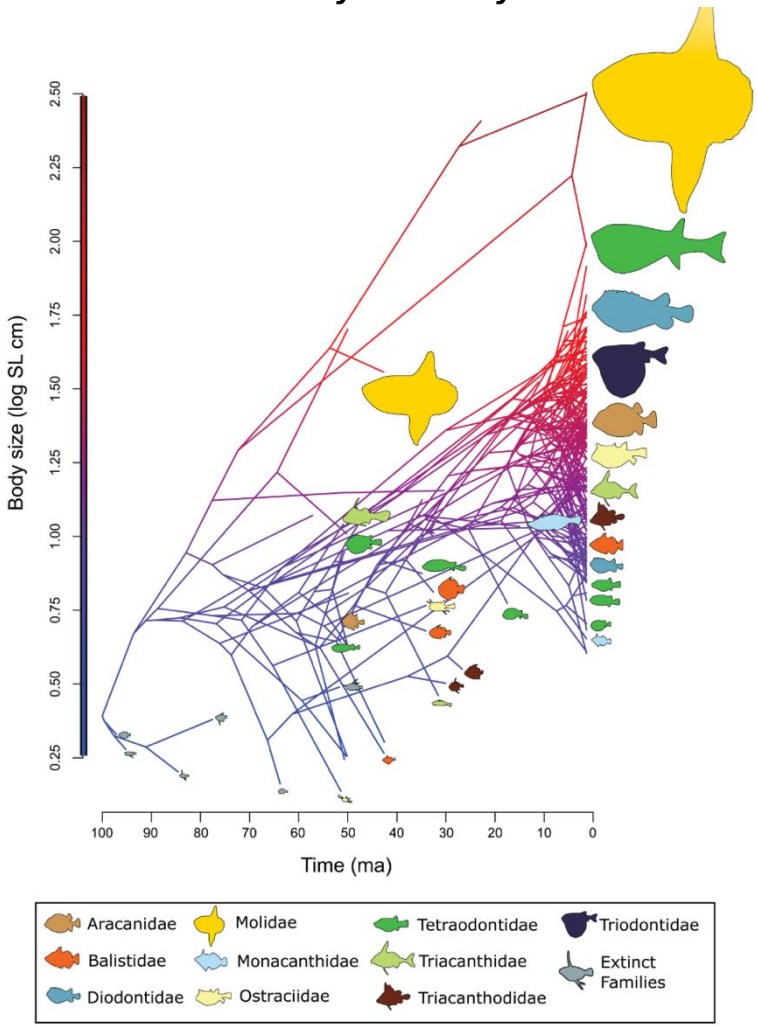
Introduction to Modeling Continuous Traits

BIO 508- Rosana Zenil-Ferguson

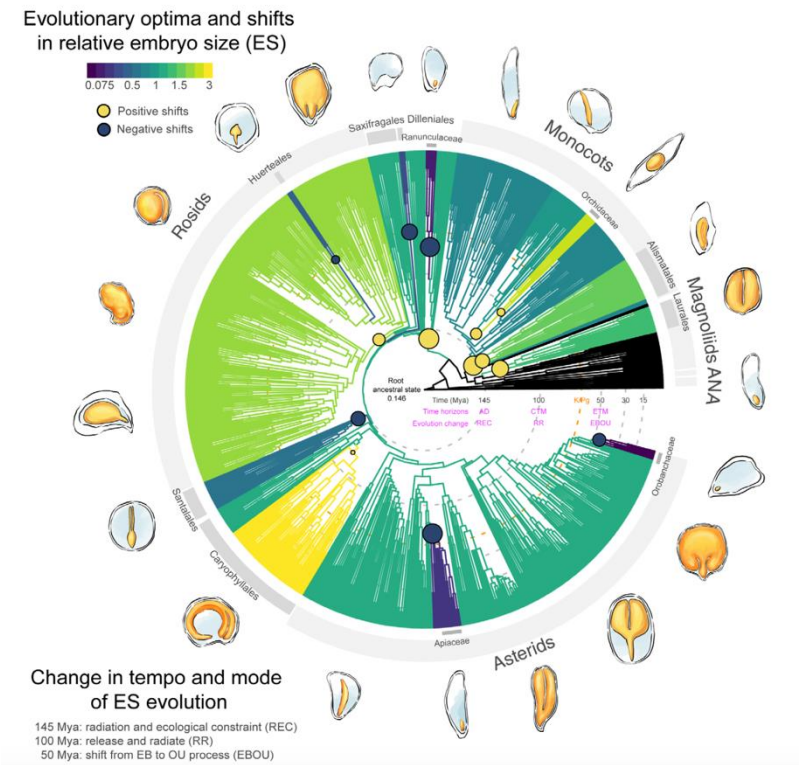
Continuous traits examples

Diversity in body size



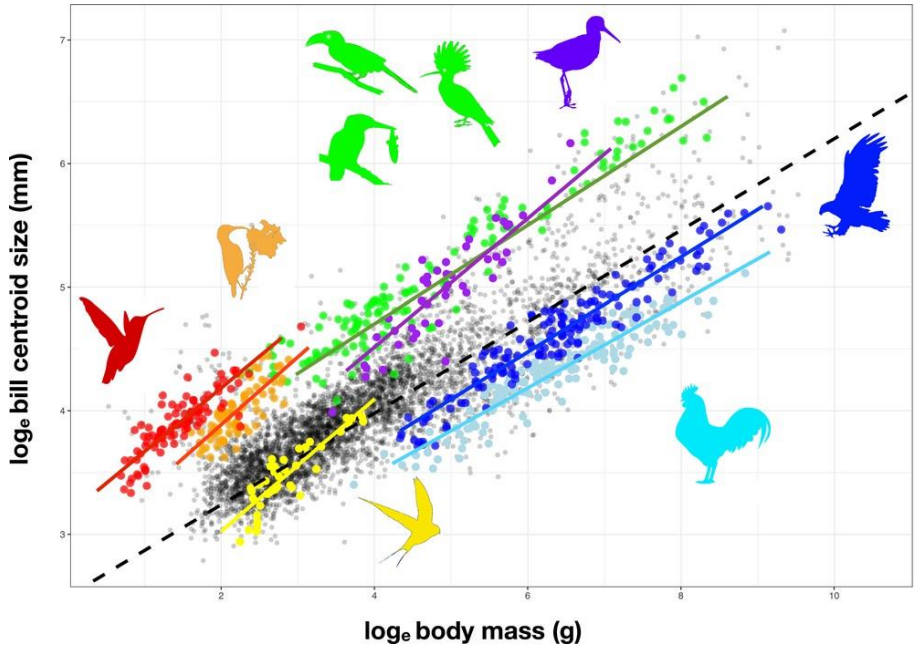
Troyer et al. 2023

Shifts in embryo size



Vandelook and Carta. 2025

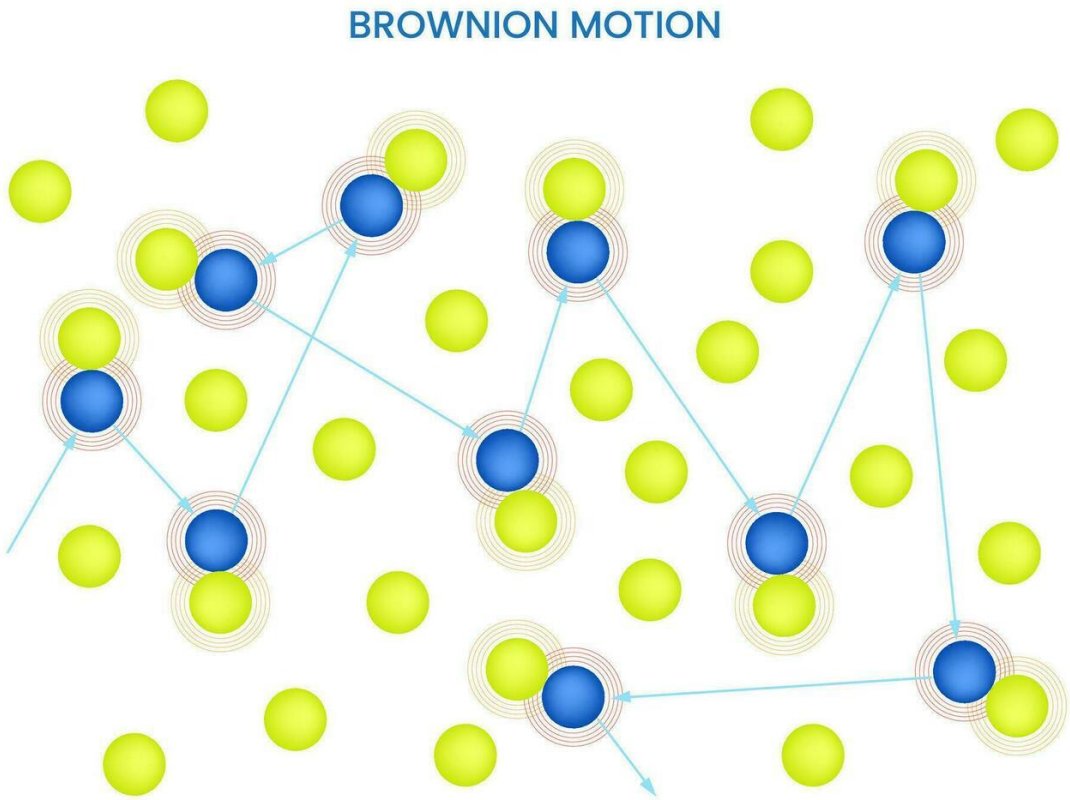
Scaling relationship beak vs. body mass



Rombaut et al. 2022

The “simplest” model- Brownian motion

- Brownian motion models the evolution of a trait through time.
- Trait value changes randomly up and down in value over time- Sometimes called a “random walk” model
- The statistical process of Brownian motion was originally invented to describe the motion of particles suspended in a fluid.



The motion of the object is due to the sum of a large number of very small random forces

- Brownian motion is a popular model in comparative biology
- It capture the way traits might evolve under a reasonably wide range of scenarios.
- Brownian motion has some very convenient statistical properties that allow relatively simple analyses and calculations on phylogenetic trees
- Brownian motion **IS NOT** genetic drift

Mathematics of Brownian motion

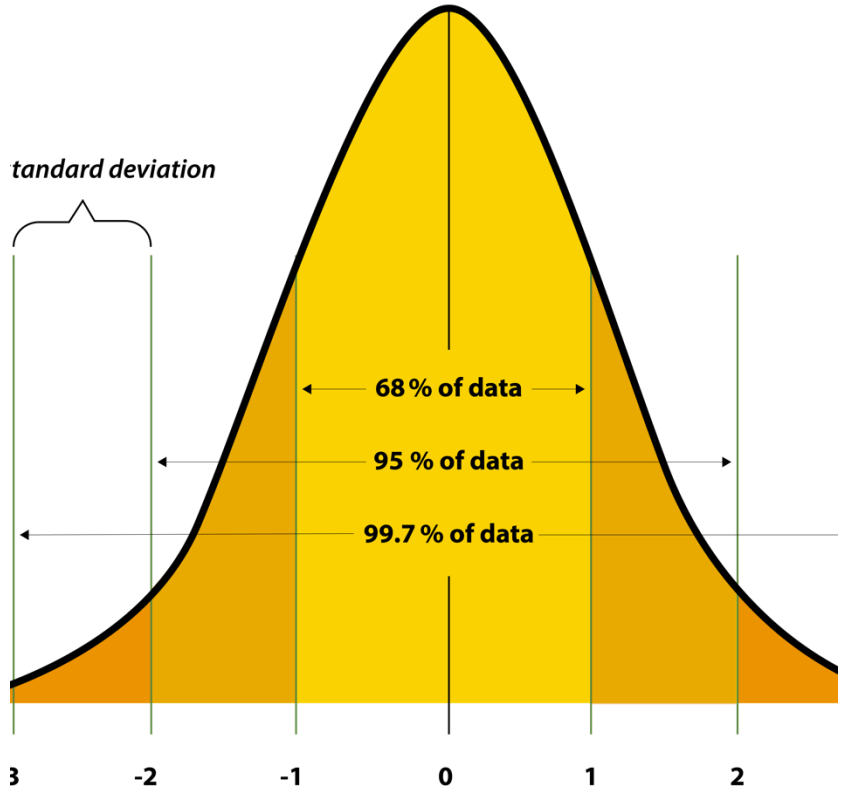
Mean value:

The mean value is the value at the root of our phylogeny (or start of the simulation) before any trait change happens

Evolutionary rate parameter:

We call this parameter “drift”, but it is not drift simply a variance on how much a trait can change.

Under Brownian motion, changes in trait values over any interval of time are always drawn from a normal distribution with mean θ and variance σ^2

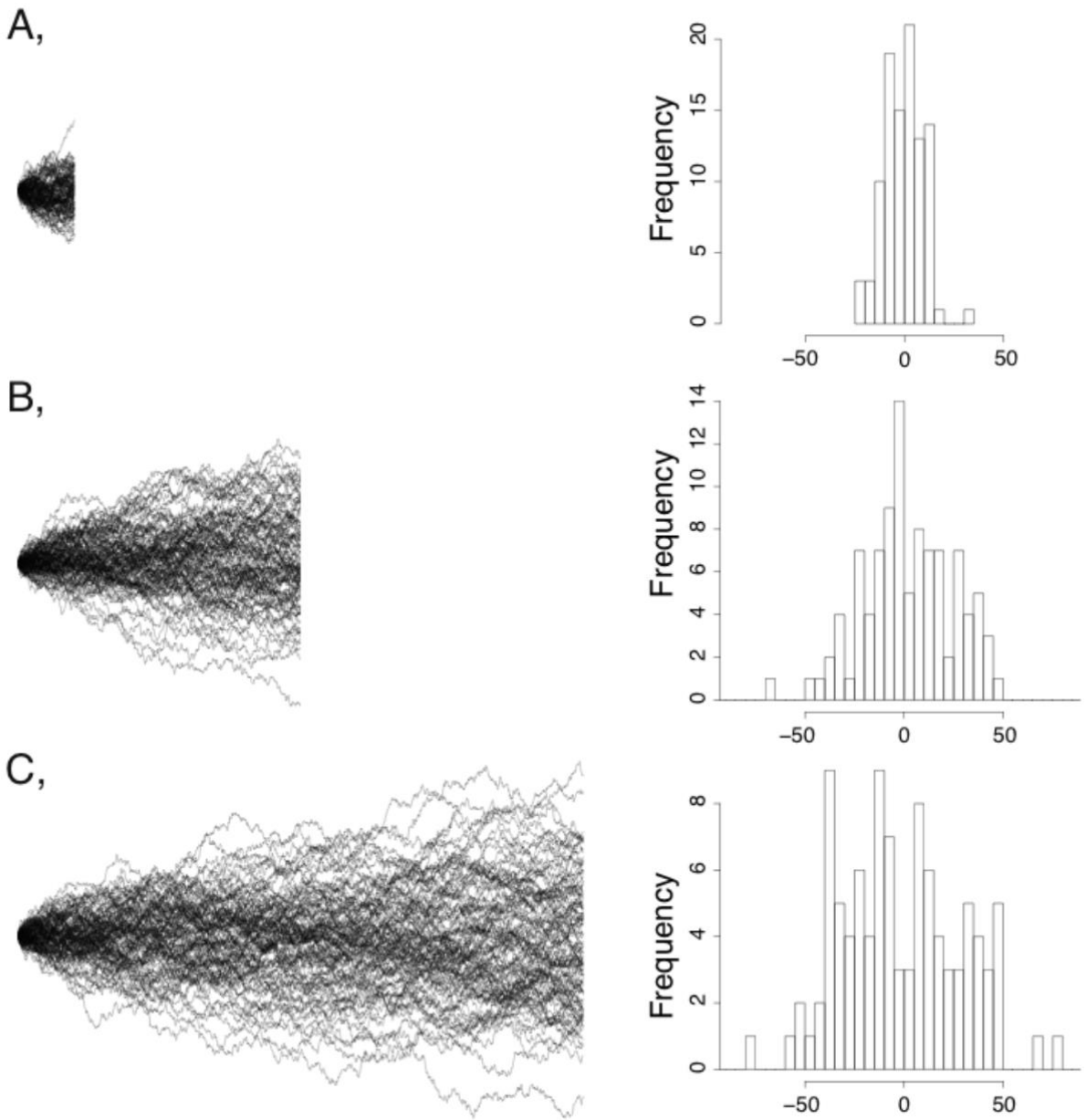


Brownian motion properties

When $X(t)$ is the value of the continuous trait at time t we have that

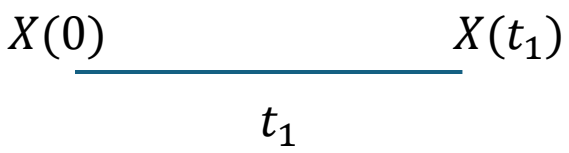
1. $E[X(t)] = \theta$
2. Each successive interval of the “walk” is independent
3. $X(t) \sim N(\theta, \sigma^2 t)$ the value of the trait is distributed Normal

Simulations of Brownian Motion
(without phylogenetic trees!)



Brownian motion over phylogenetic trees

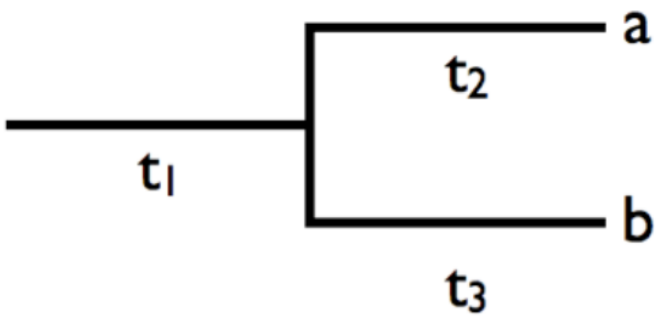
- Evolution of a trait along a single branch with length t_1



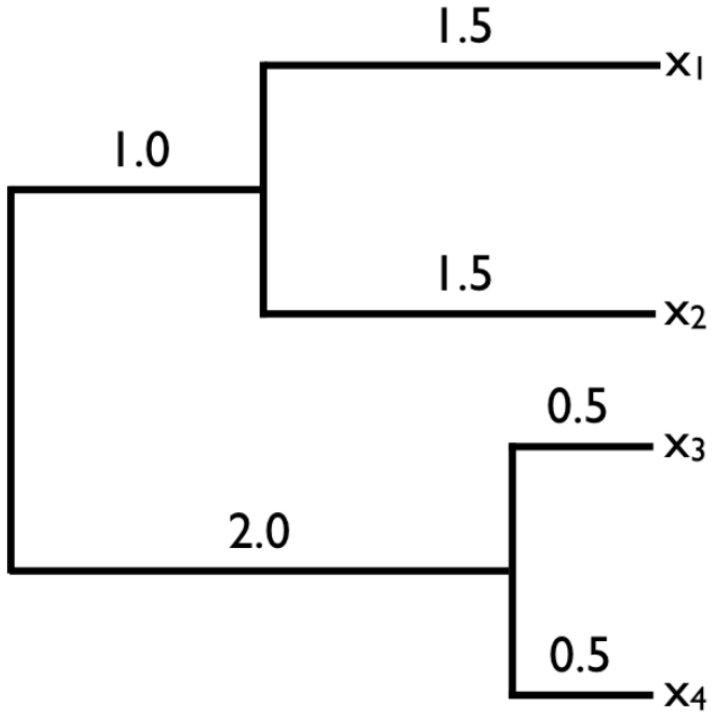
Brownian motion over phylogenetic trees

- a and b are not independent of each other. Instead, the two species share one branch in common .

- Each tip trait value can be thought of as an ancestral value plus the sum of two evolutionary changes: one (from branch 1) that is shared between the two species and one that is unique.



Variance-Covariance matrix



Simulating Brownian motion

Let’s try it with the phytools tutorial!