of household giving & receiving

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

$$\rho \sim \text{LKJCorr}(2)$$

$$\sigma \sim \text{Exponential}(1)$$

$$\alpha \sim \text{Normal}(0,1)$$

$$\begin{pmatrix} G_A \\ R_A \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \mathbf{R}_{GR}, \mathbf{S}_{GR} \right)$$

A's giving & receiving

Correlation matrix

Standard deviations

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

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$$\begin{pmatrix} G_A \\ R_A \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \mathbf{R}_{GR}, \mathbf{S}_{GR} \right)$$

$$\mathbf{R}_{GR} \sim \text{LKJCorr}(2)$$

$$\mathbf{S}_{GR} \sim \text{Exponential}(1)$$

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

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25 households

300 dyads

600 counts / 2871 transfers

602 social network parameters

53 household parameters

```

# general model
f_general <- alist(
  GAB ~ poisson( lambdaAB ),
  GBA ~ poisson( lambdaBA ),
  log(lambdaAB) <- a + T[D,1] + gr[HA,1] + gr[HB,2],
  log(lambdaBA) <- a + T[D,2] + gr[HB,1] + gr[HA,2],
  a ~ normal(0,1),

  ## dyad effects - non-centered
  transpars> matrix[N_dyads,2]:T <-
    compose_noncentered(rep_vector(sigma_T,2), L_Rho_T, Z),
  matrix[2,N_dyads]:Z ~ normal( 0 , 1 ),
  cholesky_factor_corr[2]:L_Rho_T ~ lkj_corr_cholesky( 2 ),
  sigma_T ~ exponential(1),

  ## gr matrix of varying effects
  transpars> matrix[N_households,2]:gr <-
    compose_noncentered( sigma_gr , L_Rho_gr , Zgr ),
  matrix[2,N_households]:Zgr ~ normal( 0 , 1 ),
  cholesky_factor_corr[2]:L_Rho_gr ~ lkj_corr_cholesky( 2 ),
  vector[2]:sigma_gr ~ exponential(1),

  ## compute correlation matrixes
  gq> matrix[2,2]:Rho_T <-<- Chol_to_Corr( L_Rho_T ),
  gq> matrix[2,2]:Rho_gr <-<- Chol_to_Corr( L_Rho_gr )
)
mGDGR <- ulam(f_general, data=sim_data, chains=4, cores=4, iter=2000)

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$$\rho \sim \text{LKJCorr}(2)$$

$$\sigma \sim \text{Exponential}(1)$$

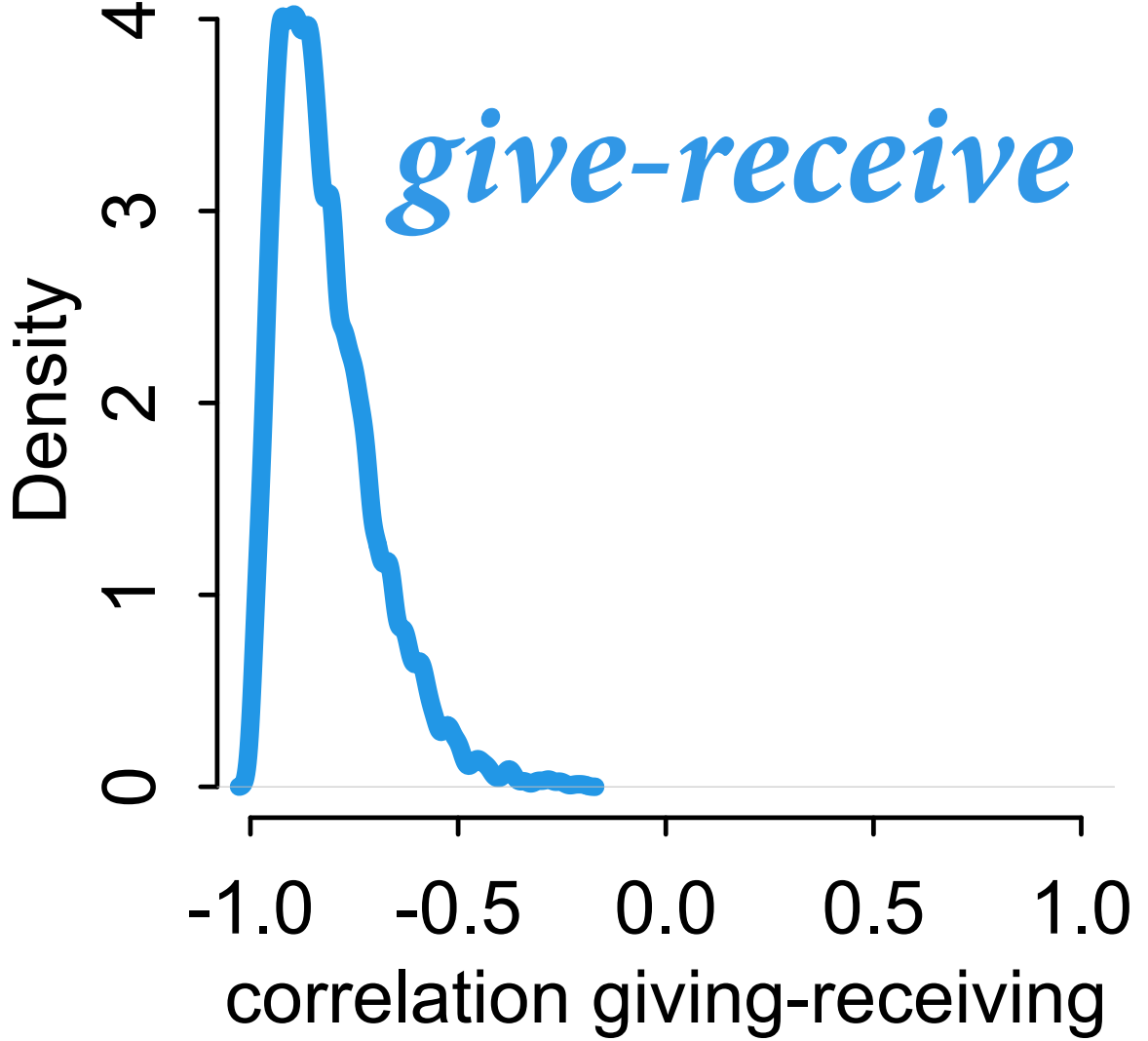
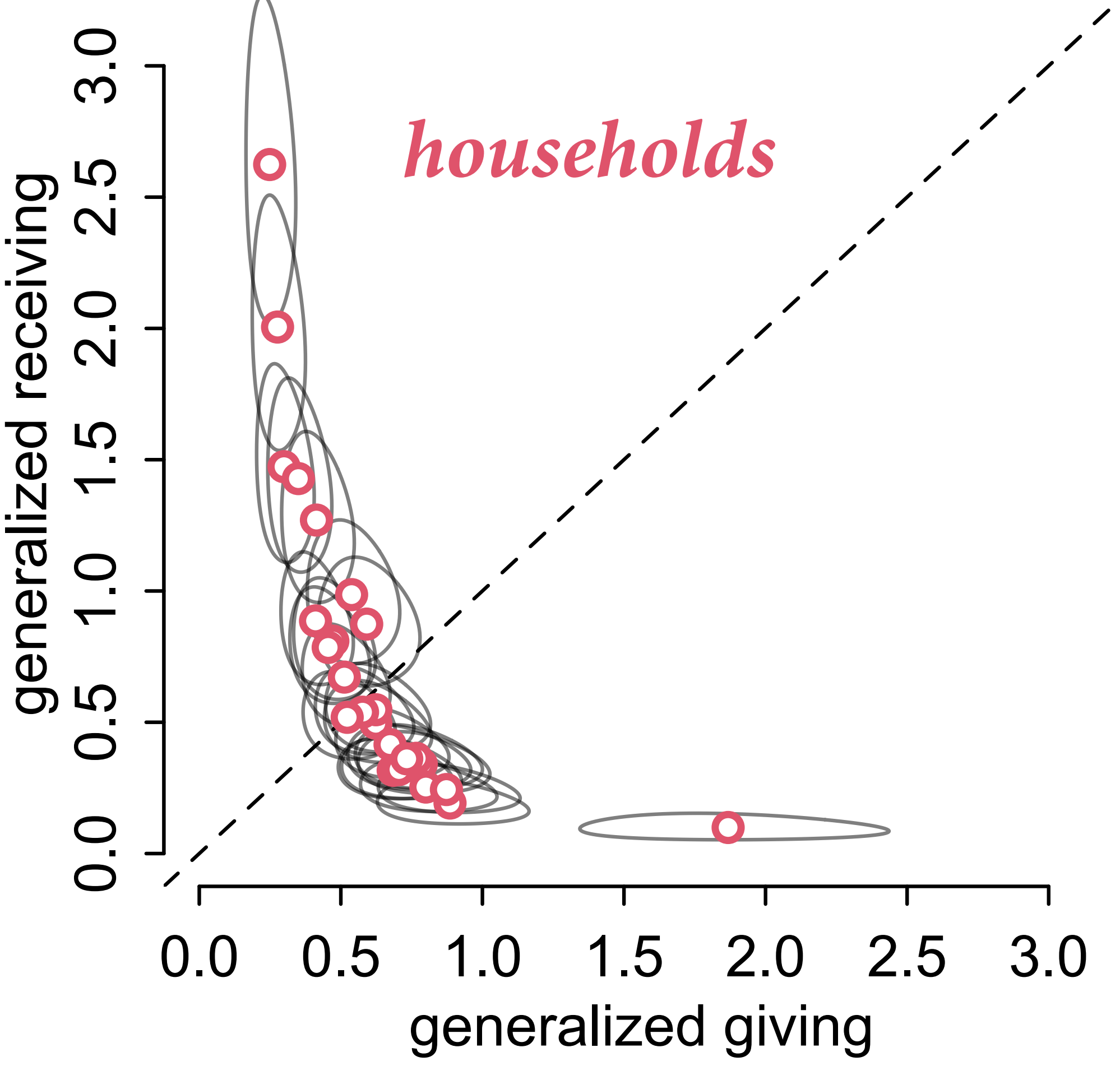
$$\alpha \sim \text{Normal}(0,1)$$

$$\begin{pmatrix} G_A \\ R_A \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \mathbf{R}_{GR}, \mathbf{S}_{GR} \right)$$

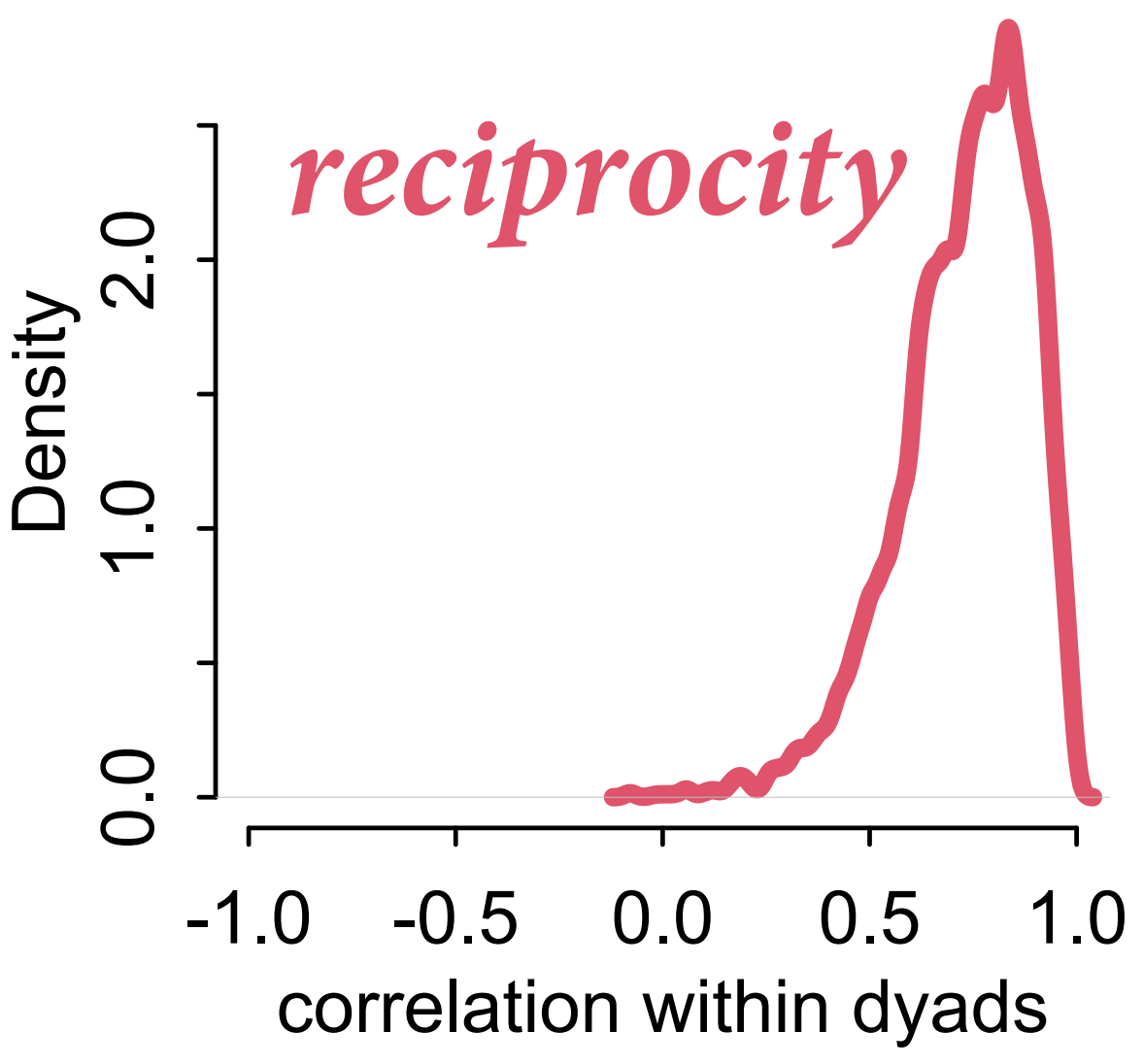
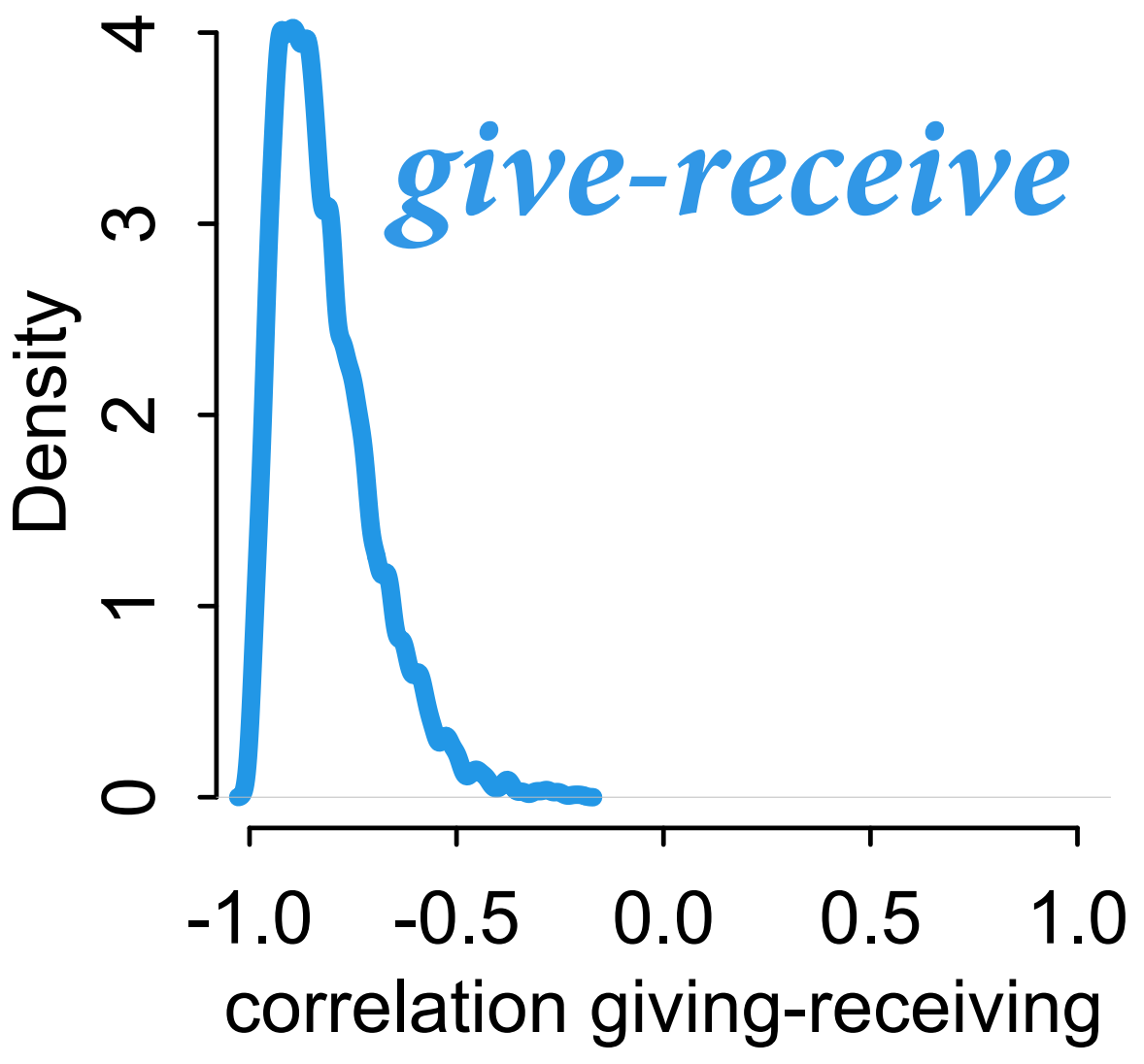
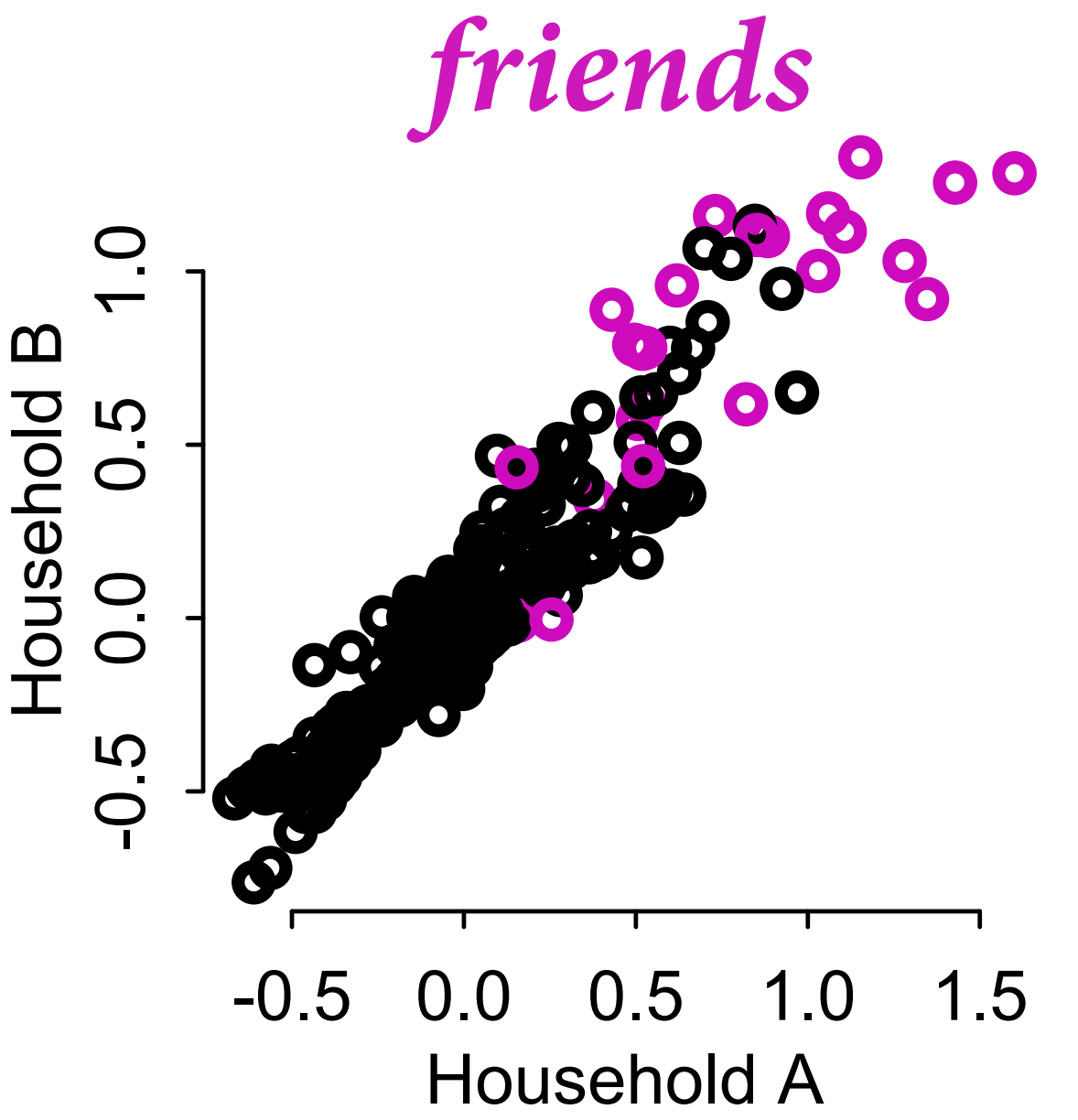
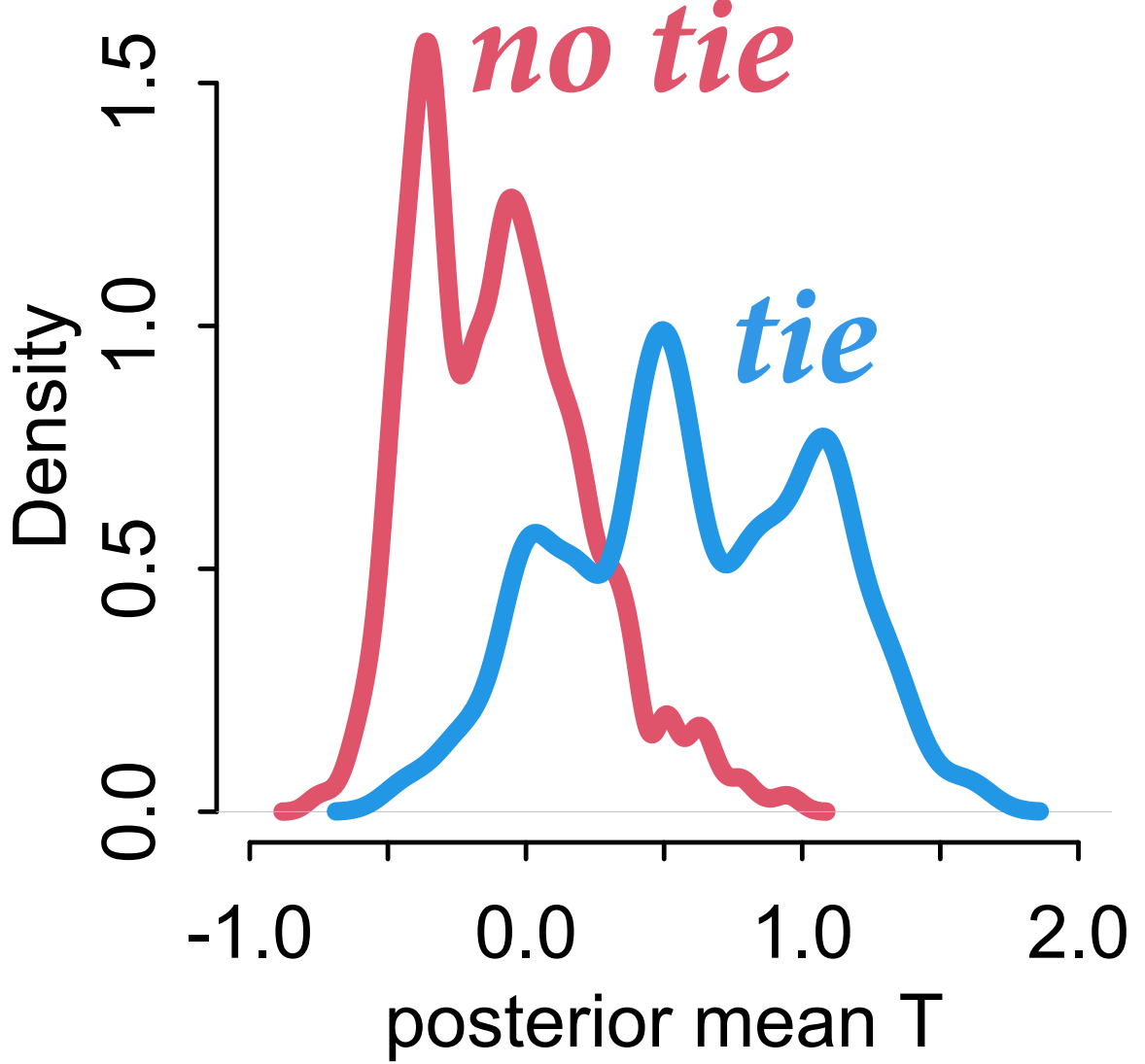
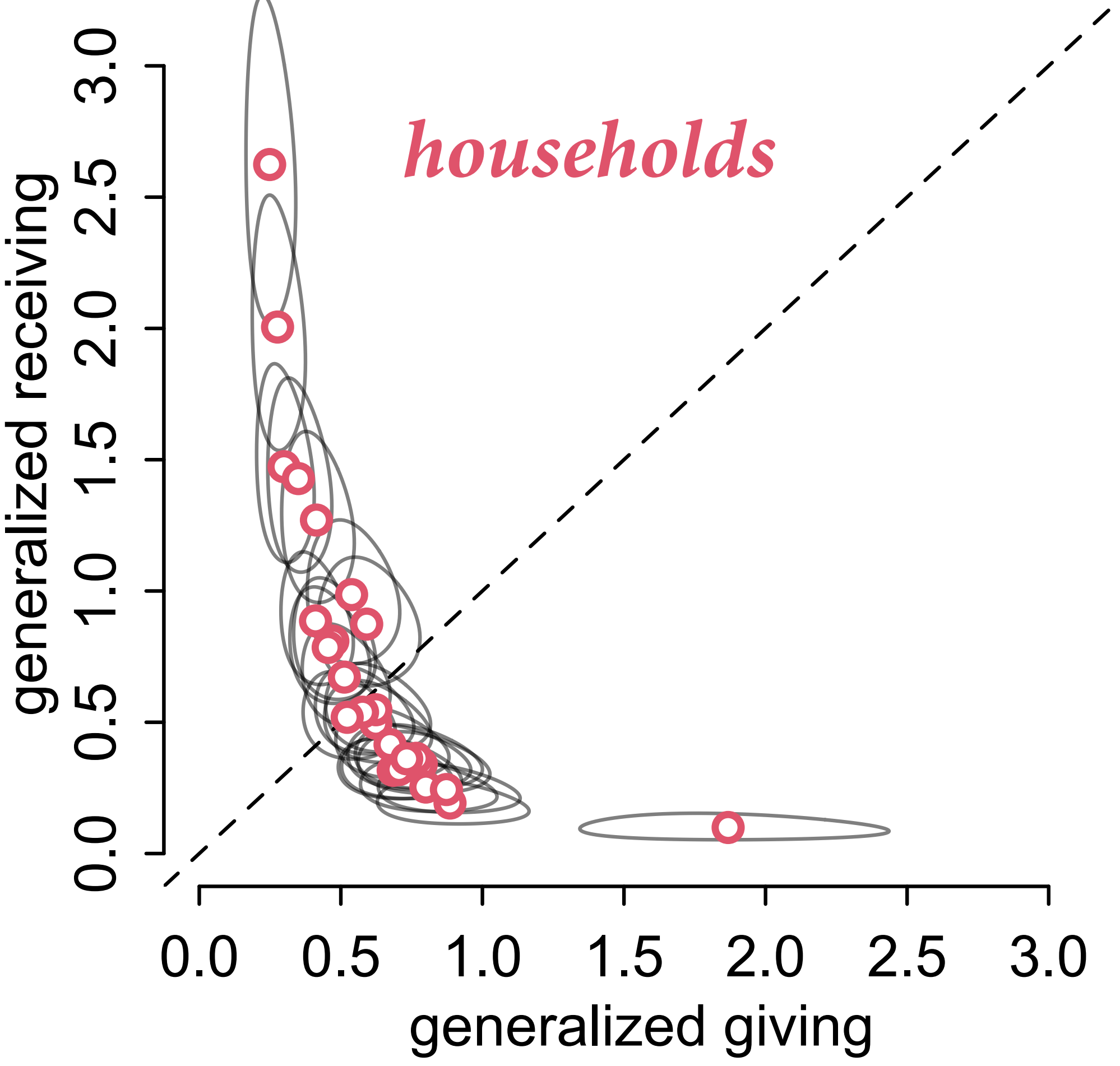
$$\mathbf{R}_{GR} \sim \text{LKJCorr}(2)$$

$$\mathbf{S}_{GR} \sim \text{Exponential}(1)$$

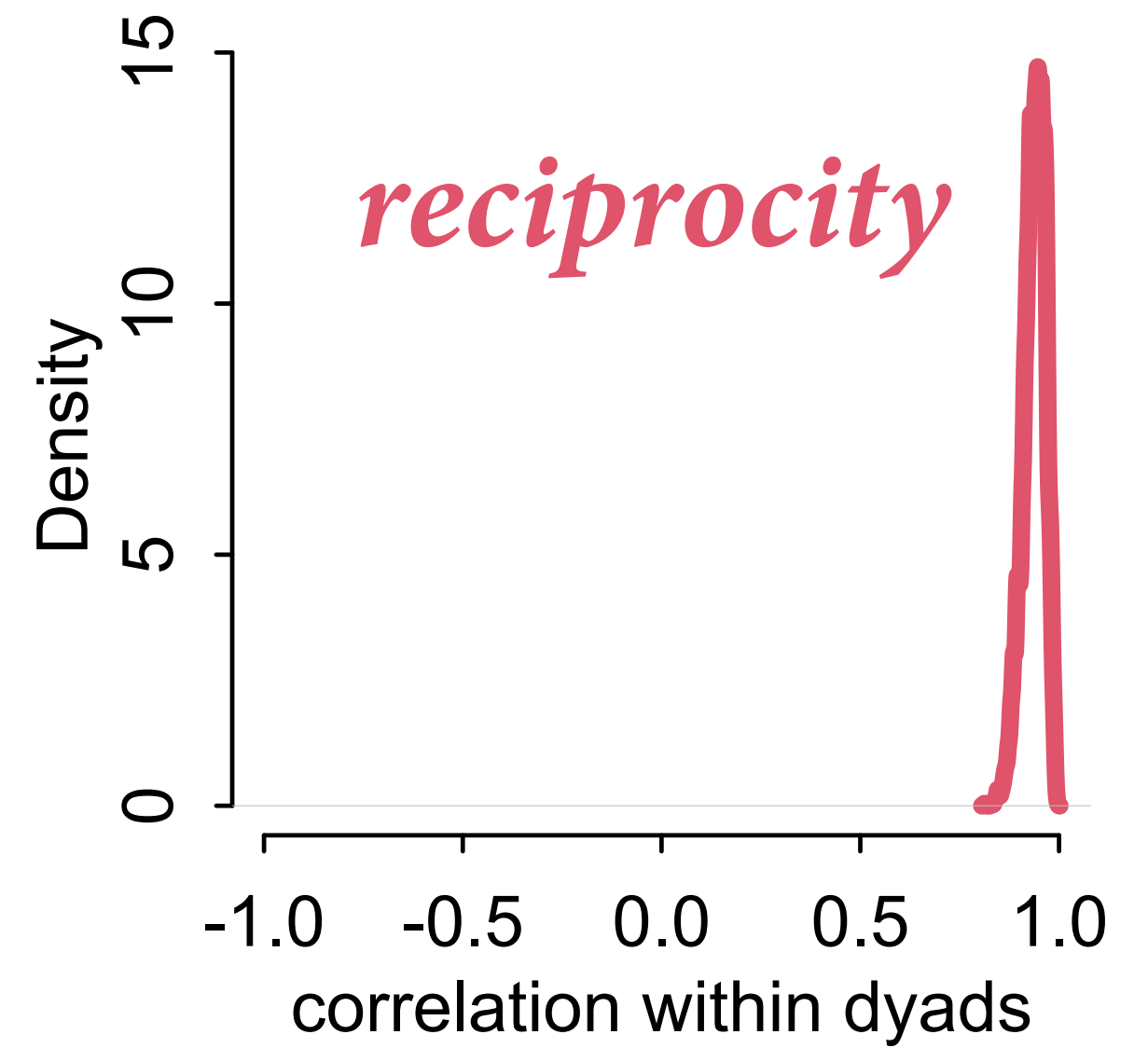
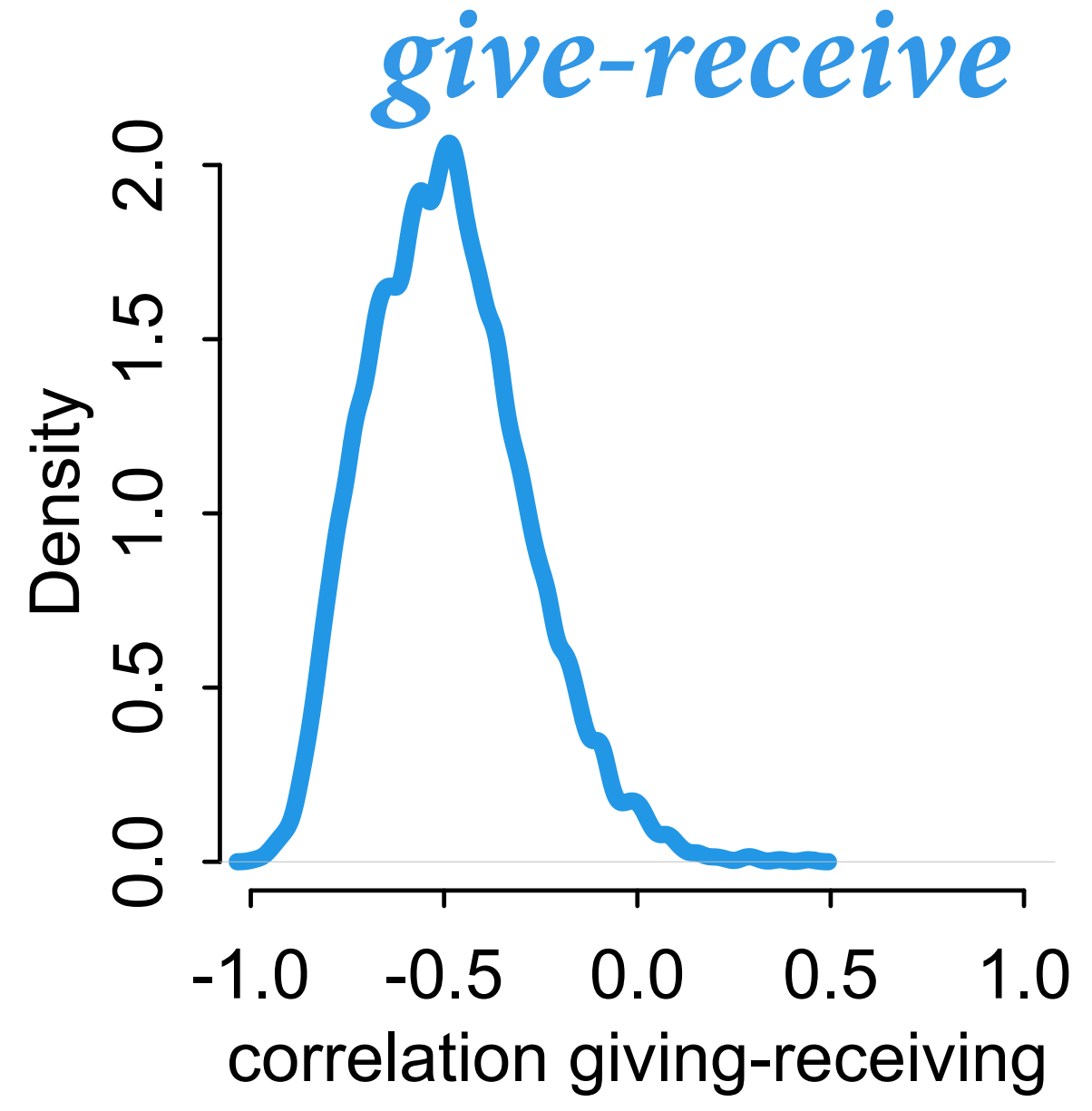
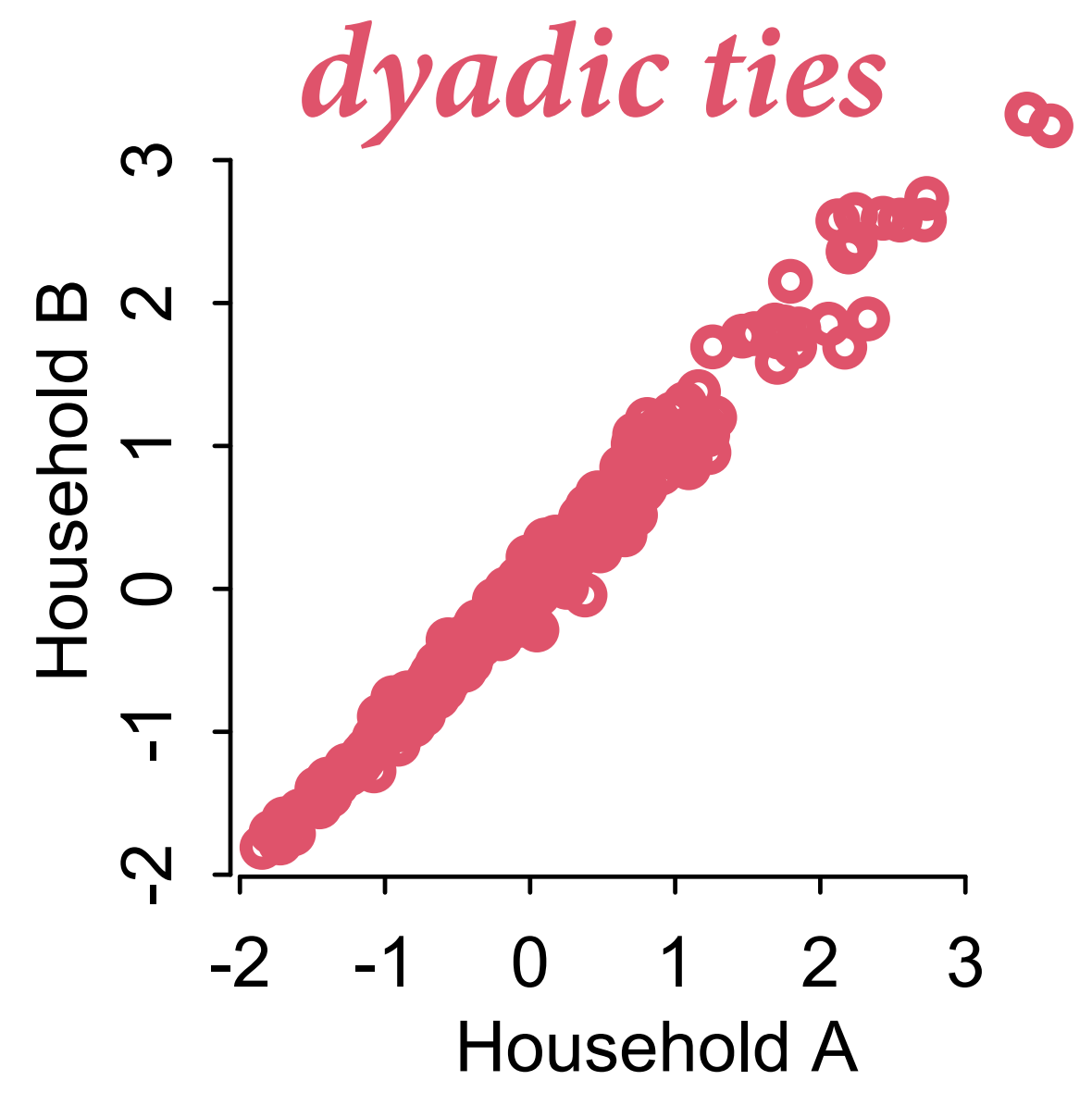
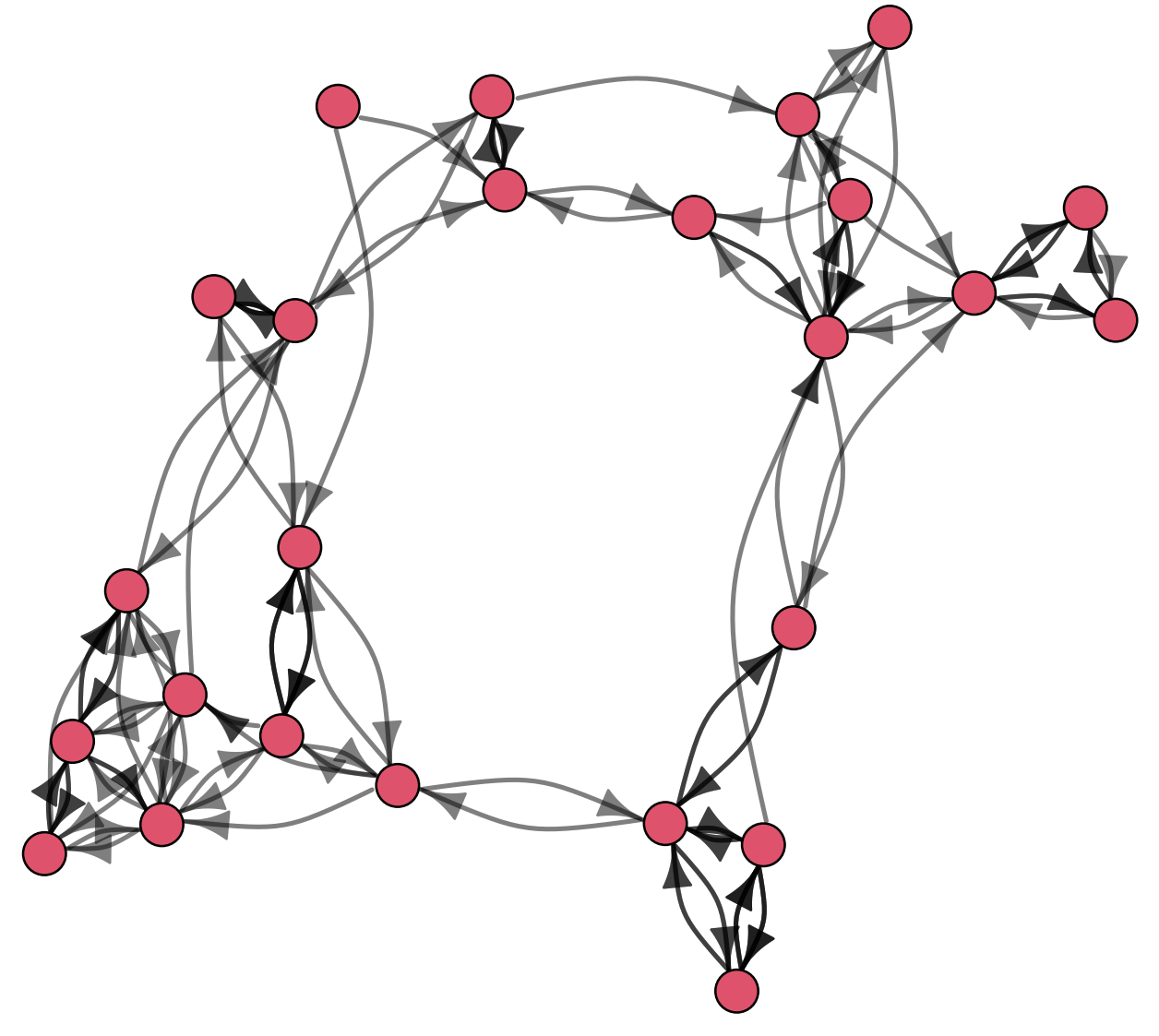
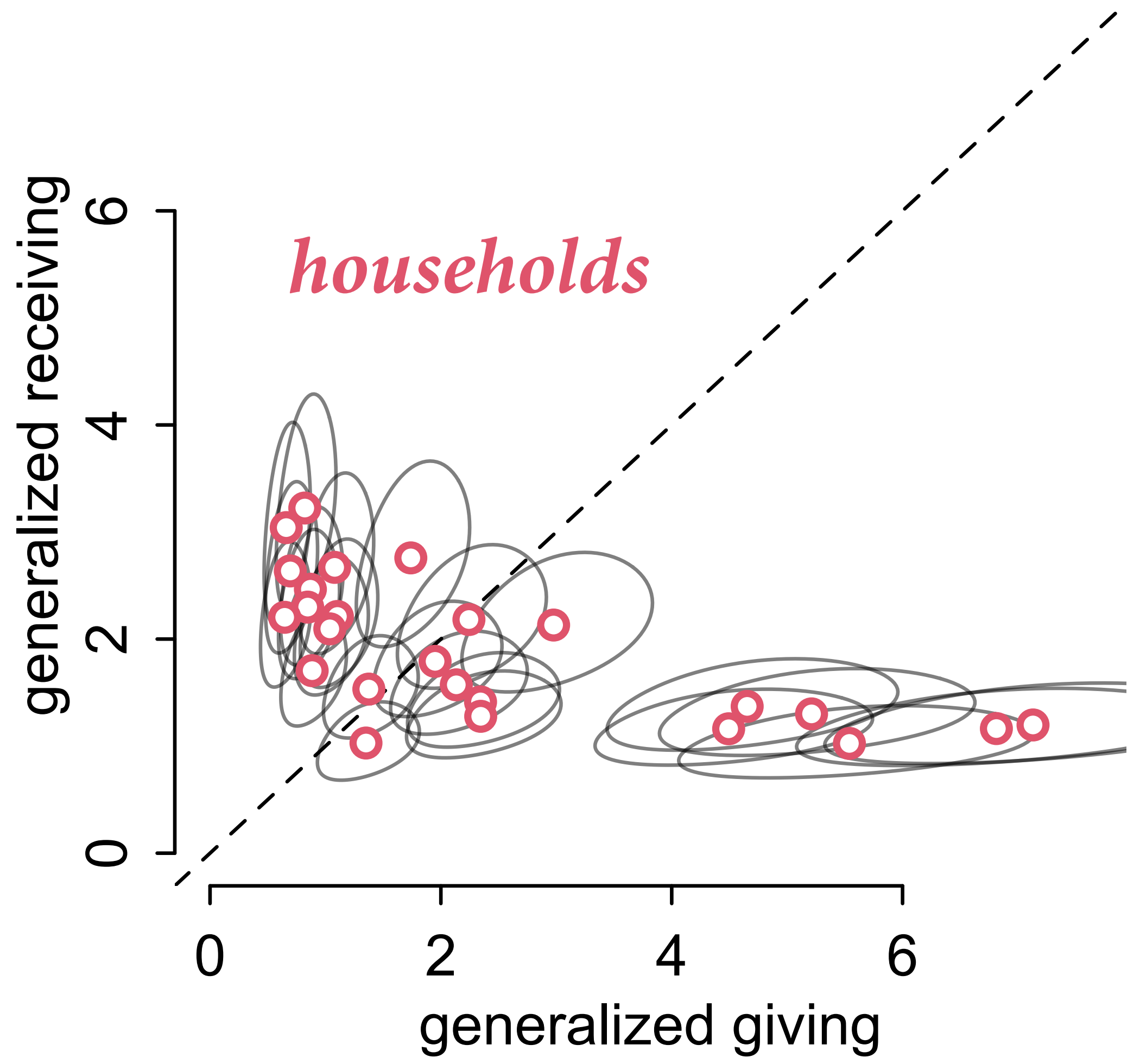
Synthetic data (validation)



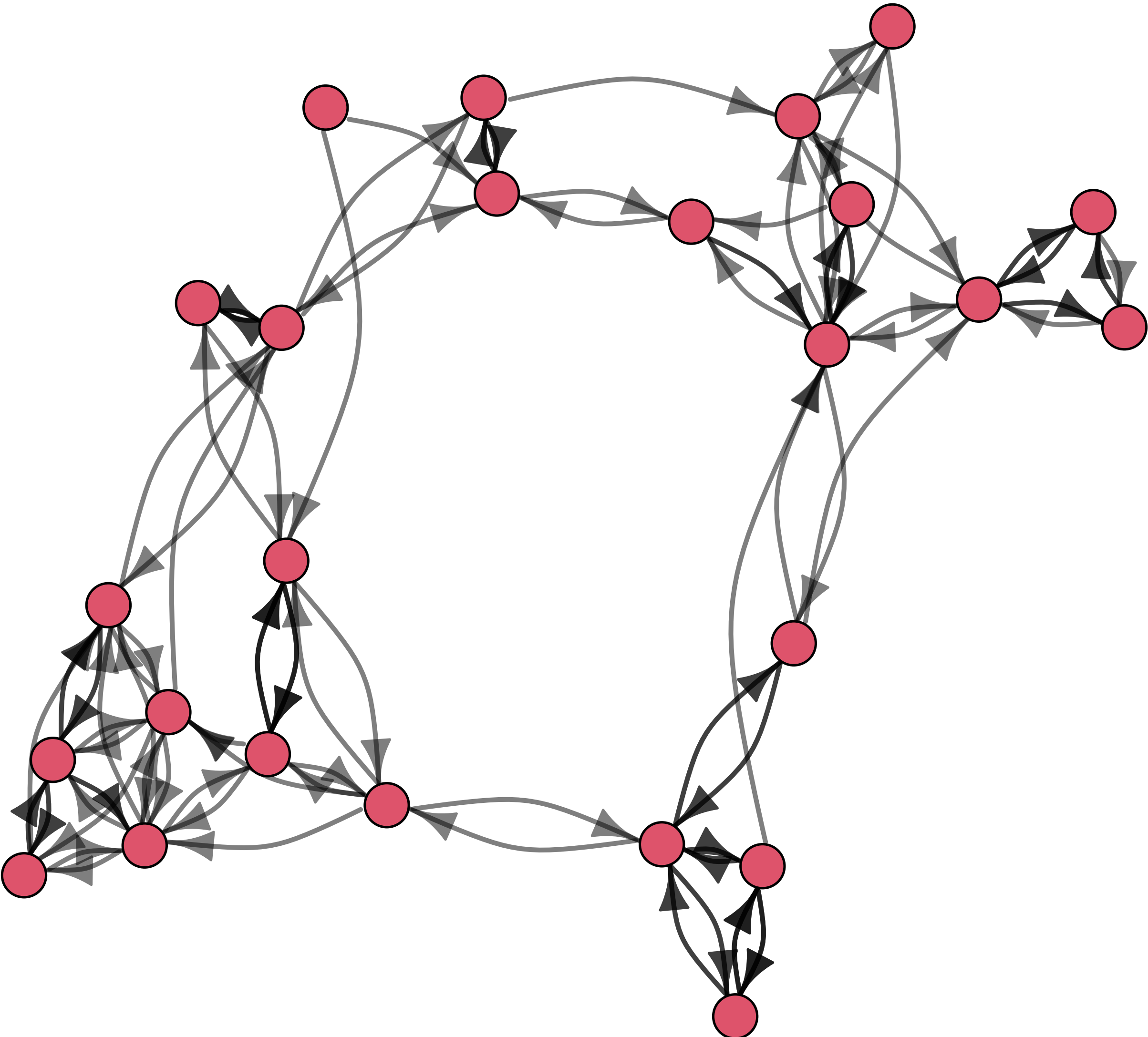
Synthetic data (validation)



Real data (analysis)

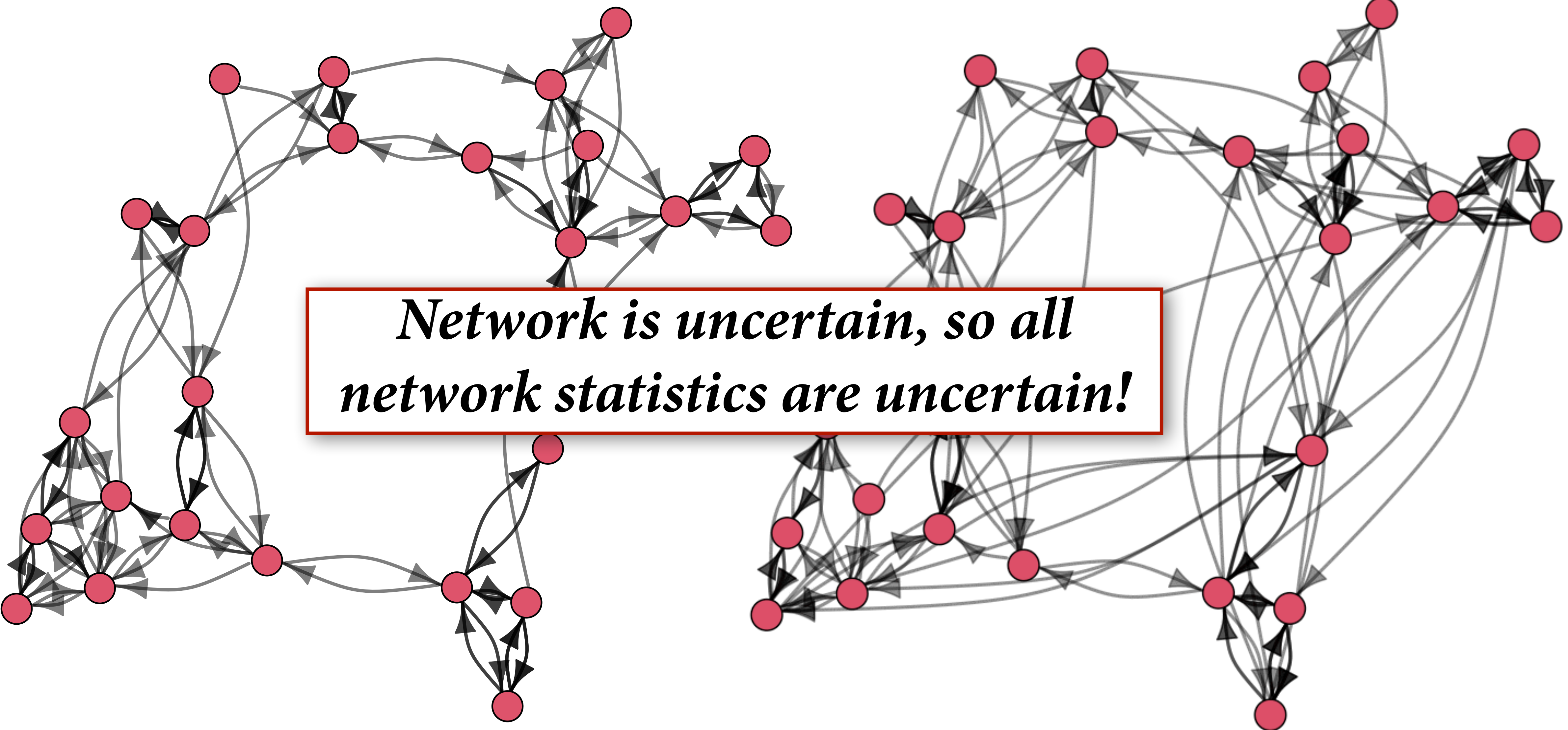


Posterior mean network

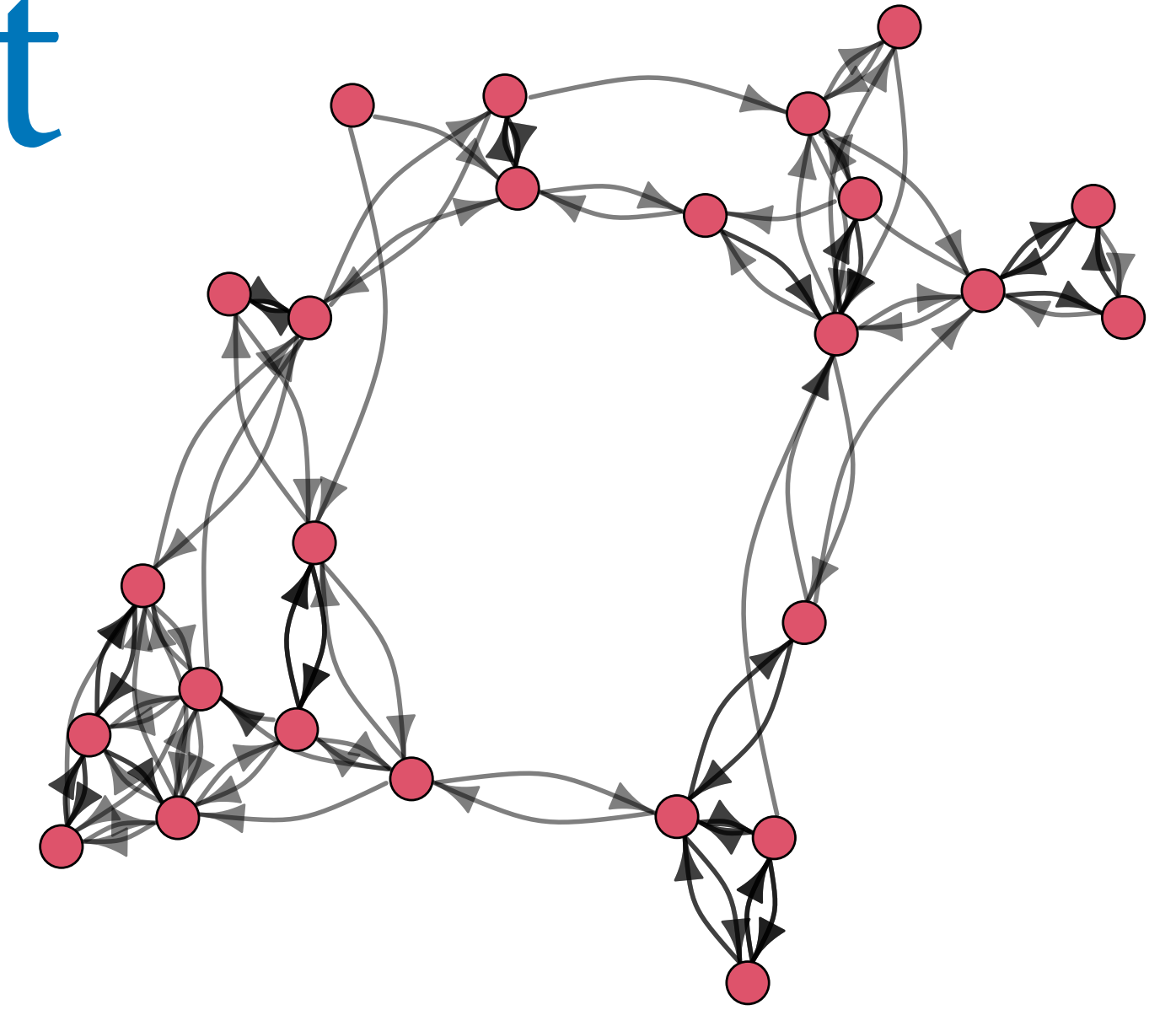


Posterior mean network

Samples from posterior



Social Networks Don't Exist



Varying effects are placeholders

Can model the network ties
(using dyad features)

Can model the giving/receiving
(using household features)

Relationships can cause other
relationships



$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + T_{AB} + G_A + R_B$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

$$\rho \sim \text{LKJCorr}(2)$$

$$\sigma \sim \text{Exponential}(1)$$

$$\alpha \sim \text{Normal}(0,1)$$

$$\begin{pmatrix} G_A \\ R_A \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \mathbf{R}_{GR}, \mathbf{S}_{GR} \right)$$

$$\mathbf{R}_{GR} \sim \text{LKJCorr}(2)$$

$$\mathbf{S}_{GR} \sim \text{Exponential}(1)$$

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$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{AB} + \mathcal{G}_A + \mathcal{R}_B$$

$$\mathcal{T}_{AB} = T_{AB} + \beta_A A_{AB}$$

*linear model
for tie strength*

*varying
effect*

*effect of
association
between A&B*

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

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$$\mathcal{G}_A = G_A + \beta_{W,G} W_A$$

linear model for giving

varying effect

effect of A's wealth on giving

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{BA}) = \alpha + T_{BA} + G_B + R_A$$

$$\begin{pmatrix} T_{AB} \\ T_{BA} \end{pmatrix} \sim \text{MVNormal} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \sigma^2 & \rho\sigma^2 \\ \rho\sigma^2 & \sigma^2 \end{bmatrix} \right)$$

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$$\mathcal{T}_{AB} = T_{AB} + \beta_A A_{AB}$$

$$\mathcal{G}_A = G_A + \beta_{W,G} W_A$$

$$\mathcal{R}_B = R_B + \beta_{W,R} W_B$$

*linear model
for receiving*

*varying
effect*

*effect of B's wealth
on receiving*

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{AB} + \mathcal{G}_A + \mathcal{R}_B$$

$$\mathcal{T}_{AB} = T_{AB} + \beta_A A_{AB}$$

$$\mathcal{G}_A = G_A + \beta_{W,G} W_A$$

$$\mathcal{R}_B = R_B + \beta_{W,R} W_B$$

$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{BA} + \mathcal{G}_B + \mathcal{R}_A$$

$$\mathcal{T}_{BA} = T_{BA} + \beta_A A_{AB}$$

$$\mathcal{G}_B = G_B + \beta_{W,G} W_B$$

$$\mathcal{R}_A = R_A + \beta_{W,R} W_A$$

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{AB} + \mathcal{G}_A + \mathcal{R}_B$$

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$$\mathcal{T}_{BA} = T_{BA} + \beta_A A_{AB}$$

$$\mathcal{G}_B = G_B + \beta_{W,G} W_B$$

$$\mathcal{R}_A = R_A + \beta_{W,R} W_A$$

```
# general model with features
```

```
f_houses <- alist(
```

```
  GAB ~ poisson( lambdaAB ),
```

```
  GBA ~ poisson( lambdaBA ),
```

```
# A to B
```

```
log(lambdaAB) <- a + TAB + GA + RB,
```

```
  TAB <- T[D,1] + bA*A,
```

```
  GA <- gr[HA,1] + bW[1]*W[HA] ,
```

```
  RB <- gr[HB,2] + bW[2]*W[HB] ,
```

```
# B to A
```

```
log(lambdaBA) <- a + TBA + GB + RA,
```

```
  TBA <- T[D,2] + bA*A,
```

```
  GB <- gr[HB,1] + bW[1]*W[HB] ,
```

```
  RA <- gr[HA,2] + bW[2]*W[HA] ,
```

```
# priors
```

```
a ~ normal(0,1),
```

```
vector[2]:bW ~ normal(0,1),
```

```
bA ~ normal(0,1),
```

$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{AB} + \mathcal{G}_A + \mathcal{R}_B$$

$$\mathcal{T}_{AB} = T_{AB} + \beta_A A_{AB}$$

$$\mathcal{G}_A = G_A + \beta_{W,G} W_A$$

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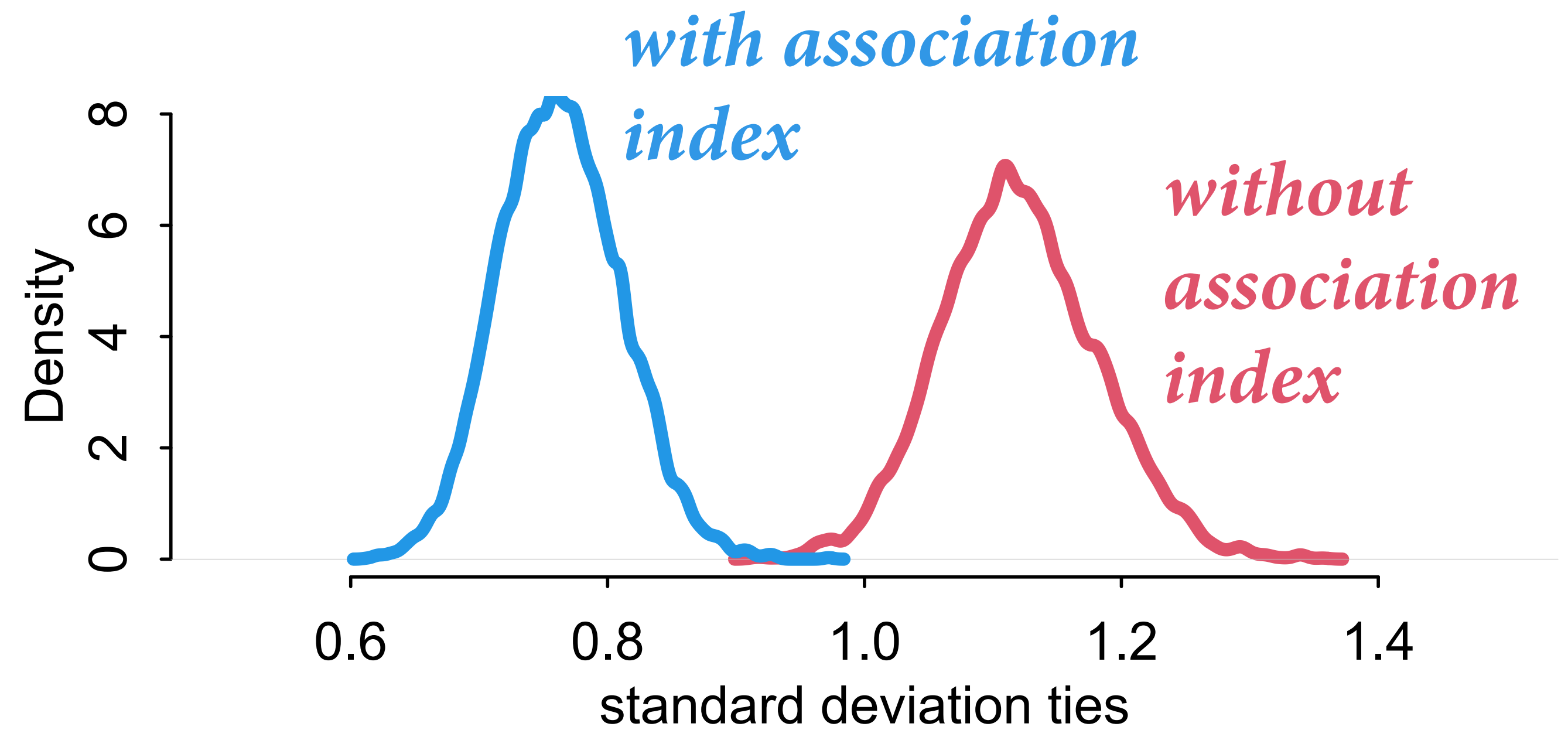
$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{BA} + \mathcal{G}_B + \mathcal{R}_A$$

$$\mathcal{T}_{BA} = T_{BA} + \beta_A A_{AB}$$

$$\mathcal{G}_B = G_B + \beta_{W,G} W_B$$

$$\mathcal{R}_A = R_A + \beta_{W,R} W_A$$



$$G_{AB} \sim \text{Poisson}(\lambda_{AB})$$

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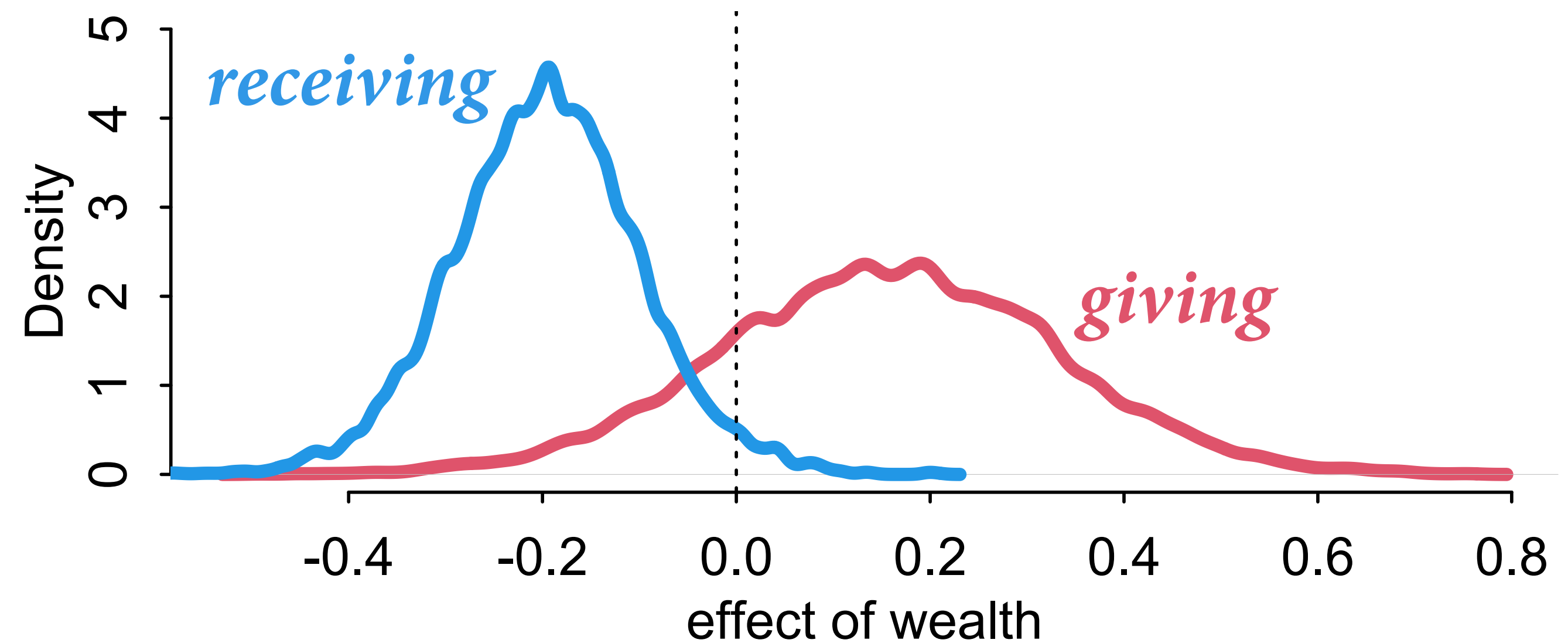
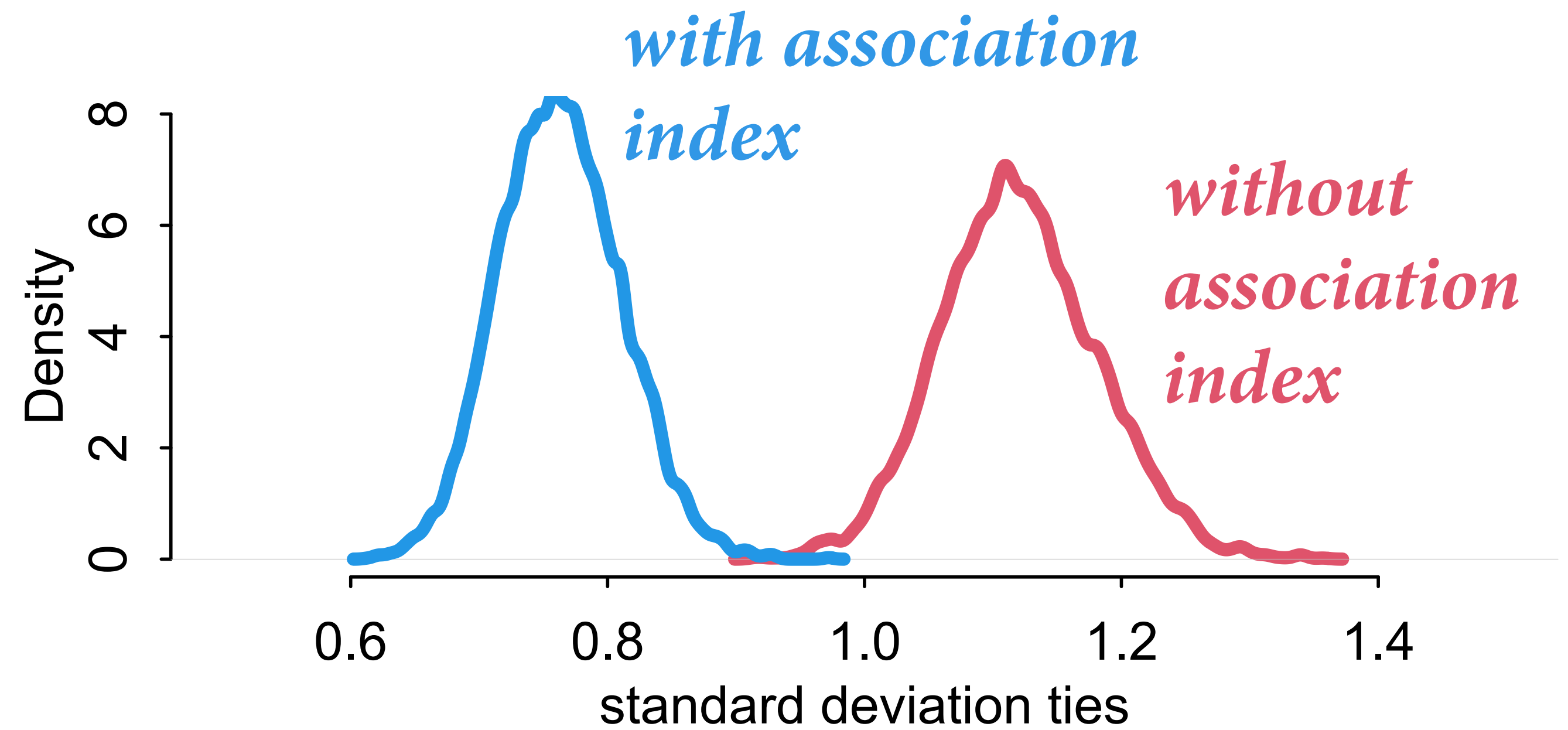
$$G_{BA} \sim \text{Poisson}(\lambda_{BA})$$

$$\log(\lambda_{AB}) = \alpha + \mathcal{T}_{BA} + \mathcal{G}_B + \mathcal{R}_A$$

$$\mathcal{T}_{BA} = T_{BA} + \beta_A A_{AB}$$

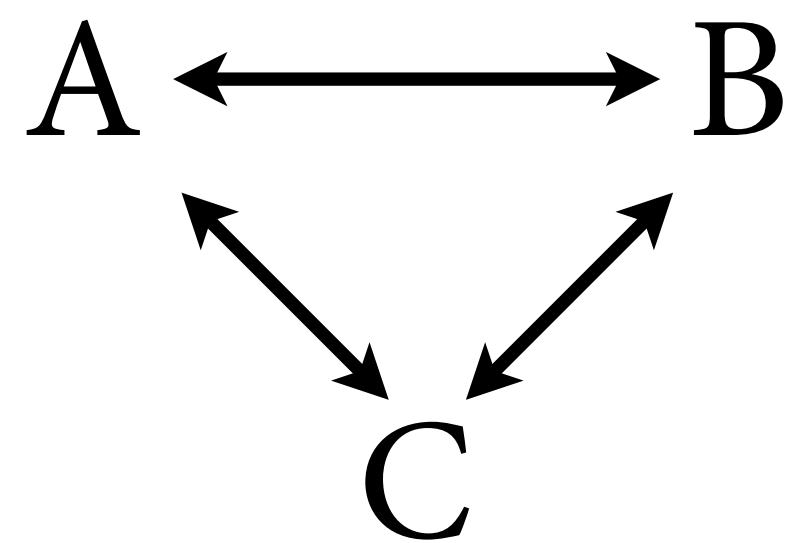
$$\mathcal{G}_B = G_B + \beta_{W,G} W_B$$

$$\mathcal{R}_A = R_A + \beta_{W,R} W_A$$



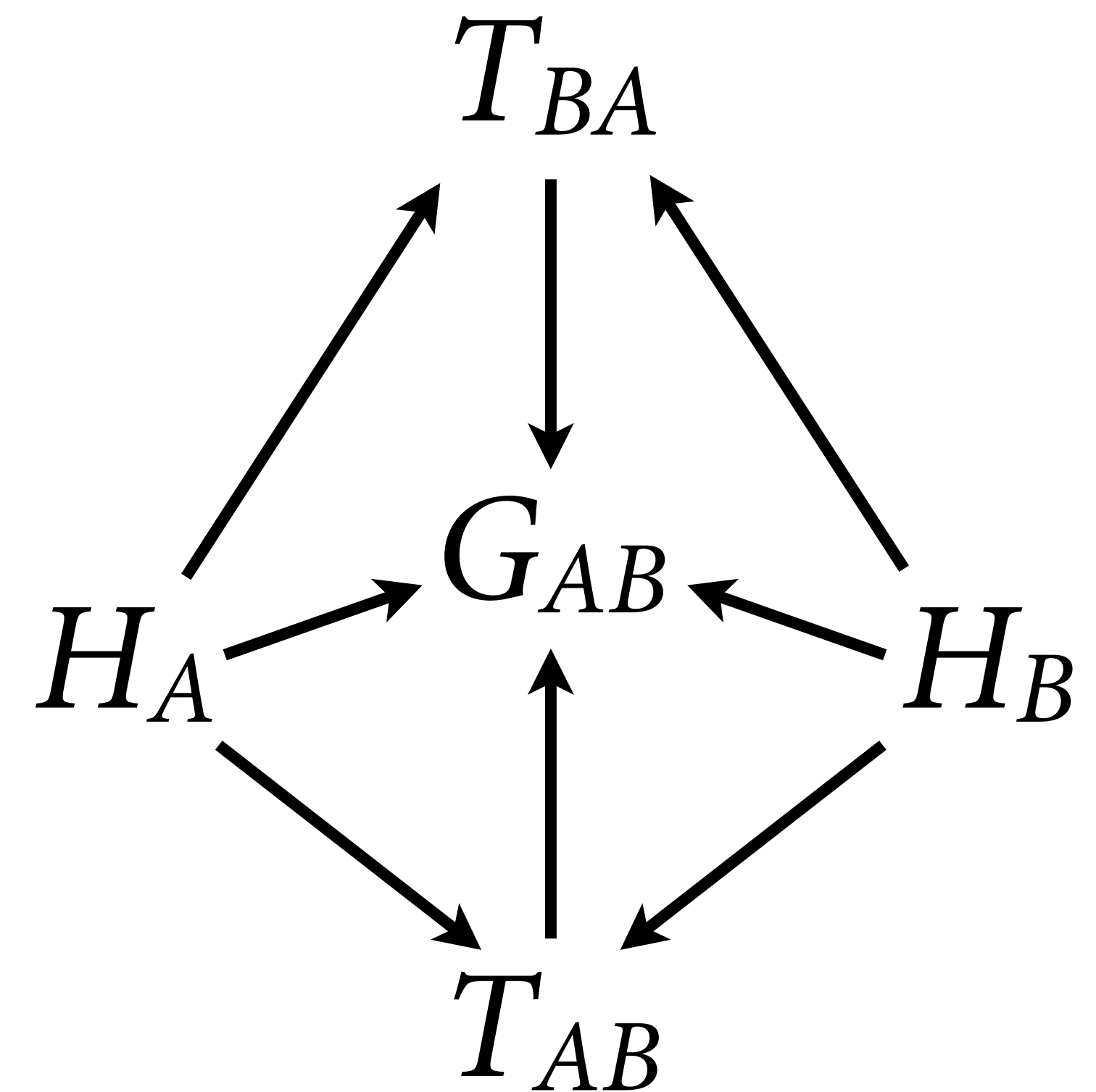
Additional Structure: Triangles

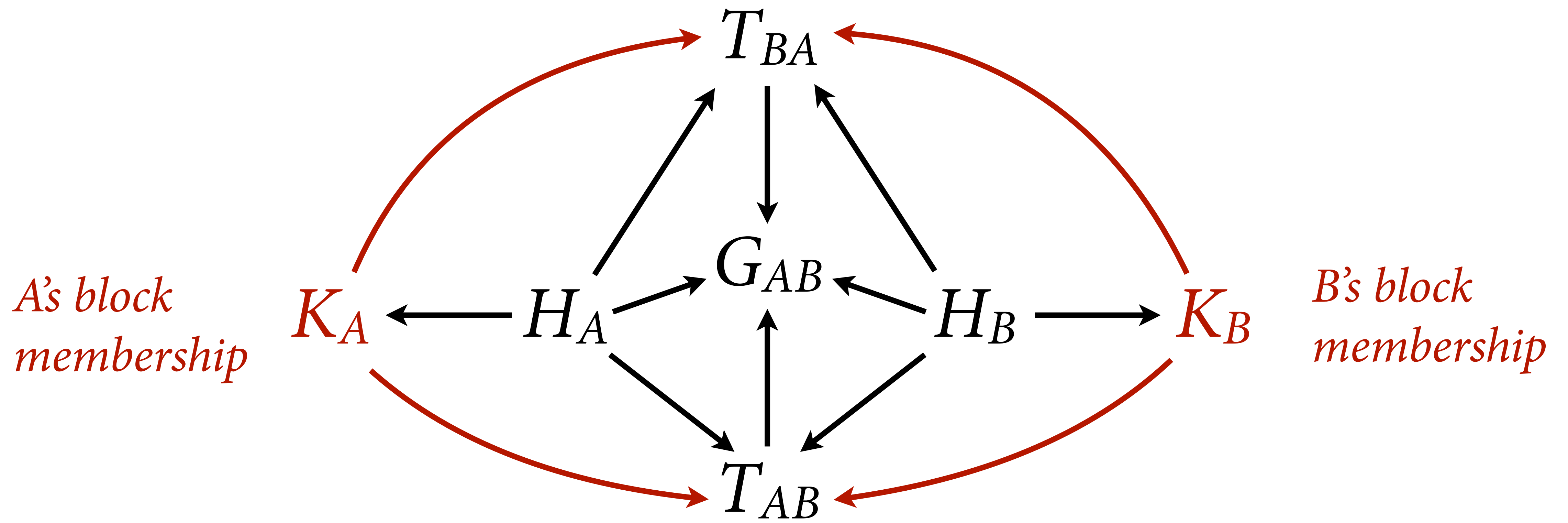
Relationships tend to come in triangles



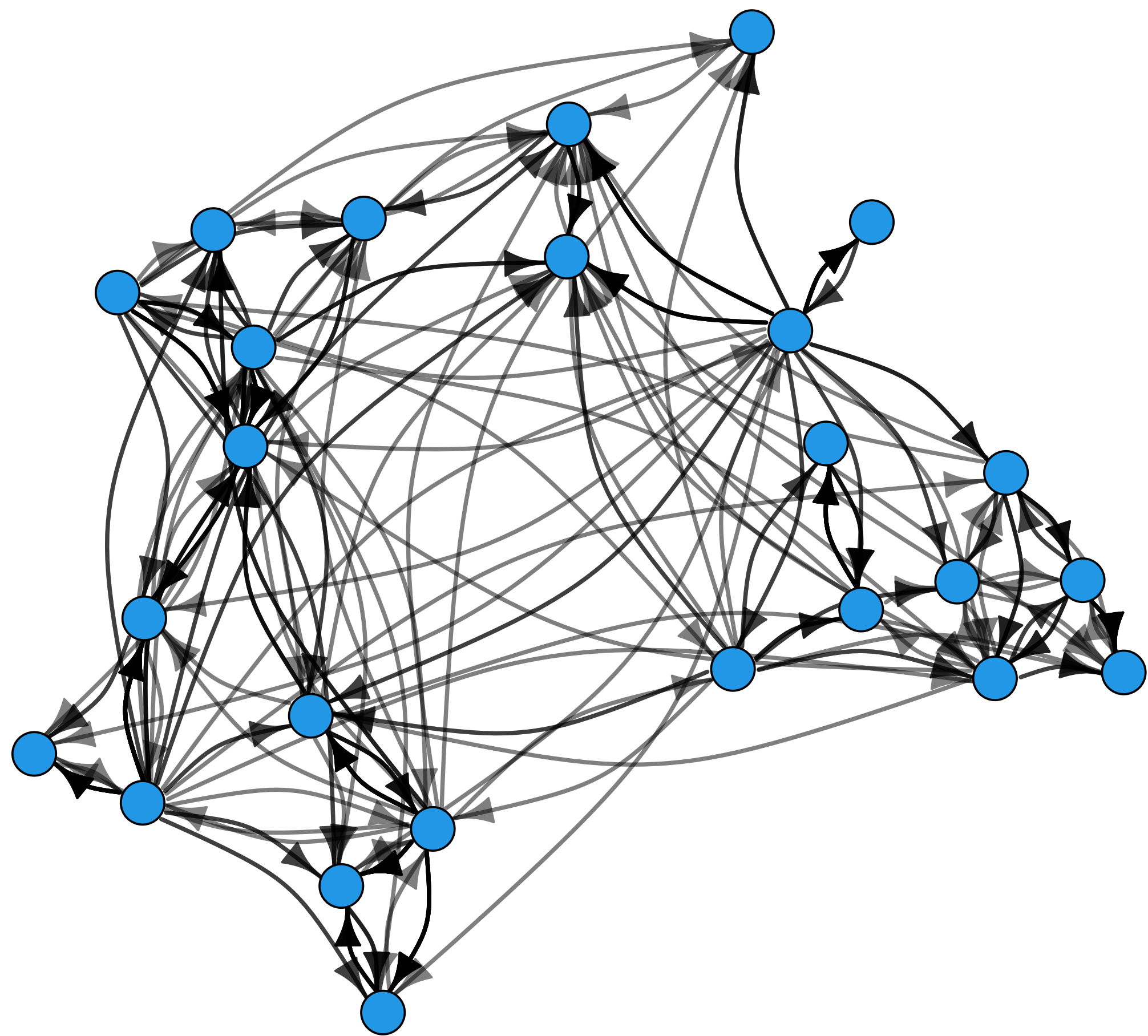
Triangle closure:

Block models: Ties more common within certain groups (family, office, *Stammtisch*)

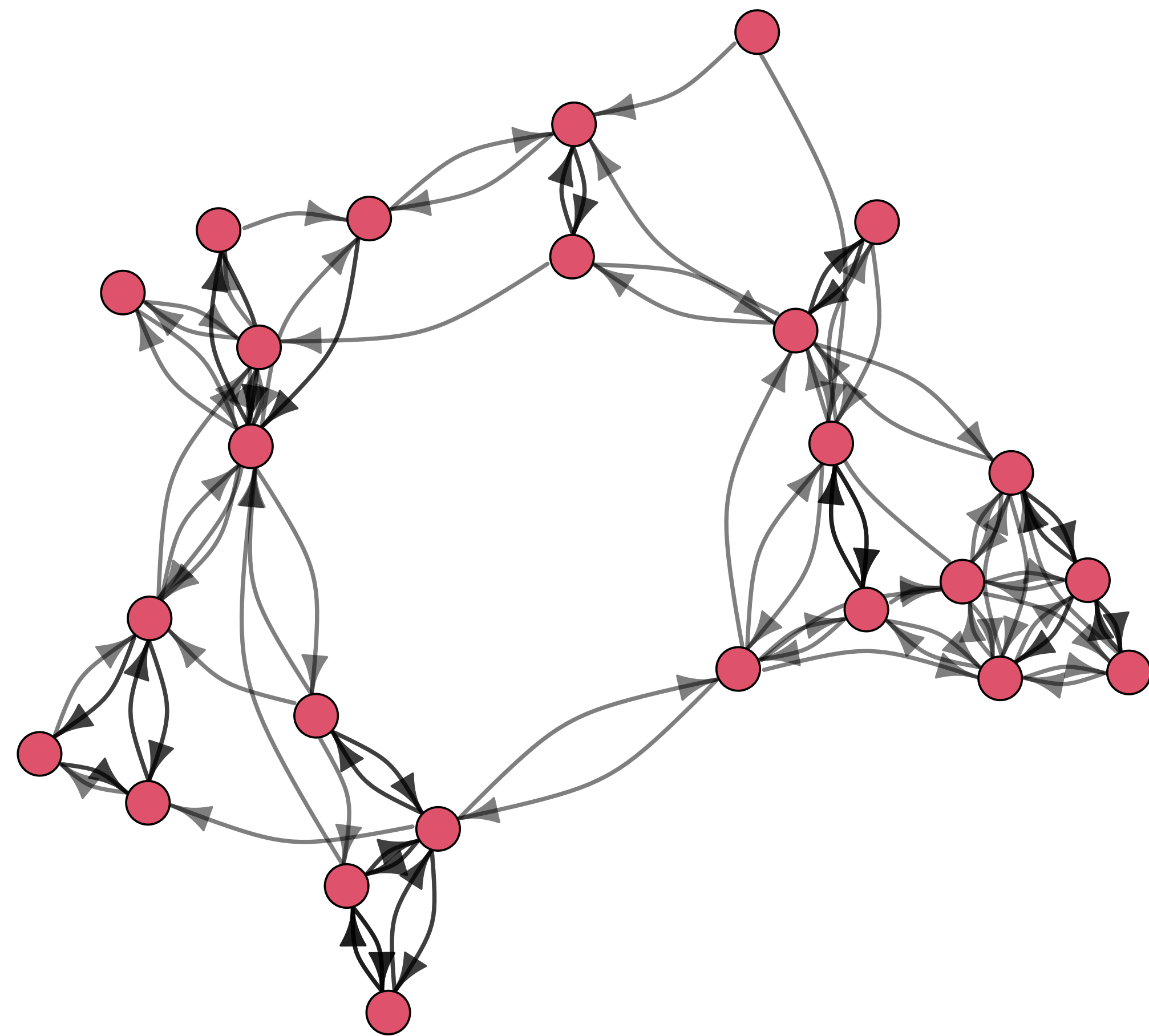




Raw data



Posterior mean network



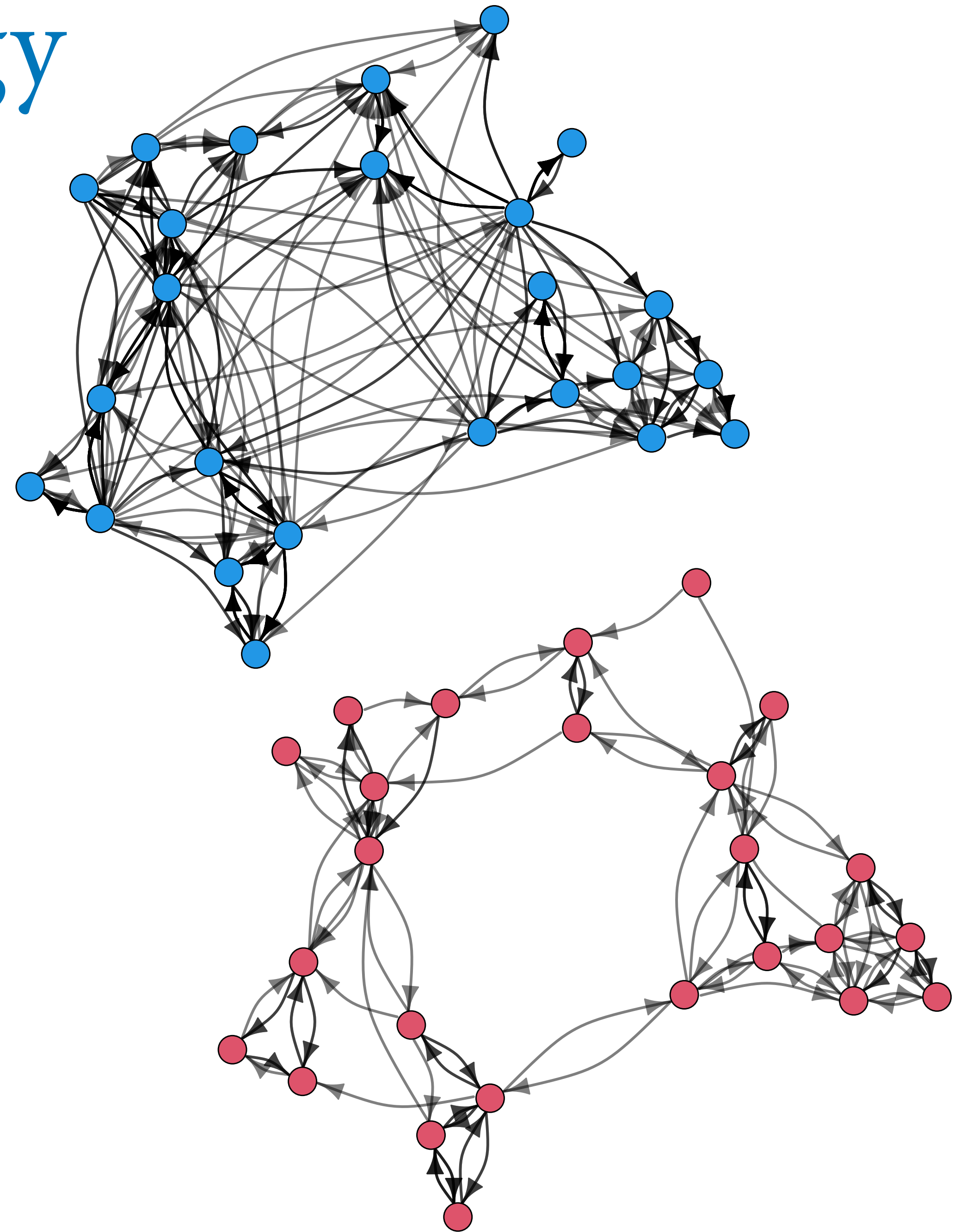
Varying effects as technology

Social networks try to express *regularities* of observations

Inferred social network is *regularized*, a structured varying effect

Analogous problems: phylogeny, space, heritability, knowledge, personality

What happens when the clusters are not *discrete* but *continuous*? Age, distance, time, similarity



Course Schedule

| | | |
|---------|--|------------------|
| Week 1 | Bayesian inference | Chapters 1, 2, 3 |
| Week 2 | Linear models & Causal Inference | Chapter 4 |
| Week 3 | Causes, Confounds & Colliders | Chapters 5 & 6 |
| Week 4 | Overfitting / MCMC | Chapters 7, 8, 9 |
| Week 5 | Generalized Linear Models | Chapters 10, 11 |
| Week 6 | Ordered categories & Multilevel models | Chapters 12 & 13 |
| Week 7 | More Multilevel models | Chapters 13 & 14 |
| Week 8 | Social Networks & Gaussian Processes | Chapter 14 |
| Week 9 | Measurement & Missingness | Chapter 15 |
| Week 10 | Generalized Linear Madness | Chapter 16 |

https://github.com/rmcelreath/stat_rethinking_2023

BONUS

Constructed Variables Are Bad

Folk tradition of building outcome variables as a back-alley form of “control”: ratios, differences, transformations

Body Mass Index (BMI) = $\text{mass}/\text{height}^2$

rates/ratios: per capita, per unit time

differences: change scores, difference from reference

All of these are usually bad

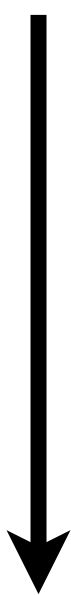
Per Capitated

Example: Dividing GDP by population does not stratify by population size

Now, using a more direct, but less fine-grained measure of economic development, **log regional GDP per capita** (mapped in Figure B.3.1), we verify the predicted association between kinship intensity and economic development. To remain consistent with the above analyses of nighttime luminosity, we estimate similar specifications, except that we now include year, year-continent, or year-country fixed effects in the models (because of the panel nature of the data), **and do not include population density** (since the dependent variable is already in per capita terms). As above, we cluster standard errors at the country level. We use the same set of control variables, constructed from the same data

population

P



GDP/P

GDP per capita



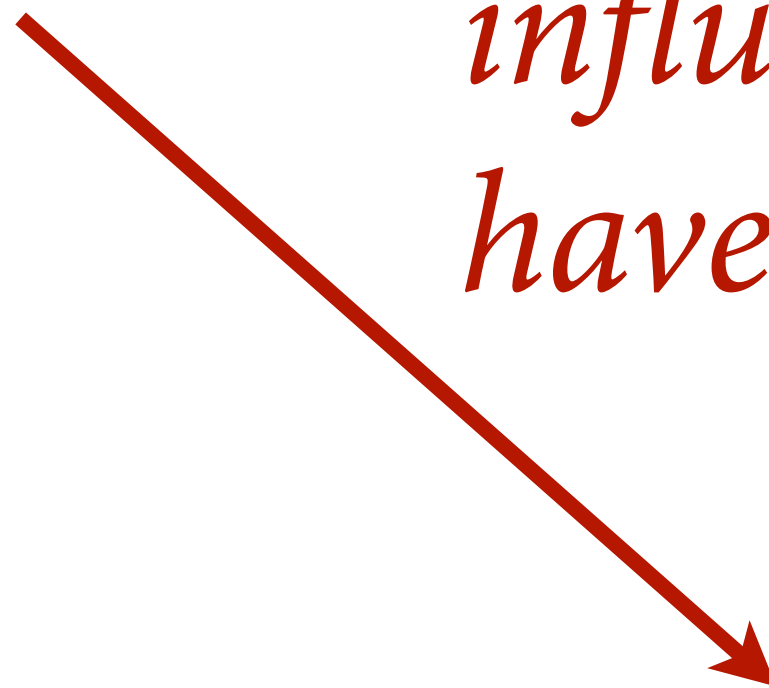
GDP

Gross Domestic Product

population

P

*influence does not
have to linear*



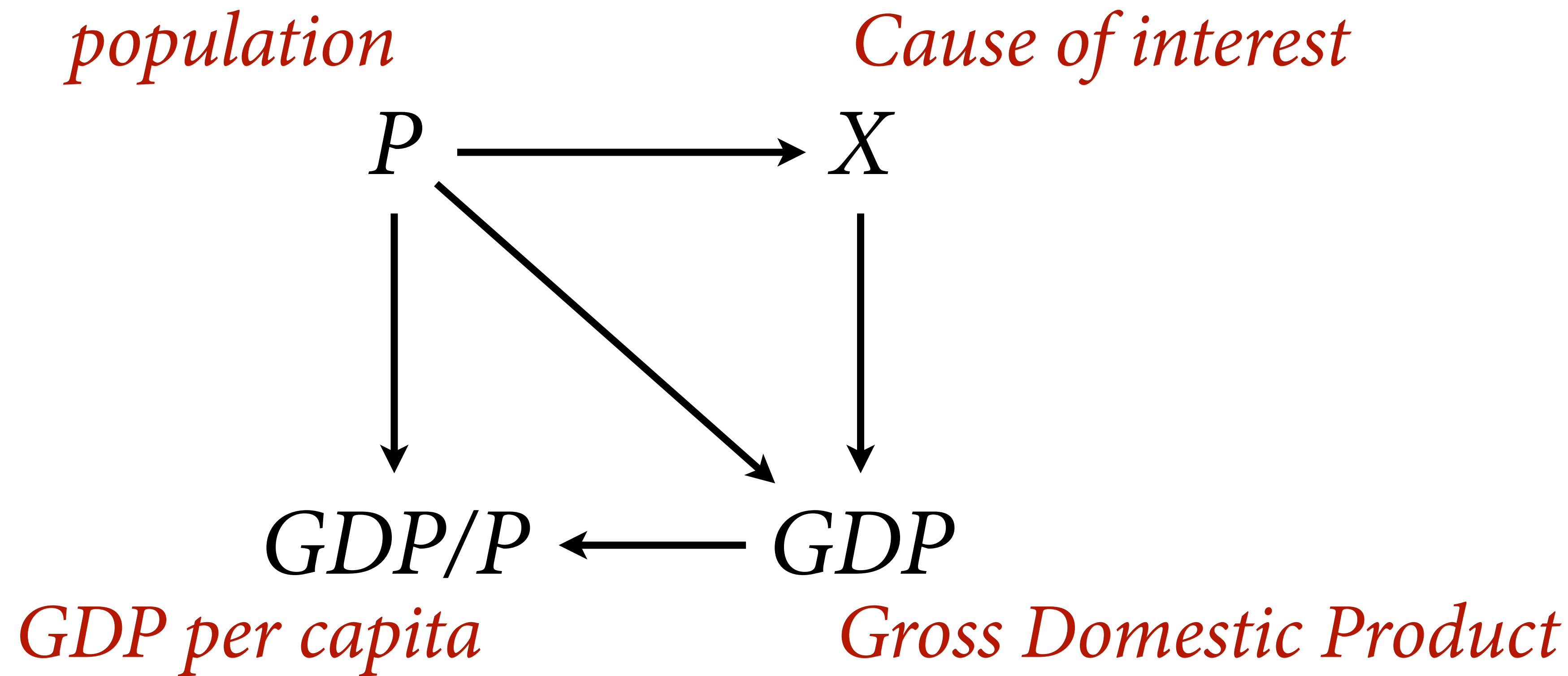
GDP/P

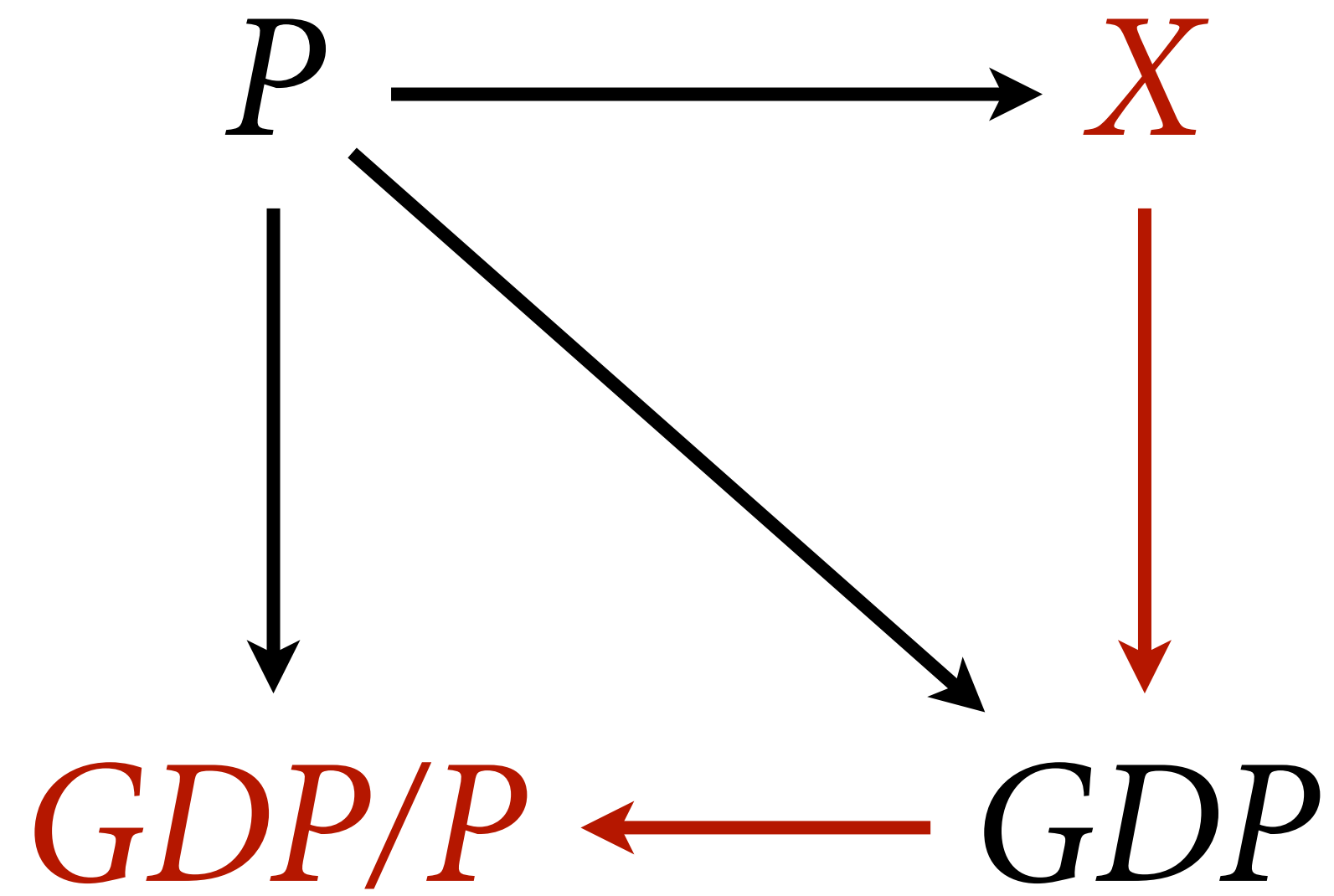


GDP

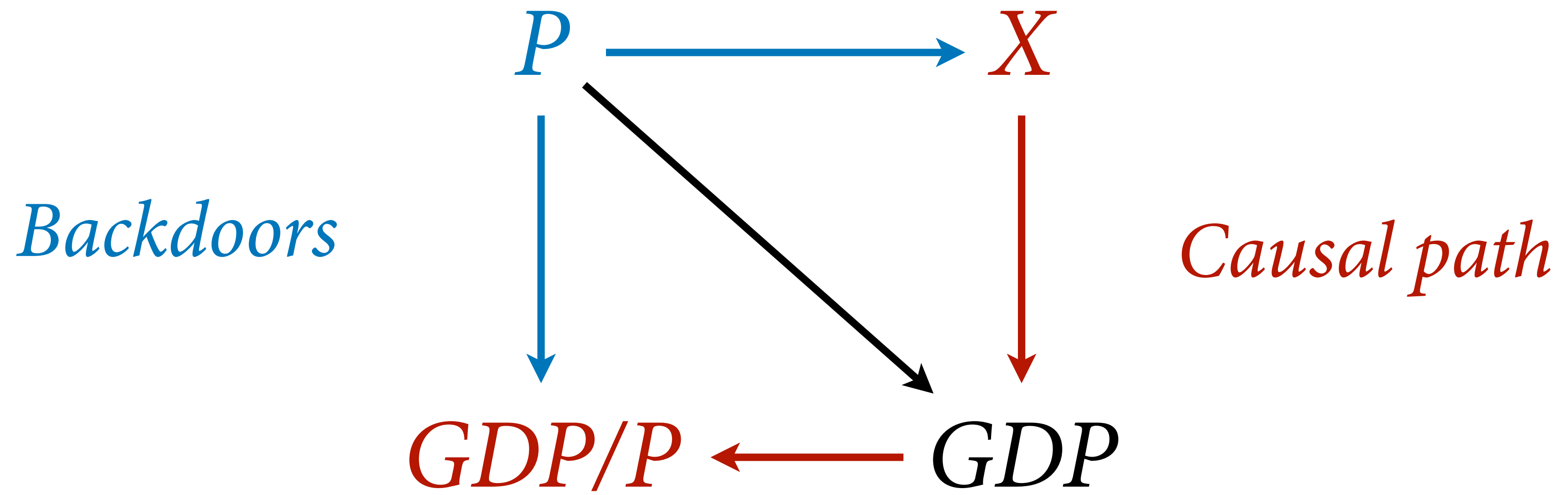
GDP per capita

Gross Domestic Product



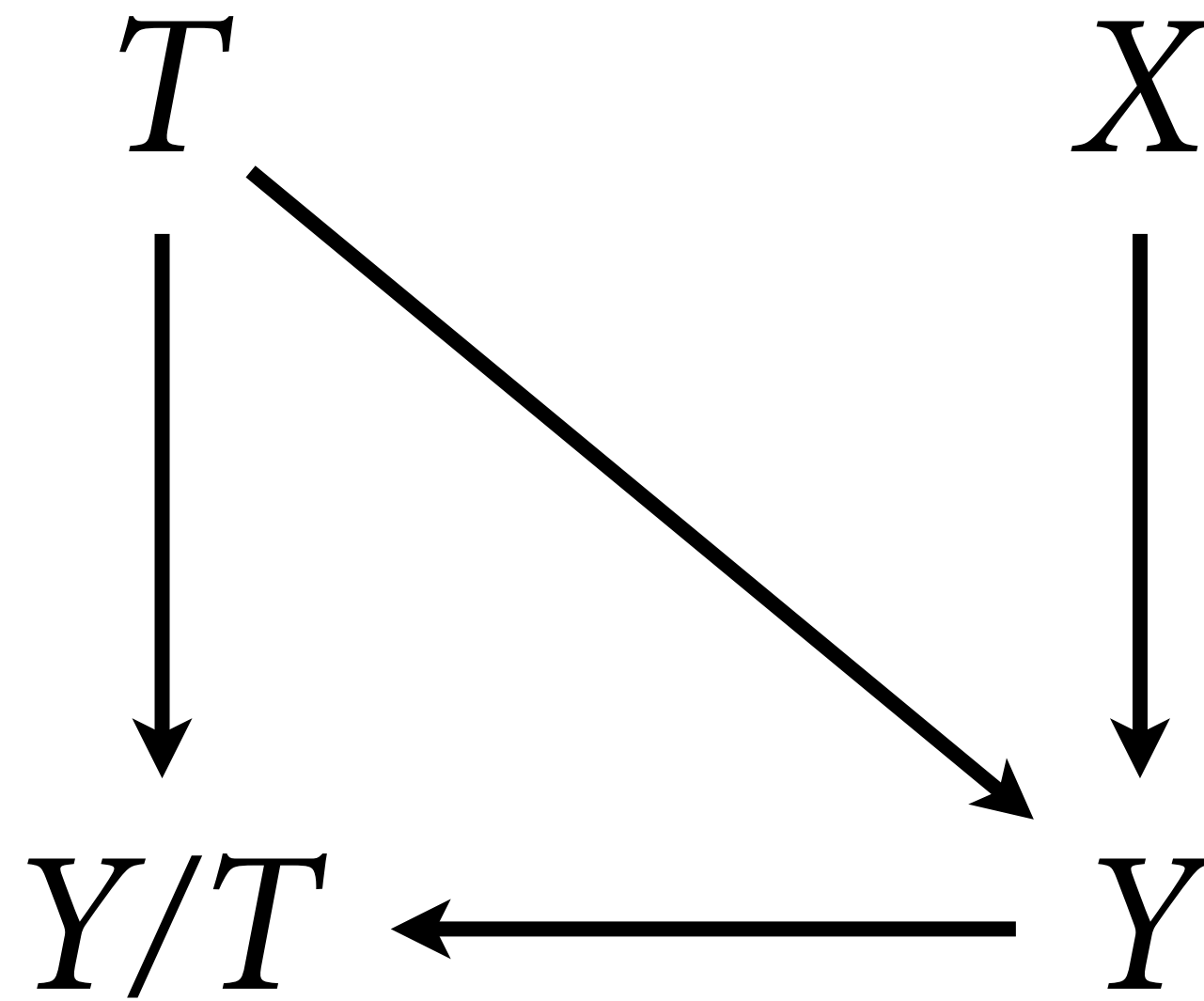


Causal path



observation time

Cause of interest



*transfers per
unit time*

number of observed transfers

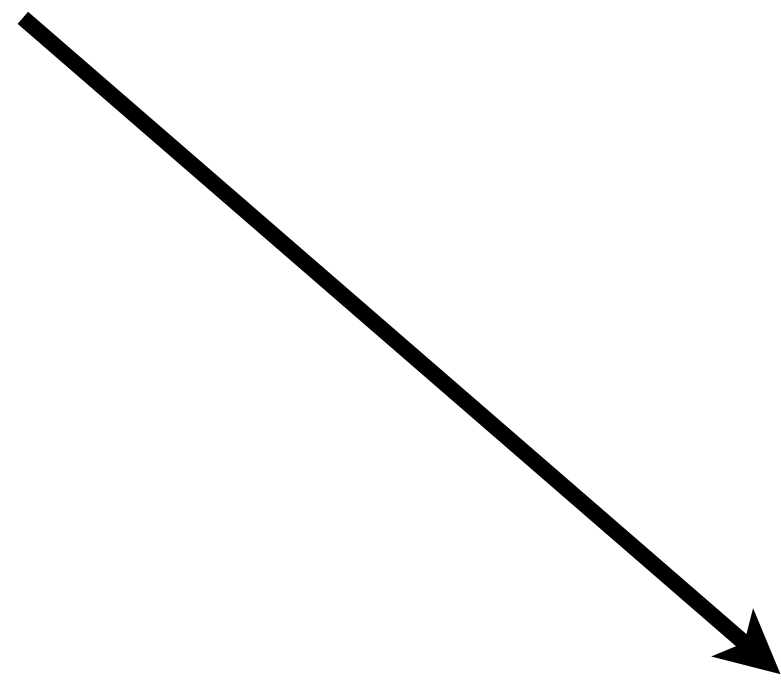
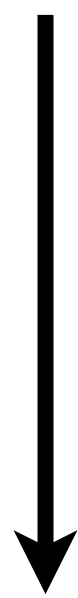
Does not account for differential precision of each Y/T

baseline height

Cause of interest

H_0

X



$H_1 - H_0$



H_1

change score

post-treatment height

Requires linear relationship, no floor/ceiling

Constructed Variables Are Bad

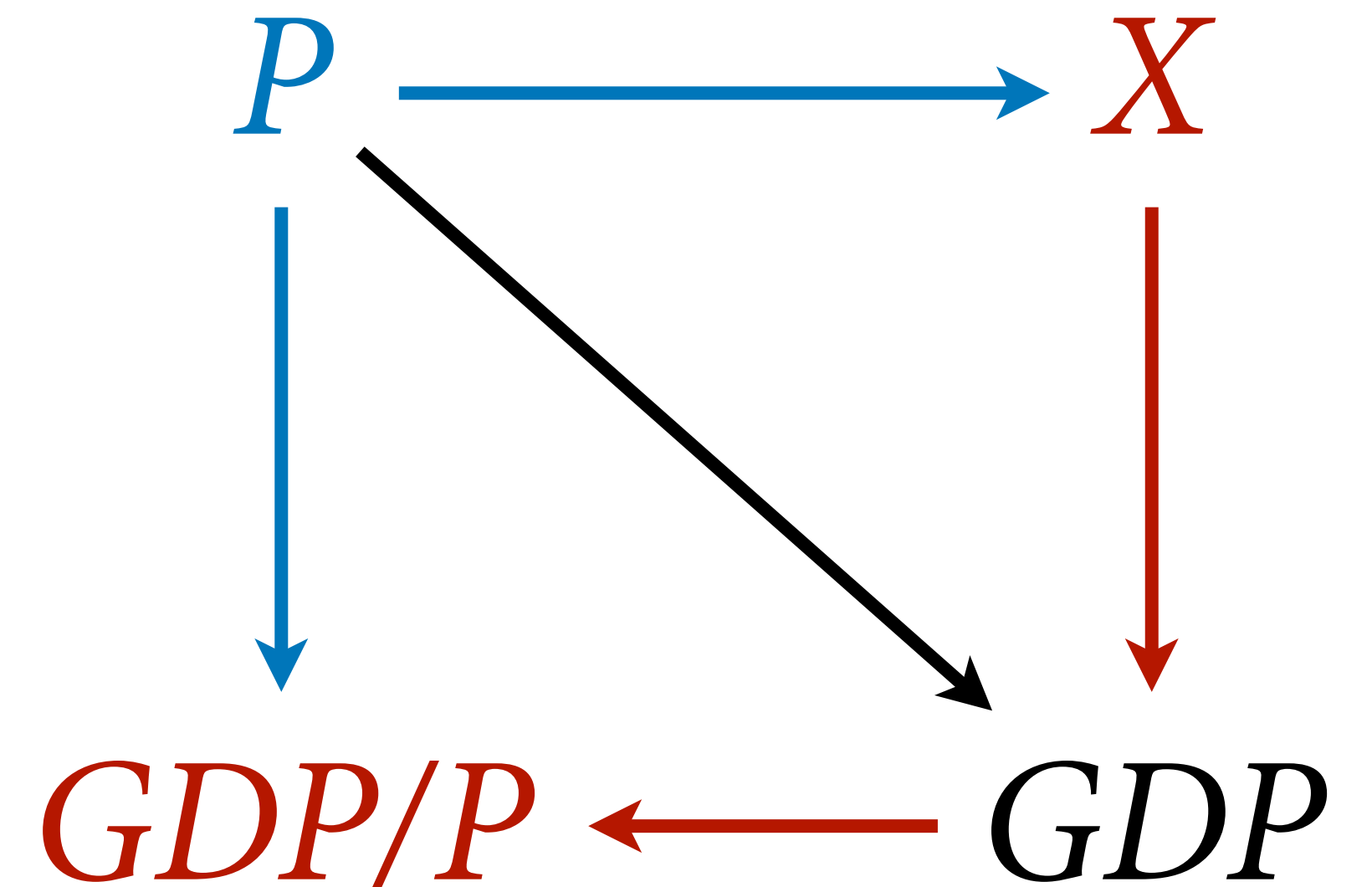
Arithmetic is not stratification

Assumes a fixed relationship, when you should estimate

Ignores uncertainty, e.g. rates

Similar: Do not use model predictions (residuals) as data

Do: Use causal logic, justify, test



Adhockery

Long tradition of *adhockery*: *ad hoc* procedures, intuition as justification

“we expect a correlation”

ad hoc procedures not justified by probability theory go wrong

Simple rule: Model what you measure



