

Re: Coevolutionary model

Francisco Escobar-Velas  
Thu 11/20/2019 12:18 PM

Hi,  
R. Escobar-Velas <resobar@eawag.ch>, Melian, Carlos <Carlos.Melian@eawag.ch>

Hi Ramon,

Yes, that's good idea, instead to see how that changes the evolution of the phenotypes, it should generate more diversity.

Cheers,

Ram

Hi Ram, 26 Nov 2018 at 16:53, Ramon F. Escobar-Velas <resobar@eawag.ch> wrote:

Hi both,

I have discussed this with Hanneke and we think it will still give the same result, no divergence, because the tendency to evolve to the intermediate phenotype (50:50) is just too strong. We think one would need some form of epistasis. The simplest form we could think of is to count a 1 only if it is followed by a 1. Then a sequence 010001 will have a very different phenotype than 000011, so the 50:50 convergence can result in very divergence in phenotypes. What do you think?

Cheers, Ramon

On 10 Nov 18 04:15, Francisco Escobar-Velas wrote:

Hi Ramon,

First sorry for my late reply, very busy here.  
I have had some solutions for the 50:50 dilemma using 1s and 0s, and keeping a quantitative genetic approach will be to sample allelic effects from a normal distribution. The phenotype of an individual will be the sum of the 8 alleles, each 1s the diploid but plus a random environmental component. Similar approaches are implemented in Quantitative software as mentioned in the following paper:  
<https://doi.org/10.1093/bioinformatics/bty184>

The aforementioned approach is widely used and I think more realistic than the additive binary genome approach.

Let me know what do you think.

Cheers,

Ram

On Wed, 12 Sep 2018 at 6:40 pm, Ramon F. Escobar-Velas <resobar@eawag.ch> wrote:

Hi Ram,

I discussed this with Hanneke and the had already played with these options, and, unless we build in some strong divergence (e.g., due to strong competition for resources), this will not give us formation of clusters. The reason is that the additive genetic architecture has the strong tendency to equilibrate at a 50:50 division of 0s and 1s and hence at the intermediate phenotype. What might solve the problem is

1) to use a simple quantitative trait that is NOT coded by genetics, but simply doing a random walk in absence of species interactions. Then, the trait is allowed to go to all values rather than a strong tendency to go to the intermediate trait value.

2) non-additive genetics: e.g., 000001 would give us a phenotype 0.01 and 100000 would give us a phenotype 0.01. In strong options (e.g., use the frequency of 0s and 1s in 50:50 in all cases).

I think option 1) is an easy solution, which is computationally simpler, and one could argue that it makes sense to have genetics only for reproductive compatibility, not for the quantitative trait.

What do you think?

Cheers, Ramon

On 10 Sep 18 08:00, Francisco Escobar-Velas wrote:

Hi Ramon,

Yes, we can go with your plan of doing first 2 and then 1, although I think already doing 2 might be enough.

Cheers,

Ram

Hi Ram, 4 Sept 2018 at 16:46, Ramon F. Escobar-Velas <resobar@eawag.ch> wrote:

Hi Ram,

I don't think there is a point in making figures of complementarity and convergence or trying to fit to data. The problem is that all animal species converge to the same trait (within a narrow range) and all plant species converge to the same trait (that is slightly lower than that of the animals). The problem lies in the purely additive nature of the trait, the deterministic nature of the plant-animal compatibility, and the fact that there is no competition, i.e. every individual profits from being maximally connected to all individuals of the other guild.

Can we do several things:

1. We add competition for resources, e.g., that for a while the plant is unavailable after being selected by its animal. This may perhaps lead to some divergence in traits.

2. We assume that rather than a deterministic map function for compatibility of plant and animal we have to assume something more smooth where animals with a very large trait are not as compatible with a plant with a smaller trait value. This could be incorporated as a probability of compatibility in the model, rather than a precise which is currently in the model.

3. We make the trait slightly epistatic rather than fully additive, meaning that genotypes have to match in some way or another which will avoid the 50:50 division of 0s and 1s leading to the usual same mean trait value.

We may need a combination of these. I would probably start with number 2, then 1, then a combination of 1 and 2, and if that does not work, think about number 3. Let me know what you think.

Cheers, Ramon

On 04 Sep 18 08:22, Francisco Escobar-Velas wrote:

Hi Ramon,

I have discussed with Carlos the results of the model, we found them very interesting, however we think that it would be good to have the same figures that we produced for the previous model to compare both models using the same parameter combinations. Specifically, I mean the figures from our manuscript (Fig. 1 and 4), see attached pdf, about the trait distributions and the results of convergence and complementarity (compared to the empirical data). One important thing that needs to be explained is the effect of genetic distance that will surely affect speciation rates.

The new results showing phase transitions are very interesting but perhaps could go in a different paper. That paper could explore bistability, hysteresis and phase transitions in diversification and diversity patterns. There are some references exploring the genome compaction model mostly in diploids: <http://www.sciencedirect.com/science/article/pii/S1537810115000000>

I can send you the specific parameter values that I used to generate the figures and the code to calculate convergence and complementarity.

Cheers,

Ram