The first thing I want to consider is a comparison of two methods of simulating a GEM. The first is the classic GEM, which chooses an individual at random, uses a Monte Carlo algorithm to determine what happens to it based on the individual's traits, and then advances time a random amount based on the total rate of events for that individual. The second method modifies the algorithm by creating the "wheel of fortune" using the rates for every individual in the population, and then using the Monte Carlo algorithm to choose both an individual and an event from a single "spin" of the wheel. Obviously, time will advance much more slowly in the second model because the timestep is chosen using the code exp(-1/sum(events))/sum(events): since the second method sums across all events (births and deaths) for every individual in the population, the denominator is a very large number in the second method. Fig. 1 shows a comparison of the dynamics for the two models for an initial CV of 0.1 and a heritability of 0.8. It is clear that the second method (in red) shows much more high intensity fluctuation around the carrying capacity (top row) and also evolves further towards the ESS trait value (ESS = 3, bottom row), although neither actually gets very close.

Fig. 2 shows a comparison of the dynamics for the two models for an initial CV of 0.2 and a heritability of 0.9. Here, you see a similar pattern for the population dynamics, but the trait dynamics are really different. The first method shows wild fluctuations in the trait dynamics, whereas the second shows much less wild excursions, but doesn't get much closer to the ESS than it did when the CV and heritability were lower.

The question is which method is actually better. I'm not sure this question has an answer, but one way to think about it is to think about how time advances. In the first method, the size of the timestep is independent of the number of individuals in the population. The expected timestep size is given by

$$\exp(-1/(\bar{b}+\bar{d}))/(\bar{b}+\bar{d}),$$
 (1)

where \bar{b} and \bar{d} are the average birth and death rates for the population and N is the total population size. In the second method, the size of the timestep depends on the number of individuals in the population. The expected timestep size is given by

$$\exp(-1/(N*(\bar{b}+\bar{d})))/(N*(\bar{b}+\bar{d}))$$
 (2)

My recollection is that, in the standard Gillespie algorithm, time advances proportional to the number of particles in the population.

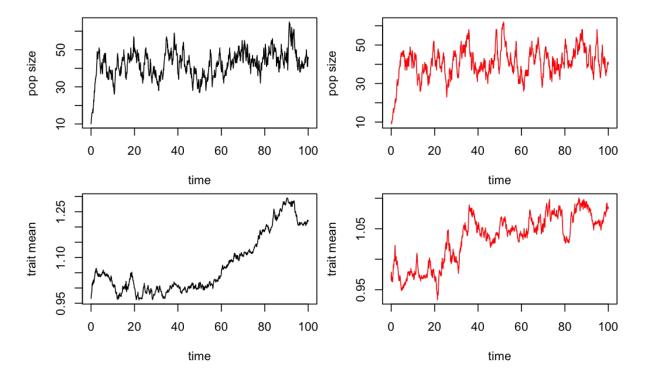


FIGURE 1. GEM simulation for the original method.

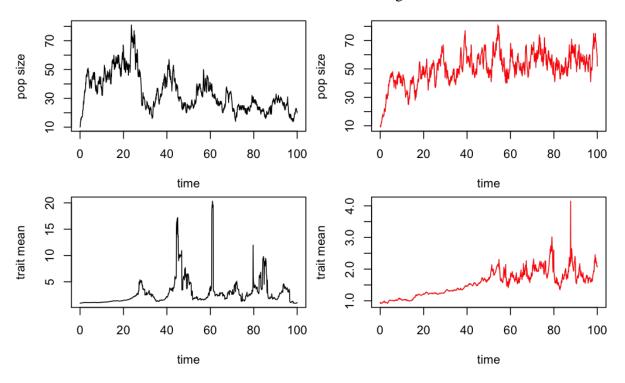


FIGURE 2. GEM simulation for the second method.

The next thing I wanted to look at was the way that offspring traits are drawn.