

CMSC 500

Topics: Artificial Life

Professor Ackles

1240-1410

T TR

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## Día 5

1. When we were using different numbers for popsize, genomesize, and n\_generations, we were able to find different tendencies. As genomesize increased, the blue line representing the best organism was linearized. As popsize increased, there seemed to be more variance in average. When we decreased n\_generations, we found that there was a decrease in the highest y value that was reached.
  2. An alternative fitness scale could be tracking patterns instead of simply the number of 1s present. For example, you could track the number of occurrences of "01".
  3. Did not complete
  4. Did not complete
  5. I think that if you use mutate instead of easy\_mutate, the results would no longer be able to be represented as a positive linear function. This is because with easy\_mutate, the changes will always be positive where if you used mutate, they may not always be positive. I believe it would be better to use a parametric approach when graphing using easy\_mutate and non-parametric when using mutate.
  6. I think the part that takes the longest is the mutate/easy\_mutate function because this must be applied to every single different genome in the population for the length of each genome.
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1. I was confused about what the difference was between popsize and genomesize. After changing the variables and seeing the example genome on the whiteboard, this makes more sense.
  2. One thing that I thought I understood was how easy\_mutate worked but now I realize that I understand the idea of what it does but I could not explain how "random.randrange(0, self.n)" worked entirely. I believe it find a random int or value from 0 to self.n, but I do not quite know what self.n is.