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**Department of
Computer Science**

PROJECT

Genetic Algorithms and Evolutionary Computing
(B-KUL-H02D1A)

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Introduction

Tasks

1.1 Task 2: Initial experiments

The impact of the following parameters on the results of the existing genetic algorithm was tested by varying them while keeping the rest of the parameters at their default values:

- number of individuals (NIND)
- maximum number of generations (MAXGEN)
- percentage of the elite population (ELITIST)
- probability of crossover (PR_CROSS)
- probability of mutation (PR_MUT)
- local loop removal (LOCALLOOP)

The tests for this task were executed on a subset of the given datasets to keep the tables readable.

1.1.1 Individuals

TODO: COMMENTS

Dataset	# Generations	Min	Mean	Max
number of individuals = 50				
rondrit016.tsp	110.0	3.93	5.61	7.07
rondrit048.tsp	110.0	12.57	17.38	21.47
rondrit067.tsp	110.0	17.46	21.76	25.39
rondrit127.tsp	110.0	26.47	30.35	33.44
number of individuals = 100				
rondrit016.tsp	107.1	3.80	4.90	6.42
rondrit048.tsp	110.0	11.80	16.51	21.15
rondrit067.tsp	110.0	16.36	20.98	24.79
rondrit127.tsp	110.0	25.24	29.61	33.18
number of individuals = 250				
rondrit016.tsp	110.0	3.75	5.32	7.25
rondrit048.tsp	110.0	11.19	16.75	22.20
rondrit067.tsp	110.0	15.64	20.89	25.46
rondrit127.tsp	110.0	24.39	29.46	33.28
number of individuals = 500				
rondrit016.tsp	110.0	3.70	5.28	7.43
rondrit048.tsp	110.0	10.89	16.52	22.17
rondrit067.tsp	110.0	15.00	20.69	26.10
rondrit127.tsp	110.0	23.65	29.08	33.24
number of individuals = 1000				
rondrit016.tsp	110.0	3.70	5.20	7.68
rondrit048.tsp	110.0	10.04	16.42	22.50
rondrit067.tsp	110.0	14.49	20.66	26.02
rondrit127.tsp	110.0	23.40	29.03	33.82

Table 1.1: Existing genetic algorithm with varying amount of individuals.

1.1.2 Generations

TODO: COMMENTS

Dataset	# Generations	Min	Mean	Max
max number of generations = 100				
rondrit016.tsp	110.0	3.99	5.57	6.95
rondrit048.tsp	110.0	12.82	17.54	21.28
rondrit067.tsp	110.0	17.41	21.66	25.29
rondrit127.tsp	110.0	26.43	30.49	33.22
max number of generations = 250				
rondrit016.tsp	271.1	3.77	5.18	6.52
rondrit048.tsp	275.0	11.72	17.00	21.24
rondrit067.tsp	275.0	16.61	21.50	24.95
rondrit127.tsp	275.0	25.66	29.95	33.01
max number of generations = 500				
rondrit016.tsp	455.7	3.76	4.74	5.99
rondrit048.tsp	550.0	11.16	16.87	20.98
rondrit067.tsp	550.0	15.85	21.02	24.38
rondrit127.tsp	550.0	25.02	29.57	32.99
max number of generations = 1000				
rondrit016.tsp	683.6	3.73	3.88	4.63
rondrit048.tsp	1100.0	10.51	16.40	20.57
rondrit067.tsp	1100.0	14.95	21.00	25.20
rondrit127.tsp	1100.0	23.50	29.18	32.57

Table 1.2: Existing genetic algorithm with varying amount of maximum generations.

1.1.3 Elitism

TODO: COMMENTS

Dataset	# Generations	Min	Mean	Max
percentage of the elite population = 0.00				
rondrit016.tsp	110.0	5.15	6.30	7.58
rondrit048.tsp	110.0	15.75	19.09	22.47
rondrit067.tsp	110.0	20.23	23.38	26.18
rondrit127.tsp	110.0	29.17	31.70	34.01
percentage of the elite population = 0.05				
rondrit016.tsp	110.0	3.94	5.65	7.21
rondrit048.tsp	110.0	12.71	17.51	20.96
rondrit067.tsp	110.0	17.35	21.71	25.04
rondrit127.tsp	110.0	26.47	30.39	33.17
percentage of the elite population = 0.15				
rondrit016.tsp	55.4	3.84	3.86	4.50
rondrit048.tsp	108.3	9.98	11.85	15.87
rondrit067.tsp	110.0	14.41	16.05	19.57
rondrit127.tsp	110.0	24.11	26.47	30.17
percentage of the elite population = 0.35				
rondrit016.tsp	56.2	3.84	3.86	4.45
rondrit048.tsp	108.0	9.99	11.09	14.44
rondrit067.tsp	107.4	14.27	15.48	18.45
rondrit127.tsp	110.0	23.16	24.46	27.44
percentage of the elite population = 0.50				
rondrit016.tsp	68.0	3.83	3.84	4.11
rondrit048.tsp	108.6	10.08	10.96	14.69
rondrit067.tsp	110.0	14.75	15.78	18.37
rondrit127.tsp	110.0	23.85	25.07	28.28
percentage of the elite population = 0.75				
rondrit016.tsp	93.7	3.92	3.97	4.47
rondrit048.tsp	110.0	11.29	12.24	15.04
rondrit067.tsp	106.0	16.31	17.05	19.70
rondrit127.tsp	110.0	24.89	25.72	28.15
percentage of the elite population = 0.95				
rondrit016.tsp	110.0	4.75	5.12	5.68
rondrit048.tsp	110.0	14.80	16.06	17.67
rondrit067.tsp	110.0	19.33	20.71	22.18
rondrit127.tsp	110.0	28.49	29.52	30.69

Table 1.3: Existing genetic algorithm with varying percentage of the elite population.

1.1.4 Crossover

TODO: COMMENTS

Dataset	# Generations	Min	Mean	Max
probability of crossover = 0.00				
rondrit016.tsp	37.8	4.91	4.91	5.26
rondrit048.tsp	81.4	13.37	13.39	13.89
rondrit067.tsp	81.5	18.96	19.11	19.48
rondrit127.tsp	91.7	28.05	28.19	28.50
probability of crossover = 0.15				
rondrit016.tsp	39.6	4.30	4.31	4.75
rondrit048.tsp	106.1	10.22	10.48	11.93
rondrit067.tsp	110.0	14.48	14.77	16.21
rondrit127.tsp	107.6	24.18	24.35	25.20
probability of crossover = 0.35				
rondrit016.tsp	41.8	4.18	4.21	4.89
rondrit048.tsp	107.6	9.09	9.48	11.64
rondrit067.tsp	107.7	13.44	13.83	15.54
rondrit127.tsp	110.0	22.97	23.56	25.66
probability of crossover = 0.50				
rondrit016.tsp	37.7	4.05	4.06	4.46
rondrit048.tsp	103.0	9.28	9.88	11.93
rondrit067.tsp	110.0	13.21	14.06	16.99
rondrit127.tsp	110.0	22.79	23.80	26.76
probability of crossover = 0.75				
rondrit016.tsp	72.3	3.88	3.89	4.44
rondrit048.tsp	110.0	10.74	13.83	17.94
rondrit067.tsp	110.0	15.31	18.32	21.76
rondrit127.tsp	110.0	24.91	27.60	30.87
probability of crossover = 0.95				
rondrit016.tsp	110.0	3.93	5.60	7.09
rondrit048.tsp	110.0	12.66	17.41	21.79
rondrit067.tsp	110.0	17.00	21.42	25.02
rondrit127.tsp	110.0	26.64	30.47	33.40

Table 1.4: Existing genetic algorithm with varying probability of crossover.

1.1.5 Mutation

TODO: COMMENTS

Dataset	# Generations	Min	Mean	Max
probability of mutation = 0.00				
rondrit016.tsp	110.0	3.92	5.60	7.30
rondrit048.tsp	110.0	12.63	17.33	21.32
rondrit067.tsp	110.0	17.01	21.54	25.30
rondrit127.tsp	110.0	26.13	30.19	33.16
probability of mutation = 0.05				
rondrit016.tsp	110.0	3.97	5.45	6.98
rondrit048.tsp	110.0	12.58	17.48	21.22
rondrit067.tsp	110.0	17.28	21.84	25.27
rondrit127.tsp	110.0	26.44	30.08	33.19
probability of mutation = 0.15				
rondrit016.tsp	110.0	3.96	5.65	7.13
rondrit048.tsp	110.0	12.61	17.44	21.61
rondrit067.tsp	110.0	17.33	21.67	25.00
rondrit127.tsp	110.0	26.40	30.46	33.12
probability of mutation = 0.35				
rondrit016.tsp	110.0	4.01	5.86	7.52
rondrit048.tsp	110.0	12.72	17.61	21.46
rondrit067.tsp	110.0	17.40	21.84	25.23
rondrit127.tsp	110.0	26.04	30.31	33.30
probability of mutation = 0.50				
rondrit016.tsp	110.0	4.07	5.95	7.50
rondrit048.tsp	110.0	12.53	17.53	21.66
rondrit067.tsp	110.0	16.70	21.78	25.31
rondrit127.tsp	110.0	26.11	30.23	33.21
probability of mutation = 0.75				
rondrit016.tsp	110.0	4.17	6.05	7.55
rondrit048.tsp	110.0	12.54	17.84	21.66
rondrit067.tsp	110.0	17.32	22.07	25.60
rondrit127.tsp	110.0	26.05	30.28	33.20
probability of mutation = 0.95				
rondrit016.tsp	110.0	4.21	6.21	7.60
rondrit048.tsp	110.0	12.80	18.11	22.43
rondrit067.tsp	110.0	17.12	22.13	25.80
rondrit127.tsp	110.0	26.50	30.61	33.61

Table 1.5: Existing genetic algorithm with varying probability of mutation.

1.1.6 Loop removal

TODO: COMMENTS

Dataset	# Generations	Min	Mean	Max
		local loop removal = 0		
rondrit016.tsp	110.0	3.98	5.37	6.75
rondrit048.tsp	110.0	12.44	17.36	21.27
rondrit067.tsp	110.0	17.43	21.88	25.77
rondrit127.tsp	110.0	26.63	30.33	33.14
		local loop removal = 1		
rondrit016.tsp	53.4	3.69	3.70	4.13
rondrit048.tsp	110.0	7.48	12.15	16.14
rondrit067.tsp	110.0	9.59	14.86	18.40
rondrit127.tsp	110.0	15.47	20.90	24.15

Table 1.6: Existing genetic algorithm with varying local loop removal.

1.1.7 Mix

TODO: some results with mixed amounts of parameters?

1.2 Task 3: Stopping criterion

To implement a new stopping criterion, we looked at the commonly used termination conditions outlined by the book. There we see the following suggestions:

1. Maximally allowed CPU time elapses.
2. Total number of fitness evaluations reaches limit.
3. Fitness improvement remains under threshold for a given period of time.
4. Population diversity drops under threshold.

The first and second criteria are useful, either to guarantee the evaluations do not go on forever, or when there is some kind of constraint on system resource usage. In the project template, we already have the guarantee of eventual termination because of the limit on the number of generations, and we do not have to account for system resource constraints.

The fourth criterion is also already present in the template and can be adjusted via the GUI. The default value is so strict (95% equal individuals), it practically is never reached.

We decided to implement the third criterion. With this condition, termination occurs when the fitness of the best individual does not improve above a threshold for a given period of time. This period of time is expressed in terms of a certain number of generations. We chose to define this number of generations to be a percentage of the specified maximum number of generations. When testing this termination condition, we see that it does succeed in avoiding computation of useless generations where the fitness does not improve for a long time. Because of the fact that improvements may still happen at a later point in time, the score will be slightly worse with this new condition.

The results of our experiments with this new termination condition are displayed in Table 1.7.

	Default stopping criterion				Custom stopping criterion			
Dataset	# Generations	Min	Mean	Max	# Generations	Min	Mean	Max
rondrit016.tsp	60.6000	3.8289	3.8405	4.3167	51.9000	3.8598	4.0645	4.9485
rondrit018.tsp	59.9000	3.6123	3.6526	4.3262	62.4000	3.5116	3.7063	4.6899
rondrit023.tsp	92.8000	3.9902	4.2086	5.2684	77.5000	4.3064	4.4586	5.5427
rondrit025.tsp	82.0000	5.3085	5.4600	6.4753	79.2000	5.3707	5.7207	7.3034
rondrit048.tsp	108.7000	7.8736	8.2540	9.5729	109.2000	8.1605	8.9541	10.9159
rondrit050.tsp	101.5000	12.3558	12.9267	14.6198	104.0000	12.0748	12.8018	14.4246
rondrit051.tsp	109.6000	11.8400	12.3779	13.6785	108.9000	11.7734	12.2508	13.6669
rondrit067.tsp	110.0000	11.5868	12.2748	13.8317	107.2000	11.4511	12.4336	14.0862
rondrit070.tsp	110.0000	17.8292	18.6919	20.5209	109.6000	18.3206	18.9595	20.7340
rondrit100.tsp	110.0000	29.6034	31.6596	34.6374	108.7000	29.1263	30.6127	33.1294
rondrit127.tsp	110.0000	19.6930	20.5928	21.9205	110.0000	19.0723	20.0230	21.4847

Table 1.7: Comparison between default and custom stopping criteria.

1.3 Task 4: Other representation

1.4 Task 5: Local optimisation

For this task, we are testing the local optimization already present in the template. This optimization takes a path and tries to remove local loops up to path length 3. With default values for other parameters, this results in major improvements to the score.

The results of our experiments with local optimisation disabled and enabled are displayed in Table 1.8.

	Local optimisation disabled				Local optimisation enabled			
Dataset	# Generations	Min	Mean	Max	# Generations	Min	Mean	Max
rondrit016.tsp	108.8	3.9087	5.3409	6.6707	63.4	3.6923	3.7783	4.4343
rondrit018.tsp	109.0	3.8205	5.9391	7.9101	82.7	3.2285	3.8159	4.8886
rondrit023.tsp	109.0	5.2503	8.0243	10.4586	109.0	3.6688	6.0516	8.2630
rondrit025.tsp	109.0	6.8383	10.5710	13.9566	109.0	4.6353	7.9255	11.2084
rondrit048.tsp	109.0	12.9322	17.3083	21.2216	109.0	7.4032	12.2117	15.8290
rondrit050.tsp	109.0	17.5460	23.0187	27.4702	109.0	10.6862	16.3413	19.9854
rondrit051.tsp	109.0	17.0520	21.6487	25.5342	109.0	9.8788	15.0773	19.2524
rondrit067.tsp	109.0	17.2930	21.6320	25.0256	109.0	9.4921	14.8637	18.2992
rondrit070.tsp	109.0	27.0916	33.4376	38.6964	109.0	14.9605	22.7446	27.9257
rondrit100.tsp	109.0	41.7305	49.6807	55.5533	109.0	22.4411	32.7396	38.8860
rondrit127.tsp	109.0	26.5206	30.3975	33.3563	109.0	15.3001	20.8402	24.3830

Table 1.8: Comparison between local optimisation disabled (left) and local optimisation enabled (right).

1.5 Task 6: Benchmark problems

1.6 Task 7: Optional tasks

1.6.1 7a: Parent selection

Additional parent selection methods we implemented are Fitness Proportional Selection and Tournament Selection. Both of them use the same parameters as the existing implementation of Stochastic Universal Sampling so we could easily swap them in.

	Stochastic Universal Sampling			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	109.0	3.9268	5.5816	6.95230040943754
rondrit018.tsp	109.0	3.8098	5.8874	7.64505139464696
rondrit023.tsp	109.0	5.2107	8.1510	10.66363338096259
rondrit025.tsp	109.0	6.9584	10.6573	13.64919455732690
rondrit048.tsp	109.0	12.5354	17.1587	20.98354804718375
rondrit050.tsp	109.0	17.6555	23.3466	27.70294938389831
rondrit051.tsp	109.0	16.8619	21.5905	24.99887566024666
rondrit067.tsp	109.0	17.3626	21.8921	25.01576819902206
rondrit070.tsp	109.0	27.3491	33.7980	39.02844367980951
rondrit100.tsp	109.0	42.5563	50.3468	56.14968388227629
rondrit127.tsp	109.0	26.3171	30.1653	32.82588637833199

Table 1.9: Results when using Stochastic Universal Sampling as parent selection method.

	Tournament Selection			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	109.0	3.8584	5.2429	6.65136434345961
rondrit018.tsp	109.0	3.8044	5.8175	7.60837957298278
rondrit023.tsp	109.0	5.0251	7.8150	10.25462477584426
rondrit025.tsp	109.0	6.8520	10.6018	13.97083528139636
rondrit048.tsp	109.0	12.3467	16.3804	20.33995051462599
rondrit050.tsp	109.0	17.7767	23.0010	26.94691760670842
rondrit051.tsp	109.0	16.6423	21.4503	24.88148805771897
rondrit067.tsp	109.0	17.4205	21.8030	24.91090949012749
rondrit070.tsp	109.0	27.0049	33.5066	38.57674586236878
rondrit100.tsp	109.0	42.1082	49.7688	55.34138052048054
rondrit127.tsp	109.0	26.5709	30.3721	33.34923179147698

Table 1.10: Results when using Tournament Selection as parent selection method.

	Fitness Proportional Selection			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	109.0	3.9268	5.5816	6.95230040943754
rondrit018.tsp	109.0	3.8098	5.8874	7.64505139464696
rondrit023.tsp	109.0	5.2107	8.1510	10.66363338096259
rondrit025.tsp	109.0	6.9584	10.6573	13.64919455732690
rondrit048.tsp	109.0	12.5354	17.1587	20.98354804718375
rondrit050.tsp	109.0	17.6555	23.3466	27.70294938389831
rondrit051.tsp	109.0	16.8619	21.5905	24.99887566024666
rondrit067.tsp	109.0	17.3626	21.8921	25.01576819902206
rondrit070.tsp	109.0	27.3491	33.7980	39.02844367980951
rondrit100.tsp	109.0	42.5563	50.3468	56.14968388227629
rondrit127.tsp	109.0	26.3171	30.1653	32.82588637833199

Table 1.11: Results when using Fitness Proportional Selection as parent selection method.

1.6.2 7b: Survivor selection

1.6.3 7c: Diversity preservation

For preserving population diversity we adapted a few of the functions in the template to work with subpopulations, simulating the island model. The results displayed in Table 1.12 through Table **??** show tests performed with 1, 2, 5, 10 and 20 subpopulations or islands.

	# subpopulations = 1			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	99.9	3.7370	5.3014	7.3443
rondrit018.tsp	120.7	3.4504	5.5736	7.9594
rondrit023.tsp	124.4	4.6149	7.6039	10.7075
rondrit025.tsp	134.5	5.8402	9.9015	13.9843
rondrit048.tsp	129.7	10.9175	16.1203	21.3953
rondrit050.tsp	194.6	14.7423	21.4762	26.9975
rondrit051.tsp	169.1	14.7132	20.3833	25.4901
rondrit067.tsp	139.0	15.3320	20.6747	25.3712
rondrit070.tsp	187.9	23.1837	31.6961	39.3717
rondrit100.tsp	174.5	38.1144	48.0221	55.8977
rondrit127.tsp	195.0	23.8434	29.0456	33.1707

Table 1.12: Results when using a single subpopulation.

	# subpopulations = 2			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	118.9	4.1112	5.6874	7.9026
rondrit018.tsp	147.5	3.8393	6.0843	8.5831
rondrit023.tsp	159.4	5.0312	8.3282	11.8303
rondrit025.tsp	152.9	6.6344	10.9143	15.5315
rondrit048.tsp	204.9	11.4129	17.6468	23.8143
rondrit050.tsp	216.0	16.5176	23.7049	29.4113
rondrit051.tsp	168.2	16.6110	22.5015	27.8662
rondrit067.tsp	203.0	16.4217	22.3292	27.4292
rondrit070.tsp	129.3	27.3049	35.4823	42.9792
rondrit100.tsp	251.9	40.3992	51.8574	60.8410
rondrit127.tsp	265.4	25.6029	31.5892	36.3884

Table 1.13: Results when using two subpopulations.

	# subpopulations = 5			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	126.6	4.1295	5.8593	7.9499
rondrit018.tsp	121.0	4.0043	6.2663	8.9579
rondrit023.tsp	138.2	5.1783	8.4623	12.0132
rondrit025.tsp	166.0	6.4178	11.0127	15.7281
rondrit048.tsp	117.9	12.4779	18.4335	24.2895
rondrit050.tsp	164.8	17.1913	24.2682	30.5998
rondrit051.tsp	166.4	17.3803	23.2727	28.6140
rondrit067.tsp	225.4	16.5562	22.6888	27.6837
rondrit070.tsp	183.2	26.8295	35.8003	42.9375
rondrit100.tsp	199.2	41.8170	53.1547	62.3695
rondrit127.tsp	218.5	26.4587	32.1475	36.5978

Table 1.14: Results when using five subpopulations.

	# subpopulations = 10			
Dataset	# Generations	Min	Mean	Max
rondrit016.tsp	97.4	4.1405	5.5019	7.7501
rondrit018.tsp	140.1	3.8233	5.5875	8.1174
rondrit023.tsp	180.4	4.7633	7.8333	11.6950
rondrit025.tsp	186.0	6.1102	10.4032	15.4008
rondrit048.tsp	276.3	10.6240	17.0398	23.1415
rondrit050.tsp	245.8	15.9304	22.8300	29.9988
rondrit051.tsp	190.7	16.0860	21.8967	27.5143
rondrit067.tsp	254.4	15.8431	21.9523	27.1892
rondrit070.tsp	272.4	24.4098	33.8360	41.4091
rondrit100.tsp	250.7	39.4631	51.1833	61.1145
rondrit127.tsp	282.1	25.3591	31.1691	36.3321

Table 1.15: Results when using ten subpopulations.

Conclusion

2.1 Weak points

There are a couple of weak points in our report:

- The speed of our Sudoku implementations in CHR are not that great. We did try to improve it with the heuristics, but we feel it is still too slow. We think this was more due to the fact that we were still novices with how CHR worked as our Hashiwokakero CHR implementation is quite fast.
- The implementation of the connectivity constraint in ECLiPSe for Hashiwokakero is also a rather weak point. Ideally we should have implemented it using disjoint sets like in CHR but we couldn't figure out how to do this correctly.
- We think that implementing a Hashiwokakero solver using a graph representation is a more logical approach than the one we have used, but we had problems with ECLiPSe and how to express the no crossing bridges constraint.

2.2 Strong points

The strong points in our report are:

- Our Hashiwokakero CHR implementation is quite fast thanks to our improvements set.
- We think we have good heuristics for Sudoku in CHR. Certainly the heuristic for the alternative viewpoint has made good improvements on the speed of the search.

2.3 Lessons learned

We have learned a lot of things during this project due to the fact we often had to re-track our steps. If we would now have to do an other project with these systems we think we would have a better idea for how to start and what to think about. We spent quite some time with both ECLiPSe and CHR so we now have a much better idea of what the strong points are and the weak points are for each system.

Appendix

We started working on this project before the Easter holiday. In the beginning we often lost quite some time, since we didn't really know how the systems worked. During the second week of the Easter holiday, we continued to work on the project each evening and we finished the Sudoku task and the ECLiPSe part of hashiwokakero before the end of the holiday. We then had to halt our work for a while since we had a deadline for a ridiculously large project for another course. As the semester was coming to an end other deadlines and an exam were coming up so we had to manage those first. Thus it was only at the start of the study period that we could continue working. From the start of the study period we tried to spend around 6 hours of work each day for this project. The work was not really divided since we were doing pair programming most of the time. Sometimes someone made individual changes when they had time but most of our work was done online using Hangouts and its screen sharing functionality. We could argue that by doing pair programming we lost quite some time, which is true, but by doing this we worked very closely together and we learned quite a lot. We have each individually put more than 100 hours in this project.

```
% run_ga.m (RUN GENETIC ALGORITHM)
%
% Input parameters:
% x, y - coordinates of the cities
% NIND - number of individuals
% MAXGEN - maximal number of generations
% ELITIST - percentage of elite population
% STOP_PERCENTAGE - percentage of equal fitness (stop criterium)
% PR_CROSS - probability for crossover
% PR_MUT - probability for mutation
% CROSSOVER - the crossover operator
% LOCALLOOP - ...
% CUSTOMSTOP - ...
% CUSTOMSS - ...
% SELECTION - the parent selection function (sus, sel_tournament,
% sel_fit_prop, ...)
% ah1, ah2, ah3 - axes handles to visualise tsp
%
% Output parameter:
% best - A vector(?) of the best result of every iteration
% mean_fits - A vector(?) of the mean result of every iteration
% worst - A vector(?) of the worst result of every iteration

function [best, mean_fits, worst] = run_ga(x, y, NIND, MAXGEN, NVAR,
    ELITIST, STOP_PERCENTAGE, PR_CROSS, PR_MUT, CROSSOVER, LOCALLOOP,
    CUSTOMSTOP, CUSTOMSS, SELECTION, SUBPOP, ah1, ah2, ah3)

```

```matlab
GGAP = 1 - ELITIST;

best = zeros(1, MAXGEN);
mean_fits = zeros(1,MAXGEN+1);
worst = zeros(1,MAXGEN+1);

Dist = zeros(NVAR,NVAR);
for i = 1:size(x,1)
    for j = 1:size(y,1)
        Dist(i,j) = sqrt((x(i)-x(j))^2+(y(i)-y(j))^2);
    end
end

% initialize population
Chrom = zeros(NIND,NVAR);
for row = 1:NIND
    Chrom(row,:) = path2adj(randperm(NVAR));
end
% evaluate initial population
ObjV = tspfun(Chrom, Dist);

% number of individuals of equal fitness needed to stop
stopN = ceil(STOP_PERCENTAGE*NIND);

gen = 0;
% generational loop
while gen < MAXGEN
    sObjV = sort(ObjV);
    best(gen+1) = min(ObjV);
    minimum = best(gen+1);
    mean_fits(gen+1) = mean(ObjV);
    worst(gen+1) = max(ObjV);
    for t = 1:size(ObjV,1)
        if (ObjV(t) == minimum)
            break;
        end
    end

    if nargin == 18
        visualizeTSP(x, y, adj2path(Chrom(t,:)), minimum, ah1, gen,
            best, mean_fits, worst, ah2, ObjV, NIND, ah3);
    end

    % stopping criterion: stop when the minimum of the last stopN
    % generations has not improved
    if CUSTOMSTOP == 1
        if (gen-0.1*MAXGEN > 1) && ((best(floor(gen-0.1*MAXGEN)) -
            minimum) <= 1e-15)
            break;
        end
    else
        if (sObjV(stopN)-sObjV(1) <= 1e-15)
            break;
            end
        end

        % assign fitness values to entire population
        FitnV = ranking(ObjV);

        % select individuals for breeding
        SelCh = select(SELECTION, Chrom, FitnV, GGAP);

        %recombine individuals (crossover)
        SelCh = crossover_tsp(CROSSOVER, SelCh, PR_CROSS, SUBPOP);
        SelCh = mutate_tsp('mut_inversion', SelCh, PR_MUT, SUBPOP);

        %evaluate offspring, call objective function
        ObjVSel = tspfun(SelCh, Dist);

        %reinsert offspring into population
        if CUSTOMSS == 0
            [Chrom, ObjV] = reins(Chrom, SelCh, SUBPOP, 1, ObjV, ObjVSel);
        else
            [Chrom, ObjV] = sur_sel_rr_tournament(Chrom, SelCh, ObjV,
                ObjVSel, 10);
        end

        Chrom = tsp_improve_population(NIND, NVAR, Chrom, LOCALLOOP, Dist)
            ;

        gen = gen+1;
    end
end
```