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1 Adding h to the trait-population evolution model

In the new version, we added a new parameter h to the model, expressing the heritability across generations. Before, we just assume it to be 1. Notice that there are two places adding h . One is in Eq.2, h^2 appears in front of the second term on the right hand side. The other one is in Eq.3, h^4 is added in front of the last term on the right hand side.

$$N_{i,t+1} = N_{i,t} R_0 e^{-\gamma(\theta - z_{i,t})^2} \cdot e^{-\beta/\beta_0} \quad (1)$$

$$z_{i,t+1} = z_{i,t} + h^2 V_{i,t} \left(2\gamma(\theta - z_{i,t}) + \frac{2\alpha}{\beta_0} \sum_j (z_{i,t} - z_{j,t}) e^{-\alpha(z_{i,t} - z_{j,t})^2} N_{j,t} \right) + \eta_{i,t} \quad (2)$$

$$V_{i,t+1} = \frac{1}{2} V_{i,t} + \frac{2N_{i,t}\nu V_{max}}{1 + 4N_{i,t}\nu} \quad (3)$$

$$+ h^4 V_{i,t}^2 \left[2\gamma(-1 + 2\gamma\theta^2) - \beta_0^{-1} \sum_j (4\alpha^2(z_{i,t} - z_{j,t})^2 - 2\alpha) e^{-\alpha(z_{i,t} - z_{j,t})^2} N_{j,t} \right.$$

$$- \left(2\gamma(2\theta - z_{i,t}) + 2\alpha\beta_0^{-1} \sum_j (z_{i,t} - z_{j,t}) e^{-\alpha(z_{i,t} - z_{j,t})^2} N_{j,t} \right)$$

$$\cdot \left. \left(2\gamma z_{i,t} - 2\alpha\beta_0^{-1} \sum_j (z_{i,t} - z_{j,t}) e^{-\alpha(z_{i,t} - z_{j,t})^2} N_{j,t} \right) \right].$$

2 Set the initial variance of the trait to be one argument of the simulation function

We would like to confirm that the initial condition doesn't affect the results. So the initial variance of the trait should be tested. Before, we have it valued in the simulation function, $V[0] = (1/\text{td.total species})$.

3 A simulation function for Drury's model

As we want to test if our model is superior than Drury's model, I applied the SMC algorithm to both our model and Drury's model. However, even though I have parallelized my code for simulation under Drury's model, the speed is still much slower like a snail compare to your code. So I am wondering if you could implement this model to C++. The model is super simpler than our model. It only contains the trait mean dynamics. The model is as follows:

$$z_{i,t+1} = z_{i,t} + \gamma(\theta - z_{i,t})dt + m \cdot \text{sign}(z_{j,t} - z_{i,t}) \cdot e^{-\alpha(z_{j,t} - z_{i,t})^2} dt + \sigma^2 dt. \quad (4)$$

I want to obtain the sim_time and the traits of the tips given a phylogenetic tree.