Bayesian nets
Meeting notes 12/07/2022

Patrick, Amber, and Zhongming met. Dennis indicated that he somehow forgot about he meting, but has been in contact since.

This was a brief 'catch-up' meeting. Amber indicated that she had programmed the randomization of single- and double- genetic algorithm mutations, as well as the 'don't change the good parts' heuristic.

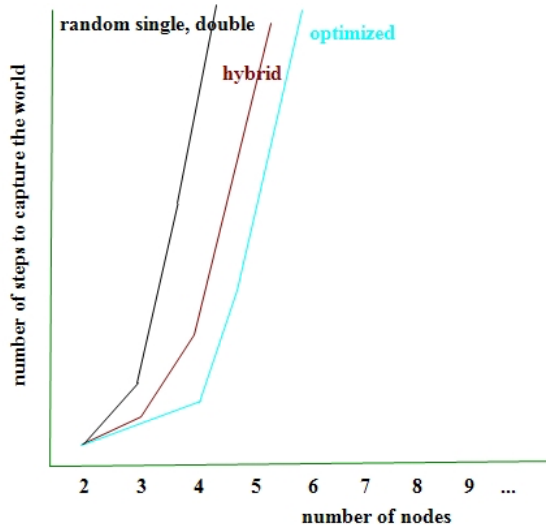
She also had some comparative results regarding average numbers of steps required for the representation to match the world, using some of these different heuristics.

Dennis is to pass programming for hybrid (crossover) genetic algorithm networks along to Amber when he has them, as well as his ideas on a 'sequential scene' representation of the evidence pattern of networks (if I have that right).

With regard to hybrid, it occurs to me that one way to do this would be to simply pick a random set of cells from the network matrix for one fairly successful network, and combine those with the *other* cells from a second successful matrix. That would avoid any problem of position bias in the matrices. But our hybrids might end up not making sense or containing loops, might they not?

Zhongming has calculated the 'space' of possible configurations of n-node networks without loops. His result is 2n! (see attached). This is clearly right for 3-node networks, but we want to be sure that it generalizes.

Patrick indicated that a useful next step, combining these two streams, would be to construct graphs of how many steps different mutation heuristics take to find the 'world' for networks of increasing numbers of nodes. Something like:



We will meet again next semester. Dennis has promised to set up a when2meet page for scheduling for meetings then.

At that point we'll also try to integrate Bayesian updating of credences and conditional probabilities in networks with the kind of structural change we've been working out in simple causal networks.

If you haven't given me a snail-mail address for a holiday card, send that along…

Patrick