

# CS/CSYS 352 F'18 GA Theory Assignment

assigned: 9/20/18

Due: softcopy of code and writeup due in blackboard by 4:00,

Zippped hardcopy of code (as m-files, NOT as pdfs!) and writeup by 4:30pm on 9/27/18

You must do this homework solo.

1. Write down the mathematical equation for the basic Schema Theorem that we derived in class for a canonical (a.k.a. simple) GA, and give an intuitive description of what each piece of it is representing.
2. What is the fundamental take-home message of the Schema Theorem (also called the “Building Block Hypothesis”)?
3. What are some important limitations of the basic Schema Theorem described above?
4. Let  $S1 = *0**11***0**$  and  $S2 = *****0*1****$  be two schemata.
  - a) What is the probability that  $S1$  and  $S2$  survive the application of both single-point crossover (with crossover rate  $P_c$ ) and bit-flip mutation (with probability of mutation  $P_m$ )?
  - b) Is it correct to call one of these two schemata a “building block”? Explain why or why not.
5. Whilst optimizing a three-bit problem, you notice that your population, of size 100, consists of 25 copies of each of strings 100 (with fitness 10), 111 (with fitness 20), 011 (with fitness 15), and 010 (with fitness 15).
  - a) What is the estimated fitness of schema  $1**$ ?
  - b) Assuming fitness proportionate selection with no crossover or mutation, calculate the estimated fitness of schema  $1**$  in the next generation (show your work).
6. Consider the following fitness function for a maximization problem (i.e., where high fitness is better):

Integer phenotypic	Fitness
0	7
1	5
2	3
3	9
4	10
5	1
6	6
7	6

- a) Perform (and show) a schema analysis assuming there is exactly one copy of each possible genotype in the population (see p. 110 in the Rothlauf Schema Analysis supplemental reading for an example of a schema analysis), and show a Hamming cube diagram (see Figure 2.13 on page 53 of the Goldberg Ch. 2 supplemental reading for a Hamming cube, and additionally label the corners with the corresponding fitness values), of this problem for both binary and gray genotypic

encodings of the integer phenotype. Use your schema analysis and Hamming cube diagrams to justify your answers to the following where helpful.

- b) Under each of these encodings, is the problem fully or partially deceptive (and, if so, type I deceptive (sign epistasis) or type II deceptive (reciprocal sign epistasis), or fully easy? (Justify how you determined this).
  - c) Are the saliences of the three bits of these two encodings for this problem uniformly scaled? (Justify how you determined this).
  - d) Comment on how and why the uniformity (or non-uniformity) of saliences can impact the GA search times and the impact this has on required population size.
  - e) Which encoding do you think makes the problem easier, and why?
  - f) Construct an alternative 3-bit encoding for which the problem is fully easy and use a schema analysis to prove that it is. Comment on the practical utility of designing such an encoding.
7. On pp. 49-50 in the Goldberg Ch 2 supplemental reading, 4 difference equations are shown for the minimal deceptive problem that consider both destructive and constructive effects of single-point crossover, assuming fitness proportionate selection, but with no mutation. Extend this analysis to account for both destructive and constructive effects of bit-flip mutation, assuming that, after crossover, each bit of each individuals is subsequently flipped with independent probability  $P_m$  (i.e., crossover and mutation are not mutually exclusive in this model, as they are in the Matlab GA toolbox). Do this by providing a second set of difference equations that compute the frequencies after mutation starting from the frequencies *after* crossover (this is MUCH more straightforward than trying to simply modify the first set of difference equations directly).
  8. The program `deceptivetakeover.m` (available on BB through 'demo codes') implements and plots Goldberg's difference equations from pp. 49-50.
    - a) Extend this program to include the constructive and destructive effects of bit-flipping mutation, based on the equations you derived in question 7.
    - b) Compare simulations for a Type 2 minimal deceptive problem both with and without mutation, playing with the various parameters such as the relative fitnesses, the initial representation of each schema, the crossover rate, the defining length, the mutation rate, etc. Can you find a circumstance in which some mutation enables convergence to find the optimum when simulations with no mutation didn't? Can you find a circumstance in which some mutation prevents convergence to the optimum when simulations with no mutation did? Include plots demonstrating these and explain why you think this is happening in each case.
    - c) After experimenting with this simulation model, what general conclusions can you reach about desirable mutation rates?