Bayesian nets
Meeting notes 11/30/2022

Amber, Dennis, Zhongming and Patrick were physically present.

1. Amber presented admirable progress with the full basic set-up:

We start with a world that generates an evidence string and a random representation scored on the basis of whether its evidence string matches that of the world. The representation breeds variations using either (a) one-point or (b) two-point mutation, with the variations again scored in terms of evidence-match. The best of those is again mutated…

A very nice feature: Amber's program registers the number of generations of this sort until there is a full match in evidence.

2. She also noted a complication in the way we were doing things, and an unexpected feature of two-point mutation.

a. The complication: These two nets return the same evidence matrix, meaning that the one on the right is taken as a 'match' for the one on the left:
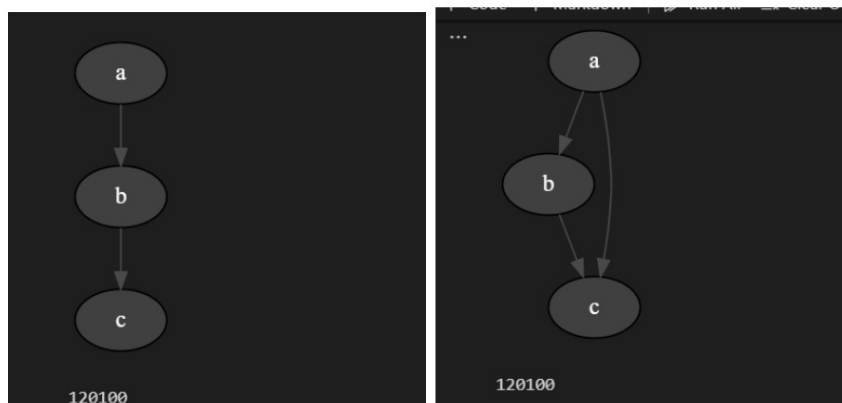
We discussed ways of remedying that. Amber worked out a fix in which recourse was made to the adjacency matrices. If those didn't match, 'try again…'

We decided it would be better if the fix could have recourse only to the evidence stream, which means we have to distinguish cases in which c is accessed at both steps 1 and 2 from the ase in which it is only accessed at step 2.

I think Dennis has an idea for a way of representing evidence streams so as to distinguish these.

b. The unexpected feature: Although double mutation is often faster, there are cases in which double mutation alone won't give us the right answer—a single mutation is needed to reach the goal, and double mutation ends up oscillating between two not-quite-right variations.

As Amber concluded, there are cases where we need an odd number of changes to match the world, and double mutation limits us to an even number of changes.

We also discussed how to address this. Amber's fix uses double unless there is a single digit incorrect, in which case run single mutation.

That may or may not work in all cases. An alternative: At each generation, randomly run a double or single mutation.

I think an argument could be made for either of these as a model of scientific theory-change. In favor of Amber's version: It seems wise to explore broadly (with double mutations), only later fine-tuning in terms of single mutation. In favor of the random model: Perhaps we don't always know on how many spots our theory is off.

3. Amber's results make it clear that there are cases where double mutation alone won't get the right result. Patrick raised the question of whether there are cases where single mutation alone wouldn't get the right result—that two simultaneous changes would be required to get there.

The abstract idea of this is that single changes, starting from a certain network, would get stuck in a 'local maximum,' not getting to the global maximum. But that's just an abstract picture that holds in other models of other things.

Whether that holds here or not, and whether it holds for simple or only more complicated nets, remains an open question. Patrick handed the question to Zhongming, promising a better outline of the question.

But at the moment he's also not sure that in phrasing the problem it might not become clear that this couldn't happen.

4. There was also some discussion of approximation algorithms, which seems another promising lead.

5. The outline for next steps:

Dennis is going to figure out coding of the evidence stream that will distinguish the cases in 2a above.

For work down the line, he's also going to try to figure out how to do a 'hybrid' genetic algorithm: Take the adjacency matrices of the two most successful networks, and make a new one that combines a section of one with the corresponding section of the other.

In addition to the explorations so far, Amber is going to explore what happens with:

(a) 'guided' mutation, where nothing that is correct is changed, and
(b) random single- and double-mutation. Here, given the randomness, how successful such a combination is will have to be gauged in terms of an average of steps required over a number of runs.

… plus any other good ideas that come up.

All good stuff. Next meeting Wednesday December 7th, same time and place.

Thanks,
Patrick