Genetic Algorithms and Local Search

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GENETIC ALGORITHMS AND LOCAL SEARCH

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ABSTRACT

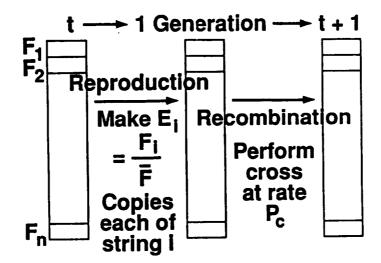
The first part of this presentation is a tutorial level introduction to the principles of genetic search and models of simple genetic algorithms. The second half covers the combination of genetic algorithms with local search methods to produce hybrid genetic algorithms. Hybrid algorithms can be modeled within the existing theoretical framework developed for simple genetic algorithms.

An application of a hybrid to geometric model matching is given. The hybrid algorithm yields results that improve on the current state-of-the-art for this problem.¹

¹Ross Beveridge collaborated in the geometric matching application. This work was supported by NSF grants IRI-9312748 and IRI-9503366 and by the Advanced Research Projects Agency (ARPA) under grant DAAH04-93-G-422 monitored by the U.S. Army Research Office.

THE CANONICAL GENETIC ALGORITHM

In the canonical genetic algorithm, fitness is defined by: f_i / \bar{f} where f_i is the evaluation associated with string *i*, and \bar{f} is the average evaluation of all the strings in the population. It is helpful to view the execution of the genetic algorithm as a two-stage process. It starts with the *current population*. Selection is applied to the current population to create an *intermediate population*. Then recombination and mutation are applied to the intermediate population to create the *next population*.



- 1. Generate a random population of strings.
- 2. Evaluate all strings in the population.
- 3. Reproduce (duplicate) strings according to fitness.
- 4. Recombine strings according to the probability of crossover.
- 5. Repeat steps 2 to 4.

AN EXAMPLE OF HYPERPLANE PARTITIONING

A function over a single variable is plotted as a one-dimensional space, with function maximization as a goal. The hyperplane 0****...** spans the first half of the space and 1****...** spans the second half of the space. Since the strings in the 0****...** partition are on average better than those in the 1****...** partition, we would like the search to be proportionally biased toward this partition. In the second graph the portion of the space corresponding to **1**...** is shaded, which also highlights the intersection of 0****...** and **1**...**, namely, 0*1*...**. Finally, in the third graph, 0*10**...** is highlighted.

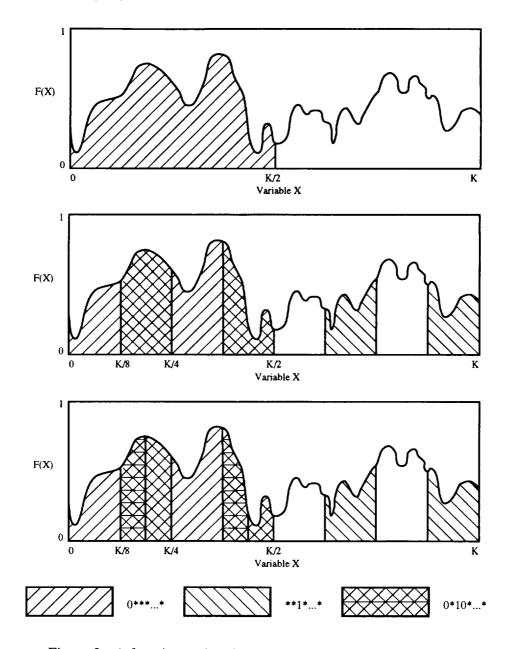


Figure 3 - A function and various partitions of hyperspace. Fitness is scaled to a 0 to 1 range in this diagram.

SELECTION IN A SAMPLE POPULATION

This example population contains only 21 (partially specified) strings. The table includes information on the fitness of each string and the number of copies to be placed in the intermediate population. This table enumerates the 27 hyperplanes (3^3) that can be defined over the first three bits of the strings in the population and *explicitly* calculates the fitness associated with the corresponding hyperplane partition. The true fitness of the hyperplane partition corresponds to the average fitness of all strings that lie in that hyperplane partition.

Strings and Fitness Values									
String-ID	String	Fitness	Random	copies					
1	001##	2.0	-	2					
2	101##	1.9	0.93	2					
3	111##	1.8	0.65	2					
4	010##	1.7	0.02	1					
5	111##	1.6	0.51	2					
6	101##	1.5	0.20	1					
7	011##	1.4	0.93	2					
8	001##	1.3	0.20	1					
9	000##	1.2	0.37	1					
10	100##	1.1	0.79	1					
11	010##	1.0	-	1					
12	011##	0.9	0.28	1					
13	000##	0.8	0.13	0					
14	110##	0.7	0.70	1					
15	110##	0.6	0.80	1					
16	100##	0.5	0.51	1					
17	011##	0.4	0.76	1					
18	000##	0.3	0.45	0					
19	001##	0.2	0.61	0					
20	100##	0.1	0.07	0					
21	010##	0 0	-	0					

Table 1 - A population with fitness assigned to strings according to rank.

PROCESSING OF HYPERPLANES

The *expected* number of strings sampling a hyperplane partition after selection can be calculated by multiplying the number of hyperplane samples in the current population before selection by the average fitness of the strings in the population that fall in that partition. The *observed* number of copies actually allocated by selection is also given. In most cases, the match between expected and observed sampling rate is fairly good: the error is a result of sampling error due to the small population size.

	Schemata and Fitness Values											
Schema	Mean	Count	Expect	Obs	Schema	Mean	Count	Expect	Obs			
101**	1.70	2	3.4	3	*0***	0.991	11	10.9	9			
111**	1.70	2	3.4	4	00***	0.967	6	5.8	4			
1*1**	1.70	4	6.8	7	0****	0.933	12	11.2	10			
*01**	1.38	5	6.9	6	011**	0.900	3	2.7	4			
1	1.30	10	13.0	14	010**	0.900	3	2.7	2			
*11**	1.22	5	6	8	01***	0.900	6	5.4	6			
11***	1.175	4	4.7	6	0*0**	0.833	6	5.0	3			
001**	1.136	3	3.5	3	*10**	0.800	5	4.0	4			
1****	1.089	9	9.8	11	000**	0.767	3	2.3	1			
0*1**	1.033	6	6.2	7	**0**	0.727	11	8.0	7			
10***	1.020	5	5.1	5	*00**	0.667	6	4.0	3			
*1***	1.010	10	10.1	12	110**	0.650	2	1.3	2			
*****	1.000	21	21.0	2.	1*0**	0.600	5	3.0	4			
		İ			100**	0.566	3	1.70	2			

Table 2 - The average fitnesses (Mean) associated with the samples from the 27 hyperplanes defined over the first three bit positions are explicitly calculated. The Expected representation (Expect) and Observed representation (Obs) are shown. Count refers to the number of strings in hyperplane H before selection.

THE VOSE AND LIEPINS MODEL

In the Vose and Liepins model, the vector $s' \in \Re$ represents the *t* th generation of the genetic algorithm and the *i* th component of s' is the probability that the string *i* is selected for the gene pool. The standard form of the executable equations corresponds to the following portion of the Liepins and Vose model (T denotes transpose):

 $s^T M s$

A permutation function, σ , is defined as follows:

$$\sigma_j < s_0, ..., s_{V-1} >^T = < s_{j \oplus 0}, ..., s_{j \oplus (V-1)} >^T$$

where the vectors are treated as columns and $V = 2^{L}$, the size of the search space.

The Vose and Liepins Model

The *i* th component of vector s^{i} is the probability that the string *i* is selected for the gene pool.

$$S_i^t = P(S_i, t) f(S_i) / \bar{f}$$

The function $r_{i,j}(k)$ is used to construct a mixing matrix M where the i, j th entry $m_{i,j} = r_{i,j}(0)$. This matrix gives the probabilities that crossing strings i and j will produce S_0 .

The proportional representation for string 0 at time t+1 is given by:

 $s^T M s$

where T denotes transpose.

If recombination is a combination of crossover and mutation then

$$r_{i,j}\left(k\oplus q\right)=r_{i\oplus k,j\oplus k}\left(q\right)$$

THE VOSE AND LIEPINS MODEL (Cont.)

A general operator \mathcal{M} can be defined over s which remaps $s^T M s$ to cover all strings in the space.

$$\mathcal{M}(s) = \langle (\sigma_0 s)^T M \sigma_0 s, ..., (\sigma_{V-1} s)^T M \sigma_{V-1} s \rangle^T$$

Fitness information is explicitly introduced to transform the population at the beginning of iteration t + 1 to the next intermediate population. A fitness matrix F is defined such that fitness information is stored along the diagonal; the *i*,*i* th element is given by f(i) where f is the evaluation function.

The transformation from the vector p^{t+1} to the next intermediate population represented by s^{t+1} is given as follows:

$$s^{t+1} = \frac{F p^{t+1}}{1^T F p^{t+1}}$$

The Vose and Liepins Model

A general operator \mathcal{M} can now be defined over *s* which remaps $s^T M s$ to cover all strings in the search space.

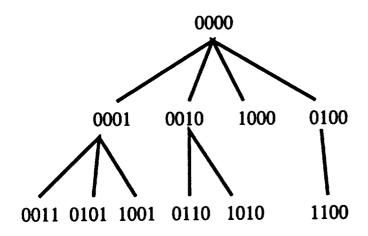
$$\mathcal{M}(s) = \langle (\sigma_0 s)^T M \sigma_0 s, ..., (\sigma_{V-1} s)^T M \sigma_{V-1} s \rangle^T$$

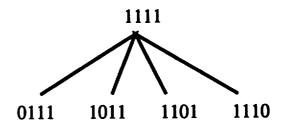
A fitness matrix *F* is defined such that fitness information is stored along the diagonal; following Vose and Wright, the $(i,i)^{th}$ element is given by f(i) where *f* is the fitness function.

$$s^{t+1} = \frac{F p^{t+1}}{1^T F p^{t+1}}$$

BASINS OF ATTRACTION

This slide illustrates the basins of attraction for a four-bit space under steepest ascent local search. Note that equivalence classes of functions are created when one considers the set of functions that have the same basins of attraction. These equivalence classes carry over into hybrid genetic algorithms that combine genetic search with local search, also referred to as Lamarckian search.





UPDATES TO REPRESENTATION UNDER LOCAL SEARCH

Local search can be added to the existing models of genetic algorithms. This slide shows how one step of steepest ascent changes the distribution of samples in the population.

How Population Distributions Change Under Lamarckian Search

```
P'(0000,t) = P(0000,t) + P(0001,t) + P(0010,t) + P(0100,t) + P(1000,t)
P'(0001,t) = P(0011,t) + P(0101,t) + P(1001,t)
P'(0010,t) = P(0110,t) + P(1010,t)
P'(0100,t) = P(1100,t)
P'(1111,t) = P(1111,t) + P(1110,t) + P(1101,t) + P(1011,t) + P(0111,t)
P'(0011,t) = 0
P'(0101,t) = 0
P'(0110,t) = 0
P'(0111,t) = 0
P'(1000,t) = 0
P'(1001,t) = 0
P'(1010,t) = 0
P'(1011,t) = 0
P'(1100,t) = 0
P'(1101,t) = 0
P'(1110,t) = 0
   Function 1:
                  e(0100) = 20
                                    e(1000) = 12
                                                      e(1100) = 4
e(0000) = 28
                                                       e(1101) = 2
                  e(0101) = 18
                                    e(1001) = 10
e(0001) = 26
                                    e(1010) = 8
                                                      e(1110) = 0
                  e(0110) = 16
e(0010) = 24
                                    e(1011) = 6
                                                      e(1111) = 30
e(0011) = 22
                  e(0111) = 14
```

The following Function is Equivalent to Function 1 Under Hybrid Search.

e(0000) = 28	e(0100) = 20	e(1000) = 18	e(1100) = 18
e(0001) = 26	e(0101) = 24	e(1001) = 24	e(1101) = 18
e(0010) = 24	e(0110) = 22	e(1010) = 22	e(1110) = 18
e(0011) = 24	e(0111) = 22	e(1011) = 22	e(1111) = 30

A MATRIX REPRESENTATION OF LOCAL UPDATES

The same redistribution of samples seen below can be captured in matrix form and used to model multiple steps of local search.

Lamarckian Updates to the p Vector

1	[10000	0
	$1 \ 0 \ 0 \ 0 \ 0$	0
	10000	0
	01000	0
	10000	0
	01000	0
	00100	0
τ	00000	0
p^T	10000	0
	01000	0
	00100	0
	00000	0
	00001	0
	00000	0
	00000	Õ
	00000	Ŭ

For one step of local search: $p^T L$ For 2 steps of local search: $(p^T L)L = p^T L^2$ For k steps of local search: $p^T L^k$

THE GEOMETRIC MATCHING PROBLEM

The geometric matching problem matches a model to a set of data. For example, the model may be a line drawing and the data might be line segments extracted from a photograph. Problems of this type arise in a number of areas and are specifically relevant to problems associated with computer vision. Variations of local search are currently being used to solve geometric matching problems in the context of semi-autonomous photo-interpretation and robot navigation.

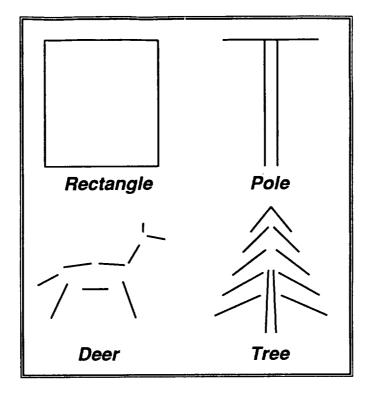


Figure 1 - Four stick figure models used in geometric matching tests.

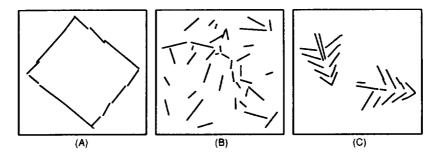


Figure 2 - Sample of synthetic test data for matching: a) rectangle model randomly placed, scaled and corrputed, b) corrupted deer model with random clutter, c) multiple corrupted instances of the tree model.

AN EXAMPLE MATCH

An example of a best match is shown for the tree model. The line segments making up the model are labeled with letters and are shown on the left. The data line segments include three instances of the tree and are shown to the right. The model is overlaid on top of the data in the best match position. The correspondence matrix indicates which pairs of model and data segments are part of this best match. Each square in the table may be thought of as representing one bit in the bit string encoding of the match. The filled in squares correspond to 1s in the bit string. Details for this application can be found in Whitley, Beveridge, Graves and Mathias (1995), "Testing Driving Three 1995 Genetic Algorithms," Journal of Heuristics.

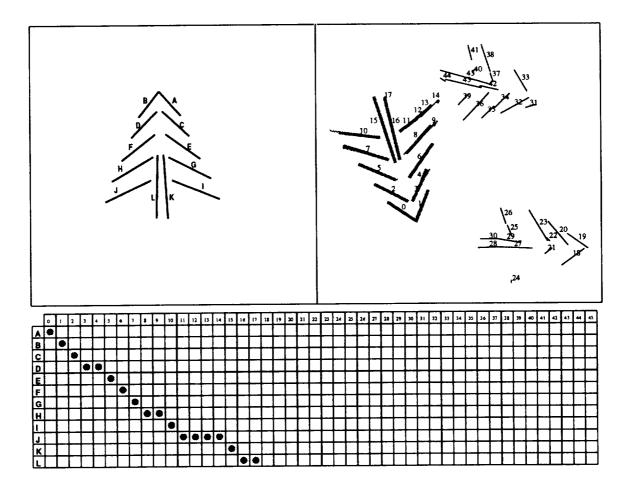


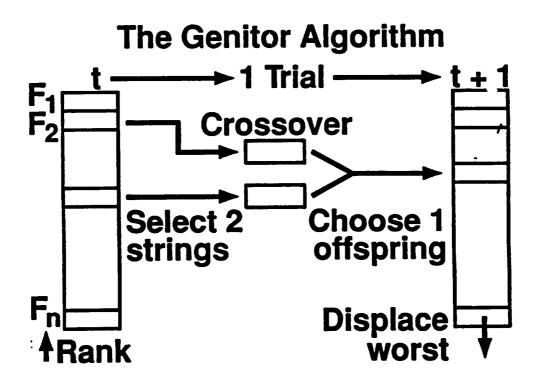
Figure 3 - Example of a best match for one of the 32 matching problems.

THE GENITOR ALGORITHM

The Genitor Algorithm. Offspring are produced one at a time and replace the worst member of the population.

Genitor

- Ranking used to determine fitness
- One-at-a-time recombination and replacement



COMPARISON OF LOCAL SEARCH AND GENITOR

Neither the local search algorithms nor the genetic algorithms converge upon the globally optimal match in all cases. Therefore, in comparing algorithms for model matching, two things must be taken into consideration. First is the likelihood that the algorithm once initiated will converge on the optimal solution. The second is how much work must be performed in order to reach convergence. LS Inc uses a fast incremental evaluation while LS Full uses a full evaluation.

		Tria	Estimated Run Time							
Model	Params	LS Inc.	LS Full	Genitor+	LS Inc. LS Full Gen			Genitor-	+	
Pole	12C	6	5	1	0.2	*	0.2	*	0.3	
Pole	24M	8	7	2	0.8	0	0.7	*	1.4	
Rectangle	28 C	6	6	3	0.6	*	0.6	*	3.6	
Pole	42 C	26	20	5	2.6	0	2.0	*	4.0	
Pole	42M	12	10	7	1.2	ο	1.0	*	9.1	
Rectangle	52M	5	5	4	1.0	*	1.5	0	7.2	
Rectangle	68C	11	9	4	1.1	*	2.7	ο	8.4	
Pole	72C	35	39	20	3.5	*	7.8	0	20.0	
Deer	81C	13	11	2	3.9	` +	8.8	ο	12.2	
Pole	81M	37	29	11	3.7	*	8.7	0	20.9	
Pole	96M	45	24	29	9.0	*	9.6	0	52.2	
Deer	99M	19	15	3	7.6	*	18.0	0	25.5	
Pole	102C	96	72	13	9.6	*	21.6		20.8	0
Rectangle	108C	47	17	8	9.4	*	10.2	ο	41.6	
Rectangle	108M	12	13	18	3.6	*	10.4	0	138.6	
Rectangle	124M	14	15	49	5.6	*	13.5	0	240.1	
Rectangle	148C	42	26	8	12.6	*	23.4	0	67.2	
Tree	156C	42	32	9	33.6	*	118.4	0	361.5	
Rectangle	168M	20	24	24	10.0	*	72.0	0	206.4	
Deer	171C	29	34	4	17.4	*	85.0	0	137.6	
Deer	180M	31	33	6	21.7	*	99.0	0	152.4	
Tree	216M	51	52	8	66.3	×	291.2	0	331.5	
Deer	261C	43	67	6	43.0	*	341.7	0	414.0	
Deer	261M	59	46	6	59.0	*	239.2	o	372.0	
Tree	276C	51	52	5	76.5	*	473.2	0	617.5	
Deer	342M	106	67	7	159.0	*	576.2	0	984.9	
Deer	351C	64	66	6	96.0	×	607.2		517.2	о
Tree	396 C	52	70	3	114.4	*	1,113.0		829.2	0
Tree	432M	135	99	7	310.5	*	1,871.1	0	2,405.2	
Tree	516C	99	96	5	297.0	*	2,438.4		$2,\!156.5$	0
Tree	552M	149	106	75	461.9	*	3,307.2	0	35,317.5	
Tree	780M	299	175	-	1,554.8	*	10,202.5	0	-	

Table 8 - Comparison of steepest ascent local search using partial incremental evaluation (LS-Inc), steepest ascent local search using full evaluation (LS-Full), and Genitor+algorithm on 32 test problems.

COMPARISON OF A HYBRID ALGORITHM

A "Hybrid Genetic Algorithm" uses local search as an operator to improve the strings in the population. The comparison in this slide suggests there is little difference in the hybrid genetic algorithm compared to local search using incremental evaluation. Aside from concerns about the execution speed of the implementations of the different algorithms, there is another factor which very much influences the results shown here: What criterion should be used to terminate genetic search when evaluation of the global optimum is unknown? This issue typically does not arise for artifically constructed test functions and this issue has not received a great deal of attention in the genetic algorithm literature.

		Success	Prob.: P.	Trials: t ₉₅		Estimated Run Time			
Model	Params	LS Inc.	Hybrid	LS Inc.	Hybrid	LS Inc.	Hybrid	% Diff.	
Pole	12C	0.42	0.94	6	2	0.2	0.2	83%	
Pole	24M	0.32	0.98	8	1	0.8	0.3	38%	
Rectangle	28C	0.44	1.00	6	1	0.6	0.5	83%	
Pole	42C	0.11	0.52	26	5	2.6	2.0	77%	
Pole	42M	0.23	0.80	12	2	1.2	1.2	100%	
Rectangle	52M	0.47	0.98	5	1	1.0	1.4	140%	
Rectangle	68C	0.24	1.00	11	1	1.1	1.1	100%	
Pole	72C	0.08	0.42	35	6	3.5	4.8	137%	
Deer	81C	0.21	0.66	13	3	3.9	7.2	185%	
Pole	81M	0.08	0.62	37	4	3.7	6.4	173%	
Pole	96M	0.07	0.40	45	6	9.0	9.6	107%	
Deer	99M	0.15	0.84	19	2	7.6	6.0	79%	
Pole	102C	0.03	0.40	96	6	9.6	8.4	88%	
Rectangle	108C	0.06	0.64	47	3	9.4	6.0	64%	
Rectangle	108M	0.23	0.94	12	2	3.6	8.0	222%	
Rectangle	124M	0.19	0.92	14	2	5.6	7.6	136%	
Rectangle	148C	0.07	0.60	42	4	12.6	14.0	111%	
Tree	156C	0.07	0.58	42	4	33.6	36.8	110%	
Rectangle	168M	0.14	0.76	20	3	10.0	1 8.3	183%	
Deer	171C	0.10	0.60	29	4	17.4	29.2	168%	
Deer	180M	0.10	0.90	31	2	21.7	16.8	77%	
Tree	216M	0.06	0.70	51	3	66.3	47.7	72%	
Deer	261C	0.07	0.52	43	5	43.0	80.5	187%	
Deer	261M	0.05	0.82	59	2	59.0	35.4	60%	
Tree	276C	0.06	0.64	51	3	76.5	78.3	102%	
Deer	342M	0.03	0.64	106	3	159.0	105.6	66%	
Deer	351C	0.05	0.54	64	4	96.0	145.2	151%	
Tree	396 C	0.06	0.80	52	2	114.4	125.2	109%	
Tree	432M	0.02	0.64	135	3	310.5	235.5	76%	
Tree	516C	0.03	0.74	99	3	297.0	390.6	132%	
Tree	552M	0.02	0.74	149	3	461.9	482.4	104%	
Tree	780M	0.01	0.46	299	5	1,554.8	1,735.0	112%	

Table 9 - Comparison of steepest ascent local search using partial evaluation (LS-Inc) and the hybrid genetic algorithm. % Diff refers to the amount of time required by the hybrid to find a solution with 95% reliability compared to local search.

EVALUATION TIME FOR THE HYBRID GA

The data presented in this slide indicates that the hybrid genetic algorithm is finding the solution to the problems long before the stopping criterion is satisfied. The data in Table 10 is broken down into the number of evaluations used by the local search algorithm (which can exploit incremental evaluation) as well as the full-evaluation calls used by the genetic algorithm after mating. The number of evaluations required to find the best solution is less than half the number of evaluations required to satisfy the stopping criterion. Cutting the number of evaluations in half can be achieved easily by picking a better stopping criteria. This would then represent a new state-of-the-art in general geometric matching.

			Best Mat	ch Found	Convergence			
Model	Params	<i>P</i> ,	Inc-Evals	Full-Evals	Inc-Evals Full-Evals		Secs	
Pole	12C	94	161.4	22.1	727.6	129.2	0.2	
Pole	24M	96	452.0	16.3	2540.8	138.0	0.5	
Rectangle	28C	100	438.8	12.2	3693.9	164.7	0.7	
Pole	42C	54	1311.2	47.6	3264.2	141.8	0.9	
Pole	42M	90	1284.0	30.2	4748.0	148.8	0.9	
Rectangle	52M	100	1462.4	13.1	11597.6	178.9	1.9	
Rectangle	68C	100	1920.9	22.1	10663.4	184.7	1.8	
Pole	72C	42	2324.5	49.8	5949.4	150.8	1.2	
Deer	81C	84	6175. 3	40.6	23095.7	252.9	3.6	
Pole	81M	72	4288.2	45.8	12057.3	162.4	2.4	
Pole	96M	56	3999.0	38.6	12707.8	163.3	2.5	
Deer	99M	92	9740.3	60.3	30829.1	280.7	4.7	
Pole	102C	48	4161.0	58.3	10026.1	163.7	2.1	
Rectangle	108C	80	4888.9	37.9	18074.7	197.9	3.4	
Rectangle	108M	96	6251.5	28.7	28152.4	205.8	5.0	
Rectangle	124M	94	6286.8	33.8	29511.1	233.6	5.7	
Rectangle	148C	62	7684.1	74.2	19792.1	227.0	4.3	
Tree	156C	68	37024.8	154.9	83272.4	505.6	13.4	
Rectangle	168M	90	8978. 0	48.0	41066.9	291.4	8.4	
Deer	171C	78	24980.9	151.2	62196.5	520 .5	10.6	
Deer	180M	88	21017.0	116.8	73928.3	602.3	12.0	
Tree	216M	74	52856.6	271.0	129904.2	897.4	21.1	
Deer	261C	62	50067.9	285.2	113533.1	796.8	20.7	
Deer	261M	84	37051.1	206.2	122304.8	925.7	22.7	
Tree	276C	72	89913.4	370.7	202536.3	1082.0	33.8	
Deer	342M	66	65857.8	274.4	184221.0	966.9	35.3	
Deer	351C	64	85626.9	371.5	179823.7	941.0	35.2	
Tree	396C	70	148512.5	504.8	332537.4	1392.8	62.9	
Tree	432M	76	175521.8	693.4	387632.3	1864.1	82.9	
Tree	516C	56	245209.8	5 39 .8	571884.2	1590.3	113.7	
Tree	552M	66	263373.7	613.2	643095.3	1937.2	130.7	
Tree	780M	42	429647.0	701.4	1032966.4	2191.5	245.9	

Table 10 - Comparison of number of evaluations required to find solutions in contrast to time required to reach the stopping criterion. This is further broken down into the incremental evaluations (Inc-Evals) used by the local search component of the hybrid algorithm and full evaluations (Full-Evals) of strings generated by recombination and mutlation.

OTHER APPLICATIONS

• Navy Air-Plane Simulator Scheduling Developed by BBN using CSU algorithms

• Poor Prototype Warehouse Scheduler

A fast evaluation function is used that approximates warehouse operations which is orders of magnitude faster than a corresponding detailed warehouse simulator.

Local methods yield poor results when the evaluation function is noisy or approximate, while genetic algorithms yield very good solutions.

Artificial Genetically Grown Neural Networks

Neural networks are grown using cell development processes for control applications. The grammar controlling the growth process is optimized rather than the neural network itself. The resulting networks have outperformed temporal difference methods on several applications.

Seismic Data Interpretation