

An Enhanced Cryptanalytic Attack on Knapsack Cipher using Genetic Algorithm

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Abstract—With the exponential growth of networked system and application such as eCommerce, the demand for effective internet security is increasing. Cryptology is the science and study of systems for secret communication. It consists of two complementary fields of study: cryptography and cryptanalysis. The application of genetic algorithms in the cryptanalysis of knapsack ciphers is suggested by Spillman [7]. In order to improve the efficiency of genetic algorithm attack on knapsack cipher, the previously published attack was enhanced and re-implemented with variation of initial assumptions and results are compared with Spillman results. The experimental result of research indicates that the efficiency of genetic algorithm attack on knapsack cipher can be improved with variation of initial assumption.

Keywords—Genetic Algorithm, Knapsack cipher, Key search.

I. INTRODUCTION

THE demand for effective internet security is increasing exponentially day by day. Businesses have an obligation to protect sensitive data from loss or theft. Such sensitive data can be potentially damaging if it is altered, destroyed, or if it falls into the wrong hands. So they need to develop a scheme that guarantees to protect the information from the attacker.

Cryptology is at the heart of providing such guarantee. Cryptology is the science of building and analyzing different encryption and decryption methods. Cryptology consists of two subfields; Cryptography & Cryptanalysis. Cryptography is the science of building new powerful and efficient encryption and decryption methods. It deals with the techniques for conveying information securely. The basic aim of cryptography is to allow the intended recipients of a message to receive the message properly while preventing eavesdroppers from understanding the message. Cryptanalysis is the science and study of method of breaking cryptographic techniques i.e. ciphers. In other words it can be described as the process of searching for flaws or oversights in the design of ciphers.

The application of genetic algorithms in the cryptanalysis of knapsack ciphers is suggested by Spillman [7].

II. KNAPSACK CIPHER

One of first knapsack cipher was proposed by Markle and

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Hellman in 1975 which utilized a NP-complete problem for its security.

The knapsack problem is formulated as follows. Let us assume the values M_1, M_2, \dots, M_n and the sum S are given. Let it be necessary to compute values b_1, b_2, \dots, b_n values, so that $S = M_1b_1 + M_2b_2 + \dots + M_nb_n$. The values of coefficient b_i can be equal 0 or 1. The 1 value shows that object will fit into the knapsack, 0 values will not in the knapsack.

The Markle-Hellman knapsack cipher encrypts a message as a knapsack problem. The plaintext block transforms into binary string (the length of block is equal number of elements in knapsack sequence). One value determines that an element will be in target sum. This sum is a ciphered message. Table I shows an example of solving the knapsack problem for the entry numbers sequence: 1 3 6 13 27 and 52.

TABLE I
EXAMPLE OF KNAPSACK ENCRYPTION

Plaintext	Knapsack sequence	Ciphertext
1 1 1 0 0 1	1 3 6 13 27 52	$1+3+6+52= 62$
0 1 0 1 1 0	1 3 6 13 27 52	$3+13+27 = 43$
0 0 0 0 0 1	1 3 6 13 27 52	$52 = 52$

The public/private key aspect of this approach lies in the fact that there are actually two different knapsack problems – referred to as the easy Knapsack and hard knapsack. The Markle-Hellman algorithm is based on this property. The private key is a sequence of number for a superincreasing knapsack problem. The public key is a sequence of number for a normal knapsack problem with the same solution.

Easy knapsacks have a sequence of numbers that are superincreasing - that is, each number is greater than the sum

of previous numbers : $a_i > \sum_{j=1}^{i-1} a_j$ for $i=2, \dots, n$ (where a_i

is i -th element of the sequence) . For example $\{1,3,6,13,27,52\}$ is a superincreasing sequence but $\{1,3,4,9,15,25\}$ is not. The knapsack solution with the superincreasing sequence proceeds as follows. The target sum is compared with a greatest number in the sequence. If the target sum is smaller, than this number, the knapsack will not fill, otherwise it will. Then the smaller element is subtracted from the target sum, and the result of the subtraction, is compared with next element. Such operation is done until the smallest number of sequence is reached. If the target sum is reduced to 0 value, than solution exists. In other case solution doesn't exist. For example, consider a total knapsack target sum is 70 and the sequence of weights of $\{2, 3, 6, 13, 27, \text{ and } 52\}$. The largest weight, 52, is less than 70, so 52 are in the

knapsack, Subtracting 52 from 70 leaves 18. The next number 27 is greater than 18, so 27 is not in the knapsack. The next weight 13 is less than 18, so 13 is in the knapsack. Subtracting 13 from 18 leaves 5. The next weight, 6, is greater than 5, so 6 are not in the knapsack. Continuing this process will show that both 2 and 3 are in the knapsack and the total weight is brought to 0, which indicates that a solution has been found. The plaintext that resulted from a ciphertext value of 70 would be 110101. The superincreasing knapsack is easy to decode, which means that it does not protect the data. Anyone can recover the bit pattern from the target sum for a superincreasing knapsack if the elements of the superincreasing knapsack are known.

Markle and Hellman suggested that such a simple knapsack be converted into a trapdoor knapsack which is difficult to break. The algorithm work as follows :

1. Select a simple knapsack sequence. Elements make a superincreasing $A' = (a'_1 + a'_2 \dots a'_n)$
2. Select an integer value m greater than sum of all elements of superincreasing sequence.
3. Select another inter w that the $\gcd(m, w) = 1$, that is number m and w are reciprocally prime.
4. Find the inverse of the $w \bmod m - w^{-1}$
5. Construct the hard knapsack sequence $A = wA' \bmod m$ i.e. $a_i = w a'_i \bmod m$

The trapdoor sequence A could be published as a public key (encryption key). The private (secret) key for this cipher consists of a simple knapsack sequence A' , so-called trapdoor, values m, w, w^{-1}

The encoding is done as follows. The message divides into n bits block (each block contains as many element as simple knapsack sequence). Values in the message block shows that the element will be in the target sum. The target sum of each block is ciphertext.

The decoding consists of the following. Each number of the ciphered message is multiplied through $w^{-1} \bmod m$ and the result of this operation is plaintext.

III. FITNESS FUNCTION

Spillman [7] proposed the fitness measure given in Equation 1.

$$\text{Fitness} = \begin{cases} 1 - \left(\frac{|T_{\text{arg et}} - \text{Sum}|}{\text{Target}} \right)^{\frac{1}{2}} & \text{if Sum} \leq \text{Target} \\ 1 - \left(\frac{|T_{\text{arg et}} - \text{Sum}|}{\text{MaxDiff}} \right)^{\frac{1}{6}} & \text{if Sum} > \text{Target} \end{cases} \quad (1)$$

Let $M = \{m_1, m_2, \dots, m_n\}$, $m_i \in \{0, 1\}$ be an arbitrary solution and the public key

$A = \{a_1, a_2, \dots, a_n\}$

$$\text{Sum} = \sum_{j=1}^n a_j m_j \quad \text{Target} = \sum_j a'_j, \quad \text{FullSum} = \sum_{j=1}^n a_j, \\ \text{MaxDiff} = \max \{ \text{Target}, \text{FullSum} - \text{Target} \}$$

IV. METHODOLOGY: AN ENHANCED CRYPTANALYTIC ATTACK ON KNAPSACK CIPHER USING GENETIC ALGORITHM

The cryptanalysis starts from cipher text, which has an integer form. Each number represents a target sum of hard knapsack problem. The goal of the genetic algorithm is to translate each number into the correct knapsack, which represents the ASCII code for the plaintext characters.

Encoding

The certain restrictions are defined on the encoding algorithm:

- (1) Only the ASCII code will be encrypted.
- (2) The superincreasing sequence will have 8 elements; these number of elements guarantee that each character has a unique encoding (There are 256 ASCII codes and 8 elements length will allow to encrypt 2^8 characters), but this length is not safe (security key has to have 100 length);
- (3) Plaintext has not more then 100 character length.

Initialization

A random population of chromosomes (binary string 0's and 1's) is generated. The size of the population has range in between 10 to 100. The number of bits in each chromosome is equal to the number of elements key (i.e. 8).

Evaluation

Based on the fitness function given in equation 1 the fitness value evaluates how the given sum is close to the target value for the knapsack. The value of the fitness function should be in the range of 0 to 1. Fitness value 1 indicates an exact match with the target sum for the knapsack. If the value of sum is greater then targets then it have a lower fitness value of chromosome, in this way it produces the infeasible solution. If the value of sum is less then target then it will produce a high fitness value and produce feasible solutions. Feasible solutions have a greater chance of being followed by the algorithm.

Selection

The important part of algorithm is selection of a new population. The convergence of the algorithm can be delayed or speed up it depends on how the criterion of selection defined. Two selection methods are applied here: elitist method and classical method. Hence, the 25% the best chromosome with parents population move to next population, the rest 75% choose after classical methods. The best chromosome of each population will preserve and not used in crossover operation or mutation process. Therefore, the results will not make it worse in the next population.

Crossover

The one-point crossover operation applied in the algorithm.

Mutation

The mutation process moves between two random points. The mutation probability has to be small. The mutation helps to prevent the algorithm from being stuck in a local optimal point.

Stop (Terminating) condition

After executing the above mentioned steps a new generation is created and the steps are repeated until the stop condition is reached. Two variants of stop conditions are applied. In the variant-I, the algorithm will stop when the fitness function reaches to the value 1. In the variant - II the algorithm will stop either the fitness function reaches to the value 1 or generates 200 populations.

Fig. 1 describes the complete steps of genetic algorithm that utilizes in the attack of knapsack cipher.

1. A random population of chromosomes (binary string 0's and 1's) is generated. The size of the population has range between 10 and 100. The number of bits in each chromosome is equal to the number of elements key (that is 8).
2. A fitness value for each chromosome in the population is determined with the help of equation 1.
3. The new population is created.
4. The crossover operation is made.
5. The mutation process is executed.
6. Repeat step 2 for the new population of chromosomes.

Fig. 1 Genetic algorithm attack on knapsack cipher

V. RESULTS AND DISCUSSIONS

An experimental result for the genetic algorithms was generated with 5 runs per data point using 'C' language. Genetic algorithm attack is run with variant-I & variant-II for each target sum mentioned in Table II. Each attack is run 5 times with constant entry parameters i.e. size of population is 75, crossover probability is 0.80, and mutation probability is 0.11 and then results are averaged.

The 8-elements (Spillman used 15 elements) sequence of hard knapsack problem (21031 63093 16371 11711 23422 58555 16615 54322) is used to encode 8 bits ASCII code. This sequence has been created from superincreasing sequence (1 3 7 13 26 65 119 267), u equal to 65423 and w integer equal 21031 ($w^{-1} = 5363$). The MACRO word has been encrypted. The Table II shows the result of encoding.

TABLE II
ENCRYPTION BY KNAPSACK

Character	ASCII Code	Target sum (ciphertext)
M	10110010	65728
A	10000010	37646
C	11000010	100739
R	01001010	103130
O	11110010	128821

The Tables III and Table IV show the experimental results with variant -I (P is population with search result, % is percentage of search space) and variant-II (P is population with search result; % is the percentage of search space, E is

the Error i.e. difference between target sum and find sum) as a stop a condition.

Table III shows that, the solution with variant -I always gives correct solution because the population is generated till the result is not erroneous. On an average 115 populations are enough for reaching to the correct results. Table IV with variant-II shows that 43 populations are enough but the solutions can be incorrect because of burdened error.

TABLE III
EXPERIMENTAL RESULTS WITH VARIANT - I

	Exp. 1		Exp. 2		Exp. 3		Exp. 4		Exp. 5		Avg	
Char	P	%	P	%	P	%	P	%	P	%	P	%
M	13	47.7	2	29.1	68	49.8	1	24.4	1	25.8	17	35.3
A	226	70.5	67	53.7	1	26.3	1	24.4	265	70.5	112	49.1
C	173	66.2	48	55.6	1	27.8	279	73.4	853	95.1	271	63.6
R	290	70.1	4	36.5	108	68.4	44	51.2	1	27.3	89.4	50.7
O	2	25.6	1	26.6	210	62.3	1	25	222	63.5	87.2	40.6
Sum											115	47.9

TABLE IV
EXPERIMENTAL RESULTS WITH VARIANT -II

	Exp.1			Exp.2			Exp.3			Exp.4			Exp.5			Avg.		
Char	P	%	E	P	%	E	P	%	E	P	%	E	P	%	E	P	%	%E
M	3	1.5	0	124	62	0	5	2.5	0	67	33.5	0	143	71.5	2635	68.4	34.2	20
A	65	32.5	0	1	0.5	2513	88	44	244	7	3.5	2513	7	3.5	244	33.6	16.8	80
C	1	0.5	0	67	33.5	0	162	81	0	2	1	0	115	57.5	0	69.4	34.7	0
R	1	0.5	244	132	66	0	1	0.5	0	1	0.5	2391	82	41	0	43.4	21.7	40
O	1	0.5	0	1	0.5	0	1	0.5	0	5	2.5	0	2	1	30229	2	1	20
Sum																43.32	21.7	32

The results shown in Table III are compared and analyzed with Spillman's results (Table V). Spillman's algorithm always gives correct results similar to results as obtained by us (Table III).

TABLE V
SPILLMAN'S RESULTS

Character	#chromosome	% of search space
M	810	2.0
A	80	0.2
C	1860	6.0
R	460	1.0
O	650	.1
Average	650	1.9

In our experiment average 115 populations gives the correct result and the average percentage of search space is near 50%. The Spillman's algorithm (Table V) searches on average less than 2% of the space. The divergence of the result is explained that the area of possible results in Spillman's work is 2^{15} i.e. 32678 and in our work it is 2^8 . The convergence of results is shown in Fig. 2.

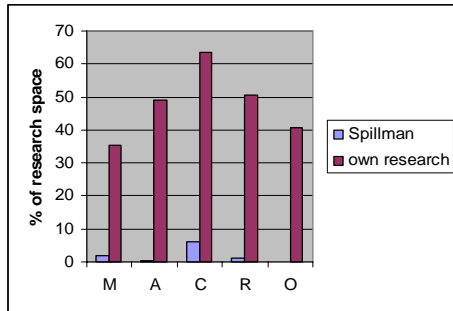


Fig. 2 The comparison of own result with Spillman's result

These results indicate that Spillman's results were distinctly suboptimal and the variation of initial assumptions could readily improve the result.

VI. CONCLUSION

This paper presents the genetic algorithm attack on the knapsack cipher. This paper also indicates that the efficiency of genetic algorithm attack on knapsack cipher can be improved by variation of initial assumptions like mutation, crossover operation and size of population. The great size of population, high crossover probability and a small mutation probability are the most optimal arrangements for GA. The results are worse when the size of population and crossover operator decreases, and when the coefficient mutation increases. Wrong coefficients destroy the chromosomes that are well-selected. In our experiment average 115 populations gives the correct result and the average percentage of search space is near 50%. The Spillman's algorithm searches on average less than 2% of the search space. Experimental results indicate that Spillman's results[7] were distinctly suboptimal and the variation of initial assumptions could readily improve the result. The genetic algorithm offers a powerful tool for the cryptanalysis of knapsack cipher.

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