Braitenbot Summer

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Outline

1. What I Did This Summer

2. Next steps

Important Summer Accomplishments

- Added to, debugged, and validated code (although this will be an ongoing process).
  - Most important addition is an algorithm that automates the performance-wise ranking and crossing of a gen.
- Developed tractable hypothesis(es) and corresponding experiment(s).
- Ran and analyzed preliminary experiments (in simulation), confirming evolution is possible in our model, among other things.
- Collected and organized code into a comprehensable document that will facilitate validation and future additions

Crossing Algorithm

Designed an algorithm that crosses organisms based on task performance.

- Organisms are placed in pools of two with the top two performers in the highest pool, the next two in the second highest, etc.
- After orgs are crossed (starting with the highets pool) they are placed in successive pools for more chances to reproduce.
  - Result is top perfromers mate multiple times with potentially many different orgs

Hypothesis

Given the mutability of the distribution and number of crossover points, we propose the following hypothesis:

H_1

The distribution of crossover points influences the robustness of an organism's traits, and thus, is directly related to evolvability, fitness, and modualrity.

Experiments

I ran multiple simulated populations in order to verify that the model is sensitive to selection pressures.

- Selected for number of 'functional' threads.
- Altered a number of genomic parameters across populations to determine how they would affect selection.

Mean results for each population type

Take Home
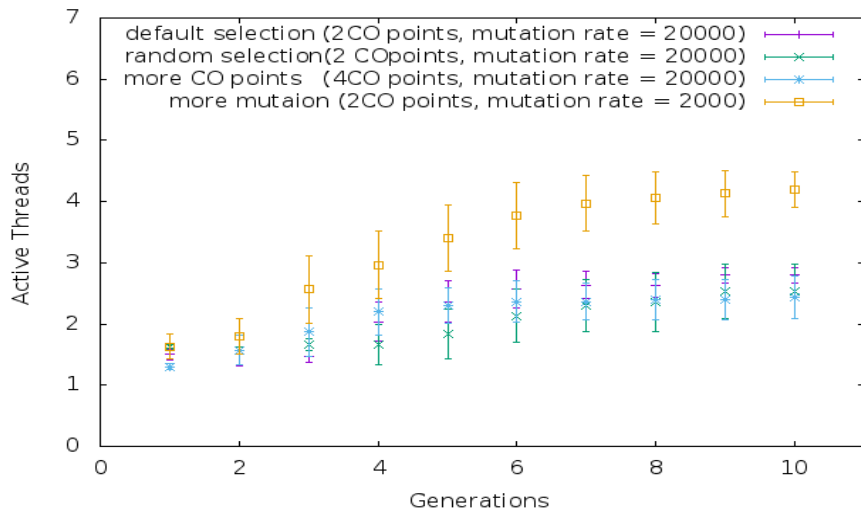
- Adaptive evolution is possible
- Due to many factors, including small population size,there is not much variation in the population
    - This is mitigated in part by a very high mutation rate (An order of magnitude larger than the default)
- Very high mutation rates are required because of the large amount of noncoding DNA
    - Likewise, more adding more crossover points did not affect performance significantly due to being distributed amongst noncoding regions.

Possible experiment/I.V.: alter noncoding region size and see how fitness modularity are affected.

Next Steps

- Firm up experimental parameters
  - What does it mean for an org to be viable?
  - Max number of threads?
- Run populations in simulation with smaller non-coding regions (Is this more or less adaptive?)
- Complete/tweak experimental protocol
- Run experiments