Problem assignment 3

Due: Wednesday, September 25, 2019

Problem 1

Variables inferred by forward checking

vars	x	у	z	w	u	t	V
domain	0,1,29	0,1,29	0,1,29	0,1,29	0,1,29	0,1,29	0,1,29
x = 2	2	0,1,29	2,5,8	0,1,29	0,1,29	0,1,29	0,1,29
y = 0	2	0	5	0,1,29	0,1,29	0,1,29	0,1,29
t = 0	2	0	5	0,1,29	0,1,29	0	0
Infer w	2	0	5	5,9	0,1,29	0	0
Infer u	2	0	5	9	0,3,6,9	0	0

For the infer of w, since u isn't assigned, we only consider the arc between w and z.

Then, the constraints would be:

$$w \mod 4 = z \mod 4 = 1$$

so $w = \{5,9\}$

For the infer of u, the constraints would be:

$$u \mod 3 = v \mod 3 = 0$$

u mod
$$3 = w \mod 3 = 5 \mod 3$$
 or $9 \mod 3 = \{0,2\}$

For the first equation, we get $u = \{0,3,6,9\}$, for the second equation, we get $u = \{0,2,3,5,6,8,9\}$, then $u = \{0,3,6,9\} \cap \{0,2,3,5,6,8,9\} = \{0,3,6,9\}$

Then since u is inferred, we should infer w again. Now the constraint for w is:

W mod
$$4 = z \mod 4 = 1$$
 -> $w = \{5,9\}$

W mod
$$3 = u \mod 3 = 0$$
 -> $w = \{0,3,6,9\}$

So the
$$w = \{5,9\} \cap \{0,3,6,9\} = 9$$
.

So, the reasonable variable groups inferred by forward checking is:

x = 2

y = 0

z = 5

w = 9

 $u = \{0,3,6,9\}$

t = 0

v = 0

Variables inferred by arc consistency

vars	X	у	z	w	u	t	V
domain	0,1,29	0,1,29	0,1,29	0,1,29	0,1,29	0,1,29	0,1,29
x = 2	2	0,1,29	2,5,8	0,1,29	0,1,29	0,1,29	0,1,29
y = 0	2	0	5	0,1,2,4,5	0,1,29	0,1,29	0,1,29
(check				,6,8,9			
arc							

z->w) t = 0 (check arc t->v,	2	0	5	5,9	0,1,29	0	0
w->u, z->w) (check arc v->u,	2	0	5	5,9	0,3,6,9	0	0
w->u) (check u->w)	2	0	5	9	0,3,6,9	0	0

So, the reasonable variable groups inferred by forward checking is:

x = 2

y = 0

z = 5

w = 9

 $u = \{0,3,6,9\}$

t = 0

v = 0

Problem 2

Part a.

Initial tour: [0, 58, 36, 53, 10, 18, 17, 2, 6, 42, 41, 19, 13, 11, 29, 4, 51, 44, 30, 15, 27, 40, 37, 22, 7, 31, 3, 54, 50, 48, 21, 23, 38, 9, 47, 33, 26, 16, 56, 43, 28, 59, 34, 52, 45, 24, 20, 8, 14, 35, 55, 46, 1, 32, 12, 5, 39, 49, 25, 57]

Initial tour distance: 306.43717

Initial temperature: 100

Number of tours tried: 100000 Number of tours accepted: 92435

The best tour found: [0, 5, 53, 32, 34, 15, 18, 33, 25, 36, 17, 3, 44, 40, 55, 20, 9, 14, 46, 2, 4, 59, 48, 10, 21, 38, 24, 26, 19, 35, 6, 52, 12, 37, 22, 8, 49, 41, 28, 13, 58, 31, 43, 57, 11, 51, 47, 23, 54, 56, 29, 7, 50, 1, 27, 45, 39, 30, 42, 16]

The best tour found distance: 103.65166

Part b.

Parameters		Initial Tour Distance	Number of Tours tried	Number of Tours Accepted	Best tour Distance
	Temperature: 10000	311.539122	100000	99838	242.586178
Steps: 100000	Temperature: 1000	300.557104	100000	98869	187.442838
	Temperature: 100	281.221808	100000	92424	102.865312

	Temperature:	304.905496	100000	8224	63.707482
	Temperature: 0.1	293.5911	100000	3672	70.27154
	Temperature: 10000	322.237354	200000	199742	214.168836
	Temperature: 1000	315.761656	200000	197847	161.578628
Steps: 200000	Temperature:	325.083958	200000	184680	85.275408
	Temperature:	334.881072	200000	15452	63.81284
	Temperature: 0.1	278.214292	200000	7408	68.78746
	Temperature: 10000	290.435064	400000	399416	207.303222
	Temperature: 1000	301.722132	400000	395590	123.624858
Steps: 400000	Temperature: 100	290.907394	400000	369320	77.615786
	Temperature:	327.964436	400000	31233	63.666698
	Temperature: 0.1	289.172244	400000	14092	67.207378
	Temperature: 10000	333.904144	800000	79880 4	165.260582
	Temperature: 1000	307.826264	800000	791020	103.25354
Steps: 800000	Temperature: 100	307.21158	800000	738602	72.957344
	Temperature:	299.86413	800000	62739	65.110992
	Temperature: 0.1	312.247572	800000	28704	67.02021
	Temperature: 10000	283.52750 4	1600000	1597645	156.056872
	Temperature: 1000	278.29668	1600000	1582088	85.168188
Steps: 1600000	Temperature:	319.700394	1600000	1477070	71.719568
	Temperature:	287.510608	1600000	124901	64.41229
	Temperature: 0.1	305.709702	1600000	58653	63.677714

With the same steps, as initial temperature decreased, the best tour distance found would decrease in general.

With the same temperature, as the steps increased, the best tour distance found would decrease in general.

The best solution appears with the parameter: steps=400000, initial_temperature=1. The best solution is 63.666698.

The red solutions are those beat the best solution in problem (72.892862).

Part c.

My cooling method for the temperature is:

$$\begin{split} T_i &= T_{init} \text{--} (T_{half} \text{/-} (0.3 \text{K})^2) * i^2 & 0 < i < 0.3 \text{K} \\ T_i &= T_{half} \text{/-} (0.7 \text{K})^2 * (i \text{--} \text{K})^2 & 0.3 \text{K} \le i < \text{K} \end{split}$$

T_{init} is the initial temperature.

T_{half} is half of the initial temperature.

K is the number of steps.

Generally, it's two part of quadratic function.

10 tries with tours accepted over 20000:

Initial	322.813	320.257	309.813	292.906	281.333	283.037	314.996	316.949	288.465	296.115
distance	260	628	396	218	09	410	344	372	31	862
Best tour	81.0421	82.3512	78.5709	79.2725	79.4346	79.6637	78.5597	83.0737	81.4297	82.8921
distance	22	88	42	02	84	48	22	36	68	66
Tours	20180	20245	20204	20169	20145	20131	20090	20115	20263	20329
accepted	20180	20245	20204	20169	20145	20131	20090	20115	20263	20329

Then, the average energy for the above 10 best distance are: 80.6290678

Problem 3.

number of generations range between 200-1000, population=500, mutation probability=0.05, culling=0.05, elite=0.05

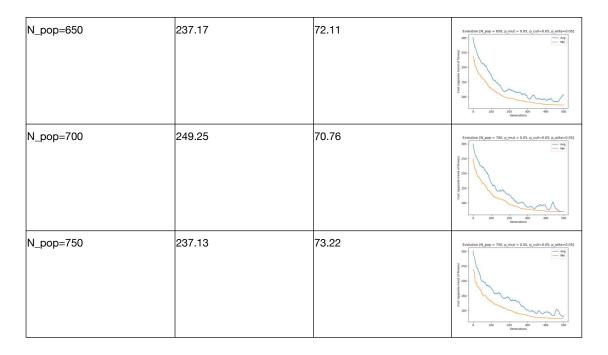
	Start state distance	Best distance found	pics
N_generations=200	248.48	105.17	Evolution (14 pag = 500, p_mixt = 0.05; p_cuit=0.05; p_cuit=0.05) 20 20 20 20 20 20 20 20 20 2
N_generations=300	258.48	80.85	Evolution IN goop = 500, p, mot = 0.05, p, cul = 0.05, p, elite = 0.05) 307

N_generations=400	253.62	78.43	Secretarion (N. prop. 5000, p. mat. = 0.001, p. cull=0.001, p. cell=0.001, p. cel
N_generations=500	259.32	74.04	Surfaction (N, pop = 500, p, mat = 0.05; p, cull=0.05; p, elete=0.05) 200 (102) (102) (102) (103) (103) (103) (104) (105) (10
N_generations=600	258.34	75.14	Eventucion (NI prop = 5000, p. must = 0.031, p. cull=0.031, p. still=0.003) 200 (02 20
N_generations=700	252.7	67.2	Seclution (RI, page 500, p, mur = 0.03, p, cul=-0.03, p, olite=-0.03) 202 202 203 204 205 205 206 206 207 208 208 208 208 208 208 208
N_generations=800	248.47	64.99	Evelution (N page 500, p. mat = 2.05, p. coll=0.05, p. elite=0.05) 200 201 202 203 204 305 205 205 205 205 205 205 205
N_generations=900	243.34	72.84	Techston (RI, pap = 500, p, mur = 0.03, p, cul=0.03, p, diffe=0.03) 20 20 20 20 20 20 20 20 20 2
N_generations=1000	254.68	69.8	Scotlation (N peop = 500, p_mat = 0.05; p_cull=0.05; p_atilin=0.05] 200 200 200 200 200 200 200

number of generations=500, population range between 250-750, mutation probability=0.05, culling=0.05, elite=0.05

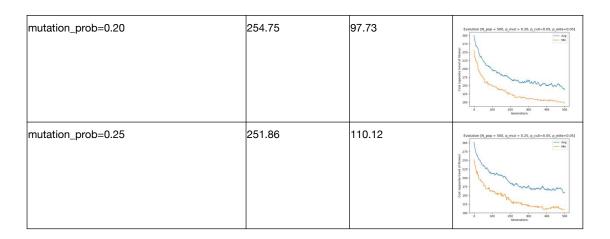
	Start state distance	Best distance found	pics
--	----------------------	---------------------	------

N non-250	250.00	77.40	
N_pop=250	259.92	77.48	Evolution IM, prop = 230, p, mut = 0.05, p, cut=0.05, p, cut=0.05) 200 30 200 30 200 30 200 30 200 30 200 30 200 30 200 30 300 400 560
N_pop=300	260.95	72.07	Evenhelm (M_ josp = 300, p_ mut = 0.03, p_ cult=0.05, p_ sites=0.05) 300 4 299 5 200 5 20
N_pop=350	257.11	73.94	Evolution (N, Jop = 350, p, mail = 0.05, p, cull=0.05, p, elite=0.05) 200
N_pop=400	250.02	77.72	Evolution (19, pop = 400), p, mod = 0.05, p, cull=0.05, p, witt=-0.05) 200
N_pop=450	250.79	74.75	Evolution (19, pop = 455), p, mod = 0.05, p, cull=0.05), p, cill=0.05) 00
N_pop=500	255.39	70.79	Evolution (N, pop = 500), p, mot = 0.05, p, cult=0.05, p, elte=0.05) 200
N_pop=550	241.84	72.85	Evolution (N, pop = 550), p, mul = 0.05, p, cull=0.05, p, eitte=0.05) 200
N_pop=600	251.63	70.52	Evalution (N, pap = 600), p, mut = 0.05, p, cull=0.05, p, elte=0.05) 200



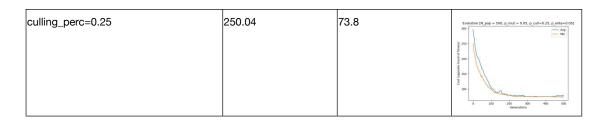
number of generations=500, population=500, mutation probability range between 0.00-0.25, culling=0.05, elite=0.05

	Start state distance	Best distance found	pics
mutation_prob=0.00	250.23	79.17	Evolution (N, pop = 500, p, max = 0.00, p, cull=0.05, p, effe=0.05) 200 - N1 200 - N1 200 300 300 300 300 300 300 30
mutation_prob=0.05	251.27	68.19	Evolution (N, po = 500, p, mot = 0.05, p, cul=0.05, p, elle=0.05) 202
mutation_prob=0.10	240.41	74.95	Evention (N, pop = 500, p, mot = 0.30, p, cull=0.05, p, eilte=0.05) 305
mutation_prob=0.15	247.96	79.87	Evolution (N, pop = 500, p, mot = 0.35, p, cull=0.05, p, eitle=0.05) 302



number of generations=500, population=500, mutation probability=0.05, culling range between 0.00-0.25, elite=0.05

	Start state distance	Best distance found	pics
culling_perc=0.00	242.99	88.26	Consider (N, page 500), p. mad = 0.00, p. cull=0.00, p. cull=0.00) The page of the page o
culling_perc=0.05	254.31	73.32	Evolution (N, pop = 500, p, mut = 0.05, p, cull=0.05, p, ell=0.05) 200
culling_perc=0.10	252.39	72.67	Condition (N, pop = 500, p, mut = 0.00, p, cull=0.10, p, ell=0.005) 300
culling_perc=0.15	250.24	70.62	Consistent (N, page = 500, p, mod = 0.00, p, cull=0.15, p, eith=0.005) 300
culling_perc=0.20	251.24	67.32	Condition (N, pop = 500, p, mod = 0.00, p, cull=0.20, p, eith=0.00) 300



number of generations=500, population=500, mutation probability=0.05, culling=0.05, elite range between 0.00-0.25

	Start state distance	Best distance found	pics
elite_perc =0.00	253.74	235.69	Evaluation (Ne. prop = 500, p. mat = 0.00, p. color-0.00) (10 p. color
elite_perc =0.05	245.17	73.7	Evolution (18 pags = 500, p, mat = 0.03, p_cull=0.05, p_elite=0.05) 200
elite_perc =0.10	245.18	65.81	Evolution (N. pop = 500, p. mut = 0.05, p. curl=0.05, p. etite=0.10) 200 300 300 300 300 300 300 3
elite_perc =0.15	250.26	69.83	Evolution (N pop = 500, p mat = 0.05, p cul = 0.05, p, either=0.15) 300
elite_perc =0.20	253.78	73.47	Foolston (N pop = 500, p, mat = 0.05, p, cul=-0.05, p, site=-0.20) 200
elite_perc =0.25	249.95	69.85	Fusikation (N pop = 500, p, mat = 0.05, p, cul=-0.05, p, sitte=-0.25) 300

Analysis and conclusion:

As the number of generations increase, the best distance result is getting smaller till n_generations=800, then the result would fluctuate around 70, which might mean the

evolution of the population is meeting the bottle-neck. However, as the number of generations increase, the average distance tend to become more closer to the best distance, which means every single "person" in the whole population tend to become the best "person".

About the population, it seems that there isn't any specific relations between the population and the best distance found. That still make sense for GA. The population only presents a sample space for the whole process. Its size somehow doesn't really matter.

The mutation probability is very interesting. Reasonable percentage of the mutation would increase the performance of the system. For out test, the mutation_prob=0.05 seems to meet the best distance, then the results become worse. Also, as the mutation probability increases, the average distance would get far away from the best distance, since more mutations means instability of the "genotype" in the population.

About the culling percentage, the best distance result appears when culling_perc=0.20. Thus, same to the mutation probability, the reasonable percentage of culling would make it closer to best distance.

And for elite percentage, something very funny happened when elite_perc=0. The whole result would fluctuate severely, which means elite is necessary in genetic algorithm. Then, the best distance result is when elite_perc=0.10. Also we need reasonable elite percentage.

Finally, for both culling and elite percentage, the higher the rate, the closer the average distances and best results are. That's easy to understand. These two parameters both means to preserve the "good gene", so as generation increases, the "genotype" would generally become as good as the best.