Statistical Rethinking
2023

16. Gaussian Processes

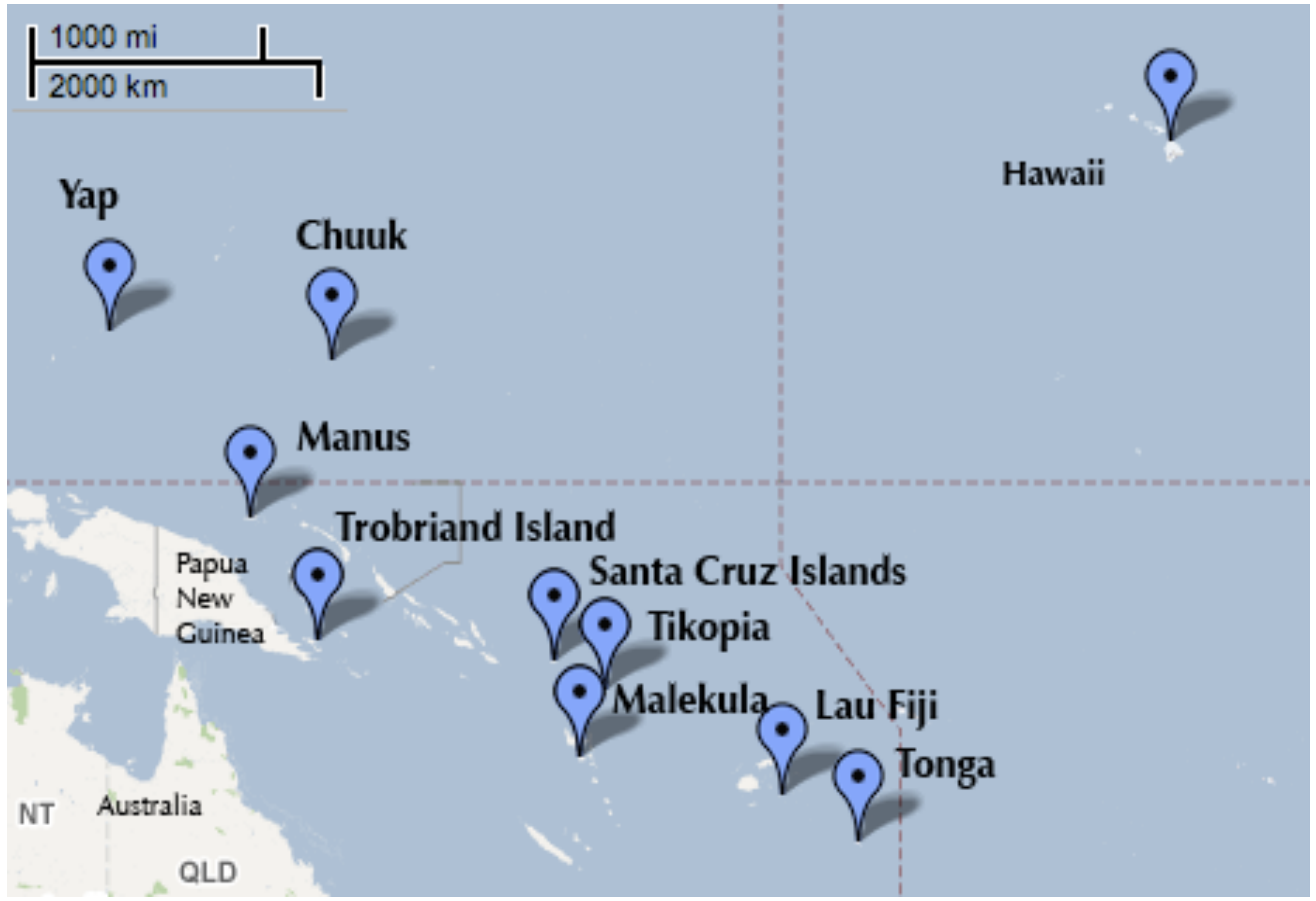
Oceanic Technology

data(Kline2)

Number of tool types associated with population size

Spatial covariation: Islands close together share unobserved confounds and innovations

Oceanic Technology



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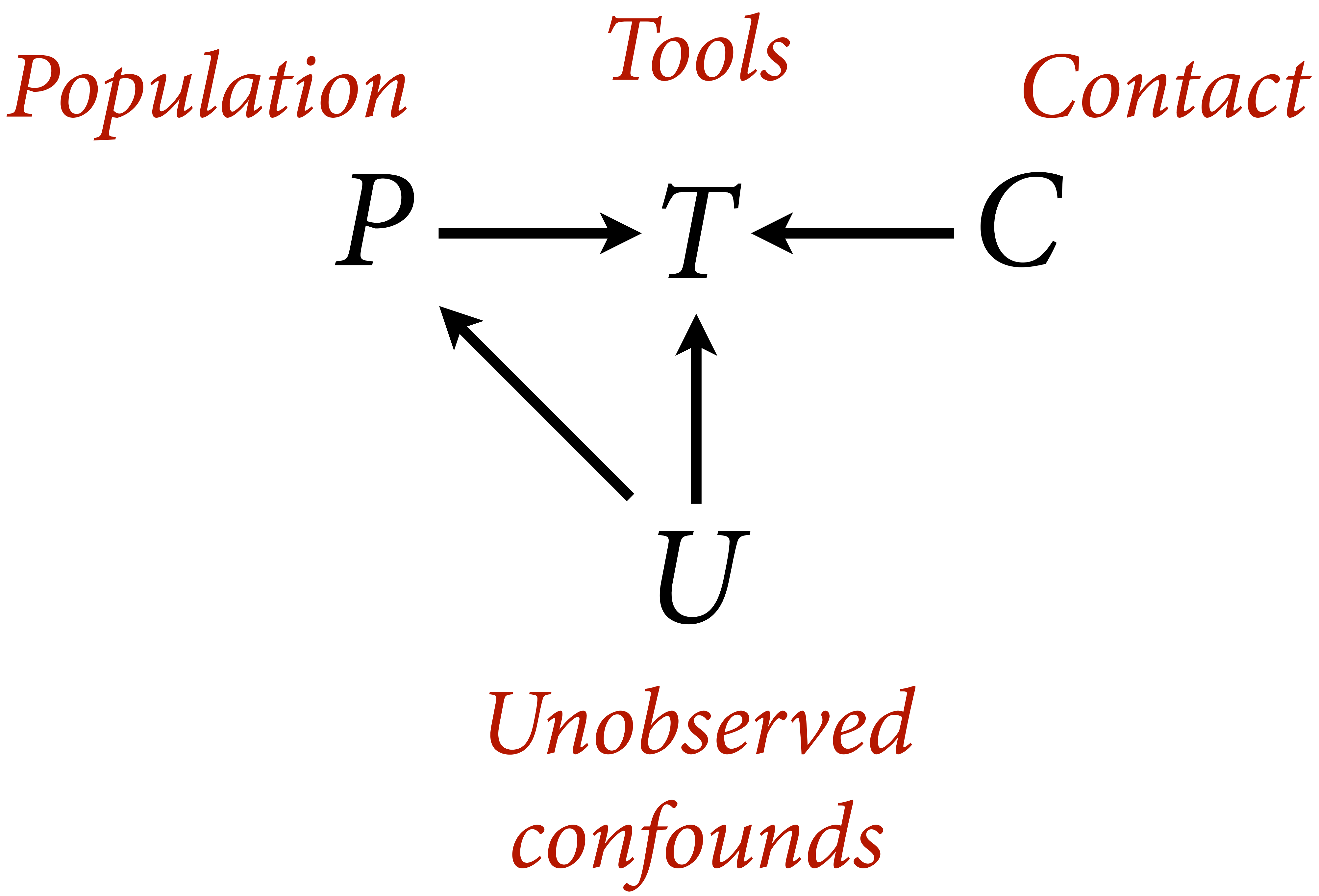
Number of tool types associated with population size

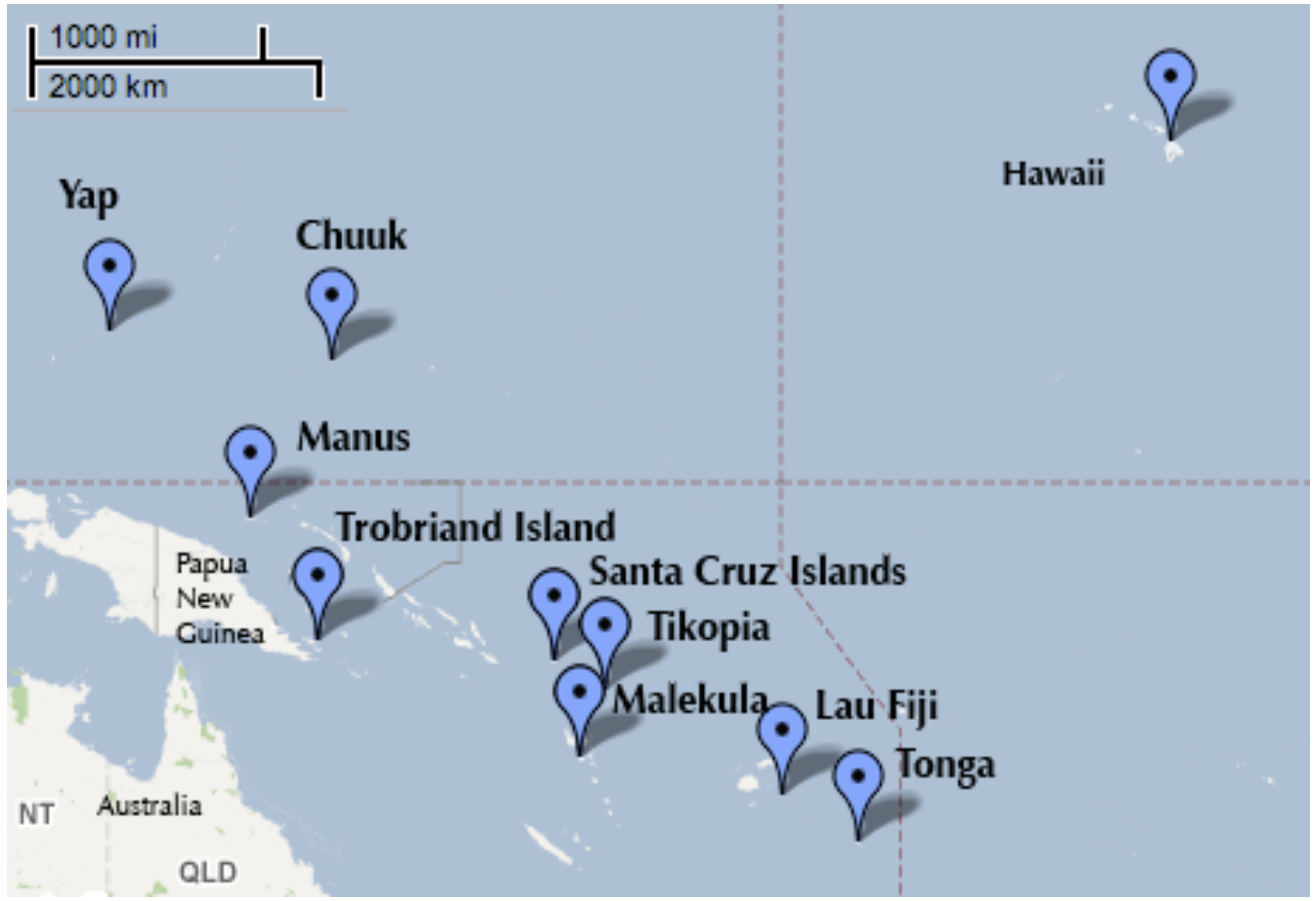
Spatial covariation: Islands close together share unobserved confounds and innovations



change in tools *innovation rate* *diminishing returns (elasticity)*

$$\Delta T = \alpha P^{\beta} - \gamma T$$

rate of loss



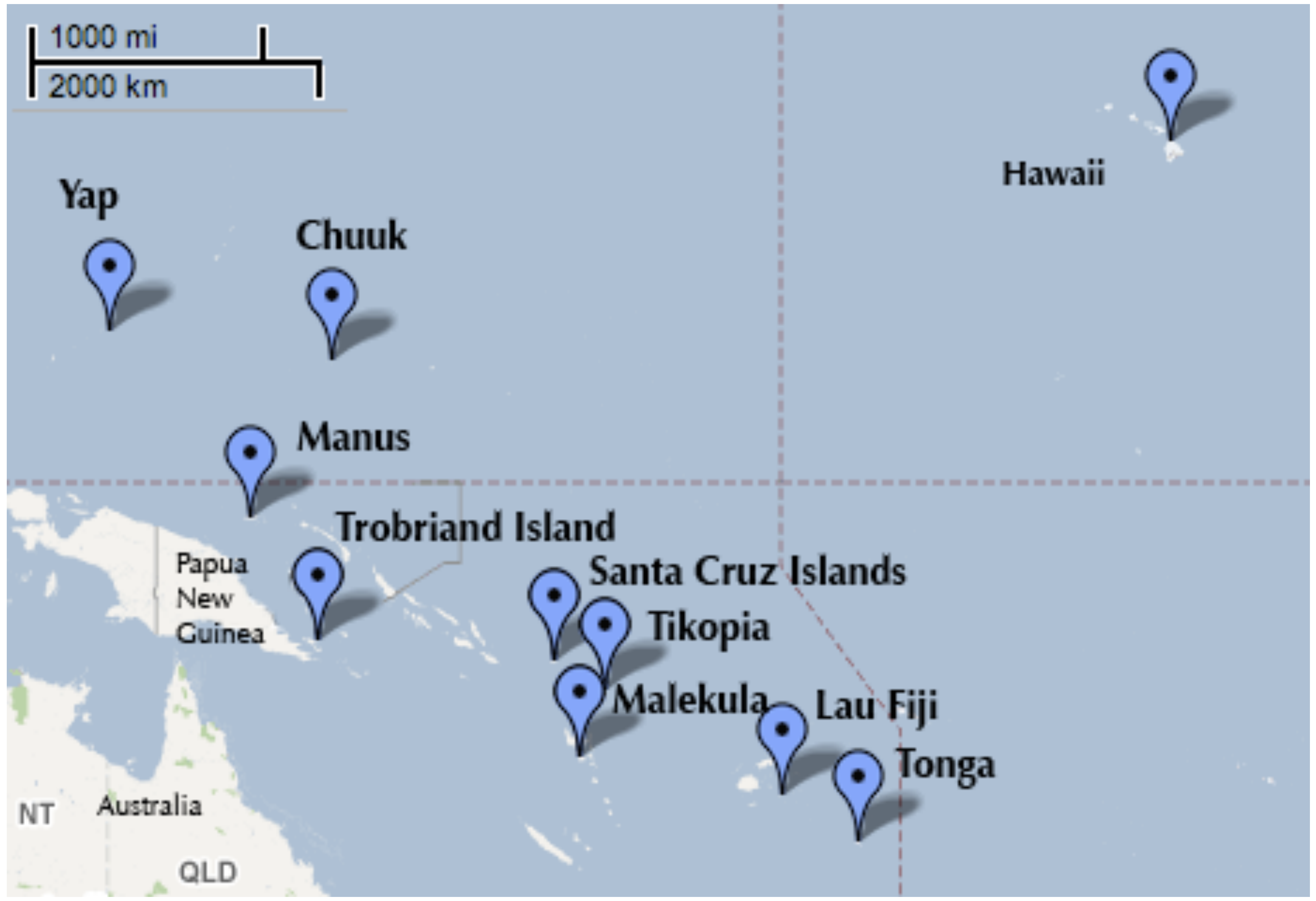
$$T_i \sim \text{Poisson}(\lambda_i)$$
$$\lambda_i = \hat{T}$$
$$\hat{T} = \frac{\alpha P^{\beta}}{\gamma}$$

Population *Tools* *Contact*

$$\begin{tikzcd} P \arrow[r] & T & C \arrow[l] \\ & U \arrow[ul] \arrow[u] & \end{tikzcd}$$

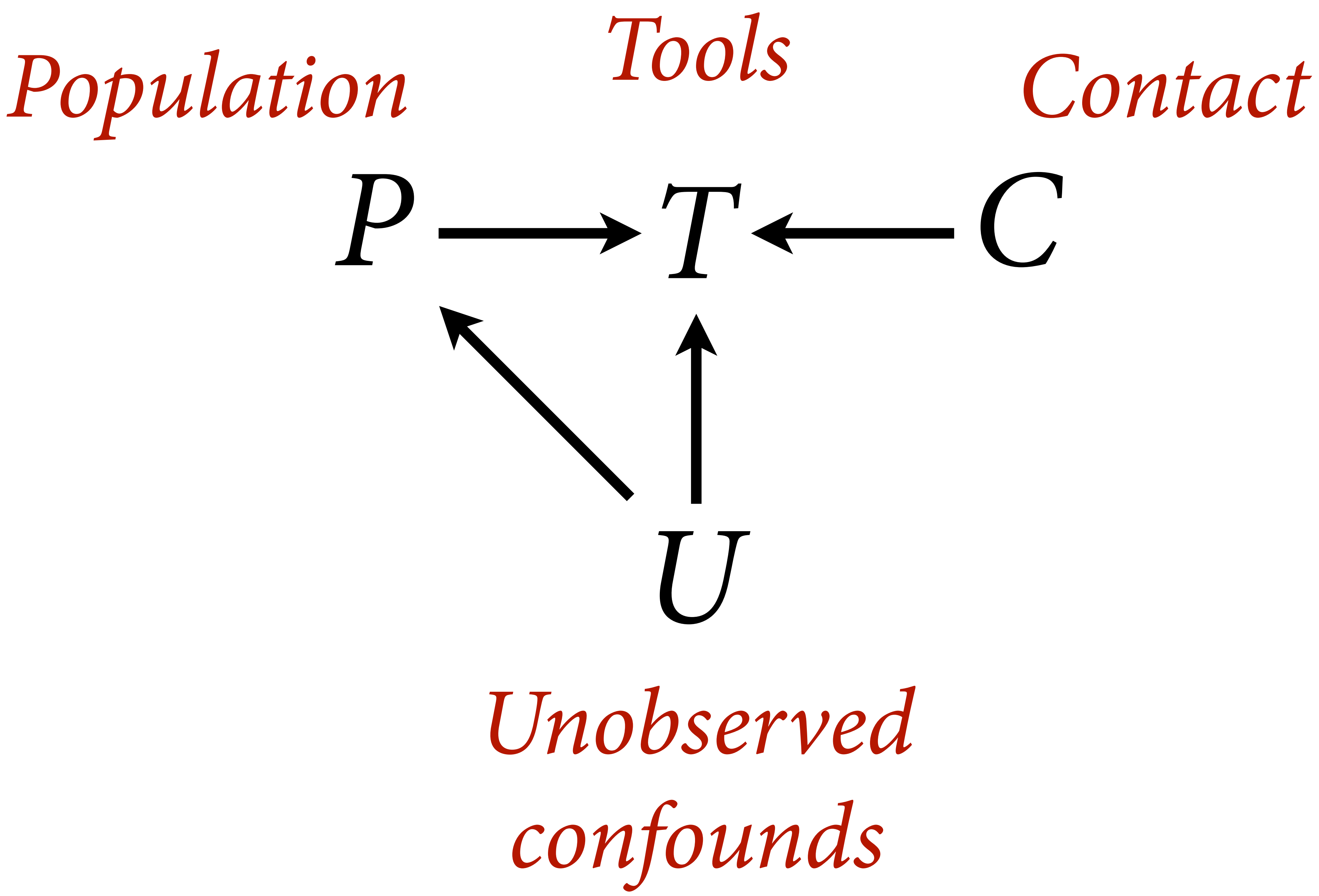
Unobserved confounds

$$T_i \sim \text{Poisson}(\lambda_i)$$
$$\lambda_i = \hat{T}$$
$$\hat{T} = \frac{\alpha P^{\beta}}{\gamma}$$



Spatial covariation: Islands close together share unobserved confounds and innovations

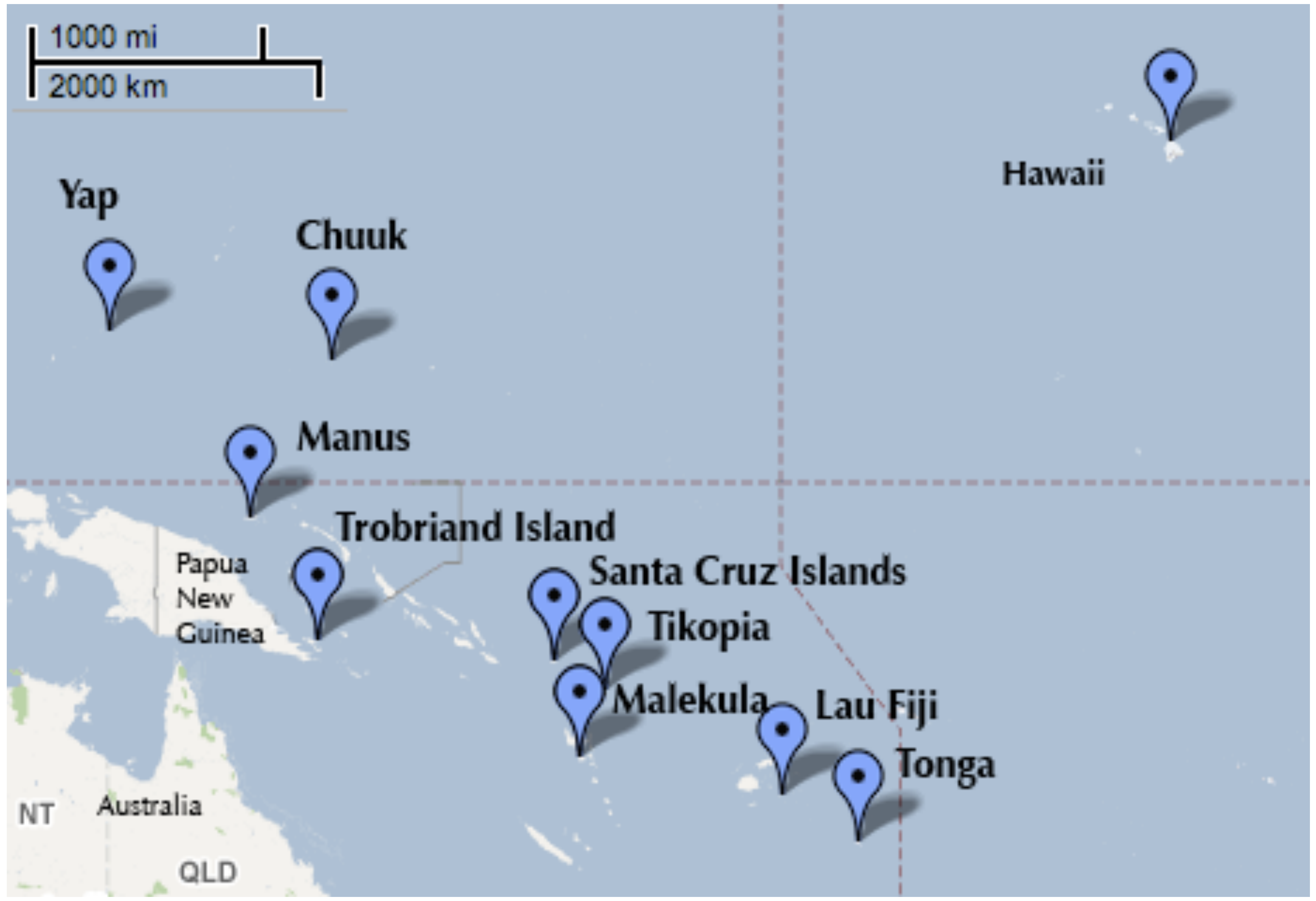
Effect of U is to make closer islands have more similar $\hat{T}$



$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\log \lambda_i = \bar{\alpha} + \alpha_{S[i]}$$

deviation log-tools in society i



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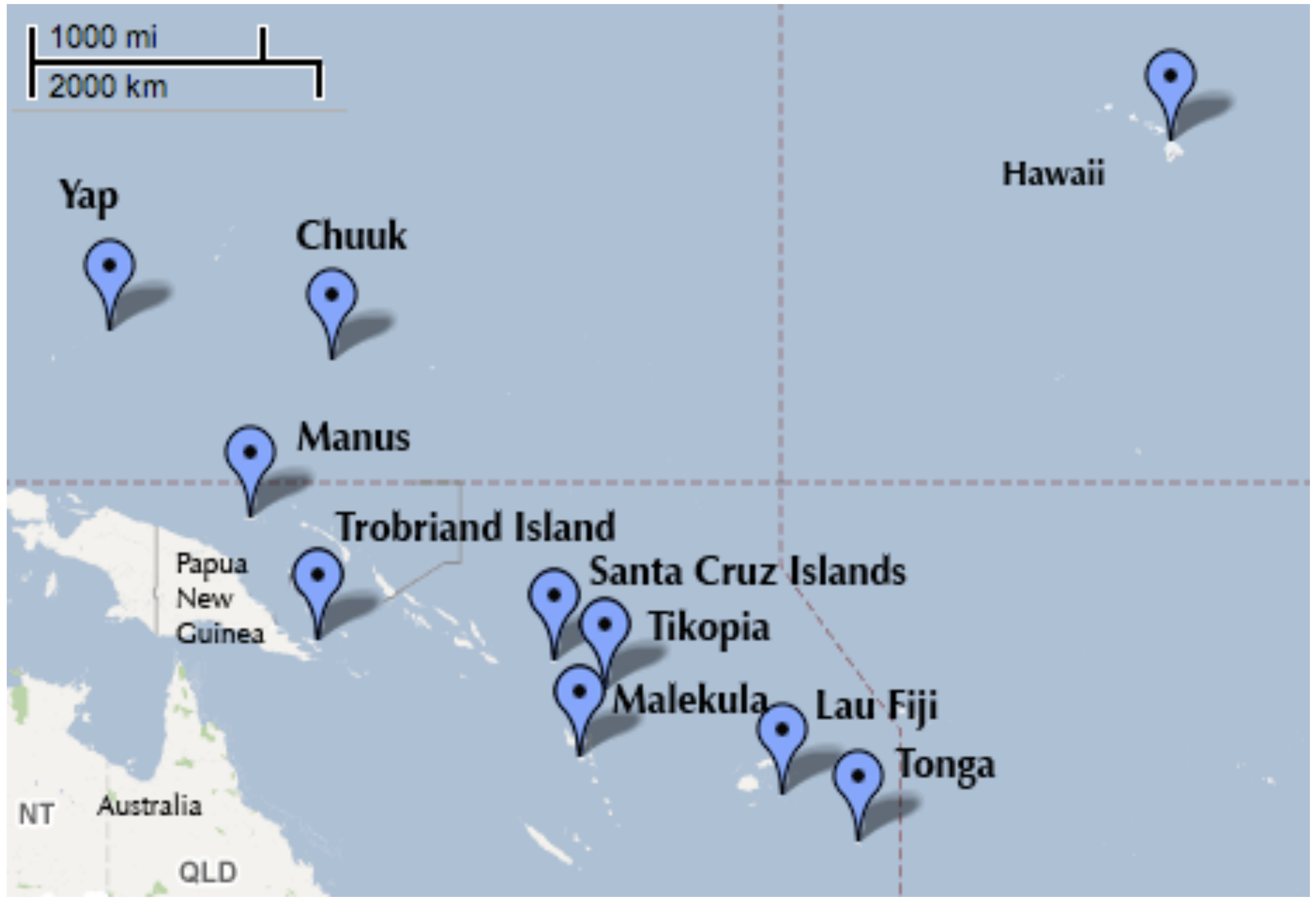
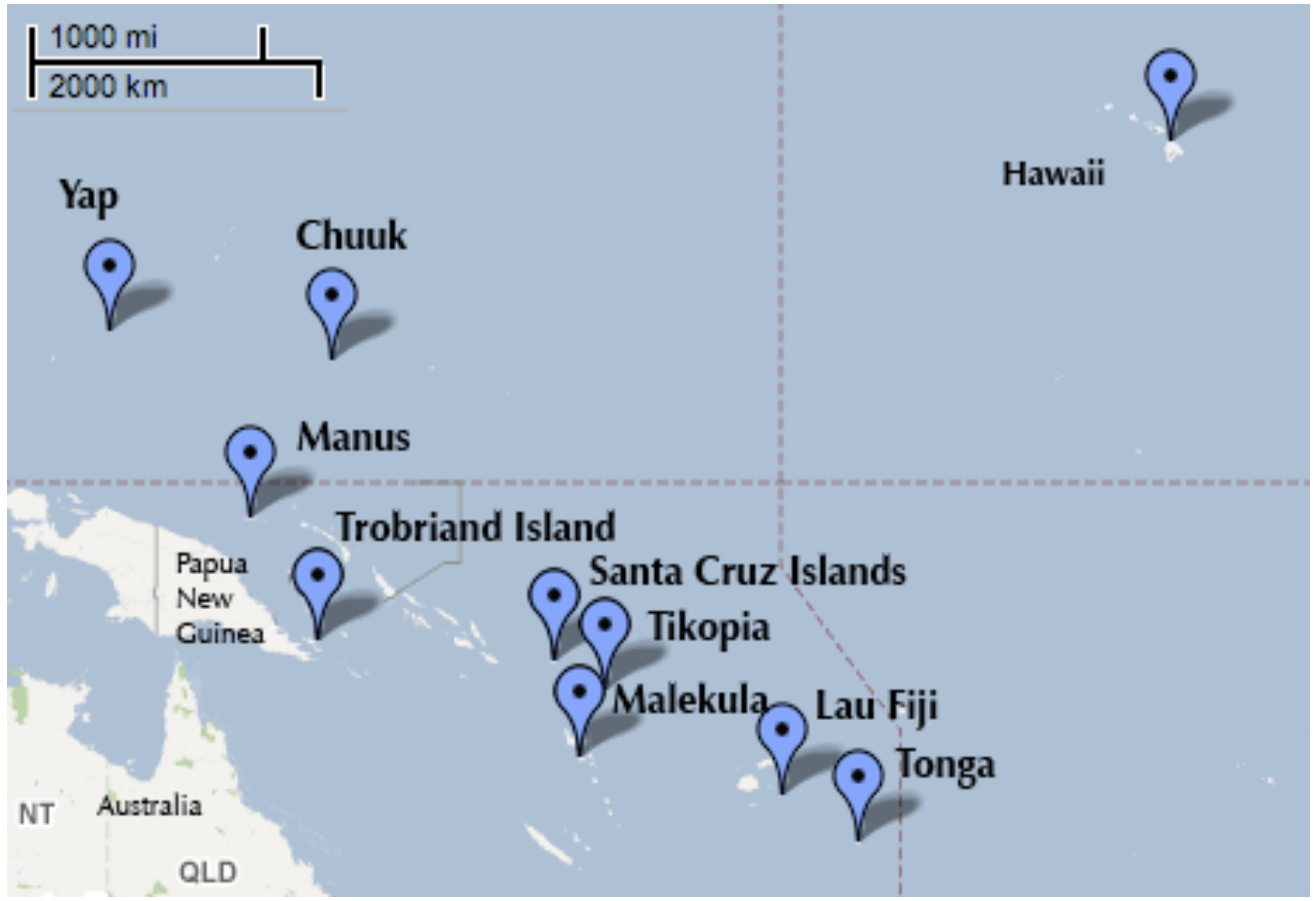


$$\begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{10} \end{bmatrix}$$

vector of all varying effects



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$$\begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{10} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \mathbf{K} \right)$$

covariance matrix, the "Kernel"

vector of all varying effects

vector of zeros

$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\log \lambda_i = \bar{\alpha} + \alpha_{S[i]}$$

$$\begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{10} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \mathbf{K} \right)$$

$$\mathbf{K} = \begin{bmatrix} \sigma^2 & k_{1,2} & k_{1,3} & k_{1,4} & k_{1,5} & k_{1,6} & k_{1,7} & k_{1,8} & k_{1,9} & k_{1,10} \\ & \sigma^2 & k_{2,3} & k_{2,4} & k_{2,5} & k_{2,6} & k_{2,7} & k_{2,8} & k_{2,9} & k_{2,10} \\ & & \sigma^2 & k_{3,4} & k_{3,5} & k_{3,6} & k_{3,7} & k_{3,8} & k_{3,9} & k_{3,10} \\ & & & \sigma^2 & k_{4,5} & k_{4,6} & k_{4,7} & k_{4,8} & k_{4,9} & k_{4,10} \\ & & & & \sigma^2 & k_{5,6} & k_{5,7} & k_{5,8} & k_{5,9} & k_{5,10} \\ & & & & & \sigma^2 & k_{6,7} & k_{6,8} & k_{6,9} & k_{6,10} \\ & & & & & & \sigma^2 & k_{7,8} & k_{7,9} & k_{7,10} \\ & & & & & & & \sigma^2 & k_{8,9} & k_{8,10} \\ & & & & & & & & \sigma^2 & k_{9,10} \\ & & & & & & & & & \sigma^2 \end{bmatrix}$$

$$\mathbf{K} = \begin{array}{cc}
\begin{array}{cccccccccc} \text{Malekula} & \text{Tikopia} & \text{Santa Cruz} & \text{Yap} & \text{Fiji} & \text{Trobriand} & \text{Chuuk} & \text{Manus} & \text{Tonga} & \text{Hawaii} \end{array} & \\
\begin{bmatrix}
\sigma^2 & k_{1,2} & k_{1,3} & k_{1,4} & k_{1,5} & k_{1,6} & k_{1,7} & k_{1,8} & k_{1,9} & k_{1,10} \\
 & \sigma^2 & k_{2,3} & k_{2,4} & k_{2,5} & k_{2,6} & k_{2,7} & k_{2,8} & k_{2,9} & k_{2,10} \\
 & & \sigma^2 & k_{3,4} & k_{3,5} & k_{3,6} & k_{3,7} & k_{3,8} & k_{3,9} & k_{3,10} \\
 & & & \sigma^2 & k_{4,5} & k_{4,6} & k_{4,7} & k_{4,8} & k_{4,9} & k_{4,10} \\
 & & & & \sigma^2 & k_{5,6} & k_{5,7} & k_{5,8} & k_{5,9} & k_{5,10} \\
 & & & & & \sigma^2 & k_{6,7} & k_{6,8} & k_{6,9} & k_{6,10} \\
 & & & & & & \sigma^2 & k_{7,8} & k_{7,9} & k_{7,10} \\
 & & & & & & & \sigma^2 & k_{8,9} & k_{8,10} \\
 & & & & & & & & \sigma^2 & k_{9,10} \\
 & & & & & & & & & \sigma^2
\end{bmatrix} & \begin{array}{l} \text{Malekula} \\ \text{Tikopia} \\ \text{Santa Cruz} \\ \text{Yap} \\ \text{Fiji} \\ \text{Trobriand} \\ \text{Chuuk} \\ \text{Manus} \\ \text{Tonga} \\ \text{Hawaii} \end{array}
\end{array}$$

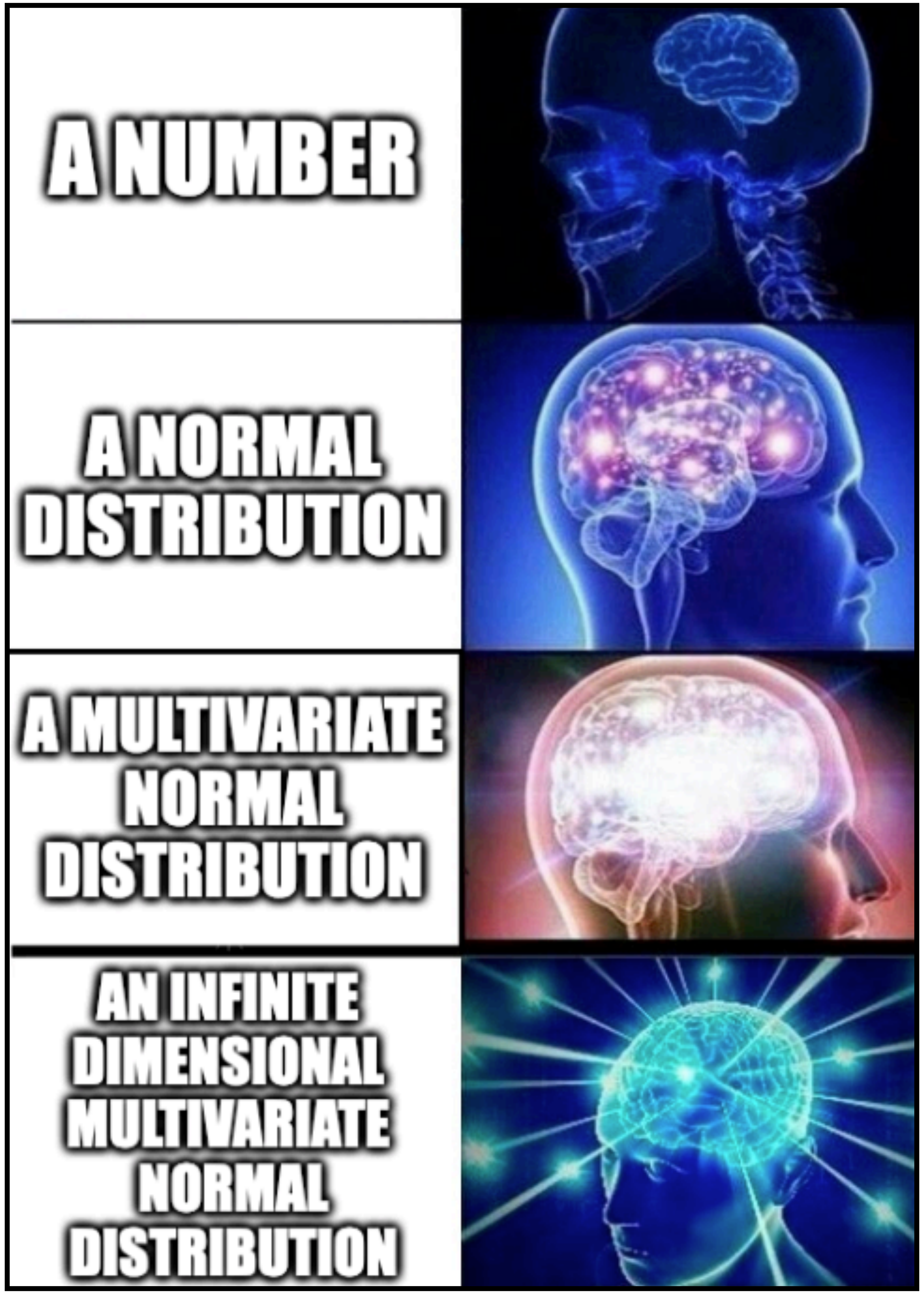
45 covariances

Gaussian Processes

A Gaussian Process is "*an infinite-dimensional generalization of multivariate normal distributions*"

What does this mean?

Instead of conventional covariance matrix, use a kernel function that generalizes to infinite dimensions/observations/predictions



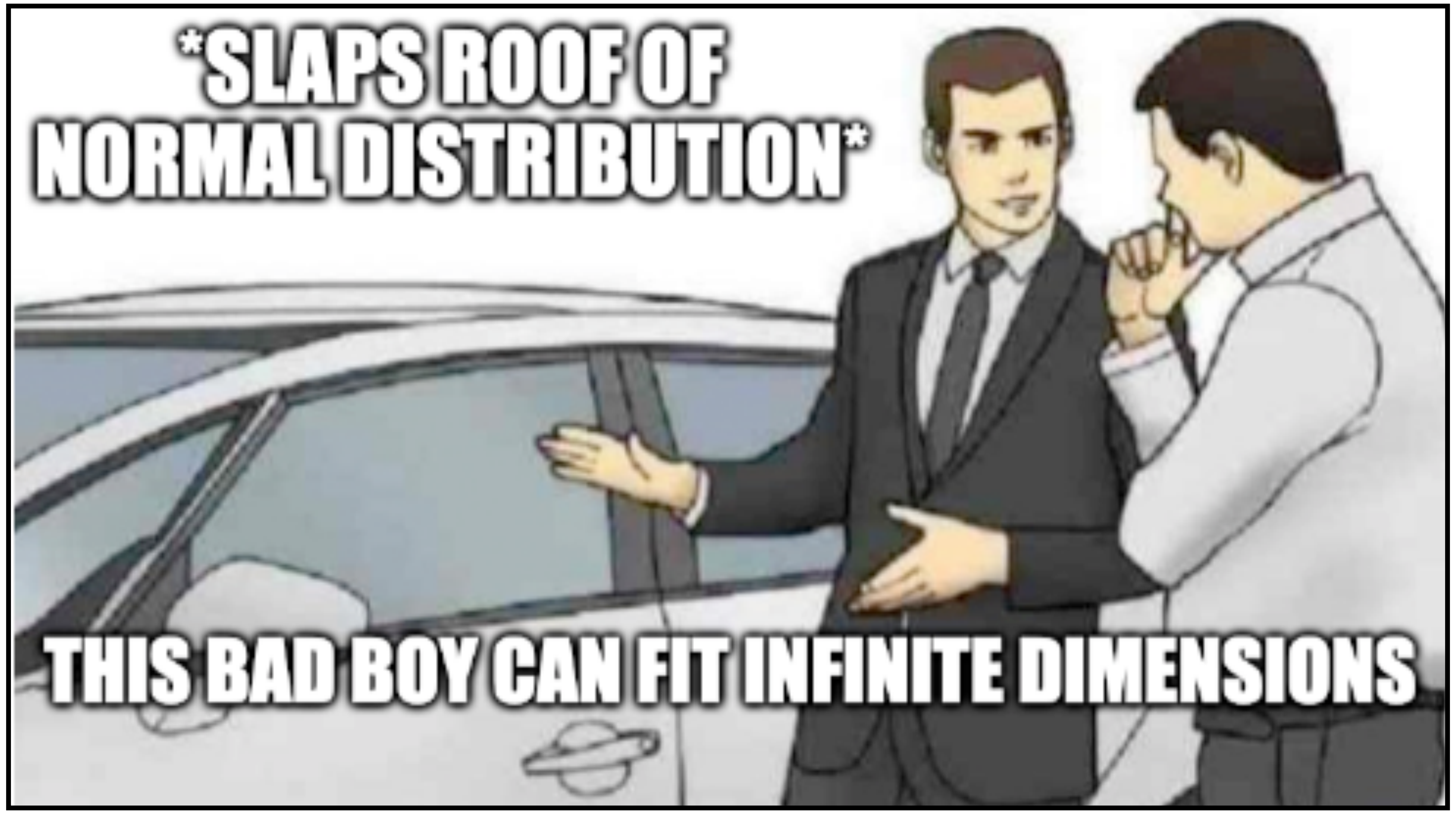
Gaussian Processes

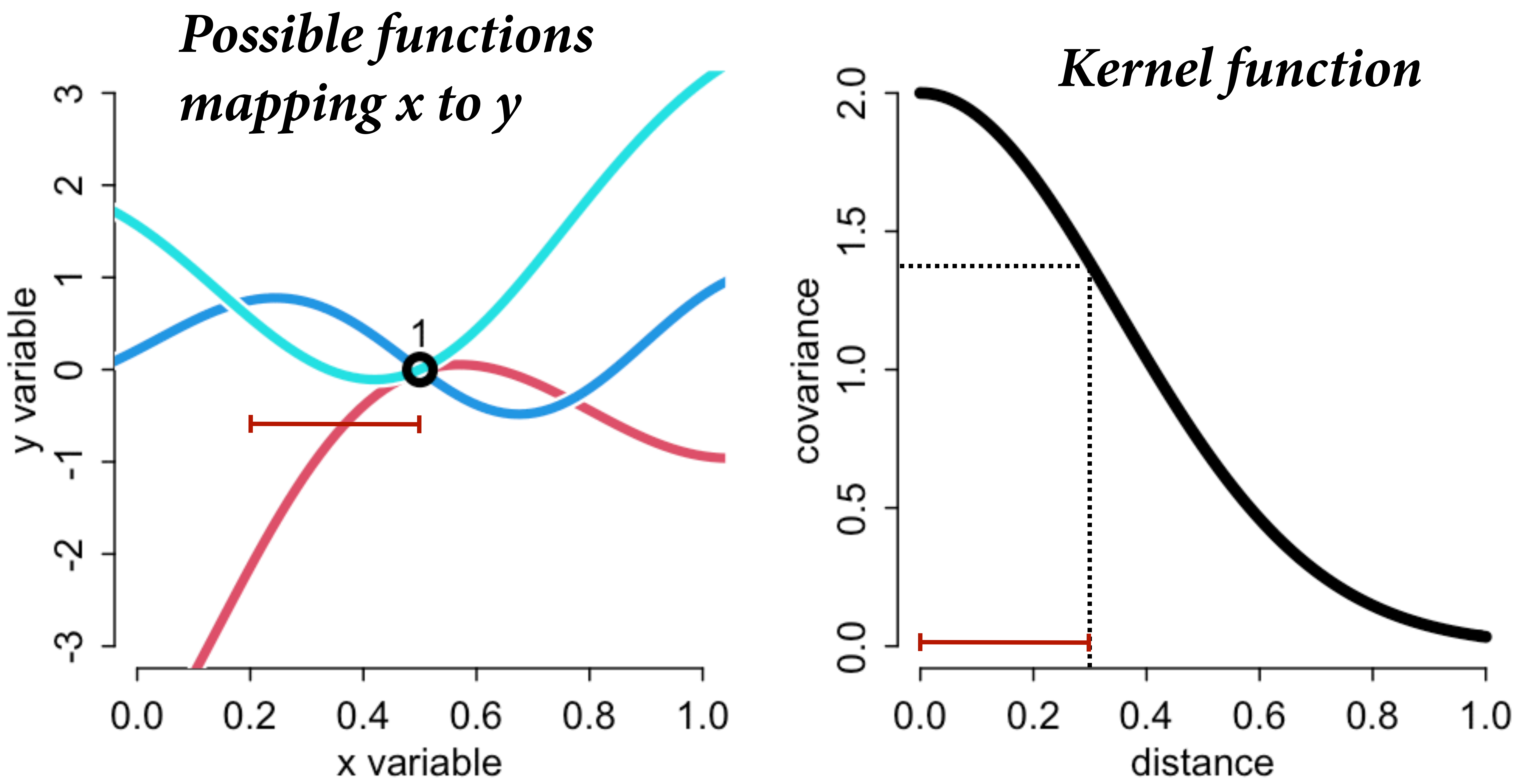
Instead of conventional covariance matrix, use a kernel function

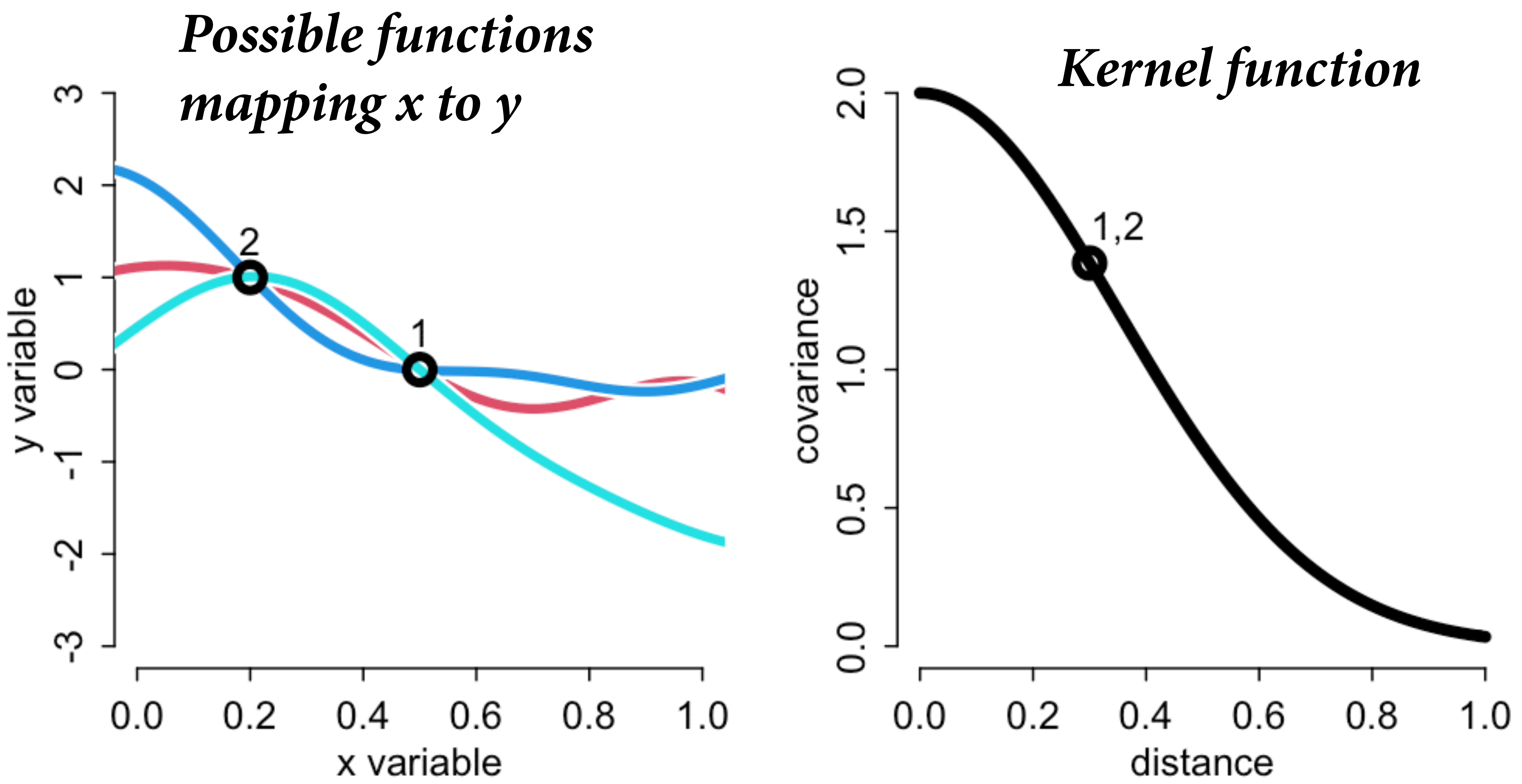
The kernel gives the covariance between any pair of points as a function of their distance

Distance can be difference, space, time, etc

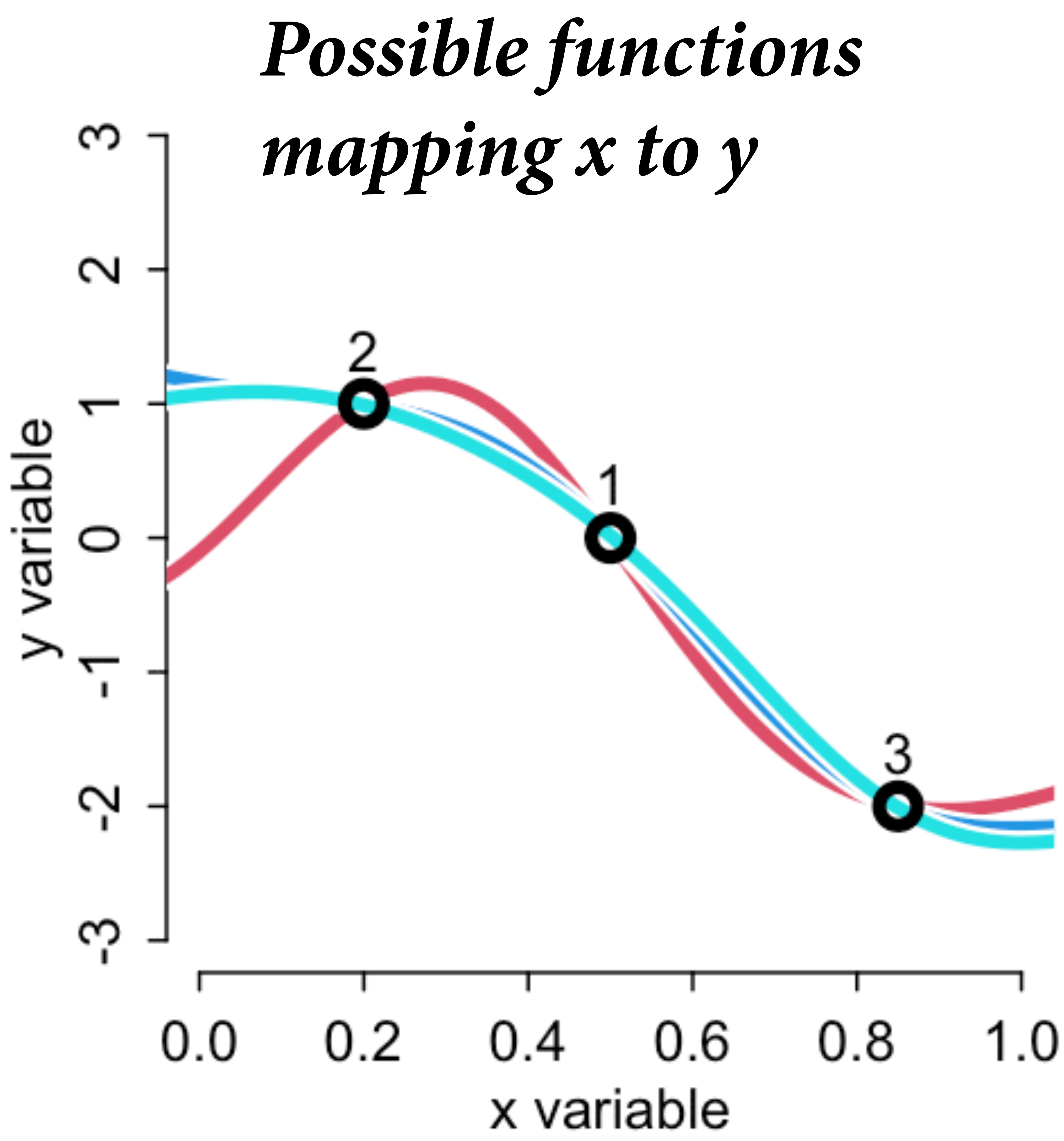
Continuous, ordered categories




Possible functions mapping x to y
3
2
1
0
-1
-2
-3
y variable
1
0.0
0.2
0.4
0.6
0.8
1.0
x variable
Kernel function
2.0
1.5
1.0
0.5
0.0
covariance
0.0
0.2
0.4
0.6
0.8
1.0
distance



Possible functions mapping x to y
y variable
x variable
2
1
Kernel function
covariance
distance
1,2



Possible functions mapping x to y
y variable
x variable
3
2
1
0
-1
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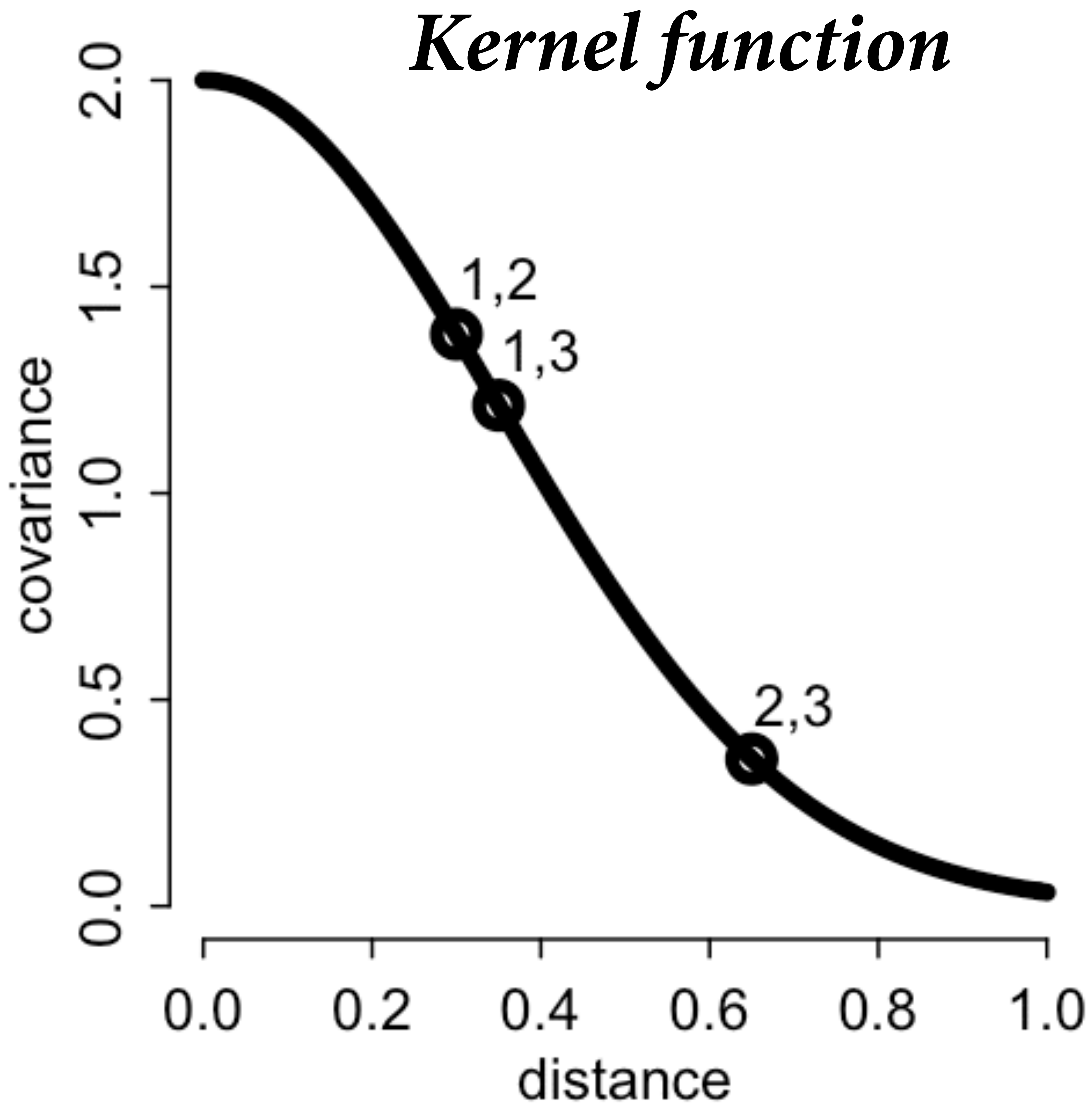
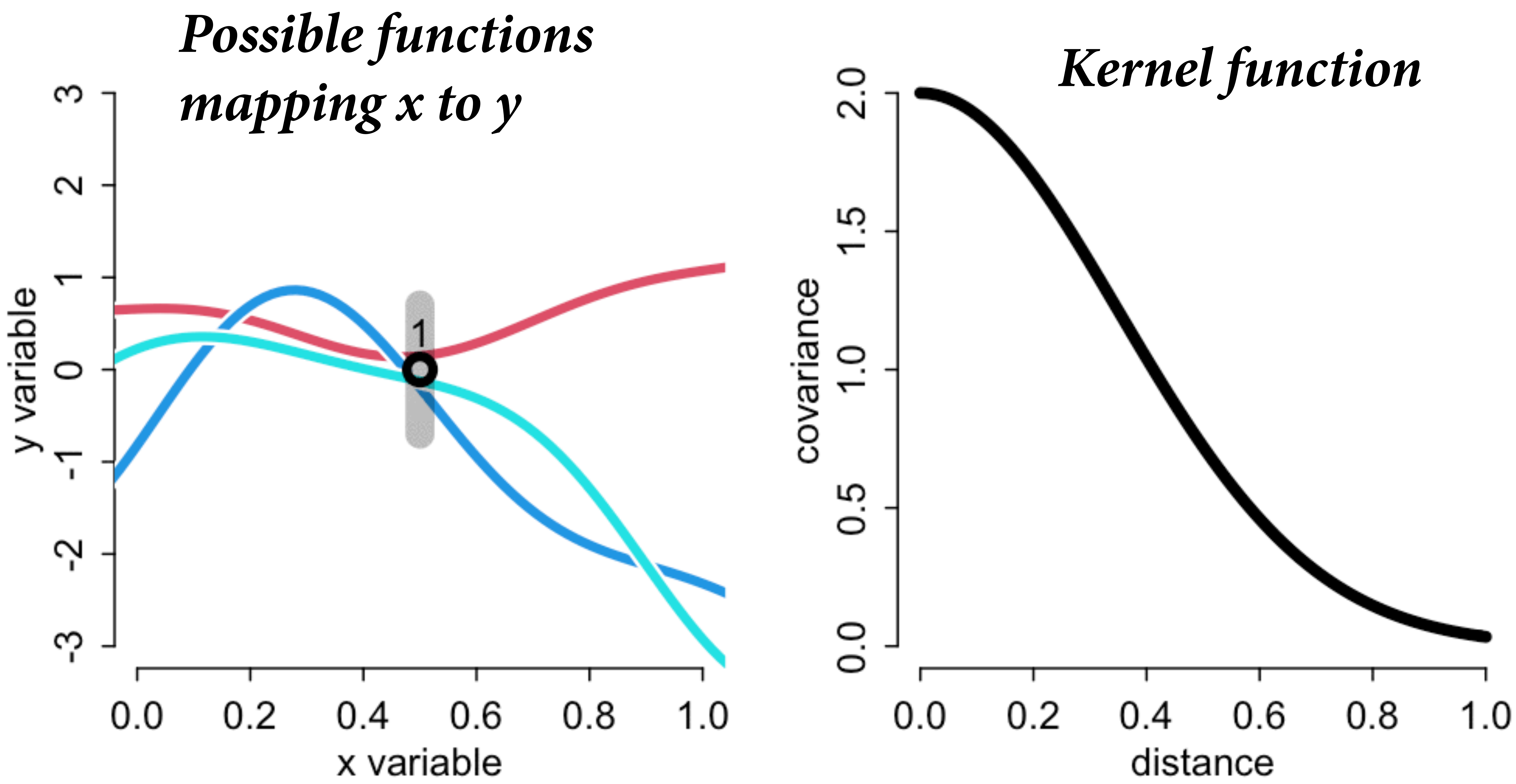
-3
0.0
0.2
0.4
0.6
0.8
1.0



Kernel function
covariance
distance
2.0
1.5
1.0
0.5
0.0
1,2
1,3
2,3
0.0
0.2
0.4
0.6
0.8
1.0



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y variable
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0.6
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x variable
Kernel function
2.0
1.5
1.0
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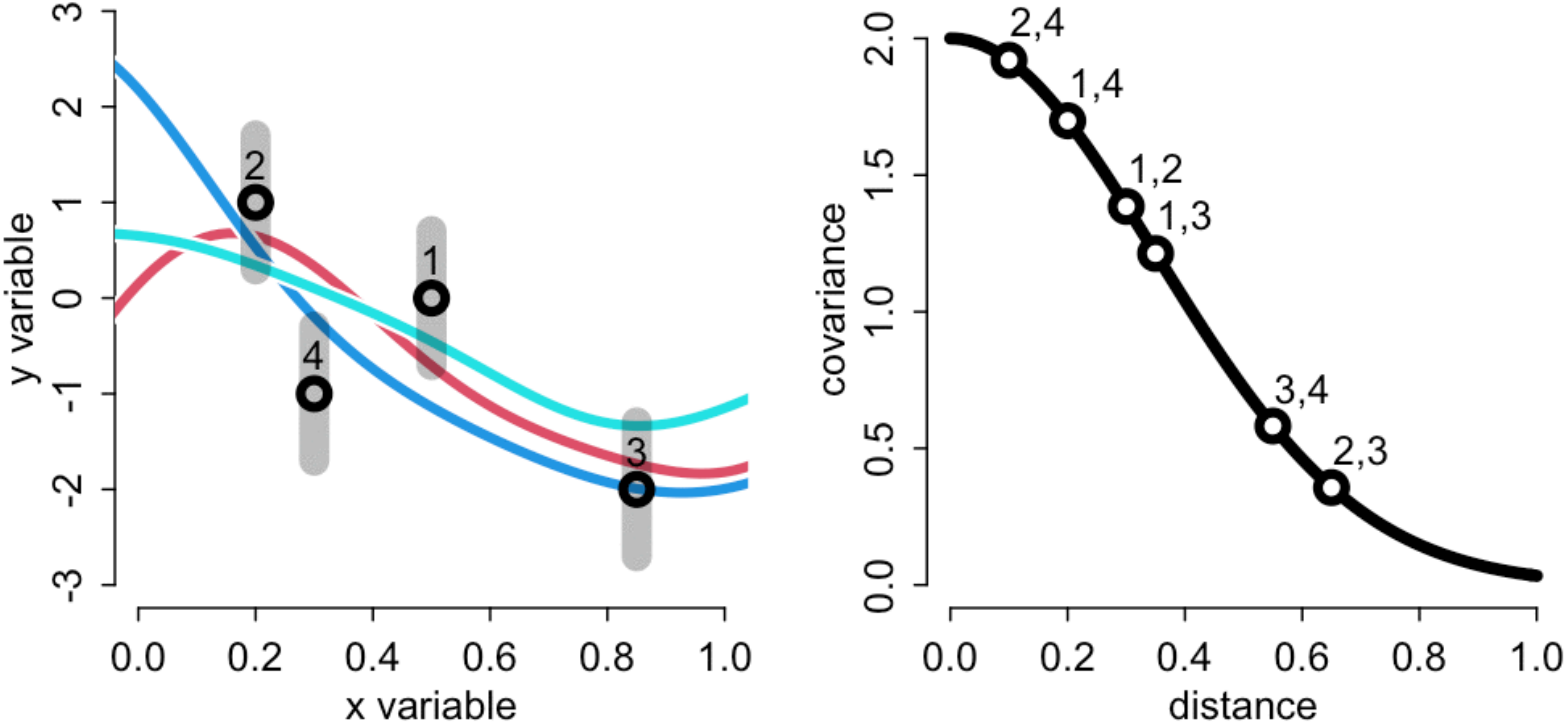
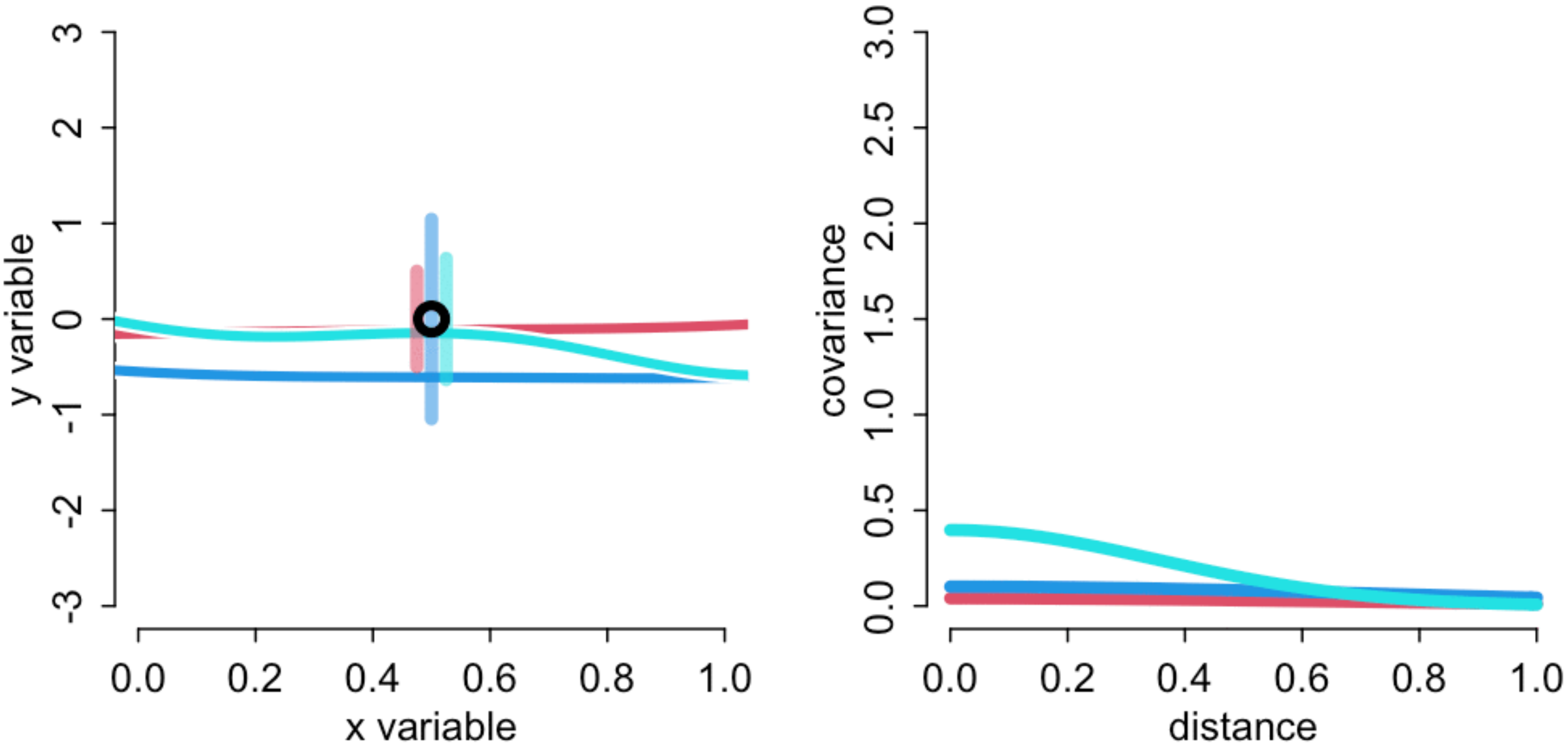
covariance
0.0
0.2
0.4
0.6
0.8
1.0
distance



y variable
x variable
3
2
1
0
-1
-2
-3
0.0
0.2
0.4
0.6
0.8
1.0
1
2
3
4
covariance
distance
2.0
1.5
1.0
0.5
0.0
2,4
1,4
1,2
1,3
3,4
2,3



y variable
3
2
1
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0.0
0.2
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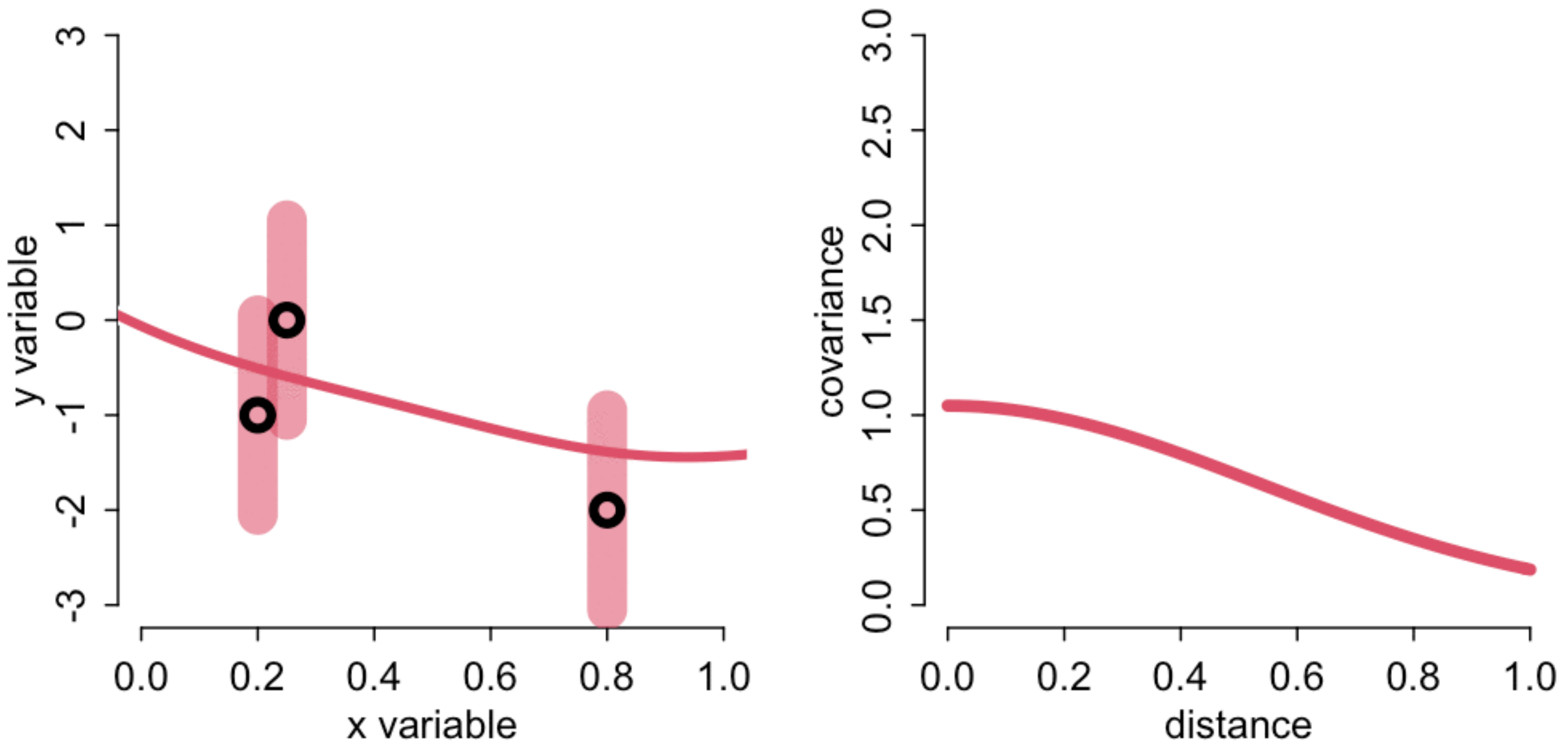

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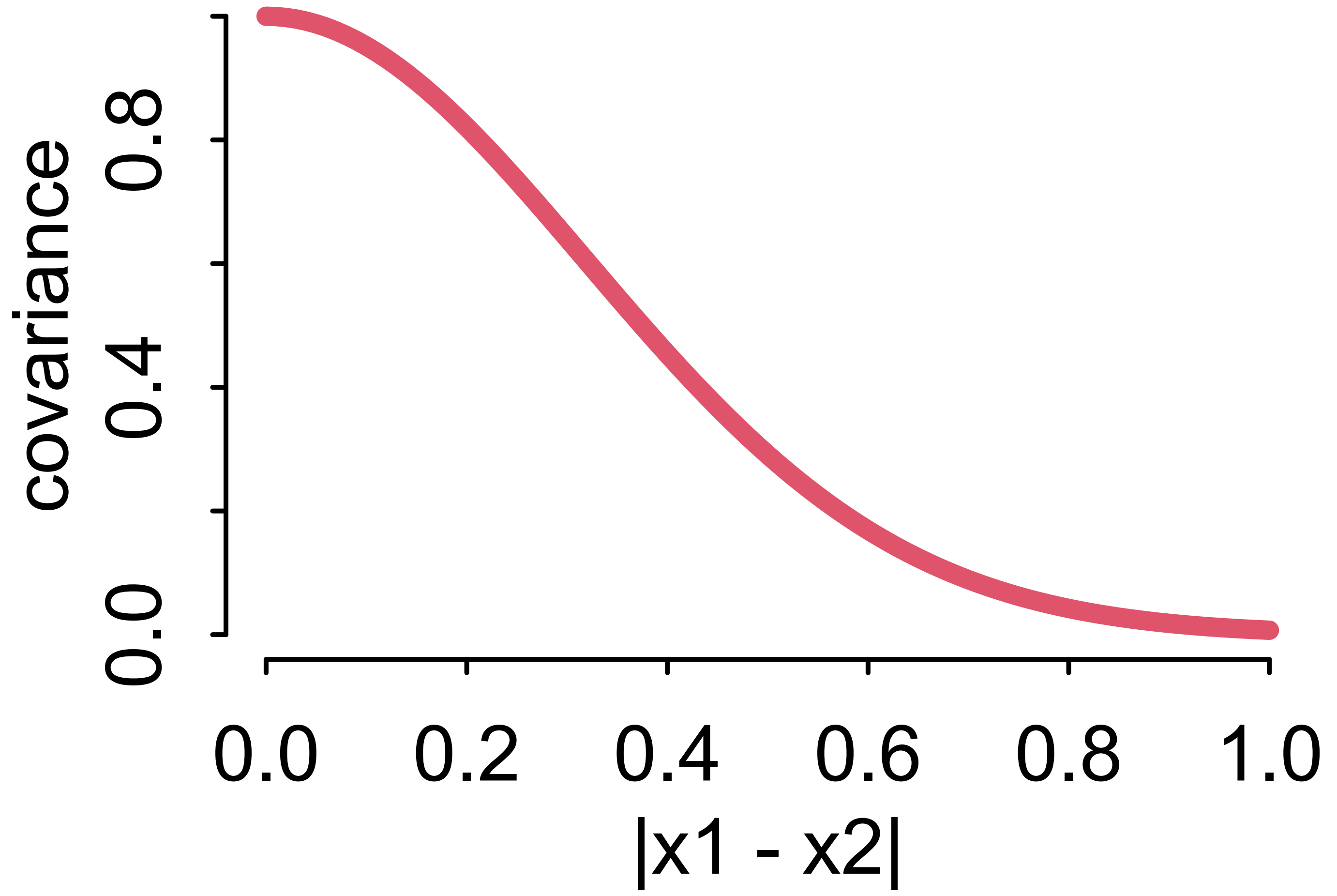
1.0
distance

Quadratic (L2)

$$k(x_1, x_2) = \alpha^2 \exp\left(-\frac{(x_1 - x_2)^2}{\sigma^2}\right)$$



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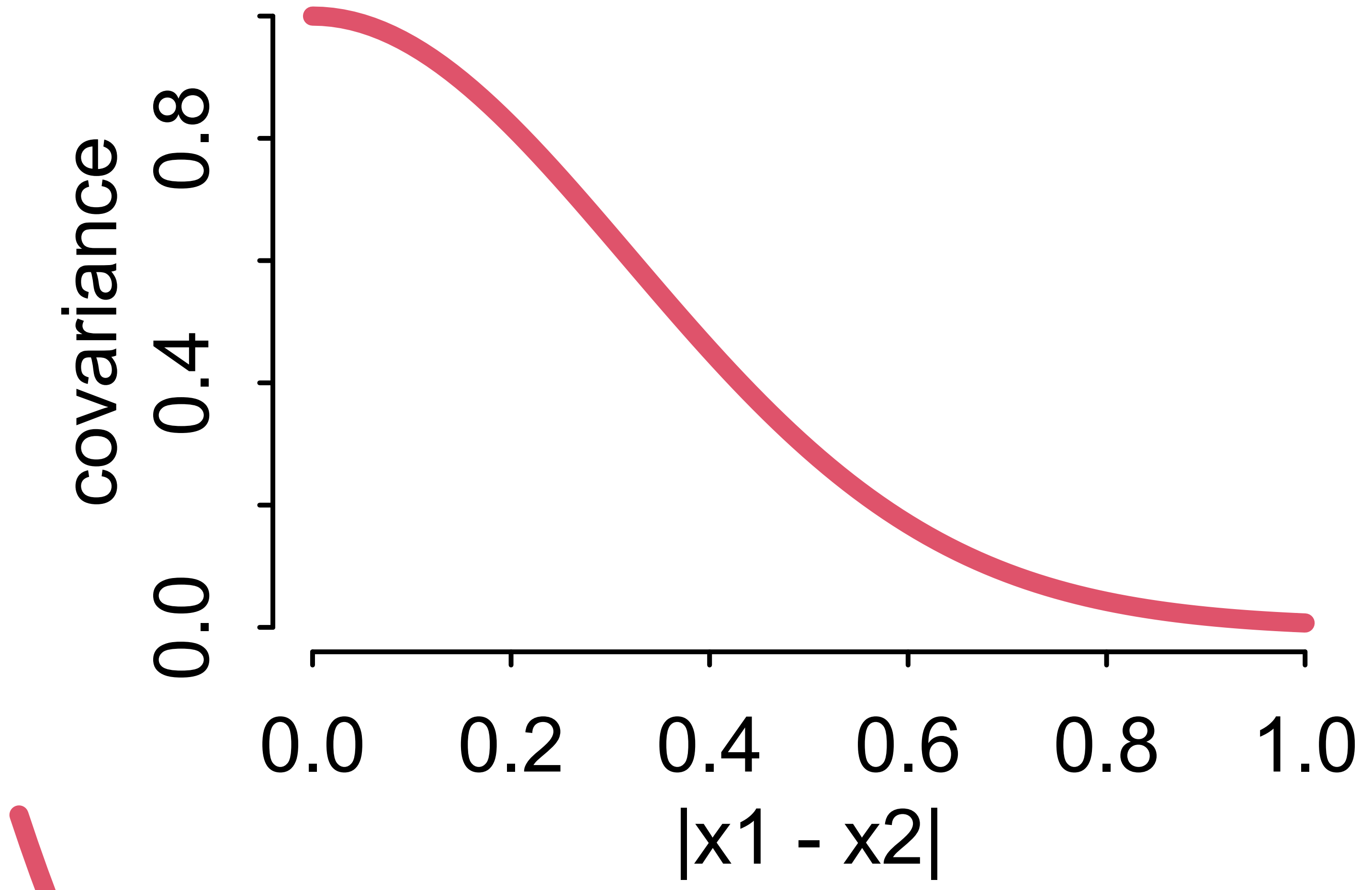
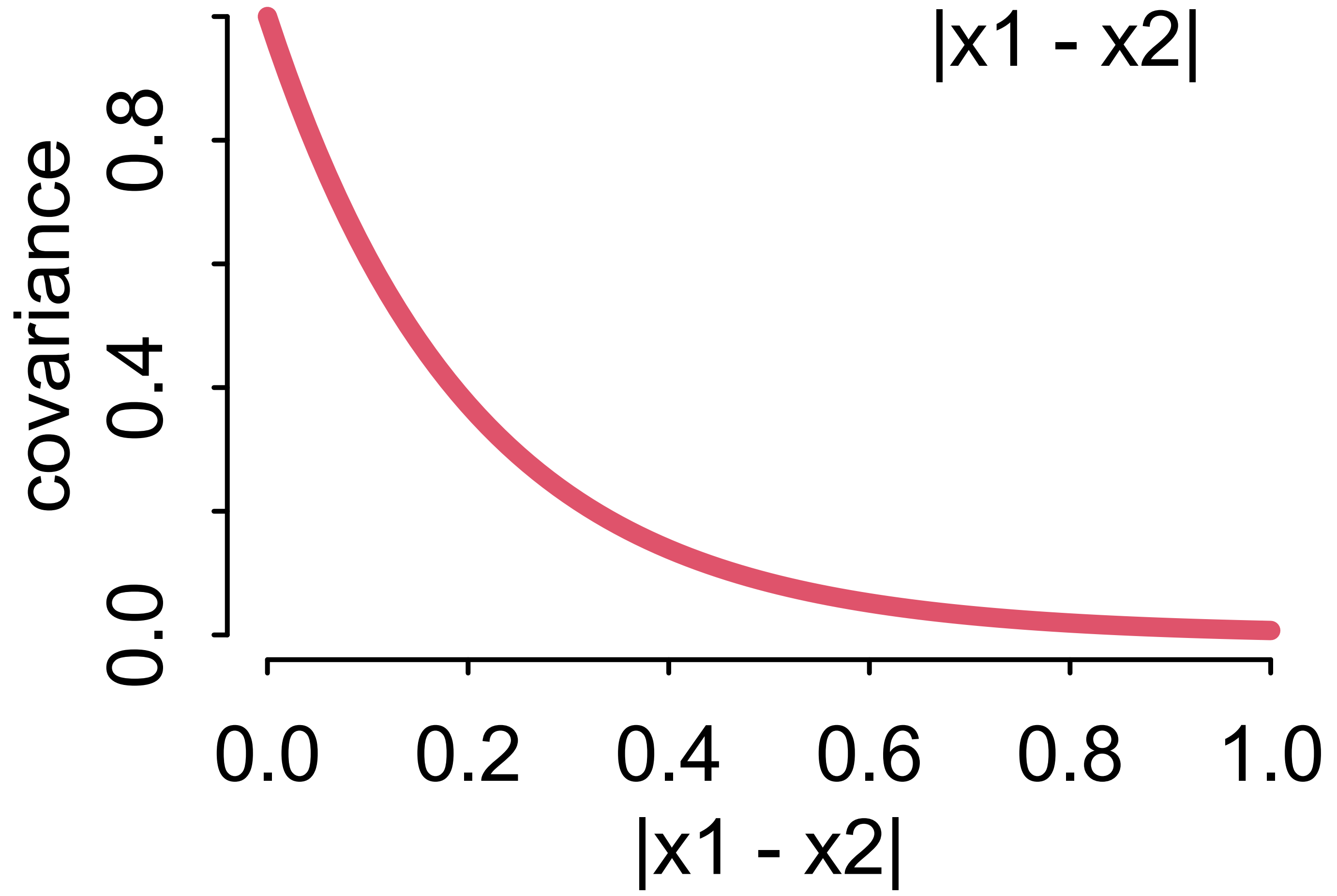


Ornstein-Uhlenbeck

$$k(x_1, x_2) = \alpha^2 \exp\left(-\frac{|x_1 - x_2|}{\sigma}\right)$$



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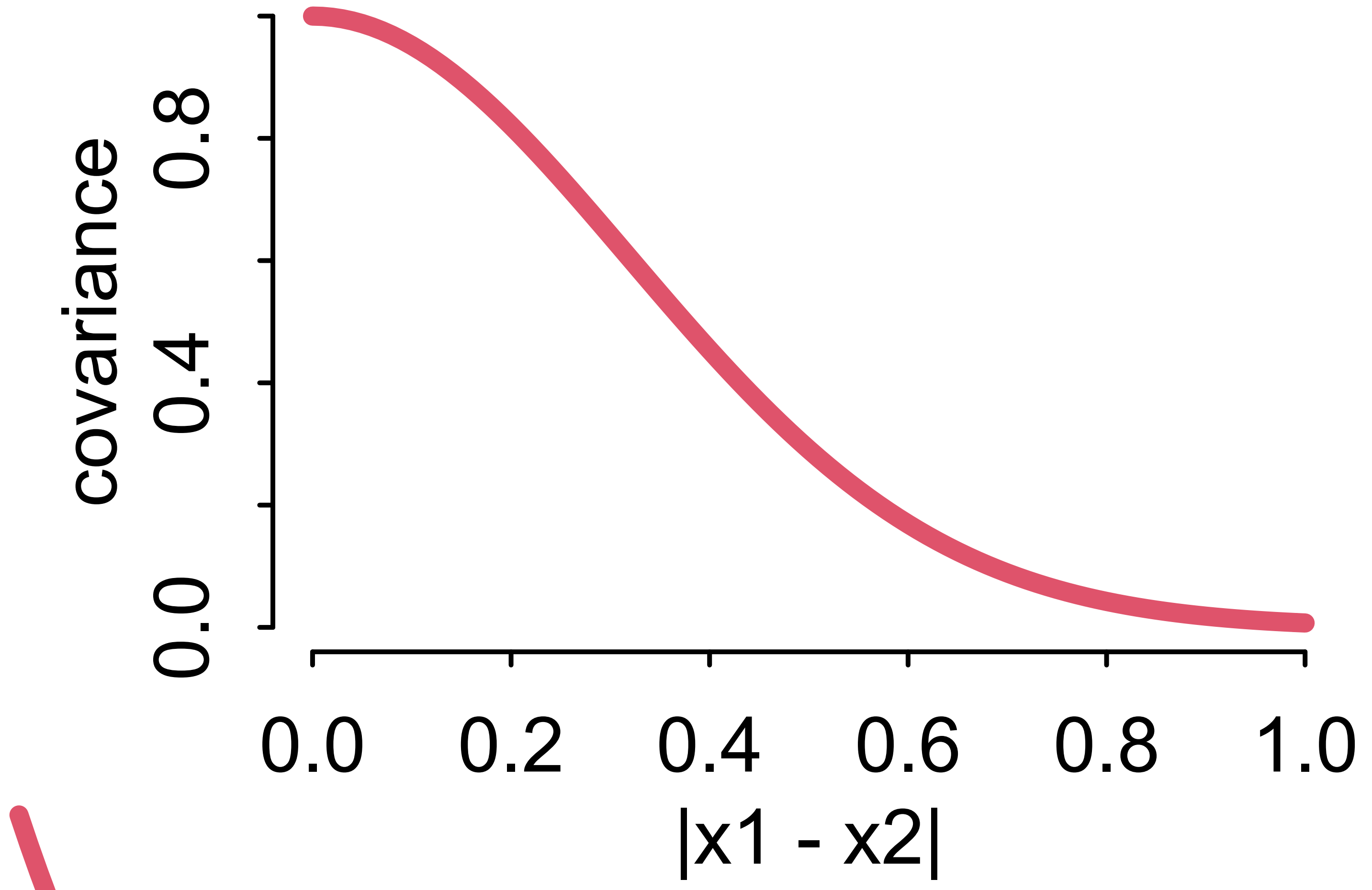

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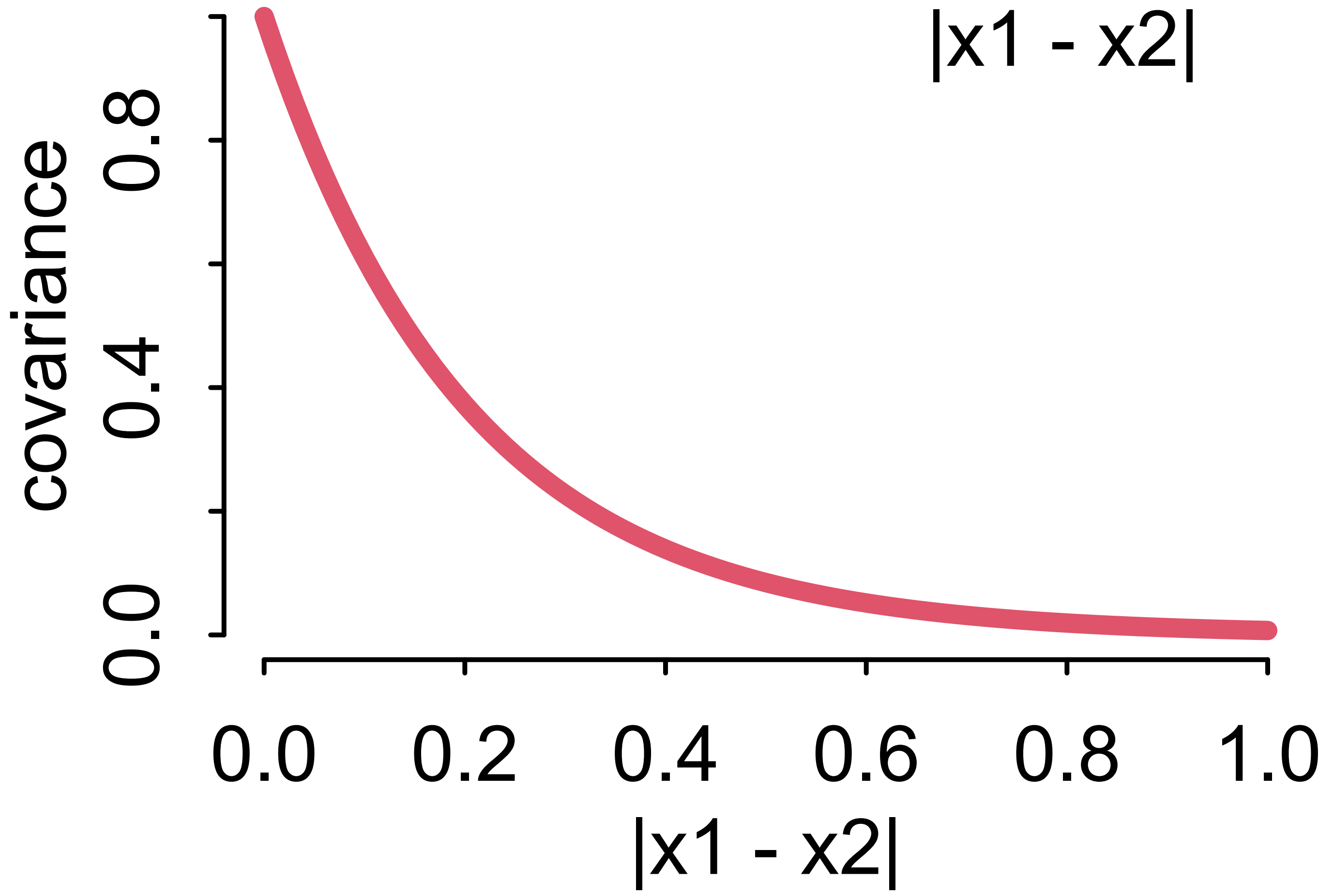
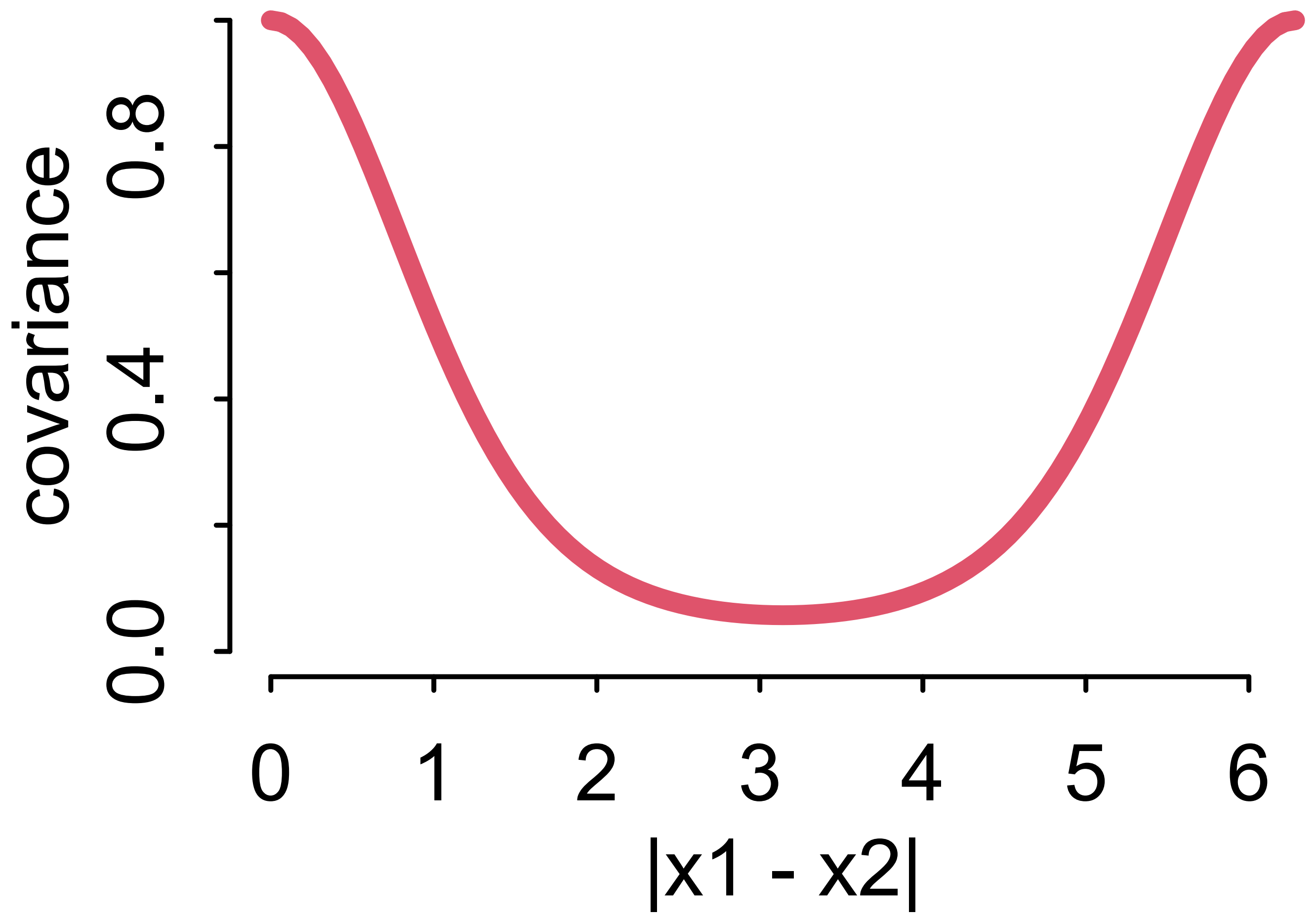


Periodic

$$k(x_1, x_2) = \alpha^2 \exp\left(-\frac{2\sin^2\left((x_1 - x_2)/2\right)}{\sigma^2}\right)$$



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$$\begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{10} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \mathbf{K} \right)$$

rate of decline

$$k_{i,j} = \eta^2 \exp\left(-\rho^2 d_{i,j}^2\right)$$

covariance

maximum covariance

distance i,j

$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\log \lambda_i = \bar{\alpha} + \alpha_{S[i]}$$

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$$k_{i,j} = \eta^2 \exp\left(-\rho^2 d_{i,j}^2\right)$$

$$\bar{\alpha} \sim \text{Normal}(3, 0.5)$$

$$\eta^2 \sim \text{Exponential}(2)$$

$$\rho^2 \sim \text{Exponential}(0.5)$$

Distance matrix (thousand km)

	Ml	Ti	SC	Ya	Fi	Tr	Ch	Mn	To	Ha
Malekula	0.0	0.5	0.6	4.4	1.2	2.0	3.2	2.8	1.9	5.7
Tikopia	0.5	0.0	0.3	4.2	1.2	2.0	2.9	2.7	2.0	5.3
Santa Cruz	0.6	0.3	0.0	3.9	1.6	1.7	2.6	2.4	2.3	5.4
Yap	4.4	4.2	3.9	0.0	5.4	2.5	1.6	1.6	6.1	7.2
Lau Fiji	1.2	1.2	1.6	5.4	0.0	3.2	4.0	3.9	0.8	4.9
Trobriand	2.0	2.0	1.7	2.5	3.2	0.0	1.8	0.8	3.9	6.7
Chuuk	3.2	2.9	2.6	1.6	4.0	1.8	0.0	1.2	4.8	5.8
Manus	2.8	2.7	2.4	1.6	3.9	0.8	1.2	0.0	4.6	6.7
Tonga	1.9	2.0	2.3	6.1	0.8	3.9	4.8	4.6	0.0	5.0
Hawaii	5.7	5.3	5.4	7.2	4.9	6.7	5.8	6.7	5.0	0.0

What do these priors imply?

$$k_{i,j} = \eta^2 \exp\left(-\rho^2 d_{i,j}^2\right)$$

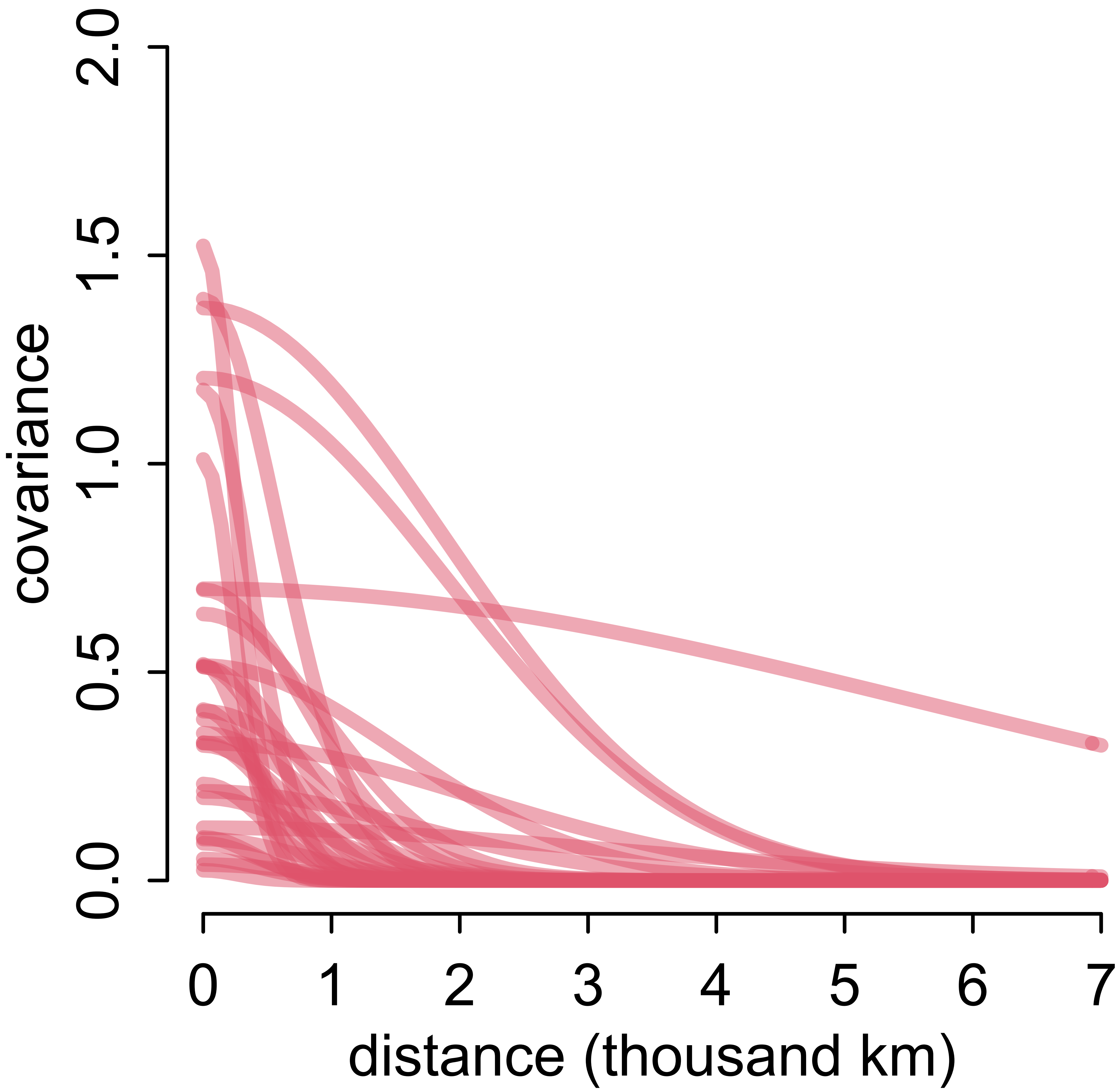
$$\eta^2 \sim \text{Exponential}(2)$$

$$\rho^2 \sim \text{Exponential}(0.5)$$

```
# sim priors for distance model
n <- 30
etasq <- rexp(n,2)
rhosq <- rexp(n,0.5)

plot( NULL , xlim=c(0,7) , ylim=c(0,2) ,
  xlab="distance (thousand km)" ,
  ylab="covariance" )

for ( i in 1:n )
    curve( etasq[i]*exp(-rhosq[i]*x^2) ,
        add=TRUE , lwd=4 ,
        col=col.alpha(2,0.5) )
```



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Santa Cruz	0.6	0.3	0.0	3.9	1.6	1.7	2.6	2.4	2.3	5.4
Yap	4.4	4.2	3.9	0.0	5.4	2.5	1.6	1.6	6.1	7.2
Lau Fiji	1.2	1.2	1.6	5.4	0.0	3.2	4.0	3.9	0.8	4.9
Trobriand	2.0	2.0	1.7	2.5	3.2	0.0	1.8	0.8	3.9	6.7
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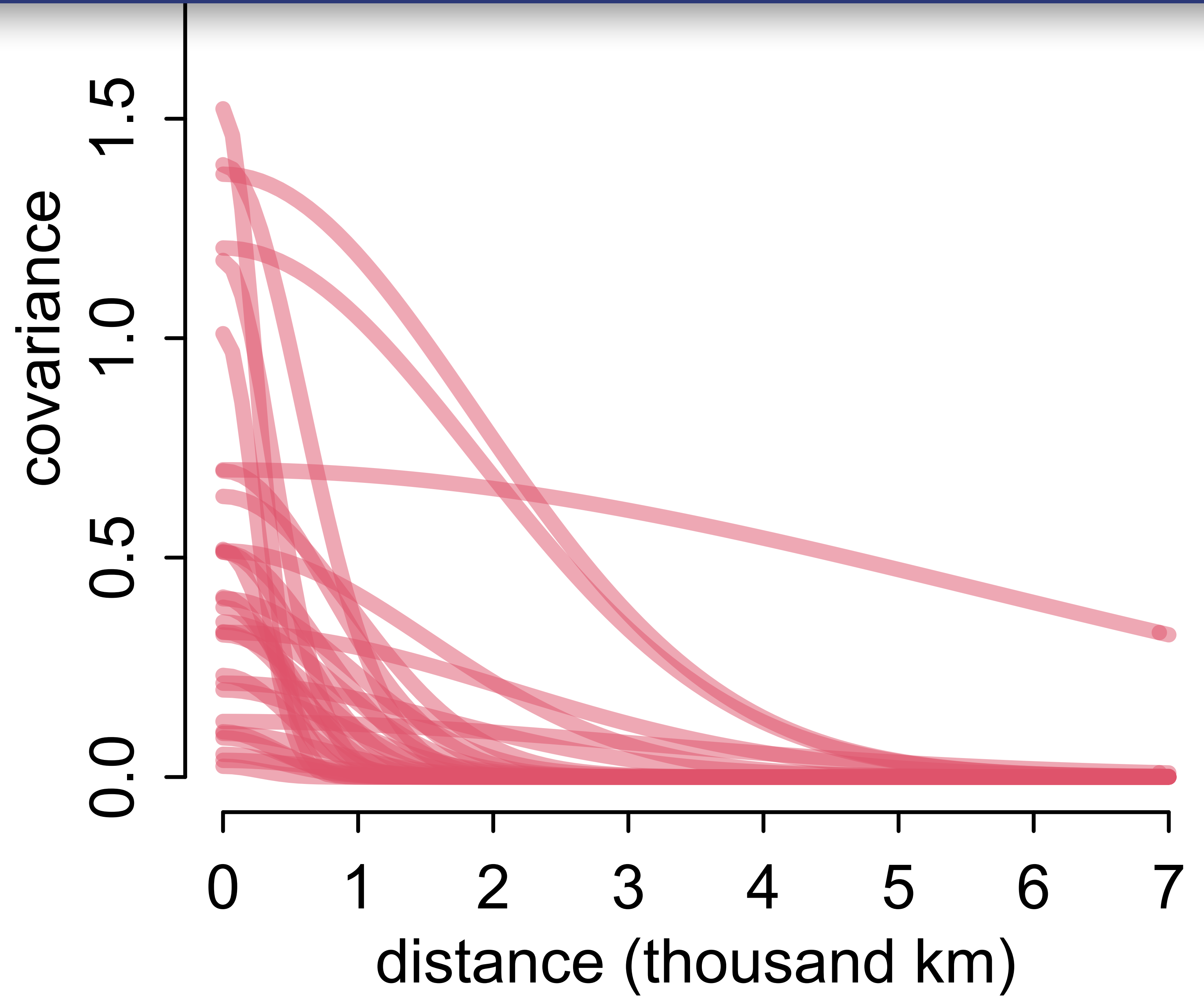

```r
data(Kline2)
d <- Kline2
data(islandsDistMatrix)

dat_list <- list(
    T = d$total_tools,
    S = 1:10,
    D = islandsDistMatrix )

mTdist <- ulam(
    alist(
        T ~ dpois(lambda),
        log(lambda) <- abar + a[S],
        vector[10]:a ~ multi_normal( 0 , K ),
        matrix[10,10]:K <- cov_GPL2(D,etasq,rhosq,0.01),
        abar ~ normal(3,0.5),
        etasq ~ dexp( 2 ),
        rhosq ~ dexp( 0.5 )
    ), data=dat_list , chains=4 , cores=4 , iter=4000 )
```

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        abar ~ normal(3,0.5),
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    ), data=dat_list , chains=4 , cores=4 , iter=4000 )
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$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\log \lambda_i = \bar{\alpha} + \alpha_{S[i]}$$

$$\begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{10} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \mathbf{K} \right)$$

$$k_{i,j} = \eta^2 \exp\left(-\rho^2 d_{i,j}^2\right)$$

$$\bar{\alpha} \sim \text{Normal}(3, 0.5)$$

$$\eta^2 \sim \text{Exponential}(2)$$

$$\rho^2 \sim \text{Exponential}(0.5)$$

$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\log \lambda_i = \bar{\alpha} + \alpha_{S[i]}$$

```r
data(Kline2)
d <- Kline2
data(islandsDistMatrix)

dat_list <- list(
    T = d$total_tools,
    S = 1:10,
    D = islandsDistMatrix )

mTdist <- ulam(
    alist(
        T ~ dpois(lambda),
        log(lambda) <- abar + a[S],
        vector[10]:a ~ multi_normal( 0
        matrix[10,10]:K <- cov_GPL2(D,e
        abar ~ normal(3,0.5),
        etasq ~ dexp( 2 ),
        rhosq ~ dexp( 0.5 )
    ), data=dat_list , chains=4 , cores
```

```
> precis(mTdist,2)
```

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a[1]	-0.67	0.31	-1.16	-0.18	1385	1
a[2]	-0.43	0.30	-0.89	0.06	1075	1
a[3]	-0.38	0.30	-0.87	0.10	1137	1
a[4]	0.24	0.28	-0.20	0.71	1133	1
a[5]	0.02	0.29	-0.44	0.49	1124	1
a[6]	-0.48	0.30	-0.96	-0.01	1303	1
a[7]	0.16	0.29	-0.28	0.63	1154	1
a[8]	-0.17	0.30	-0.65	0.29	1164	1
a[9]	0.45	0.28	0.01	0.90	1053	1
a[10]	0.73	0.27	0.30	1.18	1027	1
abar	3.49	0.25	3.08	3.88	896	1
etasq	0.38	0.27	0.12	0.87	1989	1
rhosq	1.09	1.39	0.08	3.68	3302	1

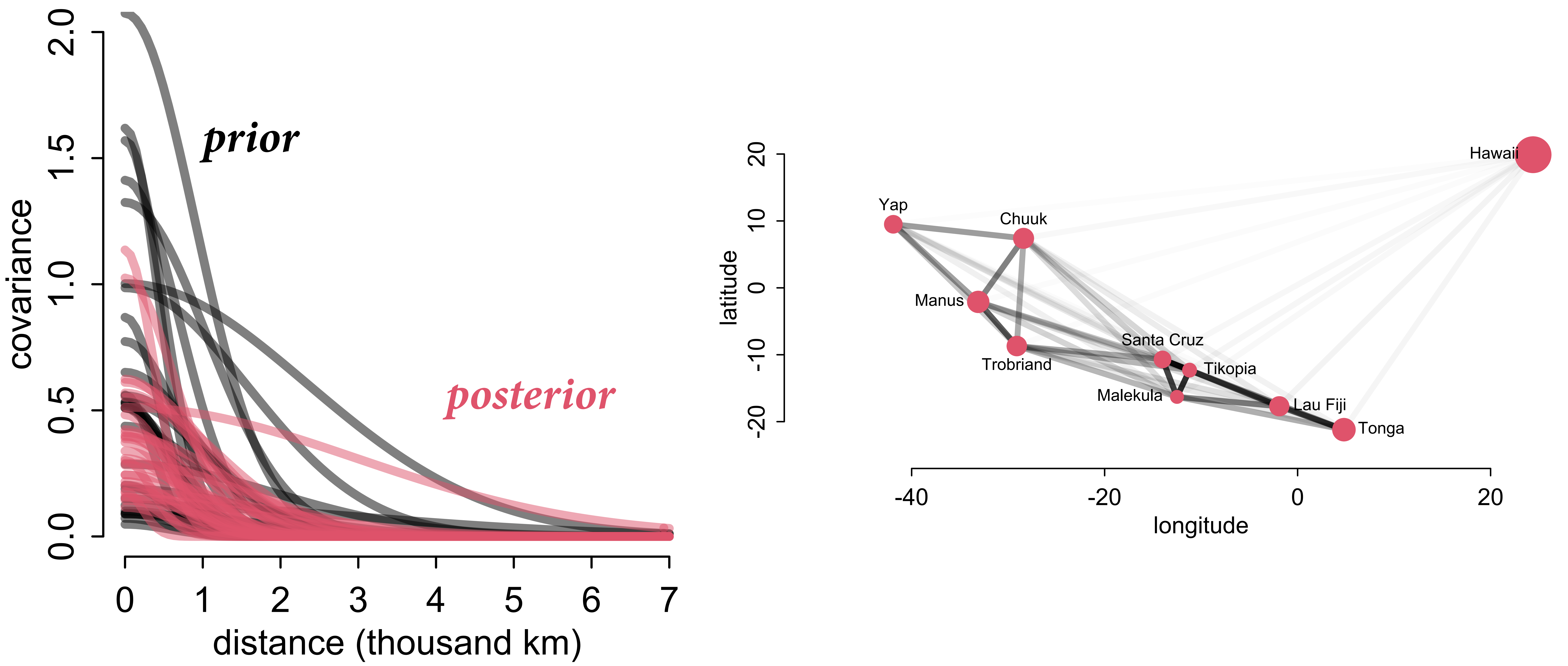
$$\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \mathbf{K} \Big)$$

$$_i\Big)$$

$$5)$$

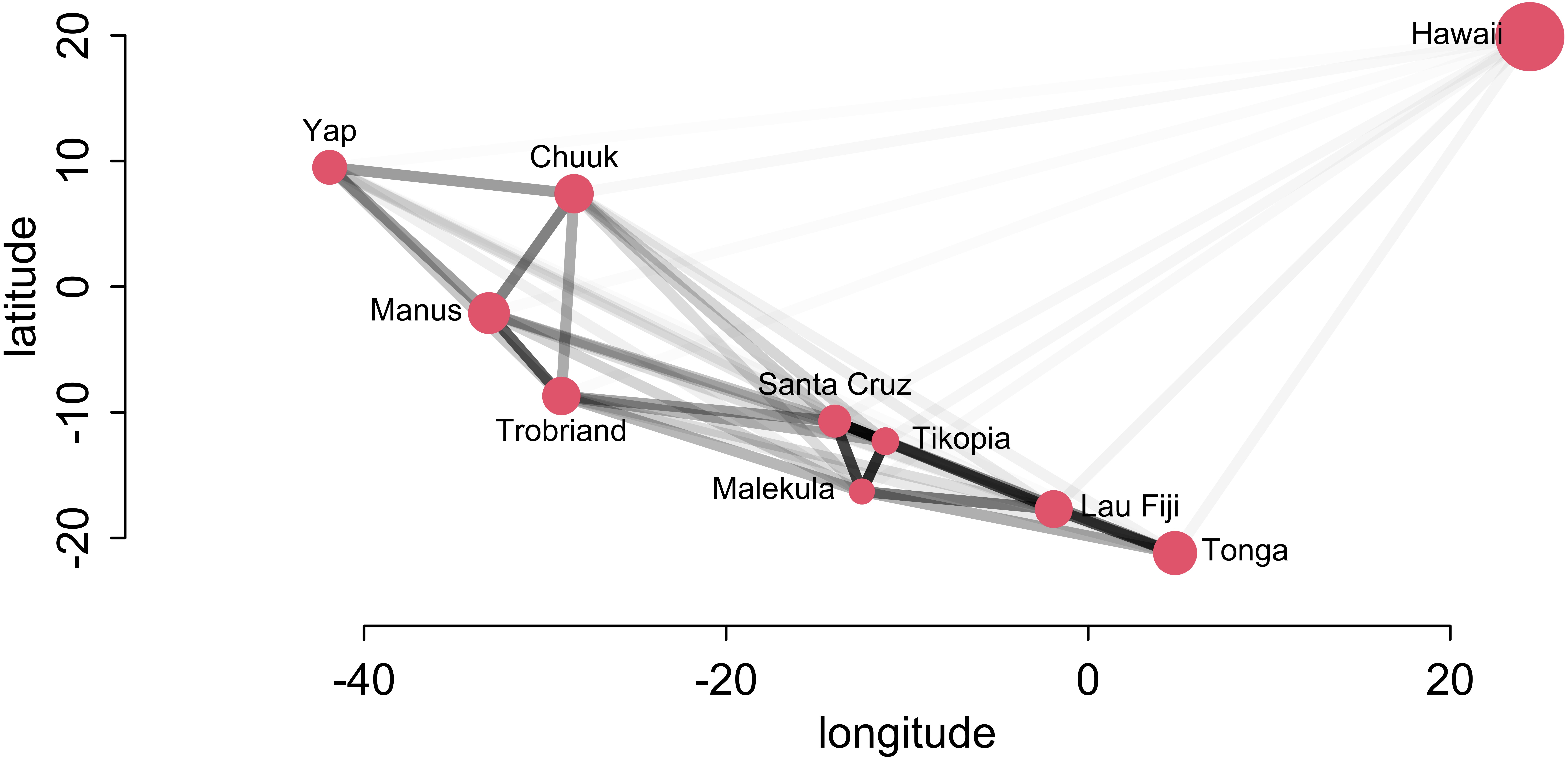
$$2)$$

$$0.5)$$



prior
posterior
covariance
distance (thousand km)
0.0
0.5
1.0
1.5
2.0
0
1
2
3
4
5
6
7
latitude
longitude
Hawaii
Yap
Chuuk
Manus
Trobriand
Santa Cruz
Tikopia
Malekula
Lau Fiji
Tonga
20
10
0
-10
-20
-40
-20
0
20

Pure spatial covariance, nothing else



Stratify by population size

```
dat_list <- list(
    T = d$total_tools,
    P = d$population,
    S = 1:10,
    D = islandsDistMatrix )

mTDP <- ulam(
    alist(
        T ~ dpois(lambda),
        lambda <- (abar*P^b/g)*exp(a[S]),
        vector[10]:a ~ multi_normal( 0 , K ),
        transpars> matrix[10,10]:K <-
            cov_GPL2(D,etasq,rhosq,0.01),
        c(abar,b,g) ~ dexp( 1 ),
        etasq ~ dexp( 2 ),
        rhosq ~ dexp( 0.5 )
    ), data=dat_list , chains=4 , cores=4 , iter=4000 )
```

$$T_i \sim \text{Poisson}(\lambda_i)$$

$$\lambda_i = \frac{\bar{\alpha} P^{\beta}}{\gamma} \exp(\alpha_{S[i]})$$

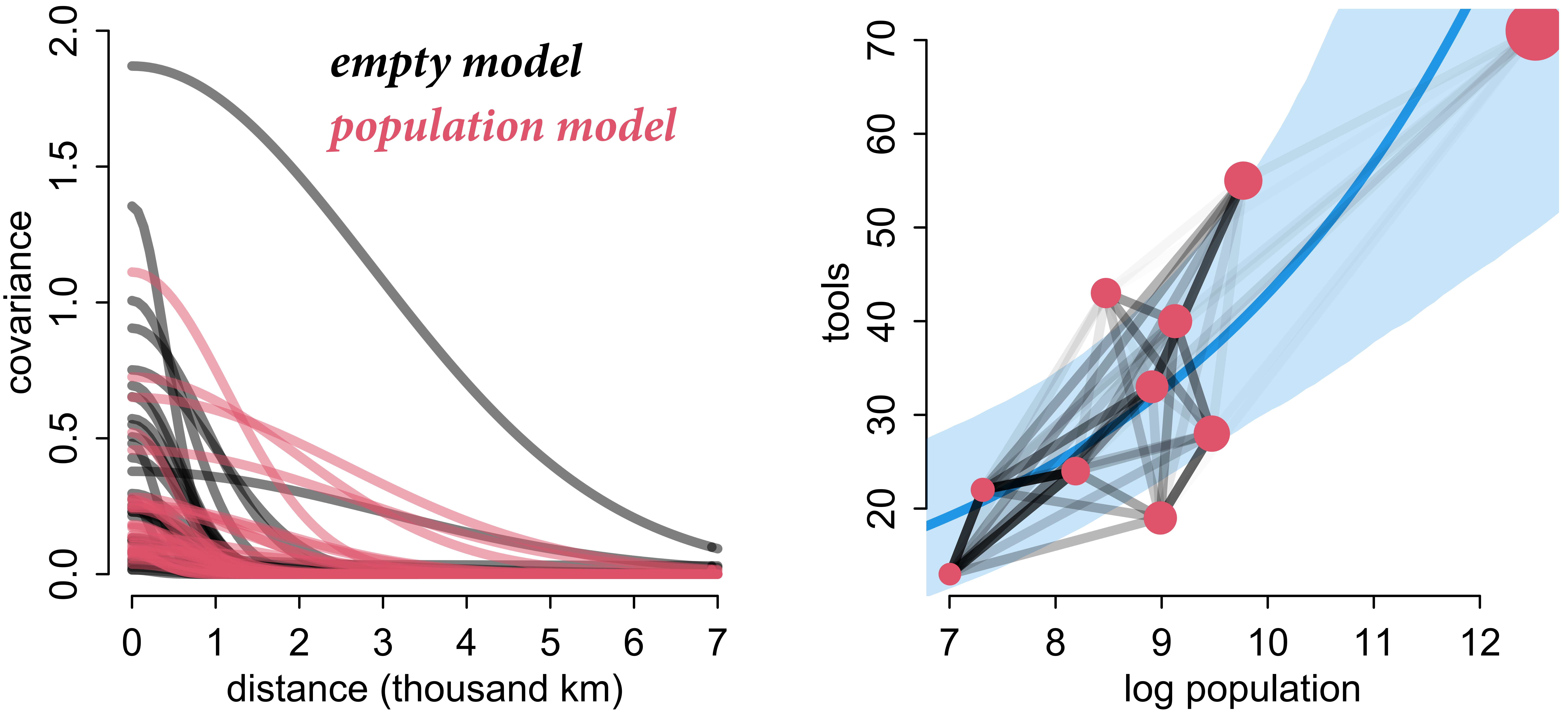
$$\begin{bmatrix} \alpha_1 \\ \alpha_2 \\ \vdots \\ \alpha_{10} \end{bmatrix} \sim \text{MVNormal}\left(\begin{bmatrix} 0 \\ 0 \\ \vdots \\ 0 \end{bmatrix}, \mathbf{K} \right)$$

$$k_{i,j} = \eta^2 \exp\left(-\rho^2 d_{i,j}^2\right)$$

$$\bar{\alpha}, \beta, \gamma \sim \text{Exponential}(1)$$

$$\eta^2 \sim \text{Exponential}(2)$$

$$\rho^2 \sim \text{Exponential}(0.5)$$



empty model
population model
covariance
distance (thousand km)
0.0
0.5
1.0
1.5
2.0
0
1
2
3
4
5
6
7
tools
log population
20
30
40
50
60
70
7
8
9
10
11
12

PAUSE

Primates


Cercopithecus diana
Cercopithecus wolfi
Cercopithecus pogonias
Cercopithecus mona
Cercopithecus campbelli lowei
Cercopithecus campbelli
Cercopithecus nictitans
Cercopithecus mitis
Cercopithecus albogularis
Cercopithecus petaurista
Cercopithecus erythrogaster erythrogaster
Cercopithecus erythrogaster
Cercopithecus ascanius
Cercopithecus erythrotis
Cercopithecus cephus ngottoensis
Cercopithecus cephus cephus
Cercopithecus cephus
Mandrillus sphinx
Mandrillus leucophaeus
Cercocebus torquatus atys
Cercocebus torquatus
Cercocebus galeritus
Cercocebus agilis
Theropithecus gelada
Lophocebus aterrimus
Lophocebus albigena
Rungwecebus kipunji
Papio ursinus
Papio cynocephalus
Papio papio
Papio hamadryas
Papio anubis
Alouatta palliata
Alouatta pigra
Alouatta belzebul
Alouatta sara
Alouatta seniculus
Alouatta caraya
Alouatta guariba
Ateles fusciceps
Ateles geoffroyi
Ateles belzebuth
Ateles paniscus
Brachyteles arachnoides
Lagothrix lagotricha
Cacajao calvus
Cacajao melanocephalus
Chiropotes satanas
Pithecia irrorata
Pithecia pithecia
Callicebus hoffmannsi
Callicebus moloch
Callicebus donacophilus
Callicebus personatus
Callicebus torquatus
Tarsius bancanus
Tarsius syrichta
Tarsius dentatus
Tarsius lariang
Microcebus bongolavensis
Microcebus ravelobensis
Microcebus danfossi
Microcebus macarthurii
Microcebus tavaratra
Microcebus jollyae
Microcebus rufus
Microcebus simmonsi
Microcebus mittermeieri
Microcebus lokobensis
Microcebus sambiranensis
Microcebus mamiratra
Microcebus griseorufus
Microcebus murinus
Microcebus berthae
Microcebus myoxinus
Microcebus lehilahytsara

Theropithecus gelada
Lophocebus aterrimus
Lophocebus albigena
Rungwecebus kipunji
Papio ursinus
Papio cynocephalus
Papio papio
Papio hamadryas
Papio anubis
Macaca sylvanus
Macaca thibetana
Macaca munzala
Macaca mulatta
Macaca fascicularis
Macaca fuscata
Macaca cyclopis
Macaca arctoides
Macaca assamensis
Macaca sinica
Macaca radiata
Macaca nemestrina
Macaca silenus
Macaca pagensis
Macaca nemestrina leonina
Macaca nemestrina siberu
Macaca leonina
Macaca nigrescens
Macaca nigra
Macaca hecki
Macaca tonkeana
Macaca maura
Macaca ochreata
Macaca brunnescens
Perodicticus potto
Arctocebus calabarensis
Arctocebus aureus
Loris tardigradus
Loris lydekkerianus
Nycticebus pygmaeus
Aotus azarai
Aotus azarai boliviensis
Aotus infulatus
Aotus nigriceps
Aotus brumbacki
Aotus vociferans
Aotus nancymaae
Aotus lemurinus
Aotus trivirgatus
Aotus lemurinus griseimembra
Cebus albifrons
Cebus olivaceus
Cebus capucinus
Cebus apella
Cebus xanthosternos
Saimiri oerstedii
Saimiri sciureus
Saimiri ustus
Saimiri boliviensis
Alouatta palliata
Alouatta pigra
Alouatta belzebul
Alouatta sara
Alouatta seniculus
Alouatta caraya

Apes

Colobus satanas
Colobus angolensis palliatus
Colobus angolensis
Colobus guereza
Colobus vellerosus
Hylobates agilis
Hylobates klossii
Hylobates moloch
Hylobates muelleri
Hylobates lar
Hylobates pileatus
Symphalangus syndactylus
Nomascus leucogenys
Nomascus siki
Nomascus gabriellae
Nomascus concolor
Nomascus nasutus
Bunopithecus hoolock
Pan troglodytes schweinfurthii
Pan troglodytes troglodytes
Pan troglodytes vellerosus
Pan troglodytes verus
Pan paniscus
Homo sapiens
Homo sapiens neanderthalensis
Gorilla beringei
Gorilla gorilla graueri
Gorilla gorilla gorilla
Pongo abelii
Pongo pygmaeus
Callithrix argentata
Callithrix emiliae
Callithrix humeralifera
Callithrix mauesi
Callithrix pygmaea
Callithrix kuhli
Callithrix penicillata

African & Asian monkeys

American monkeys

Tarsiers

Lemurs etc


Lepilemur manasamody
Lepilemur otto
Lepilemur microdon
Lepilemur mustelinus
Lepilemur seali
Phaner furcifer pallescens
Phaner furcifer
Propithecus coquereli
Propithecus tattersalli
Propithecus deckenii
Propithecus verreauxi
Propithecus diadema
Propithecus edwardsi
Avahi cleesei
Avahi occidentalis
Avahi unicolor
Avahi laniger
Archaeolemur majori
Indri indri
Eulemur fulvus albifrons
Eulemur fulvus sanfordi
Eulemur fulvus fulvus
Eulemur fulvus mayottensis
Eulemur fulvus albocollaris
Eulemur fulvus collaris
Eulemur rubriventer
Eulemur fulvus rufus
Eulemur mongoz
Eulemur macaco flavifrons
Eulemur macaco macaco
Eulemur coronatus
Hapalemur griseus
Hapalemur griseus griseus
Hapalemur aureus
Hapalemur simus
Lemur catta
Varecia rubra
Varecia variegata variegata
Daubentonia madagascariensis
Galago moholi
Galago senegalensis
Euoticus elegantulus
Galago gallarum
Galago matschiei
Galagoides granti
Galagoides zanzibaricus
Otolemur crassicaudatus
Otolemur garnettii
Galago alleni
Galagoides demidoff
Nycticebus bengalensis
Nycticebus coucang
Nycticebus menagensis
Nycticebus javanicus
Nycticebus pygmaeus
Loris lydekkerianus
Loris tardigradus
Arctocebus aureus
Arctocebus calabarensis
Perodicticus potto
Macaca brunnescens
Macaca ochreata
Macaca maura
Galagos
Lorises

Perodicticus potto
Arctocebus calabarensis
Arctocebus aureus
Loris tardigradus
Loris lydekkerianus
Nycticebus pygmaeus
Nycticebus javanicus
Nycticebus menagensis
Nycticebus coucang
Nycticebus bengalensis
Galagoides demidoff
Galago alleni
Otolemur garnettii
Otolemur crassicaudatus
Galagoides zanzibaricus
Galago granti
Galago matschiei
Euoticus elegantulus
Galago gallarum
Galago senegalensis
Galago moholi
Daubentonia madagascariensis
Varecia variegata variegata
Varecia rubra
Lemur catta
Hapalemur simus
Hapalemur aureus
Hapalemur griseus griseus
Hapalemur griseus alaotrensis
Hapalemur griseus occidentalis
Hapalemur griseus meridionalis
Hapalemur griseus
Eulemur coronatus
Eulemur macaco macaco
Eulemur macaco flavifrons
Eulemur mongoz
Eulemur fulvus rufus
Eulemur rubriventer
Eulemur fulvus collaris
Eulemur fulvus albocollaris
Eulemur fulvus mayottensis
Eulemur fulvus fulvus
Eulemur fulvus sanfordi
Eulemur fulvus albifrons
Archaeolemur majori
Indri indri
Avahi laniger
Avahi unicolor
Avahi occidentalis
Avahi cleesei
Propithecus edwardsi
Propithecus diadema
Propithecus verreauxi
Propithecus deckenii
Propithecus tattersalli
Propithecus coquereli
Phaner furcifer pallescens
Phaner furcifer
Lepilemur seali
Lepilemur mustelinus
Lepilemur microdon
Lepilemur otto
Lepilemur manasamody
Lepilemur septentrionalis
Lepilemur sahamalazensis
Lepilemur dorsalis
Lepilemur ankaranensis
Lepilemur leucopus
Lepilemur ruficaudatus
Lepilemur hubbardorum
Lepilemur randrianasoli
Lepilemur edwardsi
Lepilemur mitsinjoensis
Lepilemur aeeclis
Cheirogaleus medius
Cheirogaleus major
Cheirogaleus crossleyi
Allocebus trichotis
Mirza zaza
Mirza coquereli
Microcebus lehilahytsara
Microcebus myoxinus
Microcebus berthae
Microcebus murinus
Microcebus griseorufus
Microcebus mamiratra
Microcebus sambiranensis
Microcebus lokobensis
Microcebus mittermeieri
Microcebus simmonsi
Microcebus rufus
Microcebus jollyae
Microcebus tavaratra
Microcebus macarthurii
Microcebus danfossi
Microcebus ravelobensis
Microcebus bongolavensis
Tarsius lariang
Tarsius dentatus
Tarsius syrichta
Tarsius bancanus
Callicebus torquatus
Callicebus personatus
Callicebus donacophilus
Callicebus moloch
Callicebus hoffmannsi
Pithecia pithecia
Pithecia irrorata
Chiropotes satanas
Cacajao melanocephalus
Cacajao calvus
Lagothrix lagotricha
Brachyteles arachnoides
Ateles paniscus
Ateles belzebuth
Ateles geoffroyi
Ateles fusciceps
Alouatta guariba
Alouatta caraya
Alouatta seniculus
Alouatta sara
Alouatta belzebul
Alouatta pigra
Alouatta palliata
Saimiri boliviensis
Saimiri ustus
Saimiri sciureus
Saimiri oerstedii
Cebus xanthosternos
Cebus apella
Cebus capucinus
Cebus olivaceus
Cebus albifrons
Aotus lemurinus griseimembra
Aotus trivirgatus
Aotus lemurinus
Aotus nancymaae
Aotus vociferans
Aotus brumbacki
Aotus nigriceps
Aotus infulatus
Aotus azarai boliviensis
Aotus azarai
Saguinus tripartitus
Saguinus fuscicollis melanoleucus
Saguinus fuscicollis
Saguinus mystax
Saguinus imperator
Saguinus leucopus
Saguinus oedipus
Saguinus geoffroyi
Saguinus bicolor
Saguinus niger
Saguinus midas
Leontopithecus chrysomelas
Leontopithecus rosalia
Leontopithecus chrysopygus
Callimico goeldii
Callithrix aurita
Callithrix geoffroyi
Callithrix jacchus
Callithrix penicillata
Callithrix kuhli
Callithrix pygmaea
Callithrix mauesi
Callithrix humeralifera
Callithrix emiliae
Callithrix argentata
Pongo pygmaeus
Pongo abelii
Gorilla gorilla gorilla
Gorilla gorilla graueri
Gorilla beringei
Homo sapiens neanderthalensis
Homo sapiens
Pan paniscus
Pan troglodytes verus
Pan troglodytes vellerosus
Pan troglodytes troglodytes
Pan troglodytes schweinfurthii
Bunopithecus hoolock
Nomascus nasutus
Nomascus concolor
Nomascus gabriellae
Nomascus siki
Nomascus leucogenys
Symphalangus syndactylus
Hylobates pileatus
Hylobates lar
Hylobates muelleri
Hylobates moloch
Hylobates klossii
Hylobates agilis
Colobus satanas
Colobus angolensis palliatus
Colobus angolensis angolensis
Colobus guereza
Colobus vellerosus
Colobus polykomos
Procolobus verus
Piliocolobus badius
Piliocolobus foai
Piliocolobus preussi
Piliocolobus pennantii
Piliocolobus kirkii
Piliocolobus gordonorum
Piliocolobus tholloni
Piliocolobus tephrosceles
Piliocolobus rufomitratus
Presbytis melalophos
Presbytis comata
Nasalis larvatus
Pygathrix nemaeus
Pygathrix cinerea
Rhinopithecus bieti
Rhinopithecus brelichi
Rhinopithecus roxellana
Rhinopithecus avunculus
Semnopithecus johnii
Semnopithecus entellus
Trachypithecus vetulus
Trachypithecus pileatus
Trachypithecus geei
Trachypithecus obscurus
Trachypithecus cristatus
Trachypithecus germaini
Trachypithecus auratus
Trachypithecus phayrei
Trachypithecus laotum
Trachypithecus delacouri
Trachypithecus poliocephalus
Trachypithecus francoisi
Allenopithecus nigroviridis
Miopithecus talapoin
Erythrocebus patas
Cercopithecus solatus
Cercopithecus preussi
Cercopithecus lhoesti
Chlorocebus sabaeus
Chlorocebus pygerythrus cynosurus
Chlorocebus pygerythrus
Chlorocebus tantalus
Chlorocebus aethiops
Cercopithecus hamlyni
Cercopithecus neglectus
Cercopithecus diana
Cercopithecus wolfi
Cercopithecus pogonias
Cercopithecus mona
Cercopithecus campbelli lowei
Cercopithecus campbelli
Cercopithecus nictitans
Cercopithecus mitis
Cercopithecus albogularis
Cercopithecus petaurista
Cercopithecus erythrogaster erythrogaster
Cercopithecus erythrogaster
Cercopithecus ascanius
Cercopithecus erythrotis
Cercopithecus cephus ngottoensis
Cercopithecus cephus cephus
Cercopithecus cephus
Mandrillus sphinx
Mandrillus leucophaeus
Cercocebus torquatus atys
Cercocebus torquatus
Cercocebus galeritus
Cercocebus agilis
Theropithecus gelada
Lophocebus aterrimus
Lophocebus albigena
Rungwecebus kipunji
Papio ursinus
Papio cynocephalus
Papio papio
Papio hamadryas
Papio anubis
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Macaca fascicularis
Macaca fuscata
Macaca cyclopis
Macaca arctoides
Macaca assamensis
Macaca sinica
Macaca radiata
Macaca nemestrina
Macaca silenus
Macaca pagensis
Macaca nemestrina leonina
Macaca nemestrina siberu
Macaca leonina
Macaca nigrescens
Macaca nigra
Macaca hecki
Macaca tonkeana
Macaca maura
Macaca ochreata
Macaca brunnescens

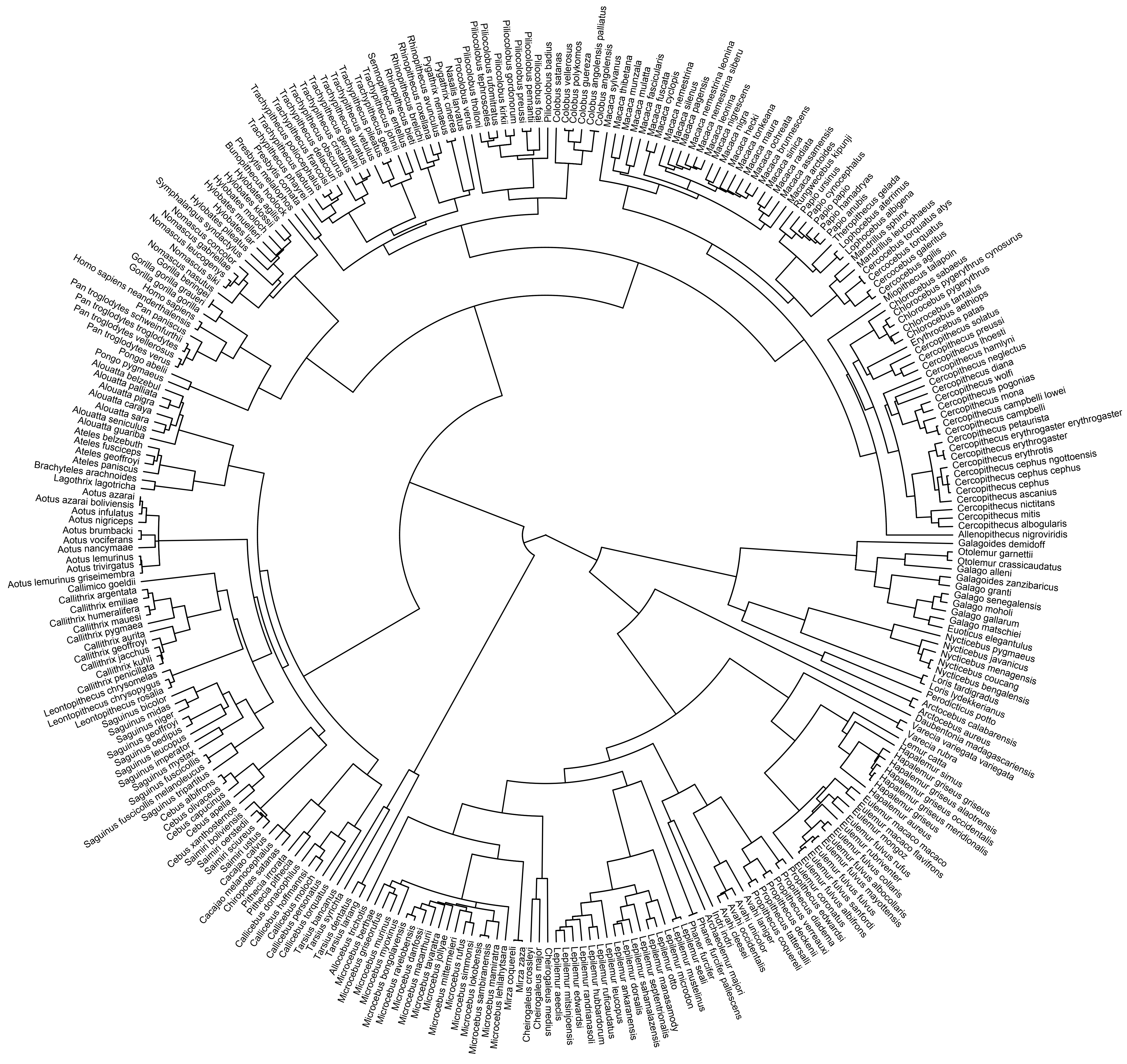
Phylogenetic regression

data(Primates301)

Life history traits

Mass g, brain cc, group size

Much missing data, measurement error, unobserved confounding



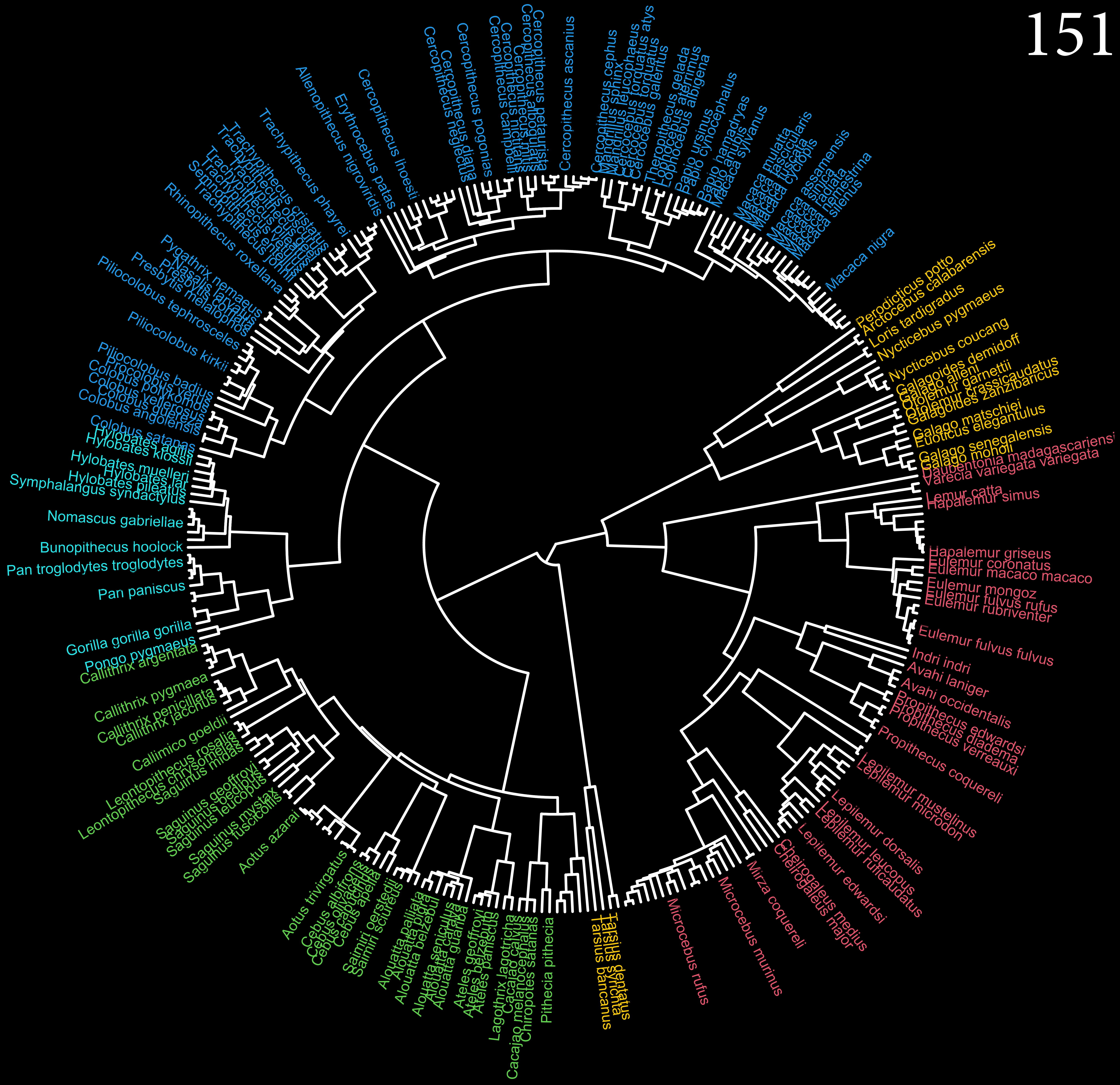
Street et al 2017 Coevolution of cultural intelligence, extended life history, sociality, and brain size in primates

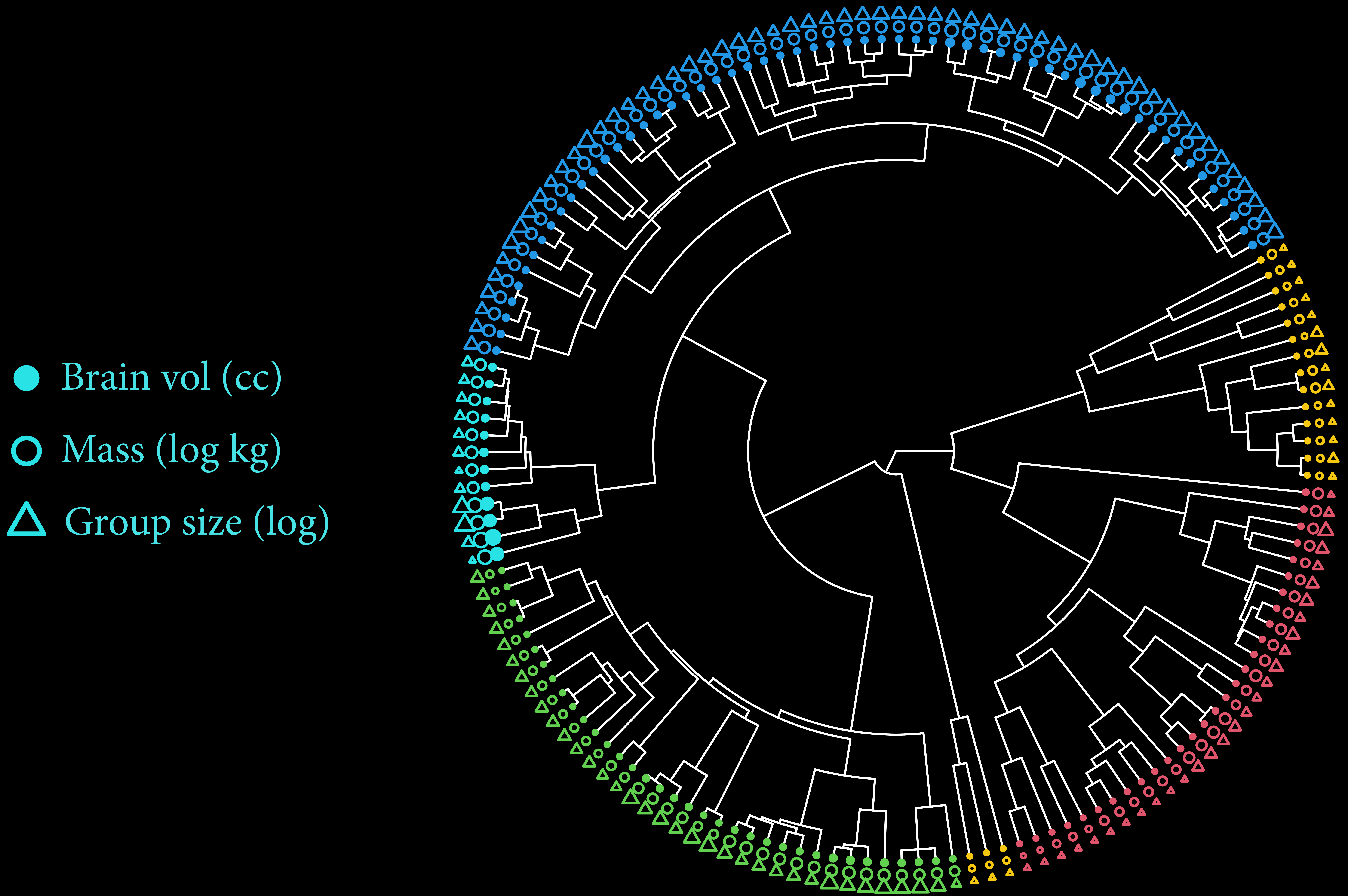
301 species

Daubentonia madagascariensis
Varecia variegata variegata
Varecia rubra
Lemur catta
Hapalemur simus
Hapalemur aureus
Hapalemur griseus griseus
Hapalemur griseus alaotrensis
Hapalemur griseus
Eulemur coronatus
Eulemur macaco macaco
Eulemur macaco flavifrons
Eulemur mongoz
Eulemur fulvus rufus
Eulemur fulvus collaris
Eulemur fulvus albocollaris
Eulemur fulvus mayottensis
Eulemur fulvus sanfordi
Eulemur fulvus albifrons
Colobus angolensis
Symphalangus syndactylus
Nomascus leucogenys
Nomascus concolor
Nomascus nasutus
Bunopithecus hoolock
Pan troglodytes schweinfurthii
Pan troglodytes troglodytes
Pan troglodytes vellerosus
Pan troglodytes verus
Pan paniscus
Homo sapiens
Pongo pygmaeus
Saguinus fuscicollis
Aotus lemurinus
Tarsius bancanus
Tarsius syrichta

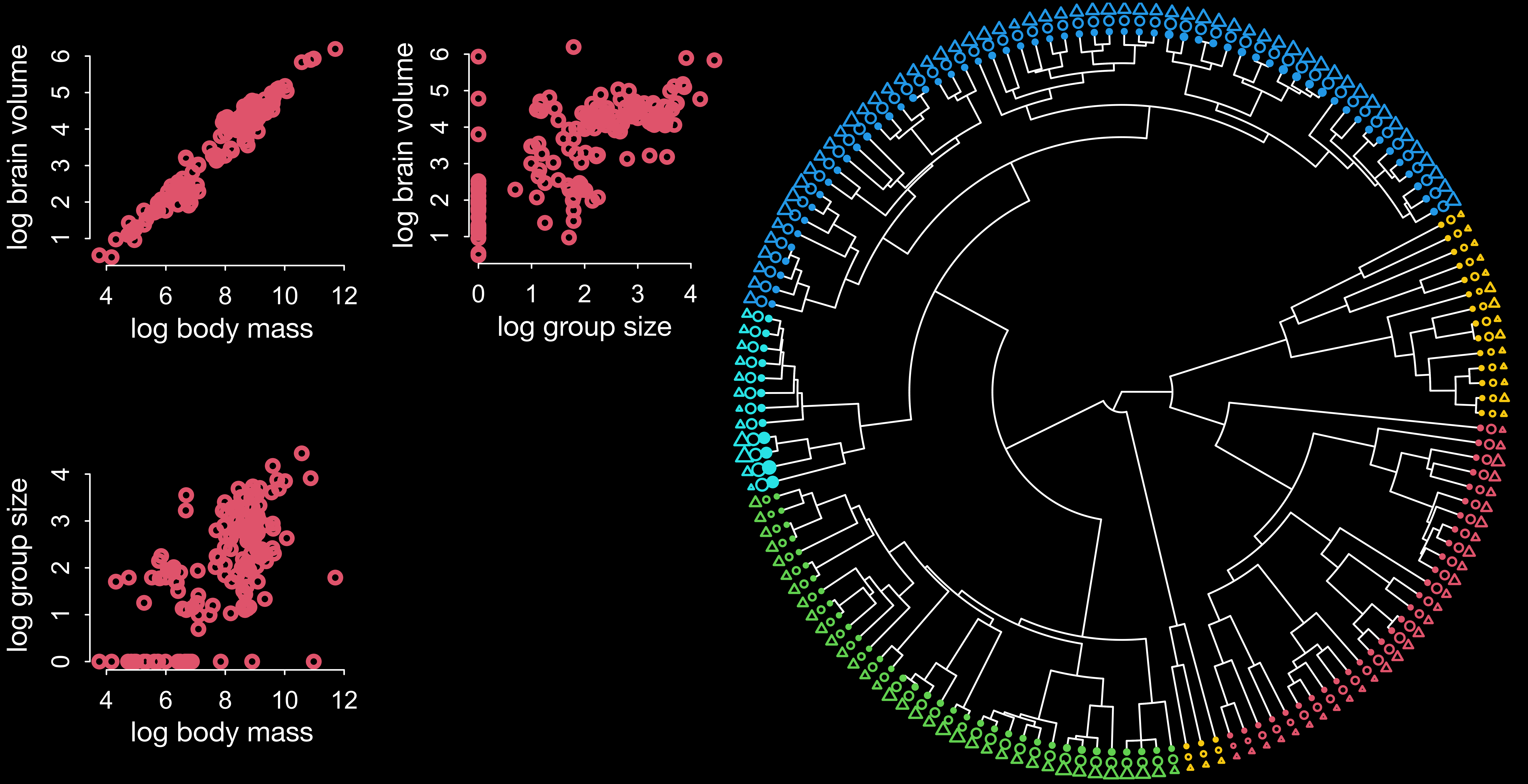
301 species

151 complete cases





Brain vol (cc)
Mass (log kg)
Group size (log)



log brain volume
log body mass
log brain volume
log group size
log group size
log body mass

Causal Salad in Evolutionary Ecology

Phylogenetic comparative methods dominated by causal salad

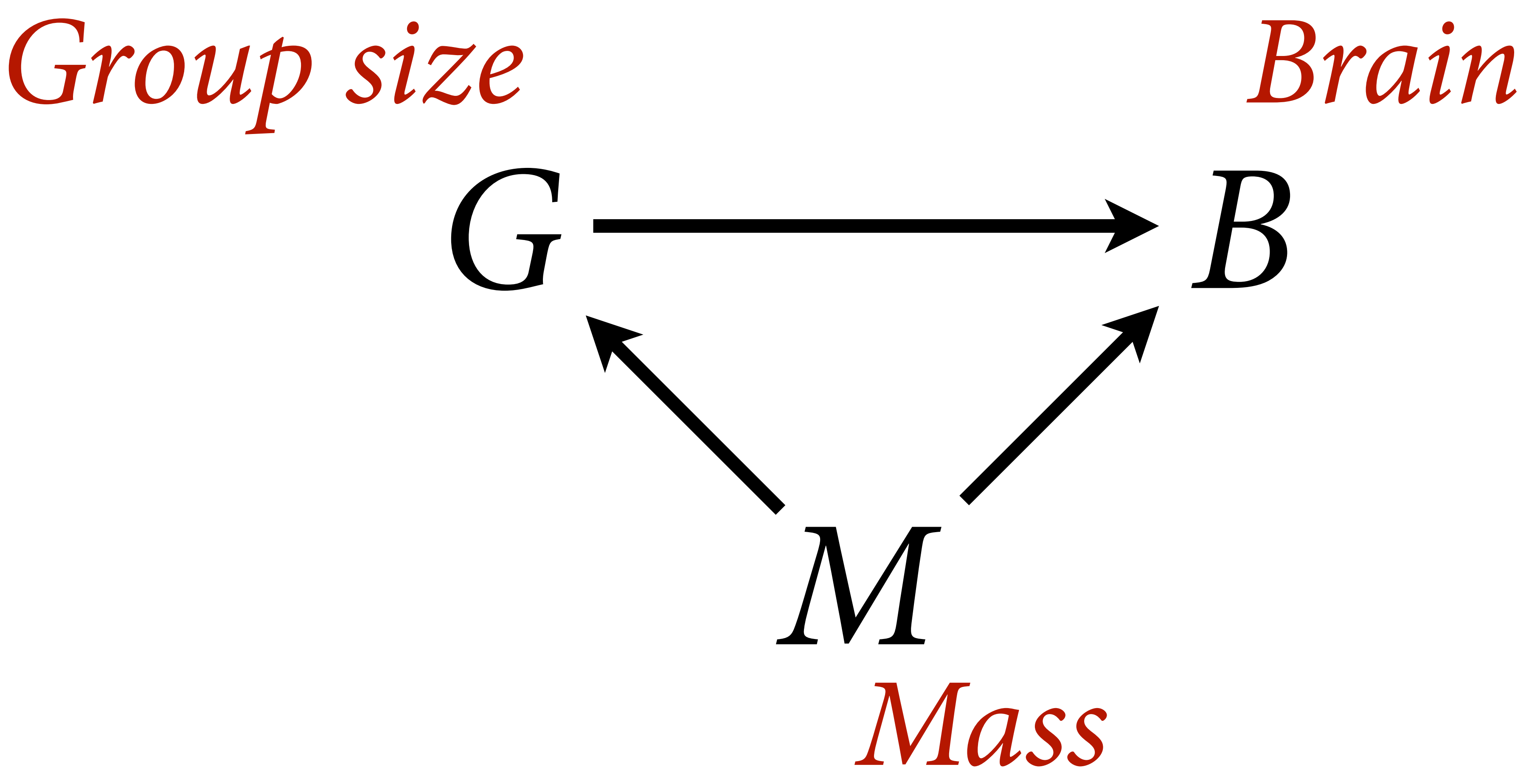
Causal salad: Tossing factors into regression and interpreting every coefficient as causal

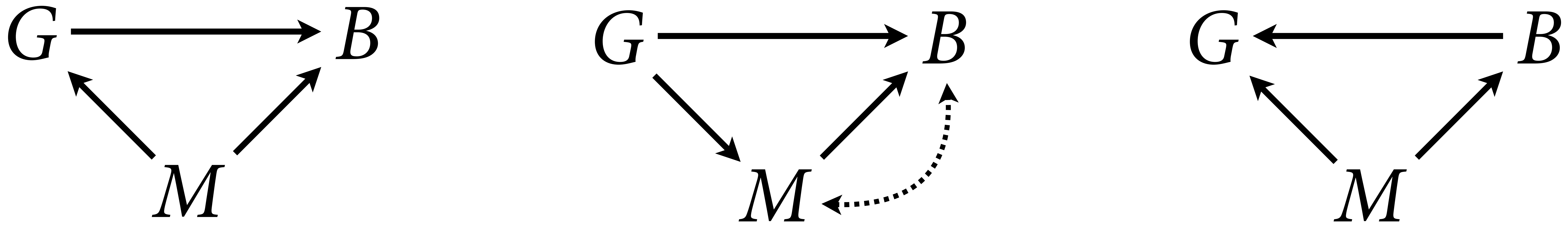
"Controlling for phylogeny": Required but mindless

Regression + phylogeny still requires causal model

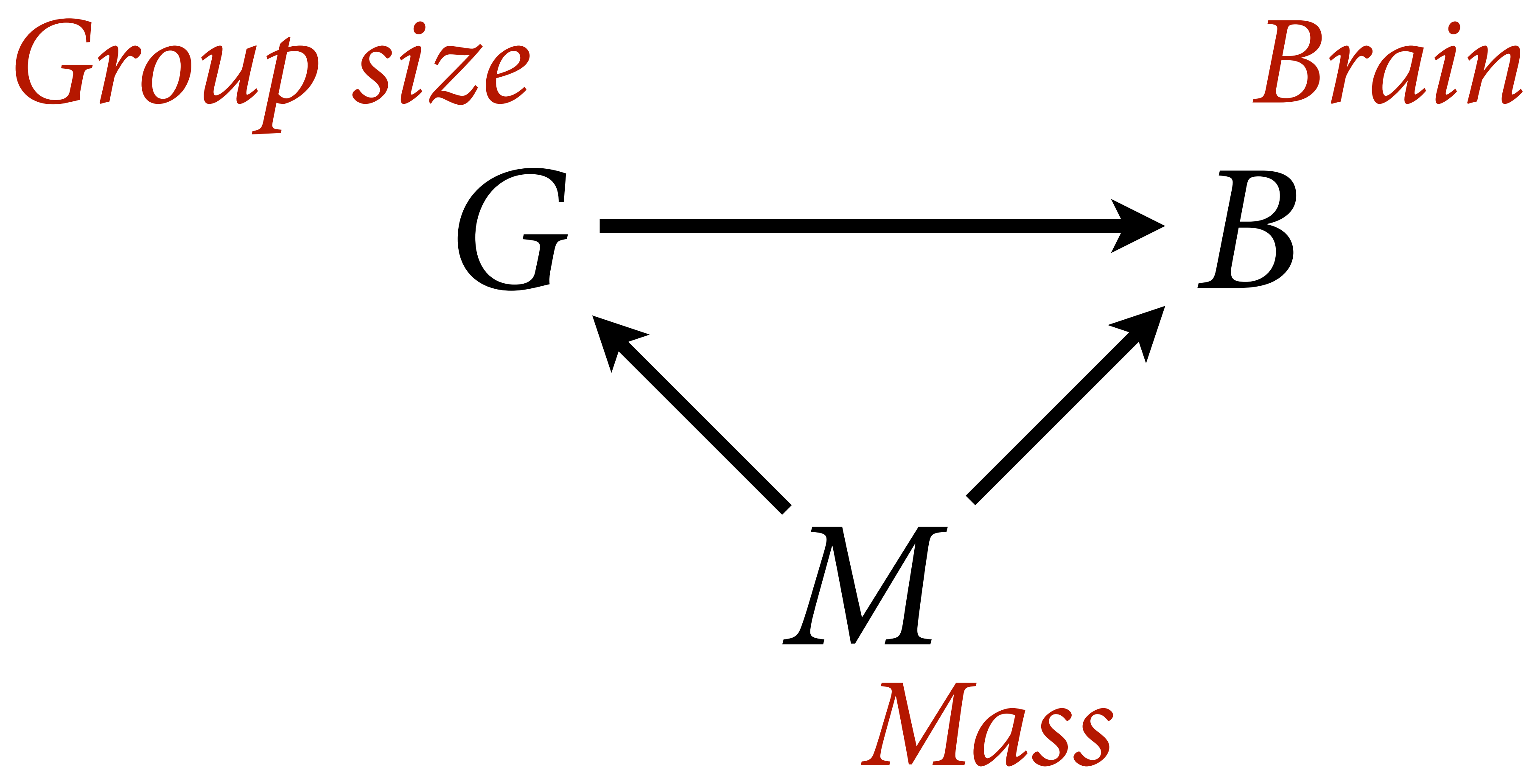
Illustration by Julia Suits

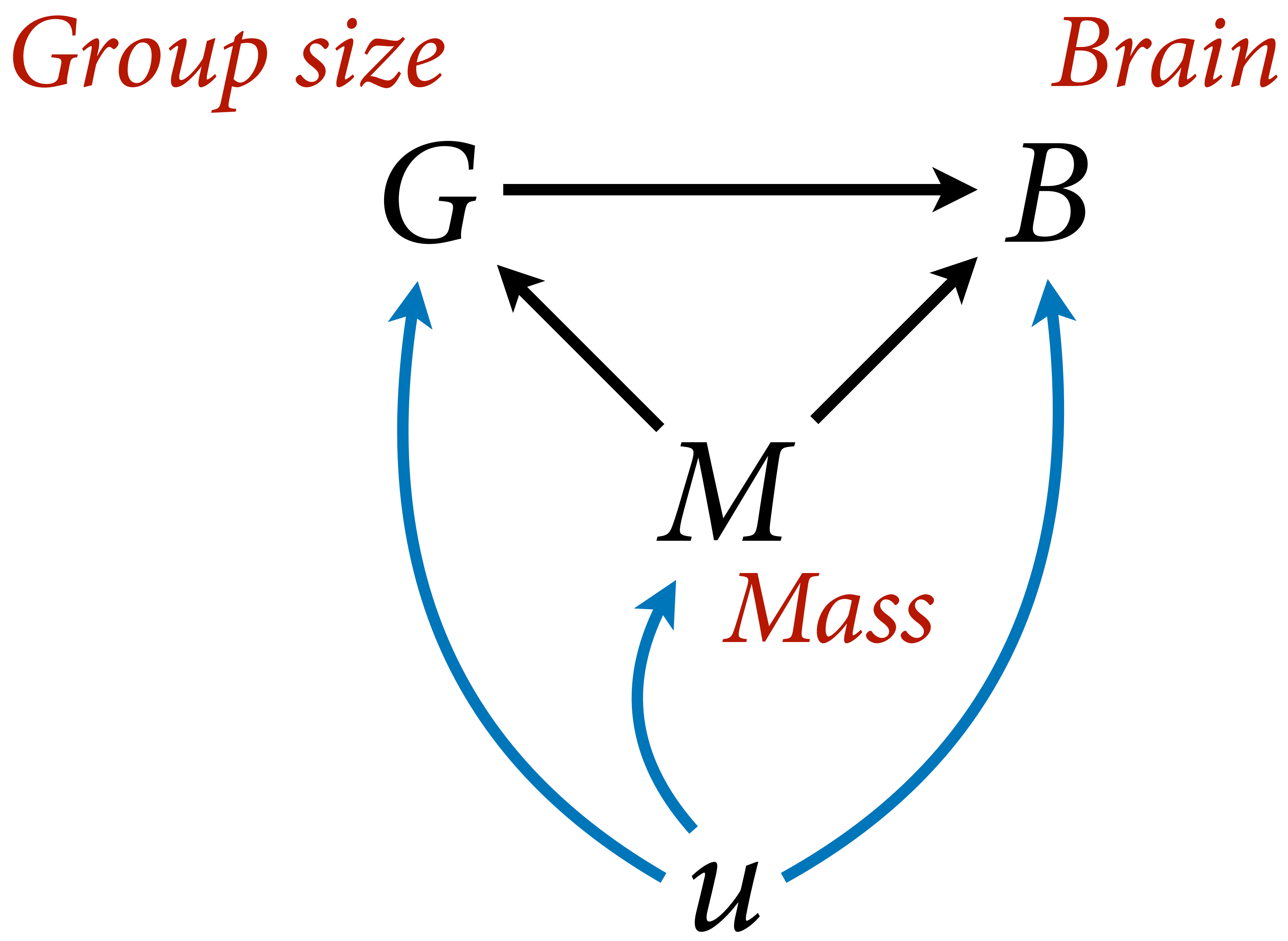
Social brain hypothesis

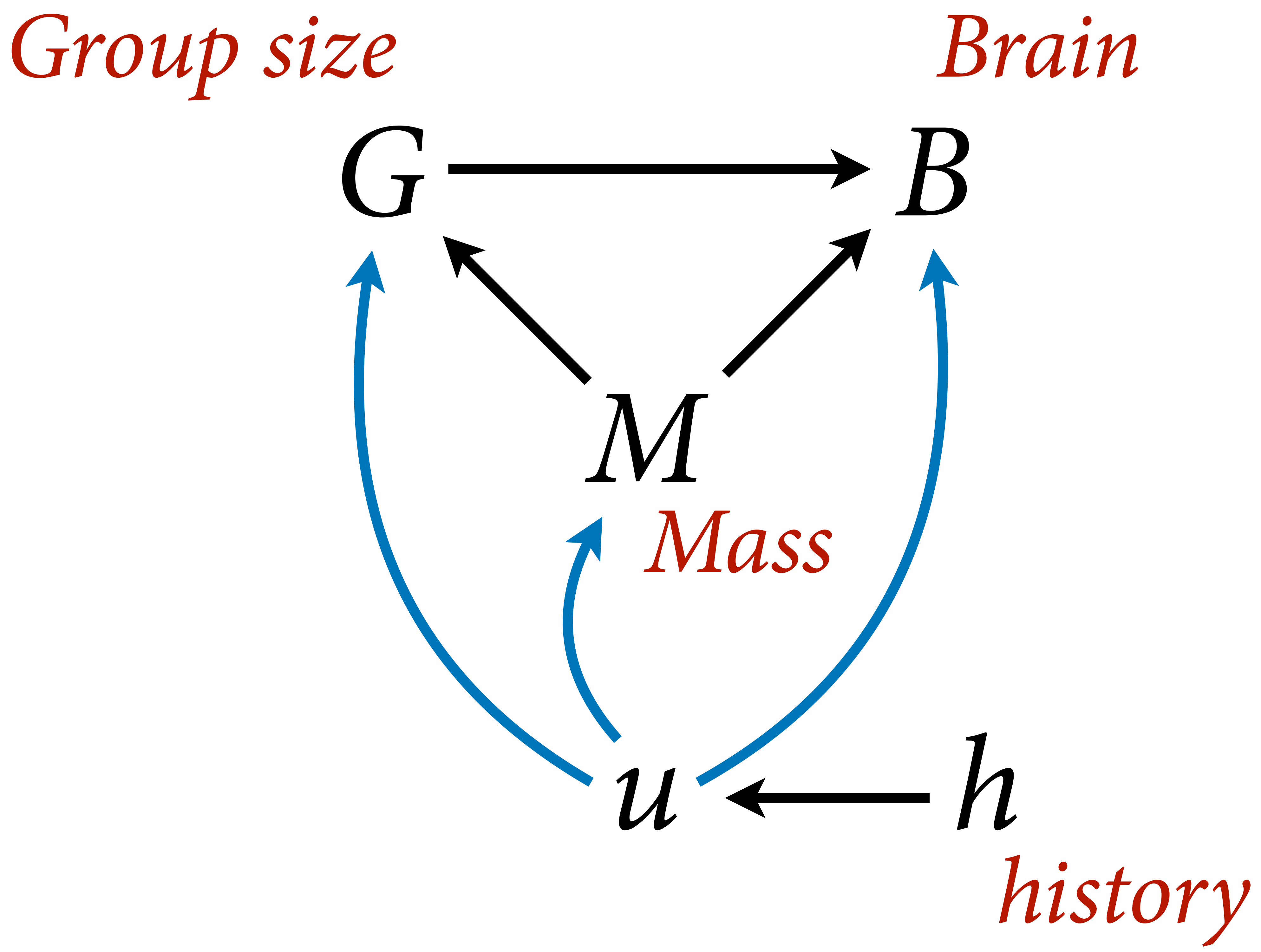




No interpretation without causal representation

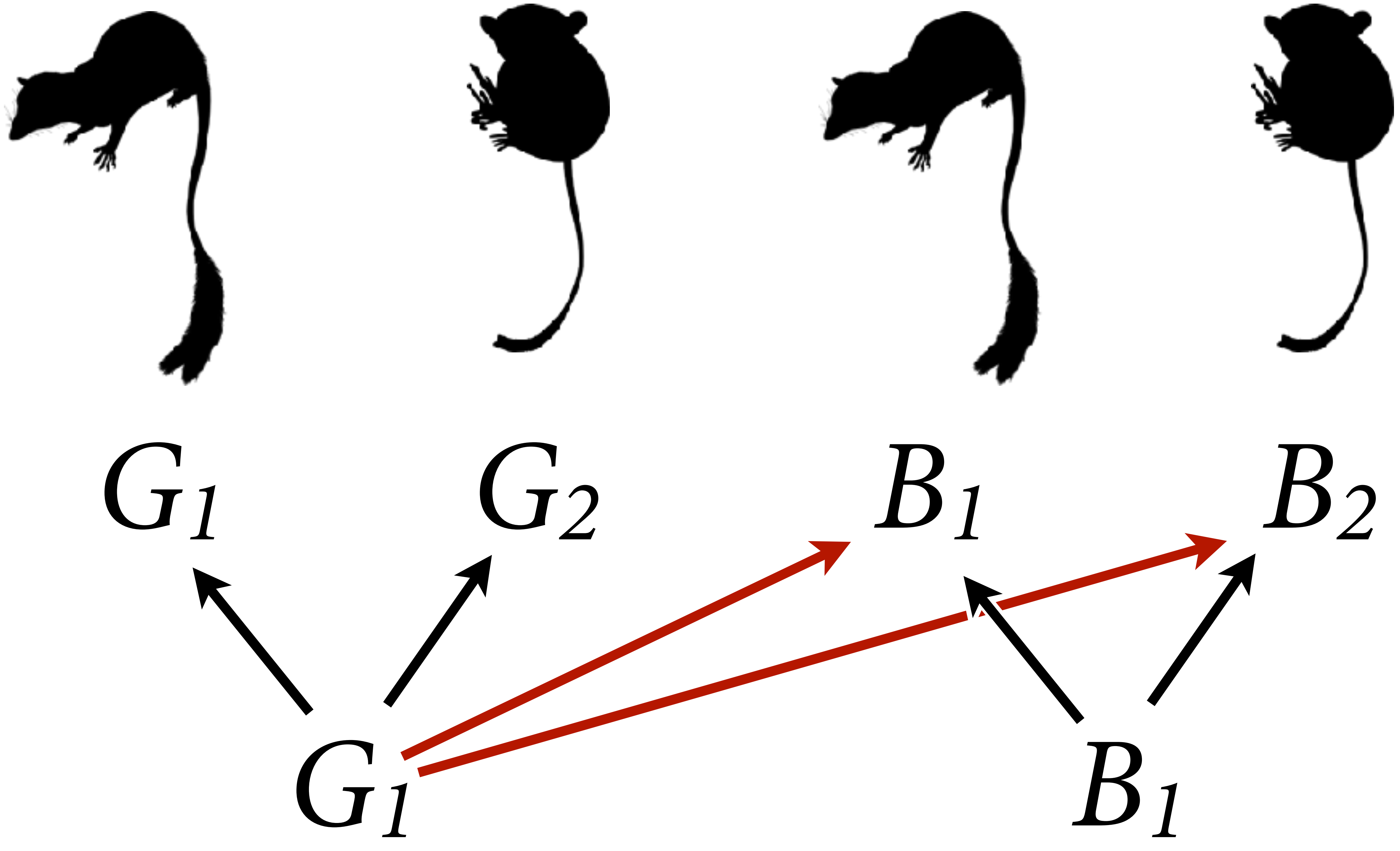

Group size
Brain
G
B
M
Mass


Group size
Brain
G
B
M
Mass
u

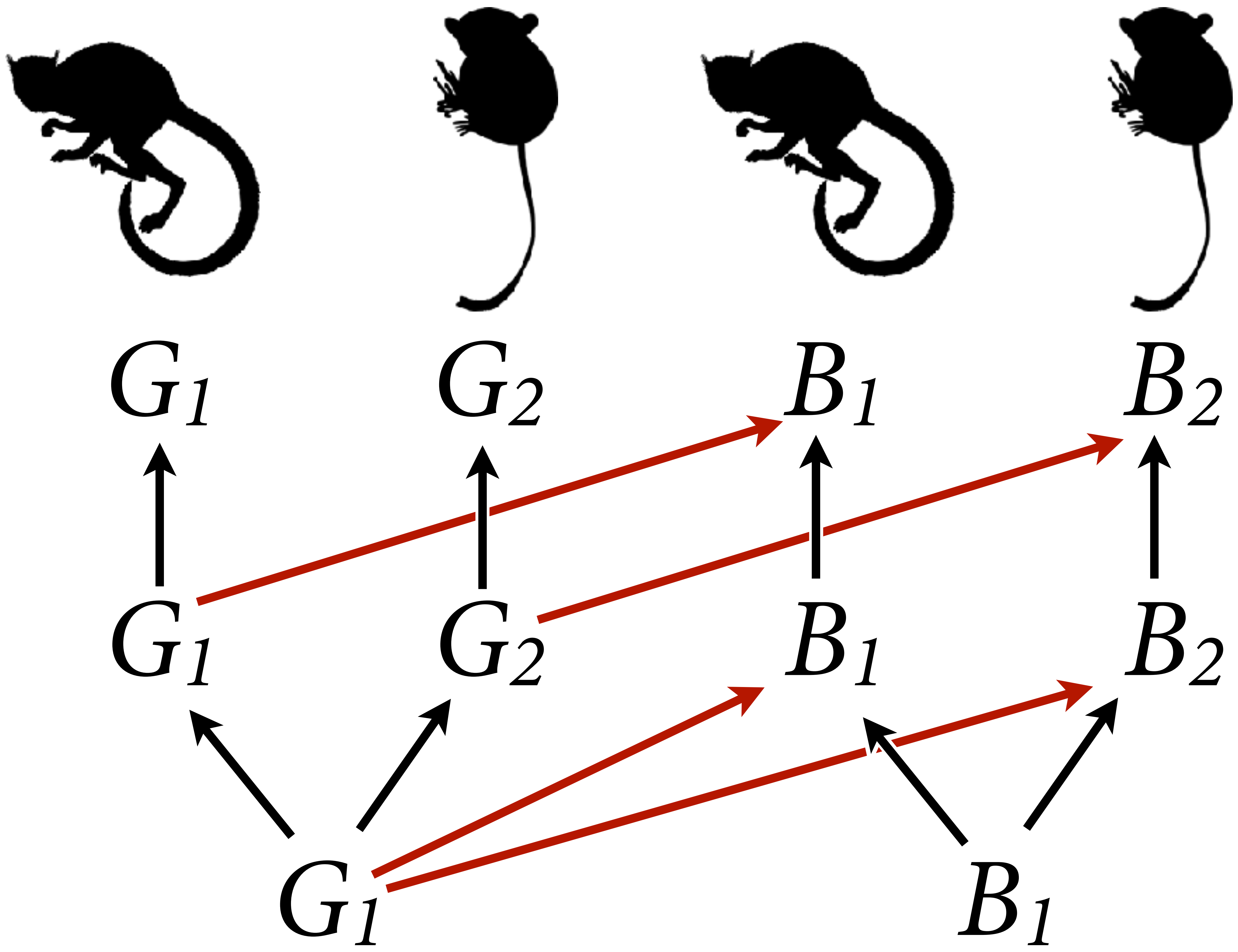

Group size
Brain
G
B
M
Mass
u
h
history

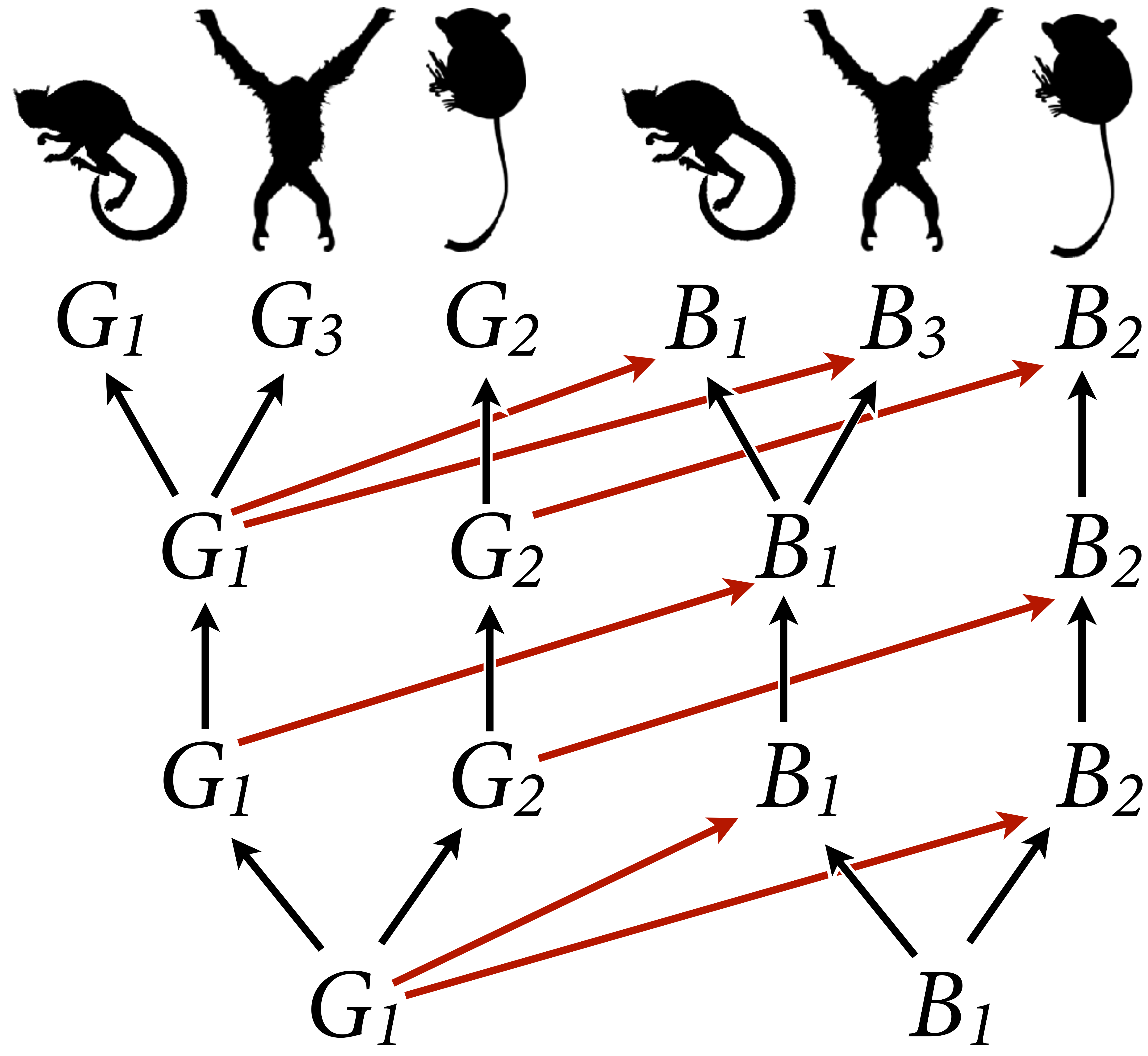
G_1

B_1

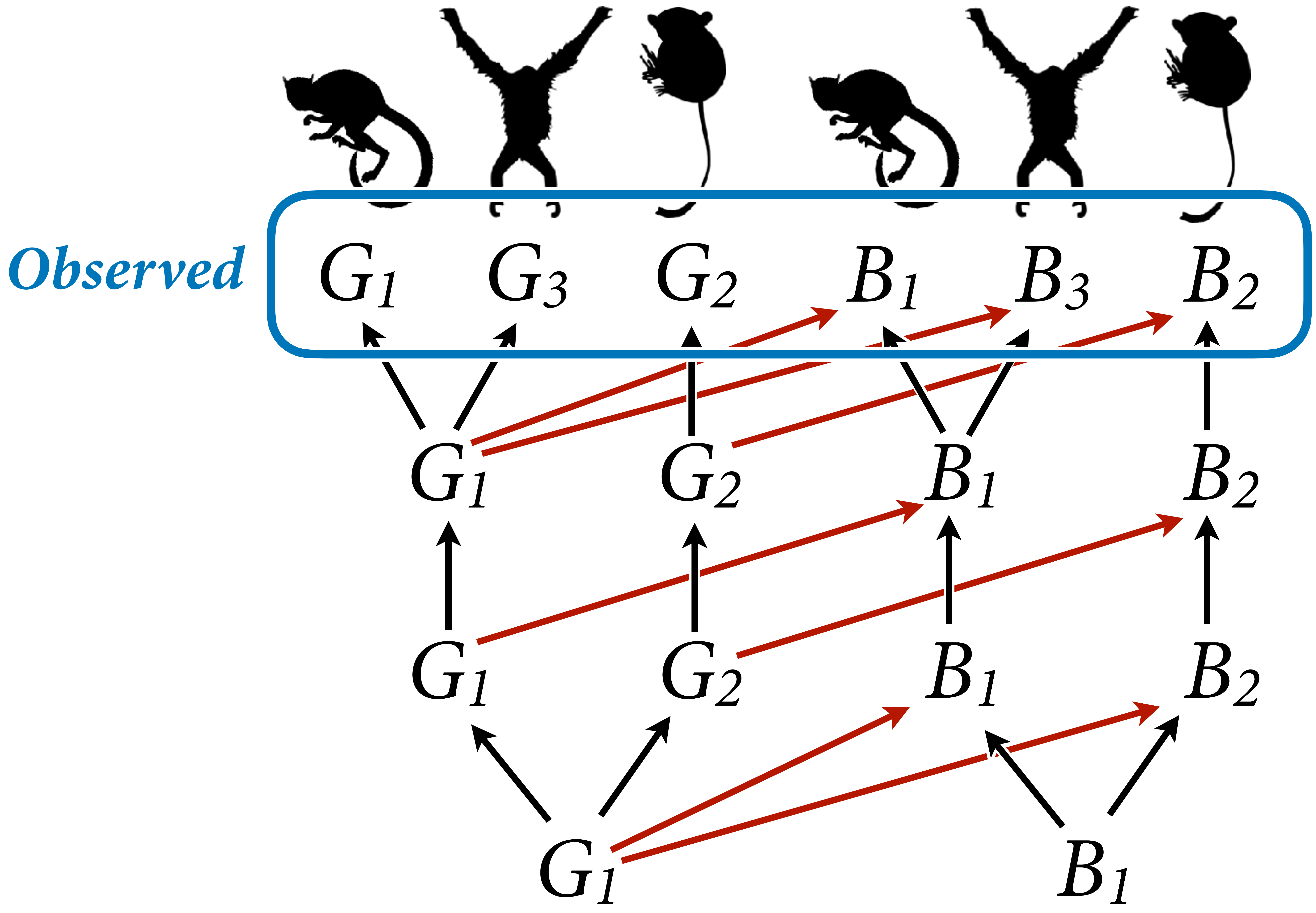


G_1
G_2
B_1
B_2
G_1
B_1

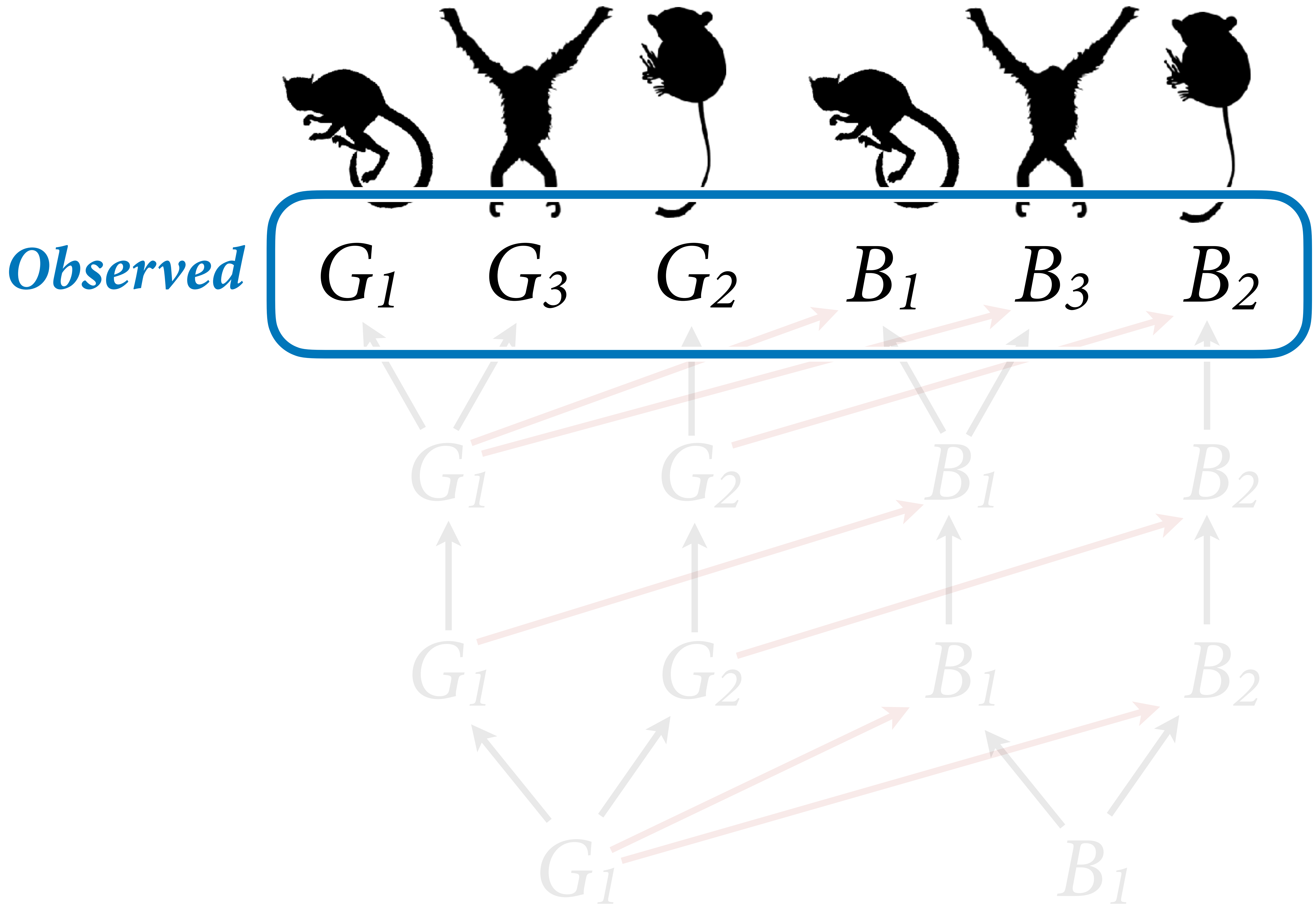

G_1
G_2
B_1
B_2
G_1
G_2
B_1
B_2
G_1
B_1



G1
G3
G2
B1
B3
B2
G1
G2
B1
B2
G1
G2
B1
B2
G1
B1



Observed
G_1 G_3 G_2 B_1 B_3 B_2
G_1 G_2 B_1 B_2
G_1 G_2 B_1 B_2
G_1 B_1



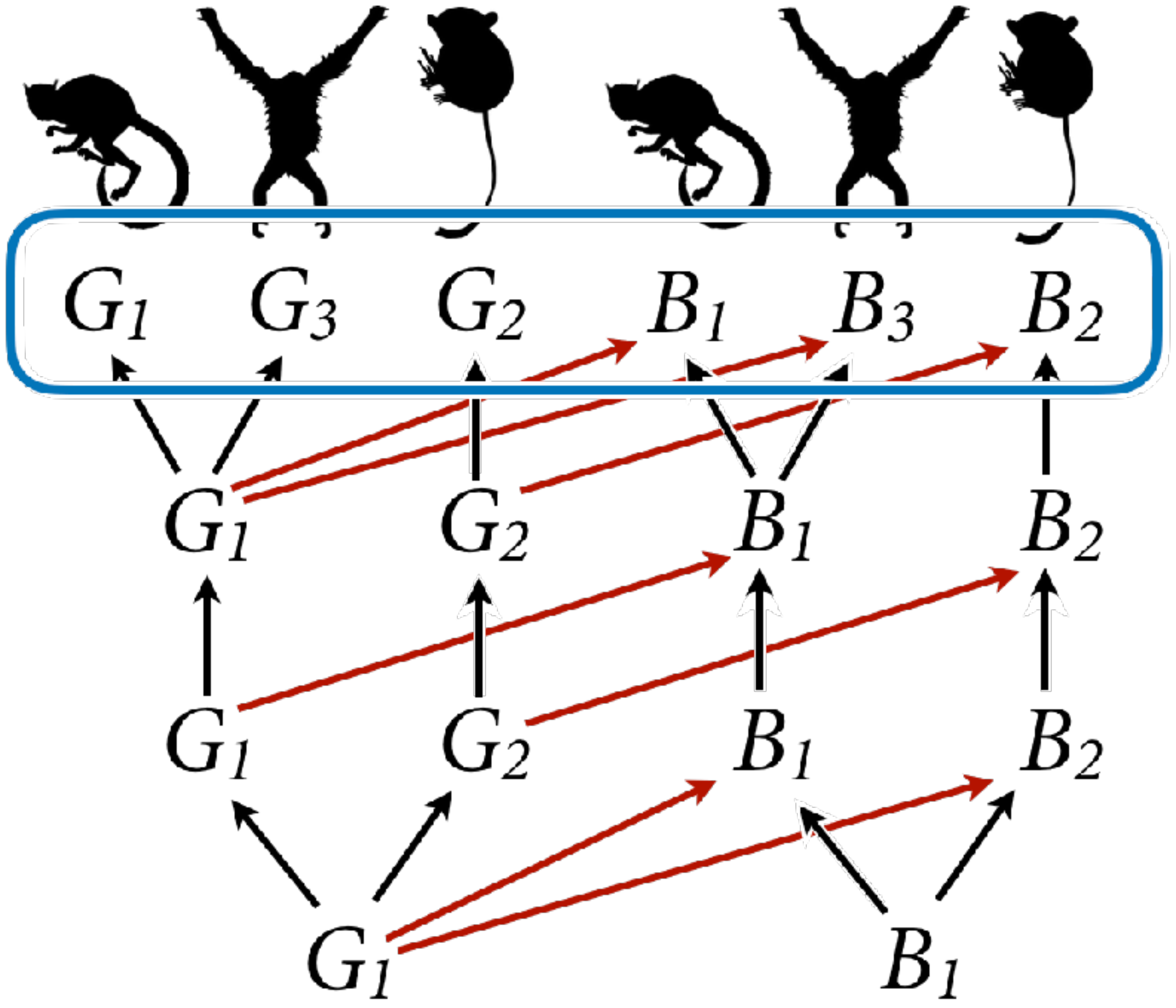
Observed
G_1 G_3 G_2 B_1 B_3 B_2
G_1 G_2 B_1 B_2
G_1 G_2 B_1 B_2
G_1 B_1

Phylogenetic regression

Two conjoint problems

(1) What is the history (phylogeny)?

(2) How to use it to model causes?



Phylogenetic regression

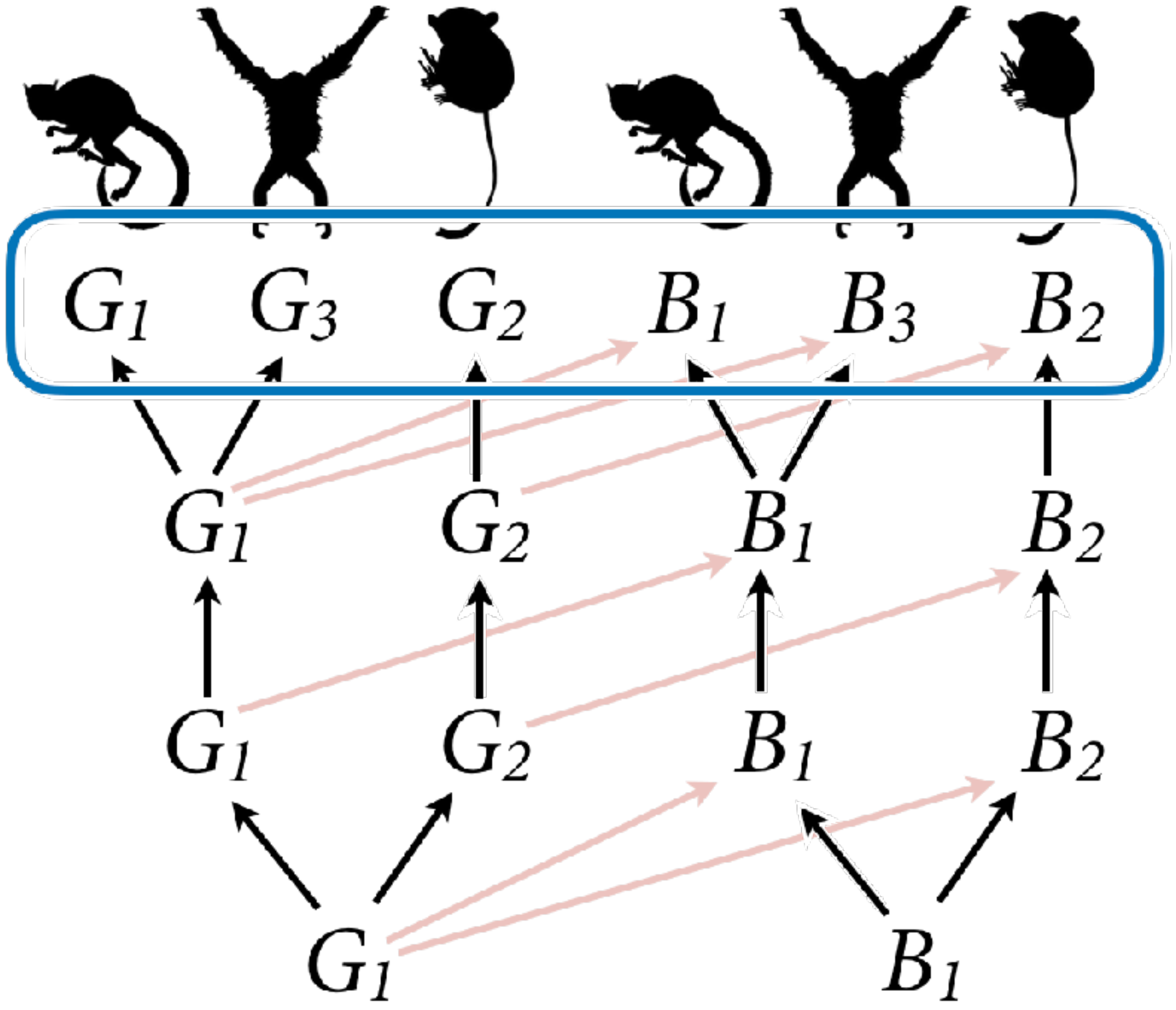
(1) What is the history (phylogeny)?

Gotten much better with genomics BUT

Problems: Huge uncertainty in best case, process not stationary, no one phylogeny correct for all traits

Cultural/linguistic phylogenies unconvincing, need new inference tools

Basic truth: Phylogenies do not exist



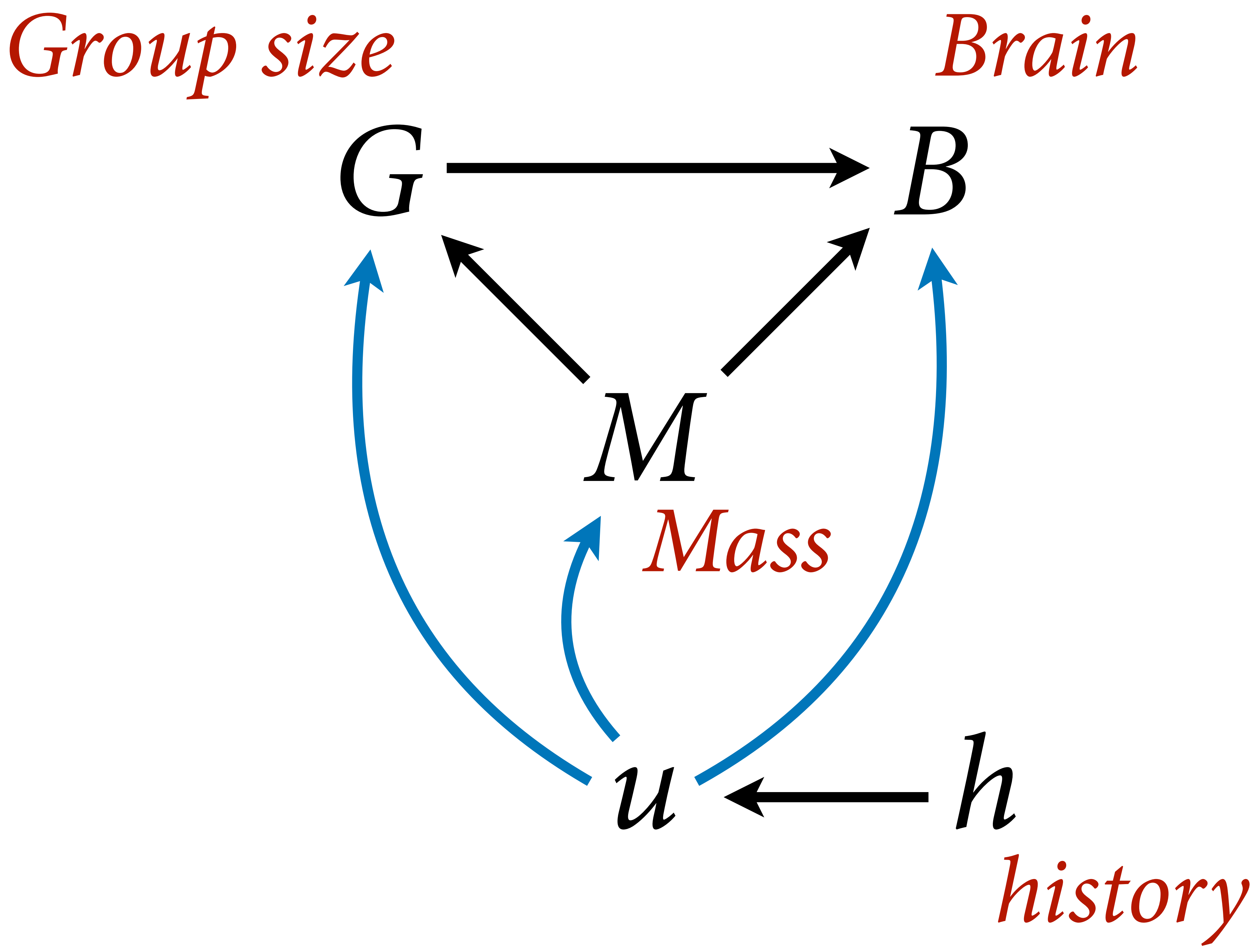
Phylogenetic regression

(2) How to use it to model causes?

Suppose we have a phylogeny.
Now what?

No universally correct approach

Default approach is a Gaussian process regression



$$
\begin{aligned}
B_i &\sim \text{Normal}(\mu_i, \sigma) \\
\mu_i &= \alpha + \beta_G G_i + \beta_M M_i \\
\alpha &\sim \text{Normal}(0,1) \\
\beta_G, \beta_M &\sim \text{Normal}(0,0.5) \\
\sigma &\sim \text{Exponential}(1)
\end{aligned}
$$

$$
\begin{tikzcd}
G \arrow[rr] & & B \\
& M \arrow[ul] \arrow[ur] &
\end{tikzcd}
$$

$$B \sim \mathrm{MVNormal}(\mu, \mathbf{K})$$

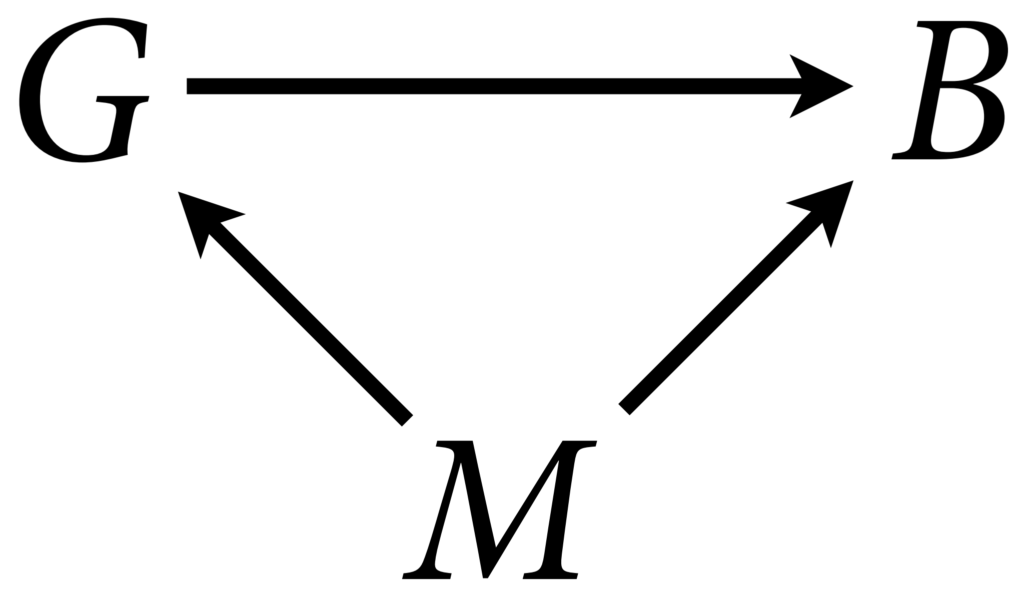
$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i$$

$$\mathbf{K} = \mathbf{I}\sigma^2$$

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

$$\beta_G, \beta_M \sim \mathrm{Normal}(0,0.5)$$

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



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$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i$$

$$\mathbf{K} = \mathbf{I}\sigma^2$$

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

$$\beta_G, \beta_M \sim \text{Normal}(0,0.5)$$

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

$$\mathbf{I} = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 0 & 1 & 0 & \dots & 0 \\ 0 & 0 & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & 0 \\ 0 & 0 & 0 & \dots & 1 \end{bmatrix}$$

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i$$

$$\mathbf{K} = \mathbf{I}\sigma^2$$

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

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$$\mathbf{I} = \begin{bmatrix} 1 & 0 & 0 & \dots & 0 \\ 0 & 1 & 0 & \dots & 0 \\ 0 & 0 & 1 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & 0 \\ 0 & 0 & 0 & \dots & 1 \end{bmatrix}$$

$$\mathbf{K} = \begin{bmatrix} \sigma^2 & 0 & 0 & \dots & 0 \\ 0 & \sigma^2 & 0 & \dots & 0 \\ 0 & 0 & \sigma^2 & \dots & 0 \\ \vdots & \vdots & \vdots & \ddots & 0 \\ 0 & 0 & 0 & \dots & \sigma^2 \end{bmatrix}$$

$$B_i \sim \text{Normal}(\mu_i, \sigma)$$

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

```
dat_list <- list(
    N_spp = nrow(dstan),
    M = standardize(log(dstan$body)),
    B = standardize(log(dstan$brain)),
    G = standardize(log(dstan$group_size)),
    Imat = diag(nrow(dstan)) )

# classical regression form
mBMG0 <- ulam(
    alist(
        B ~ normal( mu , sigma ),
        mu <- a + bM*M + bG*G,
        a ~ normal( 0 , 1 ),
        c(bM,bG) ~ normal( 0 , 0.5 ),
        sigma ~ exponential( 1 )
    ), data=dat_list , chains=4 , cores=4 )
```

```
# multivariate form
mBMG <- ulam(
    alist(
        B ~ multi_normal( mu , K ),
        mu <- a + bM*M + bG*G,
        matrix[N_spp,N_spp]:K <- Imat*(sigma^2),
        a ~ normal( 0 , 1 ),
        c(bM,bG) ~ normal( 0 , 0.5 ),
        sigma ~ exponential( 1 )
    ), data=dat_list , chains=4 , cores=4 )
```

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$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

```
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# classical regression form
mBMG0 <- ulam(
    alist(
        B ~ normal( mu , sigma ),
        mu <- a + bM*M + bG*G,
```

```
> precis( mBMG0 )
       mean   sd  5.5% 94.5% n_eff Rhat4
a      0.00 0.02 -0.03  0.03  1740     1
bG     0.12 0.02  0.09  0.16  1491     1
bM     0.89 0.02  0.86  0.93  1439     1
sigma  0.22 0.01  0.20  0.24  1706     1
```

```
# multivariate form
mBMG <- ulam(
    alist(
        B ~ multi_normal( mu , K ),
        mu <- a + bM*M + bG*G,
        matrix[N_spp,N_spp]:K <- Imat*(sigma^2),
```

```
> precis( mBMG )
       mean   sd  5.5% 94.5% n_eff Rhat4
a      0.00 0.02 -0.03  0.03  1880     1
bG     0.12 0.02  0.09  0.16  1384     1
bM     0.89 0.02  0.86  0.93  1395     1
sigma  0.22 0.01  0.20  0.24  1433     1
```

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

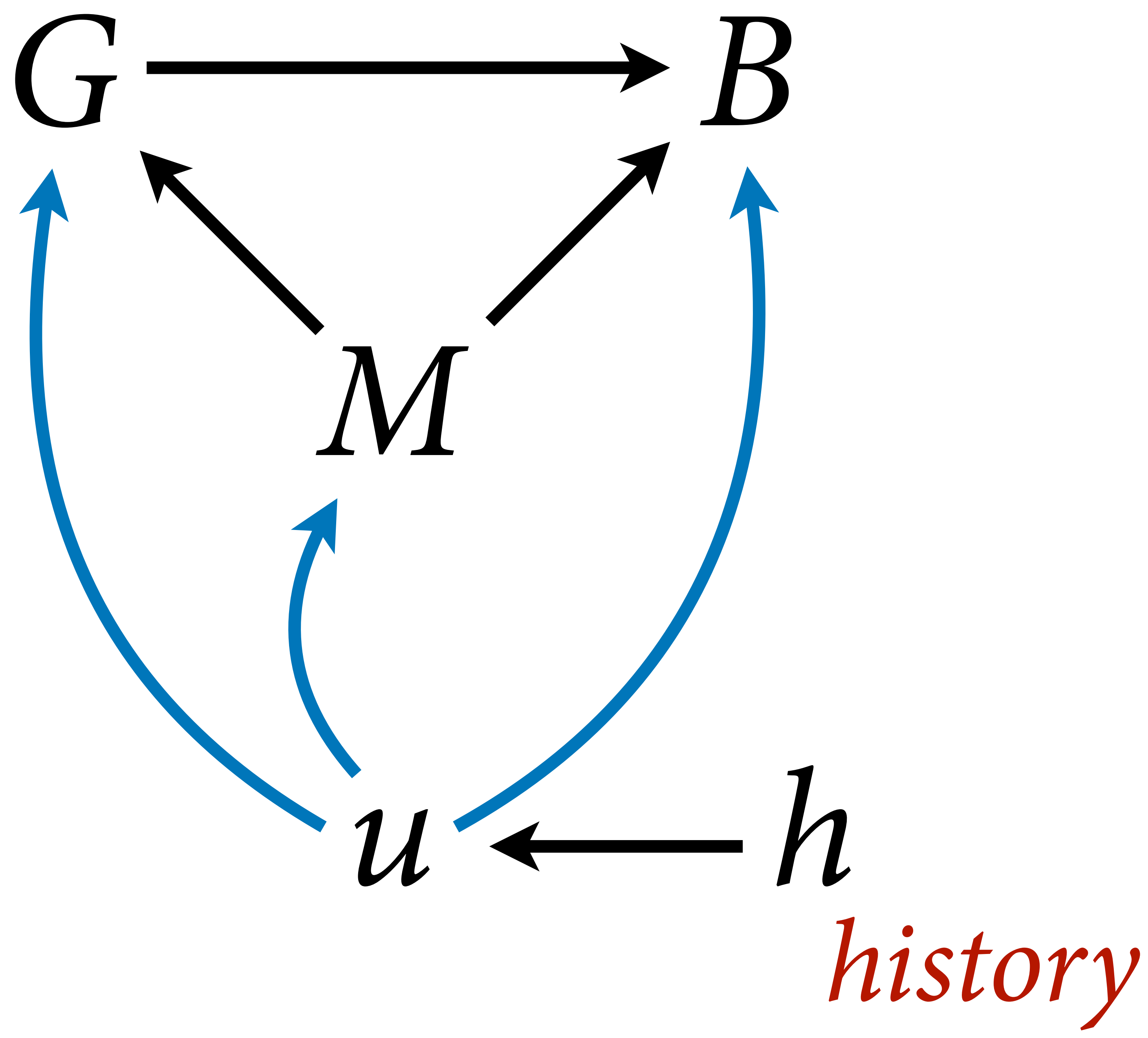
$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i + u_i$$

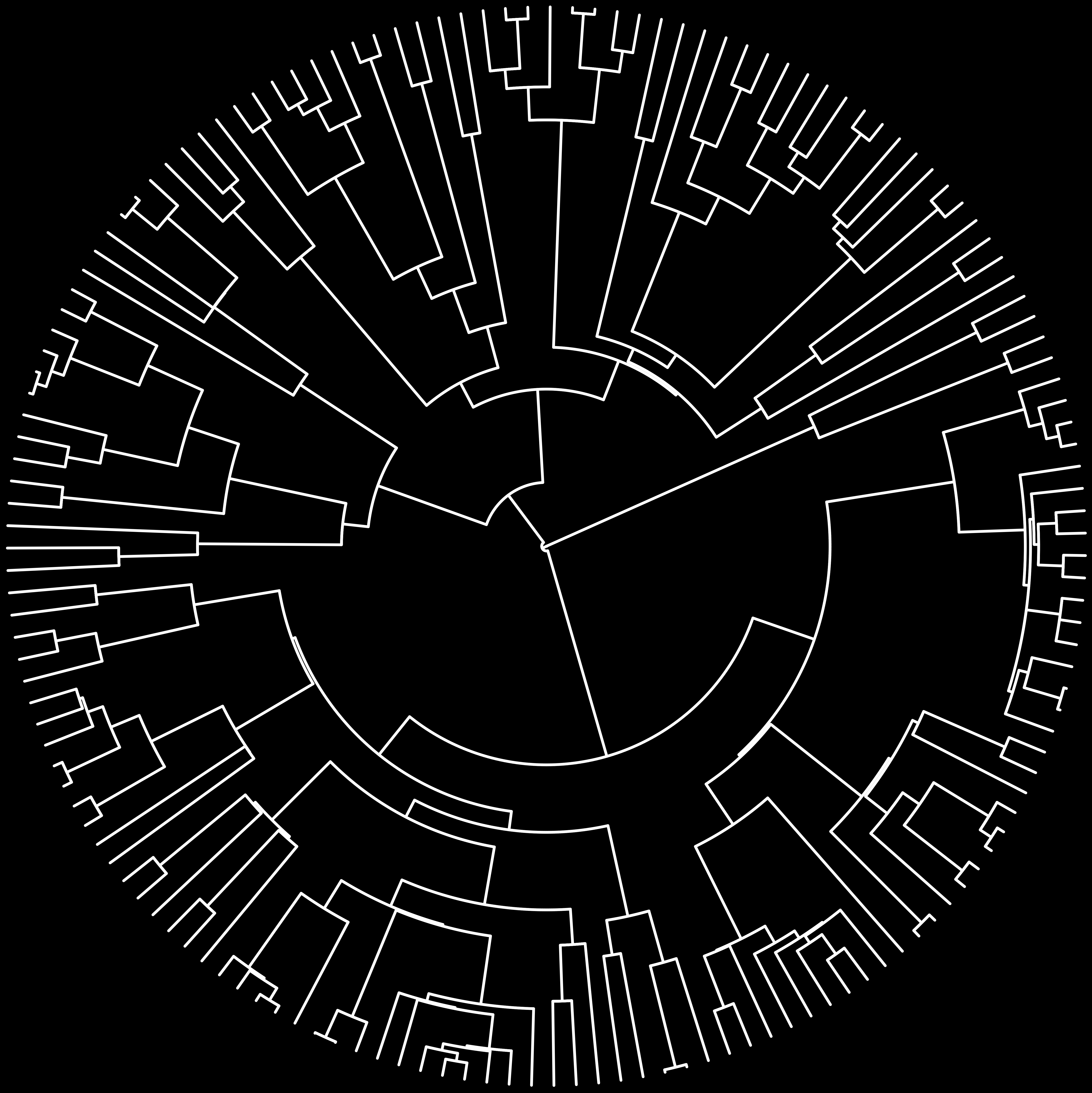
$$\mathbf{K} = \mathbf{I}\sigma^2$$

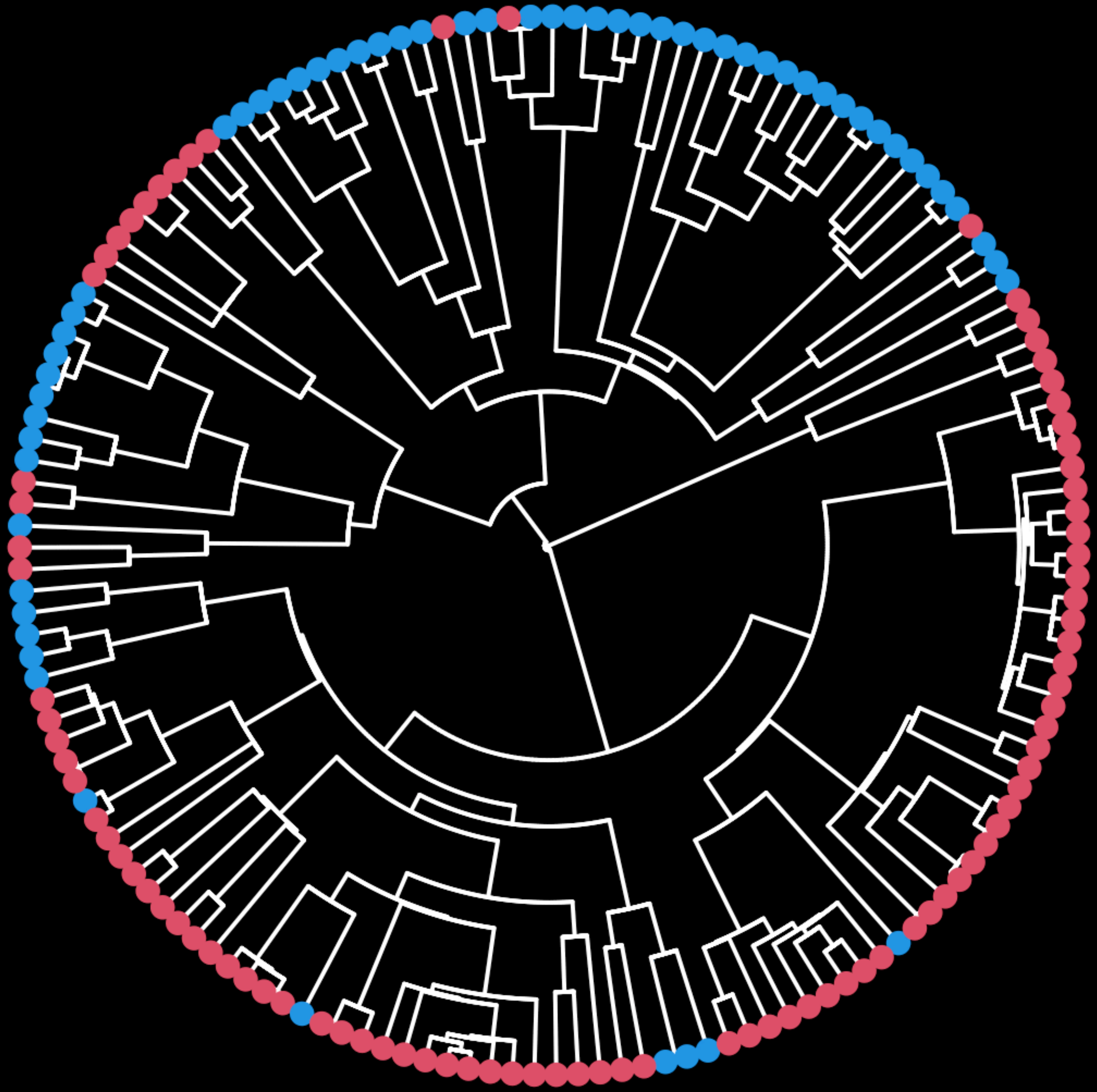
$$\alpha \sim \text{Normal}(0,1)$$

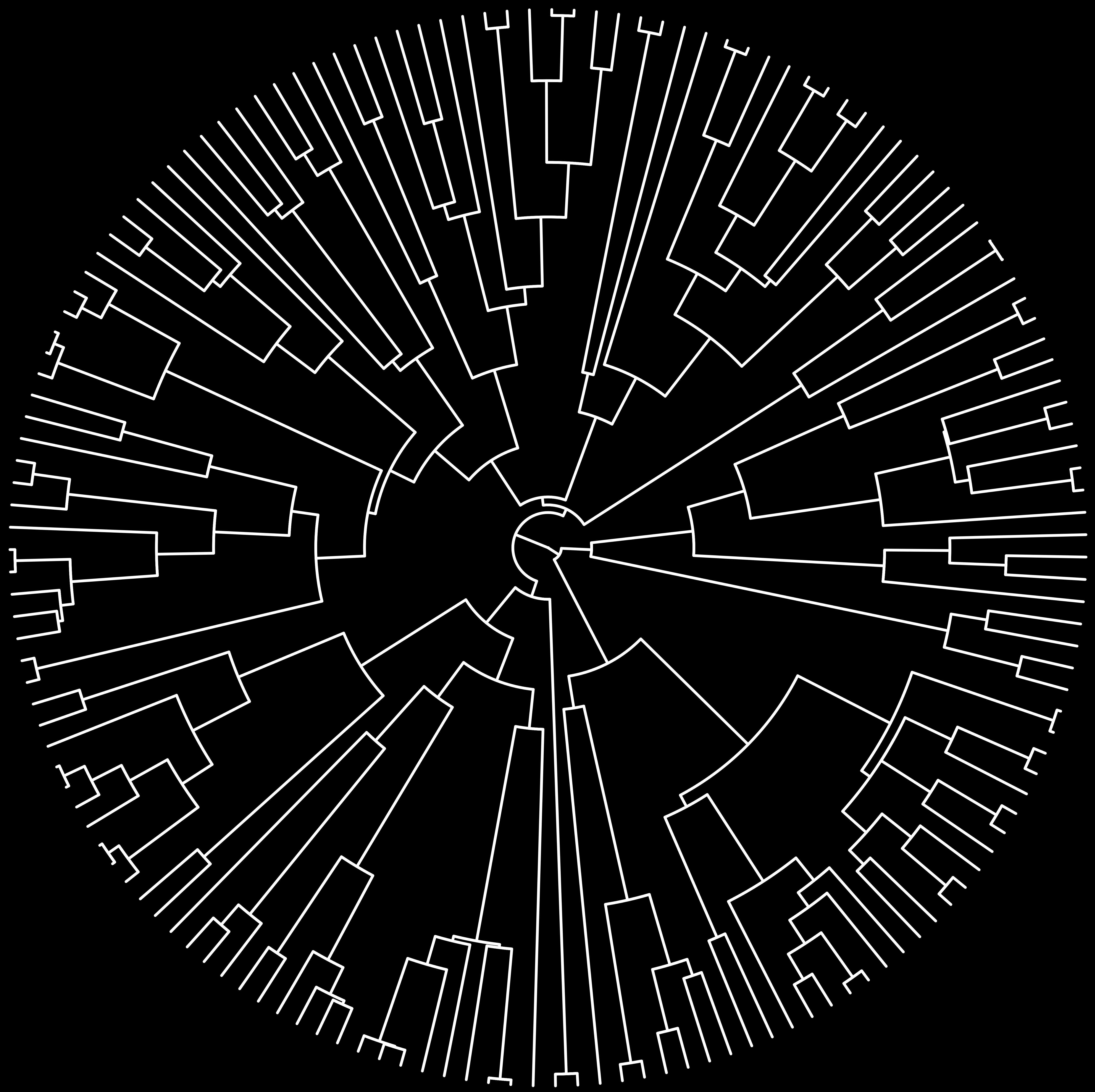
$$\beta_G, \beta_M \sim \text{Normal}(0,0.5)$$

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







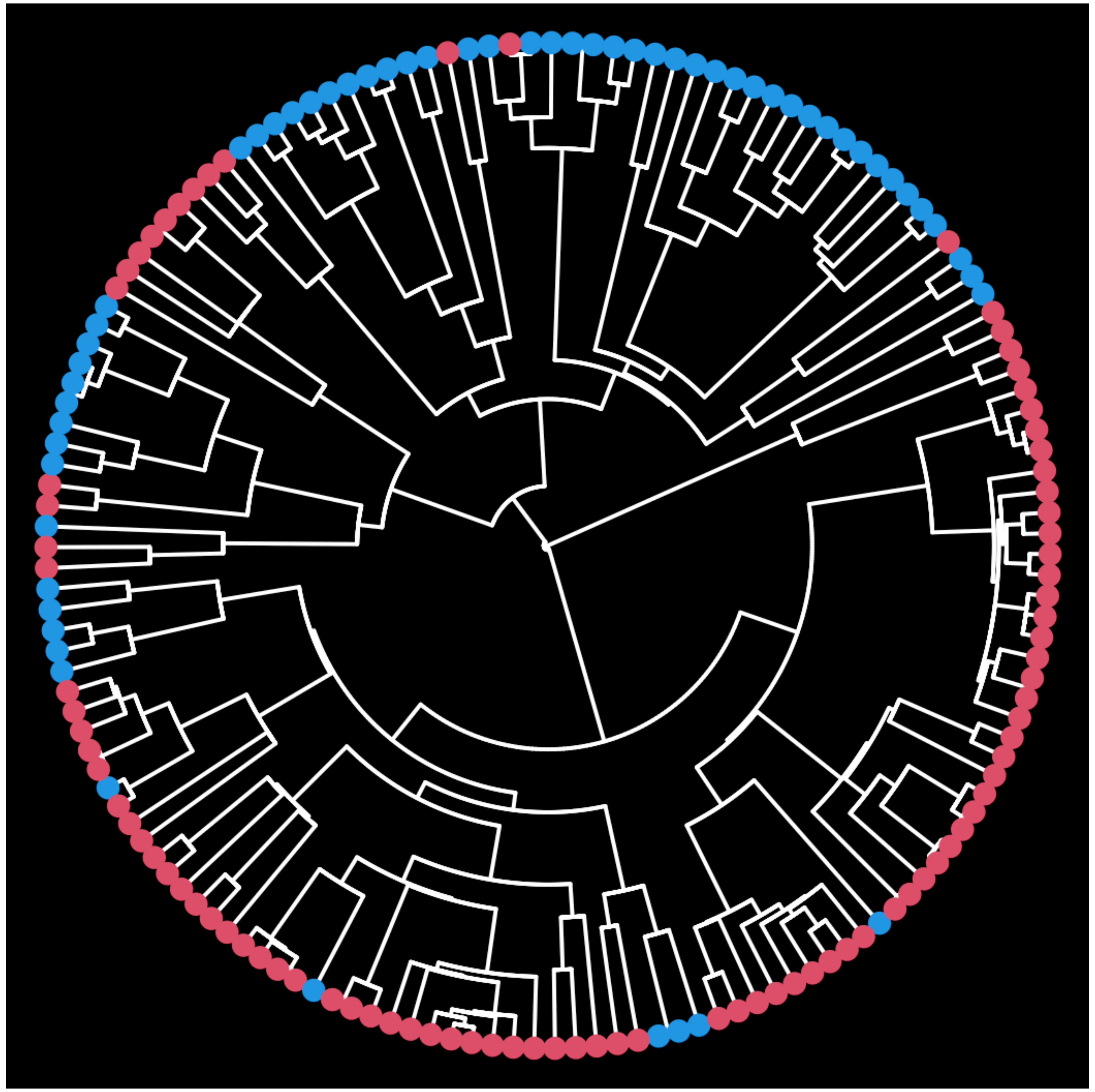


From Model to Kernel

Evolutionary model + tree structure
= pattern of covariation at tips

Covariance declines with
phylogenetic distance

Phylogenetic distance: Branch length
from one species to another



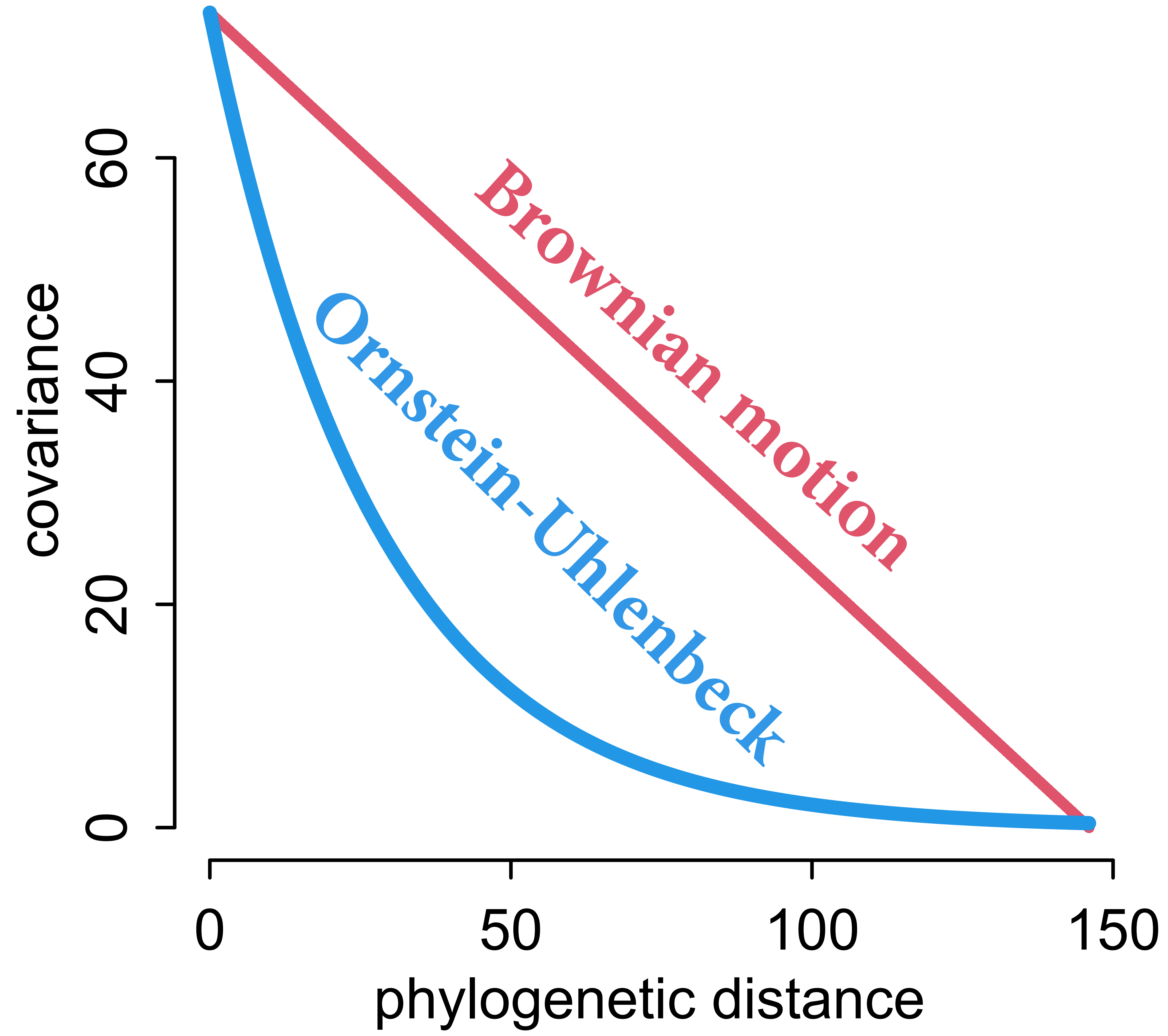
From Model to Kernel

Evolutionary model + tree structure
= pattern of covariation at tips

Common simple models:

Brownian motion

Ornstein-Uhlenbeck (damped
Brownian motion)



$$
\begin{aligned}
B &\sim \mathrm{MVNormal}(\mu, \mathbf{K}) \\
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\sigma &\sim \mathrm{Exponential}(1)
\end{aligned}
$$

$$B \sim \mathrm{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i$$

$$\mathbf{K} = \eta^2 \exp(-\rho d_{i,j})$$ *Ornstein-Uhlenbeck kernel*

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

$$\beta_G, \beta_M \sim \mathrm{Normal}(0,0.5)$$

$$\eta^2 \sim \mathrm{HalfNormal}(1,0.25)$$ *Maximum covariance prior*

$$\rho \sim \mathrm{HalfNormal}(3,0.25)$$ *Rate prior*

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i$$

$$\mathbf{K} = \eta^2 \exp(-\rho d_{i,j})$$

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

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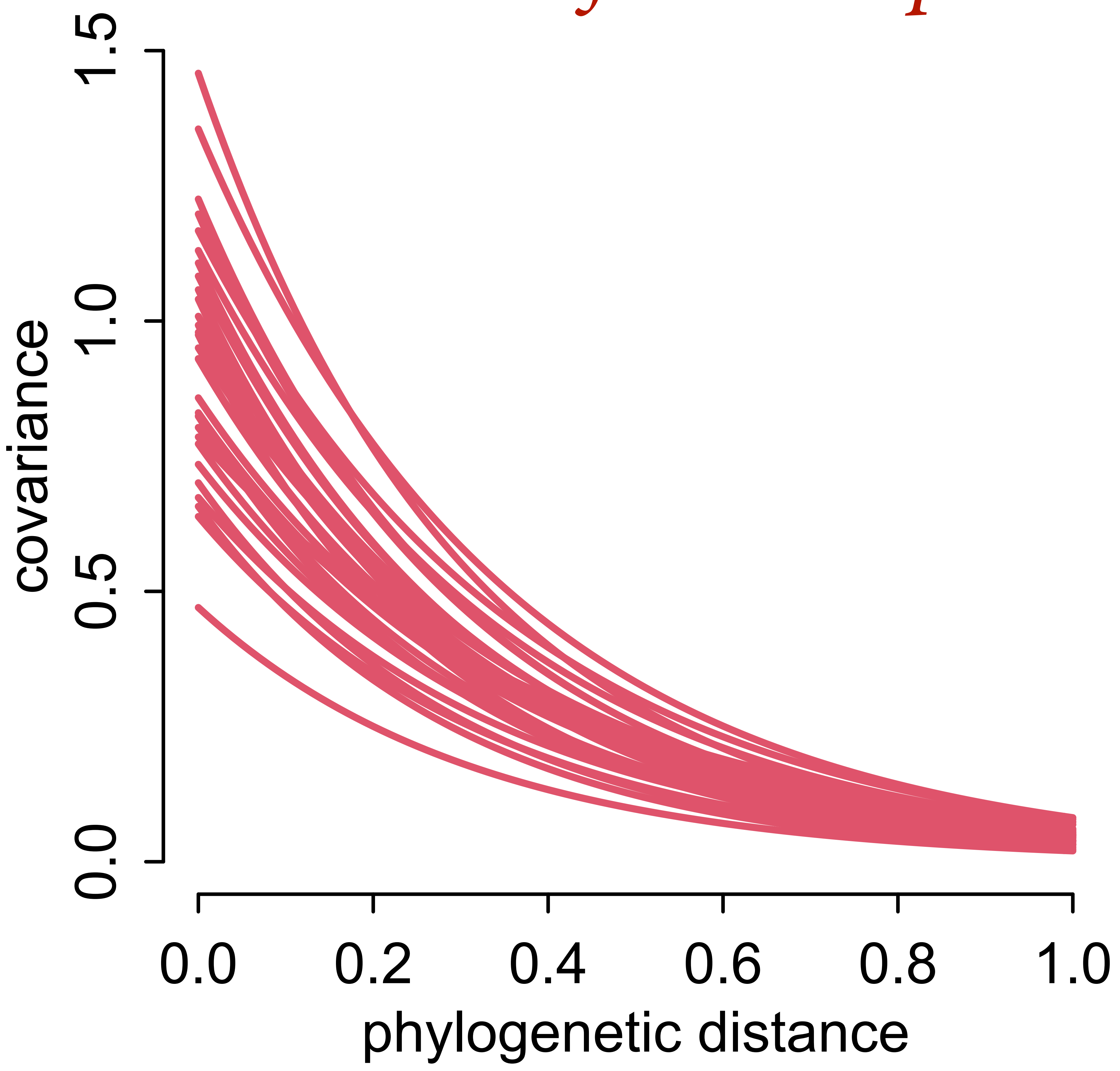
$$\rho \sim \text{HalfNormal}(3,0.25)$$

covariance function prior



$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha$$

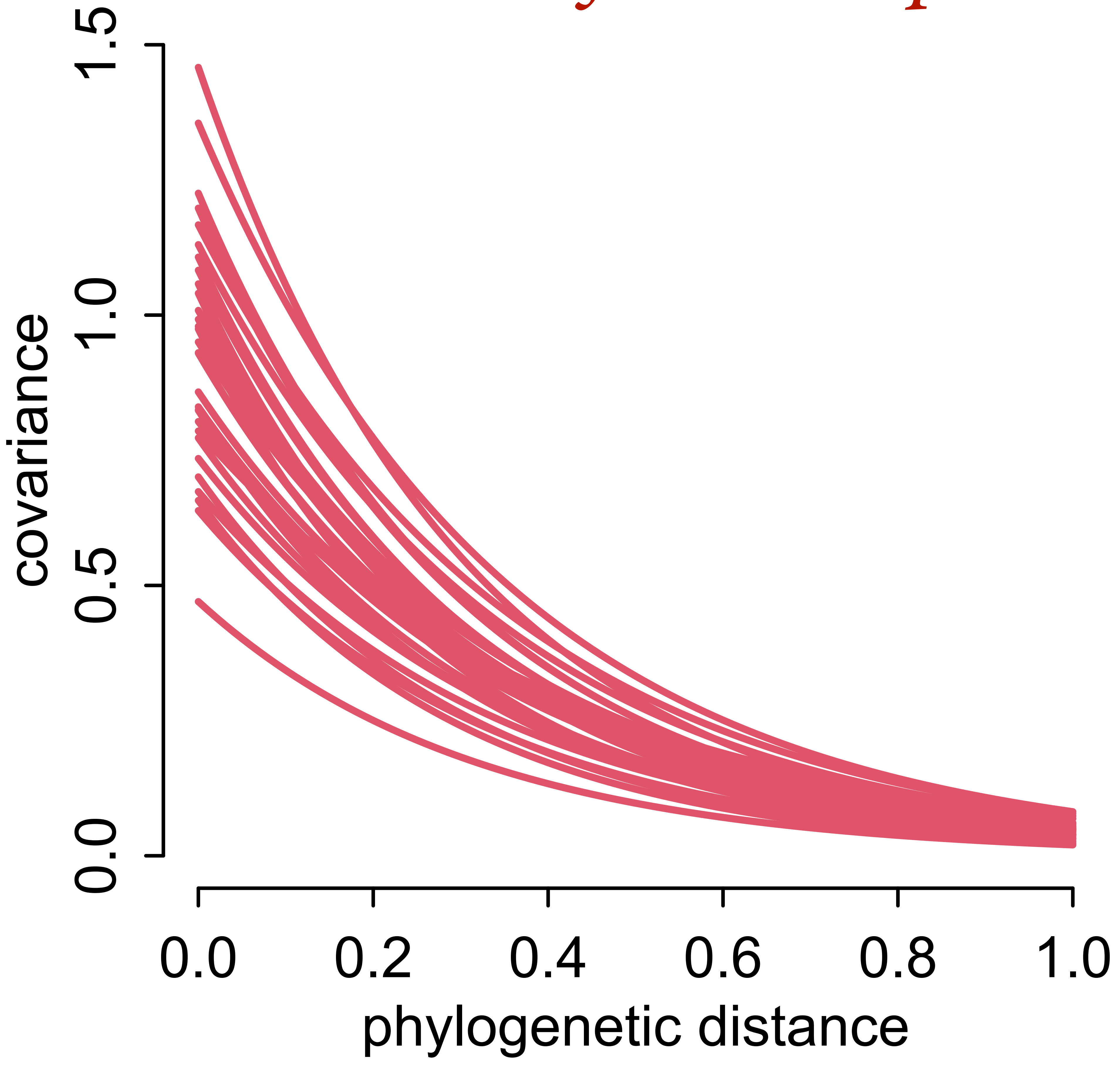
$$\mathbf{K} = \eta^2 \exp(-\rho d_{i,j})$$

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

$$\eta^2 \sim \text{HalfNormal}(1,0.25)$$

$$\rho \sim \text{HalfNormal}(3,0.25)$$

covariance function prior



```
# Ornstein-Uhlenbeck (L1 gaussian process)
# add scaled and reordered distance matrix
dat_list$Dmat <- Dmat[ spp_obs , spp_obs ] / max(Dmat)

mB_OU <- ulam(
    alist(

        B ~ multi_normal( mu , K ),
        mu <- a + 0*M,
        matrix[N_spp,N_spp]:K <- cov_GPL1(Dmat,etasq,rho,0.01),
        a ~ normal(0,1),
        etasq ~ half_normal(1,0.25),
        rho ~ half_normal(3,0.25)

    ), data=dat_list , chains=4 , cores=4 )
```

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha$$

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```r
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```

$$B \sim \mathrm{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha$$

$$\boxed{\mathbf{K} = \eta^2 \exp(-\rho d_{i,j})}$$

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

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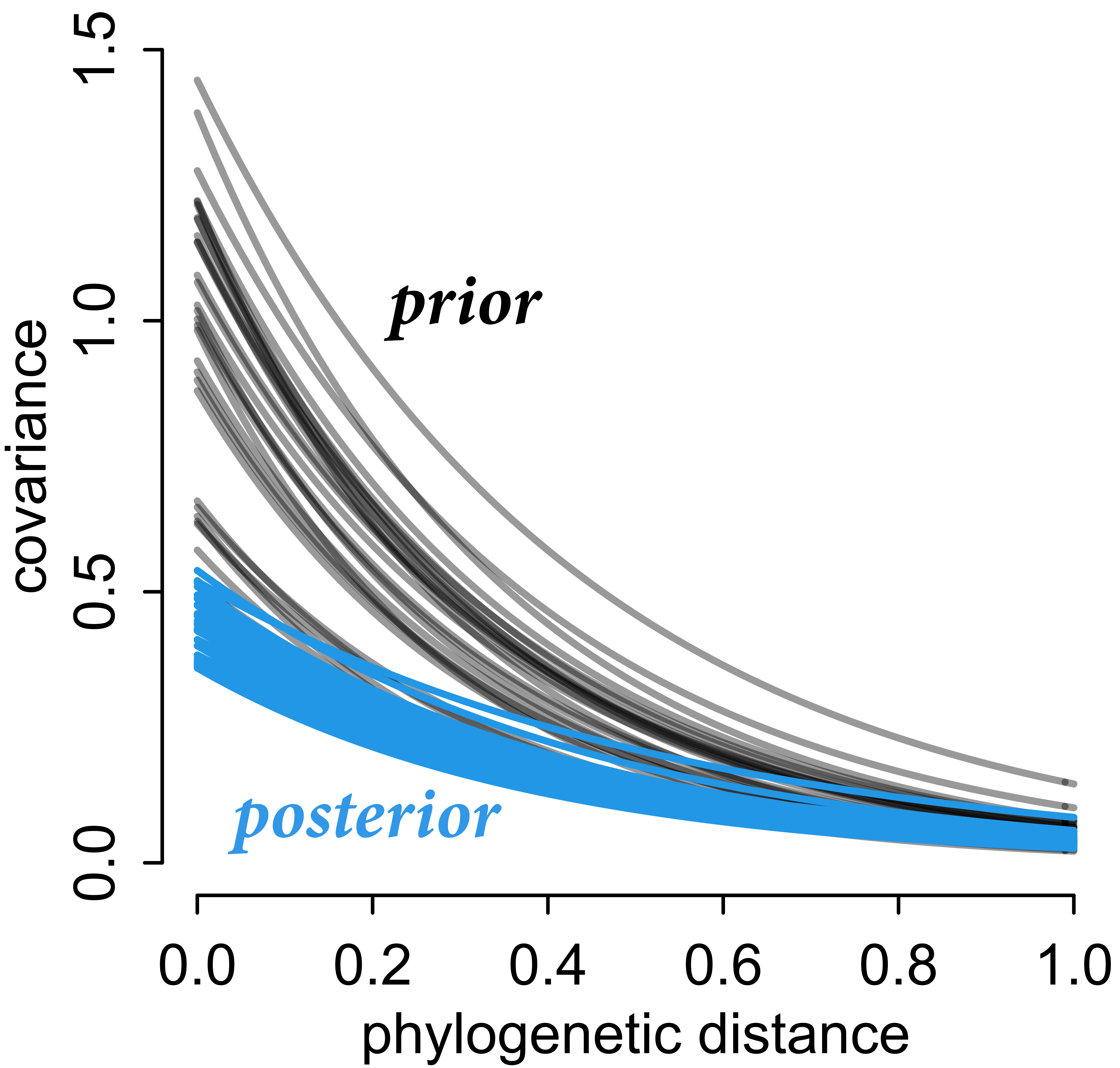
$$\rho \sim \mathrm{HalfNormal}(3,0.25)$$



$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha$$

$$\mathbf{K} = \eta^2 \exp(-\rho d_{i,j})$$

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

$$\eta^2 \sim \text{HalfNormal}(1,0.25)$$

$$\rho \sim \text{HalfNormal}(3,0.25)$$

Stratify by M and G

```
mBMG_OU <- ulam(
    alist(

        B ~ multi_normal( mu , K ),
        mu <- a + bM*M + bG*G,
        matrix[N_spp,N_spp]:K <- cov_GPL1(Dmat,etasq,rho,0.01),
        a ~ normal(0,1),
        c(bM,bG) ~ normal(0,0.5),
        etasq ~ half_normal(1,0.25),
        rho ~ half_normal(3,0.25)

    ), data=dat_list , chains=4 , cores=4 )
```

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

$$\mu_i = \alpha + \beta_G G_i + \beta_M M_i$$

$$\mathbf{K} = \eta^2 \exp(-\rho d_{i,j})$$

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

$$\beta_G, \beta_M \sim \text{Normal}(0,0.5)$$

$$\eta^2 \sim \text{HalfNormal}(1,0.25)$$

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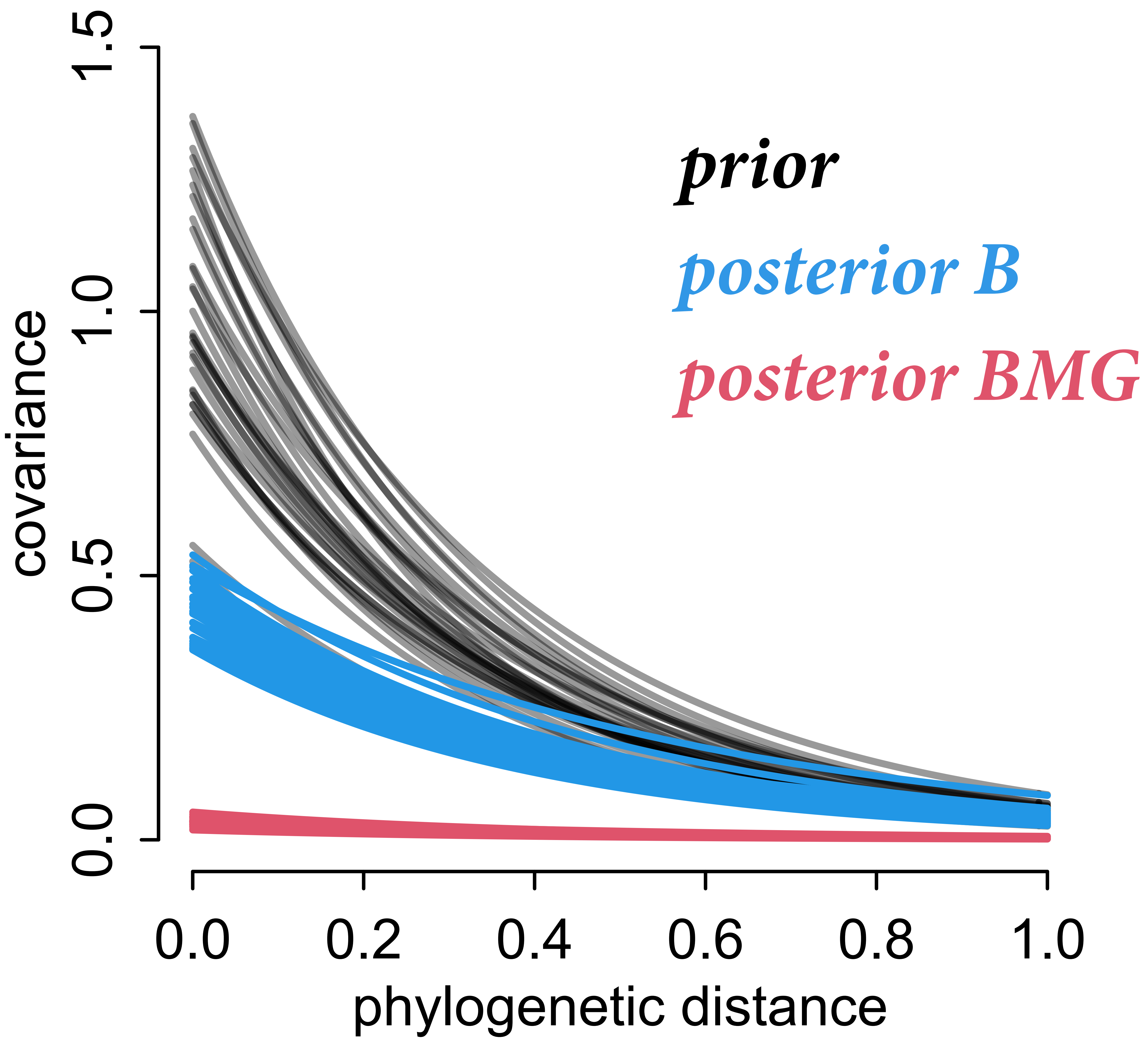

$$B \sim \text{MVNormal}(\mu, \mathbf{K})$$

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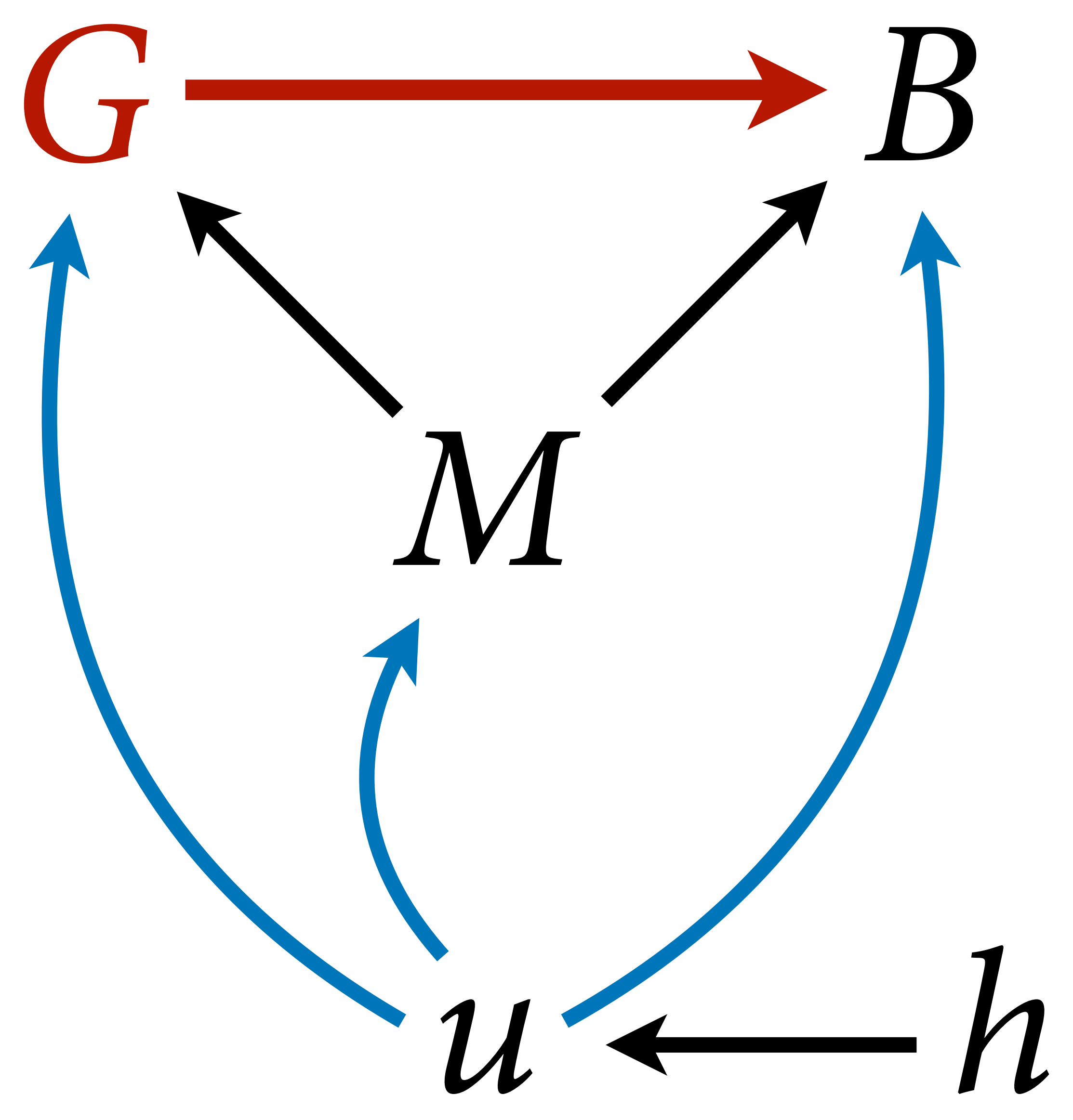
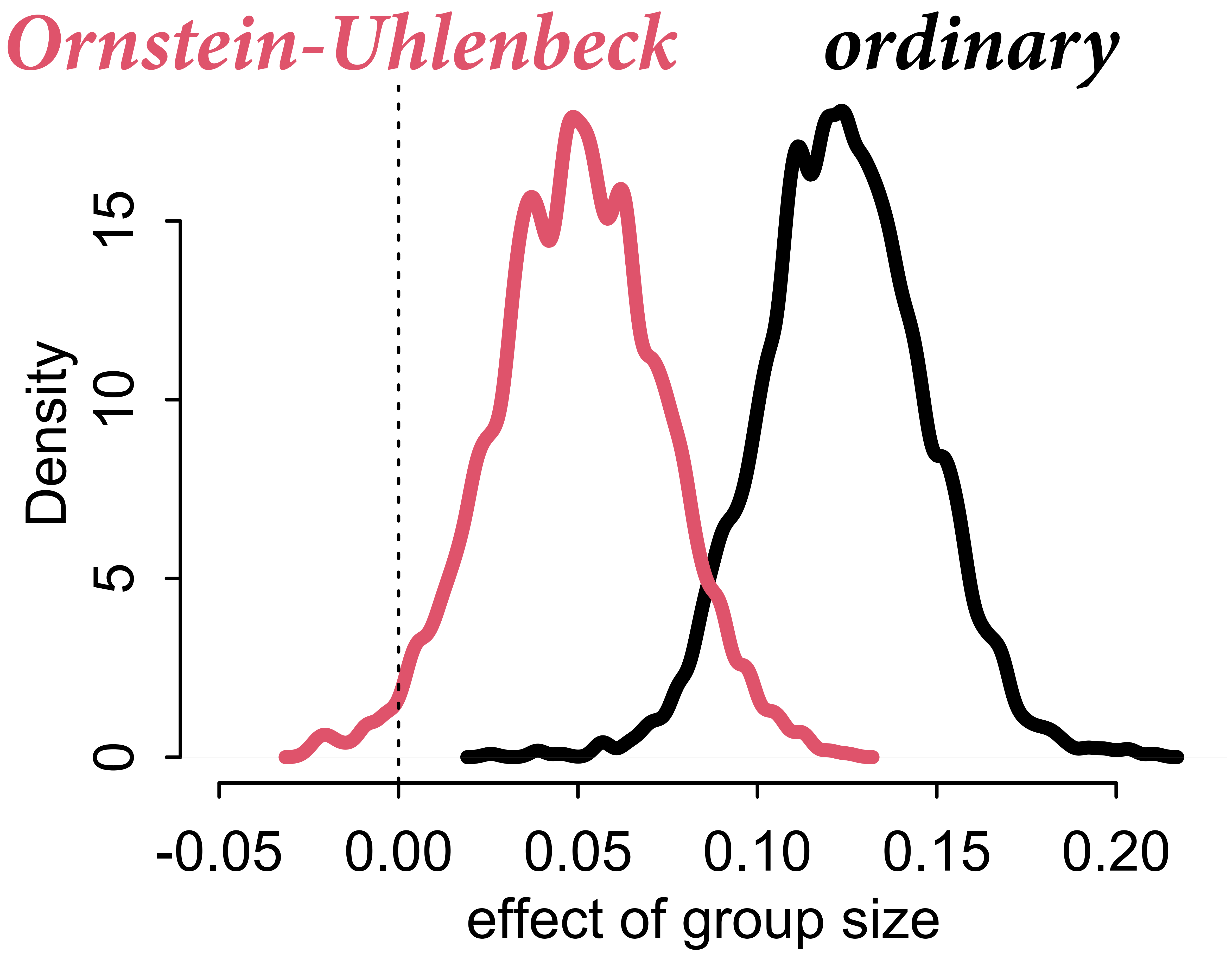


G
B
M
u
h



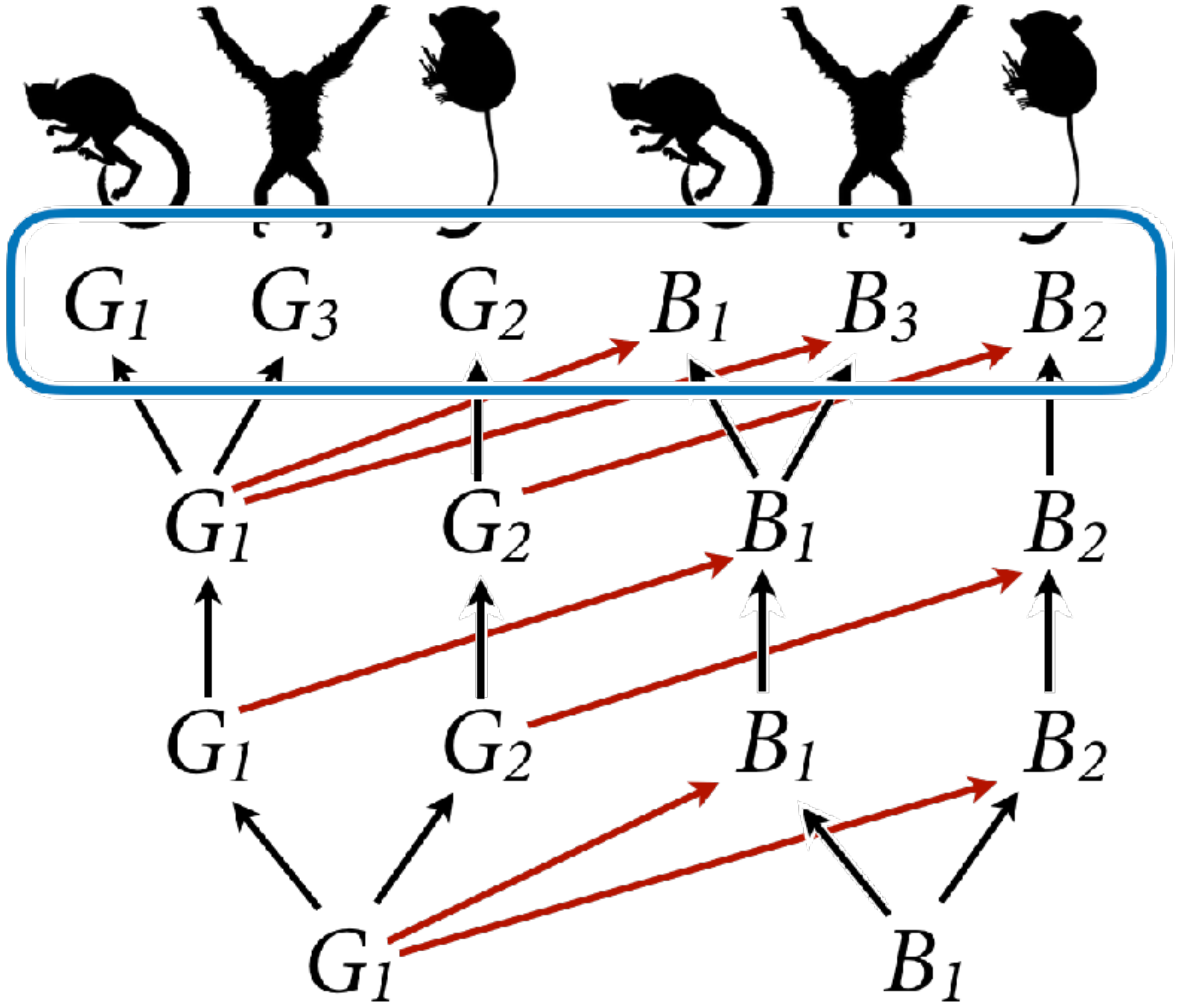
Ornstein-Uhlenbeck
ordinary
Density
0
5
10
15
-0.05
0.00
0.05
0.10
0.15
0.20
effect of group size

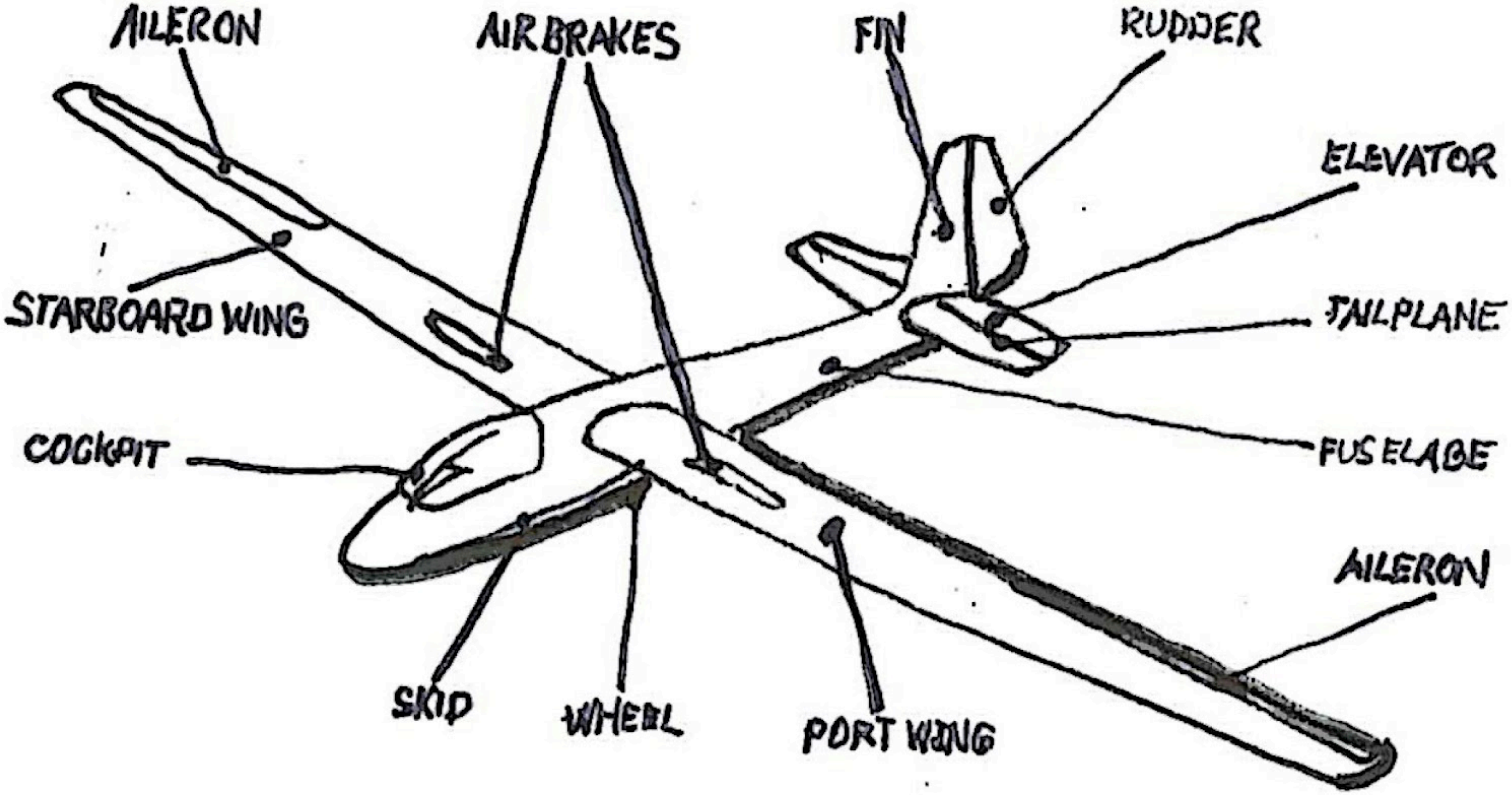
Phylogenetic regression

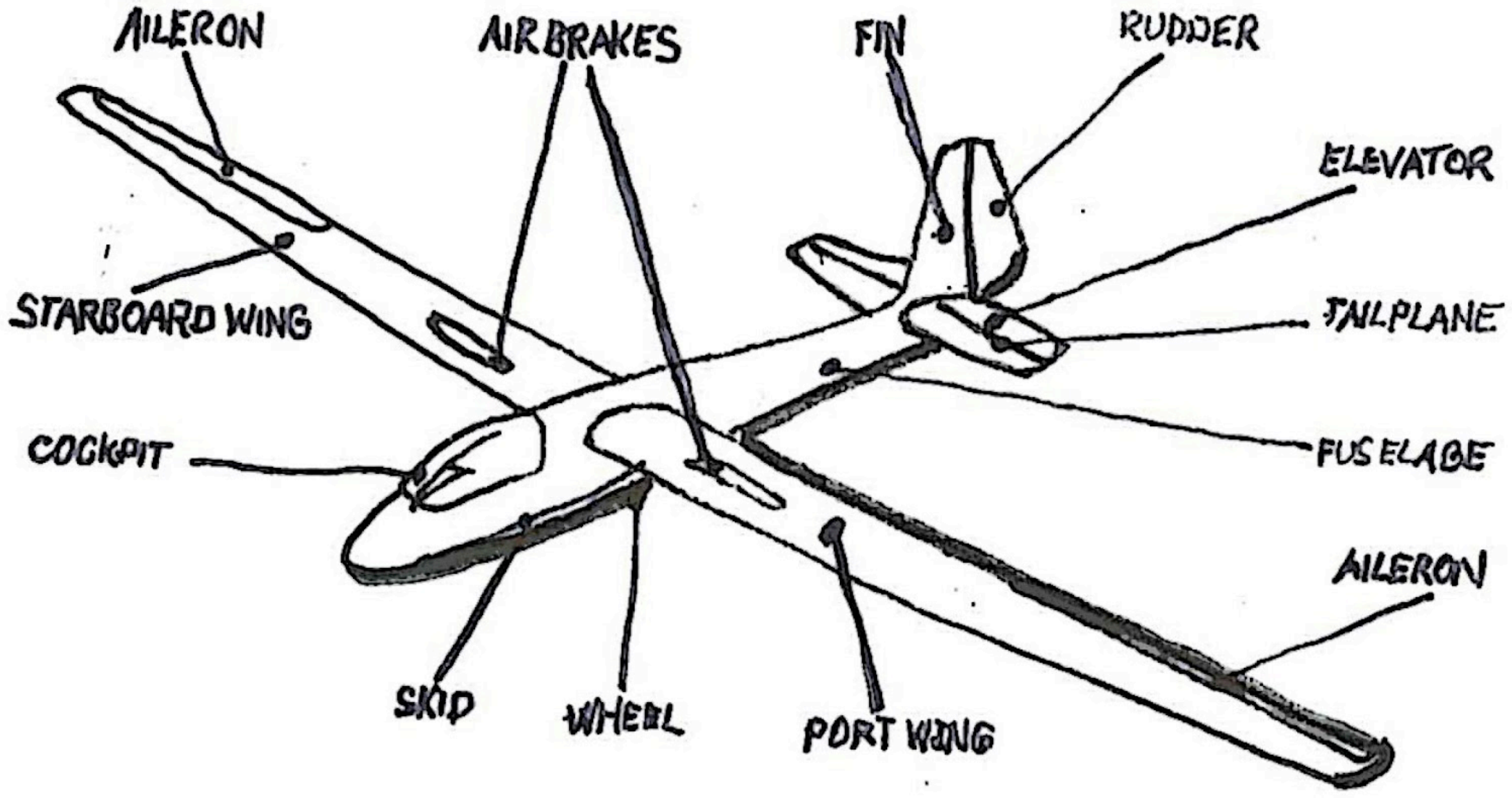
Lingering problems:

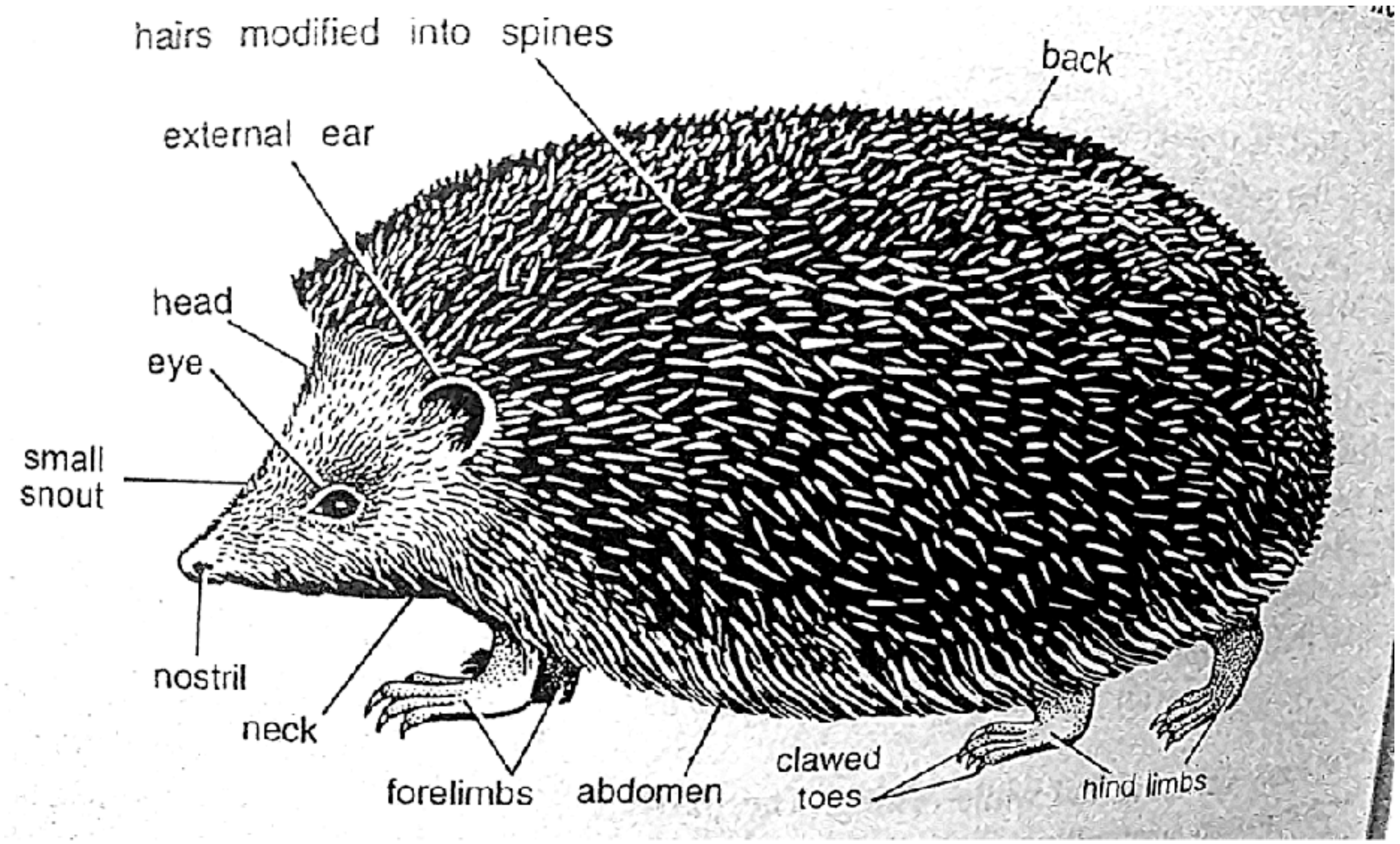
(1) What about phylogenetic uncertainty?

(2) Don't these traits influence one another reciprocally over time?




AILERON
AIR BRAKES
FIN
RUDDER
ELEVATOR
STARBOARD WING
TAILPLANE
COCKPIT
FUSELAGE
AILERON
SKID
WHEEL
PORT WING

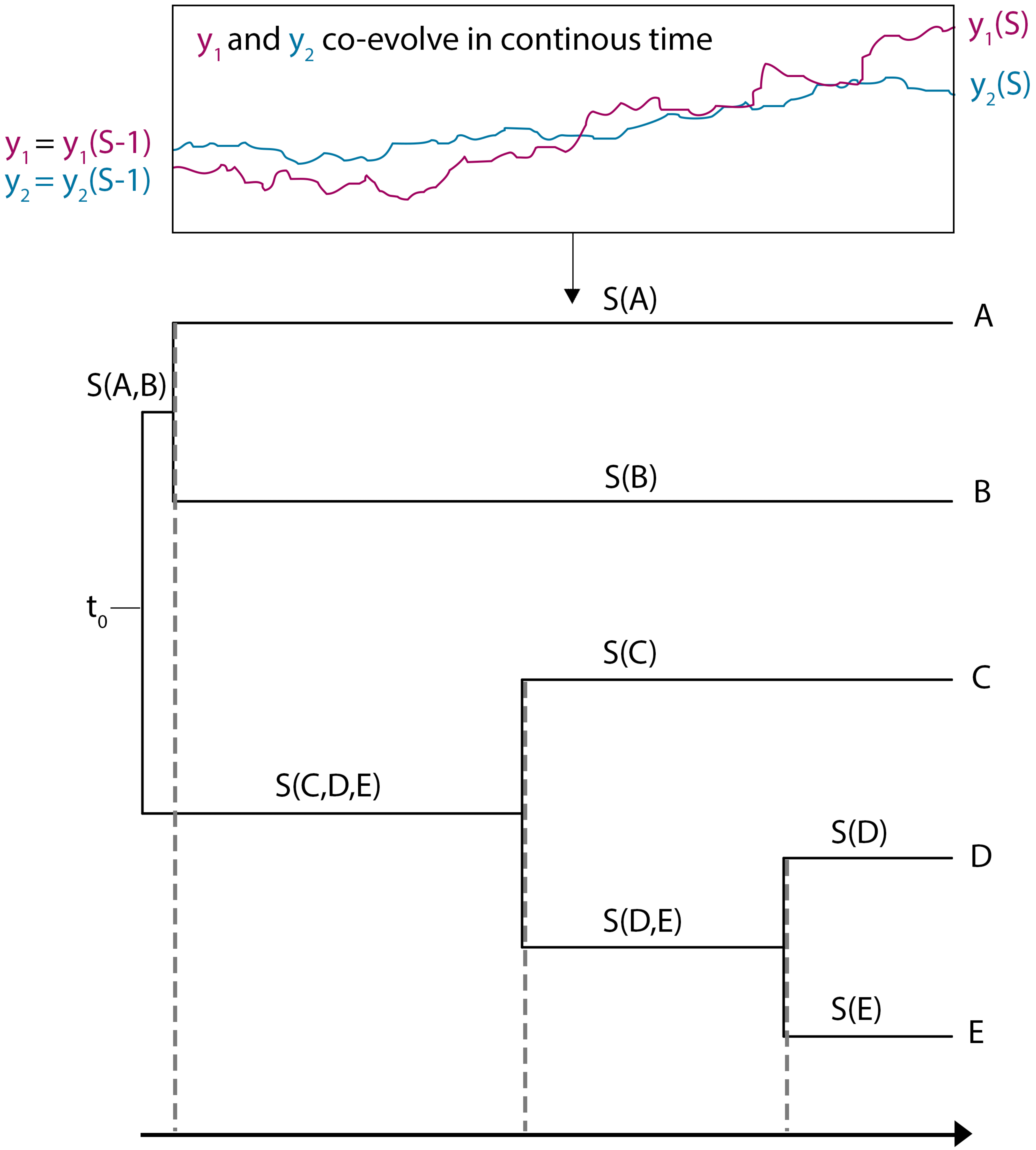




A glider knows many things. Gliders and hedgehogs are both complex machines with many mutually influencing parts. Causation in such machines involves powerful feedbacks.

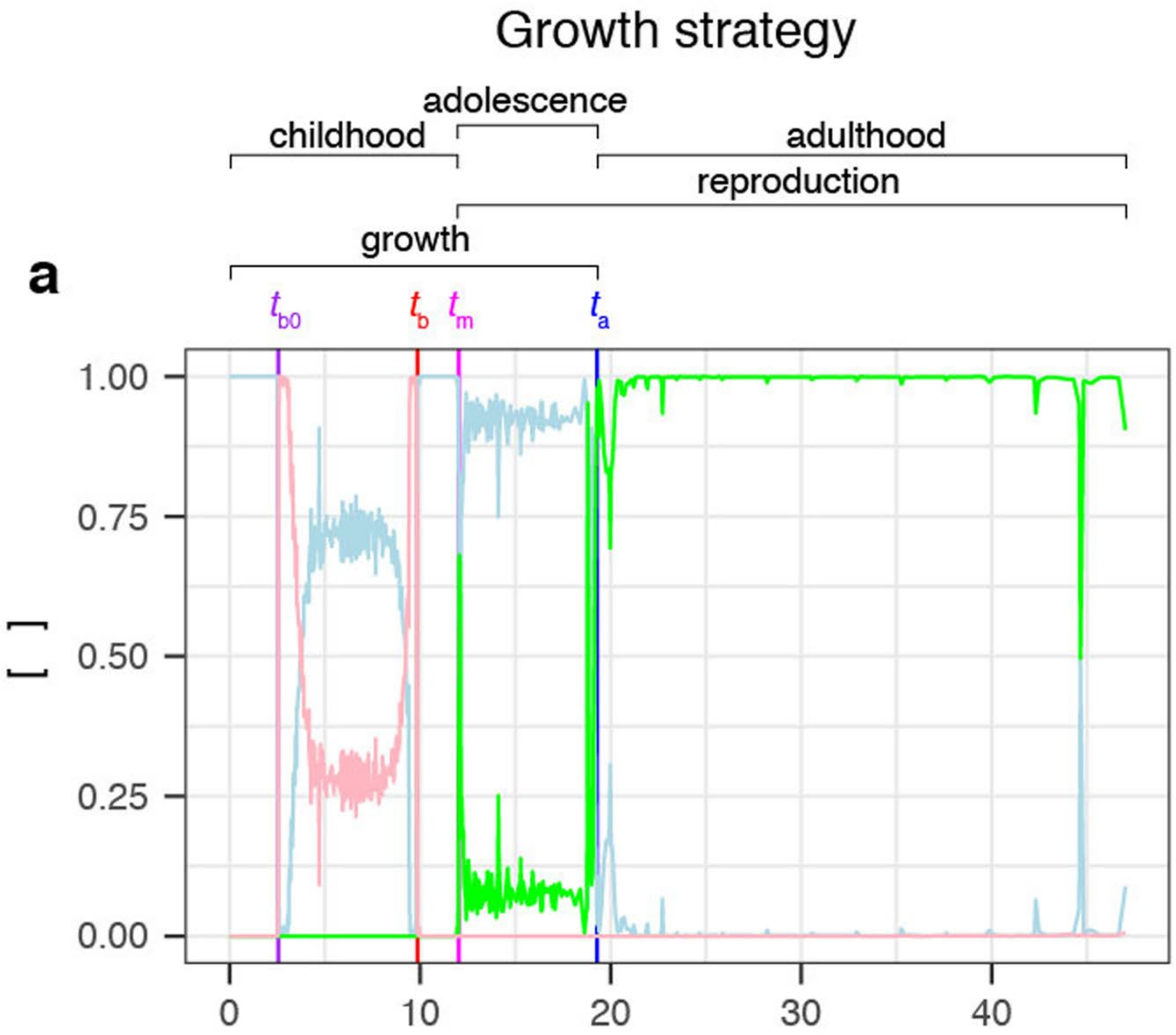
Ringen, Martin, Jaeggi 2021

Drift-coevolution dynamics



González-Forero & Gardner 2018

Optimal life history approach



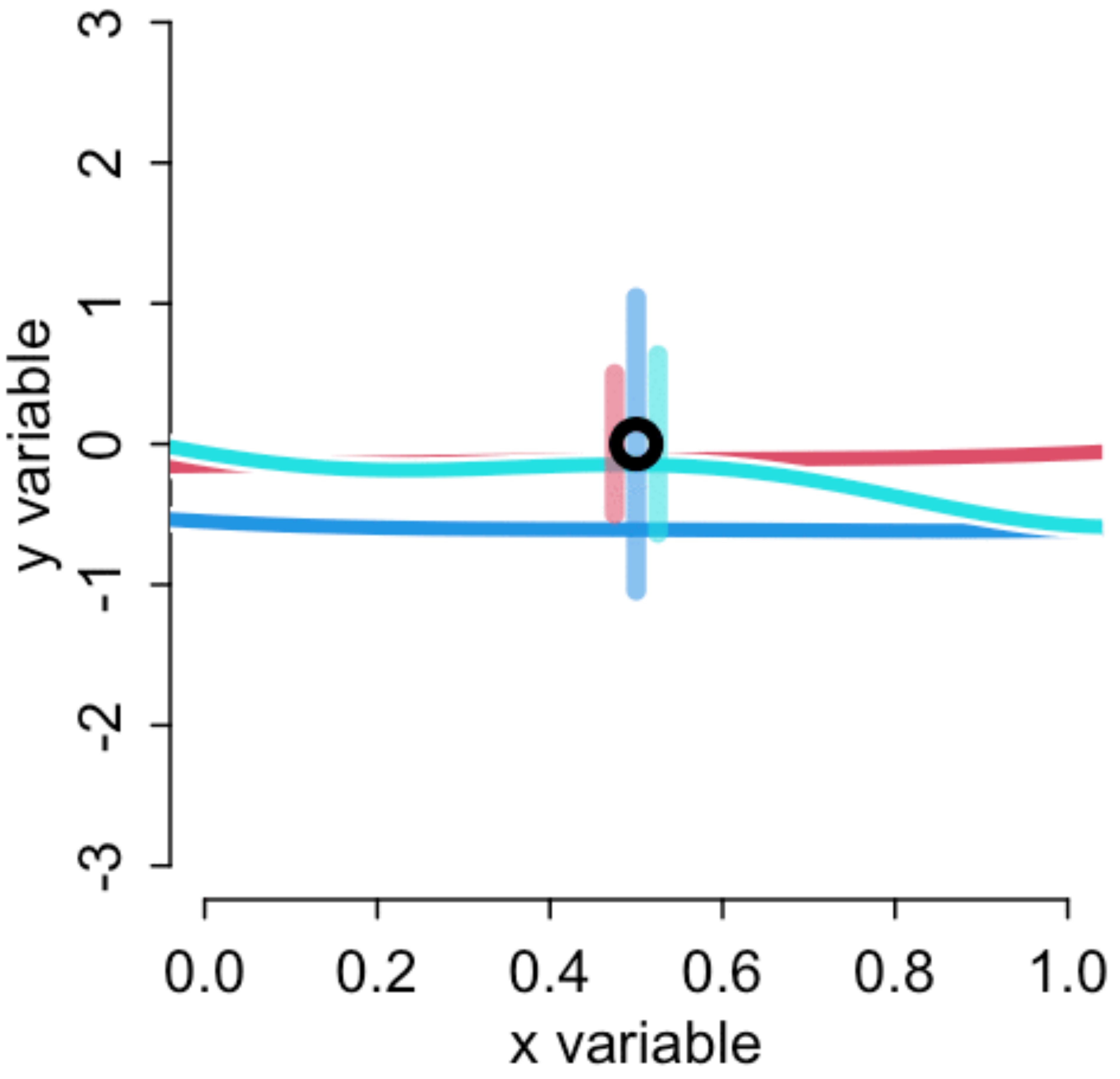
Gaussian Processes

Partial pooling for continuous categories

Very general approximation engine

Causal theory => covariance kernel

Sensitivity to kernel priors — choose wisely

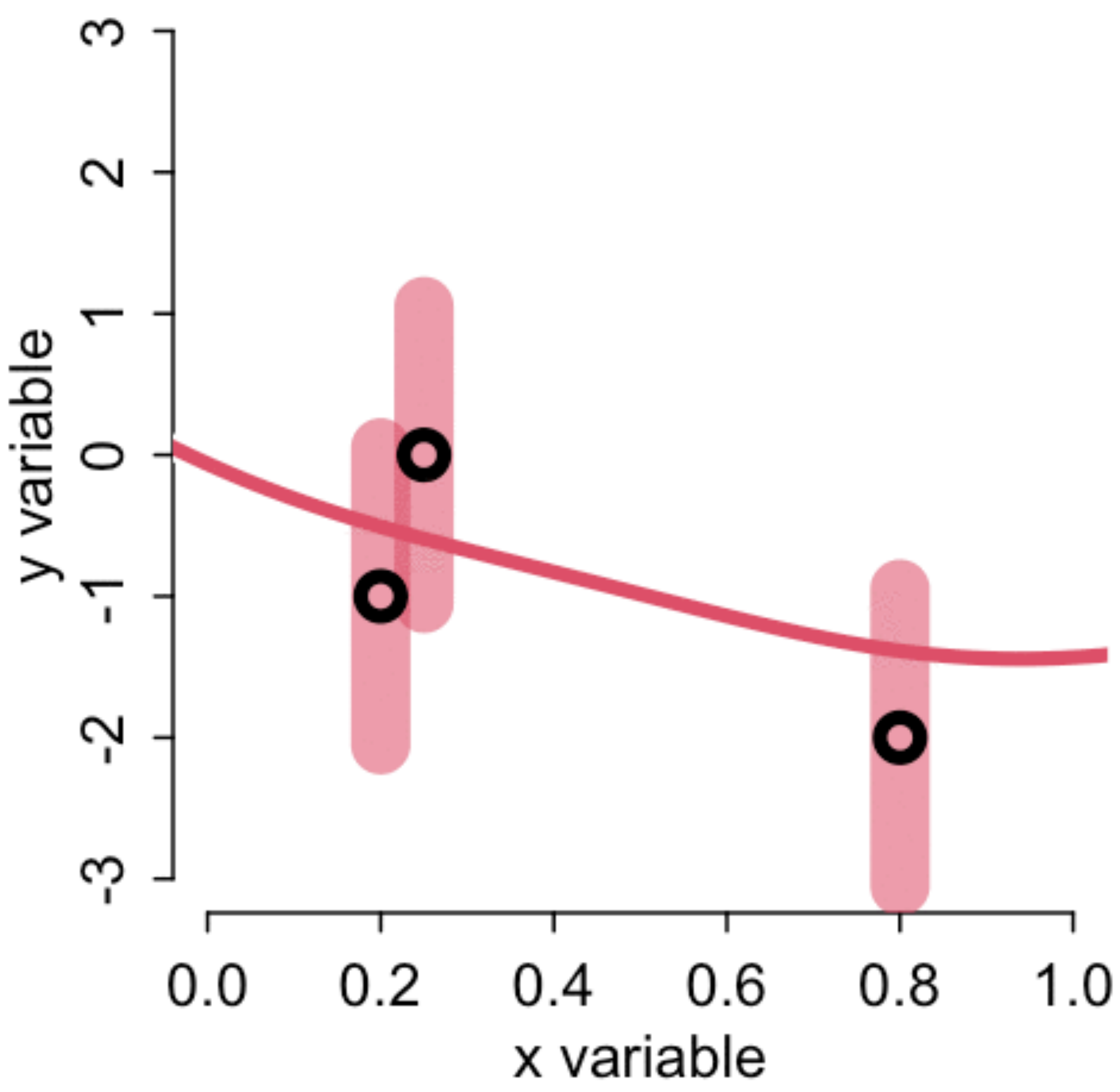


Gaussian Possibilities

Automatic relevance determination (ARD): Multiple distance dimensions inside the kernel

Multi-output Gaussian processes: Draw vectors from kernel

Telemetry, navigation: Real-time tracking and error correction (*Kálmán filter*)



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