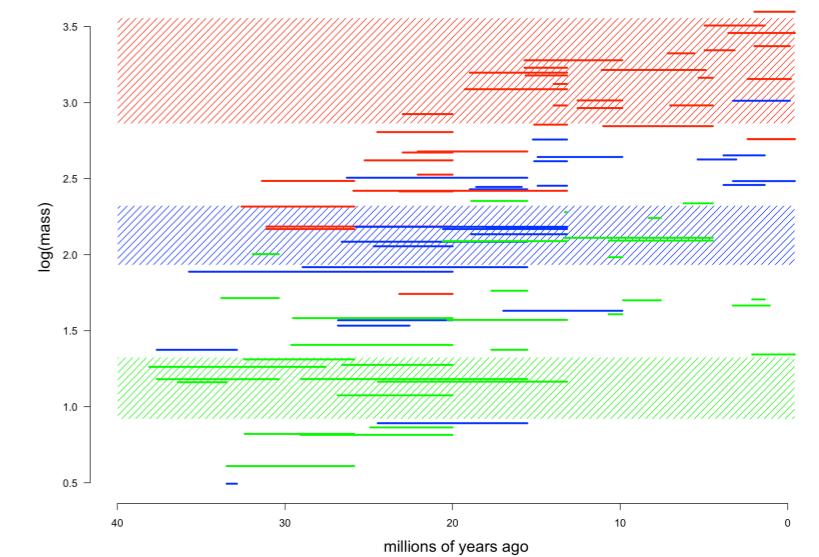
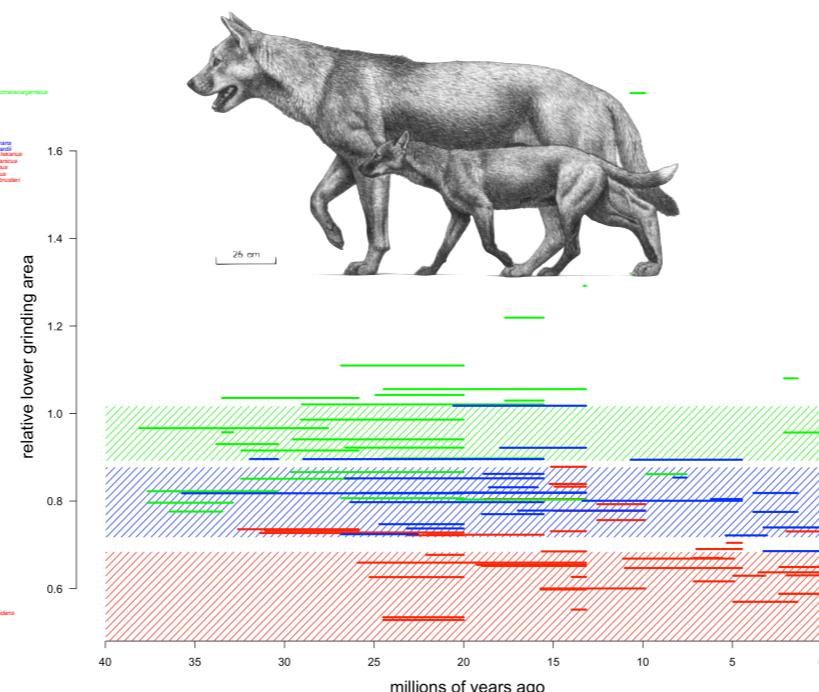
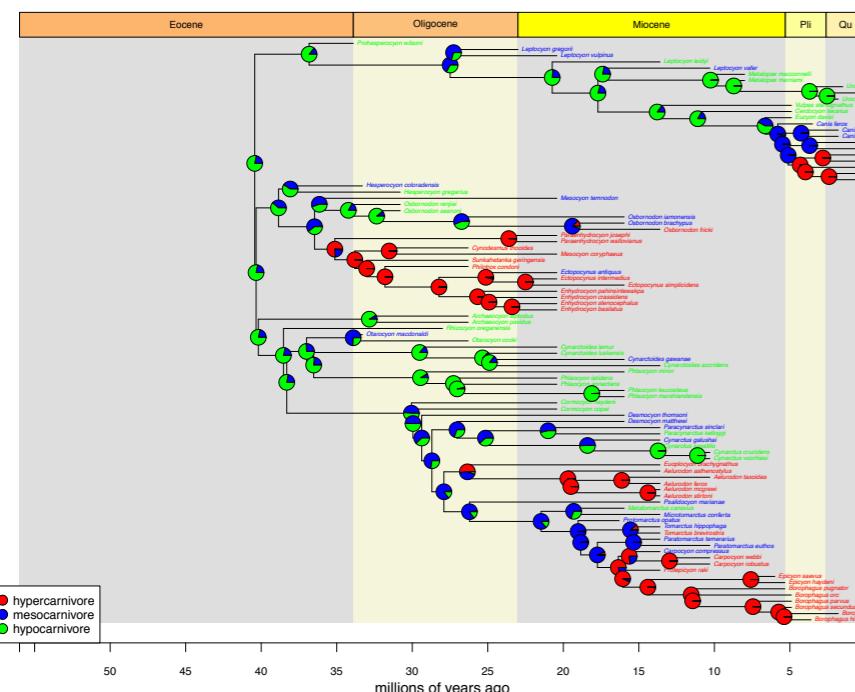
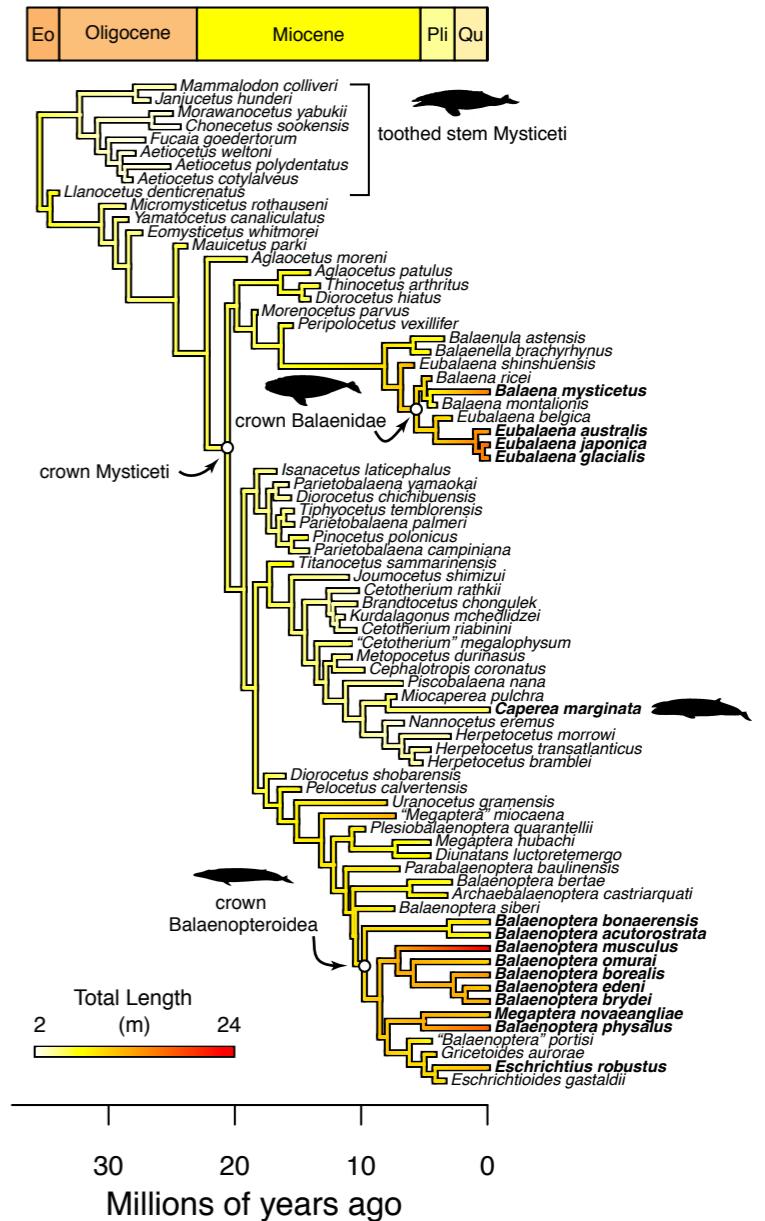
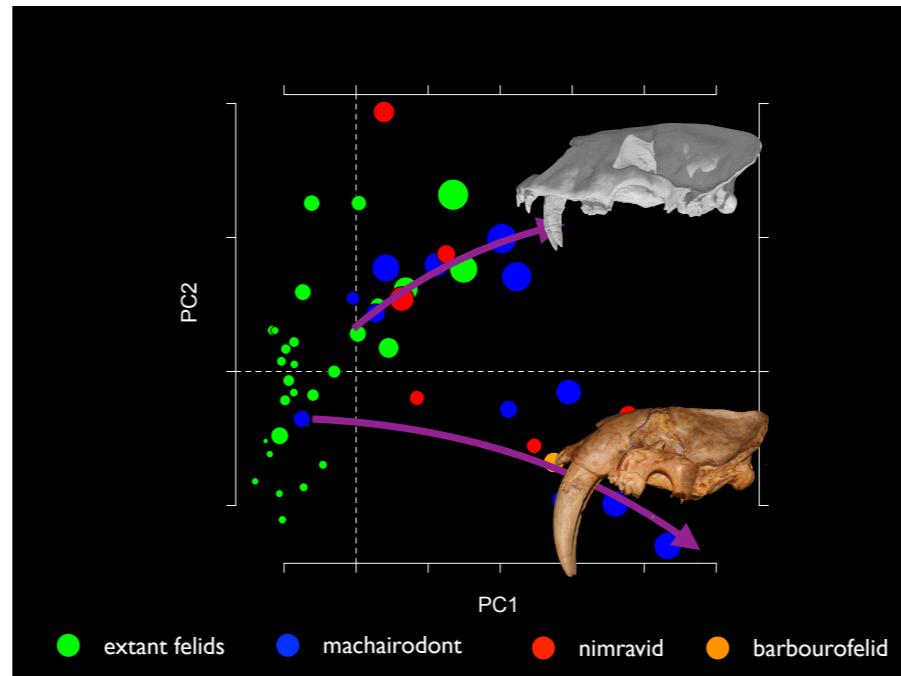
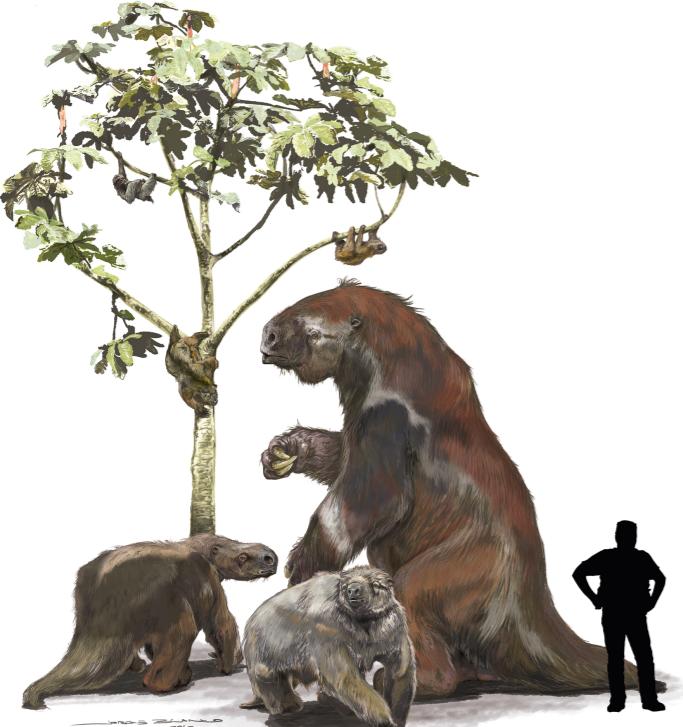


Graham Slater

University of Chicago

mammalian macroevolution



continuous trait evolution

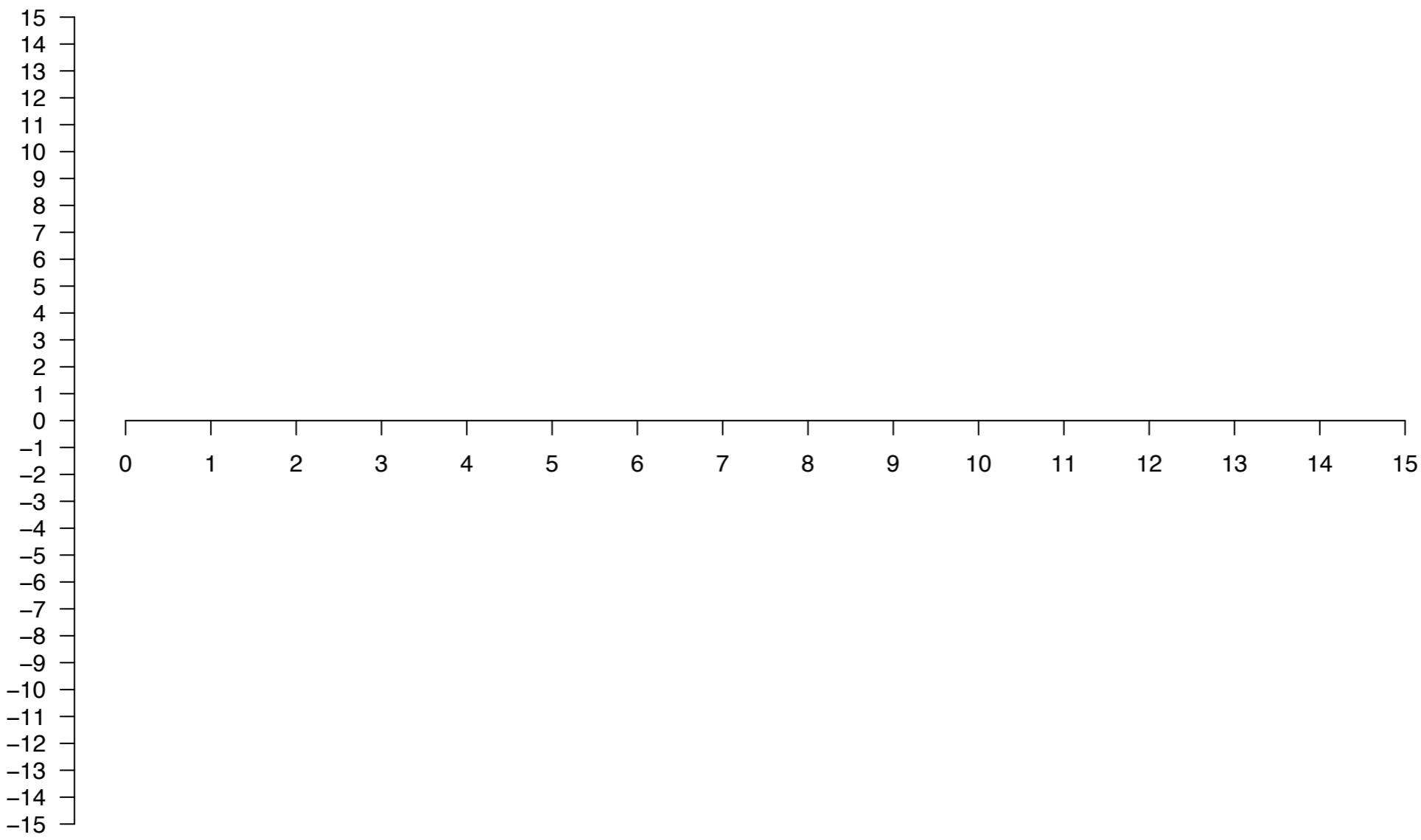




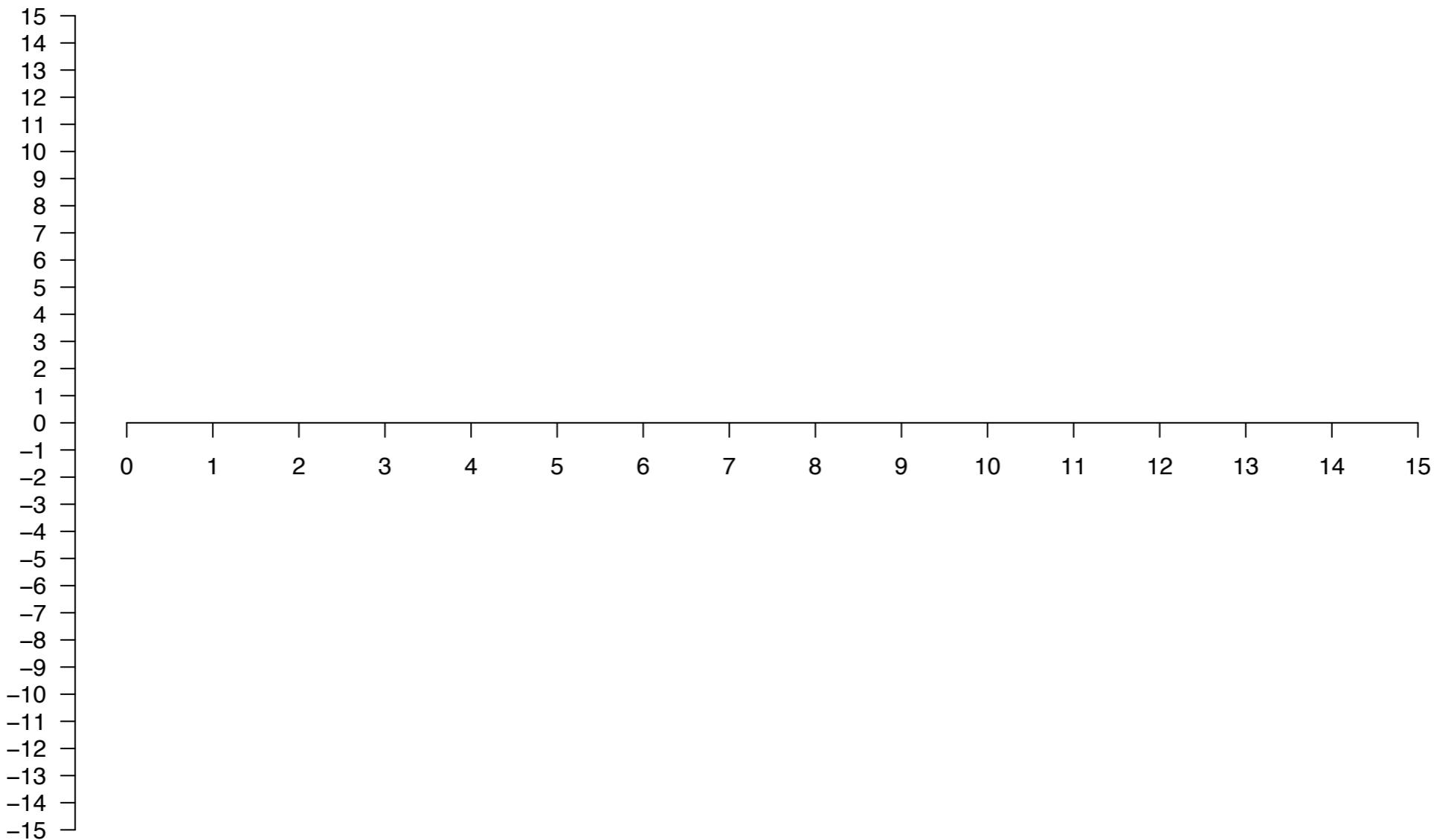
+1

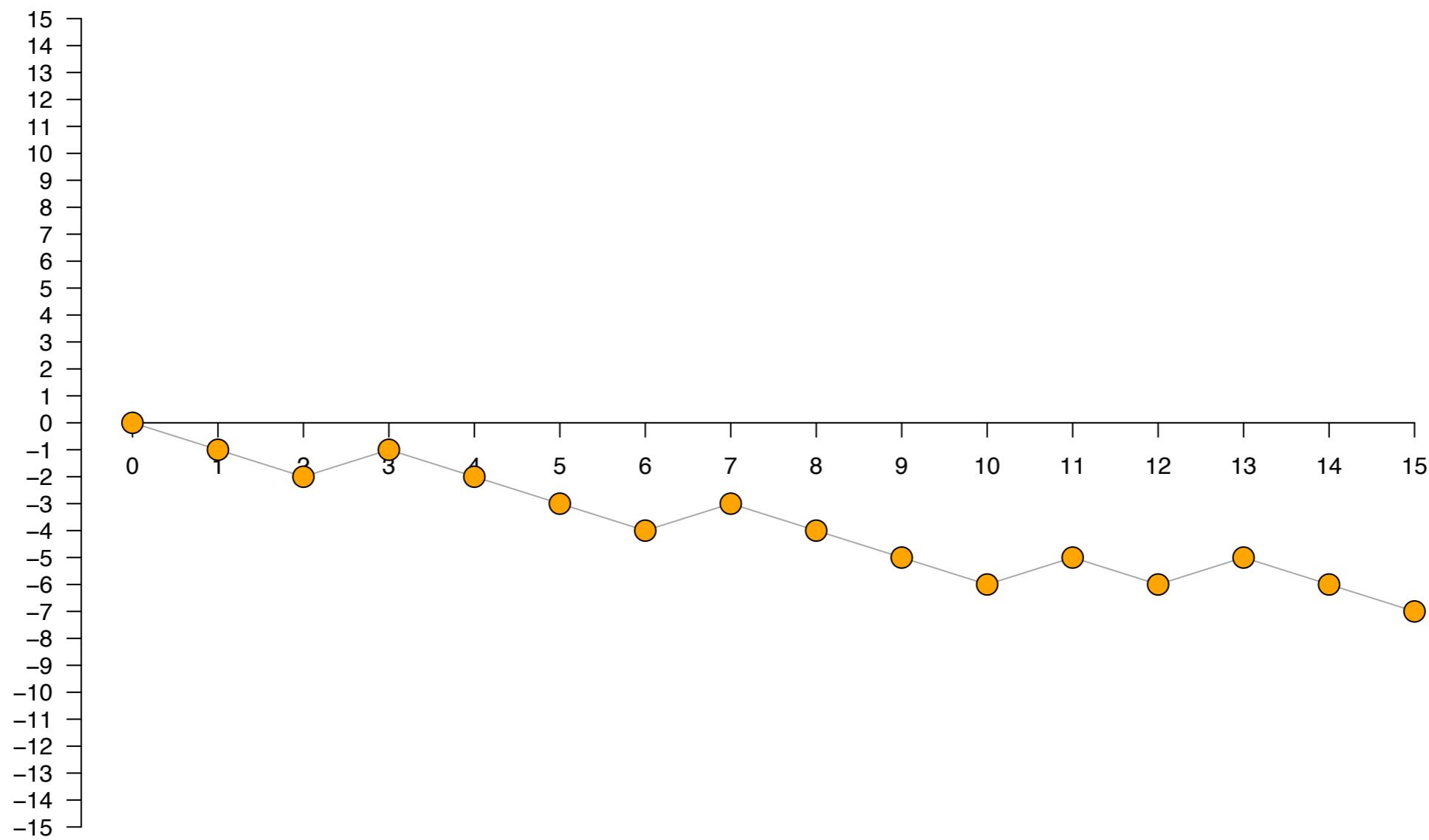


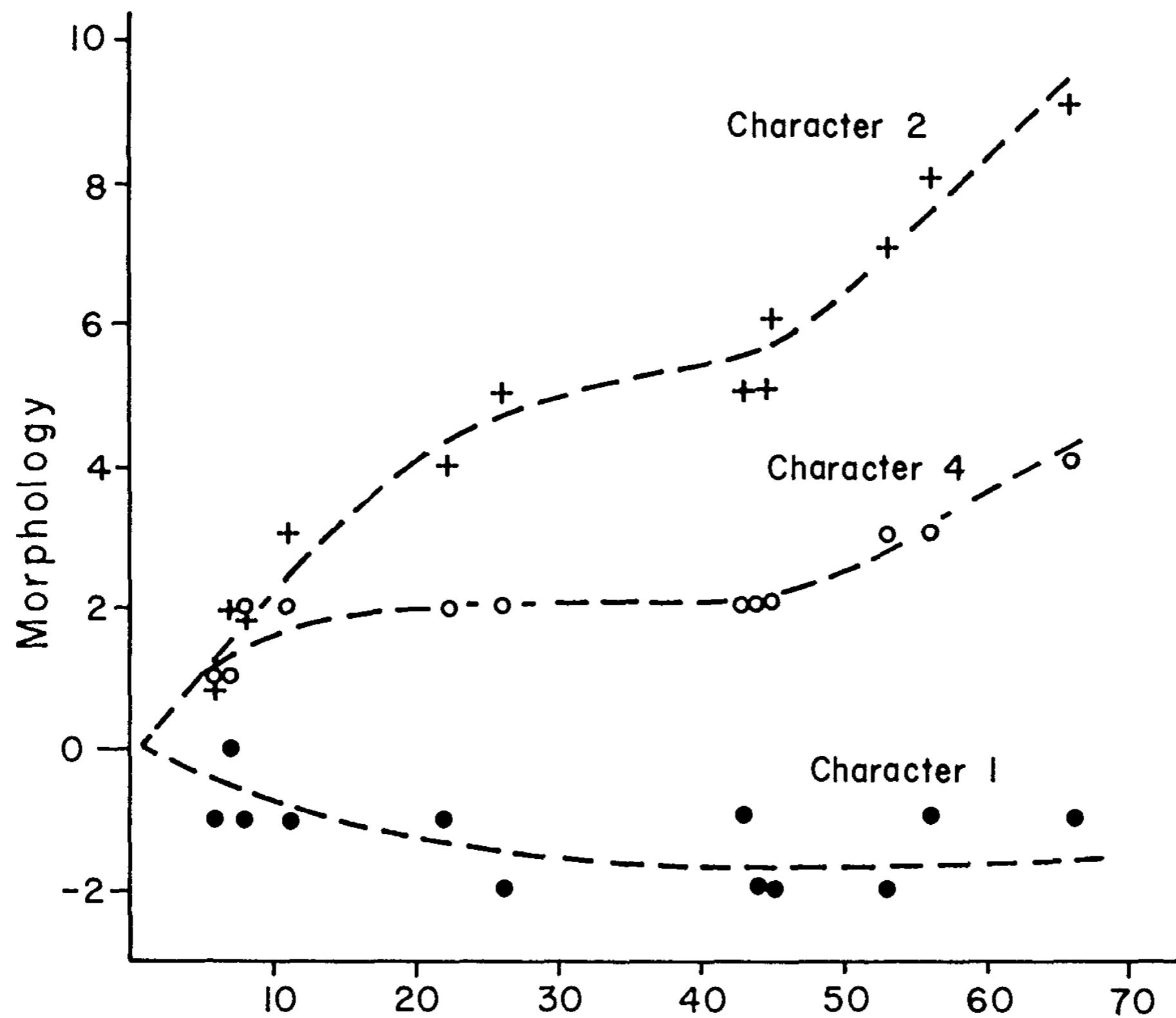
-1

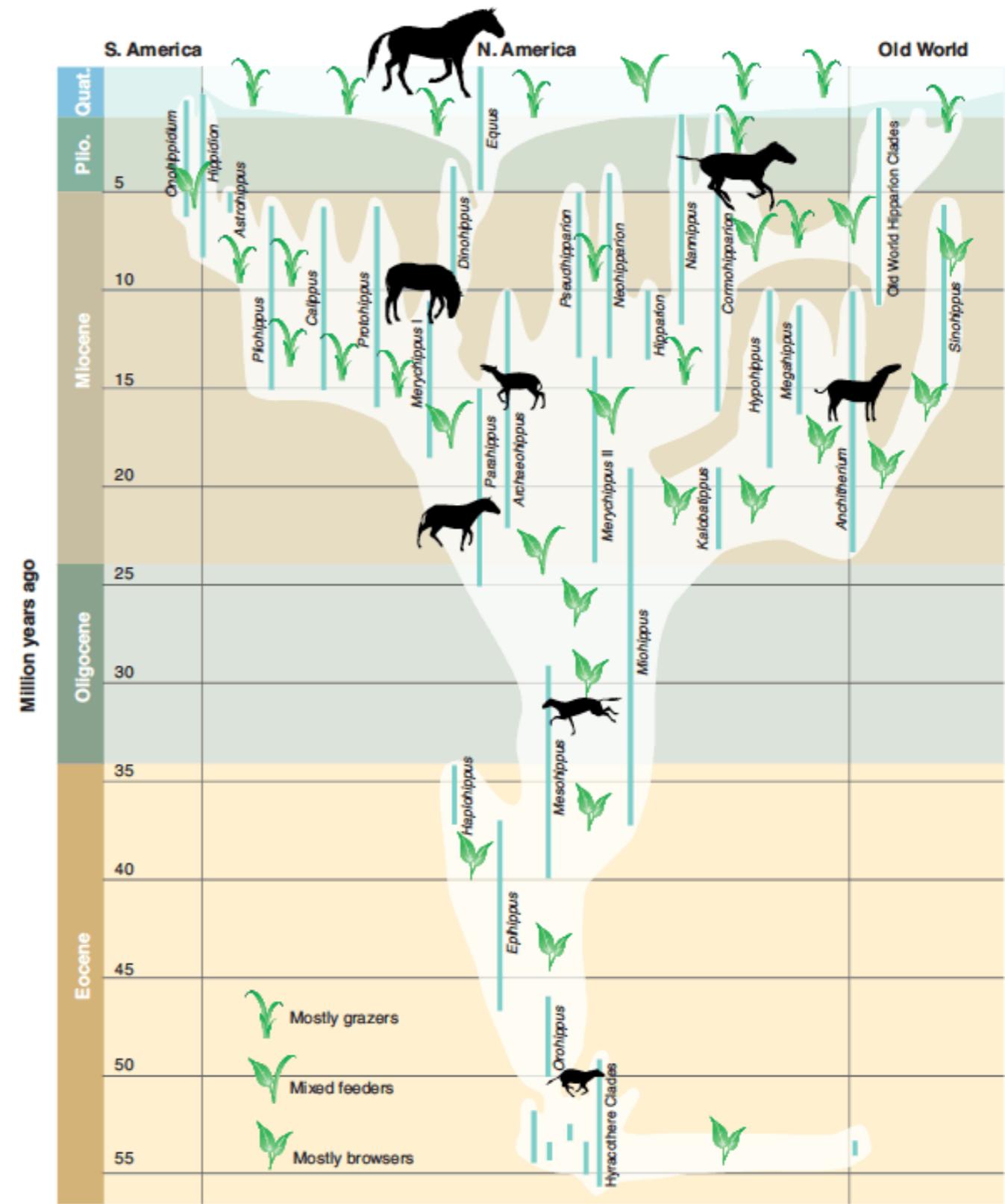
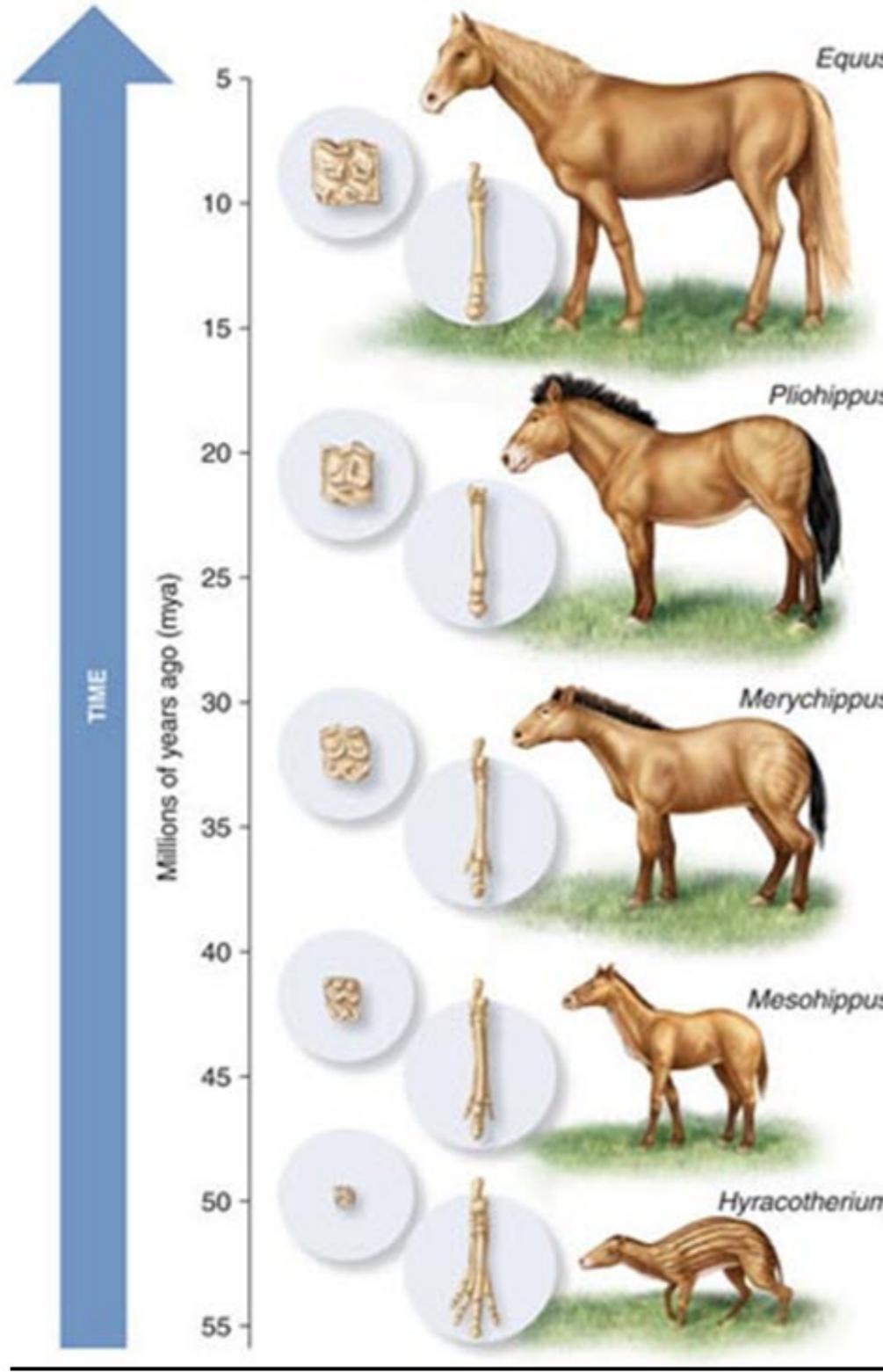


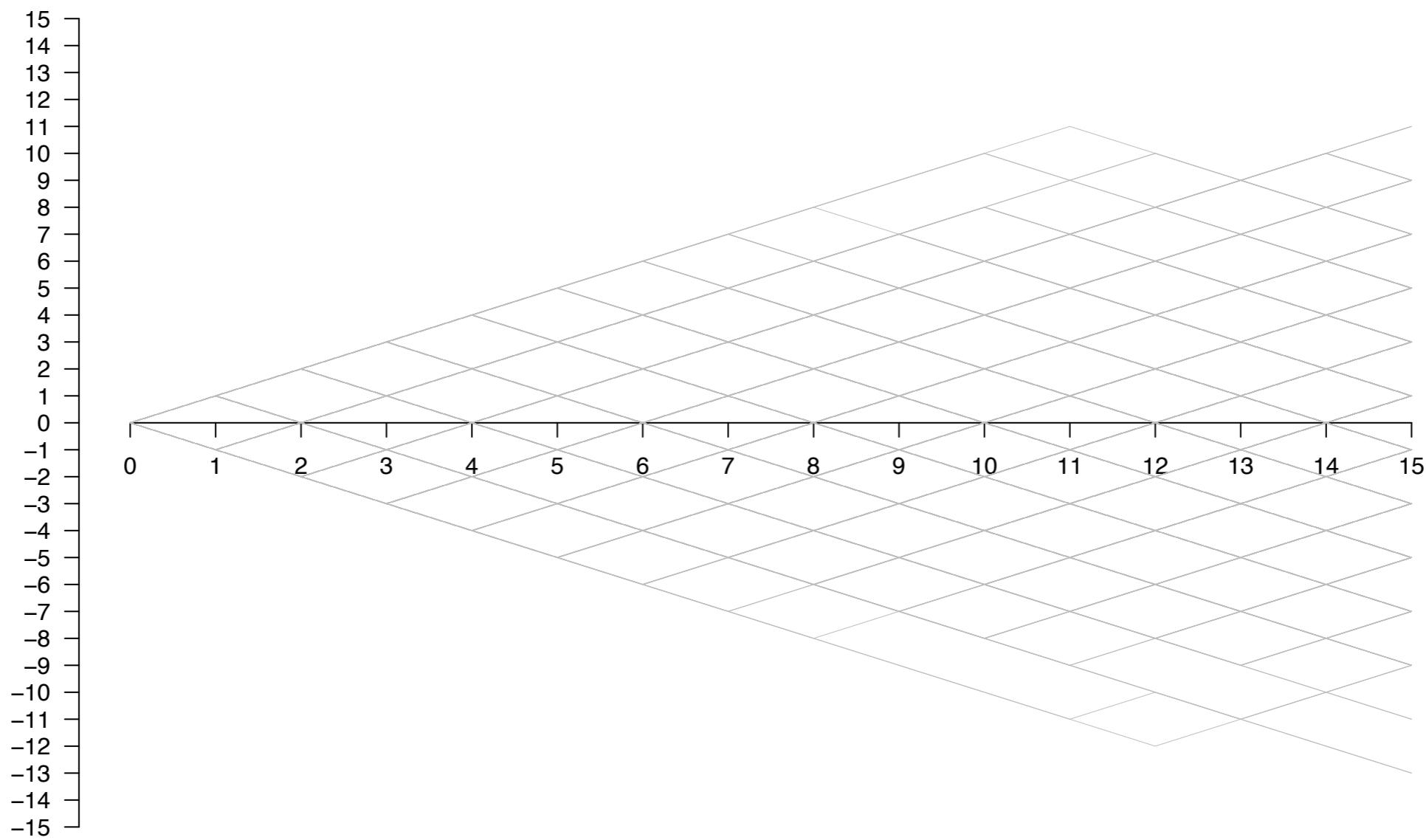
$$F_n = 0 + X_1 + X_2 + \dots + X_n$$



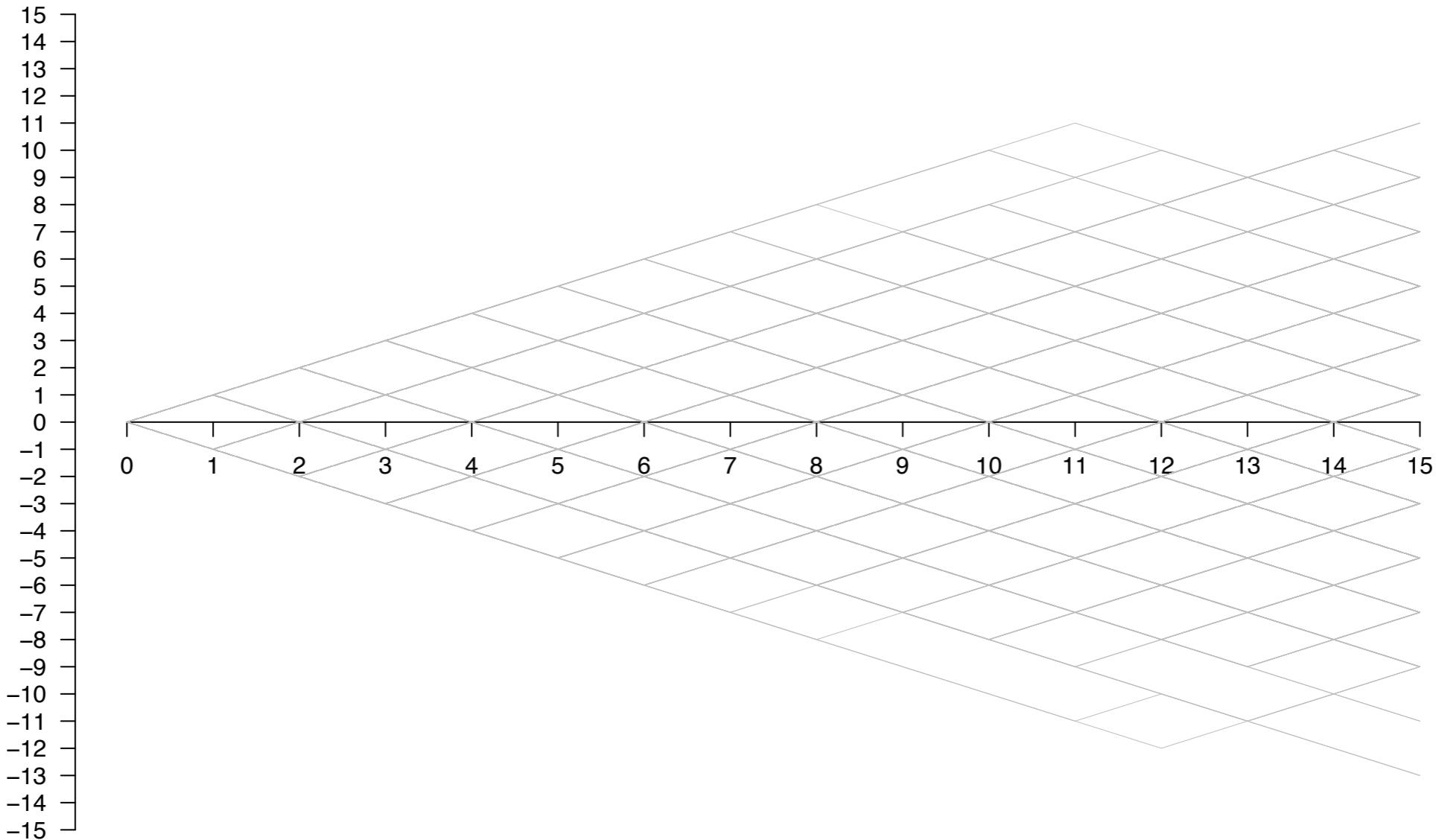




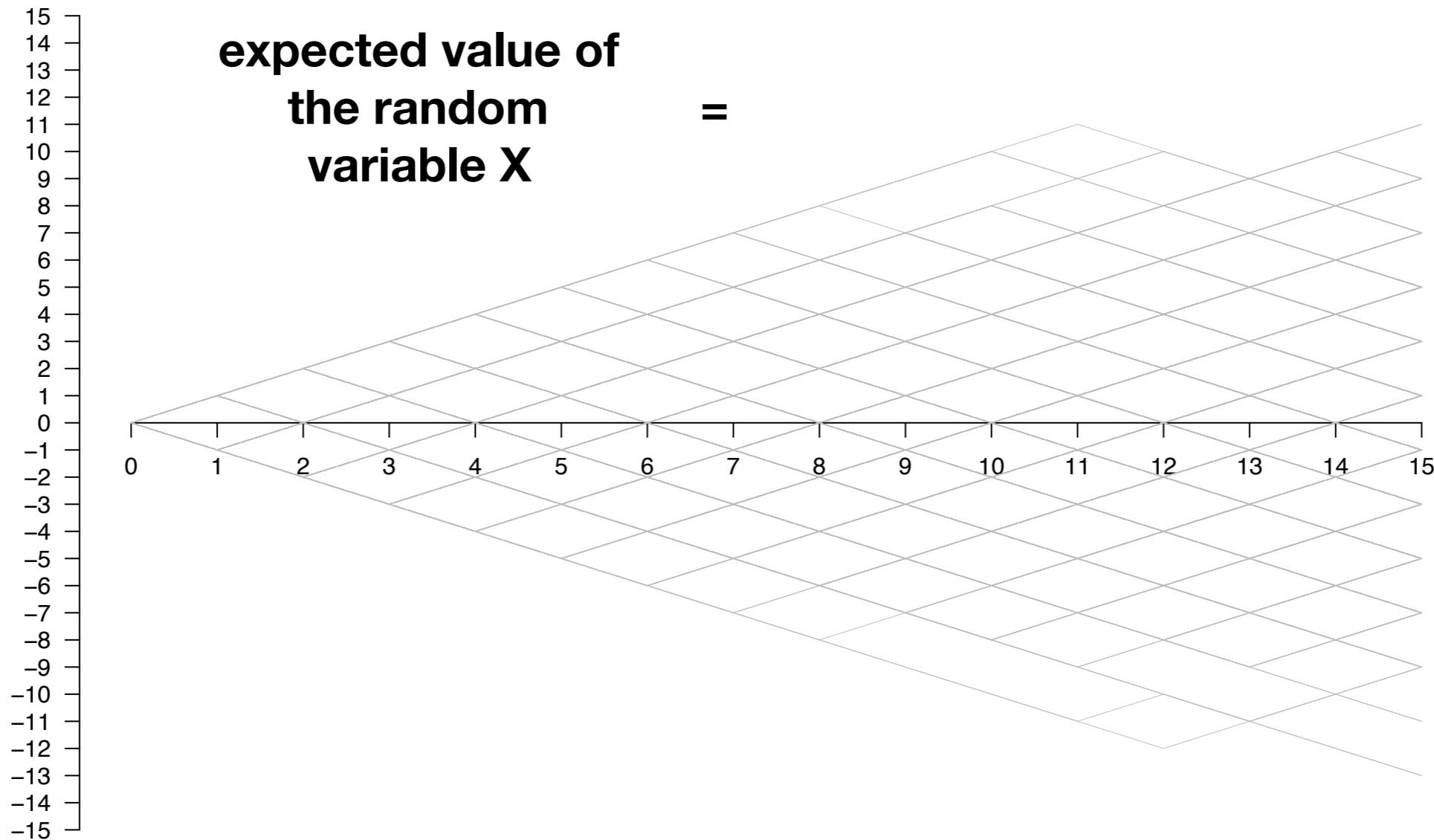




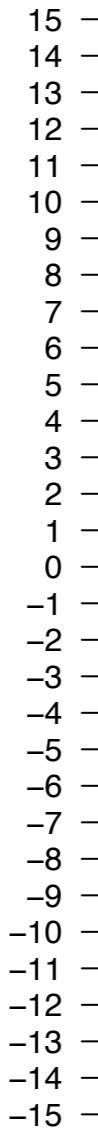
$$\mathbb{E}[X] = \sum_{i=1}^n x_i p_i$$



$$\mathbb{E}[X] = \sum_{i=1}^n x_i p_i$$



$$\mathbb{E}[X] = \sum_{i=1}^n x_i p_i$$

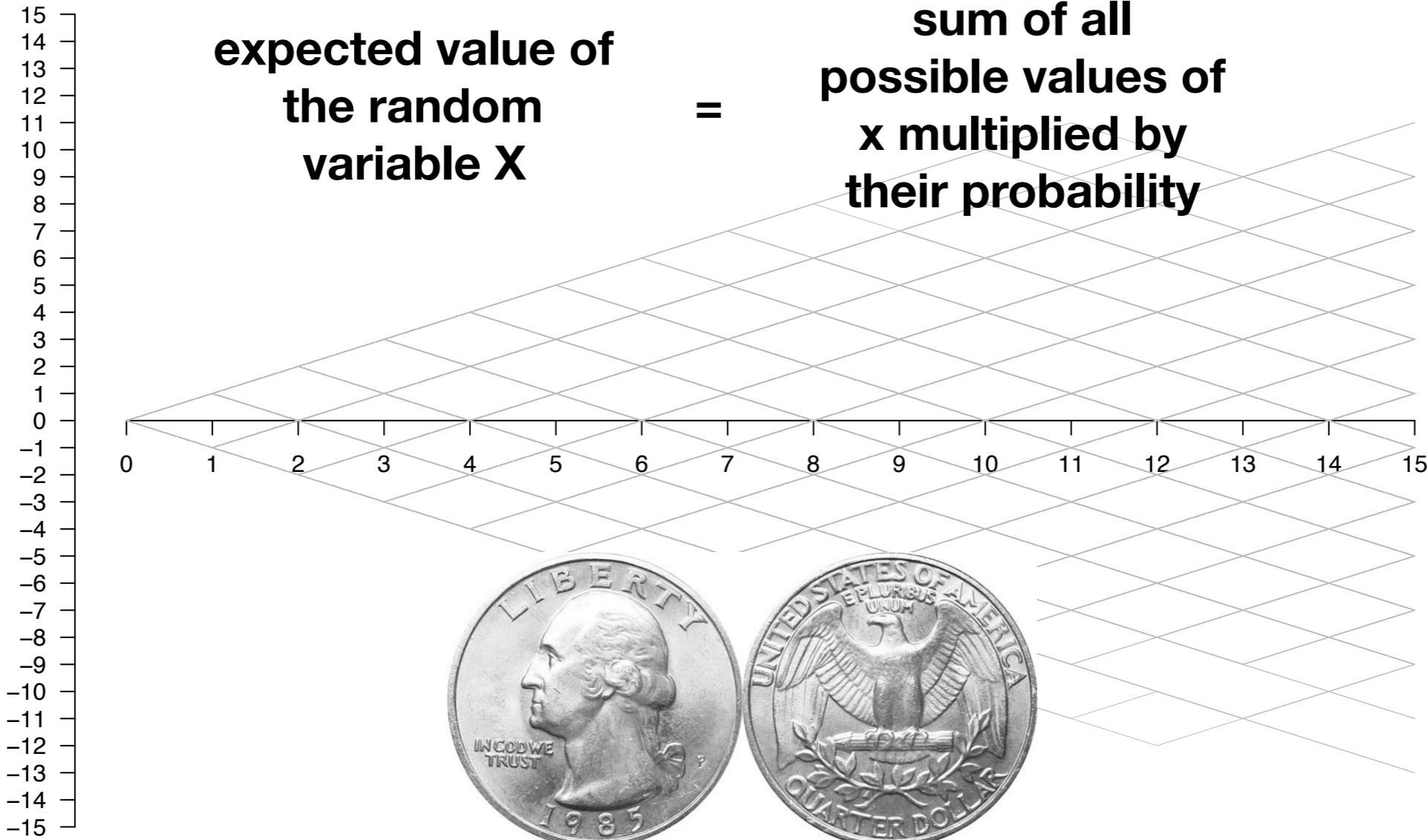


**expected value of
the random
variable X**

=

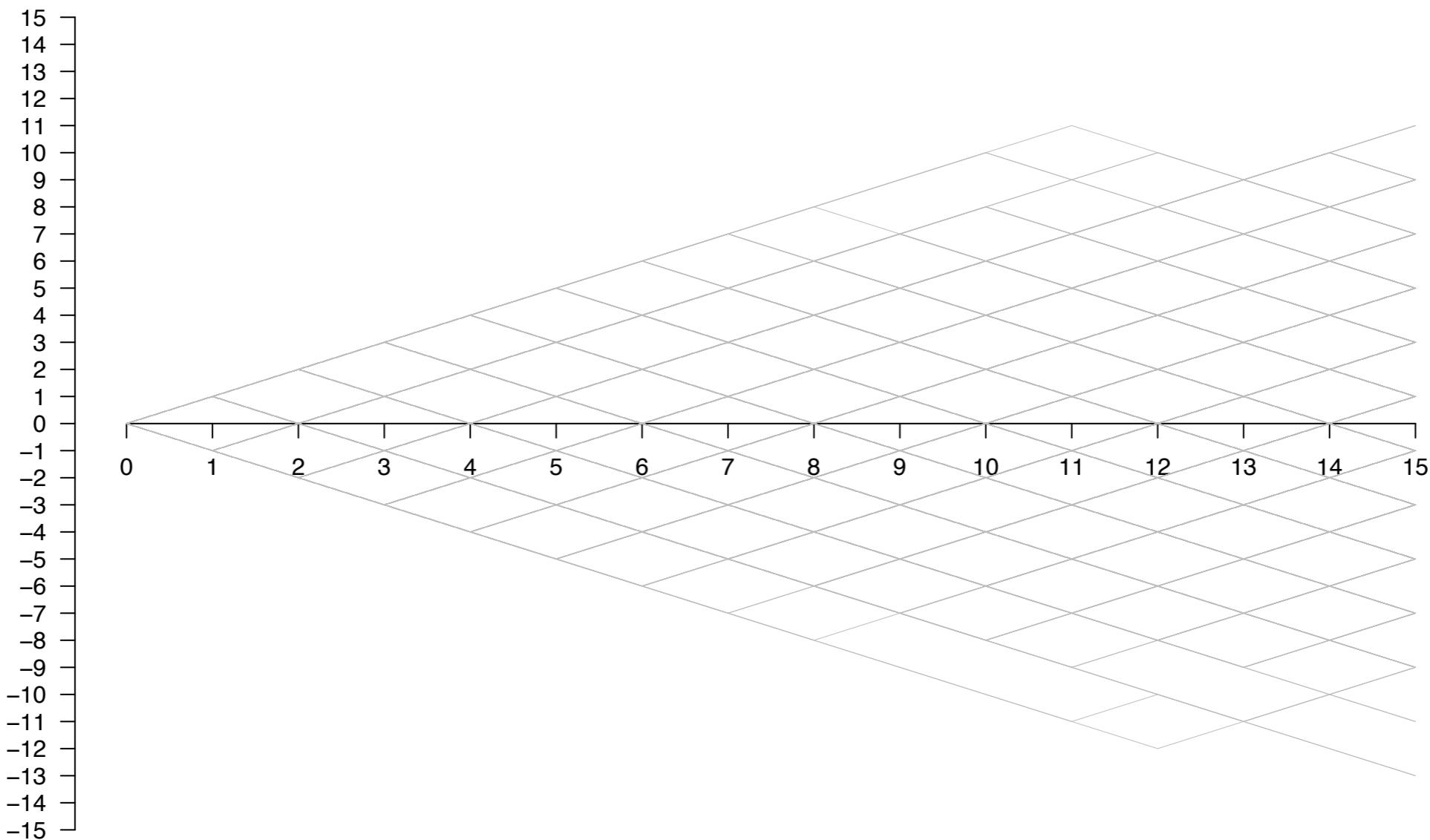
**sum of all
possible values of
 x multiplied by
their probability**

$$\mathbb{E}[X] = \sum_{i=1}^n x_i p_i$$



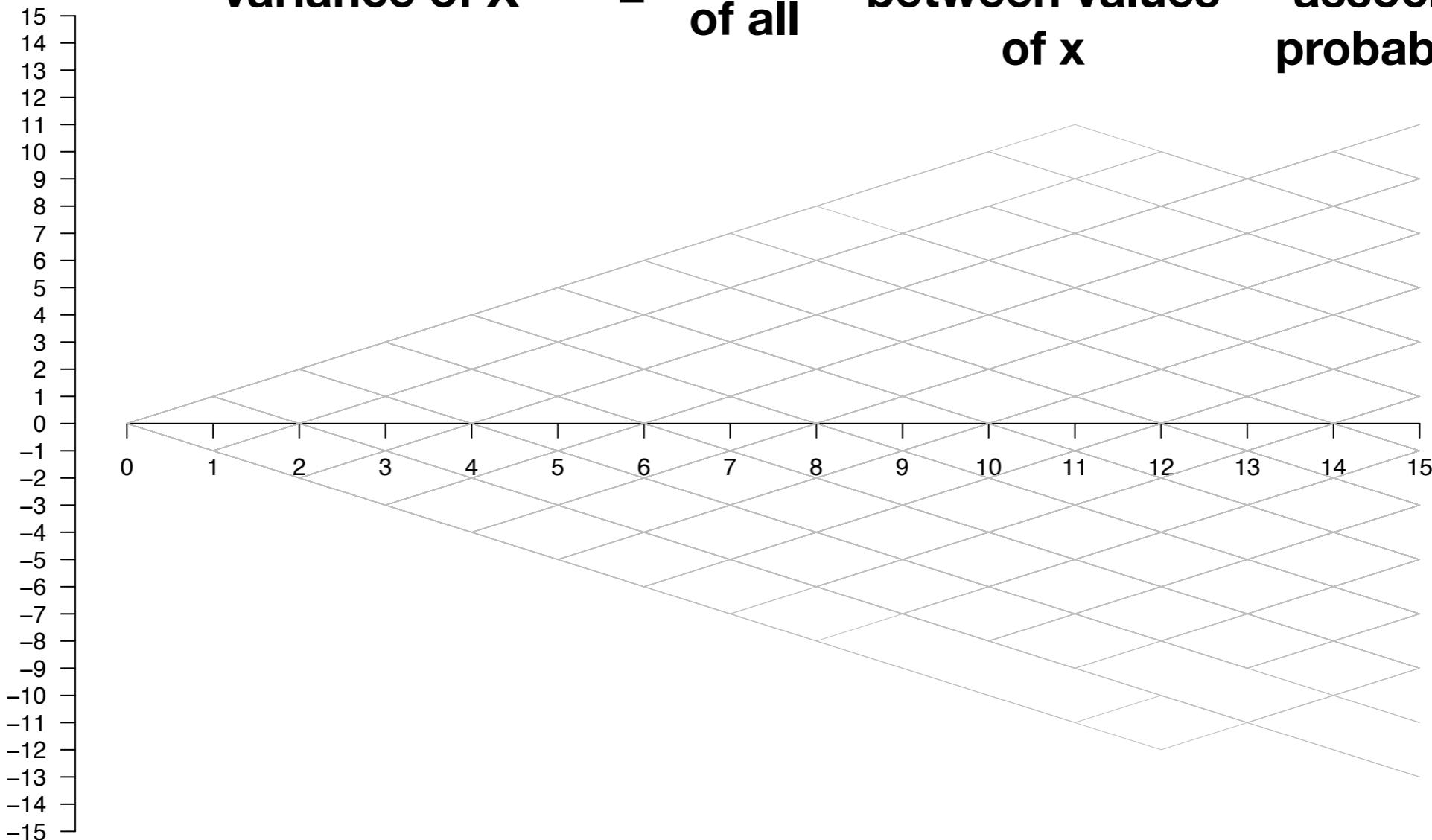
x	+1	-1
p	0.5	0.5

$$Var(X) = \sum_{i=1}^n (x_i - \mathbb{E}[X])^2 p_i$$



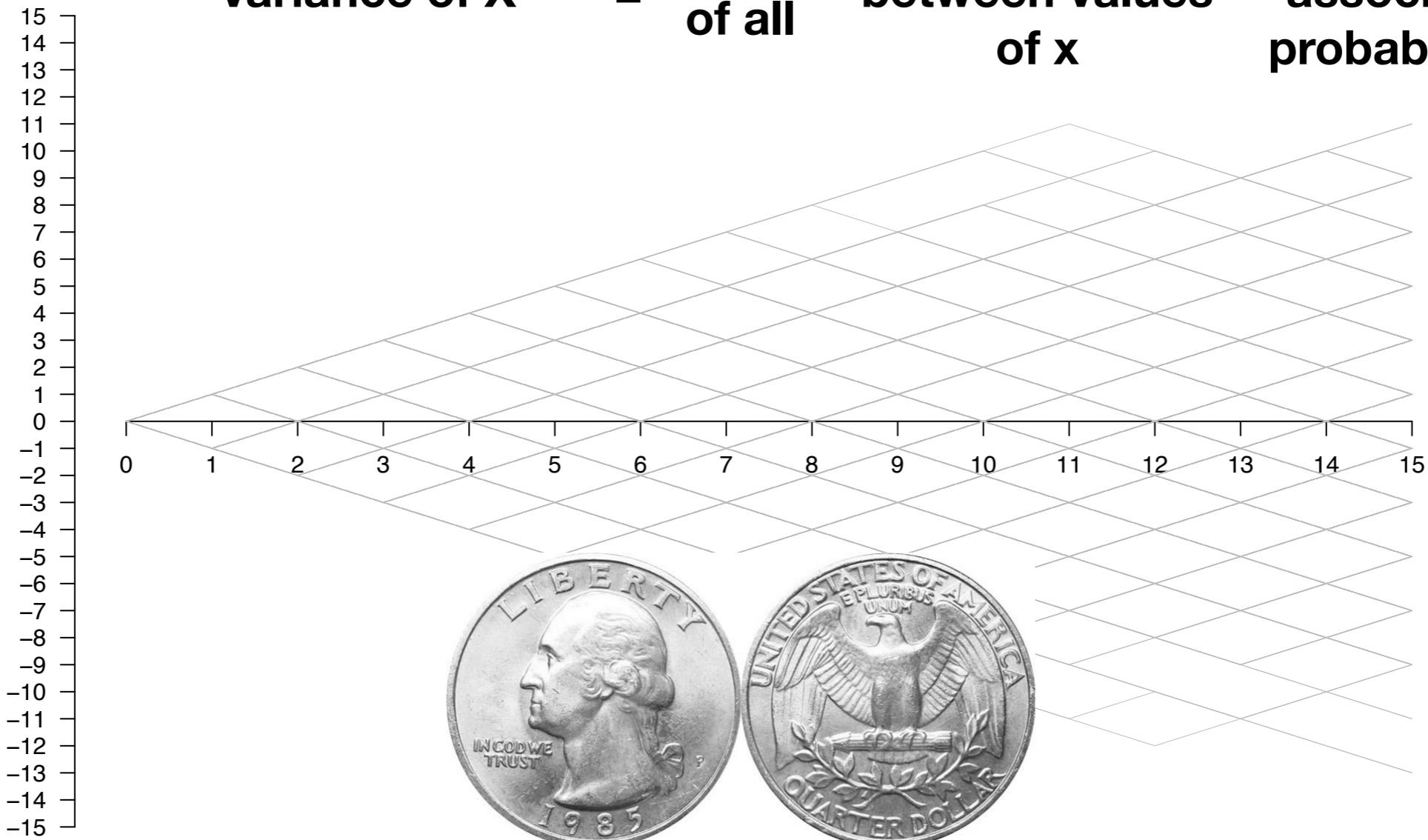
$$Var(X) = \sum_{i=1}^n (x_i - \mathbb{E}[X])^2 p_i$$

variance of X = **Sum of all** **squared diffs between values of x** **Multiplied by associated probabilities**



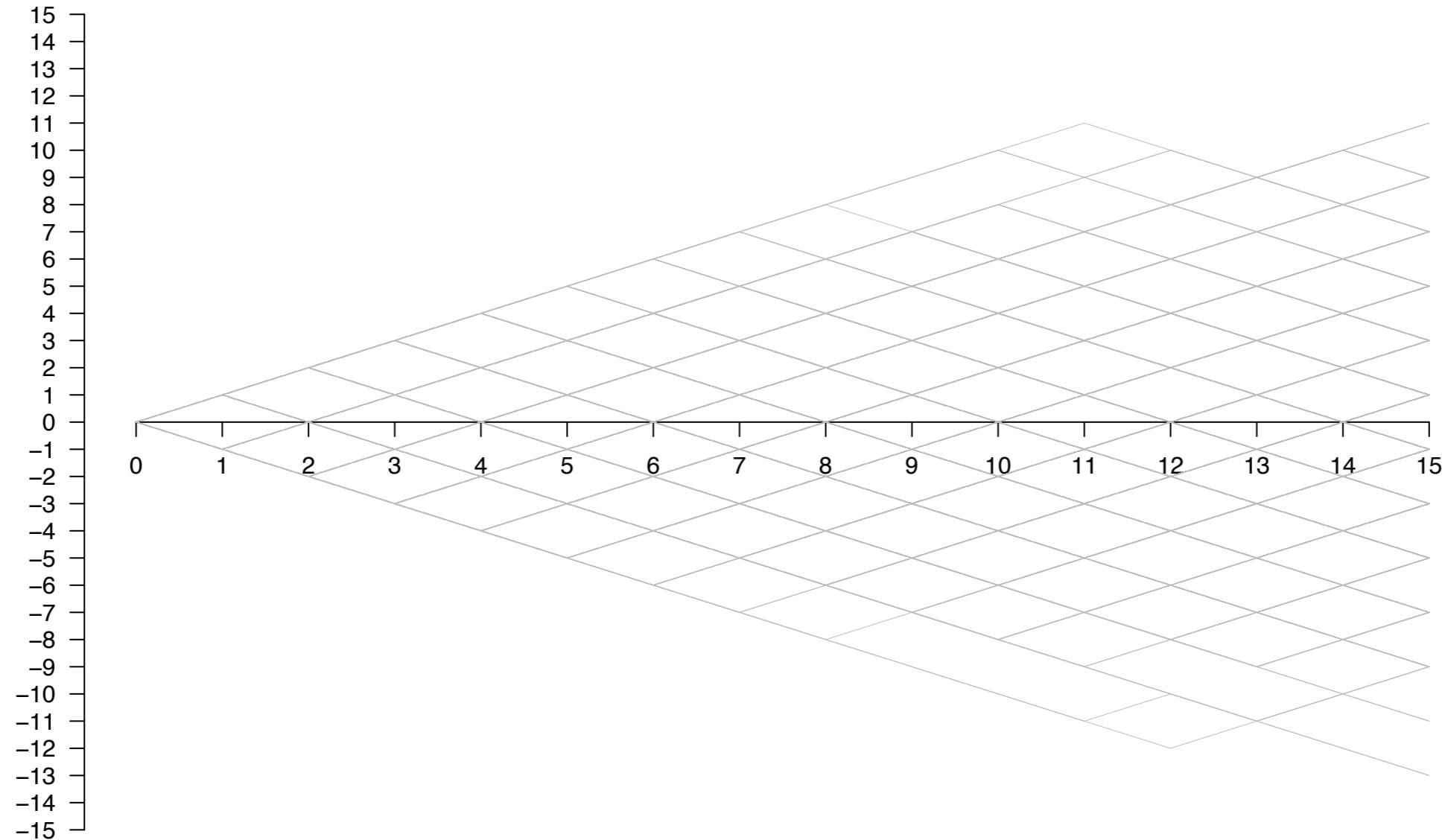
$$Var(X) = \sum_{i=1}^n (x_i - \mathbb{E}[X])^2 p_i$$

variance of X = **Sum of all** **squared diffs between values of x** **Multiplied by associated probabilities**



x	+1	-1
p	0.5	0.5

$$Var[X_1 + X_2 + \dots + X_n] = Var[X_1] + Var[X_2] + \dots + Var[X_n]$$





+0.5



-0.5

$$\mathbb{E}[X] = \sum_{i=1}^n x_i p_i$$



+0.5



-0.5

$$Var(X) = \sum_{i=1}^n (x_i - \mathbb{E}[X])^2 p_i$$



+0.5

-0.5



+0.7



-0.3

$$\mathbb{E}[X] = \sum_{i=1}^n x_i p_i$$



+0.7



-0.3

$$Var(X) = \sum_{i=1}^n (x_i - \mathbb{E}[X])^2 p_i$$



+0.7

-0.3

continuous random walks

likelihoods of random walks

likelihoods of random walks

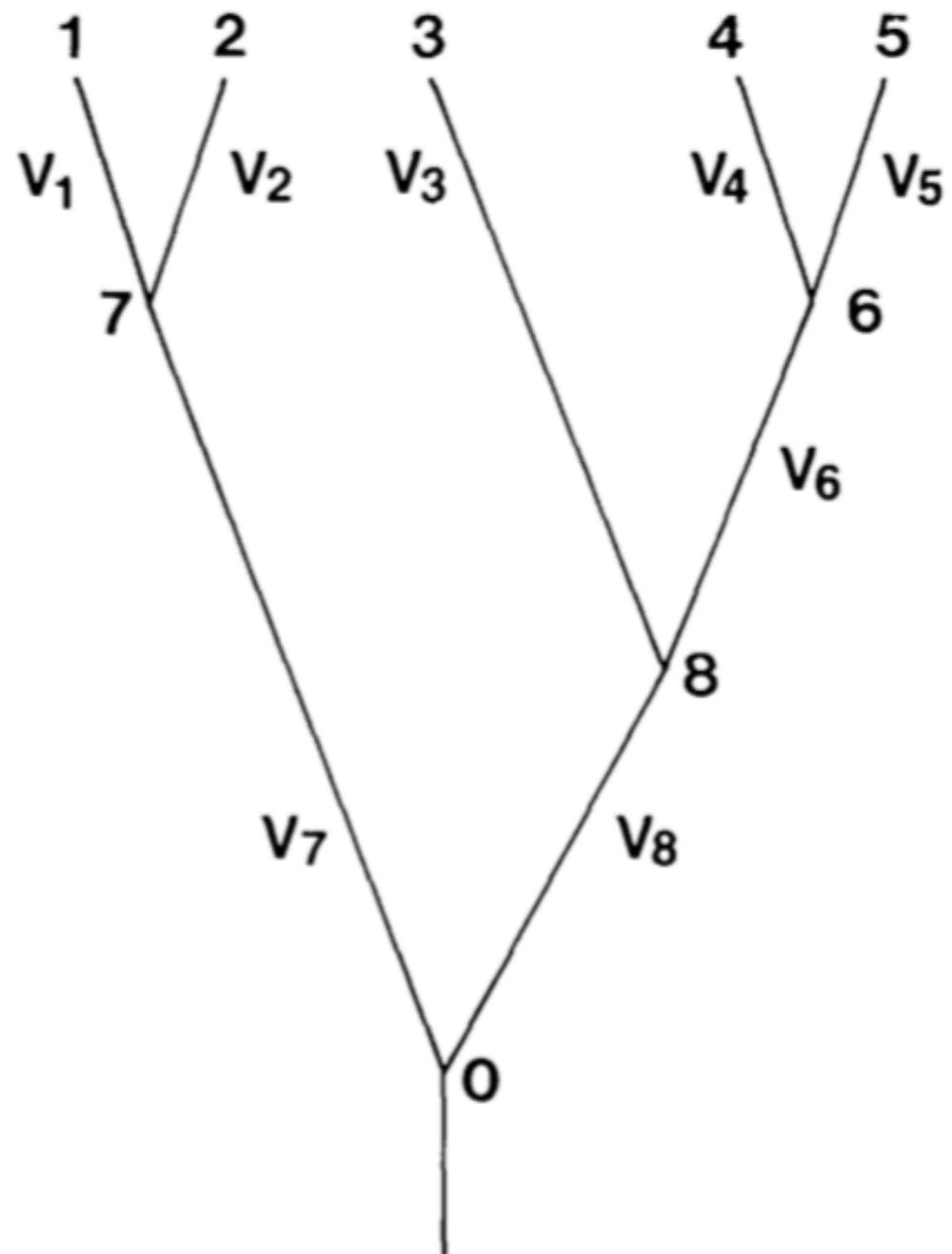
$$f(x|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{(x-\mu)^2}{2\sigma^2}}$$

likelihoods of random walks

$$f(x|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{(x-\mu)^2}{2\sigma^2}}$$

$$\mathcal{L}(X|\mu, \sigma^2) = \prod_{i=1}^n \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{(x_i-\mu)^2}{2\sigma^2}}$$

Independent contrasts



THE FOUR CONTRASTS EXTRACTED FROM THE PHYLOGENY
SHOWN IN FIGURE 9, EACH WITH ITS VARIANCE, ALL
COMPUTED USING STEPS 1-4 IN THE TEXT

CONTRAST	VARIANCE
$X_1 - X_2$	$v_1 + v_2$
$X_4 - X_5$	$v_4 + v_5$
$X_3 - X_6$	$v_3 + v'_6$
$X_7 - X_8$	$v'_7 + v'_8$

where

$$X_6 = \frac{v_4 X_5 + v_5 X_4}{v_4 + v_5}$$

$$v'_6 = v_6 + v_4 \, v_5 / (v_4 + v_5)$$

$$X_7 = \frac{v_2 X_1 + v_1 X_2}{v_1 + v_2}$$

$$v'_7 = v_7 + v_1 \, v_2 / (v_1 + v_2)$$

$$X_8 = \frac{v'_6 X_3 + v_3 X_6}{v_3 + v_6}$$

$$v'_8 = v'_7 + v_3 \, v'_6 / (v_3 + v'_6)$$

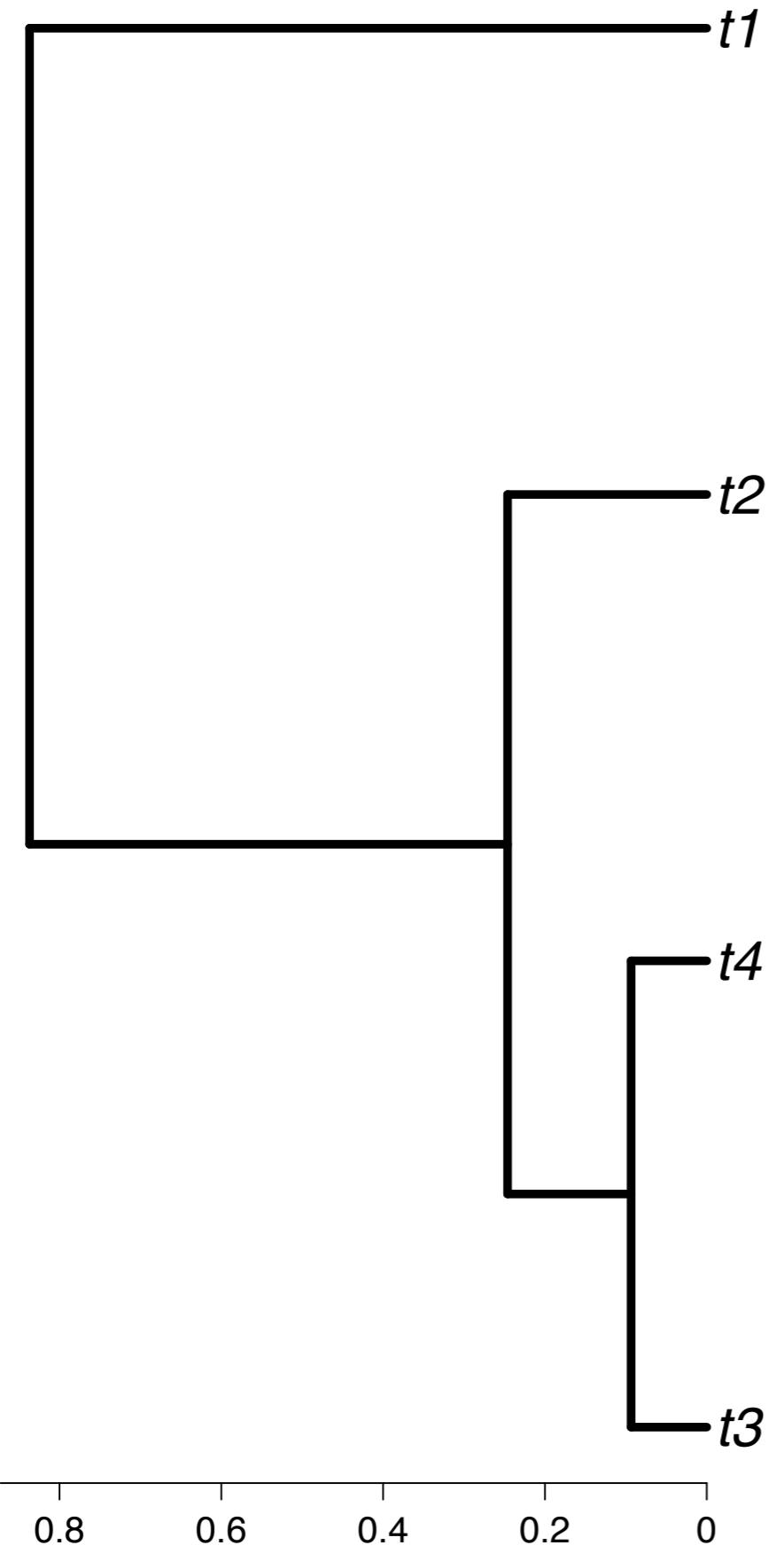
likelihoods of random walks with a covariance structure - the multivariate normal distribution

$$f(x_1, x_2, \dots, x_k) = \frac{e^{-0.5[\mathbf{x}-\boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1} (\mathbf{x}-\boldsymbol{\mu})]}{\sqrt{(2\pi)^k \det(\boldsymbol{\Sigma})}}$$

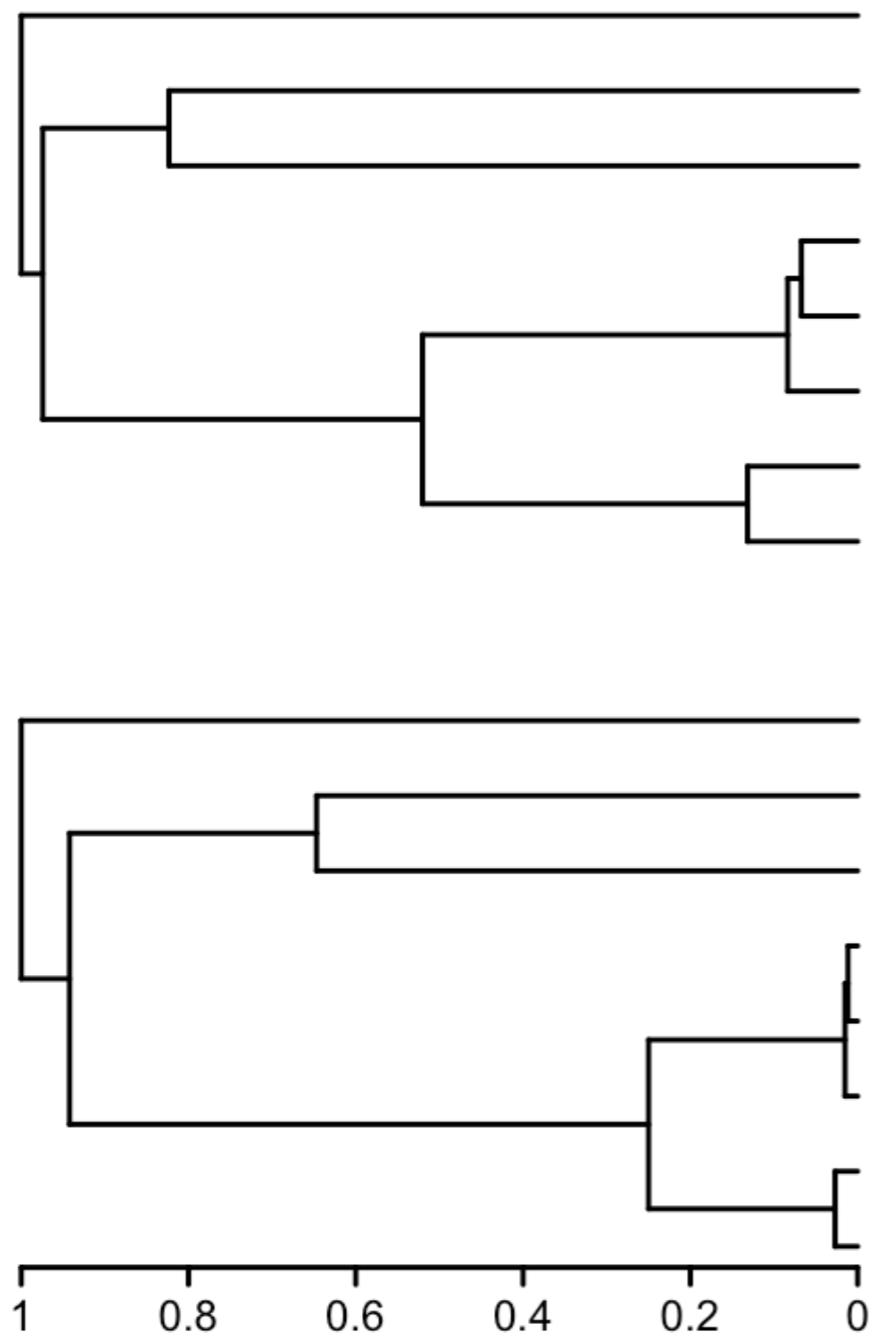
likelihoods of random walks with a covariance structure - the multivariate normal distribution

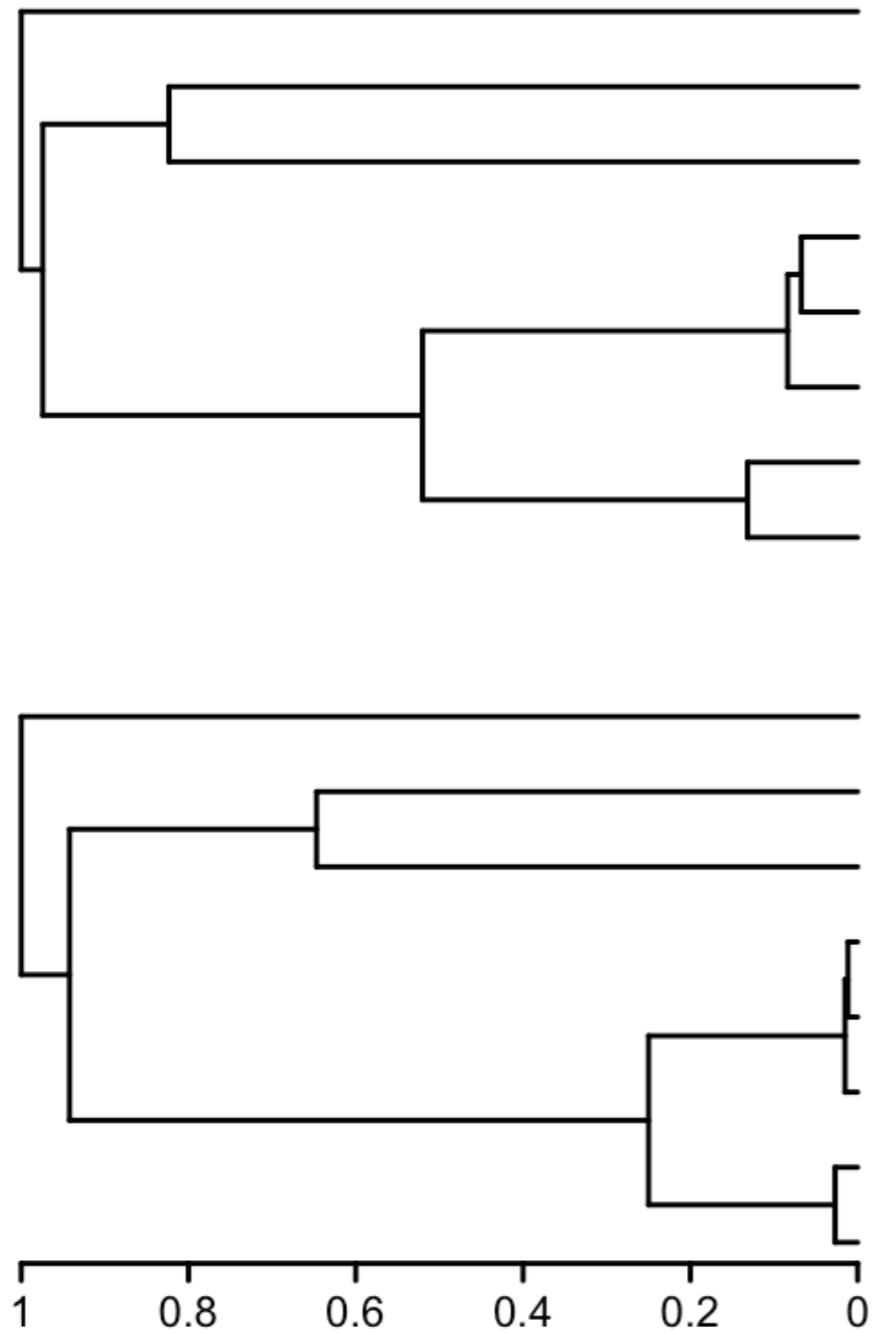
$$f(x_1, x_2, \dots, x_k) = \frac{e^{-0.5[\mathbf{x}-\boldsymbol{\mu})^T \boldsymbol{\Sigma}^{-1} (\mathbf{x}-\boldsymbol{\mu})]}}{\sqrt{(2\pi)^k \det(\boldsymbol{\Sigma})}}$$

$$f(x|\mu, \sigma^2) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{\frac{(x-\mu)^2}{2\sigma^2}}$$

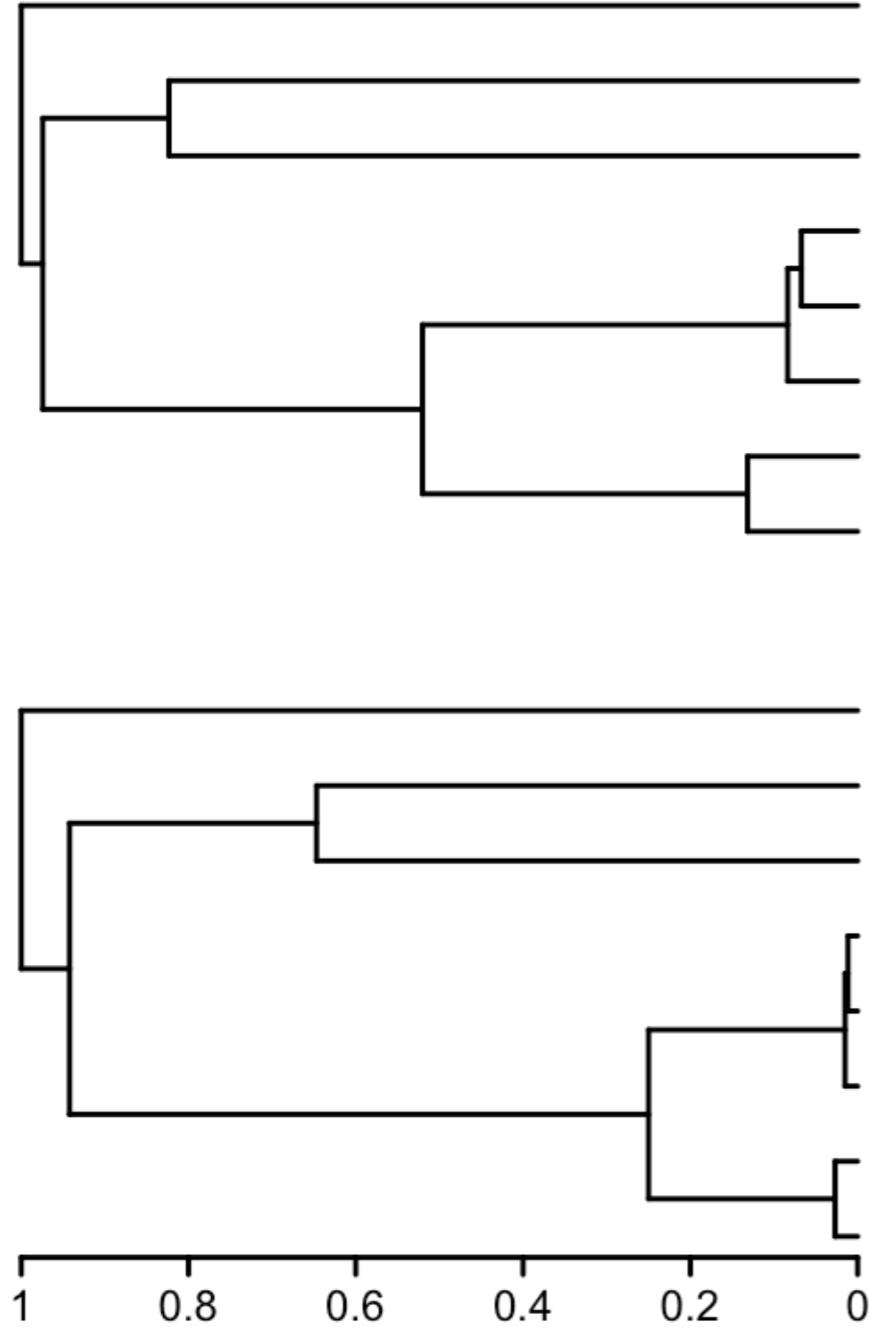


	t_3	t_4	t_2	t_1
t_3	0.84	0.74	0.59	0.00
t_4	0.74	0.84	0.59	0.00
t_2	0.59	0.59	0.84	0.00
t_1	0.00	0.00	0.00	0.84



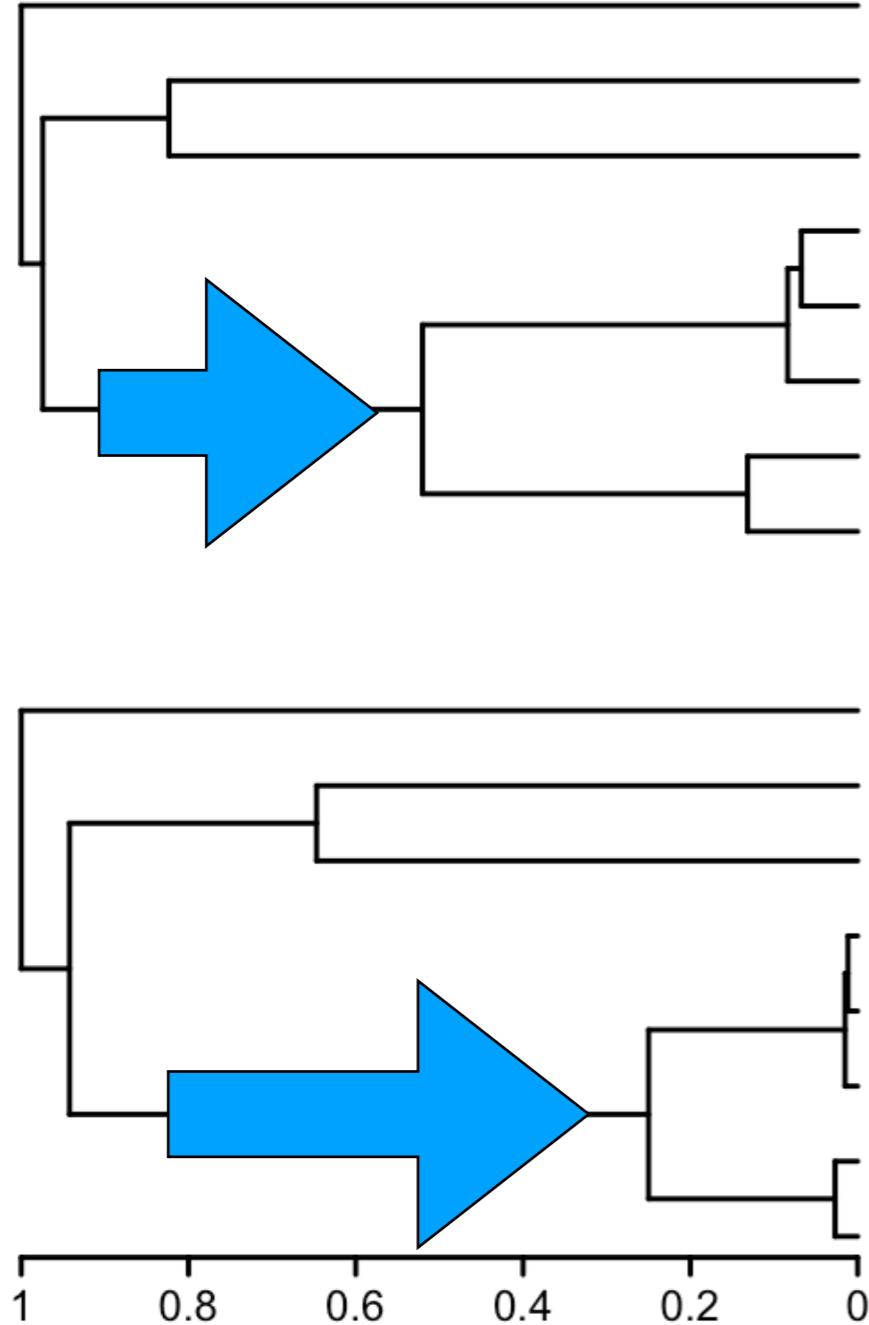


$$E(\text{disparity}) = \sigma^2 \left[\frac{1}{N} \text{tr}(\mathbf{C}) - \frac{1}{N^2} \mathbf{1}' \mathbf{C} \mathbf{1} \right]$$



rate * independent evolution

$$E(\text{disparity}) = \sigma^2 \left[\frac{1}{N} \text{tr}(\mathbf{C}) - \frac{1}{N^2} \mathbf{1}' \mathbf{C} \mathbf{1} \right]$$

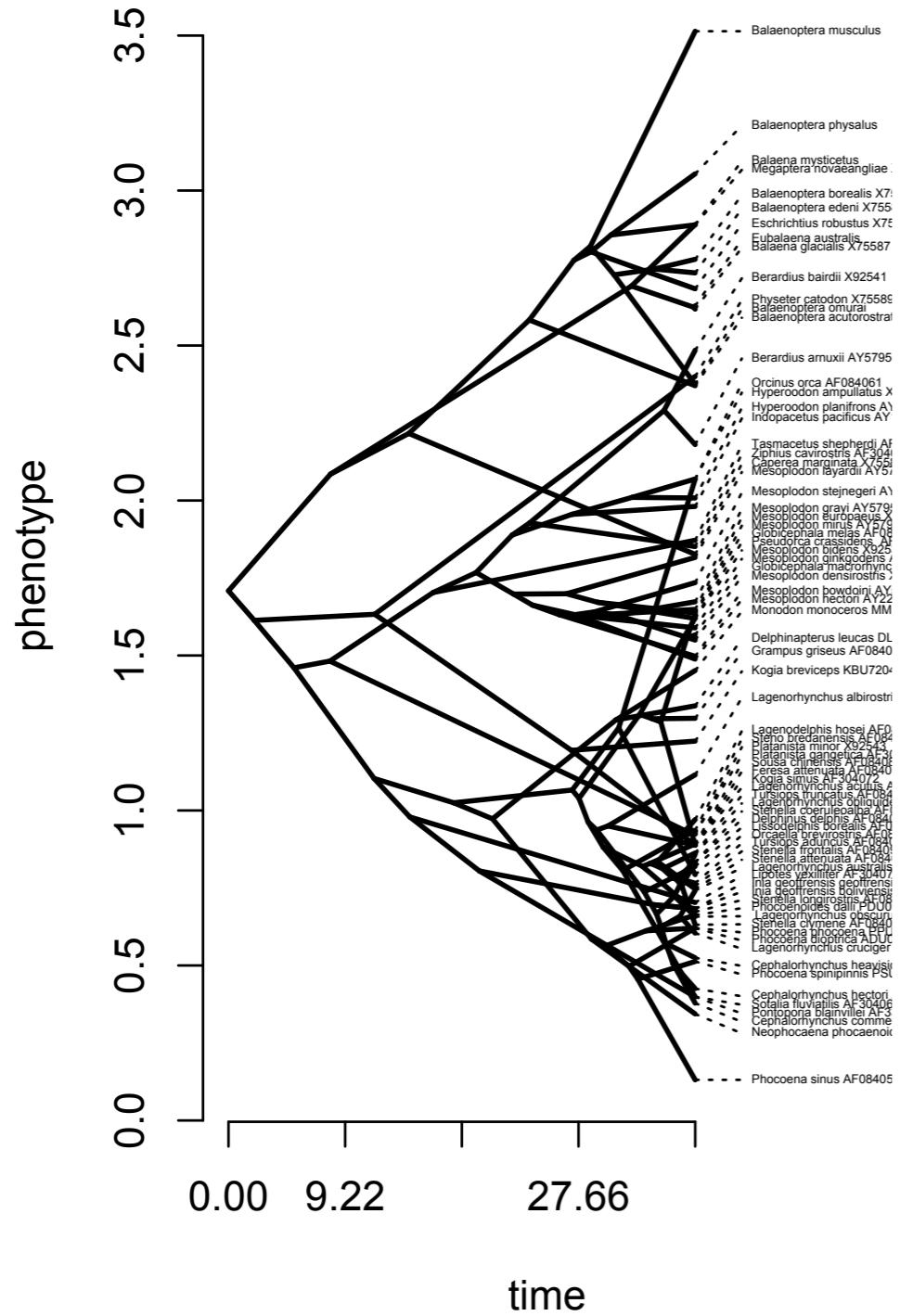


rate * independent evolution

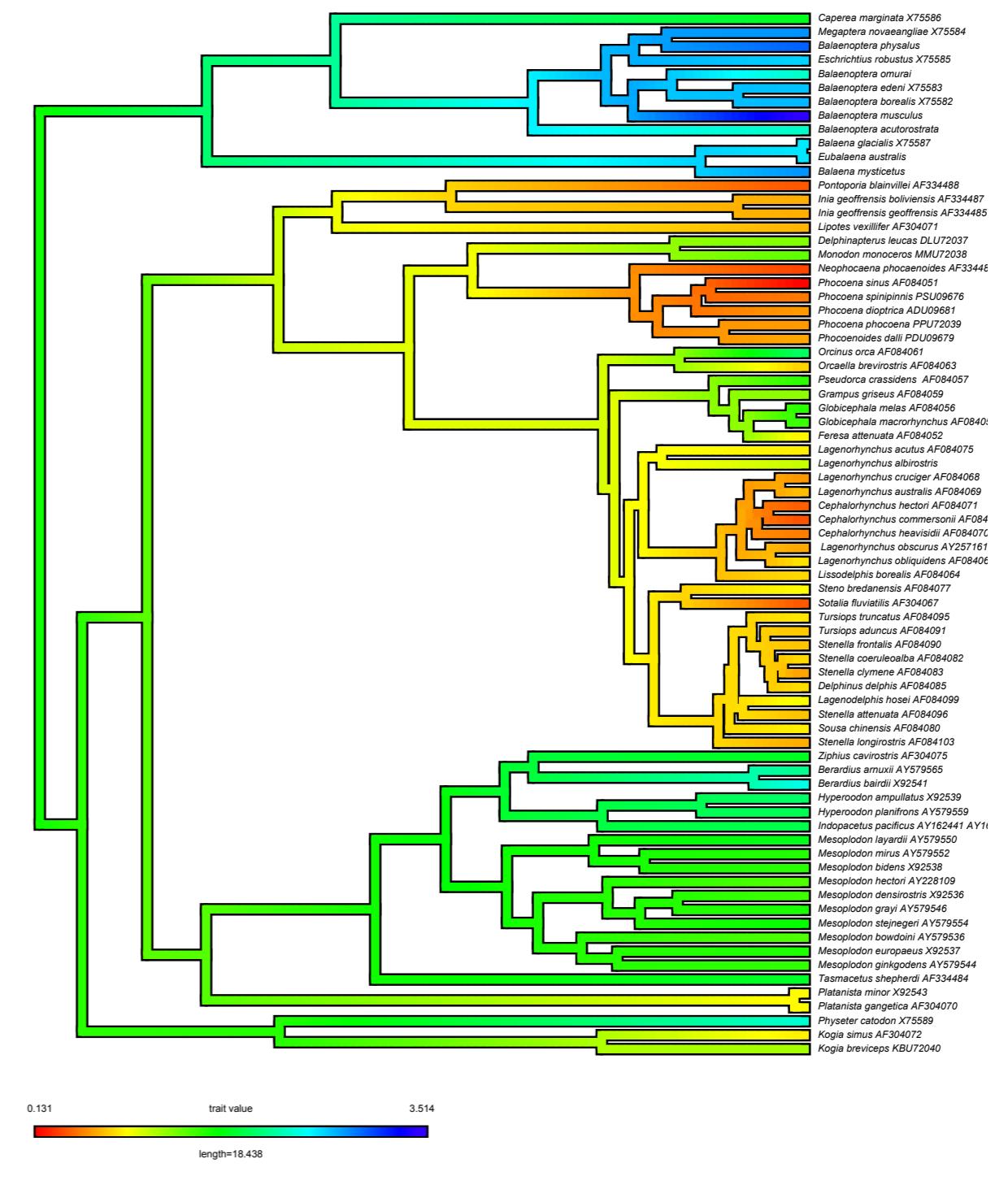
$$E(\text{disparity}) = \sigma^2 \left[\frac{1}{N} \text{tr}(\mathbf{C}) - \frac{1}{N^2} \mathbf{1}' \mathbf{C} \mathbf{1} \right]$$

**fitting a Brownian motion model to
phylogenetic data**

ancestral states

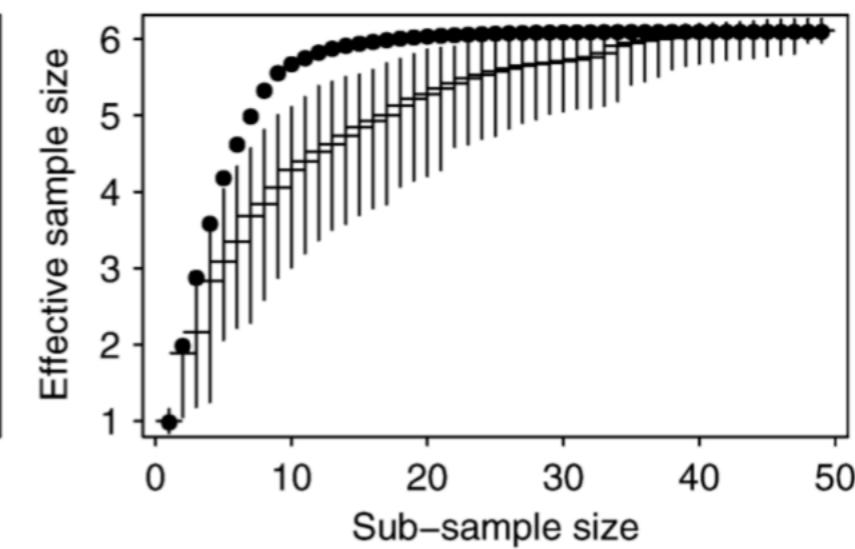
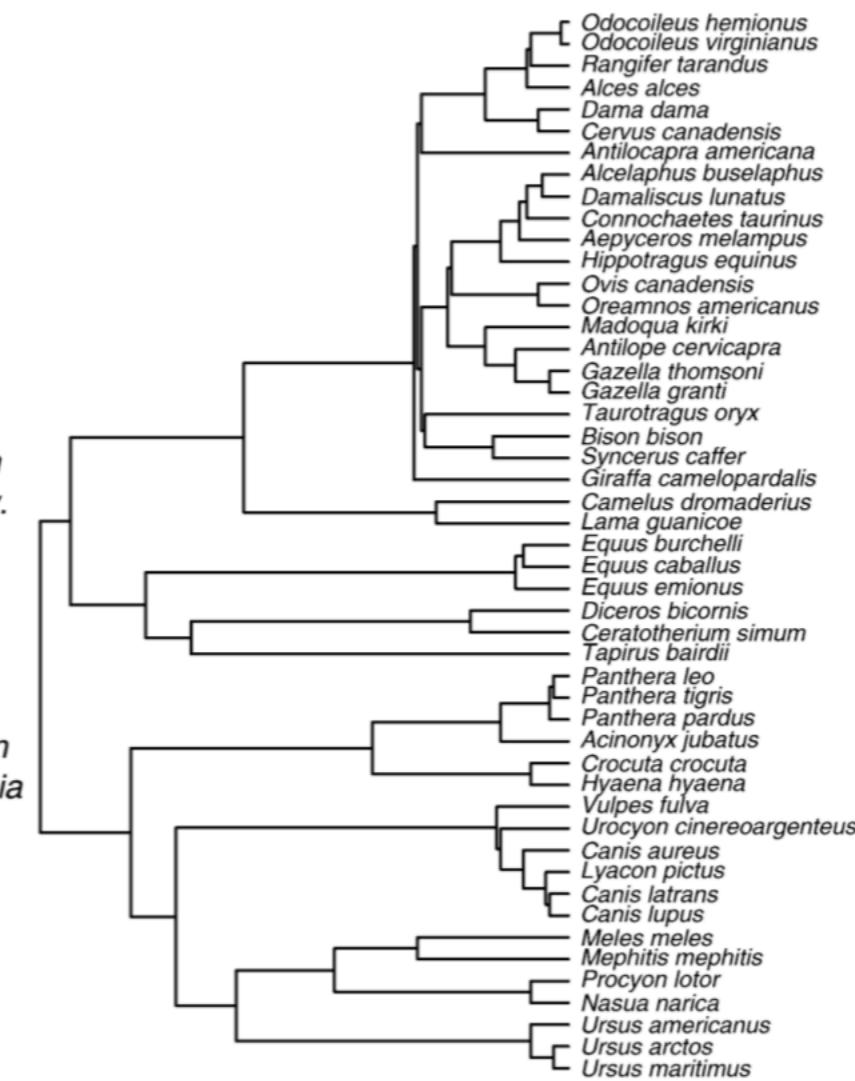
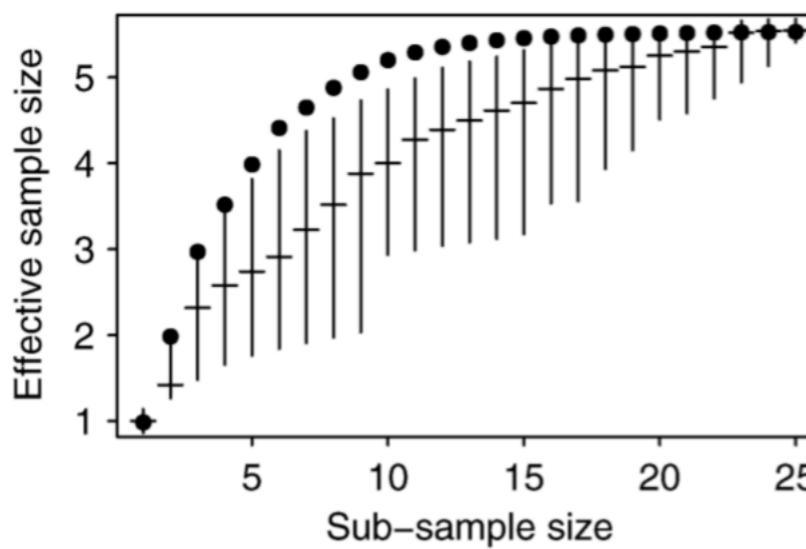
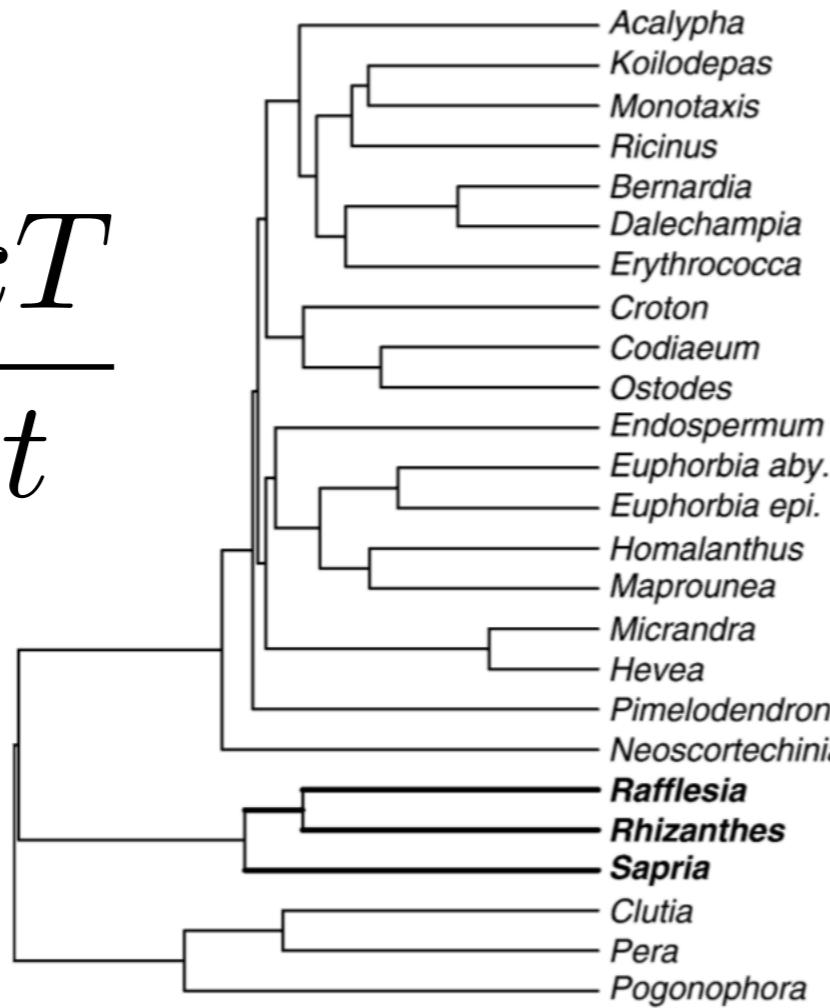


Phytools:::phenogram

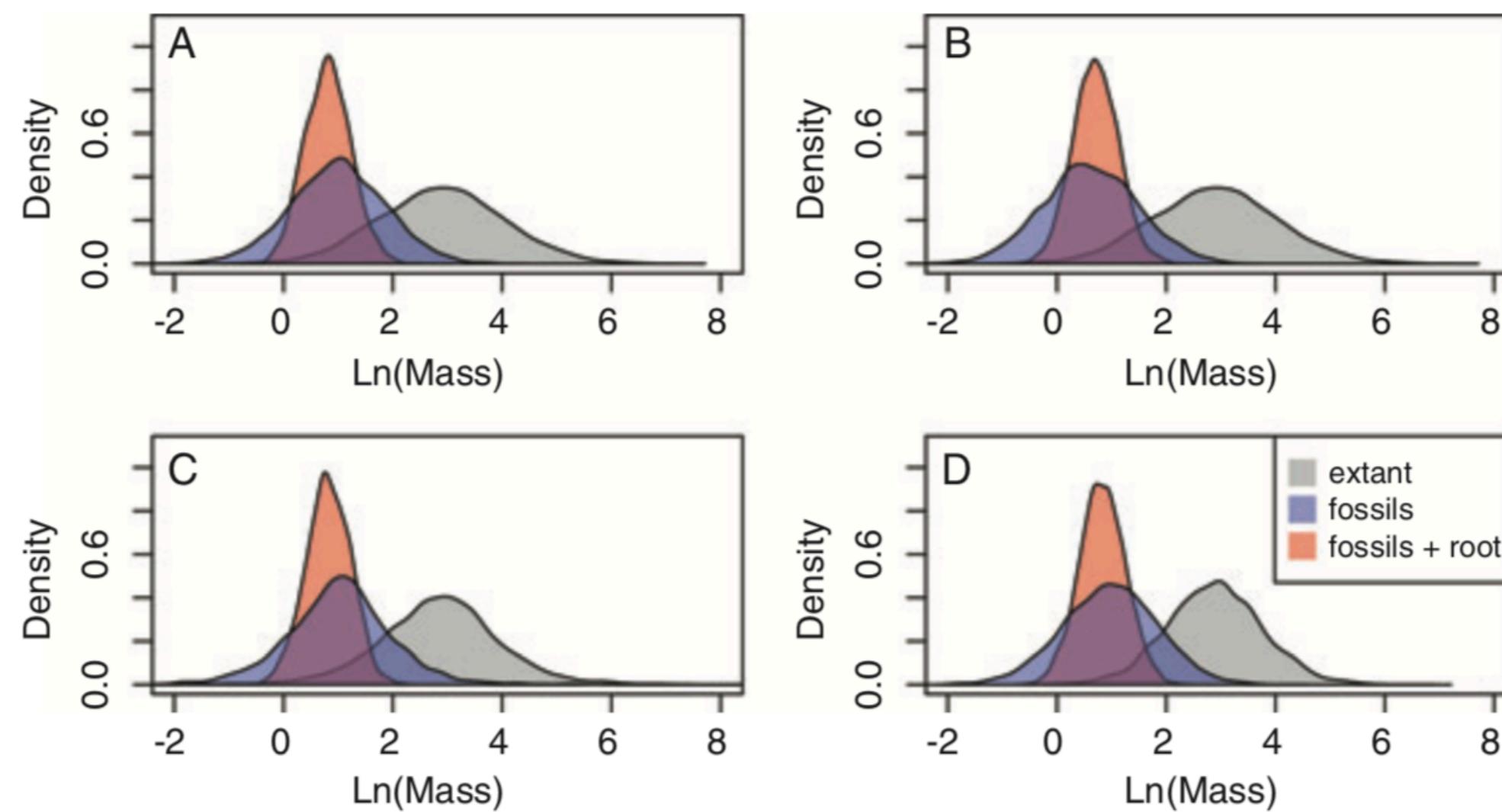


Phytools:::contmap

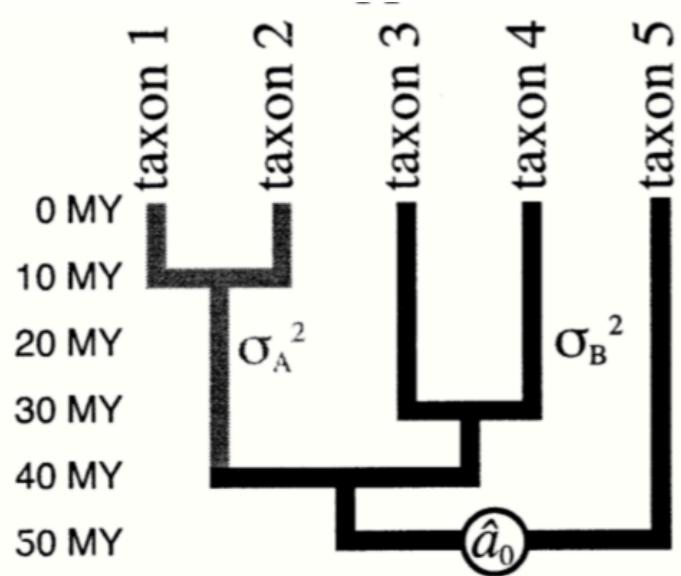
$$n_e < \frac{kT}{t}$$



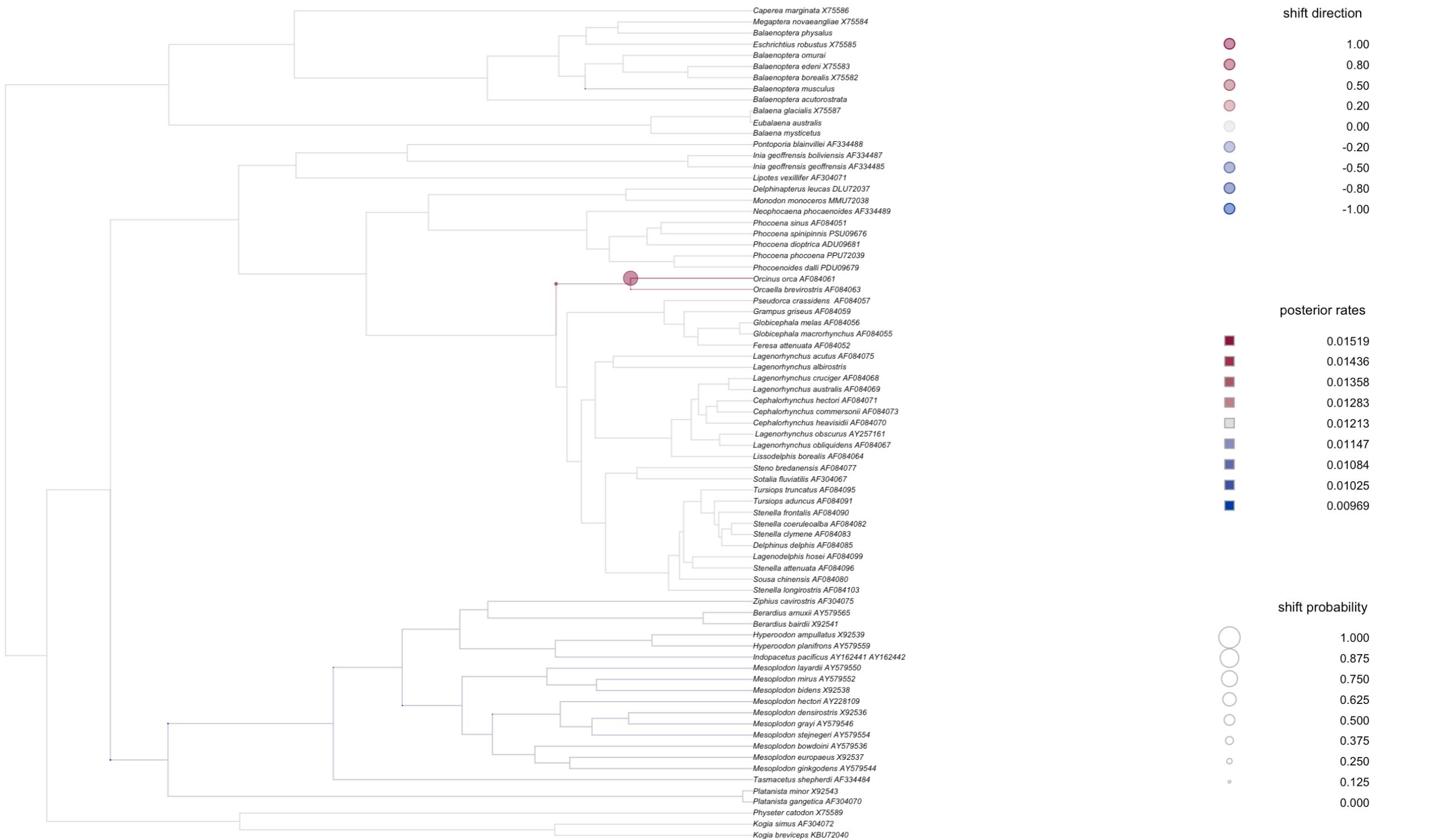
fossil data improve ancestral state estimates



extending Brownian motion

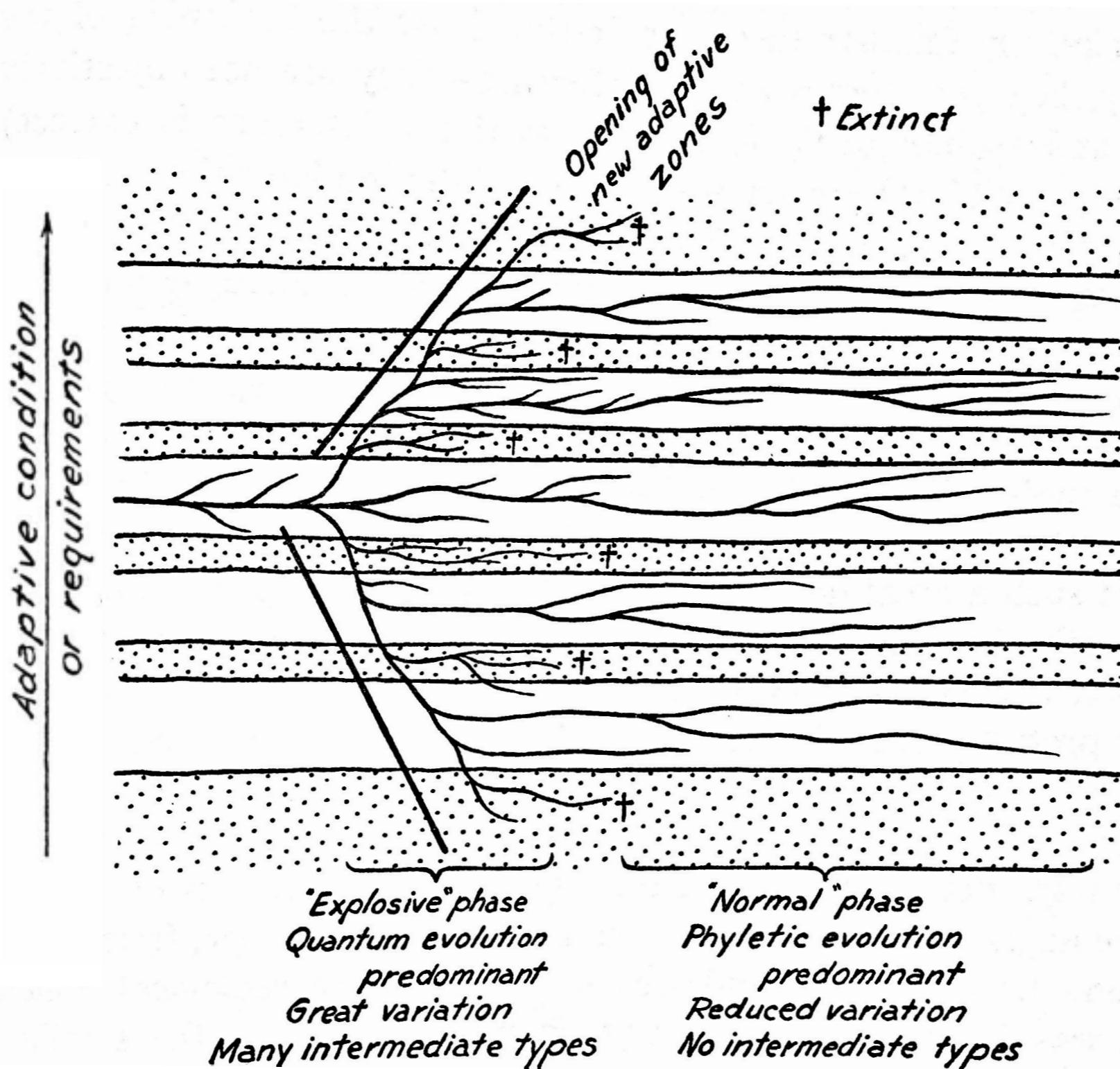


	taxon 1	taxon 2	taxon 3	taxon 4	taxon 5	$E(\mathbf{X})$
taxon 1	$40\sigma_A^2 + 10\sigma_B^2$	$30\sigma_A^2 + 10\sigma_B^2$	$10\sigma_B^2$	$10\sigma_B^2$	0	\hat{a}_0
taxon 2	$30\sigma_A^2 + 10\sigma_B^2$	$40\sigma_A^2 + 10\sigma_B^2$	$10\sigma_B^2$	$10\sigma_B^2$	0	\hat{a}_0
taxon 3	$10\sigma_B^2$	$10\sigma_B^2$	$50\sigma_B^2$	$20\sigma_B^2$	0	\hat{a}_0
taxon 4	$10\sigma_B^2$	$10\sigma_B^2$	$20\sigma_B^2$	$50\sigma_B^2$	0	\hat{a}_0
taxon 5	0	0	0	0	$50\sigma_B^2$	\hat{a}_0



geiger:::auteur

Simpson's model of "Quantum Evolution"

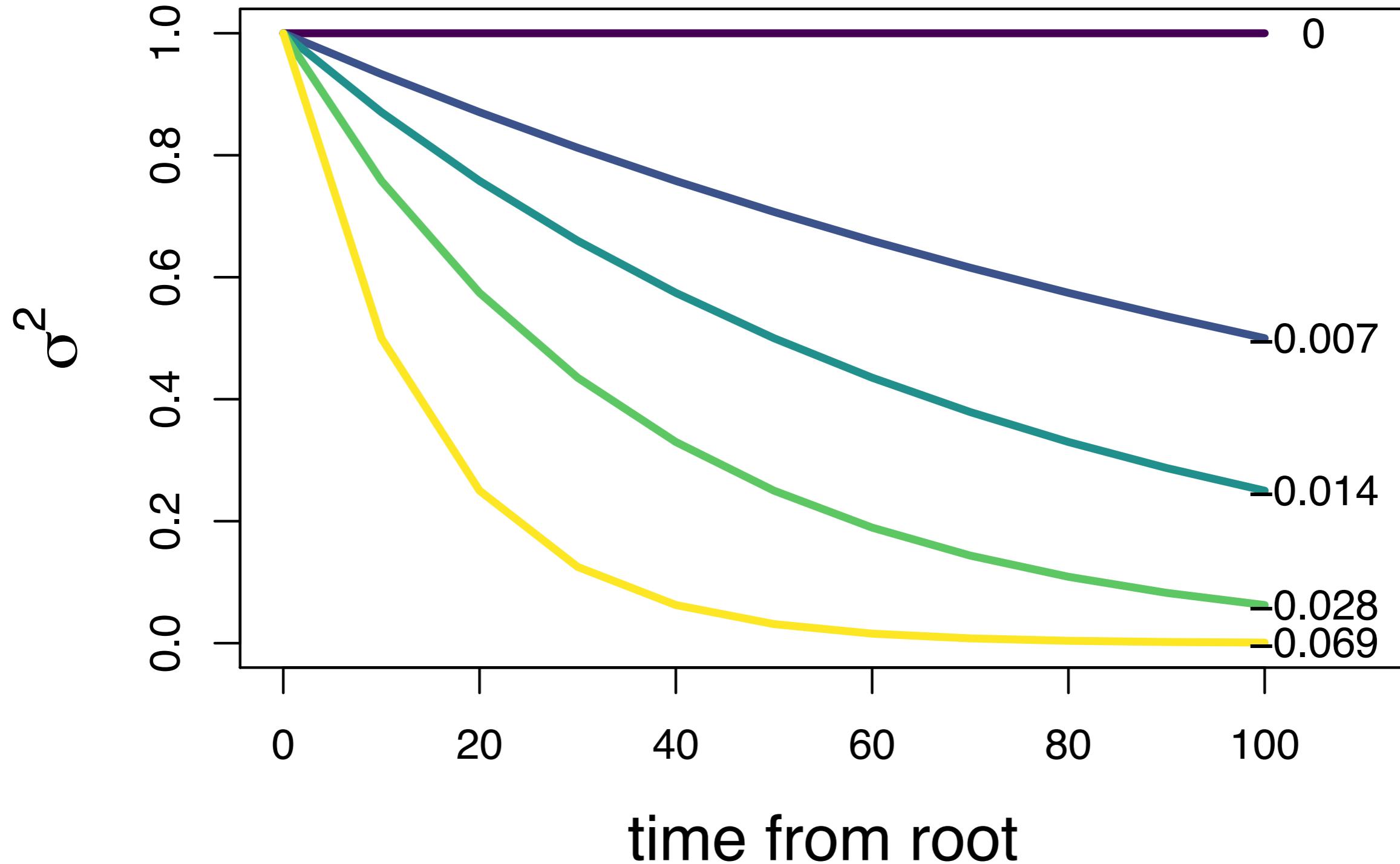


Early Bursts

$$\sigma_t^2 = \sigma_0^2 e^{rt}$$

Early Bursts

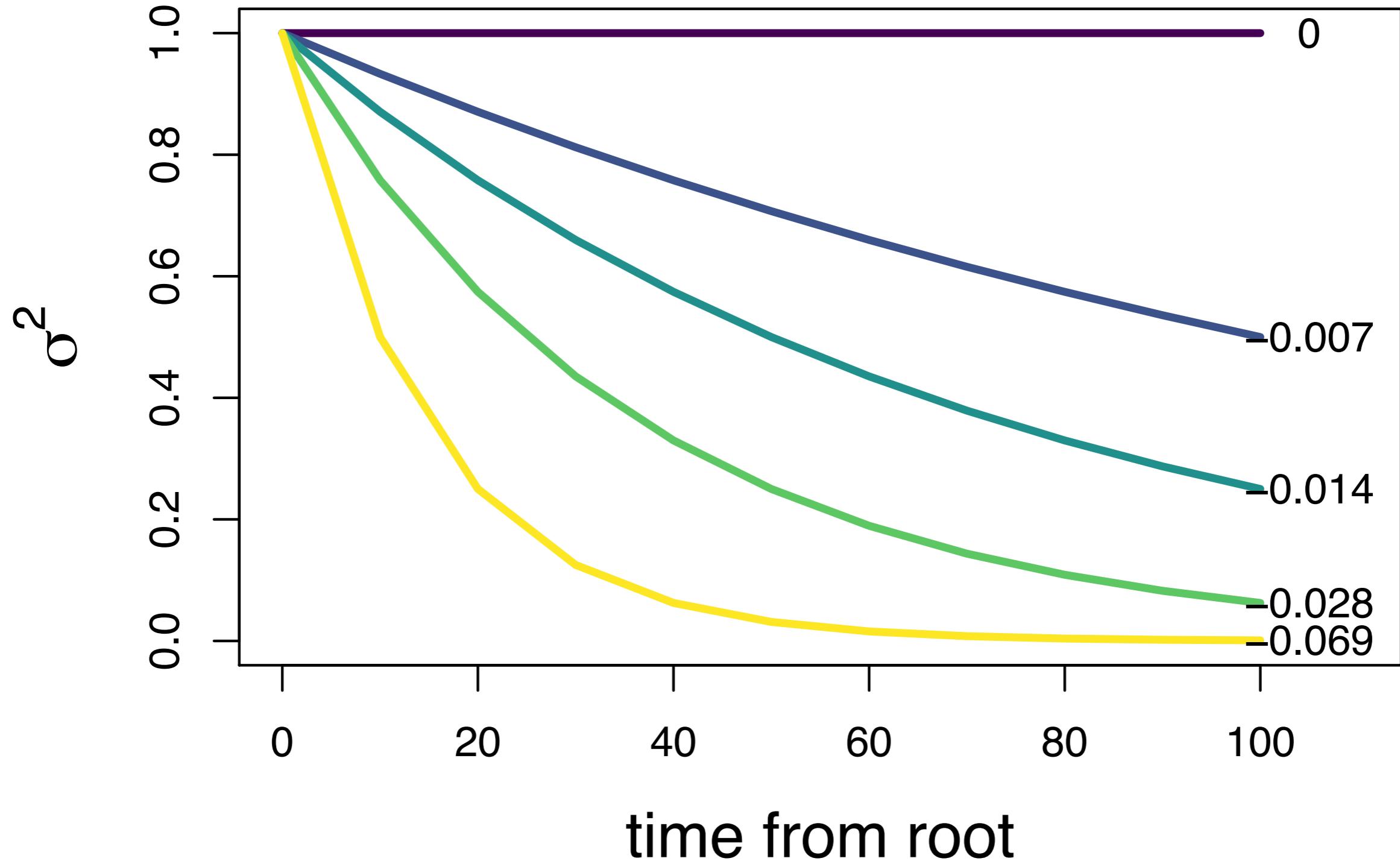
$$\sigma_t^2 = \sigma_0^2 e^{rt}$$



Early Bursts

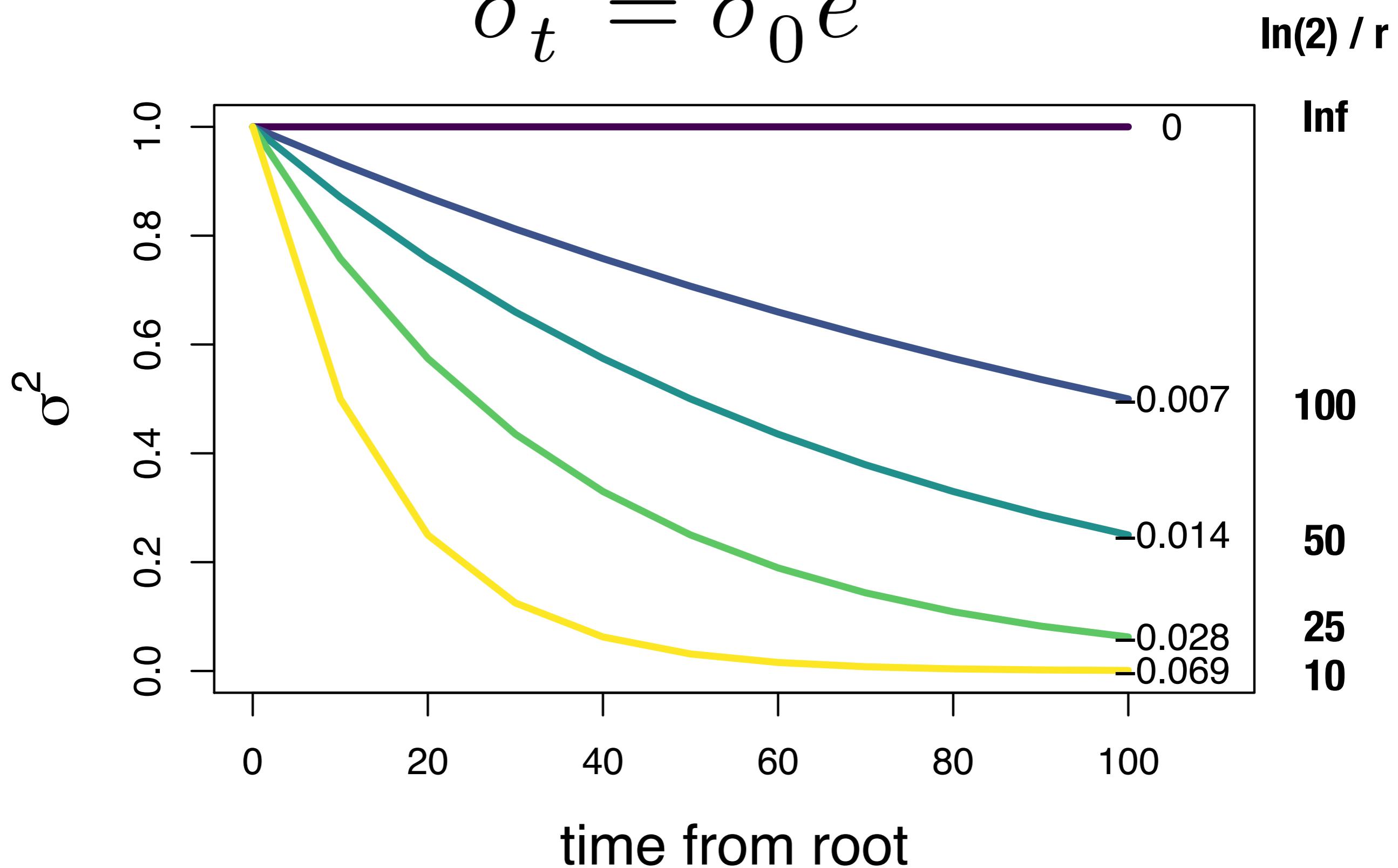
$$\sigma_t^2 = \sigma_0^2 e^{rt}$$

$\ln(2) / r$



Early Bursts

$$\sigma_t^2 = \sigma_0^2 e^{rt}$$



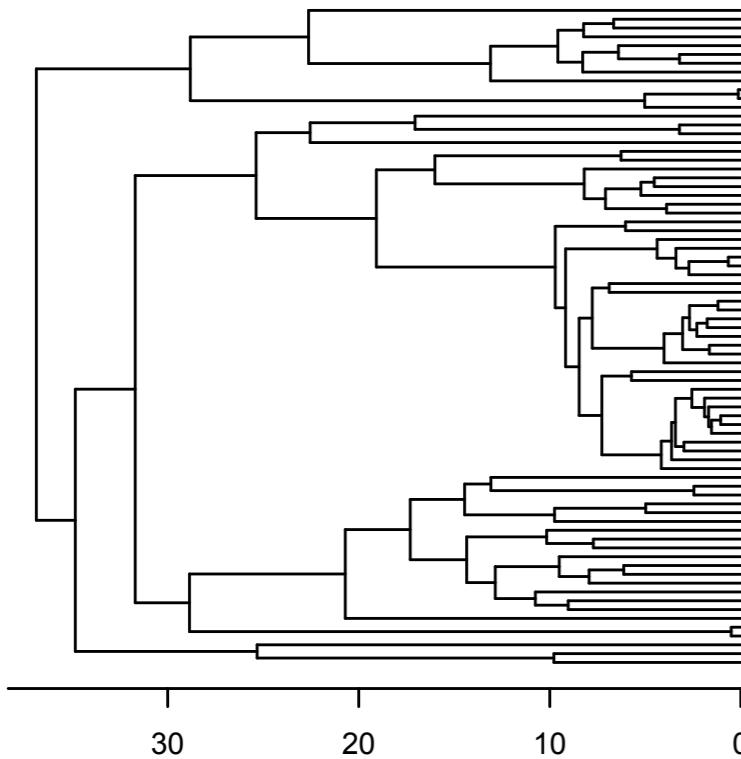
early bursts on trees

$$\begin{aligned}\mathbf{V}_{i,j} &= \sigma_0^2 * \int_0^{\mathbf{C}_{i,j}} e^{rt} d(t) \\ &= \sigma_0^2 * \frac{e^{r\mathbf{C}_{i,j}} - 1}{r}\end{aligned}$$

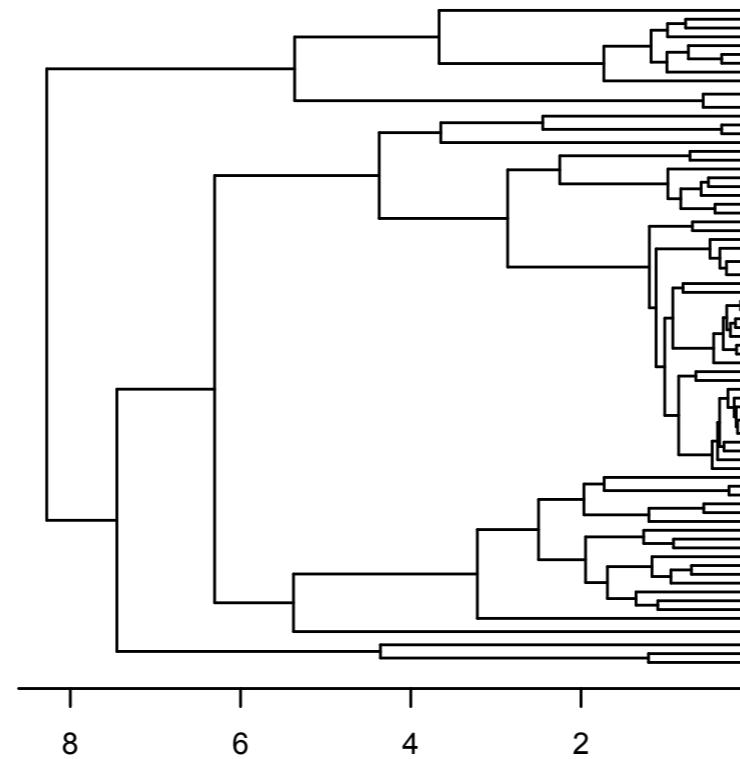
early bursts on trees

$$\mathbf{V}_{i,j} = \sigma_0^2 * \int_0^{\mathbf{C}_{i,j}} e^{rt} d(t)$$
$$= \sigma_0^2 * \frac{e^{r\mathbf{C}_{i,j}} - 1}{r}$$

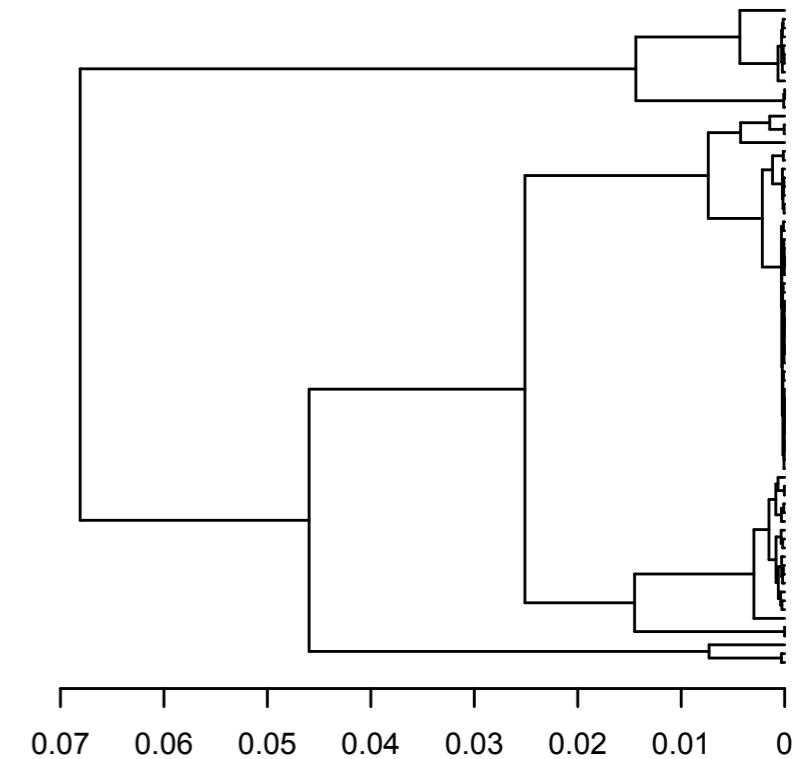
BM



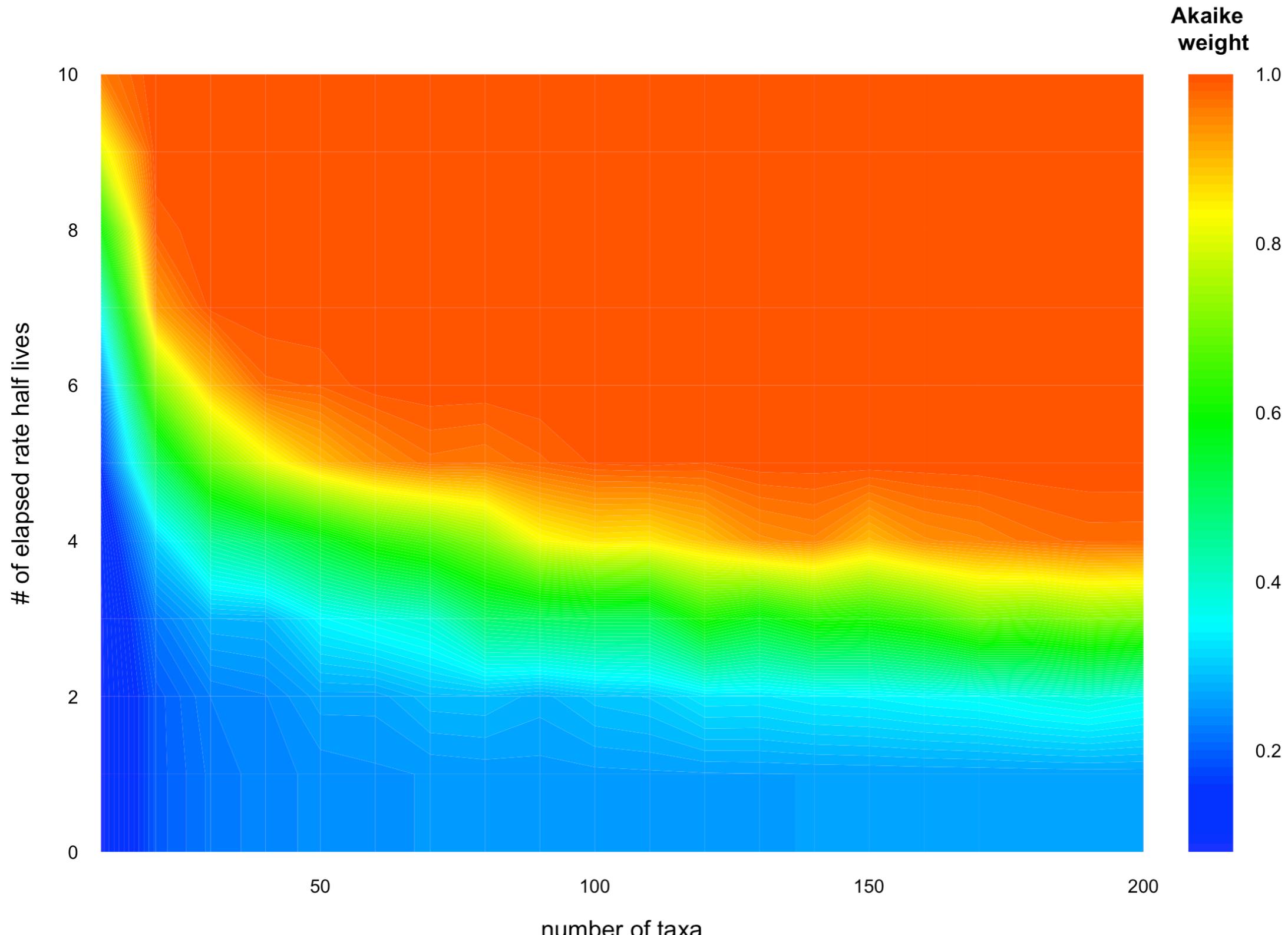
1 rate half-life



10 rate half-life

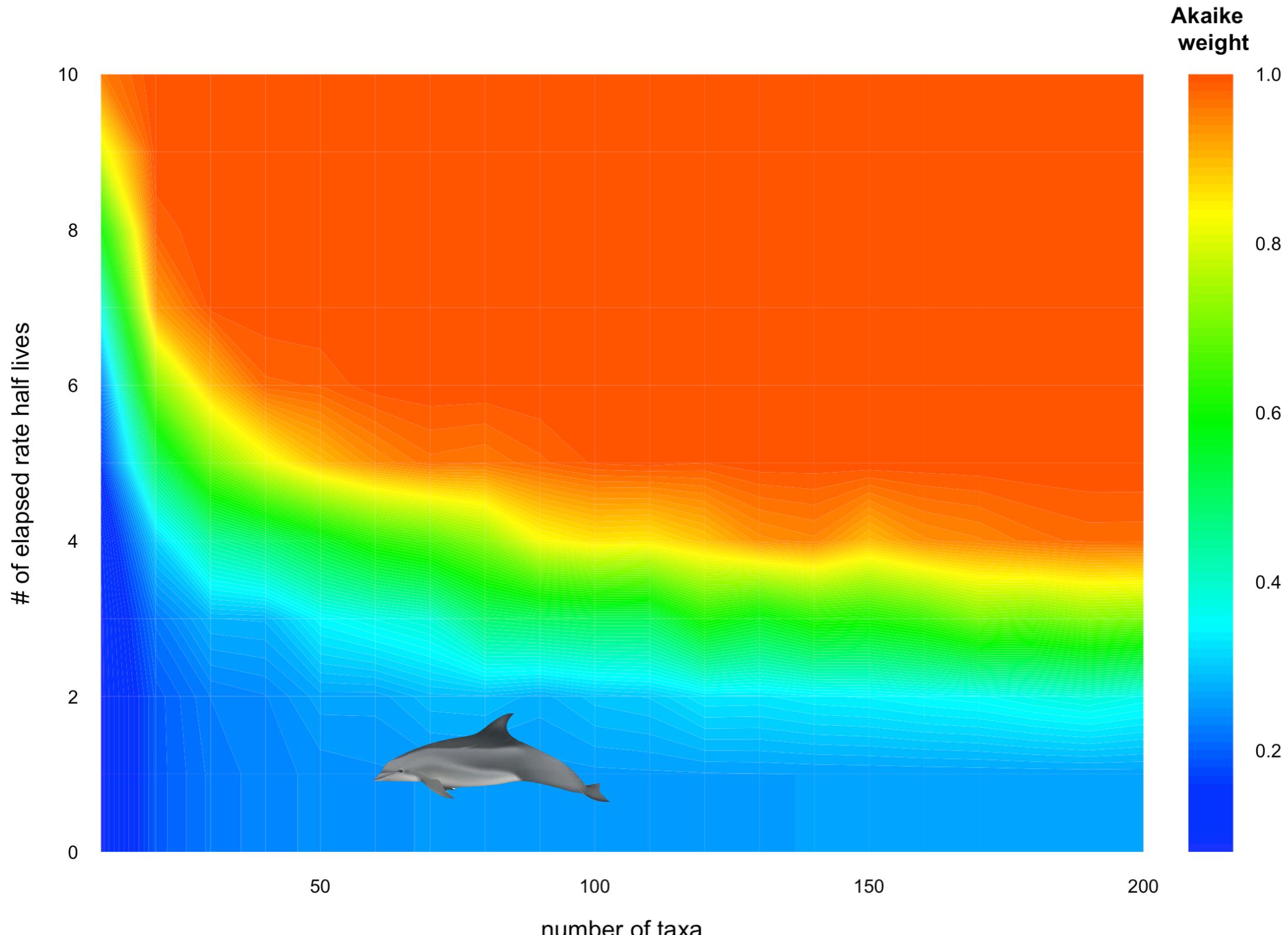


early bursts are difficult to detect*



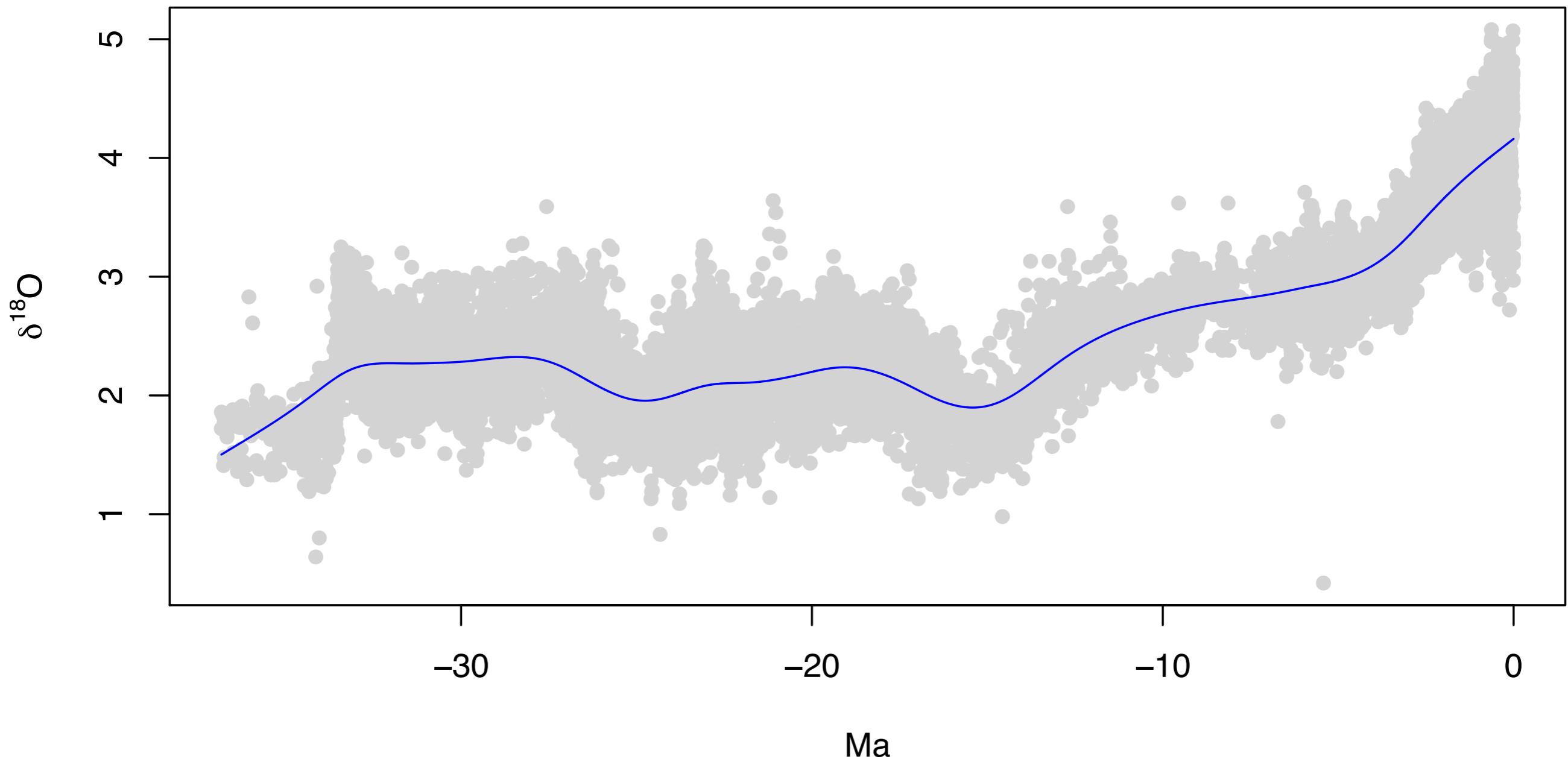
* when you only have extant taxa

early bursts are difficult to detect*



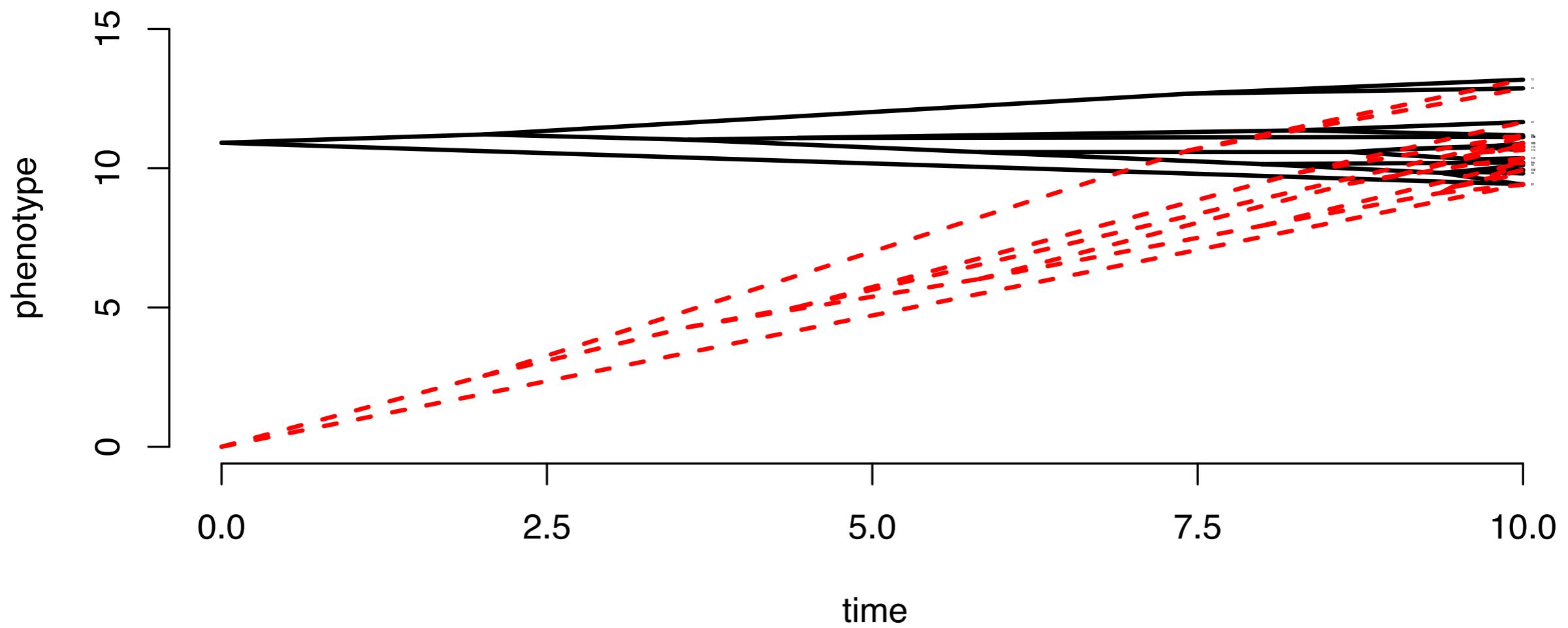
* when you only have extant taxa

environmentally - determined rates



Data from Zachos et al 2008

trends screw up your ancestral states (and maybe your rates)



Model Selection!

Model Selection!

$$AIC = 2k - 2LnLk$$

Model Selection!

$$AIC = 2k - 2LnLk$$

$$AICc = 2k - 2LnLk + \frac{2k^2 + 2k}{n - k - 1}$$

Model Selection!

$$AIC = 2k - 2LnLk$$

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$$\Delta AIC_i = AIC_i - AIC_{min}$$

Model Selection!

$$AIC = 2k - 2LnLk$$

$$AICc = 2k - 2LnLk + \frac{2k^2 + 2k}{n - k - 1}$$

$$\Delta AIC_i = AIC_i - AIC_{min}$$

$$AICW_i = \frac{e^{-0.5\Delta AIC_i}}{\sum_{j=1}^n e^{-0.5\Delta AIC_j}}$$

Ornstein-Uhlenbeck models - adaptation and constraint

Ornstein-Uhlenbeck models - adaptation and constraint

$$\mathbb{E}[dX] = -\alpha(X - \theta)$$

Ornstein-Uhlenbeck models - adaptation and constraint

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the expected change in X

Ornstein-Uhlenbeck models - adaptation and constraint

$$\mathbb{E}[dX] = -\alpha(X - \theta)$$

the expected change in X

**X-the “optimal” value
(θ)**

Ornstein-Uhlenbeck models - adaptation and constraint

$$\mathbb{E}[dX] = -\alpha(X - \theta)$$

the expected change in X

**multiplied by the
negative of the strength
of selection (α)**

**X-the “optimal” value
(θ)**

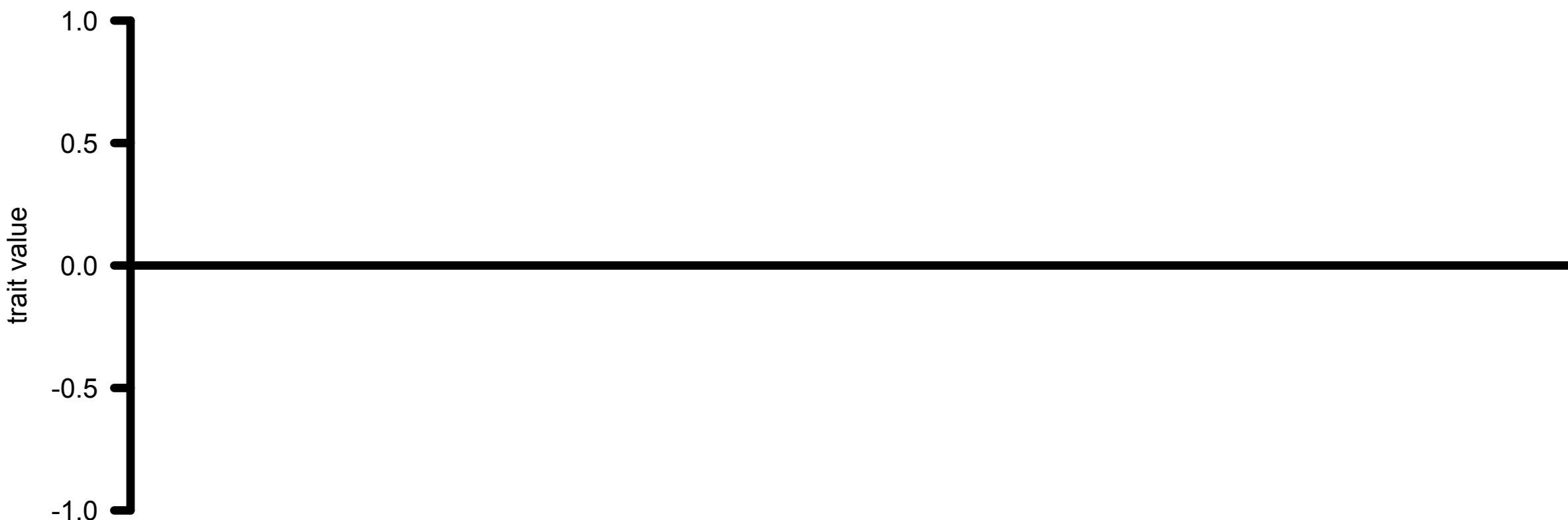
Ornstein-Uhlenbeck models - adaptation and constraint

$$\mathbb{E}[dX] = -\alpha(X - \theta)$$

the expected change in X

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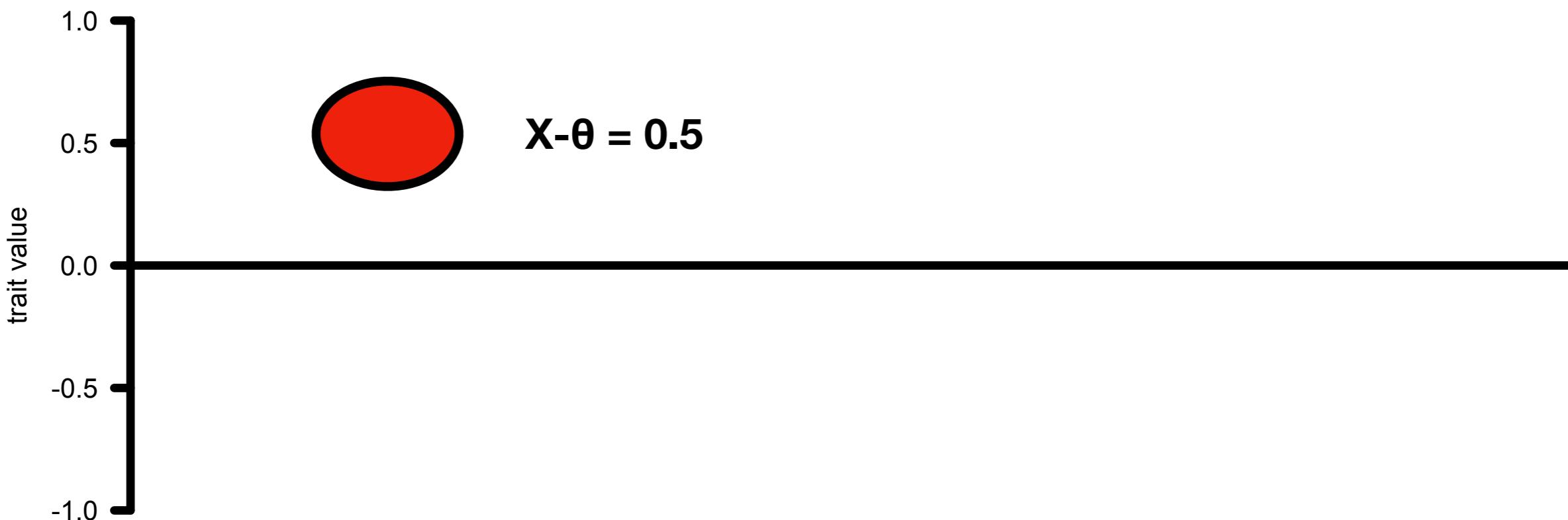
Ornstein-Uhlenbeck models - adaptation and constraint

$$\mathbb{E}[dX] = -\alpha(X - \theta)$$

the expected change in X

**multiplied by the
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**X -the “optimal” value
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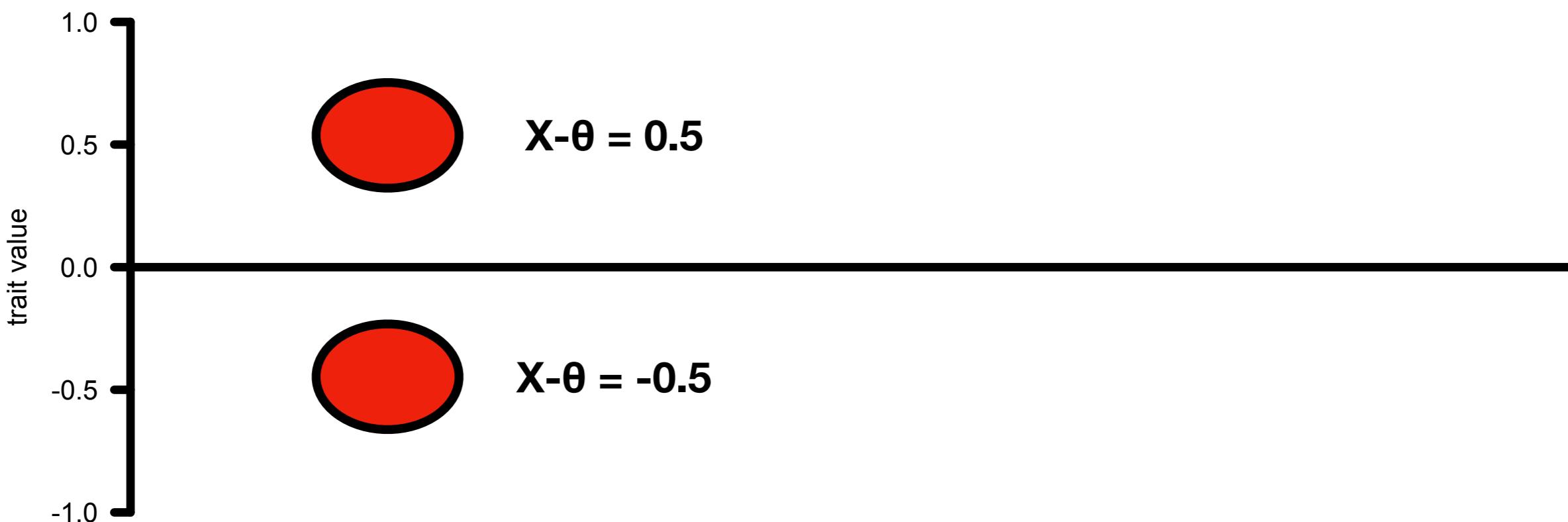
Ornstein-Uhlenbeck models - adaptation and constraint

$$\mathbb{E}[dX] = -\alpha(X - \theta)$$

the expected change in X

**multiplied by the
negative of the strength
of selection (α)**

**X -the “optimal” value
(θ)**



long term behavior of an OU process

$$\mathbb{E}[X_t | X_0] = [1 - e^{-\alpha t}] \theta + e^{-\alpha t} X_0$$

$$Var[X_t | X_0] = \frac{\sigma^2}{2\alpha} [1 - e^{-2\alpha t}]$$

long term behavior of an OU process

$$\mathbb{E}[X_t | X_0] = [1 - e^{-\alpha t}] \theta + e^{-\alpha t} X_0$$

Influence of optimum

$$Var[X_t | X_0] = \frac{\sigma^2}{2\alpha} [1 - e^{-2\alpha t}]$$

long term behavior of an OU process

$$\mathbb{E}[X_t | X_0] = [1 - e^{-\alpha t}] \theta + e^{-\alpha t} X_0$$

Influence of optimum

Influence of root

$$Var[X_t | X_0] = \frac{\sigma^2}{2\alpha} [1 - e^{-2\alpha t}]$$

long term behavior of an OU process

$$\mathbb{E}[X_t | X_0] = [1 - e^{-\alpha t}] \theta + e^{-\alpha t} X_0$$

Influence of optimum

Influence of root

$$Var[X_t | X_0] = \frac{\sigma^2}{2\alpha} [1 - e^{-2\alpha t}]$$

**equilibrium
variance**

write an OU process simulator

- 1. what happens when the root state and θ are the same?**

- 2. If the root state and θ differ and $\sigma^2 = 0.1$, how strong does a have to be for the trait to get to θ in 10 time units? How about in 5? How about in 1?**

- 2. Using the example above with any a that gets you to the optimum, what happens if you increase σ^2 once you ?**

OU on trees

OU on trees

$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-\alpha t_{ij}} [1 - e^{-2\alpha C_{ij}}]$$

OU on trees

$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-\alpha t_{ij}} [1 - e^{-2\alpha C_{ij}}]$$

**equilibrium
variance**

OU on trees

$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-\alpha t_{ij}} [1 - e^{-2\alpha C_{ij}}]$$

equilibrium variance

co-variance accumulated by the common ancestor

OU on trees

$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-\alpha t_{ij}} [1 - e^{-2\alpha C_{ij}}]$$

equilibrium variance

co-variance accumulated by the common ancestor

OU on trees

$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-\alpha t_{ij}} [1 - e^{-2\alpha C_{ij}}]$$

**t_{ij} = branch length
accumulated since
divergence**

**equilibrium
variance**

**co-variance
accumulated by the
common ancestor**

OU on trees

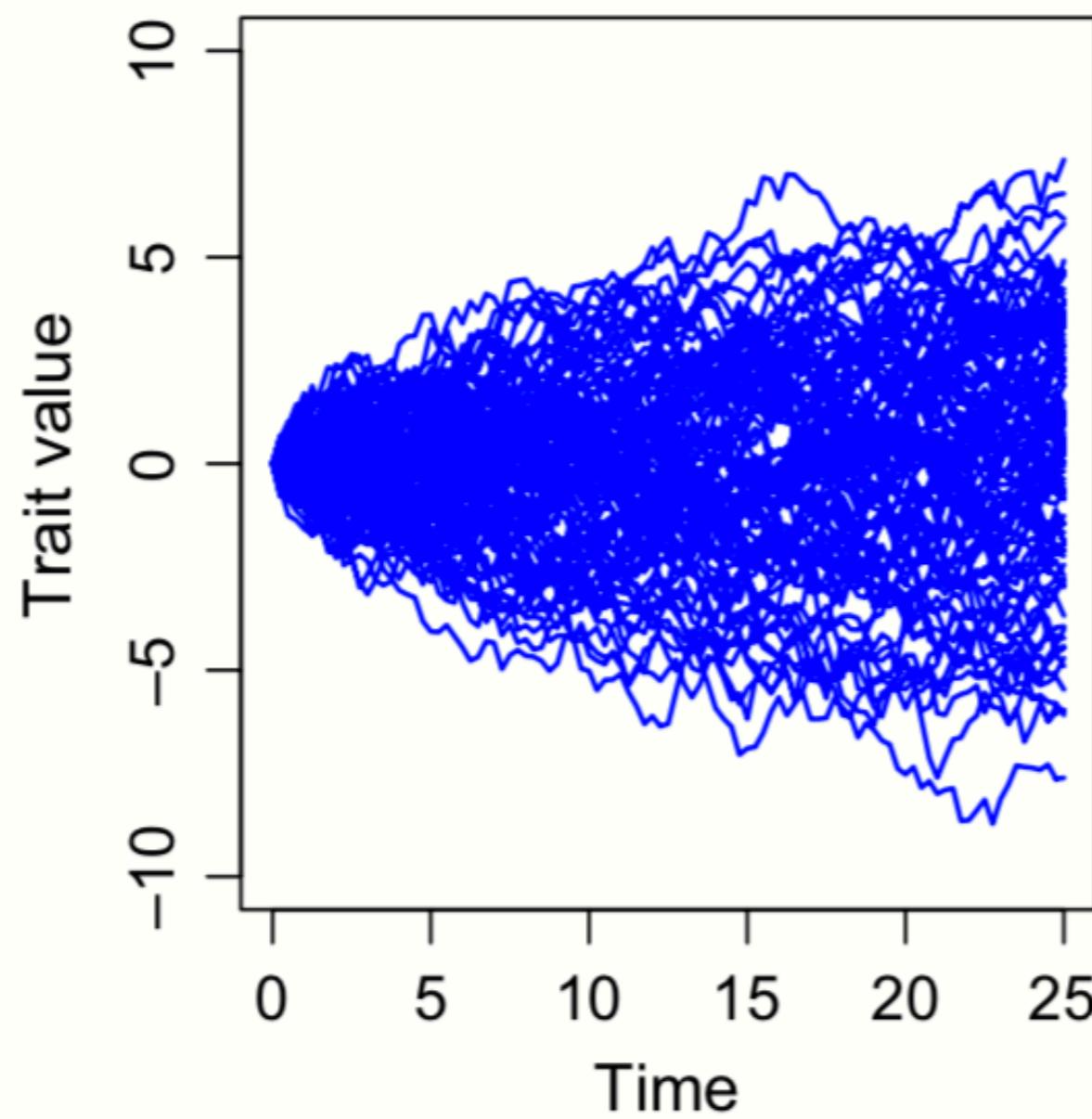
$$V_{ij} = \frac{\sigma^2}{2\alpha} e^{-\alpha t_{ij}} [1 - e^{-2\alpha C_{ij}}]$$

t_{ij} = branch length accumulated since divergence

equilibrium variance **co-variance lost due to independent evolution** **co-variance accumulated by the common ancestor**

(a)

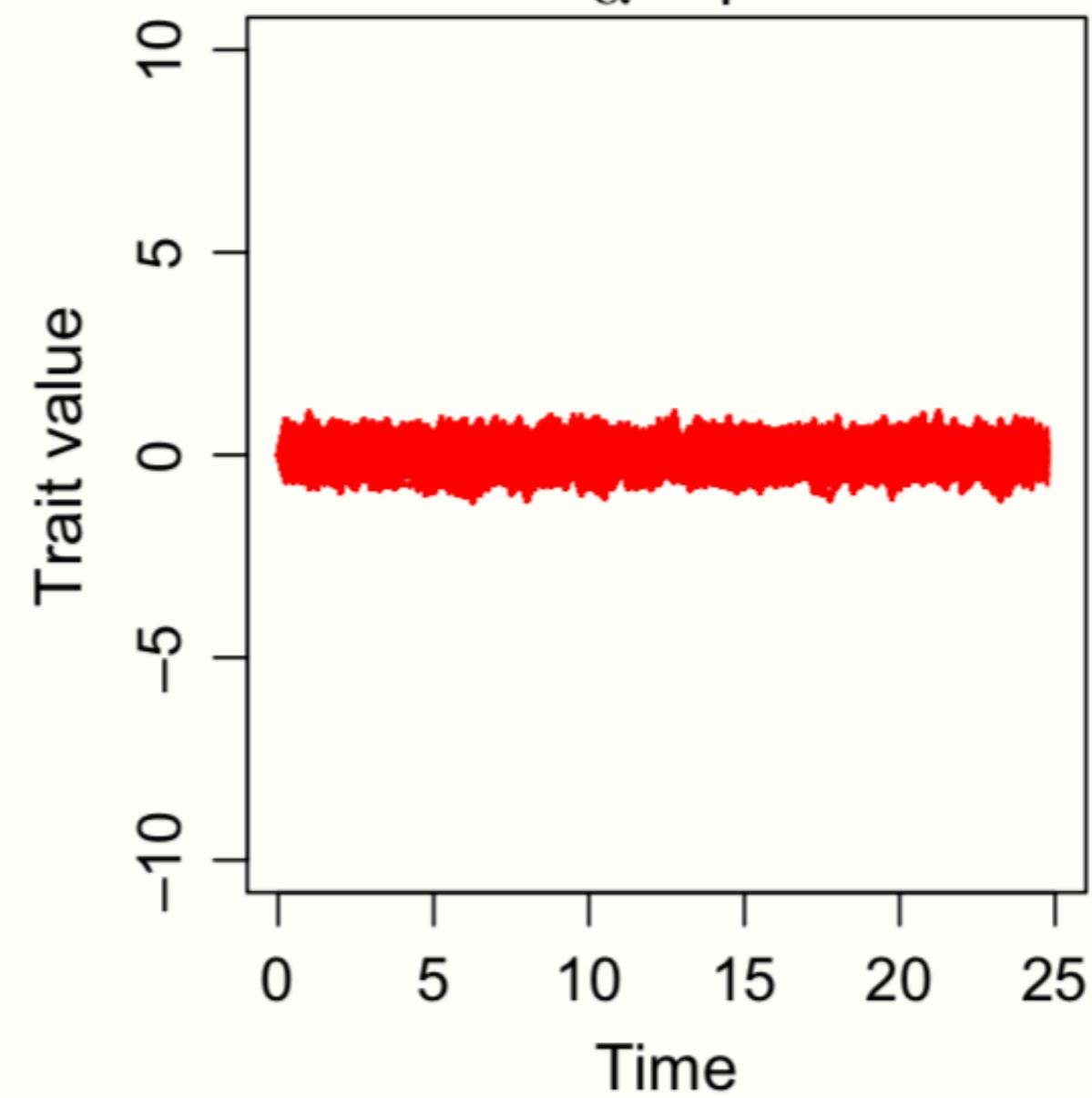
$$\sigma^2 = 0.5$$



(b)

$$\sigma^2 = 0.5$$

$$\alpha = 1$$



flavors of phylogenetic OU models

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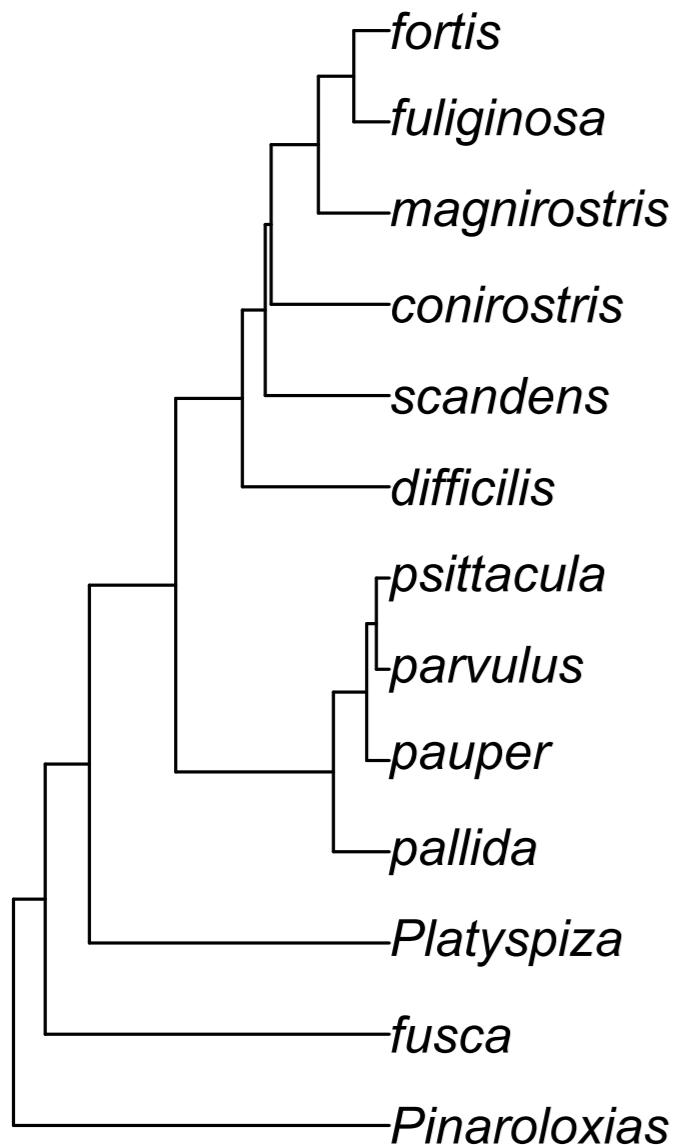
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flavors of phylogenetic OU models

- **root state and θ are the same [aka single stationary peak] (geiger, mvMORPH)**
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- **θ , α , and/ or σ^2 differ based on some user defined regimes (OUwie, OUCH, mvMORPH)**
- **θ , α , and/ or σ^2 differ based on regimes that are unknown a priori (bayou [rjMCMC], l1ou [lasso regression])**

multivariate data

multivariate data



	wingL	tarsusL	culmenL	beakD	gonysW
fuliginosa	4.13	2.81	2.09	1.94	1.85
fortis	4.24	2.89	2.41	2.36	2.22
magnirostris	4.40	3.04	2.72	2.82	2.68
conirostris	4.35	2.98	2.65	2.51	2.36
scandens	4.26	2.93	2.62	2.14	2.04
difficilis	4.22	2.90	2.28	2.01	1.93
pallida	4.27	3.09	2.43	2.02	1.95
parvulus	4.13	2.97	1.97	1.87	1.81
psittacula	4.24	3.05	2.26	2.23	2.07
pauper	4.23	3.04	2.19	2.07	1.96
Platyspiza	4.42	3.27	2.33	2.35	2.28
fusca	3.98	2.94	2.05	1.19	1.40
Pinaroloxias	4.19	2.98	2.31	1.55	1.63

multivariate data

$$\mathcal{L}(\mathbf{X}|\mathbf{R}, \boldsymbol{\mu}) = \frac{e^{-0.5[\mathbf{X}-\boldsymbol{\mu}]^T \mathbf{V}^{-1} [\mathbf{X}-\boldsymbol{\mu}]}}{\sqrt{(2\pi)^{nr} \det(\mathbf{V})}}$$

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**V is the outer
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**R is the “evolutionary
rate matrix”**

**V is the outer
product $\mathbf{R} \otimes \mathbf{C}$**

