

# Stochastic processes on trees: Brownian motion and beyond

Paul Bastide<sup>1</sup>, Miraine Dávila Felipe<sup>2</sup>

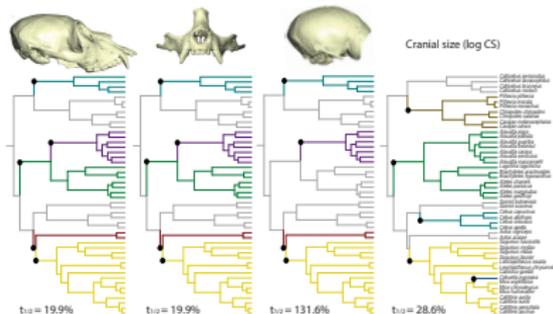
<sup>1</sup> IMAG, Université de Montpellier, CNRS

<sup>2</sup> LMAC, Université de Technologie de Compiègne

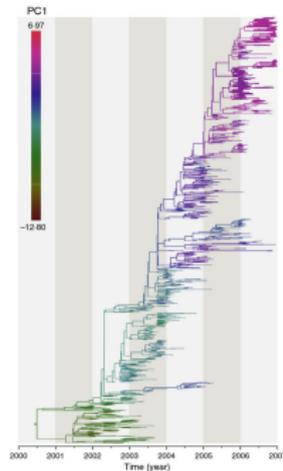
December 2021



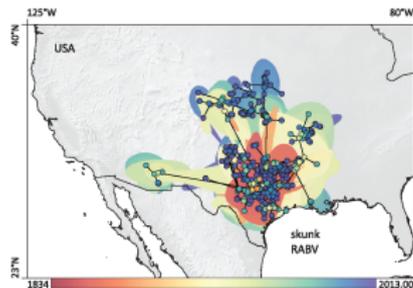
# Phylogenetic Comparative Methods



Aristide et al. (2018)



Vrancken et al. (2015)



Dellicour et al. (2017)

- Various time scales: Myr – decade.
- Various traits: morpho, geo, viral.

**Question:** Trait dynamics for an evolving organism ?

# Outline

## Today

- Models of trait evolution.
- The phylogenetic regression.
- Application: HIV virulence heritability.

## Tomorrow

- Multivariate and heterogeneous models.
- Bayesian inference.
- Application: phylogeography.

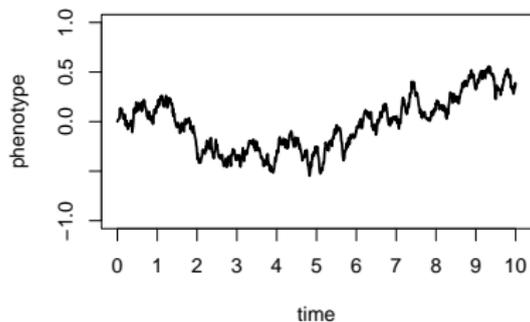
# Models of trait evolution

- ① Brownian Motion
- ② Ornstein-Uhlenbeck
- ③ Gaussian Models
- ④ General Diffusion Models

# Outline

- 1 Brownian Motion
  - Brownian Motion
  - Distribution
  - Modelling
- 2 Ornstein-Uhlenbeck
- 3 Gaussian Models
- 4 General Diffusion Models

# Brownian Motion

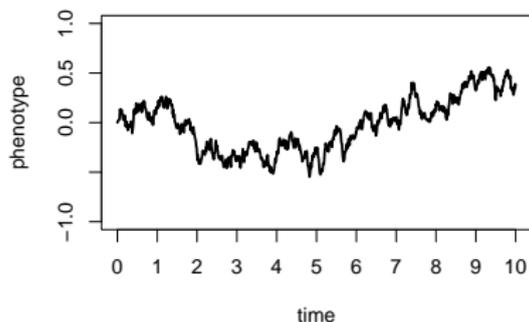


$$X_0 = \mu; \quad dX_t = \sigma dB_t$$

## Brownian Motion:

- Continuous time process.

# Brownian Motion

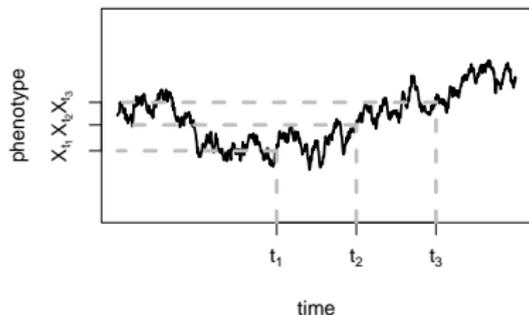


$$X_0 = \mu; \quad dX_t = \sigma dB_t$$

## Brownian Motion:

- Continuous time process.
- Continuous trajectory (almost surely)

# Brownian Motion

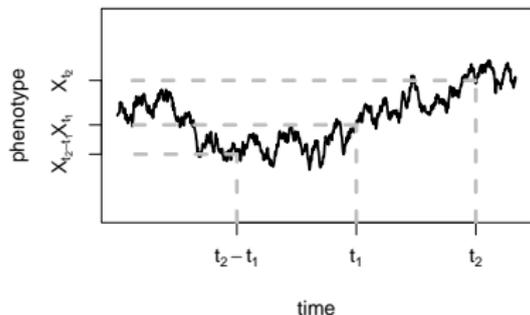


$$X_0 = \mu; \quad dX_t = \sigma dB_t$$

## Brownian Motion:

- Continuous time process.
- Continuous trajectory (almost surely)
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$

# Brownian Motion

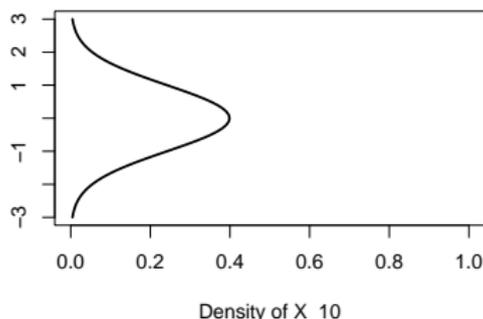
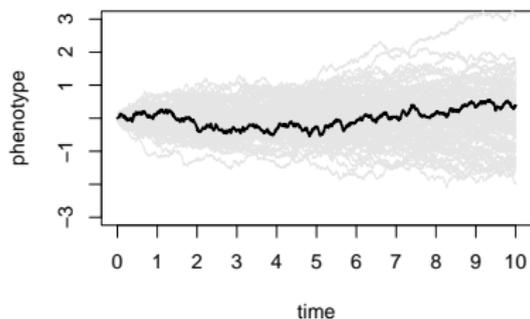


$$X_0 = \mu; \quad dX_t = \sigma dB_t$$

## Brownian Motion:

- Continuous time process.
- Continuous trajectory (almost surely)
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$
- Stationary increments:  $(X_{t_2} - X_{t_1}) \sim X_{t_2-t_1} - X_0$

# Brownian Motion

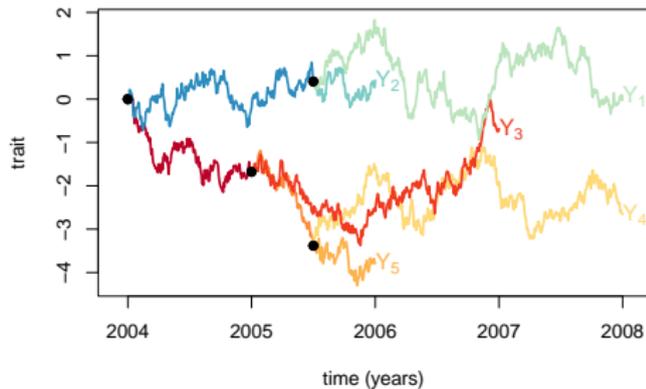
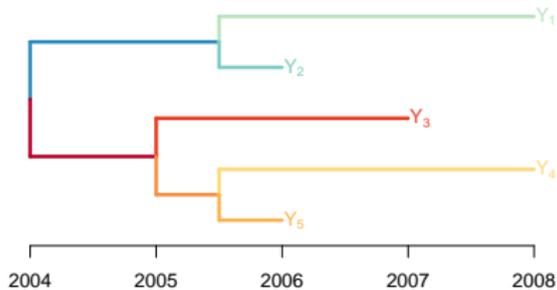


## Brownian Motion:

- Continuous time process.
- Continuous trajectory (almost surely)
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$
- Stationary increments:  $(X_{t_2} - X_{t_1}) \sim X_{t_2-t_1} - X_0$
- Gaussian:  $X_t \sim \mathcal{N}(X_0, \sigma^2 t)$

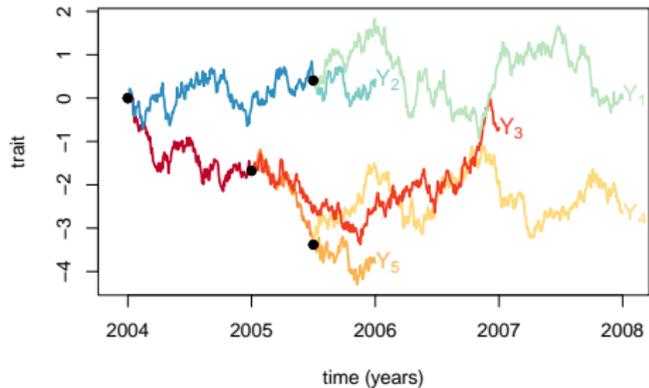
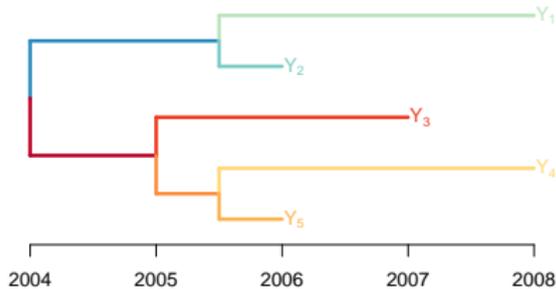
# Brownian Motion on a Tree

(Felsenstein, 1985)



# Brownian Motion on a Tree

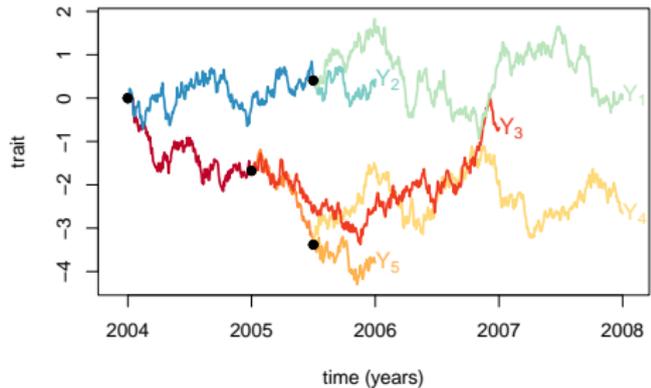
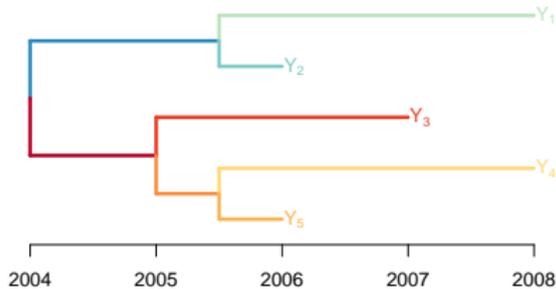
(Felsenstein, 1985)



- The trait evolves like a BM in time

# Brownian Motion on a Tree

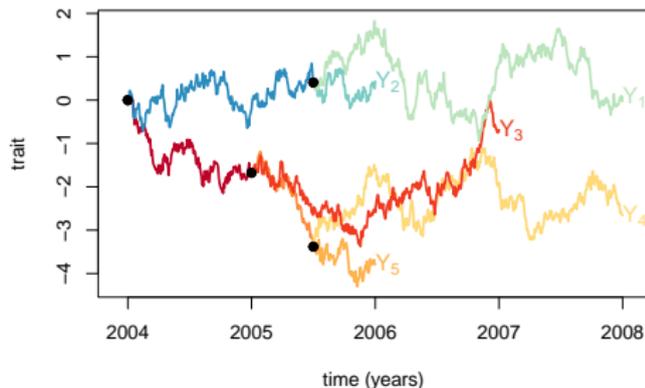
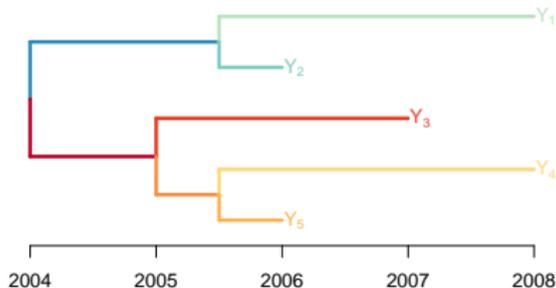
(Felsenstein, 1985)



- The trait evolves like a BM in time
- Speciation → two independent processes

# Brownian Motion on a Tree

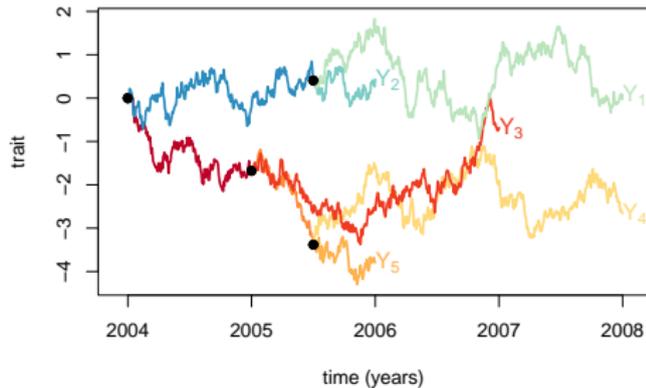
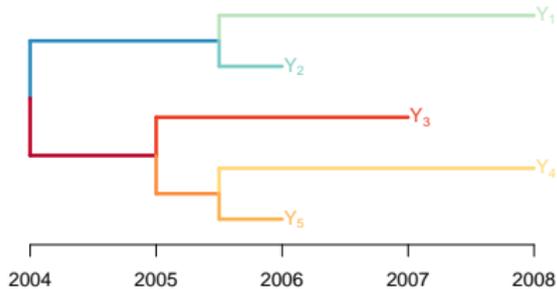
(Felsenstein, 1985)



- The trait evolves like a BM in time
- Speciation → two independent processes
- Only **tip values** are measured

# Brownian Motion on a Tree

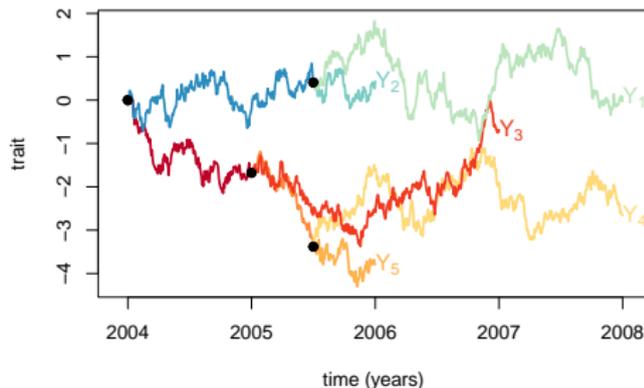
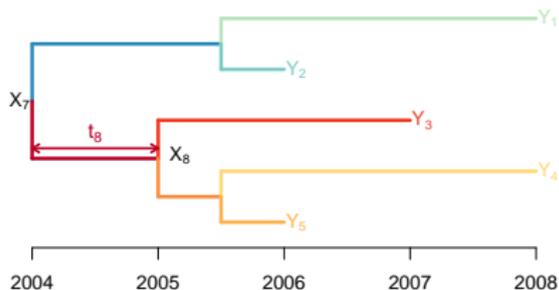
(Felsenstein, 1985)



- SDE:  $dX_t = \sigma dB_t$

# Brownian Motion on a Tree

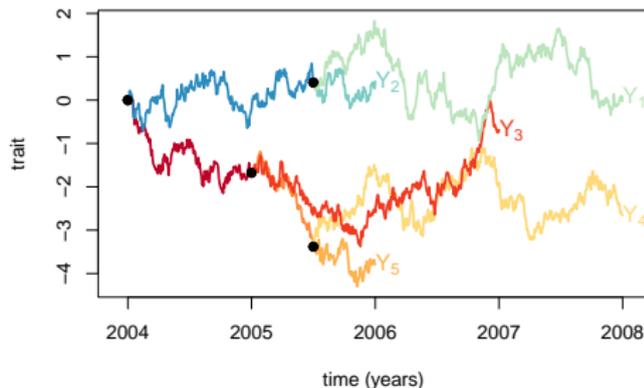
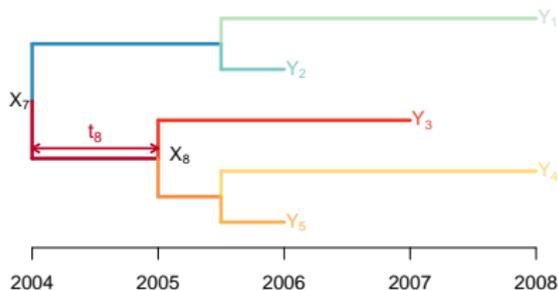
(Felsenstein, 1985)



- SDE:  $dX_t = \sigma dB_t$
- Heredity:  $X_8 | X_7 \sim \mathcal{N}(X_7, \sigma^2 t_8)$

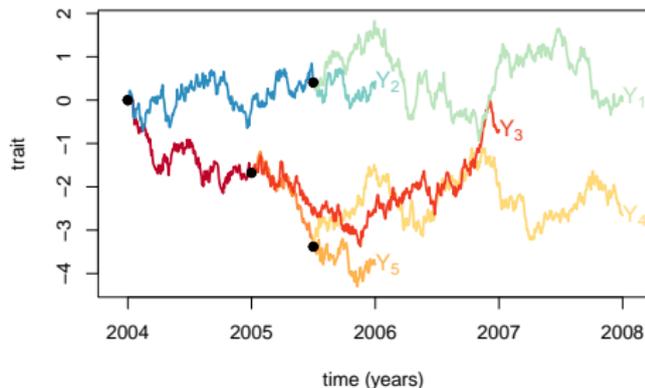
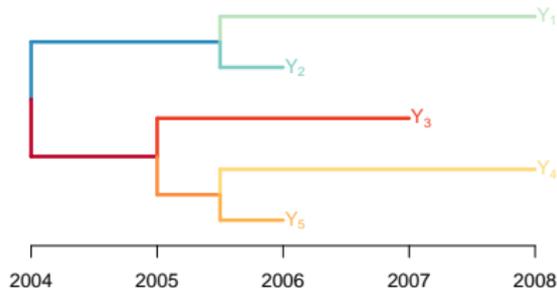
# Brownian Motion on a Tree

(Felsenstein, 1985)



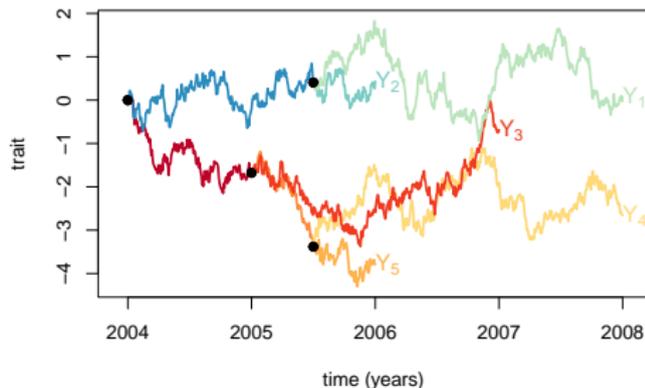
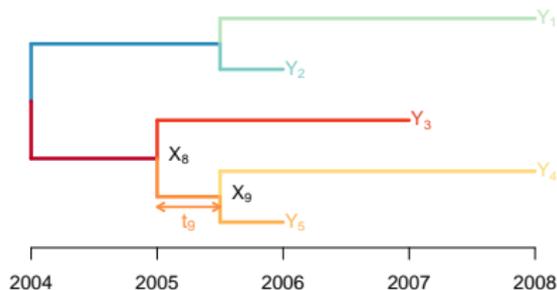
- SDE:  $dX_t = \sigma dB_t$
- Heredity:  $X_8 | X_7 \sim \mathcal{N}(X_7, \sigma^2 t_8)$
- Root:  $X_\rho = \mu$

# Variance Structure



Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

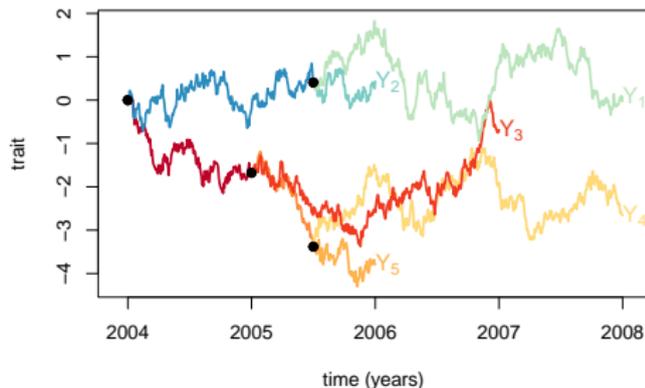
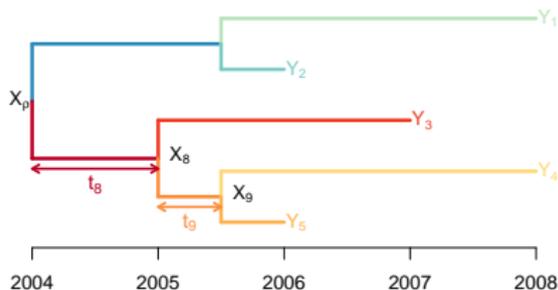
## Variance Structure



Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

$$\text{Var}(X_9) = \text{Var}(X_8) + \sigma^2 t_9$$

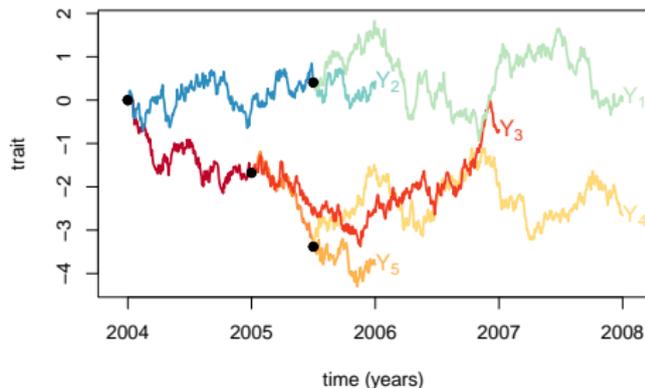
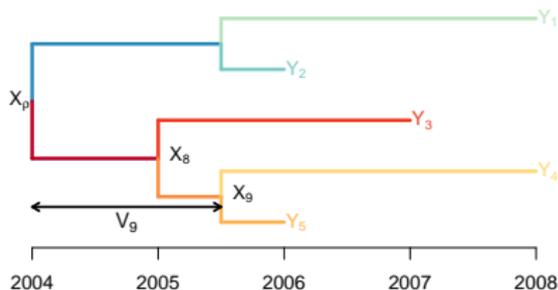
# Variance Structure



Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

$$\begin{aligned}\text{Var}(X_9) &= \text{Var}(X_8) + \sigma^2 t_9 \\ &= \sigma^2 t_8 + \sigma^2 t_9\end{aligned}$$

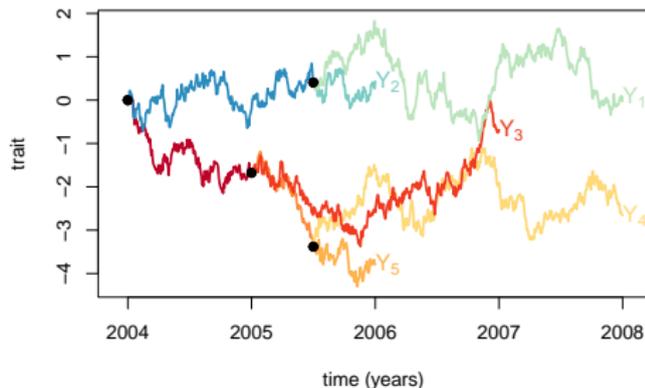
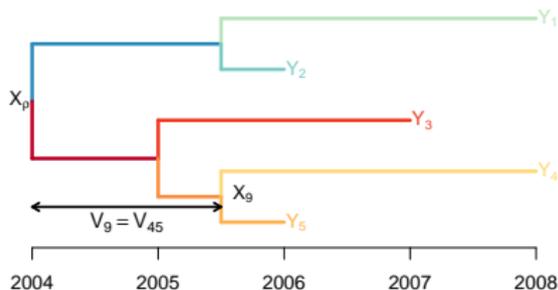
## Variance Structure



Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

$$\begin{aligned}\text{Var}(X_9) &= \text{Var}(X_8) + \sigma^2 t_9 \\ &= \sigma^2 t_8 + \sigma^2 t_9 \\ &= \sigma^2 V_9\end{aligned}$$

## Variance Structure

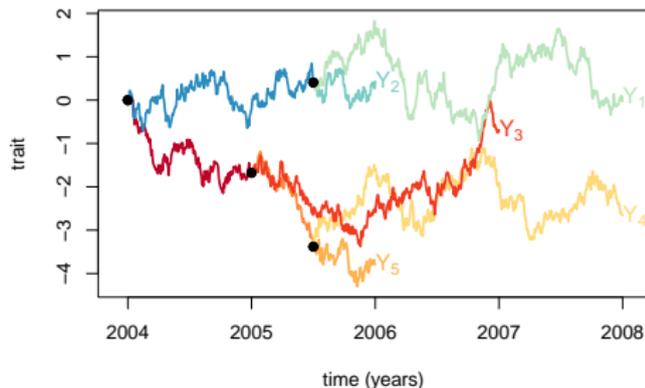
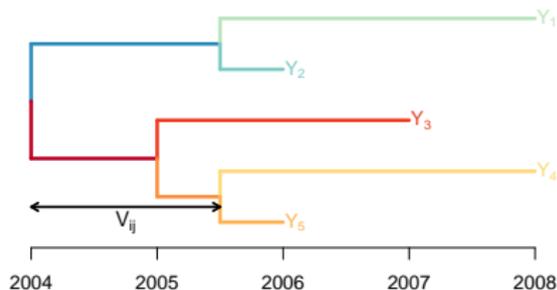


Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

$$\mathbb{V}\text{ar}(X_9) = \sigma^2 V_9$$

$$\text{Cov}(Y_4, Y_5) = \mathbb{V}\text{ar}(X_9) = \sigma^2 V_9 = \sigma^2 V_{45}$$

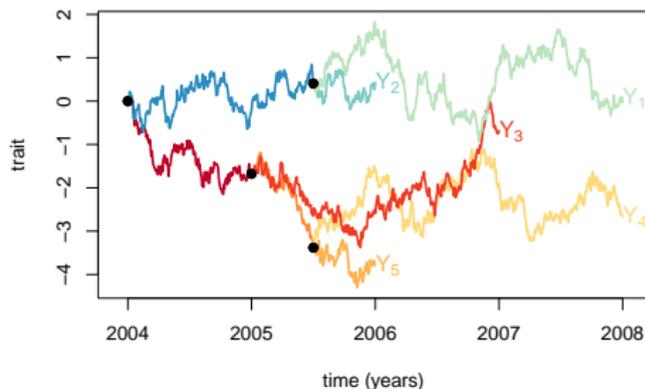
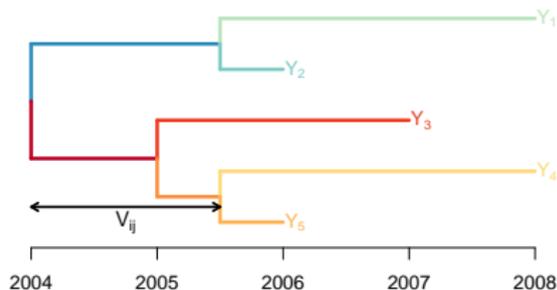
# Variance Structure



Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

Covariances:  $\text{Cov}(Y_i, Y_j) = \sigma^2 V_{ij}$

## Variance Structure

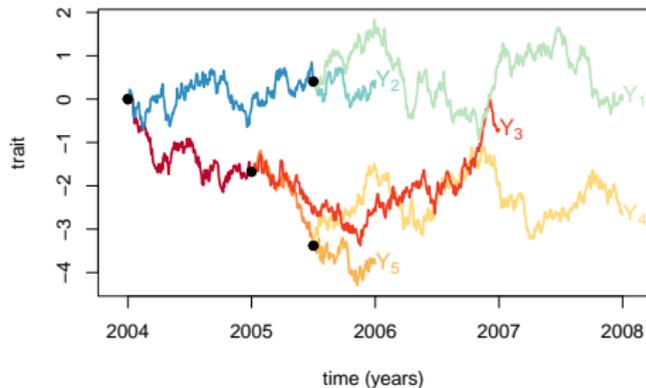
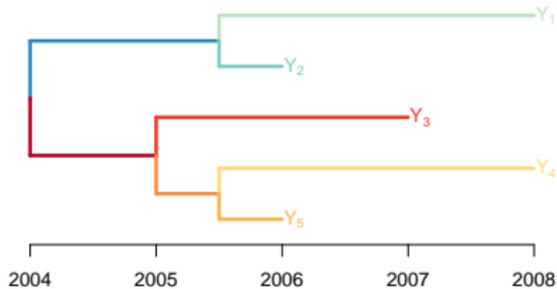


Structure:  $X_i = X_{\text{pa}(i)} + \sigma\sqrt{t_i} \times \epsilon_i$ , with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid

Covariances:  $\text{Cov}(Y_i, Y_j) = \sigma^2 V_{ij}$

Distribution:  $\mathbf{Y} \sim \mathcal{N}(\mu \mathbf{1}_n, \sigma^2 \mathbf{V})$  Gaussian Multivariate

# Modelling



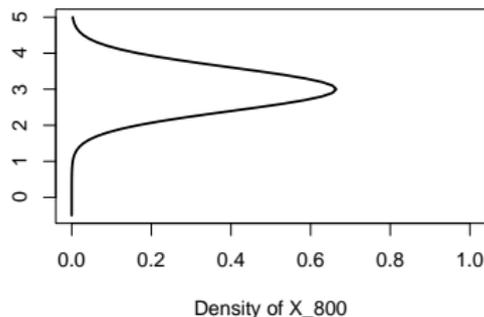
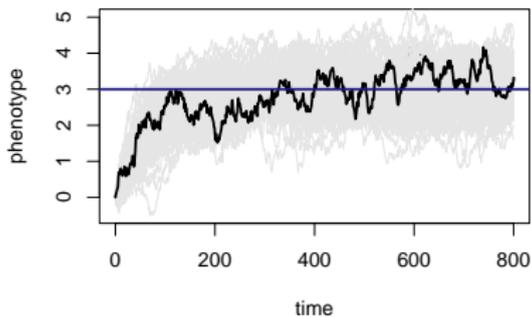
- Unbounded variance
- No direction

# Outline

- 1 Brownian Motion
- 2 Ornstein-Uhlenbeck
  - Ornstein-Uhlenbeck
  - Variance
  - Modelling
- 3 Gaussian Models
- 4 General Diffusion Models

# Ornstein-Uhlenbeck

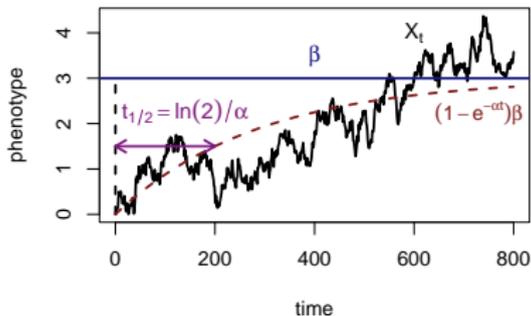
$$dX_t = \alpha[\beta - X_t]dt + \sigma dB_t$$



## Brownian with purpose:

- Gaussian:  $X_t \sim \mathcal{N}(e^{-\alpha t}X_0 + (1 - e^{-\alpha t})\beta, (1 - e^{-2\alpha t})\frac{\sigma^2}{2\alpha})$
- Stationary state  $\mathcal{N}(\beta, \frac{\sigma^2}{2\alpha})$
- Bounded variance.

# Ornstein-Uhlenbeck



$$dX_t = \alpha[\beta - X_t]dt + \sigma dB_t$$

## Deterministic part:

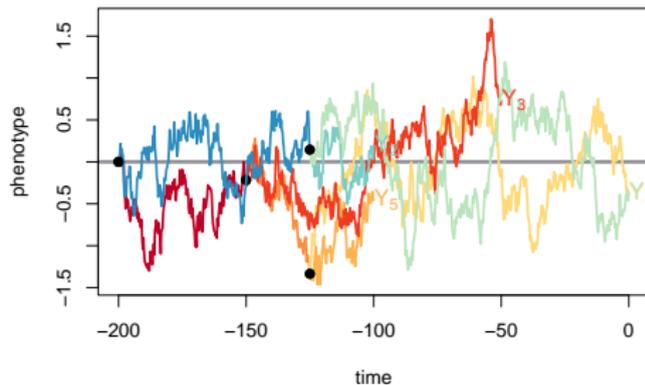
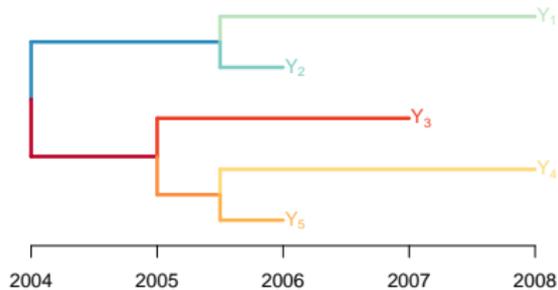
- $\beta$ : primary optimum (mechanistically defined).
- $\ln(2)/\alpha$ : phylogenetic half live.

## Stochastic part:

- $X_t$ : trait value (actual optimum).
- $\sigma dB(t)$ : Brownian fluctuations.

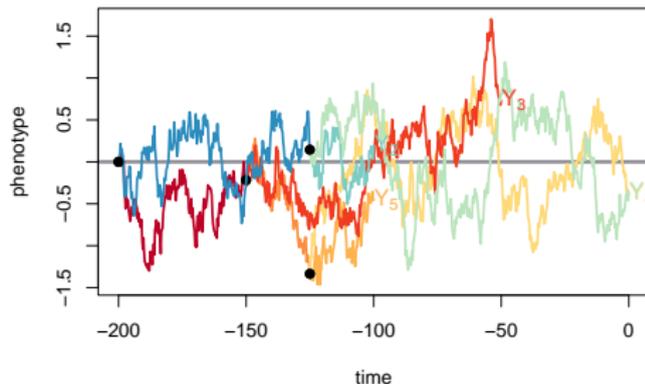
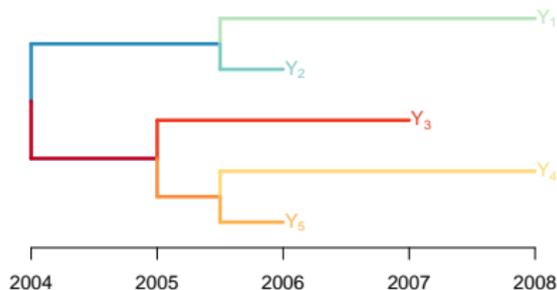
# OU on a Tree

(Hansen, 1997)



## OU on a Tree

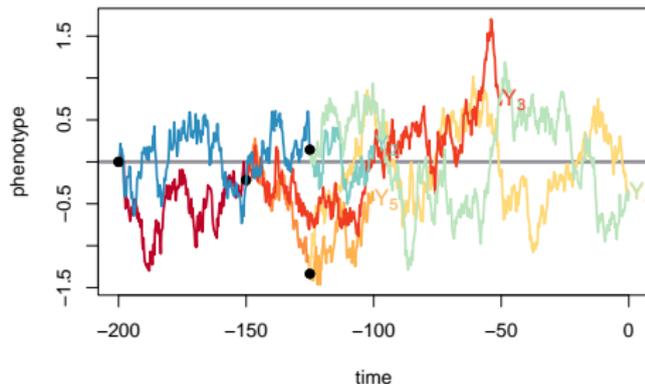
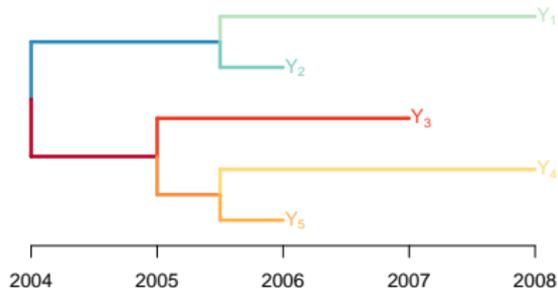
(Hansen, 1997)



- The trait evolves like a OU in time
- Speciation  $\rightarrow$  two independent processes
- Only **tip values** only are measured

# OU on a Tree

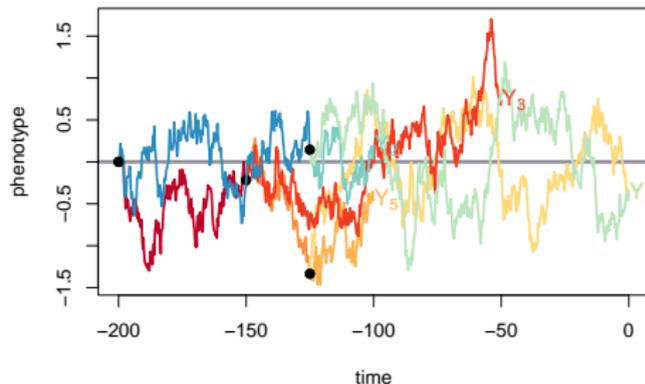
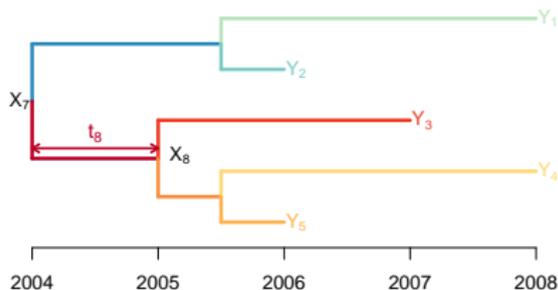
(Hansen, 1997)



- SDE:  $dX_t = \alpha[\beta - X_t] dt + \sigma dB_t$

# OU on a Tree

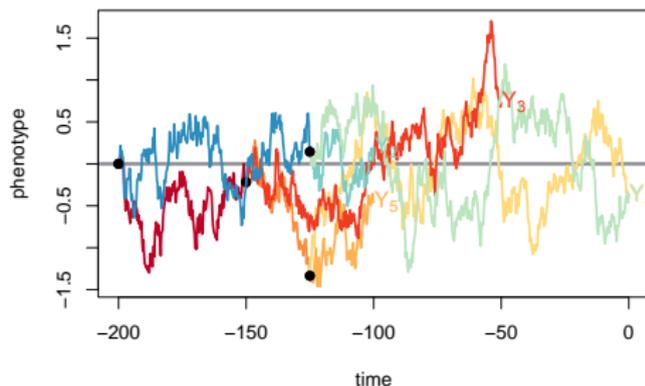
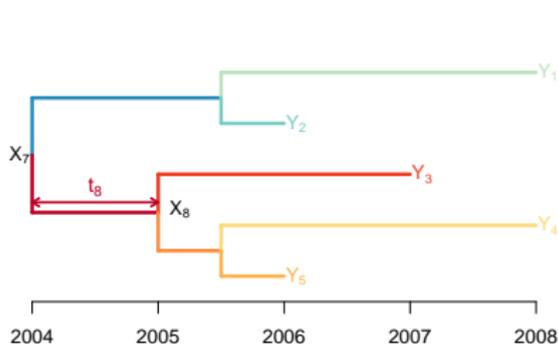
(Hansen, 1997)



- **SDE:**  $dX_t = \alpha[\beta - X_t] dt + \sigma dB_t$
- **Heredity:**  $X_8 | X_7 \sim \mathcal{N}(e^{-\alpha t_8} X_7 + (1 - e^{-\alpha t_8})\beta, (1 - e^{-2\alpha t_8}) \frac{\sigma^2}{2\alpha})$

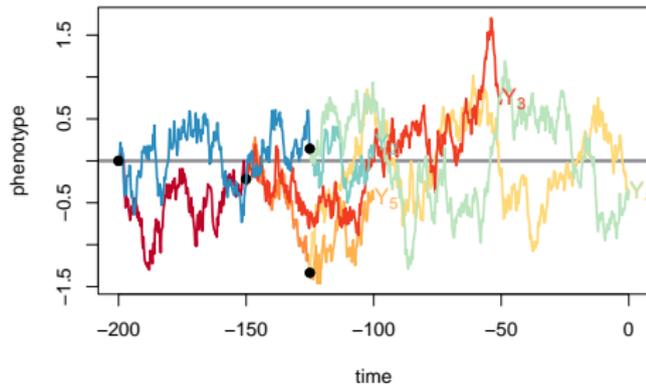
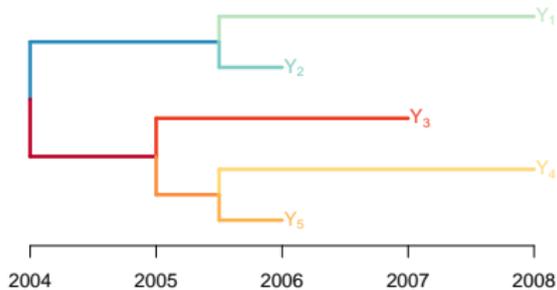
## OU on a Tree

(Hansen, 1997)

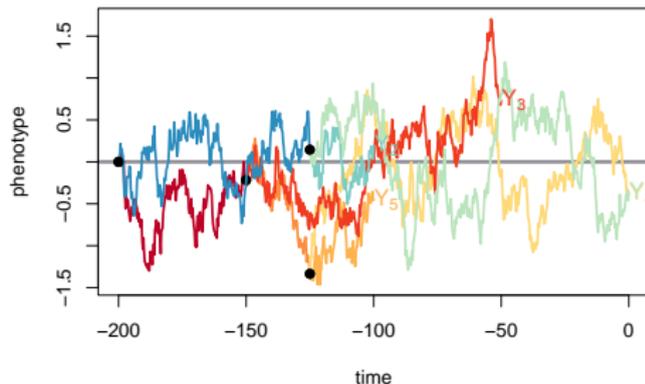
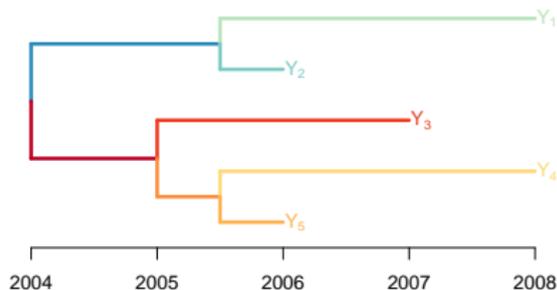


- SDE:  $dX_t = \alpha[\beta - X_t]dt + \sigma dB_t$
- Heredity:  $X_8|X_7 \sim \mathcal{N}(e^{-\alpha t_8} X_7 + (1 - e^{-\alpha t_8})\beta, (1 - e^{-2\alpha t_8})\frac{\sigma^2}{2\alpha})$
- Root:  $X_\rho = \mu = \beta$

# Distribution of an OU

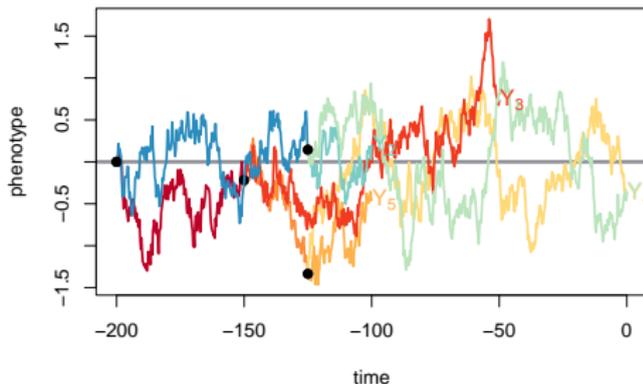
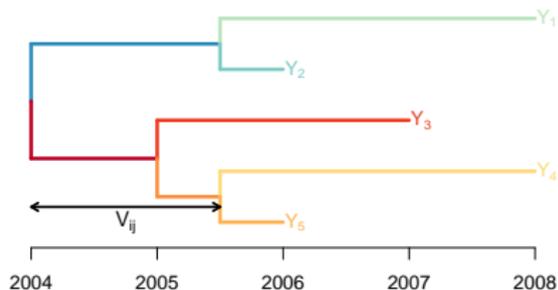


# Distribution of an OU



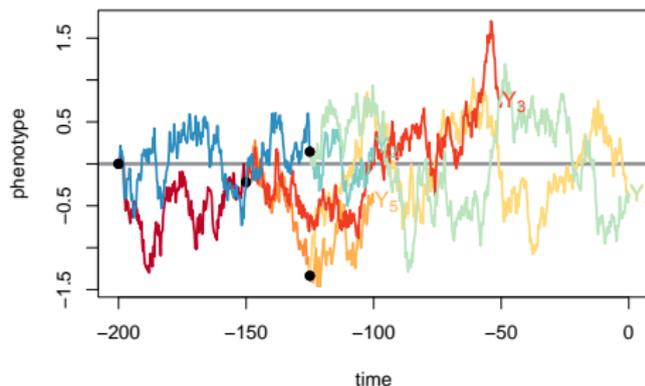
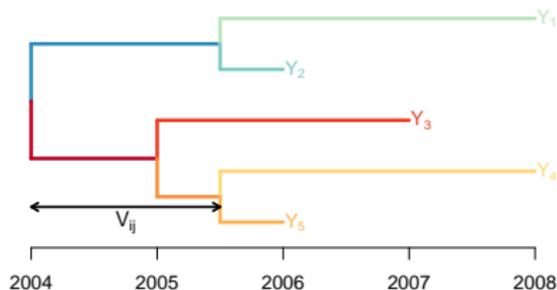
**Structure:**  $X_i = e^{-\alpha t_i} X_{\text{pa}(i)} + (1 - e^{-\alpha t_i})\beta + \sqrt{(1 - e^{-2\alpha t_i})\frac{\sigma^2}{2\alpha}} \times \epsilon_i$   
with  $\epsilon_i \sim \mathcal{N}(0, 1)$  iid.

## Distribution of an OU



Covariances:  $\text{Cov}[Y_i; Y_j] = \frac{\sigma^2}{2\alpha} e^{-\alpha(V_i+V_j)} (e^{2\alpha V_{ij}} - 1)$

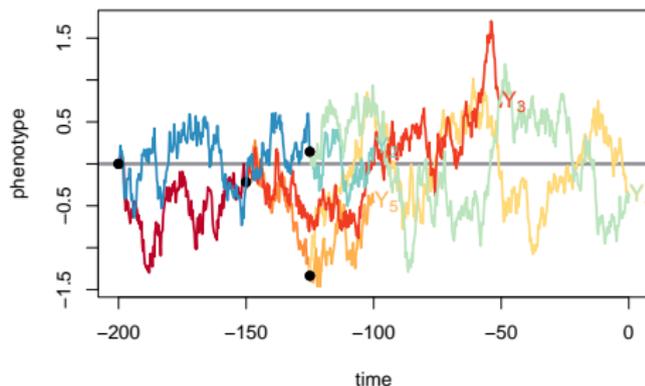
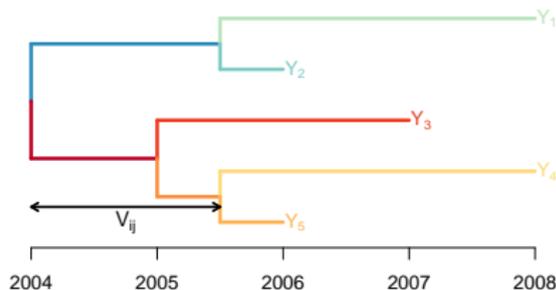
## Distribution of an OU



Covariances:  $\text{Cov}[Y_i; Y_j] = \frac{\sigma^2}{2\alpha} e^{-\alpha(V_i+V_j)} (e^{2\alpha V_{ij}} - 1)$

Expectation:  $\mathbb{E}[Y_i] = \mu e^{-\alpha V_i} + \beta(1 - e^{-\alpha V_i})$

## Distribution of an OU

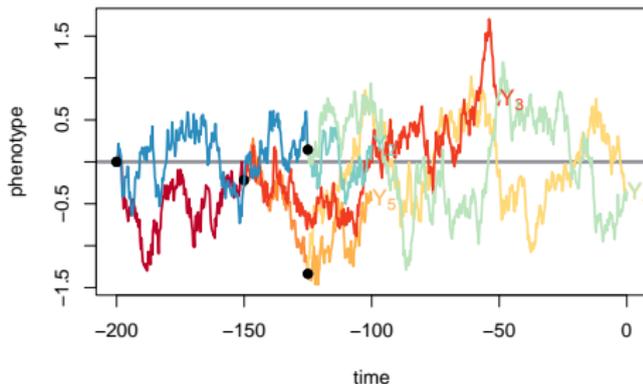
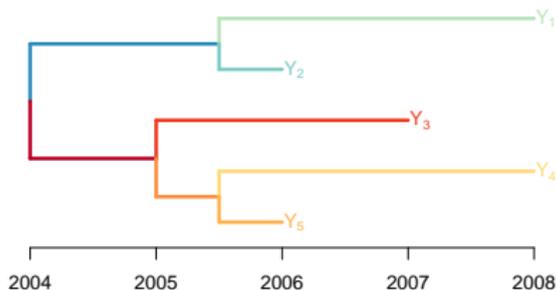


Covariances:  $\text{Cov}[Y_i; Y_j] = \frac{\sigma^2}{2\alpha} e^{-\alpha(V_i+V_j)} (e^{2\alpha V_{ij}} - 1)$

Expectation:  $\mathbb{E}[Y_i] = \mu e^{-\alpha V_i} + \beta(1 - e^{-\alpha V_i})$

Distribution:  $\mathbf{Y}$  still Gaussian Multivariate.

# Modelling



- Bounded variance  $\gamma^2 = \frac{\sigma^2}{2\alpha}$
- Stationary state
- Stabilizing selection

## Non-Identifiability on an Ultrametric Tree

Ultrametric tree:  $h = V_i$  for all tip  $i$ .

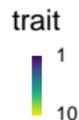
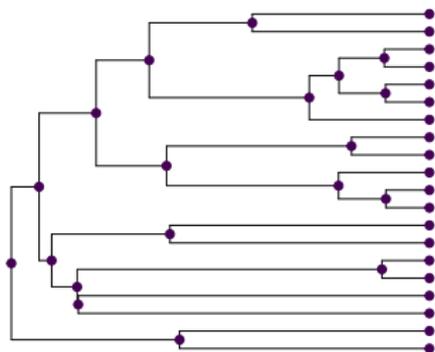
Expectation: All tips have the same expectation

$$\mathbb{E}[Y_i] = \mu e^{-\alpha h} + \beta(1 - e^{-\alpha h})$$

Non-Identifiability  $\mu$  and  $\beta$  cannot be identified separately.

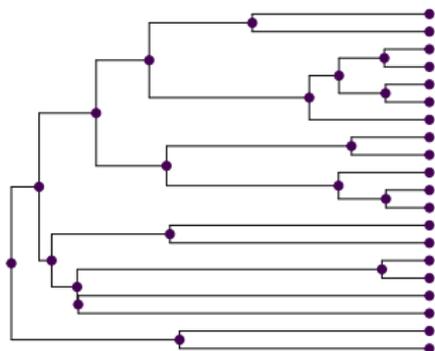
Only  $\lambda = \mu e^{-\alpha h} + \beta(1 - e^{-\alpha h})$  is identifiable.

# Non-Identifiability on an Ultrametric Tree

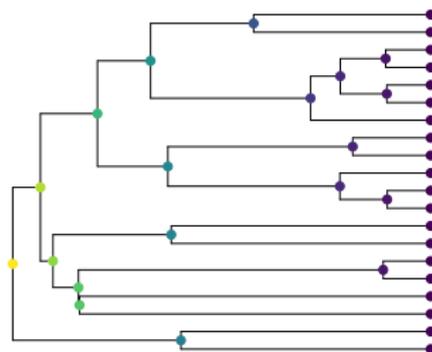


- $\lambda = \mu = \beta = 1$
- Root in stationary state
- Tips expectation: 1.

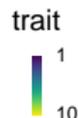
## Non-Identifiability on an Ultrametric Tree



- $\lambda = \mu = \beta = 1$
- Root in stationary state
- Tips expectation: 1.



- $\lambda = 1, \mu = 10, \beta = -2$
- Out of equilibrium.
- Tips expectation: 1.



## Interpretation and time scale

Short Time Scale: Quantitative genetics (Lande, 1976)

## Interpretation and time scale

Short Time Scale: Quantitative genetics (Lande, 1976)

- BM: limit of a genetic additive random drift on a flat landscape

## Interpretation and time scale

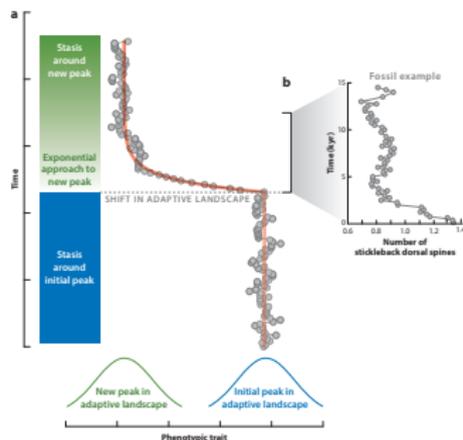
Short Time Scale: Quantitative genetics (Lande, 1976)

- BM: limit of a genetic additive random drift on a flat landscape
- OU: on an adaptation landscape with one peak

## Interpretation and time scale

### Short Time Scale: Quantitative genetics (Lande, 1976)

- BM: limit of a genetic additive random drift on a flat landscape
- OU: on an adaptation landscape with one peak
- *Gasterosteidae*: trait optimum change in  $\sim 1000$  years



Hunt and Rabosky (2014)

## Interpretation and time scale

Long Time Scale: Random fluctuations (Felsenstein, 2004)

## Interpretation and time scale

Long Time Scale: Random fluctuations (Felsenstein, 2004)

- Adaptation is almost instantaneous

## Interpretation and time scale

Long Time Scale: Random fluctuations (Felsenstein, 2004)

- Adaptation is almost instantaneous
- BM: fluctuations of the environment ("secondary optimum")

## Interpretation and time scale

Long Time Scale: Random fluctuations (Felsenstein, 2004)

- Adaptation is almost instantaneous
- BM: fluctuations of the environment ("secondary optimum")
- OU: secondary optimum itself goes to a "primary optimum"

## Interpretation and time scale

Long Time Scale: Random fluctuations (Felsenstein, 2004)

- Adaptation is almost instantaneous
- BM: fluctuations of the environment ("secondary optimum")
- OU: secondary optimum itself goes to a "primary optimum"
- Empirical, no theoretical justification.

## Interpretation and time scale

Long Time Scale: Random fluctuations (Felsenstein, 2004)

- Adaptation is almost instantaneous
- BM: fluctuations of the environment ("secondary optimum")
- OU: secondary optimum itself goes to a "primary optimum"
- Empirical, no theoretical justification.
- "Paradox of stasis" (Hansen and Houle, 2004)

# Outline

① Brownian Motion

② Ornstein-Uhlenbeck

③ Gaussian Models

- Accelerating / Decelerating Model
- General Gaussian Model
- Intra-species Variations

④ General Diffusion Models

## Accelerating / Decelerating Model

(Blomberg et al., 2003)

AC/DC: Exponentially increasing / decreasing variance

$$dX_t = \sigma_0 e^{rt/2} dB_t$$

## Accelerating / Decelerating Model

(Blomberg et al., 2003)

AC/DC: Exponentially increasing / decreasing variance

$$dX_t = \sigma_0 e^{rt/2} dB_t$$

$r < 0$  : "Early Burst" model (Harmon et al., 2010)

→ variance decreases in time: ecological radiation

# Accelerating / Decelerating Model

(Blomberg et al., 2003)

AC/DC: Exponentially increasing / decreasing variance

$$dX_t = \sigma_0 e^{rt/2} dB_t$$

$r < 0$  : "Early Burst" model (Harmon et al., 2010)

→ variance decreases in time: ecological radiation

Variance:

$$\text{Cov}(Y_i, Y_j) = \sigma_0^2 \frac{e^{rV_{ij}} - 1}{r}$$

# Accelerating / Decelerating Model

(Blomberg et al., 2003)

AC/DC: Exponentially increasing / decreasing variance

$$dX_t = \sigma_0 e^{rt/2} dB_t$$

$r < 0$  : "Early Burst" model (Harmon et al., 2010)

→ variance decreases in time: ecological radiation

Variance:

$$\text{Cov}(Y_i, Y_j) = \sigma_0^2 \frac{e^{rV_{ij}} - 1}{r}$$

Note: Equivalent to a single peak OU in some cases.

## General Model

BM, OU: Instance of a general Gaussian propagation model.

## General Model

BM, OU: Instance of a general Gaussian propagation model.



$$\mathbf{z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma}) \quad \text{root}$$

$$\mathbf{z}^j \mid \mathbf{z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j) \quad \text{nodes}$$

BM:  $\mathbf{q}_j = 1$ ,  $\mathbf{r}_j = 0$ ,  $\boldsymbol{\Sigma}_j = \sigma^2 \mathbf{t}_j$ .

# General Model

BM, OU: Instance of a general Gaussian propagation model.



$$\mathbf{z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma})$$

root

$$\mathbf{z}^j \mid \mathbf{z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j)$$

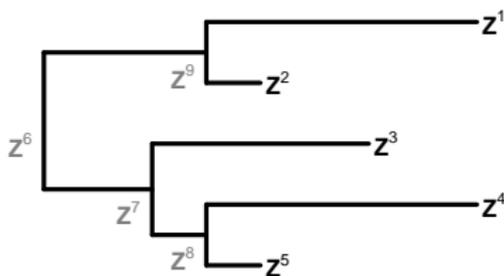
nodes

BM:  $\mathbf{q}_j = 1$ ,  $\mathbf{r}_j = 0$ ,  $\boldsymbol{\Sigma}_j = \sigma^2 \mathbf{t}_j$ .

OU:  $\mathbf{q}_j = e^{-\alpha \mathbf{t}_j}$ ,  $\mathbf{r}_j = (1 - e^{-\alpha \mathbf{t}_j})\boldsymbol{\beta}$ ,  $\boldsymbol{\Sigma}_j = \frac{\sigma^2}{2\alpha}(1 - e^{-2\alpha \mathbf{t}_j})$ .

## General Model

BM, OU: Instance of a general Gaussian propagation model.



$$\mathbf{z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma}) \quad \text{root}$$

$$\mathbf{z}^j \mid \mathbf{z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j) \quad \text{nodes}$$

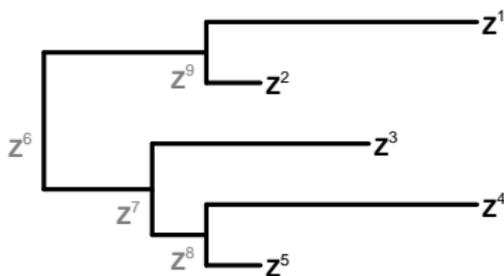
BM:  $\mathbf{q}_j = 1$ ,  $\mathbf{r}_j = 0$ ,  $\boldsymbol{\Sigma}_j = \sigma^2 \mathbf{t}_j$ .

OU:  $\mathbf{q}_j = e^{-\alpha \mathbf{t}_j}$ ,  $\mathbf{r}_j = (1 - e^{-\alpha \mathbf{t}_j})\boldsymbol{\beta}$ ,  $\boldsymbol{\Sigma}_j = \frac{\sigma^2}{2\alpha}(1 - e^{-2\alpha \mathbf{t}_j})$ .

Drift, shifts, Integrated OU...

## General Model

BM, OU: Instance of a general Gaussian propagation model.



$$\mathbf{z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma}) \quad \text{root}$$

$$\mathbf{z}^j \mid \mathbf{z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j) \quad \text{nodes}$$

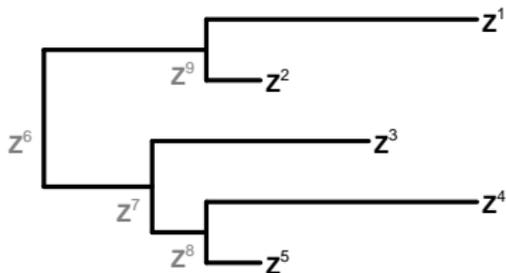
BM:  $\mathbf{q}_j = 1$ ,  $\mathbf{r}_j = 0$ ,  $\boldsymbol{\Sigma}_j = \sigma^2 t_j$ .

OU:  $\mathbf{q}_j = e^{-\alpha t_j}$ ,  $\mathbf{r}_j = (1 - e^{-\alpha t_j})\boldsymbol{\beta}$ ,  $\boldsymbol{\Sigma}_j = \frac{\sigma^2}{2\alpha}(1 - e^{-2\alpha t_j})$ .

Drift, shifts, Integrated OU...

Easy computations (Kalman filter)

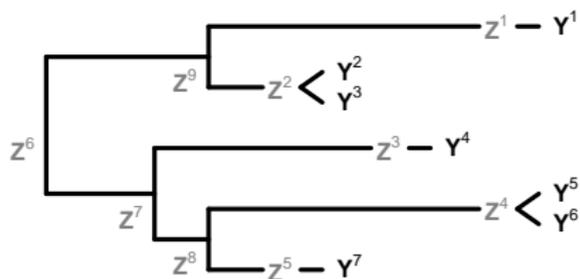
# Intra-species variations Model



$$\mathbf{z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma}) \quad \text{root}$$

$$\mathbf{z}^j \mid \mathbf{z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j) \quad \text{nodes}$$

# Intra-species variations Model



$$\mathbf{Z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma})$$

root

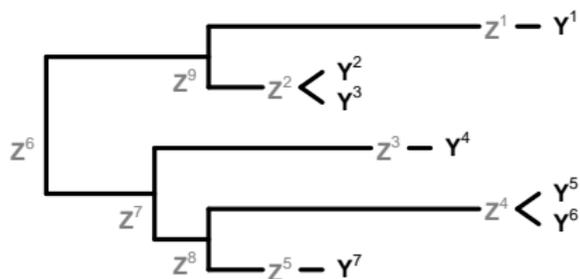
$$\mathbf{Z}^j \mid \mathbf{Z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{Z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j)$$

nodes

$$\mathbf{Y}^i \mid \mathbf{Z}^{\text{pa}(i)} \sim \mathcal{N}(\mathbf{Z}^{\text{pa}(i)}, \mathbf{S}_i)$$

obs

## Intra-species variations Model



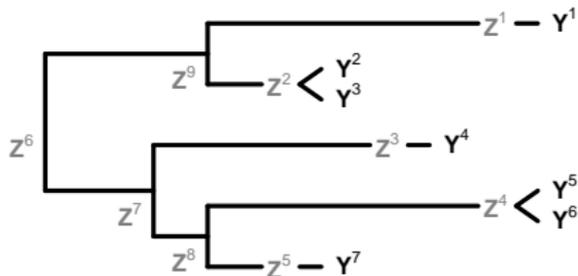
$$\mathbf{Z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma}) \quad \text{root}$$

$$\mathbf{Z}^j \mid \mathbf{Z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{Z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j) \quad \text{nodes}$$

$$\mathbf{Y}^i \mid \mathbf{Z}^{\text{pa}(i)} \sim \mathcal{N}(\mathbf{Z}^{\text{pa}(i)}, \mathbf{S}_i) \quad \text{obs}$$

Measurement Errors, Non phylogenetic variations, intra-species variations, ...

## Intra-species variations Model



$$\mathbf{Z}^r \sim \mathcal{N}(\boldsymbol{\mu}, \boldsymbol{\Gamma})$$

root

$$\mathbf{Z}^j \mid \mathbf{Z}^{\text{pa}(j)} \sim \mathcal{N}(\mathbf{q}_j \mathbf{Z}^{\text{pa}(j)} + \mathbf{r}_j, \boldsymbol{\Sigma}_j)$$

nodes

$$\mathbf{Y}^i \mid \mathbf{Z}^{\text{pa}(i)} \sim \mathcal{N}(\mathbf{Z}^{\text{pa}(i)}, \mathbf{S}_i)$$

obs

Measurement Errors, Non phylogenetic variations, intra-species variations, ...

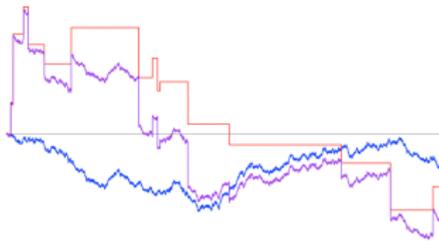
“Heritability”:

$$h^2 = \frac{V(\mathbf{Z}_{\text{tips}})}{V(\mathbf{Y})}$$

# Outline

- 1 Brownian Motion
- 2 Ornstein-Uhlenbeck
- 3 Gaussian Models
- 4 General Diffusion Models
  - Lévy processes
  - General diffusions

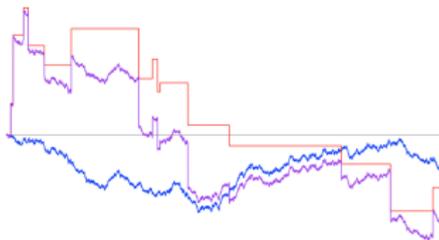
# Lévy processes



## Lévy processes

- Continuous time process.

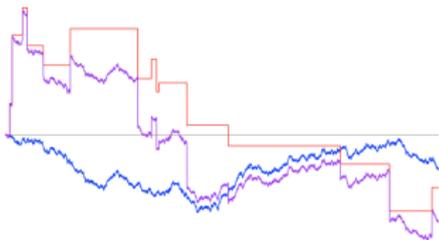
# Lévy processes



## Lévy processes

- Continuous time process.
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$

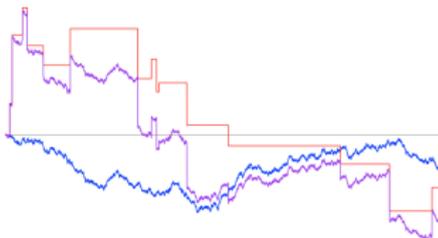
# Lévy processes



## Lévy processes

- Continuous time process.
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$
- Stationary increments:  $(X_{t_2} - X_{t_1}) \sim X_{t_2-t_1}$

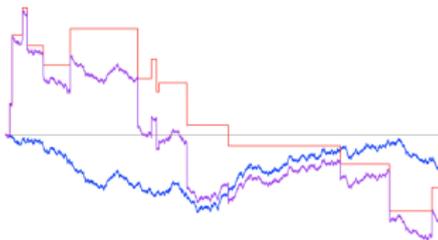
# Lévy processes



## Lévy processes

- Continuous time process.
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$
- Stationary increments:  $(X_{t_2} - X_{t_1}) \sim X_{t_2-t_1}$
- Càdlàg trajectory (almost surely)

# Lévy processes

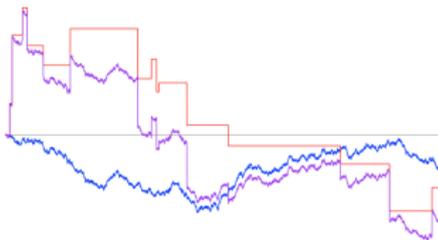


- BM is a Lévy process

## Lévy processes

- Continuous time process.
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$
- Stationary increments:  $(X_{t_2} - X_{t_1}) \sim X_{t_2-t_1}$
- Càdlàg trajectory (almost surely)

# Lévy processes



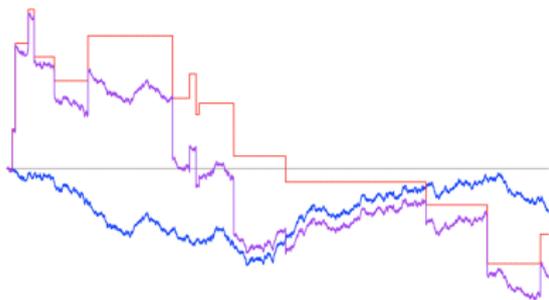
- BM is a Lévy process
- OU is not a Lévy process

## Lévy processes

- Continuous time process.
- Independent increments:  $(X_{t_3} - X_{t_2})$  ind.  $(X_{t_2} - X_{t_1})$
- Stationary increments:  $(X_{t_2} - X_{t_1}) \sim X_{t_2-t_1}$
- Càdlàg trajectory (almost surely)

## Lévy processes

(Landis et al., 2013; Duchen et al., 2017)



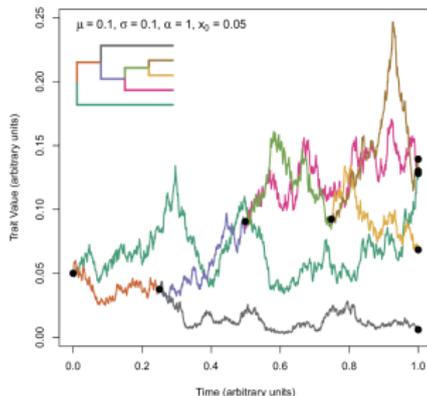
Lévy-Ito decomposition:  $X = B + J$

- $B$  and  $J$  are independent
- $B$  is a BM with rate  $\sigma^2$ ,  $B(0) = \mu$
- $J$  compound Poisson process, rate  $\lambda$ , jumps  $\sim \mathcal{N}(0, s_1^2)$

$$\mathbb{E}(X_i) = \mu \quad \text{and} \quad \text{Cov}(X_i, X_j) = V_{ij}(\sigma^2 + \lambda s_1^2)$$

## General diffusions

(Blomberg et al., 2020)



$$dX_t = b(X_t, t)dt + \sigma(X_t, t)dB_t$$

*Brownian motion is a poor model, and so is Ornstein-Uhlenbeck, but just as democracy is the worst method of organizing a society “except for all the other”, so these two models are all we’ve really got that is tractable. Critics will be admitted to the event, but only if they carry with them another tractable model. J. Felsenstein, 2008.*

# Bibliography

- Aristide, Bastide, dos Reis, et al. 2018. *Evolution*. 72:2697–2711.
- Blomberg, Garland, Ives. 2003. *Evolution*. 57:717–745.
- Blomberg, Rathnayake, Moreau. 2020. *The American Naturalist*. 195:145–165.
- Dellicour, Rose, Faria, et al. 2017. *Molecular Biology and Evolution*. 34:2563–2571.
- Duchen, Leuenberger, Szilágyi, et al. 2017. *Systematic Biology*. 66:950–963.
- Felsenstein. 1985. *The American Naturalist*. 125:1–15.
- Felsenstein. 2004. Sunderland, Massachusetts: Sinauer Associates.
- Hansen. 1997. *Evolution*. 51:1341.
- Hansen, Houle. 2004. In: Pigliucci, Preston, editors, Phenotypic integration: studying the ecology and evolution of complex phenotypes, New York: Oxford University Press, chapter 6, pp. 130–154.
- Harmon, Losos, Davies, et al. 2010. *Evolution*. 64:2385–2396.
- Hunt, Rabosky. 2014. *Annual Review of Earth and Planetary Sciences*. 42:421–441.
- Lande. 1976. *Evolution*. 30:314.
- Landis, Schraiber, Liang. 2013. *Systematic Biology*. 62:193–204.
- Vrancken, Lemey, Rambaut, et al. 2015. *Methods in Ecology and Evolution*. 6:67–82.

Thank you for listening



Institut Montpelliérain Alexander Grothendieck

# Appendices