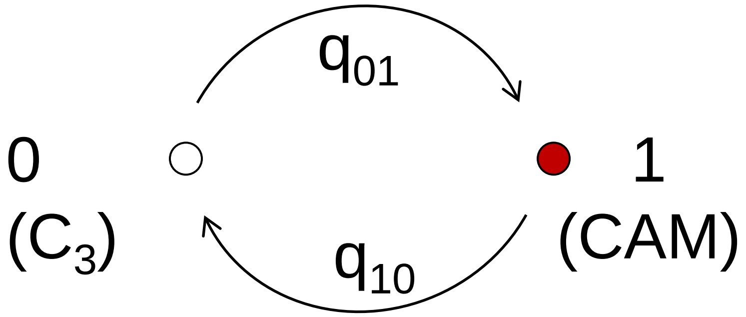
Markov Process for 1 discrete trait

Basic case: a single trait *Y*, only 2 states: 0,1.

Markov process: needs

- transition rates q_{01} (gain) and q_{10} (loss)
- probability of each state at the root: π_0, π_1



q_{01}

0 ○ ● 1

(C_3) (CAM)

q_{10}

Similar to evolutionary models for DNA, but only a single ‘column’ of data.

1. Maximum Likelihood: estimate rates

Choose gain (q_{01}) and loss (q_{10}) rates so as to maximize the likelihood:

P(tip data | rates q_{01} q_{10}, prior frequency at root)

Possible prior frequencies at the root:

- equal: $\pi_0 = \pi_1 = 0.5$
- equilibrium: $\pi_0 = q_{10} / (q_{10} + q_{01})$, $\pi_1 = q_{01} / (q_{10} + q_{01})$

Possible constraints on rates:

- none
- equal: $q_{01} = q_{10}$
- fixed value for gain rate. Ex: $q_{01} = 0.1$

2. Maximum Likelihood: ancestral states

Conditioned on the estimated rates, estimate ancestral states using the posterior probabilities:

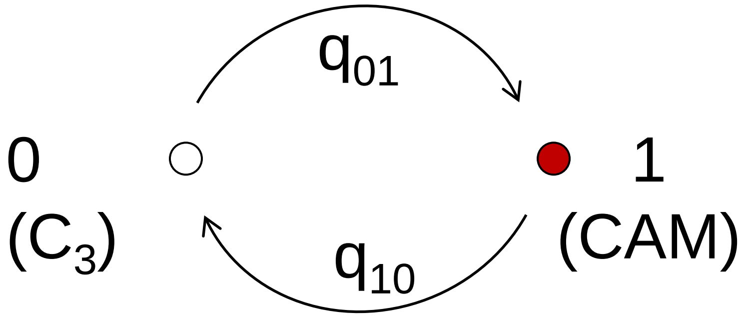
P(0 at node j | tip data, rates q_{01},q_{10}, prior π_0,π_1 at root)
P(1 at node j | tip data, rates q_{01},q_{10}, prior π_0,π_1 at root)

and plot these as a pie chart.

Choices made in Silvera et al.

In Silvera et al. and Mesquite:

"Mk1" = Markov, k-state trait, 1 parameter: $q_{01} = q_{10}$
"Asymmetric Mk" = Markov, 2-state trait, 2 parameters
"bias" = q_{01}/q_{10}.Used the constraint bias<1 i.e. $q_{01} < q_{10}$



Choices made in Silvera et al.

Continuous data analysis:

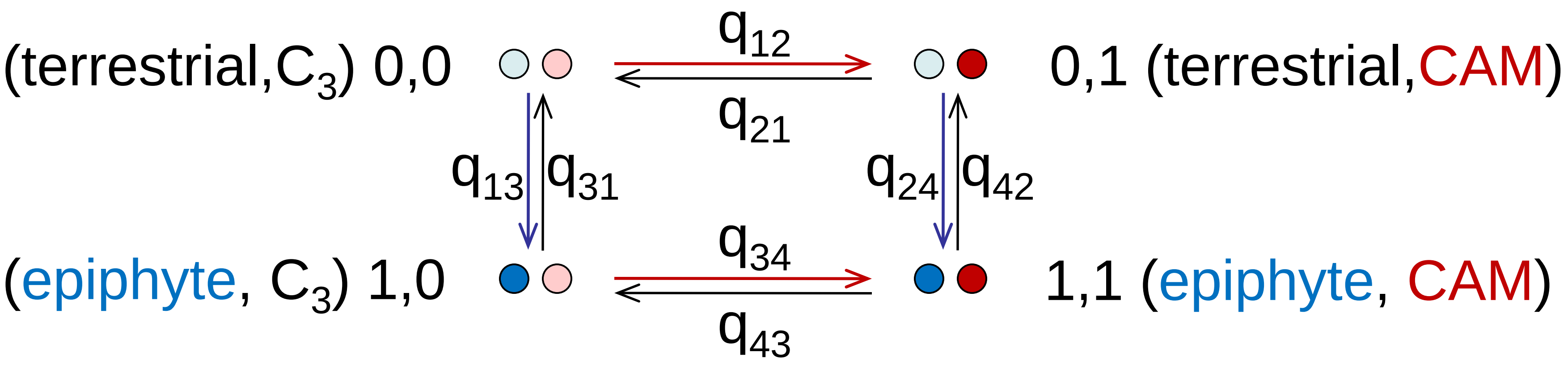
“Correlated divergence analysis was performed by constructing a 0-intercept linear regression between divergence in trait 1 (δ^{13}C) and divergence in trait 2 (epiphytism) […]. We used divergence width instead of independent contrasts as a measure of absolute trait radiation because the SD (divergence width) can be used when polytomies are present in the phylogeny)”

“divergence width” = SD across daughter nodes compared to their parent (Phylocom). For resolved nodes: divergence ~ absolute value of non-standardized contrast.

Markov Process for 2 discrete traits

Basic case: traits *X* and *Y*, 2 states each : 0,1.

Markov process: needs
- transition rates q’s
- probability of each state at the root: π’s



(terrestrial,C_3) 0,0

0,1 (terrestrial,CAM)

(epiphyte, C_3) 1,0

1,1 (epiphyte, CAM)

Maximum Likelihood

Same as with 1 trait: get rates (q values) that maximize the likelihood:

P(tip data | rates q's, prior frequency at root)

Possible prior frequencies at the root:

- equal: $\pi_{00} = \pi_{10} = \pi_{10} = \pi_{11} = 0.25$
- equilibrium: π = some function f(q's)

- For better accuracy or numeric stability: Fix small value for "first gain" rates. Ex: $q_{12} = q_{13} = 0.1$

Testing correlation with ML

- Independent evolution for the 2 traits: parallel arrows have equal rates:

$q_{12} = q_{34}$, $q_{21} = q_{43}$, $q_{13} = q_{24}$, $q_{31} = q_{42}$

If any of these equalities does not hold, then correlated evolution.

- Likelihood Ratio Test for correlation:

ℓ_0 = logL(tip data | independence equalities enforced)
ℓ_1 = logL(tip data | independence equalities NOT enforced)

Compare $2*(\ell_1 - \ell_0)$ to a chi-square distribution.