

Brownian motion models and phylogenies.

Wright-Fisher Model: everything deterministic.

↳ only n places can survive (random sampling succeed becoming adults for the next generation).

~~###~~ Brownian motion: moving along a scale and in any given moment there's a constant variance of the places that you will go to. ~~not~~

Edwards and Cavalli-Sforza's approximation.

modeling gene frequency change

needing to compute the probability of going from one gene frequency to another in a certain branch of the tree of a certain length in lineage.

approximate gene frequency change by Brownian motion model.

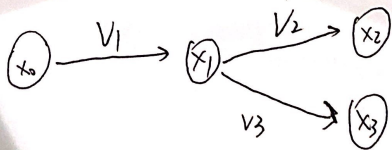
Brownian motion along a tree

for time t has expectation 0 and variance σ^2 per unit time.

displacement after time t is normal with expectation 0 and variance $\sigma^2 t$

Displacements in successive periods are independent.

$$\sigma^2(t_1 + t_2 + t_3)$$



displacement normally distributed independently
 $\Delta x_1 = x_1 - x_0$
 $\Delta x_2 = x_2 - x_1$
mean 0 and variance V_i

The covariance (noting that x_0 is constant and drops out)

$$x_2 = \Delta x_1 + \Delta x_2 + x_0, \quad x_3 = \Delta x_1 + \Delta x_3 + x_0.$$

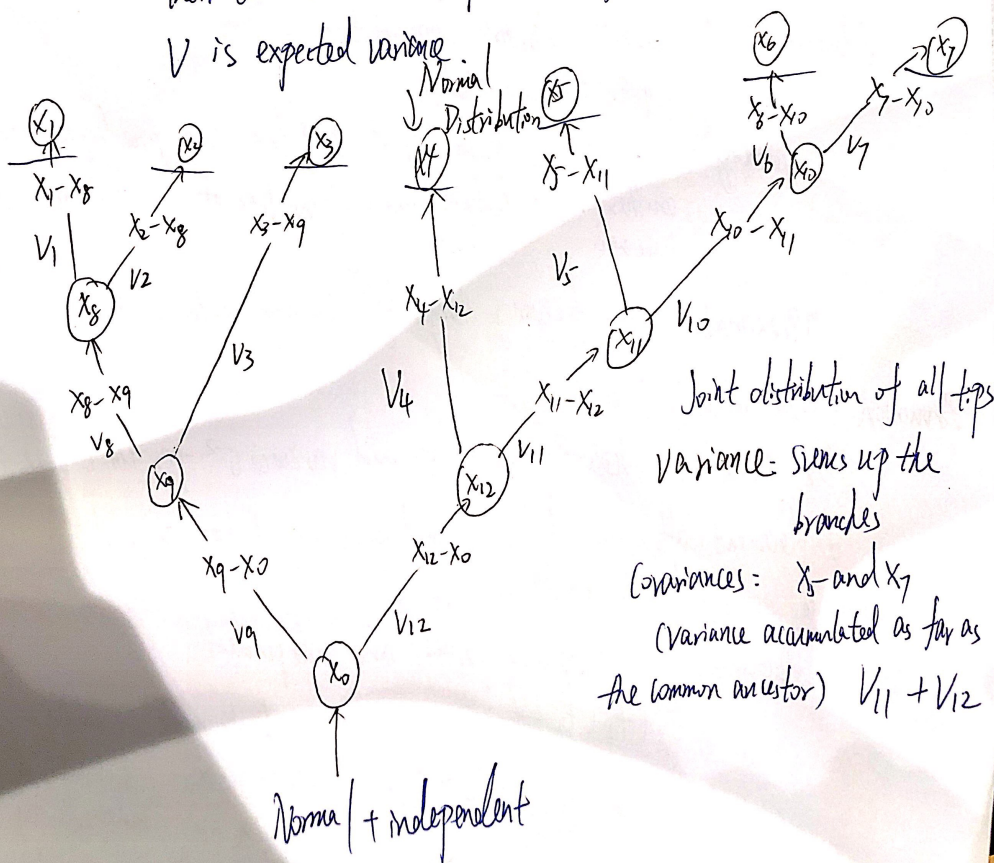
$$\text{Cov}(x_2, x_3) = \text{Cov}(\Delta x_1 + \Delta x_2, \Delta x_1 + \Delta x_3)$$

since changes in different branches are independent

$$\text{Cov}(x_2, x_3) = \text{Var}(\Delta x_1) = V_1.$$

~~the~~ the covariance between two tips is the ^{variance} accumulated up their common ancestor up the line as far as their common ancestor.

V is expected variance.



Phylogeny.

The evolutionary history of the relationships between all living things.

— all evolved from a common ancestor —

Derived trait — trait that is shared among a group of organisms
make their group unique.

clade — all evolutionary descendants of a common ancestor.