Stochastic optimization algorithms 2020-09-08

Matlab programming for SOAs: Notes

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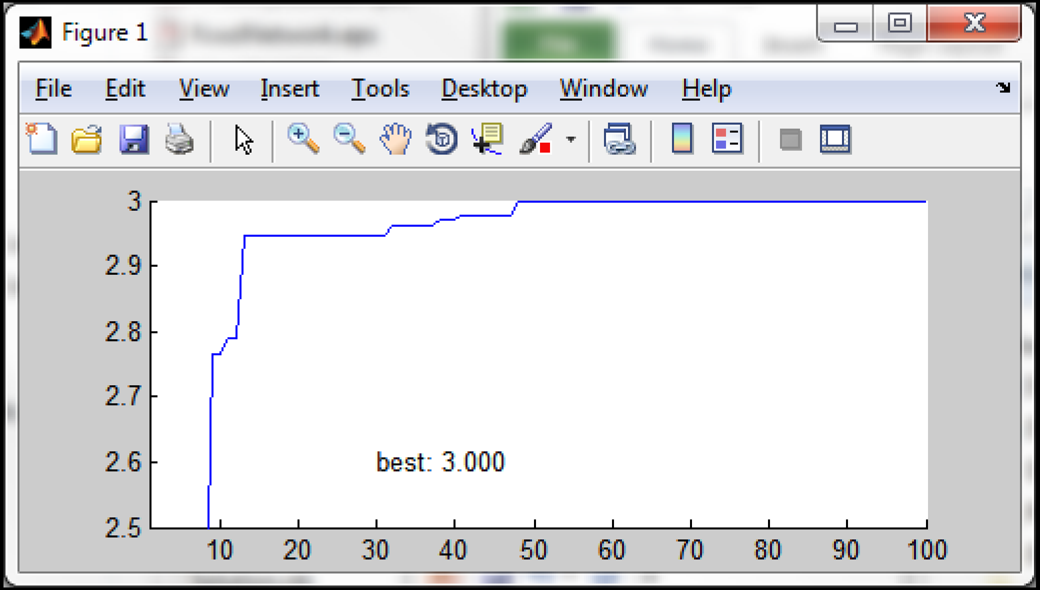
General comments

- Please make sure to implement the code in the instruction file (FFR105_MatlabIntroduction.pdf).
- Implement it *yourself* – this document is intended for individual work.
- Do not just copy the text from the PDF. There is ***a very strong correlation*** between implementing the code (without copying) and doing well in the course!
- (Parts of) the code can serve as a starting point for HP1.3 as well as some later home problems (in Set 2).

Program performance

- Make sure that your code runs properly, i.e. that (with the 2D graphics) the outcome looks (roughly) like this:



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Program performance

- SOAs are stochastic, so the result will look different from run to run, but it should look roughly as above, i.e. the program should easily reach the maximum fitness (3.0) with default settings.
- If it does not, please check carefully the list of common errors (below) and correct the code until it works as intended.
- If there appears to be remaining errors, do not hesitate to ask us. At *that* stage, you can also perhaps copy-paste from the PDF, but do write the code yourself, first.

Program performance

- When your code works as intended, take a moment to reflect on what you have implemented:
  - What does the GA do?
  - How does it do it? (Refer back to the biological background and the basic GA description in today's lecture, as well as Chapter 3 in the course book).
  - Note how it easily escapes local optima.
  - Note that the exact outcome is stochastic, i.e. it will differ slightly from run to run.

Common errors

- **Errors in DecodeChromosome:**
  - Writing 2^(j) instead of 2^(-j),
  - forgetting the "+nHalf" for x(2), writing 2^(nHalf) instead of 2^(-nHalf),
  - copy-pasting incorrectly (so that x(2) becomes x(1) in one or more locations) etc.
  - Another common (general) error is to write "for j = nHalf" instead of "for j = 1:nHalf" (or similar, for other for-loops). Check carefully!

Common errors

- **Incorrect objective function (EvaluateIndividual)**
  - Check carefully that you have written it *exactly* as in the document (p. 5).
- **Errors in TournamentSelect:**
  - Make sure to obtain the populationSize as size(fitness,1). (**Check** that the function gives the correct value, by temporarily removing the “;”).
  - Also, make sure that the “iTmp1” and “iTmp2”are used exactly as in the document (when finding iSelected).

Common errors

- **Errors in Cross:**
  - Make sure to obtain the nGenes as size(chromosome1,2). (**Check** that the function gives the correct value, by temporarily removing the “;”).
  - Once again, the limits on the for-loop. Write “for j = 1:nGenes”, not “for j = nGenes”.
  - (Very common!) Make sure to write “tempPopulation(i,:)”. It should be “i” not “1”, and don’t forget the “:”!
  - Avoid copy-paste errors here: Check carefully where it shold be “chromosome1(j)” and where it should be “chromosome2(j)”.

Common errors

- **Errors in Mutate:**
  – Make sure to obtain the nGenes as size(chromosome,2). (**Check** that the function gives the correct value, by temporarily removing the “;”).
  – Once again, the limits on the for-loop. Write “for j = 1:nGenes”, not “for j = nGenes”.

Common errors

- **(Very common) errors in Elitism:**
  - Make sure to place the elitism code *at the correct location in FunctionOptimization.m*. Check carefully (on p. 11 in the document) where it should be placed!
  - (very, very common!) Do not forget the line that copies the best individual into the population (line 61 on p. 12)! Make sure to place it at the correct location in the file!
  - Note also that here is should be “tempPopulation(1,:)” not ”(i,:)”. It is the first individual that should be overwritten!
  - Make sure to write chromosome = population(i,:) (line 20, p.11)! Here, it should be “(i,:)” *not* (1,:)!