

Experimental Comparison of Different Techniques to Generate Adaptive Sequences ^{*}

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Abstract. The focus of this paper is to present the results of a set of experiments regarding the construction of an adaptive sequence by a genetic algorithm and other techniques in order to reach a goal state in a non-deterministic finite state machine.

1 Introduction

Testing ([6,2]) is one of the most important tasks to be undertaken in software engineering. Its development and application covers a high percentage of the total cost of development in any process of software engineering.

Reaching a specific state is a fundamental part of the testing process because it allows the tester to move the implementation to that state and continue the testing of a certain part of a system, such as a specific component of an embedded system. In the case that the tester is confronted with a *non-deterministic finite state machine* (from now on *ndFSM*) this problem belongs to the EXPTIME complete category. Therefore, heuristic methods are used to present a solution.

A non-deterministic finite state machine is, informally, a set of states and labeled transitions with pairs input/output, the characteristic that makes it non-deterministic is that from the same state there can be several transitions labeled with the same input. We restrict our work to observable *ndFSMs*, that is, to machines in which two transitions departing from the same state cannot have the same combination of input/output.

Adaptive sequences [4,3,1] is a method used to reach a state in a non-deterministic setting. An *adaptive sequence* is a tree such that the unique edge that leaves its root will be labeled by an input (to be applied to the *ndFSM*), and it will reach a state such that from this state outgoing edges labeled by outputs (returned from the *ndFSM*) arrives at one state each from where a new input will depart and so on.

We have presented in a previous work [5], the use of a genetic algorithm to create an adaptive sequence to reach deterministically a goal state in a *ndFSM*. The interested

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reader is referred to the aforementioned paper for a more complete understanding of our approach, detailed explanations of the evolution of our GA and a formal definition of the elements present in the system. The goal of this paper is to present a set of experiments regarding the achievement of our genetic algorithm and some other techniques to an extent in which we can assure its validity.

The rest of the paper is organized as follows. In Section 2 we summarize the main aspect of the evolution of our GA. In Section 3 we show the results of our experiments and in Section 4 we present our conclusions.

2 Description of our GA

In this section we summarize the main concepts behind the evolution of our genetic algorithm. A more detailed description can be found in the aforementioned paper [5].

The inhabitants from the population create, based on their random coefficients, a new adaptive sequence which is their DNA.

This DNA is mutated once every generation, the way this is achieved is by traversing randomly the adaptive sequence and when the algorithm finds a node with no children then it adds a subtree to the adaptive sequence, or deletes the subtree to which the node belongs to (each with a 50% probability). The positive point about using this method to select a node is that it has a similar probability of being chosen as when executing the *ndFSM*. This allows to always modify the nodes that influence in a greater extent the overall functioning of the adaptive sequence.

Crossover is done by selecting the individuals with a higher heuristic value through *roulette wheel selection* and then traversing randomly both instances to try to find a node that represents the same node in the *ndFSM*. If this node is found then the algorithm exchanges the subtree of both adaptive sequences and creates two children that are added to the population. If no node is found following this procedure, then no crossover is performed.

In the beginning of the next generation, all the specimens are judged by a sampling procedure (running 100 times its adaptive sequence), and the algorithm performs a selection of the fittest, maintaining a constant number in the population by eliminating those individuals with the worst heuristic value. The selection of the fittest is an elitist selection, which means that the best individual from the last generation is copied directly into the next one without any mutation or crossover, to make sure that the GA does not lose the best solution found until that moment.

3 Experimental comparison

The number of experiments that we have conducted was established by taking into account the amplitude of the oscillation in the averaged heuristic values of the runs of different GAs against a series of *ndFSMs*. This value tends to stabilize around 50 experiments. This is one of the main motivations for having extended our experimental setup with respect to our previous work, since, before, we only performed 20 experiments and, as one can see in Figure 1, the value fluctuates at that point greatly.

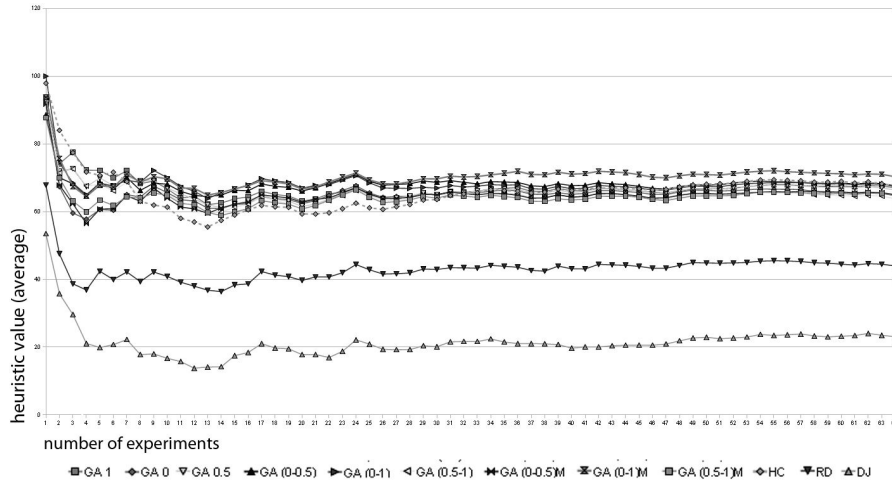


Fig. 1. Evolution of the average heuristic values for several techniques, including various kinds of GAs. The hillclimbing methodology appears in dotted lines.

We were also able to increase the speed of the algorithm, which has led to a modification in the heuristic values and of the total size of the resulting specimens.

3.1 Description of the experimentation

The experiments were run in a Intel Core2 Duo CPU T7300 at 2.00GHz with 2 GB of RAM.

The different techniques were given separate runs of 200 seconds each to find a solution. The GA was started with a population of 50 individuals, a crossover rate of 25 (half of the population was reproducing and producing new offspring), and a mutation rate of 1 (each individual was mutated once every generation). The highest individual was transferred into the next generation following the normal procedure for elitist evolution.

The hillclimbing specimen mutates as many times as it needs in order to find an specimen with a higher value and then continue its evolution, adding new nodes to its adaptive sequence.

The dijkstra individual is initiated once. In order to do so, first the Dijkstra's shortest path algorithm is ran in the *ndFSM* in order to calculate the distance from each state to the goal state. The algorithm as is proposed in this paper starts by creating a graph that is an inverted copy of the *ndFSM*, that is, a graph in which for a transition $s_i \xrightarrow{i/o} s_j$ existing in the *ndFSM* there exist one transition $s_j \rightarrow s_i$ in the inverted graph. Then we use the goal state as the initial state and calculate Dijkstra's shortest path algorithm.

The random individual mutates a random number of times between 0 and the total number of states in the *ndFSM*.

The heuristic that is used is the same for every type of evolution present in the system. The adaptive sequence of each specimen is used a hundred times to run the *ndFSM*, then the *ndFSM* returns its current state and we apply add of n (where n is the number of states), if it is the goal state, we subtract $n/2$ if it is a node from where the goal is unreachable, or subtract the value of its distance to the goal in any other case. Since the adaptive sequence is applied a hundred times, the total amount of heuristic value that an individual can have is 10000 points, that is considered being 100% fit, which means that every reachable end node of its adaptive sequence is the goal state. A drawback of this heuristic method is that using a sampling rating method, creates a fluctuation in the values for the same adaptive sequence, which makes evolution more complicated.

3.2 Comparison between GAs

The first set of experiments are focused on comparing different GAs, with different random coefficients, and that traverse the *ndFSM* in a distinctive manner (the results from the experiments are shown in Figure 2). The random coefficient is a number that expresses how likely the GA will mutate using the shortest distance to the goal state. A random coefficient of 0 will behave randomly, and a coefficient of 1 will traverse the *ndFSM* using the minimum distance, between these values, the specimen will choose some times at random and sometimes the closest node to the goal.

There are three ways of selecting the random coefficient for a new specimen. The first one is that every specimen in the population has a steady coefficient, for example in *GA 0.5* the whole population has 0.5 as its coefficient. The second manner is that it is started randomly from an interval, which is for example the case for *GA (0-0.5)*. And the third approach consist in a hereditary option, in which it is the average of its parents with a small amount of random added, which will be the case for *GA (0-1)m*. Every population labeled with an m (*mixed*) behaves in this last manner.

The population that achieved better results was the one started in the range of $(0-1)$ with the hereditary coefficient (*GA (0-1)m*). This population created, in average, adaptive sequences that reached 70.32% of the times the goal state, and obtained the lowest average distance with respect to the maximum achieved by any other method ($\mu = 9.41$, where $\mu = \sqrt{\frac{\sum_{i=0}^n (x_i - \max\{\cup_{j=0}^{11} \text{technique}_j\})^2}{n}}$). This behaves as expected since this population tries every possible random coefficient value and, depending on the configuration of the *ndFSM* (how much non-determinism contains, how much branching towards the goal following the shortest path) the individuals with highest results pass their configuration to their offspring. The second best population is the one started in the range $(0-0.5)$, this is the population that appeared to behave best in the few experiments that we presented in our previous paper.

The overall values are lower than in Section 3.3 because given the high number of populations, we restricted highly the time that we allowed the populations to evolve.

Comparison												
HEURISTIC VALUE (%)												
#	1	0	0.5	(0-0.5)	(0-1)	(0.5-1)	(0-0.5)m	(0-1)m	HC	RD	DJ	
0	93.86	92.77	93.85	88.6	100.0	92.75	91.75	93.81	87.71	97.92	67.86	53.5
1	54.47	42.05	50.09	51.5	48.94	50.15	43.93	57.67	52.16	70.13	27.23	18.05
2	84.38	43.95	74.3	64.62	56.42	74.95	51.3	50.78	49.46	64.2	21.0	17.34
3	56.35	52.47	51.35	53.57	54.69	52.61	39.0	55.76	50.65	54.63	31.43	-4.56
4	71.88	71.91	80.17	85.38	81.99	69.69	78.01	81.19	77.05	66.68	64.56	15.25
5	58.98	59.41	56.27	56.29	63.6	56.78	61.15	64.33	54.11	76.4	27.57	24.8
6	84.54	92.78	86.11	90.73	79.2	84.37	87.54	93.8	79.29	52.35	55.84	31.36
7	41.81	59.18	60.58	39.64	64.67	30.83	51.9	52.15	61.57	22.07	19.34	-13.26
8	75.16	93.38	70.02	85.5	100.0	85.58	97.92	83.45	77.74	53.04	64.83	19.57
9	45.66	48.21	47.12	65.26	51.02	53.34	37.49	64.03	58.78	56.15	29.27	4.95
10	37.42	42.52	47.91	44.68	41.64	39.89	35.29	39.92	38.08	24.82	21.93	6.25
11	70.06	59.52	46.87	52.12	50.17	49.29	54.47	65.79	58.47	45.29	25.19	-7.81
12	32.8	35.45	42.12	59.73	38.1	37.45	44.29	40.98	31.24	37.73	22.71	18.28
13	68.17	59.0	49.87	71.18	87.7	59.99	81.48	75.41	48.3	82.53	30.83	15.14
14	81.42	79.46	75.17	86.54	83.45	82.45	78.1	82.37	73.88	81.44	65.67	63.95
15	73.17	65.68	81.31	63.52	83.88	75.22	72.05	81.32	76.28	83.52	44.19	31.75
16	91.77	96.93	88.7	100.0	100.0	100.0	98.97	92.85	100.0	82.45	100.0	63.25
17	49.78	54.23	44.37	56.12	58.05	42.61	56.14	61.62	52.7	54.36	23.23	-2.32
18	56.06	59.24	53.38	61.2	59.96	46.76	56.68	58.77	54.78	58.73	32.8	15.07
19	34.66	39.88	31.36	45.75	35.66	29.49	37.51	37.56	33.95	21.91	18.4	-14.39
20	76.68	79.94	76.95	86.34	83.33	83.33	82.1	79.97	82.2	59.36	62.13	17.82
21	96.89	97.94	93.76	94.84	73.08	94.79	72.16	100.0	95.84	67.08	39.94	-1.02
22	75.86	97.94	100.0	100.0	100.0	97.93	98.94	100.0	100.0	87.55	69.59	59.05
23	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
24	15.22	14.3	19.72	20.84	17.3	16.74	22.49	20.61	12.41	28.03	5.61	-9.54
25	31.68	31.88	34.59	39.65	28.52	31.39	30.63	41.11	23.06	49.36	10.25	-18.26
26	66.05	71.37	73.07	72.77	65.65	78.09	66.09	65.78	70.42	81.97	44.25	15.1
27	80.33	64.73	79.23	74.24	65.77	65.35	69.84	86.1	78.13	79.57	48.22	20.68
28	94.74	91.75	94.72	92.66	74.7	86.89	90.52	94.77	91.64	100.0	75.25	52.0
29	50.88	47.65	44.38	55.89	61.25	55.89	62.37	68.11	51.91	68.44	39.0	12.19
30	92.7	90.64	91.65	85.41	90.68	89.69	88.55	94.86	89.58	100.0	58.54	64.3
31	59.04	61.49	56.16	62.56	54.13	53.13	51.1	63.15	55.32	80.33	42.71	24.85
32	76.97	67.46	86.4	84.64	74.84	55.88	84.49	74.41	53.83	77.3	40.29	21.25
33	87.69	79.42	81.57	89.7	83.14	85.16	80.4	87.65	84.15	95.9	71.28	47.5
34	75.04	80.73	72.69	65.61	62.63	78.16	61.37	85.42	52.11	56.92	34.73	8.45
35	75.13	56.26	58.42	64.52	71.79	62.66	47.79	93.84	51.51	59.71	33.62	4.3
36	25.43	28.58	30.52	30.72	24.53	23.33	33.51	37.83	26.62	45.9	8.35	21.73
37	63.92	60.53	63.42	59.46	62.39	64.29	67.14	66.67	59.75	76.22	35.57	17.38
38	100.0	86.49	100.0	100.0	100.0	97.94	100.0	100.0	93.75	100.0	100.0	12.78
39	42.03	48.09	37.8	46.55	37.08	34.6	38.32	49.86	49.79	49.1	12.55	-21.52
40	63.9	76.38	80.41	71.12	75.27	78.35	72.15	77.22	72.2	87.68	41.44	34.3
41	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	74.45	100.0	19.41
42	57.66	66.83	63.96	54.41	57.37	53.5	66.21	63.64	63.74	73.28	37.7	35.52
43	59.53	54.29	59.53	57.81	61.82	53.09	51.02	61.69	66.75	64.78	38.42	27.12
44	50.08	51.91	51.29	44.86	49.93	47.22	45.82	46.78	52.01	56.59	29.83	21.52
45	43.0	39.63	36.09	41.25	40.73	29.9	36.7	34.71	32.36	49.33	18.3	20.2
46	55.69	64.75	63.74	56.68	62.8	64.85	68.89	61.65	48.44	73.31	44.74	36.77
47	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	82.53	66.01
48	91.68	93.8	93.8	94.82	92.77	92.83	91.3	92.74	92.7	98.97	85.54	63.6
49	64.2	61.01	67.49	62.89	61.9	64.33	63.78	64.91	67.53	78.71	38.62	33.85
50	71.01	56.26	56.72	75.15	63.64	60.47	55.54	63.88	64.35	75.99	42.08	0.1
51	75.34	74.22	89.7	92.85	95.91	73.03	73.12	94.87	72.19	76.94	48.37	34.48
52	91.7	76.8	86.55	89.62	86.54	83.42	75.63	92.8	89.63	96.45	52.58	36.76
53	87.52	82.2	80.06	78.14	77.86	76.96	79.58	86.39	89.6	89.6	65.62	64.64
54	76.2	61.8	72.98	59.72	75.09	70.12	73.09	81.37	63.79	73.85	51.35	7.66
55	67.7	65.53	67.71	66.52	68.17	63.55	60.4	54.23	63.48	60.2	42.78	33.74
56	56.52	61.6	57.58	58.02	69.91	53.2	73.93	62.67	61.52	61.43	35.57	38.05
57	54.1	36.59	53.28	59.99	51.13	33.67	62.2	60.22	49.14	44.82	23.62	-9.34
58	66.55	58.43	59.45	60.44	60.46	56.34	55.25	62.25	59.36	70.68	38.33	5.35
59	74.69	64.15	70.35	76.8	74.75	63.11	70.67	66.34	78.87	82.88	26.74	35.1
60	55.95	49.47	55.47	50.53	52.75	50.6	44.29	51.8	45.05	37.38	30.43	35.23
61	86.48	80.08	86.48	85.45	81.15	79.0	83.03	87.17	89.59	92.82	67.44	63.6
62	60.0	43.24	43.35	57.56	60.84	53.73	59.4	64.92	55.56	32.13	36.29	-10.08
63	33.02	20.77	27.09	25.49	22.72	14.16	26.32	24.4	27.98	12.95	10.56	-4.58
64	67.05	64.76	66.39	67.63	67.4	63.83	65.02	70.32	64.75	67.41	43.98	23.08
65	12.61	15.25	13.61	12.69	12.74	15.69	15.29	9.41	15.99	16.15	35.95	57.69

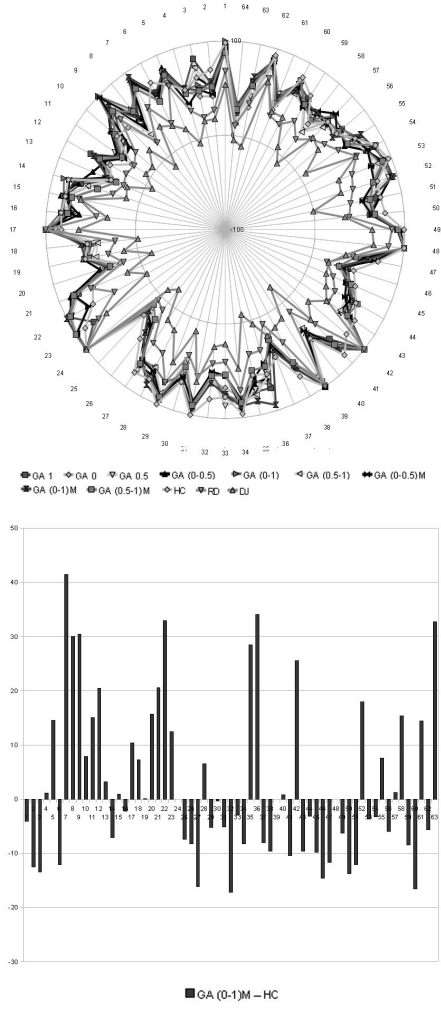


Fig. 2. Heuristic values of the comparisons between different GA methodologies, hillclimbing, random and dijkstra. Graphical representation of the heuristic values (upper right) and difference of the best GA and hillclimbing (GA-HC) (lower right).

3.3 Results of the main techniques

Next, we will present and comment, the experiments conducted by applying the adaptive sequences, obtained by the main techniques, to *ndFSMs* of different sizes and connection rates.

The connection rate specifies a maximum number of transitions, for example in a *ndFSM* with a hundred states and a connection level of 3 the average number of transitions is 255 and in a *ndFSM* with five hundred states and a connection level of 3 the average number of transitions is 1280.

The experiments were run against *ndFSMs* of 100, 500 and 1000 states, and two connection levels 3 and 4. The results for the connection level 4 are shown in Figure 3 and the results from connection level 3 can be found under <http://www.carlosmolineri.com/GAforAdapSeq.htm>.

As we can see by taking a look at the averages (\bar{x}) and the average distances to the maximum (μ), GA outperforms the rest of the methodologies. The value of the average of the heuristic value (\bar{x}) depends highly on the number of states, and in a lower percentage in the connection rate. In fact, as expected, the higher the number of states and therefore, of transitions, and the higher connection level (which also influences in the number of transitions) the more difficult it becomes to find a valid adaptive sequence. On the other hand, the distance to the maximum (μ) remains a quasi-constant value for each methodology no matter the *ndFSM* that it is applied to. The lower μ is, the larger the number of times that the technique achieved the maximal heuristic value, it also represents the difference in heuristic value that the technique had when it was not the highest. For our GA $\mu = 3.1$ in average (this average is computed taking into account all the experiments performed) while the hillclimbing method had $\mu = 11.08$.

After performing some scatter plots of the relationships between the heuristic values of the techniques, we realized that GA and hillclimbing has a positive correlation with the random heuristic value. In the case of the GA that uses the random method and the dijkstra method as specimens inside its population this was expected, but the hillclimbing methodology never uses the random specimen, or a random approach, still they have a correlation. In the case of hillclimbing the trendline is defined by the equation $heurVal(random) * 1.3 + 10$ and in the case of GA the trendline responds to the equation $heurVal(random) * 1.3 + 15$. This scatter plots are presented in Figure 4.

Another thing that we can observe in the scatter plots, is that although hillclimbing and GA behaved proportionally, the samples that are away from the *trendline* behave differently, which is one of the factors that impact on its relative fitness. In the case of hillclimbing, those samples away from the trendline behave worst than expected (they fall mostly in the right lower sector from the trendline) while in the GA they behave better than expected (they locate in the upper left sector from the trendline)

4 Conclusions and future work

We have presented in this paper a series of experiments undertaken in the context of our previous work [5]. The purpose of these experiments is to test whether a evolutionary methodology composed of genetic algorithms is able to find *adaptive sequences* that

Comparison																										
#	HEURISTIC VALUE (%)				SIZES				#	HEURISTIC VALUE (%)				SIZES												
	GA	HC	RD	DJ	GA	HC	RD	DJ		GA	HC	RD	DJ	GA	HC	RD	DJ									
0	94.85	89.22	79.87	52.0	1158.0	8160.0	261.0	2.0	0	57.97	59.38	39.67	39.75	2335.0	5701.0	1320.0	11.0	0	17.78	12.21	0.48	6.14	2527.0	4578.0	2659.0	67.0
1	87.44	92.82	59.1	36.16	1696.0	6948.0	265.0	9.0	1	82.1	63.45	40.85	1.69	1135.0	6800.0	1302.0	15.0	1	42.85	34.23	23.11	35.1	2726.0	3181.0	2552.0	30.0
2	100.0	97.94	81.46	0.26	12469.0	2642.0	233.0	8.0	2	45.6	40.47	22.74	13.97	1851.0	6345.0	1306.0	14.0	2	40.0	33.07	16.18	14.87	2366.0	5254.0	2571.0	16.0
3	83.38	74.29	50.4	22.02	33972.0	1214.0	257.0	8.0	3	40.58	43.98	16.99	4.04	2210.0	5490.0	1290.0	16.0	3	48.31	35.73	20.77	15.5	4518.0	4804.0	2585.0	12.0
4	97.95	96.44	82.92	32.08	789.0	7759.0	263.0	9.0	4	73.59	76.19	51.13	4.71	983.0	6930.0	1312.0	15.0	4	22.76	17.35	1.45	0.25	3790.0	4340.0	2636.0	16.0
5	97.93	87.26	49.81	13.12	2996.0	6723.0	266.0	15.0	5	57.77	51.24	30.36	15.48	1202.0	6533.0	1312.0	18.0	5	60.18	60.52	49.8	39.58	1719.0	7089.0	2594.0	11.0
6	59.24	51.45	32.88	10.02	2088.0	7016.0	268.0	17.0	6	54.73	42.91	27.95	11.76	1363.0	6358.0	1321.0	15.0	6	24.66	22.62	8.01	9.75	2459.0	6113.0	2640.0	13.0
7	67.89	71.29	36.51	21.62	4990.0	5223.0	265.0	10.0	7	45.79	45.04	23.67	7.88	1219.0	6462.0	1271.0	19.0	7	53.6	52.46	36.75	19.96	2097.0	5131.0	2589.0	12.0
8	91.73	98.98	65.39	24.08	1465.0	7309.0	271.0	12.0	8	70.33	80.09	43.12	36.26	1872.0	6265.0	1323.0	15.0	8	20.9	19.53	8.83	1.1	2272.0	6802.0	2635.0	20.0
9	40.86	31.24	15.76	11.77	40213.0	1244.0	277.0	14.0	9	48.03	54.49	36.51	37.62	1278.0	7141.0	1335.0	13.0	9	54.66	47.64	35.01	12.4	1780.0	7121.0	2627.0	20.0
10	23.6	30.72	2.76	16.14	1771.0	7288.0	272.0	20.0	10	36.16	44.48	19.6	5.86	1315.0	7006.0	1310.0	15.0	10	28.53	28.9	15.2	35.15	2899.0	5528.0	2545.0	23.0
11	98.97	92.34	64.89	39.03	2295.0	6196.0	265.0	9.0	11	29.04	33.27	15.69	15.87	1311.0	6081.0	1315.0	21.0	11	80.11	82.65	61.27	65.76	1336.0	7455.0	2644.0	14.0
12	57.85	57.37	40.66	35.69	6214.0	5310.0	266.0	13.0	12	41.36	32.48	28.45	18.27	1356.0	6538.0	1309.0	12.0	12	49.99	57.23	32.7	10.4	2371.0	6047.0	2600.0	28.0
13	100.0	100.0	73.03	39.54	1205.0	6775.0	260.0	11.0	13	82.3	83.52	67.31	21.91	867.0	7554.0	1258.0	10.0	13	37.45	33.78	16.03	19.44	2886.0	4510.0	2596.0	16.0
14	63.37	58.5	19.71	6.82	5249.0	3943.0	266.0	15.0	14	49.56	41.1	24.14	8.33	2660.0	5631.0	1284.0	17.0	14	28.55	16.23	11.78	6.55	2445.0	5445.0	2631.0	21.0
15	35.25	34.16	12.26	17.09	4857.0	5221.0	271.0	17.0	15	45.54	54.21	31.72	17.2	2360.0	6593.0	1271.0	12.0	15	42.87	30.32	25.81	1.64	2516.0	5466.0	2589.0	14.0
16	83.97	73.63	41.17	3.25	19724.0	2686.0	265.0	10.0	16	31.33	19.89	5.21	17.45	1746.0	6474.0	1348.0	22.0	16	46.39	43.84	23.91	2.56	7992.0	2765.0	2551.0	14.0
17	100.0	85.04	75.24	12.1	931.0	7769.0	276.0	12.0	17	84.3	86.47	66.66	10.6	1133.0	6762.0	1266.0	17.0	17	65.96	74.06	54.36	24.62	2363.0	6280.0	2593.0	7.0
18	95.82	73.63	41.17	3.25	19724.0	2686.0	265.0	10.0	18	63.36	70.87	39.84	42.09	1300.0	7057.0	1306.0	17.0	18	100.0	100.0	100.0	0.0	850.0	7.0	2590.0	7.0
19	65.73	61.16	43.14	2.14	24934.0	1902.0	267.0	25.0	19	49.74	24.62	17.65	8.0	2418.0	6164.0	1336.0	17.0	19	57.56	52.16	44.97	40.15	1657.0	6492.0	2567.0	27.0
20	88.48	89.72	56.17	34.7	20182.0	2150.0	263.0	13.0	20	62.79	36.93	29.67	-12.25	929.0	6811.0	1310.0	16.0	20	40.59	48.57	23.57	23.12	1267.0	6546.0	2597.0	10.0
21	79.35	77.47	41.91	3.48	6162.0	4523.0	267.0	12.0	21	55.35	37.5	34.99	11.64	12114.0	2858.0	1281.0	10.0	21	24.28	20.18	10.75	1.19	2361.0	5588.0	2641.0	16.0
22	83.01	77.92	53.88	40.18	5688.0	5844.0	280.0	7.0	22	61.44	59.83	37.25	11.56	2288.0	6669.0	1309.0	15.0	22	46.48	41.53	18.75	21.27	4118.0	3790.0	2579.0	20.0
23	82.26	75.76	62.67	35.56	5495.0	1003.0	262.0	9.0	23	55.72	49.96	32.73	22.82	1317.0	6467.0	1315.0	12.0	23	30.54	23.66	11.76	1.37	2692.0	6065.0	2646.0	20.0
24	75.11	47.01	34.81	12.12	4207.0	5519.0	273.0	10.0	24	81.24	82.93	69.26	68.5	1053.0	7806.0	1317.0	18.0	24	17.72	25.46	8.42	4.48	1904.0	6176.0	2625.0	18.0
25	76.07	70.59	42.27	15.71	4038.0	4839.0	267.0	12.0	25	41.72	50.61	25.06	2.82	1130.0	7073.0	1319.0	17.0	25	40.59	33.62	19.28	26.21	2591.0	5170.0	2619.0	34.0
26	82.32	68.43	53.03	38.08	3796.0	5571.0	261.0	7.0	26	63.26	72.46	43.89	12.28	784.0	7214.0	1319.0	18.0	26	50.71	57.1	32.17	7.79	2372.0	6823.0	2630.0	49.0
27	72.08	51.55	37.13	10.82	89619.0	9992.0	266.0	11.0	27	86.4	85.42	71.96	67.45	707.0	7867.0	1303.0	8.0	27	46.99	35.34	21.26	2.85	2622.0	4882.0	2626.0	12.0
28	48.14	51.8	20.74	4.94	1331.0	7590.0	271.0	13.0	28	44.3	41.73	27.69	-0.04	1183.0	7099.0	1319.0	16.0	28	32.35	39.64	15.49	4.58	1552.0	5849.0	2582.0	19.0
29	55.1	44.85	25.88	20.33	12127.0	4924.0	272.0	12.0	29	70.44	58.64	32.06	10.43	3888.0	4823.0	1297.0	11.0	29	45.77	44.43	31.86	19.36	3352.0	4910.0	2618.0	19.0
30	87.51	58.42	23.33	6.67	3637.0	5668.0	278.0	14.0	30	82.04	66.02	67.91	5.21	953.0	7364.0	1308.0	13.0	30	47.11	32.56	28.73	0.38	2400.0	4924.0	2585.0	19.0
31	82.21	77.67	52.99	1.7	1359.0	7236.0	266.0	13.0	31	40.02	27.37	19.3	9.84	892.0	6564.0	1332.0	17.0	31	39.26	25.05	8.14	22.12	2102.0	4624.0	2645.0	37.0
32	69.86	62.48	26.7	4.8	23292.0	1848.0	267.0	14.0	32	17.6	14.39	0.84	-16.62	1028.0	6936.0	1342.0	21.0	32	40.43	35.34	16.96	10.37	14366.0	1863.0	2624.0	40.0
33	46.53	46.33	11.16	13.8	6481.0	4422.0	278.0	16.0	33	36.19	22.5	20.29	3.64	1652.0	6645.0	1332.0	18.0	33	35.73	25.86	19.98	27.36	3748.0	4017.0	2614.0	40.0
34	80.07	44.61	30.25	20.18	43219.0	1286.0	272.0	12.0	34	32.36	35.66	19.81	19.14	1204.0	7082.0	1341.0	12.0	34	33.8	27.29	19.61	6.25	18806.0	1407.0	2546.0	17.0
35	73.05	69.37	45.39	17.36	40626.0	1226.0	248.0	11.0	35	35.85	30.34	16.57	4.96	1159.0	7150.0	1323.0	16.0	35	45.4	44.15	27.5	9.46	2387.0	6024.0	2649.0	16.0
36	90.75	79.53	49.21	7.35	6071.0	4404.0	269.0	15.0	36	37.48	84.39	51.48	36.65	1143.0	6423.0	1321.0	15.0	36	57.84	44.53	34.53	2.28	2347.0	6243.0	2573.0	21.0
37	92.76	64.74	43.57	9.16	38569.0	1163.0	271.0	8.0	37	57.39	56.07	35.28	22.2	2470.0	5151.0	1311.0	16.0	37	36.11	18.76	8.56	16.88	2324.0	5069.0	2633.0	21.0
38	100.0	100.0	90.7	36.4	1129.0	6709.0	257.0	9.0	38	46.02	32.06	31.15	-12.67	1457.0	6658.0	1318.0	28.0	38	70.36	62.78	32.87	14.82	7568.0	2582.0	2581.0	16.0
39	100.0	100.0	76.96	15.51	1328.0	7465.0	268.0	10.0	39	40.53	27.24	28.52	-17.42	12179.0	1992.0	1297.0	17.0	39	55.79	66.11	29.16	3.88	2196.0	6073.0	2570.0	15.0
40	100.0	100.0	100.0	64.64	1428.0	8079.0	263.0	6.0	40	53.84	51.13	29.58	-6.26	5989.0	4624.0	1277.0	17.0	40	22.03	32.42	7.7	14.13	2399.0	6003.0	2591.0	16.0
41	100.0	86.66	54.44	36.41	2182.0	6727.0	263.0	7.0	41	86.32	87.07	72.36	64.3	708.0	7824.0	1313.0	4.0	41	70.04	63.44	45.17	6.79	2163.0	7312.0	2620.0	16.0
42	100.0	85.6	75.19	20.21	2433.0	7034.0	269.0	10.0	42	68.34	73.39	44.11	15.18	1689.0	7223.0	1289.0	13.0	42	17.07	15.68	5.43	4.24	2025.0	5994.0	2632.0	18.0
43	94.83	91.75	70.64	38.45	5342.0	5580.0	259.0	11.0	43	67.62	79.35	47.22	39.81	1353.0	6963.0	1277.0	9.0	43	74.72	38.38	65.28	5.06	2367.0	6841.0	2659.0	14.0
44	95.88	83.21	55.83	21.61	32788.0	1839.0	264.0	10.0	44	52.77	31.66	35.2	6.14	4991.0	4080.0	1356.0	16.0	44	54.59	28.27	12.84	4.7	2351.0	5389.0	2637.0	16.0
45	40.5	23.55	7.06	-23.96	3610.0	6644.0	281.0	24.0																		

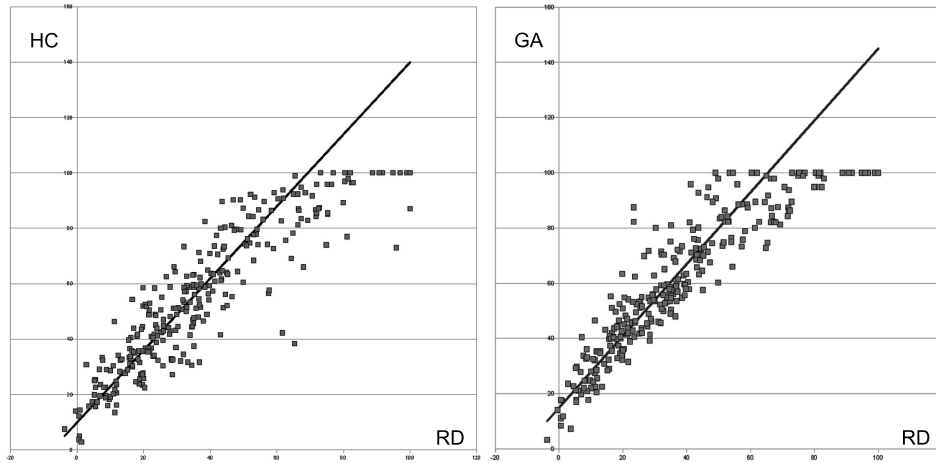


Fig. 4. Representation of the scatter plots of Hillclimbing with respect to Random, and of GA with respect to Random.

allow to reach a certain goal state in a deterministic fashion in a non-deterministic context.

The comparison with other methodologies such as the hillclimbing or random, was satisfactory in the sense that GA showed a better general performance, and with a higher consistency. In general we can say that the hillclimbing algorithm performs well in most cases, but its results are less consistent than those of the genetic algorithm.

We have experimented with *ndFSMs* of different sizes and connection levels. As the number of transitions increased there was a decrease in the heuristic values of the adaptive sequences since a higher number of states with a high degree of non-determinism, creates a high level of branching and the existence of a perfect solution becomes more complicated, as well as its discovery.

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