

Determinism in SLiM

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18/05/2020

Introduction

I've been noticing some strange behaviour with my output when modelling two traits: certain values keep cropping up for the same seed, which indicates the deterministic nature of SLiM and the effect that each parameter has on affecting that determinism. In particular, the same pleiotropy values (which are the covariance values used in the variance-covariance matrix sigma used when pulling values for phenotypes 0 and 1 from a multivariate normal) result in the same phenotypes for trait 0. Below are some examples of this.

```
> slim_out[slim_out$mean0 == 0.030587500, ]
```

	gen	mean0	var0	mean1	var1	cov	pear	seed	r	delmu	pleio
1	100	0.0305875	0.0564421	-0.01489140	0.0281072	-0.02748320	-0.690012	929413209	1e-08	0	0.000
2	100	0.0305875	0.0564421	-0.01489140	0.0281072	-0.02748320	-0.690012	929413209	0e+00	0	0.000
1335	100	0.0305875	0.0564421	-0.01095120	0.0217330	-0.02021240	-0.577105	929413209	0e+00	0	0.125
1617	100	0.0305875	0.0564421	-0.01095120	0.0217330	-0.02021240	-0.577105	929413209	1e-08	0	0.125
3208	100	0.0305875	0.0564421	-0.00677167	0.0165729	-0.01249990	-0.408702	929413209	0e+00	0	0.250
3459	100	0.0305875	0.0564421	-0.00677167	0.0165729	-0.01249990	-0.408702	929413209	1e-08	0	0.250
5053	100	0.0305875	0.0564421	0.00239741	0.0113898	0.00441993	0.174323	929413209	0e+00	0	0.500
5303	100	0.0305875	0.0564421	0.00239741	0.0113898	0.00441993	0.174323	929413209	1e-08	0	0.500

What this says to me is that linkage between gene regions (r) from 0 to 1e-08 doesn't have any appreciable effect on the simulation to affect the determinism of the simulation at a certain seed, but 0.5 (which is my third level for linkage) does. Deleterious mutation has an effect on determinism when they are included (shown by all of the values listed here having the same delmu value). Interesting that mean0 remains the same for all of them, whereas mean1 changes between runs with different levels of pleiotropy. This could be related to how SLiM processes pulls from multivariate normal distributions somehow? The pulls may be sequential, with the second (from which mean1 is calculated) being dependent on the first. This would explain the result, as the pleiotropic effect which is affecting mean1's constituents (the individual mutation effects) but not mean0's is pulled after mean0 (or rather, the constituent effects of mean0) is already stored. I think this means that there's no reason to include 1e-08 as a treatment level, it should be replaced with a higher recombination rate, something like 1e-05? Will have to test. What is annoying about this is that for each level of r and deleterious mutations (which do affect mean0 at a given seed), they will have an identical mean0 for each level of pleio (which doesn't affect it!).

We'll look at another example for r = 0.5:

```
> slim_out[slim_out$mean0 == -0.000966824, ]
```

	gen	mean0	var0	mean1	var1	cov	pear	seed	r	delmu	pleio
39	100	-0.000966824	0.000233219	0.00814330	0.0165451	-0.00196434	-1	929413209	0.5	0	0.000
1885	100	-0.000966824	0.000233219	0.00795858	0.0158030	-0.00191978	-1	929413209	0.5	0	0.125
3735	100	-0.000966824	0.000233219	0.00764301	0.0145747	-0.00184366	-1	929413209	0.5	0	0.250
5582	100	-0.000966824	0.000233219	0.00656890	0.0107660	-0.00158456	-1	929413209	0.5	0	0.500

Because this r value (0.5) results in a different mean0 than the other levels for the same generation and seed, clearly it does have an effect on the determinism of the simulation. This particular mean0 value appears 4 times, one for each level of pleiotropy, indicating the same thing as before: each level of pleiotropy has an effect on the determinism of mean1 but not mean0.

We'll look at a different deleterious mutation rate and see what happens:

```
> slim_out[slim_out$mean0 == 0.005640700, ]
```

	gen	mean0	var0	mean1	var1	cov	pear	seed	r	delmu	pleio
516	100	0.0056407	0.013333	-0.00706205	0.0263014	0.0111262	0.594147	929413209	1e-08	0.1	0.000
2208	100	0.0056407	0.013333	-0.00630157	0.0288585	0.0127055	0.647729	929413209	0e+00	0.1	0.125
2451	100	0.0056407	0.013333	-0.00630157	0.0288585	0.0127055	0.647729	929413209	1e-08	0.1	0.125
3796	100	0.0056407	0.013333	-0.00542762	0.0308773	0.0141061	0.695224	929413209	0e+00	0.1	0.250
4057	100	0.0056407	0.013333	-0.00542762	0.0308773	0.0141061	0.695224	929413209	1e-08	0.1	0.250
5583	100	0.0056407	0.013333	-0.00329556	0.0326949	0.0163020	0.780799	929413209	0e+00	0.1	0.500
5838	100	0.0056407	0.013333	-0.00329556	0.0326949	0.0163020	0.780799	929413209	1e-08	0.1	0.500

Only 7 values here: for whatever reason, with 0 pleiotropy, no linkage (r) does have an effect on determinism of mean1 compared to $1e-08$ linkage. The rest is pretty much the same as before though - same seed, same generation, same mean0 with mean1 differing between pleiotropy values.

Now lets confirm this with a different seed:

```
> slim_out[slim_out$mean0 == -0.052997300, ]
```

	gen	mean0	var0	mean1	var1	cov	pear	seed	r	delmu	pleio
21763	100	-0.0529973	0.053311	0.005995120	0.01165690	-0.01222490	-0.490394	676365814	0e+00	0.1	0.000
22015	100	-0.0529973	0.053311	0.005995120	0.01165690	-0.01222490	-0.490394	676365814	1e-08	0.1	0.000
23640	100	-0.0529973	0.053311	-0.000676563	0.00927547	-0.00546512	-0.245767	676365814	0e+00	0.1	0.125
23901	100	-0.0529973	0.053311	-0.000676563	0.00927547	-0.00546512	-0.245767	676365814	1e-08	0.1	0.125
25511	100	-0.0529973	0.053311	-0.007444570	0.00834192	0.00149107	0.070706	676365814	0e+00	0.1	0.250
25781	100	-0.0529973	0.053311	-0.007444570	0.00834192	0.00149107	0.070706	676365814	1e-08	0.1	0.250
27312	100	-0.0529973	0.053311	-0.021306700	0.01148340	0.01606850	0.649428	676365814	0e+00	0.1	0.500
27572	100	-0.0529973	0.053311	-0.021306700	0.01148340	0.01606850	0.649428	676365814	1e-08	0.1	0.500

Once again, 8 different results each with the same mean0, showing no effect of $r = 0$ vs $1e-08$ on the deterministic nature of SLiM affecting mean0, and also 4 results showing pleio only affecting mean1. So this isn't just one seed.

Conclusion

The pleiotropy value appears to affect only mean1, implying values are pulled sequentially from the `rmvnorm()` function in SLiM, dependent on the first value (which is averaged to give mean0). The result of this is that for any given combination of r and `delmu` treatments, mean0 is the exact same for every single level of pleio, invalidating any comparisons between mean0 and mean1, or var0 and var1; basically any look into covariance or correlation as a result of pleio doesn't make any sense because all the seeds with a given parameter set (minus pleio) give the same values for mean0 regardless of pleio. On the bright side, this has shown that I should choose a different level for r in future. I guess this means I should randomise pleiotropic effects per mutation and stop looking at its individual effects, because clearly that doesn't make any sense.