Re:
Coevolutionar
y model

Francisco Encinas-Viso
Thu 11/29/2018 12:18 PM

To:
R.S.Etienne <rs.etienne@rug.nl>; Melian, Carlos <Carlos.Melian@eawag.ch>;

Hi Rampal,

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

Cheers,

Fran

El lun., 26 nov. 2018 a las 19:33, Rampal S. Etienne (<rs.etienne@rug.nl>) escribió:

> Hi both,
>
> I have discussed this with Hanno 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 01010101 will have a very different phenotype than 00001111, so the 50-50 convergence can result in very divergence in phenotypes. What do you think?
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> Cheers, Rampal
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> On 12-Nov-18 04:11, Francisco Encinas-Viso wrote:
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> > Hi Rampal,
> >
> > First sorry for very late reply, very busy here.
> > I think that one solution for the 50-50 division using 0s and 1s, and keeping a quantitative genetic approach will be to sample allelic effects from a normall distribution. The phenotype (z) of an individual will be the sum of the X allelic values at the N diploid loci plus a random environmental component. Similar approaches are implemented in Quantitenno software as mentioned in the following paper:
> >
> > https://link.springer.com/content/pdf/10.1007%2Fs10530-010-9544-6.pdf
> >
> > The aforementioned approach is widely used and I think more realistic than the additive binary genome approach.
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> > Let me know what do you think,
> >
> > Cheers,
> >
> > Fran
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> > On Wed, 12 Sep 2018 at 6:40 pm, Rampal S. Etienne (<s.etienne@rug.nl>) wrote:
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> > > Hi Fran,
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> > > I discussed this with Hanno, and he 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.
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> > > 2) non-additive genetics, e.g. 00000111 would give us a phenotype of 0, 01010101 would give us a phenotype of 0.5 and 11110000 would give us a phenotype of 1, i.e. strong epistasis (as you see the frequency of 0s and 1s is 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.
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> > > What do you think?
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> > > Cheers, Rampal
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> > > On 10-Sep-18 08:58, Francisco Encinas-Viso wrote:
> > >
> > > > Hi Rampal,
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> > > > Yes, we can go with your plan of doing first 2 and then 1, although I think already doing 2 might be enough.
> > > >
> > > > Cheers,
> > > >
> > > > Fran
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> > > > El mar., 4 sept. 2018 a las 18:49, Rampal S. Etienne (<s.etienne@rug.nl>) escribió:
> > > >
> > > > > Hi Fran,
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> > > > > 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 this 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.
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> > > > > So we can several changes:
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> > > > > 1. We add competition for ressources, e.g. that for a while the plant is unavailable after being visited by an animal. This may perhaps lead to some divergence in traits,
> > > > >
> > > > > 2. We assume that rather than a deterministic step 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 small trait as an animal with a smaller trait value. This could be incorporated as a probability of compatibility in the model, rather than a yes/no 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 overall same mean trait value.
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> > > > > 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.
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> > > > > Cheers, Rampal
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> > > > > On 04-Sep-18 08:22, Francisco Encinas-Viso wrote:
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> > > > > > Hi Rampal,
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> > > > > > I have discussed with Carlos the results of the model, we found them very interesting. Howewer,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 3 and 7, 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 explored is the effect of genetic distance that will surely affect speciation rate.
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> > > > > > **The new results showing phase transition are very interesting but perhaps could go in a different paper. That paper could explore histeresis, bistability and phase transitions in diversification and diversity patterns. There are some references exploring the genome congealing model mostly in diploids.** https://www.nature.com/articles/s41559-017-0082
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> > > > > > **I can send you the specific parameter values that I used to generate the figures and the code to calculate convergence and complementarity.**
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> > > > > > **Cheers,**
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> > > > > > **Fran**