Optimisation Heuristics for Cryptology

by

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Automated cryptanalysis, cryptography, cryptology, simulated annealing, genetic algorithm, tabu search, polyalphabetic substitution cipher, transposition cipher, stream cipher, nonlinear combiner, Merkle-Hellman knapsack, Boolean function, nonlinearity.

Abstract

The aim of the research presented in this thesis is to investigate the use of various optimisation heuristics in the fields of automated cryptanalysis and automated cryptographic function generation. These techniques were found to provide a successful method of automated cryptanalysis of a variety of the classical ciphers. Also, they were found to enhance existing fast correlation attacks on certain stream ciphers. A previously proposed attack of the knapsack cipher is shown to be flawed due to the absence of a suitable solution evaluation mechanism. Finally, a new approach for finding highly nonlinear Boolean functions is introduced.

Three search heuristics are used predominantly throughout the thesis: simulated annealing, the genetic algorithm and the tabu search. The theoretical aspects of each of these techniques is investigated in detail. The theory of NP-completeness is also reviewed to highlight the need for approximate search heuristics.

Many automated attacks have been proposed in the literature for cryptanalysing classical substitution and transposition type ciphers. New attacks on these ciphers are proposed which utilise simulated annealing and the tabu search. Existing attacks which make use of the genetic algorithm and simulated annealing are compared with the new simulated annealing and tabu search techniques. Extensive experimental comparisons show that the tabu search is more effective than the other techniques when used in the cryptanalysis of these ciphers.

The use of parallel search heuristics in the field of cryptanalysis is a largely untapped area. Parallel heuristics can provide a linear speed-up based upon the number of computing processors available or required. A parallel genetic algorithm is proposed for attacking the polyalphabetic substitution cipher by solving each of the key positions simultaneously. This new approach is shown (using experimental evidence) to be highly efficient as well as effective in solving polyalphabetic ciphers even with a large period.

A number of modifications to the fast correlation attack are proposed and implemented in attacks against an LFSR-based stream cipher known as the nonlinear combiner. It is shown that considerable improvement can be achieved over the original attack of Meier and Staffelbach by updating only a subset of the error probability vector elements in each iteration. Subset selection is performed based on deterministic and random heuristics. Simulated annealing is also incorporated as a technique for selecting candidate update positions. A new technique called "fast resetting" is proposed which defines conditions under which the error probability vector should be reset. By carefully choosing the resetting criteria a highly effective attack can be obtained. The fast resetting technique is shown to be more effective than MacKay's recently proposed *free energy minimisation* technique.

An attack on the Merkle-Hellman cryptosystem proposed by Spillman (using the genetic algorithm) is shown to be flawed due to the weakness of the key evaluation technique. Experimental results are presented which show that the knapsack-type ciphers are essentially secure from attacks which attempt to naively decrypt an encoded message using the public key. The problem with Spillman's approach is that the proposed "fitness function" does not accurately assess each solution so that a candidate solution may have a very high fitness and yet differ from the correct solution in more than half of its bit positions. The results presented here do not impact on the widely known (and successful) attacks of the knapsack cipher which are based upon the structure of the secret key.

A new technique for finding highly nonlinear Boolean functions is presented. Nonlinearity is a desirable property for cryptographically sound Boolean functions. The technique, which is shown to be far more effective than traditional random search techniques, makes use of the Walsh-Hadamard transform to determine bits of the binary truth table of the Boolean function which can be complemented in order to generate a guaranteed increase in the nonlinearity of the function. An extension of this technique allows two bits of the truth table to be complemented so that the balance is maintained. In addition, it is shown that incorporating this technique in a genetic algorithm provides an even better method of generating highly nonlinear Boolean functions. Experimental results support the effectiveness of this technique.

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Declaration

The work contained in this thesis has not been previously submitted for a degree or diploma at any higher education institution. To the best of my knowledge and belief, the thesis contains no material previously published or written by another person except where due reference is made.

Signed: . . . . **Date:** . . . .

Previously Published Material

The following papers have been published or presented, and contain material based on the content of this thesis.

Journal Articles

[1] Andrew Clark, Ed Dawson, and Helen Bergen. Combinatorial optimisation and the knapsack cipher. *Cryptologia*, 20(1):85–93, January 1996.

[2] Andrew Clark and Ed Dawson. A parallel genetic algorithm for cryptanalysis of the polyalphabetic substitution cipher. *Cryptologia*, 21(2):129–138, April 1997.

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Some of the research presented in this thesis was performed jointly with other postgraduate students. The preliminary investigation into the use of a parallel genetic algorithm for the polyalphabetic substitution cipher (see Chapter 3) was performed by Harrie Nieuwland under my supervision. Also, the cryptanalysis of the nonlinear combiner (Chapter 4) was joint work with Mahmoud Salmasizadeh and the design of cryptographic algorithms for finding highly nonlinear Boolean functions (Chapter 6) was joint work with William (Bill) Millan.

Over the time I have spent on this thesis I have enjoyed immensely working with my fellow PhD students and I have formed many valuable friendships. I wish to thank them all for helping to provide the environment which made this work possible. They are: Gary Carter, James Clark, Ernest Foo, Dr Helen Gustafson, Dr Mark Looi, Bill Millan, Lauren Nielsen, Dr Mahmoud Salmasizadeh, Leonie Simpson and Jeremy Zellers.

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Chapter 1

Introduction

The use of automated techniques in the design and cryptanalysis of cryptosystems is desirable as it removes the need for time-consuming (human) interaction with a search process. Making use of computing technology also allows the inclusion of complex analysis techniques which can quickly be applied to a large number of potential solutions in order to weed out unworthy candidates. In this thesis a number of combinatorial optimisation heuristics are studied and utilised in the fields of automated cryptanalysis and automated cryptosystem design.

Cryptanalysis can be described as the process of searching for flaws or oversights in the design of cryptosystems (or ciphers). A typical cipher takes a clear text message (known as the plaintext) and some secret keying data (known as the key) as its input and produces a scrambled (or encrypted) version of the original message (known as the ciphertext). An attack on a cipher can make use of the ciphertext alone or it can make use of some plaintext and its corresponding ciphertext (referred to as a known plaintext attack).

The most fundamental criterion for the design of a cipher is that the key space (i.e., the total number of possible keys) be large enough to prevent it being searched exhaustively. By 1997 standards, a key should typically contain more than 80 independent bits - certainly the 56 bits utilised by the Data Encryption Standard (DES) is no longer considered secure [76]. Most designers of cryptosystems are aware of this requirement and thus cryptanalysis tends to require more detailed scrutiny of the cipher.

Due to their complexity, the task of determining weaknesses in ciphers is generally a laborious manual task and the process of exploiting the discovered weaknesses is rarely quick or simple even when computers are used to implement the exploit (unless the cipher contains a major flaw). This further highlights the importance of the use of automated techniques in cryptanalysis.

Automated techniques can also be useful in the area of cipher design. Most ciphers consist of a combination of a number of relatively simple operations: for example, substitutions and permutations. A large amount of research has been performed to determine good cryptographic properties of these operations and many cryptanalytic attacks are realised by exploiting instances where the designer has neglected to ensure that each of the cryptographic properties is satisfied. Automated search techniques can be employed to quickly search through a large number of possible cryptographic operations in order to find ones which satisfy the desired properties.

In Chapter 2 an overview of NP-completeness is given. Many optimisation problems are known to be NP-complete. The theory of NP-completeness allows the classification of such problems and can be used to show that all NP-complete problems are equally difficult to solve. The difficulty in solving NP-complete problems is so great that some ciphers use them as a basis for their security (for example, the “knapsack” cipher [51, 11]). While the theory of NP-completeness only applies to a certain type of problem (i.e., a *decision* problem which has a “Yes”/“No” answer), it can be shown that many related problems are at least as hard as the NP-complete problems to solve - these problems are often referred to as being “NP-hard”.

Although some techniques do exist for solving certain NP-complete problems (for example, branch and bound), these techniques are rarely useful for large instances of the problem. To counter this deficiency optimisation heuristics are utilised. Optimisation heuristics are usually designed to suit the particular problem being solved and make use of the structure of the problem in order to suggest “good” solutions. It is the nature of NP-complete problems that their optimal solution is rarely known. Thus, the notion of a “good” solution is used to indicate that the solution is “better than all the other solutions found.” Whether or not the “good” solution is useful depends on the purpose for which the solution is sought and the expectations and requirements for the solution in the particular application. For example, consider the case of cryptanalysis: if an optimisation heuristic is used to search for the key of a particular cipher, then an expectation might be that the key will provide sufficient information to render the decrypted message legible - if the key does not provide this much information then its "goodness" could be questioned.

An important requirement of an optimisation heuristic is a method of assessing every feasible solution to the problem being solved (i.e., a method for determining how "good" a solution is). In many cases finding such a method is the most difficult part of solving a particular problem, and is sometimes impossible due to the nature of the problem (Chapter 5 studies a particular instance of this problem). It is extremely important that the chosen method of assessing a solution provides a meaningful and accurate comparison of two arbitrary solutions, otherwise the search heuristic will not work.

Three general-purpose optimisation heuristics are described in detail in Chapter 2 - they are simulated annealing, the genetic algorithm and the tabu search. Numerous examples of applications of these techniques to mathematical and engineering-related problems have been discussed in the literature (some examples are [16, 64, 67]). Each of the three algorithms possesses different properties. For example, simulated annealing maintains and updates a single solution where as the genetic algorithm manipulates a "pool" of solutions and the tabu search is somewhere in-between with a single solution being maintained as well as a list of "tabu" solutions to encourage diversity in the search. Due to their different properties some techniques may be better suited to solving a particular problem than the others.

The classical ciphers, while simple, are often the object of new cryptanalytic techniques. An introduction to the types of classical ciphers is given in Appendix A - most fall into one of two categories: substitution-type ciphers and transposition-type ciphers. Many techniques have been devised for the cryptanalysis of classical ciphers and most concentrate on the substitution-type ciphers. Each of these techniques share the property that they are automated: that is, they are capable of recovering the original plaintext message without any human intervention. The algorithms are sufficiently intelligent, or possess sufficient information, to allow them to decrypt a hidden message without manual assistance. Typically this is achieved using the known statistics and redundancy of the language.

Examples of the previous research into the field of automated cryptanalysis are now given. In 1979 Peleg and Rosenfeld [60] suggested a *relaxation algorithm* for breaking a simple substitution cipher. Hunter and McKenzie [32] in 1983, and King and Bahler [37] in 1992 conducted further experiments with the relaxation algorithm in attacks on the simple substitution cipher. A different approach was used by Ramesh, Athithan and Thiruvengadam [63] in 1993 which involved searching a dictionary for words with the same "pattern" as the ciphertext words (assuming word boundaries are left intact during encryption - i.e., the SPACE symbol is not encrypted). This approach still required manual decryption of some of the ciphertext. Also in 1993, Spillman et al [73], presented a genetic algorithm and Forsyth and Safavi-Naini [18] utilised simulated annealing to make attacks on the simple substitution cipher (these attacks are described in detail in Section 3.1). In 1995, Jakobsen [33] presented a somewhat simplified version of the attacks presented in [73] and [18].

In 1994, King [36] presented an attack on the polyalphabetic substitution cipher which utilised the relaxation algorithm. King's approach was similar to the one used by Carroll and Robbins [9] in 1987 although more successful (due to the availability of greater computing power). An extension of the work presented in [73] to an attack on the polyalphabetic substitution cipher using a parallel genetic algorithm forms part of this thesis. In 1988 Matthews [46] presented a technique for finding the key length of periodic ciphers which is more accurate that the well-known Index of Coincidence (IC) described in Section A.2.

Matthews [47] also utilised the genetic algorithm in cryptanalysis of the transposition cipher (1993). This technique is discussed in more detail in Section 3.3.

It is only recently that the application of combinatorial optimisation algorithms (such as simulated annealing and the genetic algorithm) to the field of cryptanalysis has been considered (see [18, 47, 71]). The research in this area has shown that such techniques are highly effective in the field of cryptanalysis. In Chapter 3 of this thesis these techniques are investigated in detail. A new attack on the transposition cipher using simulated annealing is proposed and, also, the tabu search is used, possibly for the first time in the field of cryptanalysis, to break the substitution cipher and the transposition cipher. A large amount of experimental data is presented in order that the performance of the three techniques against simple substitution and transposition ciphers could be compared. Comparisons based on both time complexity and algorithm complexity are used to show that the tabu search is more effective than both of the other techniques for cryptanalysis of the substitution cipher while equally as good as the genetic algorithm and significantly better than simulated annealing in cryptanalysis of the transposition cipher.

The genetic algorithm in particular is well suited to parallel implementations. This is evident from the large number of research articles available which outline parallel heuristics for the genetic algorithm in a variety of applications (for examples see [8, 20, 28]). Chapter 3 also outlines a new attack on the polyalphabetic substitution cipher which makes use of a parallel genetic algorithm. This algorithm is implemented using a public domain software package (called PVM or Parallel Virtual Machine [62]) and experiments conducted to evaluate the technique. This parallel heuristic is able to solve the different keys of the polyalphabetic substitution cipher simultaneously and, therefore, proves to be extremely powerful with little overhead and excellent key recovery capabilities - even for polyalphabetic ciphers with a large block size.

Chapter 4 describes a new technique for incorporating the simulated annealing heuristic in a known attack on a certain class of stream cipher. These ciphers are based on the nonlinear combination of the output of a number of linear feedback shift registers and are described in Appendix B. The previously published *fast correlation attack* [48] is known to be effective in cryptanalysing such ciphers. However, in Chapter 4 new techniques are introduced which increase the effectiveness of the fast correlation attack so that keystreams with an even smaller correlation to the shift register output stream can be attacked.

The original fast correlation attack [48] updates a vector of error probabilities in each iteration (a full description is given in Chapter 4). This approach is modified so that only a subset of the error probability vector is updated in each iteration. A number of approaches for selecting the subset are considered, one of which utilises simulated annealing. Experiments were carried out for each of the suggested modifications and some were found to significantly improve the power of the fast correlation attack.

A slightly different type of modification to the fast correlation attack is also presented in Chapter 4. This second technique involves “resetting” the values of the error probability vector to their original value when certain criteria are satisfied. The new technique, called “fast resetting”, is shown through experiments, to be much more effective than the original fast correlation attack when used to recover an LFSR’s output sequence.

The modified fast correlation attack is compared with another known attack on this type of cipher which utilises a technique known as *free energy minimisation* [40]. It is shown that in almost all cases the newly proposed modifications to the fast correlation attack are superior to the free energy minimisation technique.

As alluded to above, when utilising combinatorial optimisation techniques there must exist a suitable method for assessing every feasible solution to the given problem. In Chapter 5 a previously published attack on the knapsack cipher [71] is shown to be flawed because of the non-existence of such a solution assessment method. Appendix C provides a description of the Merkle-Hellman public key cryptosystem which is attacked by Spillman [71]. Spillman's attack challenges the notion of NP-completeness by proposing a genetic algorithm for solving even large instances of the *subset sum* problem. The fact that a problem is NP-complete does not preclude it from solution-finding techniques using such an optimisation heuristic, however, in this case the attack *must find the optimum solution to the problem* in order to break the cipher. That is, the notion of a "good" solution is meaningless in this instance since it is not possible to tell if one solution is better than any other (except if it is the optimum). The non-existence of a suitable assessment method, in this case, means that the solution surface can be considered flat except for a single peak (where the optimum lies). Thus, performing an attack using one of the optimisation heuristics described in Chapter 2 will be futile. The discussion in Chapter 5 provides experimental evidence to support the claim that a suitable assessment method does not exist for solving the knapsack cipher using the public key.

As previously mentioned, an automated search for finding cryptographically sound operations is desirable. A new technique for this specific purpose is described in Chapter 6. Boolean functions have many uses in cryptography. They are used in stream ciphers (such as the ones discussed in Chapter 4) and can be used to described substitution operations (commonly termed S-boxes) in any cipher. Boolean functions and some of their cryptographic properties are discussed in Appendix D. The technique in Chapter 6 is used to improve the nonlinearity of an arbitrary Boolean function. By studying the values of the coefficients of the Walsh-Hadamard transform it is possible to determine sets of truth table positions such that complementing any one of those positions in the truth table will lead to an increase in the nonlinearity of the function.

The same approach is used to describe a similar technique which can be used to complement the truth table in two positions to increase the nonlinearity of the function and at the same time maintain its balance.

This technique is then incorporated in a genetic algorithm and, after defining the suitable parameters required of the genetic algorithm, it is shown that such an algorithm is able to find highly nonlinear Boolean functions far more efficiently and reliably than the existing random search techniques. A large number of experiments were conducted in order to highlight the effectiveness of this new approach.

Finally, the conclusion to this thesis (Chapter 7) provides a summary of the outcomes of this work with particular reference to the most positive of the results. Also, further research possibilities and other applications of the optimisation heuristics outlined in this thesis are discussed.

Chapter 2

Combinatorial Optimisation

The aim of combinatorial optimisation is to provide efficient techniques for solving mathematical and engineering related problems. These problems are predominantly from the set of NP-complete problems (see below). Solving such problems requires effort (eg., time and/or memory requirement) which increases dramatically with the size of the problem. Thus, for sufficiently large problems, finding the best (or *optimal*) solution with certainty is often infeasible. In practice, however, it usually suffices to find a “good” solution (the optimality of which is less certain) to the problem being solved. A subtle point to note is this: an algorithm designed to find “good” solutions to a problem may find the optimal solution - however it is infeasible to prove that the solution is in fact the optimal one.

Provided a problem has a finite number of solutions, it is possible, in theory, to find the optimal solution by trying every possible solution. An algorithm which tries every solution to a problem in order to find the best is known as a *brute force* algorithm. Cryptographic algorithms are almost always designed to make a brute force attack of their solution space (or key space) infeasible. For example, the key space is large enough so that it is not plausible for an attacker to try every possible key. Combinatorial optimisation techniques attempt to solve problems using techniques other than brute force since many problems contain variables which may be unbounded, leading to an infinite number of possible solutions. In the case where the number of solutions is finite it is generally infeasible to use a brute force approach to solve it so other techniques must be found.

Algorithms for solving problems from the field of combinatorial optimisation fall into two broad groups - *exact* algorithms and *approximate* algorithms. An exact algorithm guarantees that the optimal solution to the problem will be found. The most basic exact algorithm is a brute force one. Other examples are branch and bound, and the simplex method. Most of the algorithms used in this thesis are from the group of approximate algorithms. Approximate algorithms attempt to find a "good" solution to the problem. A "good" solution can be defined as one which satisfies a predefined list of expectations. For example, consider a cryptanalytic attack. If enough plaintext is recovered to make the message readable, then the attack could be construed as being successful and the solution assumed to be "good", as opposed to one which gives no information about the nature of the message being cryptanalysed.

Often it is impractical to use exact algorithms because of their prohibitive complexity (time or memory requirements). In such cases approximate algorithms are employed in an attempt to find an adequate solution to the problem. Examples of approximate algorithms (or, more generally, heuristics) are simulated annealing, the genetic algorithm and the tabu search. Each of these techniques are described in some detail in the latter sections of this chapter.

A discussion of the theory of NP-completeness follows. This is an important concept to illustrate in order to highlight the purpose of approximate algorithms in the field of combinatorial optimisation. Following the discussion on NP-completeness, an introduction to the approximate optimisation heuristics used in this research is given. The three techniques are: simulated annealing, the genetic algorithm and the tabu search. These techniques have been used broadly although only recently have they been applied to the field of cryptanalysis.

2.1 NP-Completeness

The theory of NP-completeness was devised in order to classify problems that are known to be difficult to solve. The following paragraph gives some definitions which are fundamental to the analysis of NP-completeness.

The notion of the *nondeterministic computer* plays an important role in defining NP-completeness. A nondeterministic computer is one which "has the ability to pursue an unbounded number of independent computational sequences in parallel" ([21], p.12). Such a computer (if it existed) would revolutionise the field of combinatorial optimisation as it is known today. A *decision problem* is one which has two possible solutions - either “yes” or “no”. The class of problems NP (nondeterministic polynomial) consists of all decision problems which can be solved in polynomial time by a nondeterministic computer. A problem can be solved in polynomial time if its time complexity can be represented as a polynomial in the size of the problem. The class of decision problems which can be solved in polynomial time (without requiring a nondeterministic computer) is called P (polynomial). Although not certain, it is often assumed that P $\neq$ NP.

It was shown by Cook [12] that every other problem in NP can be reduced to the “satisfiability” problem. Thus, if an algorithm can be found which solves the satisfiability problem in polynomial time then all other problems in NP can also be solved in polynomial time. Also, if any problem in NP is *intractable* (cannot possibly be solved in polynomial time) then the satisfiability problem must also be intractable. This leads to the notion that the satisfiability problem is the “hardest” in NP to solve. Since Cook’s initial work many different decision problems have been proved equivalent to the satisfiability problem. This equivalence class of the hardest problems to solve in NP is called the *NP-complete* class.

As has been discussed, the class NP only includes a specific type of problem, i.e., the decision problems. In general (and especially in the field of combinatorial optimisation), a minimum or a maximum of some objective function is sought - rather than a “yes” or “no” answer. However, it should be noted that many of the problems usually associated with combinatorial optimisation can be formulated as decision problems. As an example consider the classic combinatorial optimisation problem - the Travelling Salesman Problem (TSP). Expressed simply, the problem is this: “Given a list of N cities and a cost associated with travelling between every pair of cities, find the path through the N cities which visits every city exactly once and returns to the starting city and which has the minimum cost.”

Problems such as the TSP which aim to minimise an objective function can easily be converted to a decision problem by changing the requirement of finding an optimum to asking the question - “Does there exist a solution which has an associated cost which is less than some bound?” A decision problem variant of the TSP could be expressed thus: “Given a list of N cities and a cost associated with travelling between every pair of cities, does there exist a path through the N cities which visits every city exactly once and returns to the starting city and which has a cost less than B?" It can be shown that, provided the objective function is not expensive to evaluate, the decision problem can be no harder to solve than the corresponding optimisation problem. Thus, if it can be shown that an optimisation problem's corresponding decision problem is NP-complete then the optimisation problem is at least as hard.

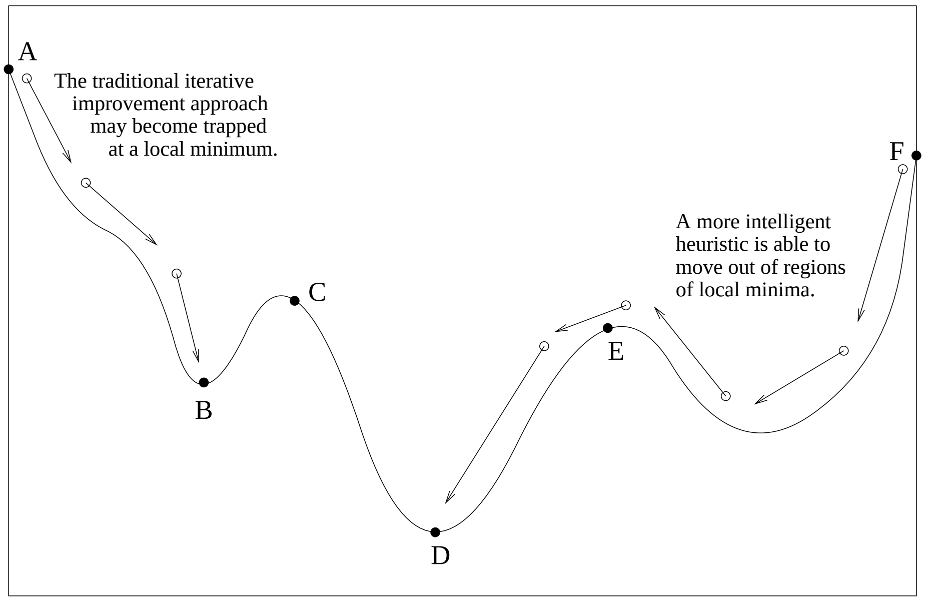
Some of the problems presented in this thesis are *NP-hard* - i.e., their corresponding decision problems are NP-complete. Others, although instinctively appearing to be so, are yet to be proven NP-hard. Proving problems to be NP-complete is difficult and does not form part of this thesis. It is, however, important to understand the basic concepts of NP-completeness in order to know why the techniques which are described in the remainder of this chapter are so important to the field of combinatorial optimisation.

By assuming that P $\neq$ NP, we are led to believe that there exists no polynomial time algorithm for solving problems which are NP-complete. Thus, for large optimisation problems we have to be satisfied that we can never find the optimal solution (or, at least, satisfied that we can never *know* that we have found the optimal solution). This exemplifies the importance of algorithms which find good solutions to problems - i.e., approximate algorithms.

2.2 Approximate Methods

Numerous approximate heuristics exist for determining (not necessarily optimal) solutions to NP-complete problems. Many of these algorithms are designed with a specific problem in mind and hence they can not be applied in all instances. The three methods presented in this chapter have been used widely in the literature and applied to a broad spectrum of optimisation problems. Their use in the field of cryptanalysis has only recently been documented.

The algorithms presented here are variations on the common approximate algorithm heuristic known as "iterative improvement". Traditional iterative improvement techniques will only undergo transitions which lead to a solution with a lower cost. Such an approach will often cause the search to become trapped at a local minimum (an undesirable condition). To illustrate this point consider the problem of finding the minimum value of the two-dimensional curve in Figure 2.1. A traditional iterative improvement technique starting at point A could easily find its way to point B, whereafter it may become trapped. It is usual to run the algorithm a number of times so that, in another instance, an algorithm starting at point C could easily reach the global minima at D. If the algorithm is allowed to make uphill steps then it is possible for the search to leave regions of local minima in order to find the global minimum (as in the search starting an point F in Figure 2.1). Two of the algorithms (simulated annealing and the genetic algorithm) which are presented in the following sections of this chapter possess the ability to lead their search in an uphill direction in order to escape regions of local minima.


A
The traditional iterative improvement approach may become trapped at a local minimum.
F
A more intelligent heuristic is able to move out of regions of local minima.
C
E
B
D
Figure 2.1: How iterative improvement techniques become stuck.

2.2.1 A Note on Objective Functions

The aim of combinatorial optimisation is always to minimise or maximise some objective function. Traditionally in simulated annealing the objective function is referred to as the *cost* function. It is usually desirable to minimise the cost associated with some problem. On the other hand, when using the genetic algorithm the objective function is often termed the *fitness* function. In this case the aim is to maximise the fitness of the solutions to the problem. It should be noted that a minimisation problem can always be converted to a maximisation one simply by negating the objective function. Additionally, it should be noted that it is generally trivial to convert a minimisation algorithm into a maximisation one simply by changing the evaluation technique of the algorithm.

2.2.2 Simulated Annealing

As indicated above, simulated annealing is based on the concept of annealing. In physics, the term annealing describes the process of slowly cooling a heated metal in order to attain a “minimum energy state”. A heated metal is said to be in a state of “high energy”. The molecules in a metal at a sufficiently high temperature move freely with respect to each other, however, when the metal is cooled, the molecules lose their thermal mobility. If the metal is cooled slowly, a “minimum energy state” will be achieved. If, however, the metal is not cooled slowly, the metal will remain in an intermediate energy state and will contain imperfections. For example, “quenching” is the process of cooling a hot metal very rapidly. Metal that has been quenched commonly has the property that it is brittle because of the unordered structure of its molecules. In order to apply the analogy of annealing in physics to the field of combinatorial optimisation it is useful to think of the slowly cooled metal as having reached a crystalline structure in which the molecules are ordered and the energy is low. This is analogous to the optimal solution to a problem which is “ordered” and represents the lowest “cost” to solve the problem being optimised (assuming, of course, that the minimum cost is sought).

In 1953, Metropolis et al [52], showed that the distribution of energy in molecules at the “minimum energy state” is governed by the Boltzmann probability distribution. This discovery was applied to determine the probability of molecules moving between different energy levels, which depends upon the temperature of the metal and the difference in the energy levels. The molecule undergoes a transition from energy level E_1 to energy level E_2 ($\Delta E = E_2 - E_1$); the temperature of the metal is T; and Boltzmann’s constant is k. If $\Delta E < 0$ the transition always occurs, otherwise it occurs with the probability indicated by Equation 2.1.

$$\Pr(E_1 \Rightarrow E_2) = e^{\left(\frac{-\Delta E}{kT}\right)} \tag{2.1}$$

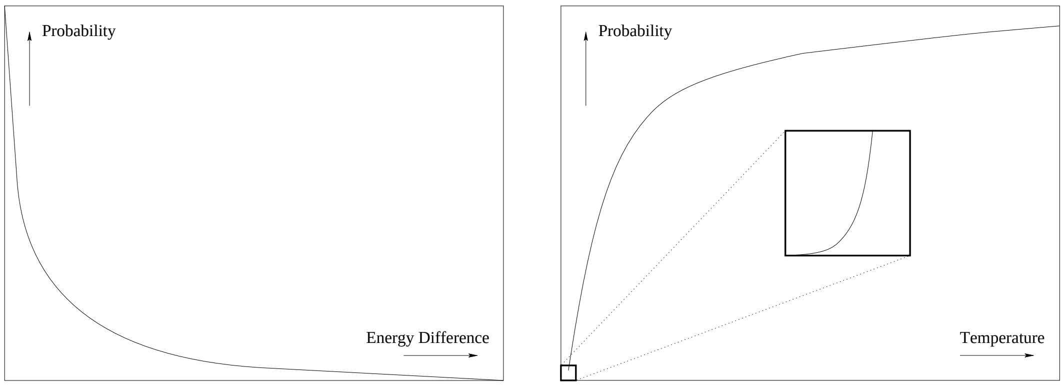


Figure 2.2: Properties of the state transition probability function.

Figure 2.2 highlights some of the properties of Equation 2.1. It can be seen that transitions occur with high probability when the energy difference (ΔE) is small and when the temperature (T) is high. When these two properties are combined the result is that a transition between energy levels with a large difference is more probable at high temperatures and, conversely, only small energy changes are likely when the temperature is low. These properties are extremely important when simulated annealing is used for solving combinatorial optimisation problems.

The idea of mimicking the annealing process to solve combinatorial optimisation problems is attributed to Kirkpatrick et al [38], who, in 1983, used such an idea to find solutions to circuit wiring and component placement problems (from an electronic engineering perspective) and also to the travelling salesman problem (a classic combinatorial optimisation problem). A generic description of the simulated annealing algorithm is given in Figure 2.3. The algorithm is (usually) initialised with a random solution to the problem being solved and a starting temperature. The choice of the initial temperature, T_0, is discussed below. At each temperature a number of attempts are made to perturb the current solution. Each proposed perturbation must be accepted by determining the change in the evaluation of the objective function (i.e., the change in the cost) and then consulting Metropolis' equation (Equation 2.1) which makes a decision based on this cost difference and the current temperature. If the proposed change is accepted then the current solution is updated. The technique used to perturb a solution is dependent on the problem being solved and the representation of the solution. For example, if the solution is represented as a binary string of fixed length, then

1. Generate a solution to the problem (randomly or otherwise) and determine its cost.
2. Initialise the temperature, $T = T_0$.
3. At temperature T, repeat J times . . .
    (a) Perturb the current solution to give a "candidate" solution.
    (b) Find the cost of the candidate and determine the difference between its cost and the cost of the current solution.
    (c) Using the cost difference (ΔE) and the current temperature (T) consult Equation 2.1 (ignore k, i.e., $k = 1$) to determine the probability that the candidate solution should be accepted. Generate a random number on the interval $[0, 1]$. If the random number is less than the probability returned by Equation 2.1 then the candidate is accepted.
    (d) If the candidate is accepted then the current solution and its cost are updated.
4. If the stopping criteria are satisfied then discontinue, otherwise reduce the temperature, T, and repeat from Step 3.

Figure 2.3: Simulated Annealing

a suitable mechanism for suggesting possible new solutions may be to complement one (or more) randomly chosen values in the bit string. Generally, the temperature is reduced when either there a predefined limit in the number of updates to the current solution has been reached or after a fixed number of attempts have been made to update the current solution. Methods for reducing the temperature are discussed below. The algorithm finishes either when no new solutions were accepted for a given temperature, or when the temperature has dropped below some predefined limit.

The variable parameters of the algorithm make up what is known as the *cooling schedule* which defines: the initial temperature, T_0; the number of iterations at each temperature, J; the temperature reduction scheme; and the stopping criteria. Each of these is now investigated in some detail.

- **The Initial Temperature.** Usually T_0 is chosen so that any candidate solution proposed in Step 3a of Figure 2.3 is accepted at Step 3c. Such a choice of T_0 is dependent upon the magnitude of typical cost values for the problem being solved, or, more specifically, the magnitude of the largest expected cost difference between two solutions to the problem being solved. To ensure that the probability that the transition occurs is close to one, T_0 must be significantly greater than the largest expected cost difference (as shown by the following equations).

$$\begin{aligned} Pr(E_1 \Rightarrow E_2) \rightarrow 1 &\Leftrightarrow e^{\left(\frac{-\Delta E}{T}\right)} \rightarrow 1 \\ &\Leftrightarrow \frac{\Delta E}{T} \rightarrow 0 \\ &\Leftrightarrow \Delta E \ll T \end{aligned}$$

The plot of Probability versus Temperature in Figure 2.2 shows the curve being relatively flat for high temperatures. It is important not to choose an initial temperature which is too high since this will cause the algorithm to run for longer than necessary since most of the useful transitions are made in the temperature ranges of the steep part of the curve.

Also, although not stated previously, it is vital that the temperature remain greater than zero since this assumption is made when calculating the probability from Equation 2.1. Hence, T_0 must be greater than zero.

- **Iterations For Each T.** The number of iterations at each temperature is equivalent to the number of candidate solutions considered for each temperature (referred to as J in Figure 2.3). The value should be large but not so large that the performance of the algorithm is hindered. One value suggested in the literature is $100N$, where N is the number of variables in the problem being solved.

  If, in Step 3a, a random alteration is made to the solution in order to generate a new candidate, the number of candidates trialled should be greater than if a more intelligent and problem specific perturbation function is used.

- **Temperature Reduction.** In theory, the rate at which temperature dissipates from a metal is governed by complicated differential equations. For the purposes of simulated annealing, two simple models are most commonly used. The first, and most simplistic, is a linear cooling model. In the linear model both an initial temperature (T_0) and a final temperature (T_∞) must be defined. The difference between these two ($T_0 - T_\infty$) is then divided by J to determine how much the temperature is reduced by at Step 4 (Figure 2.3). The temperature at iteration k is defined by Equations 2.2 and 2.3.

$$\begin{aligned} T_k &= T_0 - k \cdot \left(\frac{T_0 - T_\infty}{J} \right) \qquad (2.2) \\ &= T_{k-1} - \left(\frac{T_0 - T_\infty}{J} \right) \qquad (2.3) \end{aligned}$$

The second method of temperature reduction is exponential decay. This is a more accurate model of the true thermal dynamics in a heated metal than the linear model. At each iteration the temperature is reduced by multiplying with a factor, $\lambda < 1$. Equations 2.4 and 2.5 describe the temperature at iteration k.

$$\begin{aligned} T_k &= \lambda^k \cdot T_0 \qquad (2.4) \\ &= \lambda \cdot T_{k-1} \qquad (2.5) \end{aligned}$$

Because of its closer approximation to the expected temperature reduction in a practical sense, the exponential method is used in all work reported here.

- **Stopping Criteria.** The stopping criteria define when the algorithm should terminate. Possibilities are: a minimum temperature (eg, T_∞) has been reached; a certain number of temperature reductions have occurred; or the current solution has not changed for a number of iterations. The latter is often the best option as any candidate solutions will not be accepted (unless they are better than the current one) when the temperature is very low. This is because the probability of acceptance (as defined by Equation 2.1) is negligible.

2.2.3 Genetic Algorithms

As may be evident from the simulated annealing algorithm, mathematicians often look to other areas in search of inspiration for new techniques which can be modelled for the purpose of optimisation. While simulated annealing is derived from the field of chemical physics, the genetic algorithm is based upon another “scientific” notion, namely Darwinian evolution theory. The genetic algorithm is modelled on a relatively simple interpretation of the evolutionary process, however, it has proven to be a reliable and powerful optimisation technique in a wide variety of applications.

It was Holland [31] in his 1975 paper, who first proposed the use of genetic algorithms for problem solving. Goldberg [25] and DeJong [14] were also pioneers in the area of applying genetic processes to optimisation. Over the past twenty years numerous applications and adaptations have appeared in the literature. Three papers containing applications to the field of cryptanalysis are worthy of mention here. The first, by Matthews [47] and the second, by Spillman et al [71], are used in attacks on the transposition cipher and the substitution cipher, respectively (see Chapter 3 for more details). The third paper, by Spillman [71], attempts an attack on the knapsack cipher (this work is covered in detail in Chapter 5).

Consider a pool of genes which have the ability to reproduce, are able to adapt to environmental changes and, depending on their individual strengths, have varying life-spans. In such an environment only the fittest will survive and reproduce giving, over time, genes that are stronger and more resilient to conditional changes. After a certain amount of time the surviving genes could be considered “optimal” in some sense. This is the model used by the genetic algorithm, where the gene is the representation of a solution to the problem being optimised. Traditionally, genetic algorithms have solutions represented by binary strings. However, not all problems have solutions which are easily represented in binary (especially if the structure of the binary string is to be “meaningful”). To avoid this limiting property a more general area known as *evolutionary programming* has been developed. An evolutionary program may make use of arbitrary data structures in order to represent the solution. For simplicity all algorithms described in this thesis which use the evolutionary heuristics presented in this section are referred to as “genetic algorithms”, although, from a purist’s perspective, this may not be strictly accurate.

As with any optimisation technique there must be a method of assessing each solution. In keeping with the evolutionary theme, the assessment technique used by a genetic algorithm is usually referred to as the “fitness function”. As was pointed out above, the aim is always to maximise the fitness of the solutions in the solution pool.

Figure 2.4 gives an indication of the evolutionary processes used by the genetic algorithm. During each iteration of the algorithm the processes of selection, reproduction and mutation each take place in order to produce the next generation of solutions. The actual method used to perform each of these operations is very much dependent

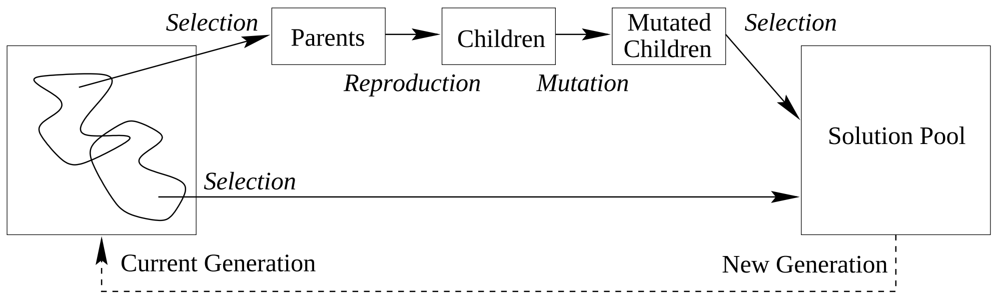


Figure 2.4: The Evolutionary Process.

upon the problem being solved and the representation of the solution. For the purposes of illustration, examples of each of these operations are now given using the traditional binary solution structure.

Example 2.1 *Consider a problem whose solutions are represented as binary strings of length $N = 7$. In this instance, a pool of M solutions is being maintained. The first phase of each iteration is the selection of a number of parents who will reproduce to give children.*

- *Selection of parents. A subset of the current solution pool is chosen to be the "breeding pool". This could be a random subset of the current solution pool, or in fact the entire current generation, or some other grouping. Another technique is to make the choice pseudo-randomly by giving the most fit solutions a higher likelihood of being selected, thus making the "better" solutions more likely to be involved in the creation of the new generation while at the same time not prohibiting the less fit solution from being involved in the breeding process.*

Once the breeding pool has been created, parents are paired for the reproduction phase.

- *Reproduction. A commonly used mating technique for solutions represented as a binary string is the "crossover" where a random integer in the range $[1, \ldots, N-1]$ is generated and all bits in the binary string after this position are swapped between the two parents. Consider the two parents P_1 and P_2 with the random chosen position 3.*

```
P1  1 0 1 1 1 1 0
P2  0 1 0 0 1 0 1
```

The two children created by this operation are C_1 and C_2.

```
C1  1 0 1 0 1 0 1
C2  0 1 0 1 1 1 0
```

As can be seen, each of the children has inherited characteristics from each of its parents.

Finally, the newly generated children undergo mutation. Here, the solutions are randomly adjusted in a further attempt to increase the diversity of the new solution pool.

- *Mutation. The most simple mutation operation for binary strings is complementation of some of the bits in the child. The probability that a bit is complemented is given by the "mutation probability", p_m. For example, if $p_m = 0.15 \approx \frac{1}{7}$, for the case when $N = 7$, one would expect that, on the average, one bit of each child would be complemented. If bit 3 of C_1 were complemented then C_1 would become as follows.*

```
C1  1 0 0 0 1 0 1
```

An algorithmic representation of the genetic algorithm is given in Figure 2.5. This description is independent of any solution representation, fitness function, selection scheme, reproduction scheme and mutation scheme. Each of these will be described in detail where the genetic algorithm has been applied.

2.2.4 Tabu Search

The final method for optimisation which is discussed in this chapter is the tabu search. The use of the tabu search was pioneered by Glover who from 1985 onwards has published many articles discussing its numerous applications (for examples see [23, 24]). Others were quick to adopt the technique which has been used for such purposes as sequencing [64], scheduling [2, 13, 61, 6], oil exploration [30] and routing [67, 6].

The properties of the tabu search can be used to enhance other procedures by preventing them from becoming stuck in the regions of local minima. The tabu search,

1. Initialise algorithm variables: G the maximum number of generations to consider, M the solution pool size and any other problem dependent variables.

2. Generate an initial solution pool containing M candidate solutions. This initial pool can be generated randomly or by using a simple known heuristic for generating solutions to the problem at hand. This solution pool is now referred to as the *current* solution pool.

3. For G iterations, using the current pool:

   (a) Select a breeding pool from the current solution pool and make pairings of parents.

   (b) For each parental pairing, generate a pair[a] of children using a suitable mating function.

   (c) Apply a mutation operation to each of the newly created children.

   (d) Evaluate the fitness function for each of the children.

   (e) Based on the fitness of each of the children and the fitness of each of the solutions in the current pool, decide which solutions will be placed in the new solution pool. Copy the chosen solutions into the new solution pool.

   (f) Replace the current solution pool with the new one. So, the new solution pool becomes the current one.

4. Choose the most fit solution of the final generation as the best solution, or, depending on the selection heuristic in Step 3e, keep an internal recording of the best solution found and report it now.

[a]In some cases the breeding process may generate a single child, or even more than two children but traditionally two children result.

Figure 2.5: The Genetic Algorithm

like the genetic algorithm, introduces memory structures into its workings. In this case the purpose of the memory is multi-faceted. The genetic algorithm utilises its solution pool as a mechanism for introducing diversity into the breeding process. The tabu search utilises memory for an additional purpose, namely to prevent the search from returning to a previously explored region of the solution space too quickly. This is achieved by retaining a list of possible solutions that have been previously encountered. These solutions are considered *tabu* - hence the name of the technique. The size of the tabu list is one of the parameters of the tabu search.

The tabu search also contains mechanisms for controlling the search. The tabu list ensures that some solutions will be unacceptable, however, the restriction provided by the tabu list may become too limiting in some cases causing the algorithm to become trapped at a locally optimum solution. The tabu search introduces the notion of *aspiration criteria* in order to overcome this problem. The aspiration criteria over-ride the tabu restrictions making it possible to broaden the search for the global optimum.

Much of the implementation of the tabu search is problem specific - i.e., the mechanisms used depend heavily upon the type of problem being solved. Figure 2.6 gives a general description of the tabu search. An initial solution is generated (usually randomly). The tabu list is initialised with the initial solution. A number of iterations are performed which attempt to update the current solution with a better one, subject to the restrictions of the tabu list. In each iteration a list of candidate solutions is proposed. These solutions are obtained in a similar fashion to the perturbation technique used in simulated annealing and the mutation operation used in the genetic algorithm. The most admissible solution is selected from the candidate list using the five steps in item 2b in Figure 2.6. The current solution is updated with the most admissible one and the new current solution is added to the tabu list. The algorithm stops after a fixed number of iterations or when a better solution has been found for a number of iterations.

2.3 Summary

This chapter has introduced the reader to several of the essential concepts involved in the field of combinatorial optimisation. Evidence justifying the need for combinatorial optimisation algorithms has been presented and a number of algorithms detailed.

The theory of NP-completeness has been introduced. This theory describes a bound on the difficulty of solving a class of problems, namely the NP-complete decision problems. This theory is necessary in order to understand the need for optimisation heuristics which, although seeming ad-hoc in some ways, are the only known methods for finding suitable solutions to problems which are NP-hard.

The difference between exact and approximate optimisation algorithms is discussed, along with the reasoning behind the suitability of each of these techniques for particular applications. Exact algorithms are usually computationally intensive and, therefore, infeasible for many applications. Approximate algorithms, on the other hand, apply search heuristics designed to scan the solution space in a meaningful manner, avoiding regions of local minima, to find a suitable solution. Three such algorithms have been described in detail: simulated annealing, the genetic algorithm and the tabu search. The amount of detail given should be sufficient to enable the implementation of any of these techniques in any suitable application. Each of the three techniques possesses unique properties which make it useful in a broad spectrum of applications. References to published material relating to the theory and applications of these techniques have also been documented.

Simulated annealing mimics the process of annealing in metals using the analogy of a solution to the structure of the molecules in the heated metal. When the temperature is high the molecules move at random and appear to have little order. This may represent an initial random guess at a solution to an optimisation problem. After some time, as the temperature slowly cools, the molecules move toward a more ordered structure, the aim of annealing being to produce a crystalline structure in the molecules. The analogy to optimisation is still present so that as the algorithm progresses a more ordered solution (hopefully one similar to the optimum) is obtained.

The genetic algorithm is an attempt to use Darwin's evolutionary model in the field of optimisation which has proven to be remarkably successful. A pool of solutions breed, and mutate in a survival of the fittest regime. Solutions not considered suitable (classified by the optimisation problem's objective function) die off so that, over time, the solution pool contains good solutions to the problem. Initially intended to operate on problems whose solutions could be represented as a binary string, the genetic algorithm has grown to cover the field known as "evolutionary programming" where an arbitrary solution representation can be utilised, provided suitable genetic operators can be created.

The tabu search incorporates techniques for ensuring that the solutions considered in the search are diverse. This is achieved by maintaining a tabu list which contains a list of solutions which have been visited by the search previously and may not be accepted again, at least not until a certain amount of time has passed. However, by specifying aspiration criteria, the tabu list can be overridden in order to ensure that solutions which are believed to be good may be accepted.

The techniques presented in this chapter will be utilised throughout the remainder of this thesis, in both cryptanalytic and cryptographic applications. In Chapter 3 the classical substitution and transposition-type ciphers are cryptanalysed. In Chapter 4 it is shown that these techniques can be incorporated with other, more specialised algorithms, in order to obtain some improvement. Chapter 5 presents an example of an application where these techniques are of little use. This further belies the necessity for understanding which applications are suited to combinatorial optimisation. This is especially true in the field of cryptology since ciphers are designed to be infeasible to solve. A method of systematically generating highly nonlinear Boolean functions using a genetic algorithm is presented in Chapter 6.

1. Generate an initial solution to the problem and calculate its cost. Add this solution to the tabu list and, also, record it as the current solution.

2. For some number of iterations perform the following steps.

   (a) By transforming the current solution generate a list of candidate solutions to the problem.

   (b) Evaluate the candidate list to find the best admissible move by performing the following steps on each of the candidates in turn.

      i. Determine if the current candidate has a lower cost than the current best admissible solution. If not go to Step 2(b)iv.

      ii. If the candidate is tabu (i.e., it is contained in the tabu list) check to see if any of the aspiration criteria are satisfied. If none of the aspiration criteria are satisfied jump to Step 2(b)iv.

      iii. Mark this candidate as the best admissible candidate.

      iv. If the list of candidate solutions is exhausted decide if the list needs to be extended and if so generate more candidate solutions. If not go to Step 2c.

      v. If there exist more candidate solutions return to Step 2(b)i.

   (c) Make the best admissible candidate the current solution. Update the tabu list by adding the new solution to the list (providing it is not already in the list).

   (d) Update the overall best solution if the current solution is better than the current overall best solution.

   (e) Determine if the stopping condition is satisfied - i.e., has the maximum number of iterations been reached or have there been a large number of iterations since the best solution was found?

3. The best solution found is output as a solution to the problem.

Figure 2.6: The Tabu Search

Chapter 3

Classical Ciphers

Classical ciphers were first used hundreds of years ago. So far as security is concerned, they are no match for today's ciphers, however, this does not mean that they are any less important to the field of cryptology. Their importance stems from the fact that most of the ciphers in common use today utilise the operations of the classical ciphers as their building blocks. For example, the Data Encryption Standard (DES), an encryption algorithm used widely in the finance community throughout the world, uses only three very simple operators, namely substitution, permutation (transposition) and bit-wise exclusive-or (admittedly, in a rather complicated fashion). Given their simplicity, and the fact that they are used to construct other ciphers, the classical ciphers are usually the first ones considered when researching new attack techniques such as the ones discussed in this chapter.

Many flavours of classical ciphers exist, although most fall into one of two broad categories: substitution ciphers and transposition (permutation) ciphers. In this chapter three specific examples of ciphers are considered. Two of the ciphers considered fall into the category of substitution ciphers: the simple (or monoalphabetic) substitution cipher and the polyalphabetic substitution cipher; and the other is an example of a transposition cipher. Detailed descriptions of each of these ciphers are given in Appendix A. The appendix also provides worked examples of each of the different ciphers.

Previously, Forsyth and Safavi-Naini (in [18]) have published an attack on the simple substitution cipher using simulated annealing and Spillman et al (in [73]) presented an attack (again, on the simple substitution cipher) using a genetic algorithm. Also, an attack on the transposition cipher was proposed by Matthews (in [47]) using a genetic algorithm. These attacks have been re-implemented in this chapter in order to obtain a comparison of the techniques and also to evaluate a third technique, namely the tabu search. Attacks on both the simple substitution cipher and the transposition cipher were implemented using all three optimisation heuristics described in Chapter 2: i.e., simulated annealing, the genetic algorithm and the tabu search. This involved the design of an attack on the substitution cipher using the tabu search and the design of attacks on the transposition cipher using simulated annealing and the tabu search. The previously published attacks were enhanced and modified in order that an accurate comparison of the three techniques could be obtained. Attacks on the simple substitution cipher are described in detail in Section 3.1 and attacks on the transposition cipher are described in Section 3.3.

Each of the three techniques was compared based on three criteria: the amount of known ciphertext available to the attack; the number of keys considered before the correct solution was found; and the time required by the attack to determine the correct solution. The results are presented graphically in order to achieve a clear comparison. The results for the simple substitution cipher are given in Section 3.1.5 and the results for the transposition cipher are given in Section 3.3.5.

In addition to the comparison of the three optimisation heuristics for attacks on the simple substitution cipher and the transposition cipher, a new attack is presented on the polyalphabetic substitution cipher. Because of the structure of the cipher, it is well suited to an attack based on a parallel heuristic. In Section 3.2 a parallel technique for attacking the polyalphabetic substitution cipher is presented which makes use of a parallel genetic algorithm. Although parallel genetic algorithms have been applied widely in other areas, especially numerical optimisation (see [8, 20] for examples), this is the first application to the field of cryptanalysis (to the best of the author's knowledge). This technique is shown to be highly effective and the results are presented in Section 3.2.2.

Techniques for determining the period of a polyalphabetic substitution cipher are described in Appendix A. In Section 3.2 an additional technique is described which makes use of the parallel heuristic described in the same section. Results highlighting the effectiveness of this approach are also given.

Note that all experiments presented in this chapter were performed on text using a 27 character alphabet, i.e., A – Z, and the space character. All punctuation and structure (sentences/paragraphs) has been removed from the text before encryption. Any two words are separated by a single space character.

3.1 Attacks on the Simple Substitution Cipher

The general strategy with the two substitution ciphers is to substitute symbols from the plaintext alphabet with different symbols from the ciphertext alphabet(s). The weakness with this strategy is that character frequency distributions are not significantly altered by the encryption process. Thus, most attacks on substitution ciphers attempt to match the character frequency statistics of the encrypted message with those of some known language (for example, English). Character frequency statistics (or n-grams) indicate the frequency distribution of all possible instances of n adjacent characters (for example, THE is a very common 3-gram (or *trigram*) in the English language). Examples A.1 and A.2 (from Appendix A) illustrate how the n-gram statistics are maintained during encryption.

The attack on the simple substitution cipher is particularly simple since the frequency of any n-gram in the plaintext (or unencrypted) message will correspond *exactly* to the frequency of the corresponding encrypted version in the ciphertext. The search for the corresponding n-gram frequencies can be automated using combinatorial optimisation algorithms such as those described in Chapter 2. Here, a number of methods are utilised in attacks in the simple substitution cipher. As previously indicated, a method of assessing intermediate solutions (in the search for the optimum) is required.

A major factor influencing the success of an attack on the simple substitution cipher (or any cipher where the attack is based on n-gram statistics of the language) is the length of the intercepted ciphertext message which is being cryptanalysed. The amount of ciphertext required in order to recover the entire key (with a high degree of certainty) varies depending on the type of cipher. From Figure 3.1 it can be seen that for a message of 1000 characters it is possible to recover 26 out of the 27 key elements on the average. Note that in practice it is impossible to find a simple substitution cipher key which differs in exactly one place from the correct key. However it is not necessary to recover every element of the key in order to obtain a message that is readable. Table 3.1 shows the relative frequency of each of the characters in a sample of English taken from the book “20000 Leagues Under the Sea” by Jules Verne. A fact evident in almost all attacks on substitution ciphers is that the most frequent characters are decrypted first. Table 3.1 also shows the amount of message that will have been recovered after each of the characters is discovered (making the unrealistic assumption that the characters are discovered in order from most frequent to least frequent). It can be seen that approximately fifty percent of the message can be recovered by correctly determining the key element for the five most frequent characters in the intercepted message. Also, the eleven most infrequent characters account for only ten percent of the message (on the average).

3.1.1 Suitability Assessment

Naturally, the technique used to compare candidate keys to the simple substitution cipher is to compare n-gram statistics of the decrypted message with those of the language (which are assumed known). Equation 3.1 is a general formula used to determine the suitability of a proposed key (k) to a simple substitution cipher. Here, $\mathcal{A}$ denotes the language alphabet (i.e., for English, $\{\mathsf{A}, \ldots, \mathsf{Z}, \_\}$, where _ represents the space symbol), K and D denote known language statistics and decrypted message statistics, respectively, and the indices u, b and t denote the unigram, bigram and trigram statistics, respectively. The values of α, β and γ allow assigning of different weights to each of the three n-gram types.

$$\begin{aligned} C_k &= \alpha \cdot \sum_{i \in \mathcal{A}} \left| K^u_{(i)} - D^u_{(i)} \right| \\ &+ \beta \cdot \sum_{i,j \in \mathcal{A}} \left| K^b_{(i,j)} - D^b_{(i,j)} \right| \\ &+ \gamma \cdot \sum_{i,j,k \in \mathcal{A}} \left| K^t_{(i,j,k)} - D^t_{(i,j,k)} \right| \end{aligned} \tag{3.1}$$

Forsyth and Safavi-Naini, in their simulated annealing attack on the substitution cipher [18] and Jakobsen in his attack [33] use a very similar evaluation, namely the one in Equation 3.2. This formula is based purely upon bigram statistics which is often

		Frequency (%)	
Order	Letter	Relative	Cumulative
1	_	18.4820	18.4820
2	E	10.3320	28.8140
3	T	7.8395	36.6535
4	A	6.6284	43.2819
5	O	6.0091	49.2909
6	I	5.7941	55.0850
7	N	5.7526	60.8376
8	S	5.3997	66.2373
9	H	4.8210	71.0583
10	R	4.5744	75.6327
11	D	3.4530	79.0857
12	L	3.2366	82.3223
13	U	2.4719	84.7941
14	C	2.2742	87.0683
15	M	1.9853	89.0537
16	F	1.9242	90.9778
17	W	1.9183	92.8961
18	P	1.5438	94.4399
19	G	1.4424	95.8823
20	Y	1.2656	97.1479
21	B	1.2026	98.3505
22	V	0.7474	99.0979
23	K	0.5482	99.6461
24	X	0.1466	99.7928
25	Q	0.0851	99.8779
26	J	0.0667	99.9445
27	Z	0.0555	100.0000

Table 3.1: English language characteristics.

sufficient for attacks on the simple substitution cipher.

$$C_k = \sum_{i,j \in \mathcal{A}} \left| K^b_{(i,j)} - D^b_{(i,j)} \right| \tag{3.2}$$

Spillman et al [73], use a different formula again (see Equation 3.3). This equation is based on unigram and bigram statistics.

$$C_k \propto \sum_{i \in \mathcal{A}} \left| K^u_{(i)} - D^u_{(i)} \right| + \sum_{i,j \in \mathcal{A}} \left| K^b_{(i,j)} - D^b_{(i,j)} \right| \tag{3.3}$$

The only difference between these assessment functions is the inclusion of different statistics (Equation 3.2 is equal to Equation 3.1 when $\alpha = \gamma = 0$). In general, the larger the n-grams, the more accurate the assessment is likely to be. It is usually an expensive task to calculate the trigram statistics - this is, perhaps, why they are omitted in Equations 3.2 and 3.3. The complexity of determining the fitness is $\mathcal{O}(N^3)$ (where N is the alphabet size) when trigram statistics are being determined, compared with $\mathcal{O}(N^2)$ when bigrams are the largest statistics being used. Following the attack description given below there are details describing a method which can be used under some circumstances for reducing the complexity of the cost calculation by a factor of N. Thus a cost based on trigram statistics can be calculated with complexity proportional to $\mathcal{O}(N^2)$.

Figure 3.1 indicates the effectiveness of using different n-grams in the evaluation of a simple substitution cipher key. The three curves in the plot represent the percentage of key recovered by an attack on a simple substitution cipher using simulated annealing (see below) versus the amount of known ciphertext used in the attack. Each curve resulted from using the cost function in Equation 3.1 with different values of the weights α, β and γ. For example, the “Unigrams only” curve was obtained with $\alpha = 1$ and $\beta = \gamma = 0$. Each data point on each curve was determined by running the attack on 200 different messages and three times for each message. Of the three runs for each message only the best result was used. The value on the curve represents the average number of key elements correctly placed (over the 200 messages). For the alphabet being used the maximum value attainable is 27.

For small amounts of known ciphertext it is interesting to note that an attack using a cost function based on bigrams alone is more effective than one which utilises only trigrams (see Figure 3.1). The crossover point of the “Bigrams only” and “Trigrams Only” curves in Figure 3.1 represents an approximate threshold value where a cost function based purely upon trigram frequencies out-performs one based only on bigram frequencies. The reason for the phenomenon can, in part, be gleaned by observing the cost function in Equation 3.1. When the length of the intercepted messages is short there are far fewer distinct bigrams or trigrams represented in the ciphertext than the total number of possible bigrams or trigrams. When $N = 27$ there are $N^3 = 19683$ possible trigrams (theoretically - of course not all trigrams are represented in the English language). The maximum number of distinct trigrams in a message of length say, 100, is 98. Thus the proportion of trigrams represented in the message

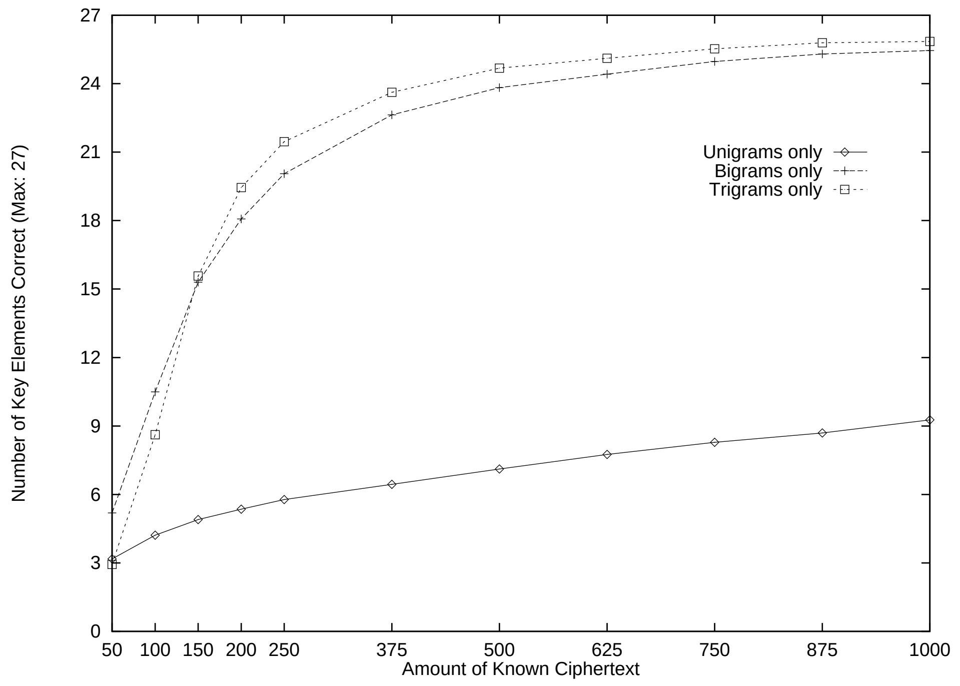


Figure 3.1: Results for cost functions using only unigrams, bigrams and trigrams, respectively.

is very small (the upper bound is $98/19683 \approx 0.005$). This means that are large number of unrepresented trigrams are effecting the evaluation of the cost function. For bigrams the proportion is much larger ($99/729 \approx 0.136$) and hence the cost function is more reliable and accurate. This effect ceases when the amount of known ciphertext is greater than approximately 150 characters.

While Figure 3.1 gives an interesting comparison of the effectiveness of each of the statistic types (i.e., unigrams, bigrams and trigrams), it is also interesting to experiment with different values of α, β and γ in order to determine how the statistics interact and in which proportions they work best. Figure 3.2 presents a comparison of different values of α, β and γ.

In the experiments used to produce Figure 3.2, the following restrictions were applied in order to keep the number of combinations of α, β and γ workable.

$$\begin{aligned} \alpha, \beta, \gamma &\in \{0.0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0\}, \text{ and} \\ \alpha + \beta + \gamma &= 1.0 \end{aligned}$$

There are 66 combinations of α, β and γ which satisfy these conditions. In order to obtain good statistical averages the same attack procedure was used as for Figure 3.1 except that only 100 different messages were used (instead of 200). The three curves represent the average number of key elements correctly placed for each of the eleven values of each of the three weights. (**NB.** "Unigram Weight" refers to α, "Bigram Weight" refers to β and "Trigram Weight" refers to γ.)

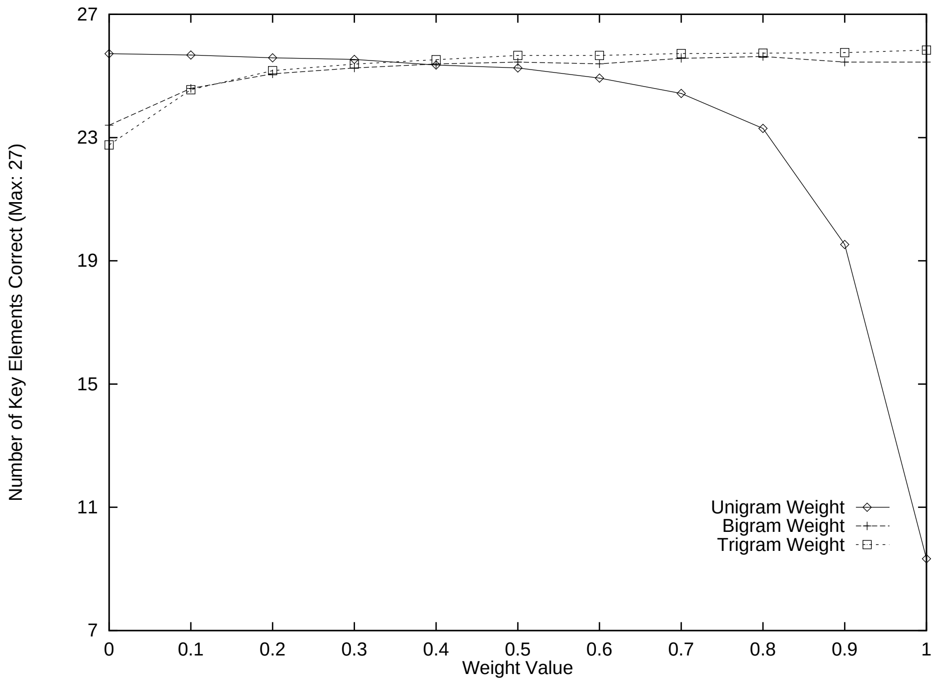


Figure 3.2: Results for cost functions with varying weights.

From Figures 3.1 and 3.2 it can be concluded that trigrams are generally the most effective basis for a cost function used in attacks on the substitution cipher. However, the benefit obtained from trigrams over bigrams is minimal. In fact, because of the complexity associated with determining trigram statistics – $\mathcal{O}(N^3)$ – it is often practical to base a fitness of a mixture of unigrams and bigrams – which has a complexity proportional to $\mathcal{O}(N^2)$. For the remainder of the work relating to simple substitution ciphers a fitness based purely on bigrams is used (i.e., Equation 3.2).

3.1.2 A Simulated Annealing Attack

The simulated annealing attack of the simple substitution cipher is relatively straightforward. Recall that the key is represented as a string of the N characters in the alphabet. A very simple way of perturbing such a key is to swap the key elements in two randomly chosen positions. This is the method utilised in the following algorithm which describes a simulated annealing attack on the simple substitution cipher.

1. The algorithm is given the intercepted ciphertext and the known language statistics as input.
2. Generate the initial solution (randomly or otherwise), K_{CURR}, and calculate its cost using Equation 3.2 (C_{CURR}). Set $T = T_0 = C_{\text{CURR}}$ and the temperature reduction factor T_{FACT}. Set MAX_ITER, the maximum number of iterations to perform.
3. Repeat MAX_ITER times (MAX_ITER temperature reductions):
    (a) Set $N_{\text{SUCC}} = 0$.
    (b) Repeat $100 \cdot N$ times:
        i. Choose $n_1, n_2 \in [1, N], n_1 \neq n_2$.
        ii. Swap element n_1 with element n_2 in K_{CURR} to produce K_{NEW}.
        iii. Calculate the cost of K_{NEW} using Equation 3.2. Call this cost C_{NEW}. Calculate the cost difference ($\Delta E = C_{\text{NEW}} - C_{\text{CURR}}$) and consult the Metropolis criterion (Equation 2.1) to determine whether the proposed transition should be accepted.
        iv. If the transition is accepted set $K_{\text{CURR}} = K_{\text{NEW}}$ and $C_{\text{CURR}} = C_{\text{NEW}}$ and increment N_{SUCC} ($N_{\text{SUCC}} = N_{\text{SUCC}} + 1$). If $N_{\text{SUCC}} > 10 \cdot N$ go to Step 3d.
    (c) If $N_{\text{SUCC}} = 0$ go to Step 4.
    (d) Reduce T ($T = T \times T_{\text{FACT}}$).
4. Output the current solution. .

The choice of $T_0 = C_{\text{CURR}}$ was made based upon experimentation. It was found that for this choice of T_0 the conditions presented in Section 2.2.2 are satisfied almost all of the time. In fact, this technique of choosing T_0 was found to be better than using a constant value since many times, when the choice of T_0 is too high, the algorithm spends a lot of time in a seemingly random search while the temperature decreases to a value which disallows some of the proposed solutions.

The values $100 \cdot N$ (Step 3b) and $10 \cdot N$ (Step 3(b)iv) are parameters of the algorithm which are arbitrary. They should, of course, be chosen so that a large number of possible solutions are assessed at each temperature, but not so large that time is wasted. By setting a limit to the number of successful updates to the solution at each temperature, the algorithm avoids assessing too many solutions when the temperature is high (since almost all suggested transitions are accepted at high temperatures).

As indicated above, there are circumstances under which it is possible to reduce the complexity of the cost calculation. One such case is when comparing the cost associated with two keys when the keys only differ in two elements (i.e., one key can be obtained from the other key simply by swapping two elements). This is exactly what happens in the simulated annealing algorithm above - two elements in the current key are swapped and the new cost calculated. The difference between the cost of the current solution and the new one (with the swapped elements) is used to determine if the new key will be accepted.

It should be clear that when two key elements are swapped only the statistics (of the decrypted message) for trigrams which contain one (or both) of the swapped elements will change. Similarly, only the statistics for bigrams which contain one (or both) of the swapped elements will change. Also, only two of the unigram statistics will change.

Making use of this property can lead to a significant increase in the efficiency of the simulated annealing attack. The improvement obtained using such a strategy is of the order of N. Table 3.2 displays the actual improvement in terms of the number of comparisons of statistics required in the evaluation of the cost difference. The numbers in brackets indicate the number of calculations required when $N = 27$. It can be seen that when $N = 27$ the complexity of determining a cost based on trigrams is not significantly reduced using this technique. However, for larger values of N - for example consider the ASCII alphabet of 256 characters - the saving is great.

This technique can be used for determining the cost difference between two keys in any system where one key is obtained from another by swapping two elements of the original key.

The results of the attack described in this section are compared with the attacks using the genetic algorithm and tabu search (described below), in Section 3.1.5.

Statistic	Exhaustive	Optimised
Unigrams	N (27)	4
Bigrams	N^2 (729)	$8(N-1)$ (208)
Trigrams	N^3 (19683)	$8(3N^2-6N+4)$ (16232)

Table 3.2: Improvement gained from optimised calculation of the cost difference.

3.1.3 A Genetic Algorithm Attack

The genetic algorithm is rather more complicated than the simulated annealing attack. This is because a pool of solutions is being maintained, rather than a single solution. An extra level of complexity is also present because of the need for a mating function.

The mating function utilised in this thesis for attacks involving substitution ciphers is similar to the one proposed by Spillman et al [73], who use a special ordering of the key. The characters in the key string are ordered such that the most frequent character in the ciphertext is mapped to the first element of the key (upon decryption), the second most frequent character in the ciphertext is mapped to the second element of the key, and so on. The correct key will then be a sorted list of the decrypted message single character frequencies. The reason for this ordering will become apparent upon inspection of the mating function. Given two parents constructed in the manner just described, the first element of the first child is chosen to be the one of the first two elements in each of the parents which is most frequent in the known language statistics. This process continues in a right to left direction along each of the parents to create the first child only. If, at any stage, a selection is made which already appears in the child being constructed, the second choice is used. If both of the characters in the parents for a given key position already appear in the child then a character is chosen at random from the set of characters which do not already appear in the newly constructed child. The second child is formed in a similar manner, except that the direction of creation is from left to right and, in this case, the least frequent of the two parent elements is chosen. An algorithmic description of this mating procedure for creating the two children is now given:

1. **Notation:** p_1 and p_2 are the parents, c_1 and c_2 are the children, $p_i(j)$ indicates character j in parent i (similarly $c_i(j)$ indicates the jth element in child i), $\{C_i^{j,k}\}$ denotes the set of elements in child i in positions j to k

(inclusive) with the limitation that if $i = N + 1$ or $j = 0$ then $\{C_i^{j,k}\} = \{\emptyset\}$ (the empty set), $f(x)$ denotes the relative frequency of character x in the known language.

2. Child 1: For $j = 1, \ldots, N$ (step 1) do
   - If $f(p_1(j)) > f(p_2(j))$ then
     - If $p_1(j) \notin \{C_1^{1,j-1}\}$ then $c_1(j) = p_1(j)$,
       else if $p_2(j) \notin \{C_1^{1,j-1}\}$ then $c_1(j) = p_2(j)$,
       else $c_1(j) =$ random element $\notin \{C_1^{1,j-1}\}$.

     else
     - If $p_2(j) \notin \{C_1^{1,j-1}\}$ then $c_1(j) = p_2(j)$,
       else if $p_1(j) \notin \{C_1^{1,j-1}\}$ then $c_1(j) = p_1(j)$,
       else $c_1(j) =$ random element $\notin \{C_1^{1,j-1}\}$.
3. Child 2: For $j = N, \ldots, 1$ (step -1) do
   - If $f(p_1(j)) < f(p_2(j))$ then
     - If $p_1(j) \notin \{C_2^{j+1,N}\}$ then $c_2(j) = p_1(j)$,
       else if $p_2(j) \notin \{C_2^{j+1,N}\}$ then $c_2(j) = p_2(j)$,
       else $c_2(j) =$ random element $\notin \{C_2^{j+1,N}\}$.

     else
     - If $p_2(j) \notin \{C_2^{j+1,N}\}$ then $c_2(j) = p_2(j)$,
       else if $p_1(j) \notin \{C_2^{j+1,N}\}$ then $c_2(j) = p_1(j)$,
       else $c_2(j) =$ random element $\notin \{C_2^{j+1,N}\}$.

This description of the mating operation for a simple substitution cipher differs from the method described in [73] where each element of the two children is chosen by taking the character from the two parents which appears *most* frequently (for both children) in the *ciphertext*. This technique is clearly less efficient since the first element of each key represents the most frequent *plaintext* character.

The mutation operation is identical to the solution perturbation technique used in the simulated annealing attack. That is, randomly select two positions in the child and swap the two characters at those positions.

The following is an algorithmic description of the attack on a simple substitution cipher using a genetic algorithm.

1. The algorithm is given the ciphertext (and its length) and the statistics of the language (unigrams, bigrams and trigrams).
2. Initialise the algorithm parameters. They are: M the solution pool size and MAX_ITER the maximum number of iterations.
3. Randomly generate the initial pool containing M solutions (keys of the simple substitution cipher). Call this pool P_{CURR}. Calculate the cost of each of the keys using Equation 3.2.
4. For iteration/generation $i = 1, \ldots,$ MAX_ITER, do
   (a) Select $M/2$ pairs of solutions from the current pool, P_{CURR}, to be the parents of the new generation. The selection should be random with a bias towards the most fit of the current generation.
   (b) Each pair of parents then mate using the algorithm above to produce two children. These M children form the new pool, P_{NEW}.
   (c) Mutate each of the children in P_{NEW} using the random swapping procedure described above.
   (d) Calculate the suitability of each of the children in P_{NEW} using Equation 3.2.
   (e) Sort P_{NEW} from most suitable (least cost) to lease suitable (most cost).
   (f) Merge P_{CURR} with P_{NEW} to give a list of sorted solutions (discard duplicates) - the size of this list will be between M and $2M$. Choose the M best solutions from the merged list to become the new P_{CURR}.
5. Output the best solution from P_{CURR}.

This genetic algorithm was implemented and results of the attack on the simple substitution cipher are given in Section 3.1.5. The genetic algorithm attack is compared with the simulated annealing attack (described above) and the tabu search attack (described now).

3.1.4 A Tabu Search Attack

The simple substitution cipher can also be attacked using a tabu search. This attack is similar to the simulated annealing one with the added constraints of the tabu list (as described in Chapter 2). The same perturbation mechanism (i.e., swapping two randomly chosen key elements) is used. The overall algorithm is described as follows:

1. The inputs to the algorithm are the known (intercepted) ciphertext and the language statistics for unigrams, bigrams and trigrams.
2. Set MAX_ITER, the maximum number of iterations, N_TABU, the size of the tabu list and N_POSS, the size of the possibilities list. Initialise the tabu list with a list of random and distinct keys.
3. For iteration $i = 1, \ldots,$ MAX_ITER, do
   (a) Find the key in the tabu list which has the lowest cost associated with it. Call this key K_{BEST}.
   (b) For $j = 1, \ldots,$ N_POSS, do
      i. Choose $n_1, n_2 \in [1, N], n_1 \neq n_2$.
      ii. Create a possible new key K_{NEW} by swapping the elements n_1 and n_2 in K_{BEST}.
      iii. Check that K_{NEW} is not already in the list of possibilities for this iteration or the tabu list. If it is return to Step 3(b)i.
      iv. Add K_{NEW} to the list of possibilities for this iteration and determine its cost.
   (c) From the list of possibilities for this iteration find the key with the lowest cost – call this key P_{BEST}.
   (d) From the tabu list find the key with the highest cost – call this key T_{WORST}.
   (e) While the cost of P_{BEST} is less than the cost of T_{WORST}:
      i. Replace T_{WORST} with P_{BEST}.
      ii. Find the new P_{BEST}.
      iii. Find the new T_{WORST}.
4. Output the best solution (i.e., the one with the least cost) from the tabu list.

Note that the choice of N_POSS must be less than $N(N-1)$ – where N is the key size – since this is the maximum number of distinct keys which can be created from K_{BEST} by swapping two elements.

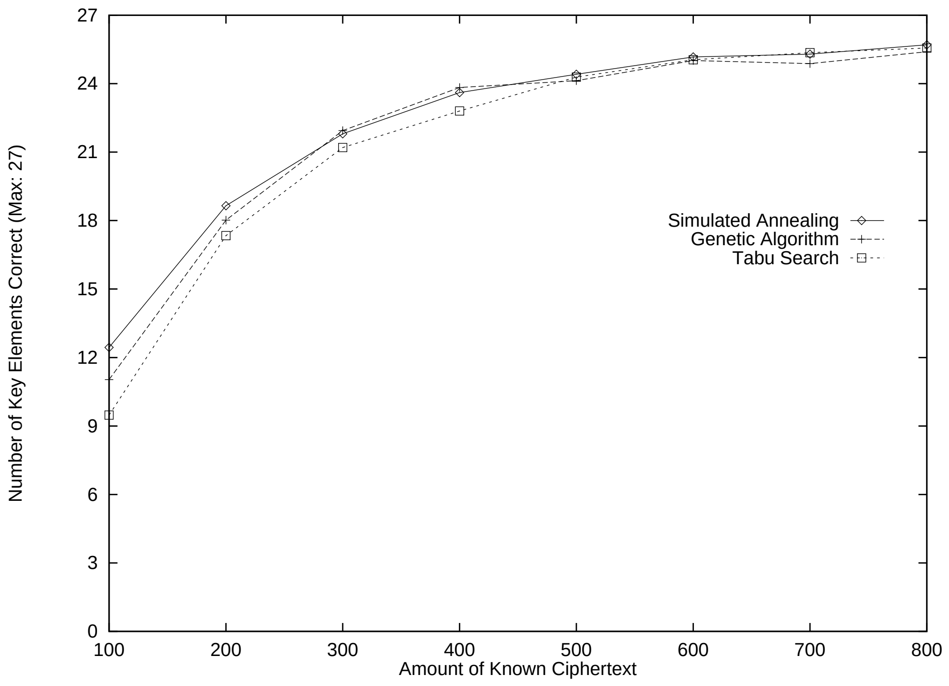


Figure 3.3: A comparison based on the amount of known ciphertext.

Number of Ciphertexts	SA		GA		TS	
	$\bar{x}$	s	$\bar{x}$	s	$\bar{x}$	s
100	10.73	4.70	7.74	4.82	6.02	4.04
200	17.70	3.40	14.17	6.13	12.76	6.32
300	21.07	2.72	18.77	6.01	17.33	6.48
400	22.86	2.27	21.72	4.61	19.45	6.34
500	23.73	2.16	22.44	4.37	21.77	5.47
600	24.50	1.86	23.69	3.68	23.50	4.14
700	24.72	1.73	23.82	3.39	23.68	4.42
800	25.08	1.59	24.64	2.23	24.18	4.12

Table 3.3: Mean and standard deviation data corresponding to Figure 3.3.

The results of the tabu search are given in the following section along with a comparison with the two alternate techniques described above.

3.1.5 Results

In this section a number of experimental results are presented which outline the effectiveness of each of the attack algorithms described above. Each of the attacks was run a number of times with a variety of parameter values. The results here are presented as

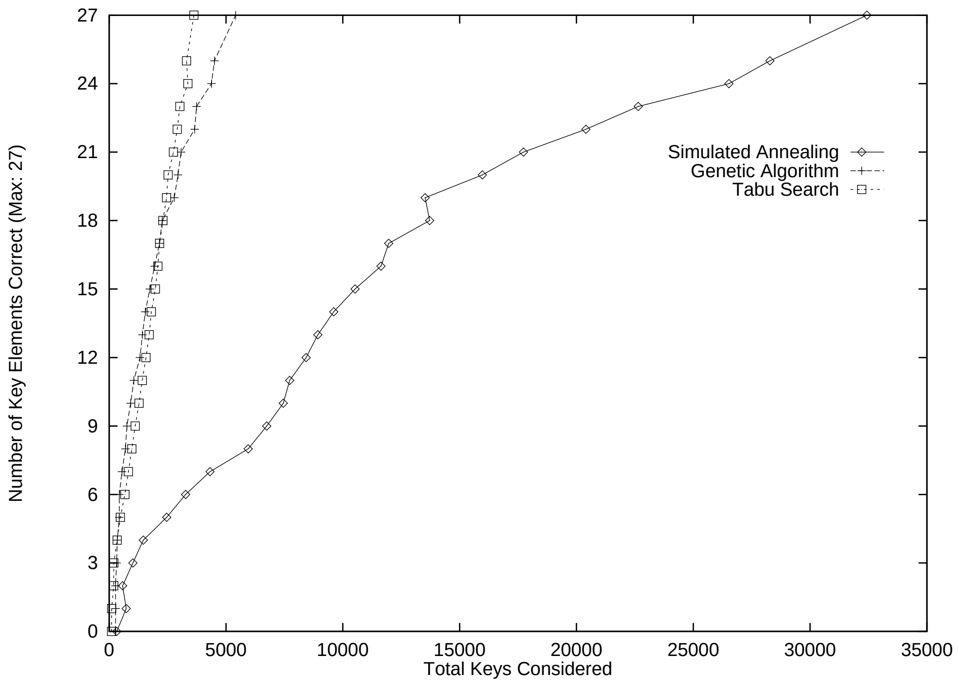


Figure 3.4: A comparison based on the number of keys considered.

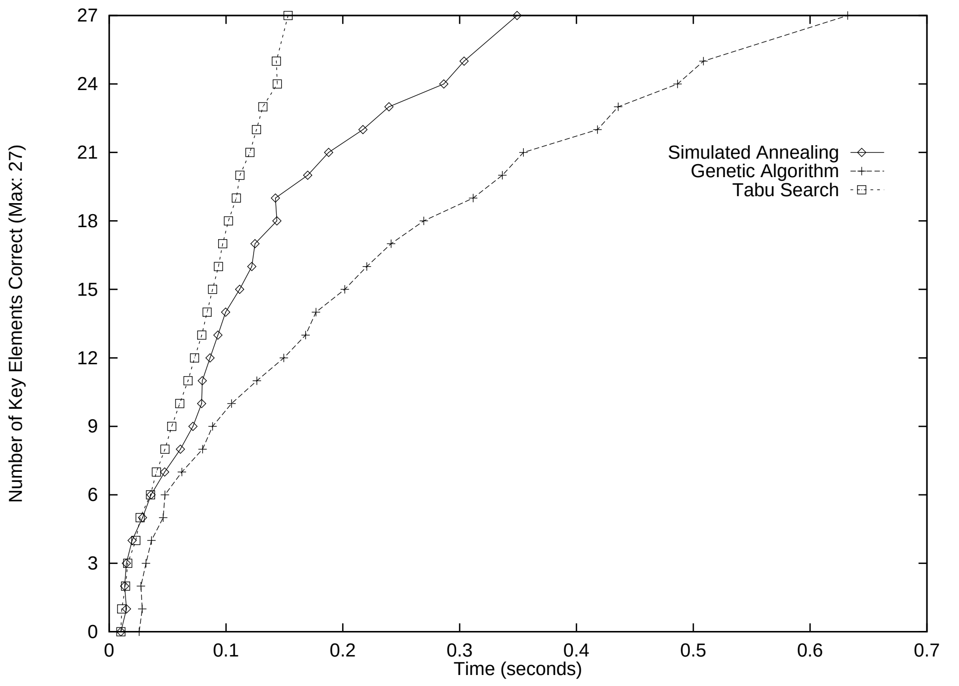


Figure 3.5: A comparison based on time.

plotted curves (Figures 3.3, 3.4 and 3.5). Each data point on these curves represents three hundred runs of the particular algorithm. One hundred different messages were generated in each case and the attack was run three times on each message. Of these three runs on each message only the best result is considered. The numerical value that is used in each of the plots is then the average over the one hundred messages of the best result for each message. Why was this technique used? It is common when using approximation algorithms to run the algorithm a number of times and then take the best result. This is because of the random nature of the algorithms. By averaging the results of a large number of independent attacks (in this case one hundred) a good representation of the algorithm's ability is obtained.

The first point to note is that each of the algorithms performed (approximately) as well as the other with regard to the ultimate outcome of the attack. This is illustrated in Figure 3.3 which compares the average number of key elements (out of 27) correctly recovered versus the amount of ciphertext which is assumed known in the attack. The plot shows results for amounts ranging from 100 to 800 known ciphertext characters. In each case the results obtained are very similar for each of the algorithms. The mean, $\bar{x}$, and standard deviation values, s, for the results in Figure 3.3 are given in Table 3.3. It can be seen that the standard deviation values for simulated annealing are less than for the other two methods. This indicates that the simulated annealing approach, as well as being slightly superior with respect to the mean values, has less variance in its results.

Each of the algorithms perform roughly equally well when the comparison is made based on the amount of ciphertext provided to the attack. It is interesting to make a comparison based on the complexity of each of the attack algorithms. The remaining results in this section aim to make a comparison of the algorithms based on complexity. In each case, the following results were obtained using cryptograms of length 1000. Figure 3.4 compares the number of correctly determined key elements with the total number of keys considered up to that point by the algorithm. It is clear that the number of keys considered by the simulated annealing technique in order to obtain the correct key is significantly greater than for the other two techniques with the genetic algorithm and the tabu search performing roughly equally in this respect. However, this comparison does not accurately indicate the relative efficiencies of the three algorithms. In Figure 3.5, which compares the number of correct key elements discovered with the amount of time used by the algorithm up to that point, it is clear that simulated annealing is actually more efficient (with respect to time) that the genetic algorithm. By comparing Figures 3.4 and 3.5 it can be concluded that the simulated annealing algorithm is able to consider a far greater number of solutions that the genetic algorithm and in much less time. It is also clear from both of these figures that the tabu search is most efficient in both respects.

3.2 Attacks on Polyalphabetic Substitution Ciphers

The level of correspondence between n-gram statistics in the plaintext and ciphertext messages for a polyalphabetic substitution cipher is not as high as for the simple substitution cipher, however, there is still a high enough correlation to achieve good results in attacks. As can be observed from the encryption process, the frequency of single characters (unigrams), *for each block position*, remains unchanged. Provided sufficient ciphertext is obtained, it is possible to find a good approximation of the correct encryption keys, for each block position, simply by determining the unigram frequencies for each block position. This, of course, assumes that the block length is known.

Methods for determining the block length were discussed in Section A.2. Another method is now presented. This (*ad hoc*) technique for determining the period of a polyalphabetic substitution cipher makes use of either a genetic algorithm or simulated annealing. Matthews (in [47]) used a similar technique for finding key lengths of transposition ciphers (see Section 3.3) with a genetic algorithm. The test procedure involves running a genetic algorithm for a small number of generations with a fixed block length B. This process is repeated for all potential values of B (the correct period). It is surmised that the cost of the best solution found for the correct period will be significantly less than the best cost found for any of the incorrect periods. The technique is described algorithmically as follows:

1. The inputs are the ciphertext and the required language statistics (unigrams, bigrams and trigrams). It is presumed that the ciphertext was created using a polyalphabetic substitution cipher of unknown period.
2. For each of a series of possible period values:
   (a) Run the attack (for example see the parallel genetic algorithm later in this section) for a small number of iterations (say 20).

b	Lowest cost
2	1.11705
3	1.02290
4	1.09631
5	1.11718
6	0.78067
7	1.06882
8	0.97778
9	0.89119
10	1.00322
11	1.00872
12	0.72703

Table 3.4: Costs for different periods. Correct period is 6.

   (b) Record the period and the cost of the best key found by the search.

3. The period of the polyalphabetic cipher used to encrypt the message (or a multiple of that period) is indicated by the lowest recorded cost.

Table 3.4 shows the results for such a technique when utilised on the polyalphabetic substitution cipher. In this case the correct period is six. Each time the parallel genetic algorithm (described later) was run for thirty iterations on the same ciphertext, each time assuming a different period. The cost function used was Equation 3.1 with $\alpha = 0.2$ and $\beta = \gamma = 0.4$ and in each case 1000 ciphertext characters were used. Results for periods up to length twelve are shown. It is of interest to note that the lowest cost obtained for an attack assuming a period of twelve was actually lower than the cost obtained for the correct value (six). This is because twelve is a multiple of the correct block size. Keys every six positions apart would be very similar indicating the shorter block size.

The polyalphabetic substitution cipher, as described in Section A.2, is simply a number of simple substitution ciphers operating on the different positions within each block. One possible attack strategy, then, is to solve each of the simple substitution ciphers in parallel. There are a number of problems with such an approach and these will be addressed presently. First some possible parallelisation techniques are investigated. The uses of parallel genetic algorithms have been widely published in the literature (see [56, 28, 8, 20]). For this reason the genetic algorithm is considered here.

3.2.1 A Parallel Genetic Algorithm Attack

There are two broad ways in which a genetic algorithm can be parallelised. The first is to parallelise the selection, mating and mutation phases in the genetic algorithm. Such a technique can be used to enhance almost any implementation of the genetic algorithm. Figure 3.6 illustrates this idea.

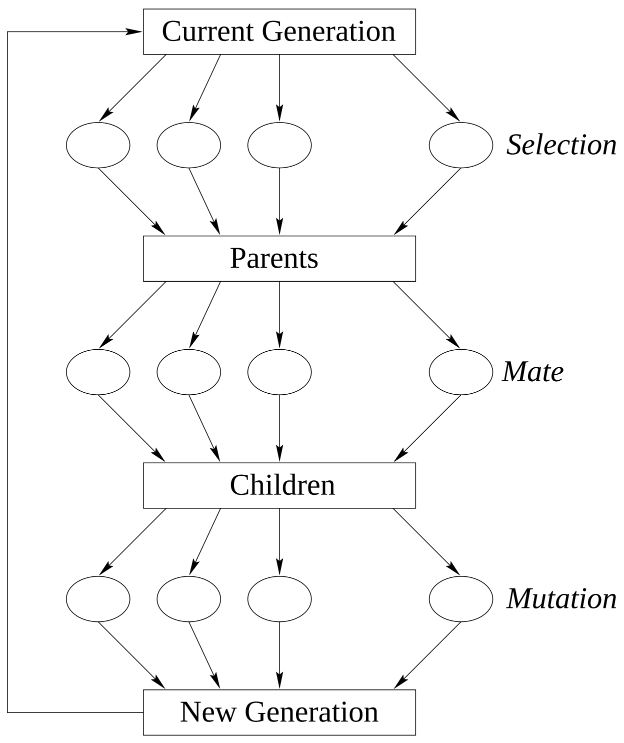


Figure 3.6: A parallel heuristic for any genetic algorithm.

When designing parallel heuristics one must be aware of the time overhead associated with transporting data to and from separate processing nodes. The heuristic presented in Figure 3.6 is only useful when dedicated hardware is available which can perform the necessary functions (eg., selection, mating, mutation and fitness/cost determination). Typically the complexity of each of these individual functions is very small, however a large number of processing nodes are required in order to gain advantage from the parallel architecture of the algorithm.

An alternative heuristic is to have a number of genetic algorithms running in parallel, each solving a different part of the problem. Figure 3.7 is a pictorial representation of this strategy with M GA's running in parallel and communicating every k iterations. The usefulness of such an approach is very much dependent on the structure of the problem being solved. Consider the polyalphabetic substitution cipher. As indicated briefly above, the polyalphabetic substitution cipher can be solved as a number of simple substitution ciphers. The key to each of these simple substitution ciphers will enable decryption of one of the positions in the block.

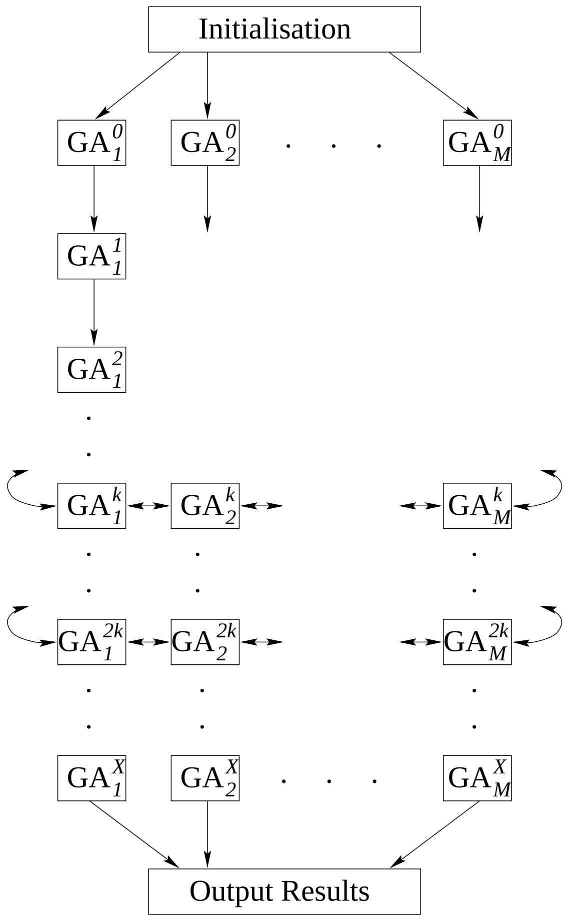


Figure 3.7: A problem specific parallel genetic algorithm heuristic.

This strategy was used to successfully attack the polyalphabetic substitution cipher. Before implementing the parallel attack a number of design problems have to be solved. Firstly, the calculation of the fitness/cost is no longer a simple task. Without knowledge of the keys for the two adjacent block positions it is impossible to determine bigram or trigram statistics. To overcome this problem the following strategy was used.

1. Initially only unigram statistics are used in determining the cost of the solutions

in any pool.

2. Every x iterations of each GA, the most fit solution in the current pool is sent to each of the neighbouring GA's. Each GA has knowledge of the entire ciphertext message so it is able to determine a fitness based on unigram, bigram and trigram statistics using ciphertext characters in its position, the position to the left and the position to the right.

In an attempt to illustrate more clearly the description of the previous paragraph the following symbolic outline is given. Consider a polyalphabetic substitution cipher consisting of B monoalphabetic or simple substitution ciphers. There will then be B genetic algorithms (call them $\text{GA}_1, \text{GA}_2, \ldots, \text{GA}_B$) solving each of the B simple substitution ciphers. Now consider GA_j $(1 < j < B)$ which is attempting to find the key to the cipher of position j. In determining the cost of each of the solutions in its pool, GA_j uses the current best key from each of its neighbours to find the bigram and trigram statistics.

The second problem to be solved when implementing a parallel GA is to determine how the different GA's will communicate between each another. The work presented here makes use of a software package called PVM (Parallel Virtual Machine) [62] which enables a number of networked computers to be linked as a virtual parallel computer in which a single application can be spread across a number of different physical computers. The use of such a package allows each of the individual GA's to communicate by sending the neighbours its current best keys.

With these design problems solved the implementation of each genetic algorithm proceeds as follows.

1. Each GA is given language statistics for unigrams, bigrams and trigrams, the ciphertext, the block size (B) and this GA's position within the block, j ($1 \leq j \leq B$), the frequency of inter-GA communications (f), the maximum number of iterations for the GA (G) and the solution pool size (M).

2. Generate a random pool of M simple substitution cipher keys for position j and calculate the cost for each using unigram statistics only. Call this pool of solutions P_{CURR}.

3. For iteration/generation i ($i = 1, \ldots, G$) do:

(a) If $i \bmod k \equiv 0$ send the best key from P_{CURR} to each of the neighbouring GA's (i.e., the GA's solving for positions $j-1$ and $j+1$). Also receive the best keys from each of these GA's.

(b) Select $M/2$ pairs of solutions from P_{CURR} to be the parents of the new generation. The selection should be biased towards the most fit of the current generation (i.e., the keys in P_{CURR}).

(c) Mate using each pair of parents with the algorithm given above. This produces M children which become the new generation (i.e., the solutions of P_{NEW}).

(d) Mutate each of the children in P_{NEW} using the same swapping procedure as described in the attack on the simple substitution cipher.

(e) Calculate the cost of each of the children in P_{NEW} using the neighbouring keys obtained in Step 3a and Equation 3.1.

(f) Select the M best keys from the two pools P_{CURR} and P_{NEW}. Replace the current solutions in P_{CURR} with these solutions.

4. Output the best key from P_{CURR}.

Experimental results obtained from this algorithm are now given. It is shown that the parallel technique is effective for polyalphabetic substitution ciphers with a variety of block sizes.

3.2.2 Results

It is clear that the parallel implementation of the attack will perform much more efficiently than a serial version since the parallel attack is solving each key of the polyalphabetic cipher simultaneously. The overhead of communication between the parallel processors is minimal leading to an attack of the polyalphabetic substitution cipher which would be expected to complete in roughly the same time as a similar attack on a monoalphabetic substitution cipher. In this section results based on the amount of ciphertext provided to the attack are given. These results can be compared with those obtained in Figure 3.3 for the simple substitution cipher.

The algorithm described above was implemented using a public domain software package called PVM (Parallel Virtual Machine) [62] which allows the development of parallel applications by sharing the processors of a number of networked computers (or

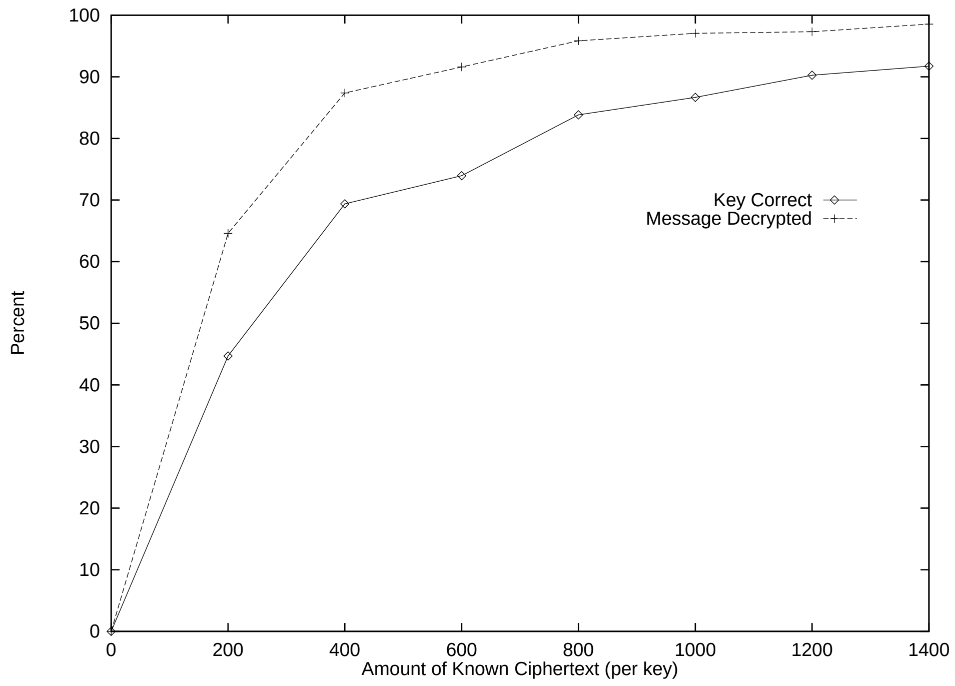


Figure 3.8: Known ciphertext versus percent recovered (key and message).

Amount of Ciphertext	PGA	
	$\bar{x}$	s
200	9.97	2.50
400	16.97	3.07
600	19.05	3.12
800	21.35	1.76
1000	22.00	2.05
1200	23.19	1.43
1400	24.11	1.58

Table 3.5: Mean and standard deviation data corresponding to Figure 3.8.

by running tasks simultaneously on a single, multitasking computer - a less efficient option). The attack was implemented with a polyalphabetic substitution cipher with a block size of three. The attack was run 100 times for each of 200, 400, 600, 800, 1000, 1200 and 1400 known ciphertext characters per key. The average results for the polyalphabetic substitution cipher are given in Figure 3.8. The mean and standard deviation statistics for the results in Figure 3.8 are given in Table 3.5. The relatively small values for the standard deviation and high values for the mean show that this technique is reliable in obtaining the indicated results. This figure presents a plot of both the amount of message recovered and the amount of key recovered as a percentage. Recall that for the simple substitution cipher (see Figure 3.3) that roughly 25 out of 27 key elements were correctly recovered after approximately 800 known ciphertext characters were provided. The parallel genetic algorithm attack of the polyalphabetic substitution cipher required about 1400 characters per key to obtain a similar result. This is to be expected because of the reduced number of trigrams available to the attack on the polyalphabetic substitution cipher.

The parallel algorithm was run on block sizes (B) ranging from 3 to 9. In each case there were 1500 characters of ciphertext *per key*. It was found that, regardless of block size, the algorithm was able to fully recover at least 99% of the original message. This result was obtained by running the algorithm using 100 different ciphertext messages for each block size and averaging the number of correctly placed key elements in each case. In each case the average number of key elements correctly placed was more than 26 out of 27 for each position in the block.

These results indicate that the parallel genetic algorithm is an extremely powerful technique for attacks on polyalphabetic substitution ciphers. It could be surmised from the experimental results given above that the attack could be used on polyalphabetic ciphers with very large periods provided that sufficient ciphertext and a parallel machine with sufficient nodes to implement the attack are available to the cryptanalyst.

3.3 Attacks on Transposition Ciphers

In this section three techniques are presented which can be utilised in attacks on the transposition cipher. These techniques make use of simulated annealing, the genetic algorithm and the tabu search, respectively. Recall that the attacks on the substitution ciphers used a perturbation mechanism which simply swapped two randomly chosen elements of the key. An additional mechanism is used in the attacks on the transposition cipher. This mechanism rotates a random (but consecutive) subsection of the key by a random amount. Possible cost functions for the attacks on the transposition cipher are now discussed.

3.3.1 Suitability Assessment

It is possible to use exactly the same cost to evaluate a key of a transposition cipher as the one used in Equation 3.1 for the simple substitution cipher. In the process of determining the cost associated with a transposition cipher key the proposed key is used to decrypt the ciphertext and then the statistics of the decrypted message are then compared with statistics of the language.

Matthews, in [47], proposed an intuitive (but never-the-less clever) alternative. Instead of using all possible bigrams and trigrams a subset of the most common ones are chosen. (Remember unigram frequencies are unchanged during the encryption process and so are ignored when evaluating a key.)

The method Matthews used was to list a number of the most common bigrams and trigrams and to assign a weight (or score) to each of them. Also, the trigram "EEE" was included in the list and assigned a negative score. The idea behind this is interesting. Since E is very common in English, it could be expected that a plaintext message might contain a relatively high number of E's. The same frequency of E's will be present in the ciphertext, but, in this case, it could be expected that, on occasion, three E's might occur simultaneously. Since these never occur normally in th English language, it makes sense to assign such a trigram a negative score.

Each weight is applied to the frequency of the corresponding bigram or trigram in the decrypted message. Note that Matthews' method (in [47]) was expressed in terms of a fitness function so the negative weight assigned to the trigram "␣␣␣" (three consecutive spaces) had the effect of reducing the fitness. Table 3.6 shows the weight table used by Matthews in his paper. The bigrams, trigrams and weights were modified for the research in this thesis to the values shown in Table 3.7. Notice that the bigram "␣␣" (two consecutive spaces) and the trigram "␣␣␣" (three consecutive spaces) have been included. Some of the other bigrams and trigrams are slightly different - due to the fact that the space symbol has been included in the encryption in this work (and was not in the work by Matthews) and also (perhaps) due to different sets of language statistics being used.

Bi/trigram	score	Bi/trigram	score
TH	+2	ED	+1
HE	+1	THE	+5
IN	+1	ING	+5
ER	+1	AND	+5
AN	+1	EEE	-5

Table 3.6: The fitness weight table proposed by Matthews.

Bi/trigram	score	Bi/trigram	score
E_	+2	__	-6
_T	+1	_TH	+5
HE	+1	THE	+5
TH	+1	HE_	+5
_A	+1	___	-10
S_	+1		

Table 3.7: The fitness weight table used in this research.

3.3.2 A Simulated Annealing Attack

In this section an attack on the transposition cipher using simulated annealing is presented. The score table from the previous section (see Table 3.7) is utilised when evaluating solutions.

Candidate solutions are generated from the current solution by either swapping two randomly chosen positions, or rotating the key a random amount. The choice of which of these two methods is made by random choice - referred to as "tossing a coin" in the algorithm description below. The algorithm can be described as follows:

1. Inputs to the algorithm are the intercepted ciphertext, the key size (permutation size or period), P, and a score table such as the one in Table 3.7.

2. The algorithm parameters are fixed – i.e, the maximum number of iterations (MAX_ITER), the initial temperature (T_0) and the temperature reduction factor (T_{FACT}). Set $T = T_0$ and generate a random initial solution (K_{CURR}) and calculate the associated cost (C_{CURR}).

3. Repeat MAX_ITER times:

   (a) Set $N_{\text{SUCC}} = 0$.

(b) Repeat $100 \cdot P$ times:
   i. Toss a coin:
      - **Heads:**
        A. Choose $n_1, n_2 \in [1, P], n_1 \neq n_2$.
        B. Swap n_1 and n_2 in K_{CURR} to create K_{NEW}.
      - **Tails:**
        A. Choose $n_1, n_2 \in [1, P], n_1 < n_2$.
        B. Choose $r \in [1, (n_2 - n_1)]$.
        C. Rotate the section from element n_1 to element n_2 in K_{CURR} r places clockwise to create K_{NEW}.
   ii. Calculate the cost C_{NEW} of K_{NEW}. Find the cost difference ($\Delta E = C_{\text{NEW}} - C_{\text{CURR}}$) and consult the Metropolis criterion (Equation 2.1) to determine whether the proposed transition should be accepted.
   iii. If the transition is accepted set $K_{\text{CURR}} = K_{\text{NEW}}$ and $C_{\text{CURR}} = C_{\text{NEW}}$ and increment N_{SUCC}. If $N_{\text{SUCC}} > 10 \cdot P$ go to Step 3d.

(c) If $N_{\text{SUCC}} = 0$ go to Step 4.

(d) Reduce T ($T = T \times T_{\text{FACT}}$).

4. Output the current solution K_{CURR}.

This simulated annealing attack was implemented and the experimental results are given below in Section 3.3.5 which compare this technique with the genetic algorithm attack described in Section 3.3.3 and the tabu search which is described in Section 3.3.4.

3.3.3 A Genetic Algorithm Attack

The mating algorithm used for the genetic algorithm attack on the transposition cipher is similar to the one used for the simple substitution cipher attack. The difference is that the language statistics are not used in this case. The technique used for mating two transposition cipher keys (to produce two more) is now given:

1. **Notation:** p_1 and p_2 are the parents, c_1 and c_2 are the children, $p_i(j)$ denotes the element j in parent i, similarly, $c_i(j)$ denotes element j in child i, $\{C_i^{j,k}\}$ denotes the set of elements in child i from positions j to k (inclusive) with the limitation that if $i = P + 1$ or $j = 0$ then $\{C_i^{j,k}\} = \emptyset$ (the empty set).

2. Child 1: For $j = 1, \ldots, P$ (step 1) do
   - If $p_1(j) \notin \{C_1^{1,j-1}\}$ then
     - $c_1(j) = p_1(j)$,

     else if $p_2(j) \notin \{C_1^{1,j-1}\}$ then
     - $c_1(j) = p_2(j)$,

     else
     - $c_1(j) =$ random element $\notin \{C_1^{1,j-1}\}$.
3. Child 2: For $j = P, \ldots, 1$ (step -1) do
   - If $p_1(j) \notin \{C_2^{j+1,P}\}$ then
     - $c_2(j) = p_1(j)$,

     else if $p_2(j) \notin \{C_2^{j+1,P}\}$ then
     - $c_2(j) = p_2(j)$,

     else
     - $c_2(j) =$ random element $\notin \{C_2^{j+1,P}\}$.

This mating technique is incorporated with the general genetic algorithm as described in Chapter 2. The same mutation operators as for the simulated annealing attack is utilised. That is, a choice (made at random) between randomly swapping two elements of the key, or rotating the key by a random amount. The algorithm can be described as follows:

1. Inputs to the algorithm are the intercepted ciphertext, the key size (permutation size or period), P, and a score table such as the one in Table 3.7.
2. The solution pool size (M) and the maximum number of generations (or iterations) (MAX_ITER) are set.
3. Generate an initial pool of solutions (randomly) – P_{CURR} – and calculate the cost of each of the solutions in the pool using the score table.
4. For MAX_ITER iterations do:
   (a) Select $M/2$ pairs of keys from P_{CURR} (the current pool) to be the parents of the new generation.

(b) Perform the mating operation described above on each of the pairs of parents to produce a new pool of solutions (P_{NEW}).

(c) For each of the M children perform a mutation by applying the same process as is used in Step 3(b)i of the simulated annealing attack algorithm described above (replace the initial representation of the child (K_{CURR}) with the new one (K_{NEW})).

(d) Calculate the cost associated with each of the keys in the new solution pool – P_{NEW}.

(e) Merge the new pool (P_{NEW}) with the current pool (P_{CURR}) and discard any duplicates in the combined list. Sort the remaining keys – based on the cost function – and choose the best M to become the new current generation (P_{CURR}).

5. Output the best solution from the current key pool (P_{CURR}).

The results of the genetic algorithm approach are given below.

3.3.4 A Tabu Search Attack

In this section an attack on the transposition cipher which utilises the tabu search is outlined. Once again the swapping/rotating mutator is used to generate candidate solutions. In each iteration the best new key found replaces the worst existing one in the tabu list. The algorithm follows:

1. Inputs to the algorithm are the intercepted ciphertext, the key size (permutation size or period), P, and a score table such as the one in Table 3.7.

2. Initialise the algorithm parameters – N_TABU, the size of the tabu list, N_POSS, the size of the list of possibilities considered in each iteration and MAX_ITER, the maximum number of iterations to perform. Initialise the tabu list with random and distinct keys and calculate the cost associated with each of the keys in the tabu list.

3. For MAX_ITER iterations do:

   (a) Find the best key (i.e., the one with the lowest cost) in the current tabu list – call this key K_{BEST}.

(b) For $j = 1, \ldots,$ N_POSS, do:

   i. Apply the perturbation mechanism described in Step 3(b)i of the simulated annealing attack algorithm above (where K_{CURR} = K_{BEST}) to produce a new key (K_{NEW}).

   ii. Check if K_{NEW} is already in the list of possibilities generated for this iteration or the tabu list. If so, return to Step 3(b)i.

   iii. Add K_{NEW} to the list of possibilities for this iteration.

(c) From the list of possibilities for this iteration find the key with the lowest cost – call this key P_{BEST}.

(d) From the tabu list find the key with the highest cost – call this key T_{WORST}.

(e) While the cost of P_{BEST} is less than the cost of T_{WORST}:

   i. Replace T_{WORST} with P_{BEST}.

   ii. Find the new P_{BEST}.

   iii. Find the new T_{WORST}.

4. Output the best solution (i.e., the one with the least cost) from the tabu list.

The experimental results obtained using all three attacks are now presented.

3.3.5 Results

The three techniques were implemented as described above and a number of results were obtained. As with all the results for the classical ciphers, the first comparison is made based upon the amount of ciphertext provided to the attack. These results are presented in Figure 3.9. Here each algorithm was run on differing amounts of ciphertext - one hundred times for each amount. The results in Figure 3.9 represent the average number of key elements correctly placed for a key size of fifteen in this case. Note that because a transposition cipher key which is rotated by one place will still properly decrypt a large amount of the message, a key element is said to be correctly placed if its right hand neighbour is correct. In this manner it is not necessary that the key obtained match exactly the original key but if each of the neighbours in an obtained key are the same as the neighbours for the correct key (except for end positions), then the

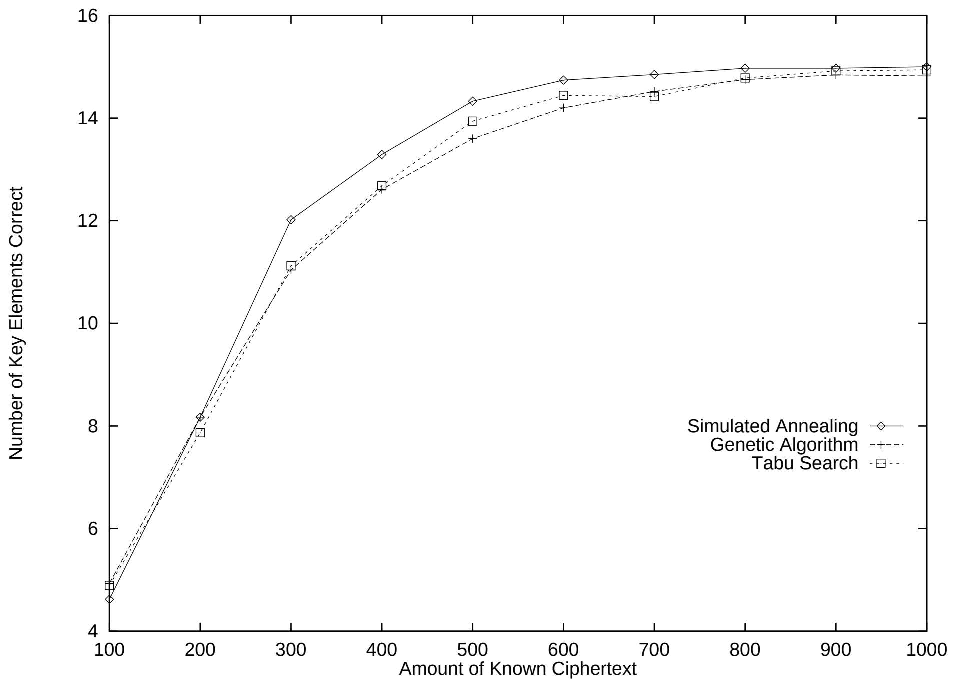


Figure 3.9: The amount of key recovered versus available ciphertext, for transposition size 15.

message will almost certainly still be readable - especially if the period of the transposition cipher is large. It can be seen from the results that each of the three algorithms performed roughly equally when the comparison is made based upon the amount of known ciphertext available to the attack. The mean and standard deviation statistics corresponding to the results in Figure 3.9 (shown in Table 3.8) once again, indicate that simulated annealing consistently finds solutions with the number of correct key elements close to the mean.

As with the simple substitution cipher in Section 3.1.5, the three techniques were also compared using the total number of keys considered and the time taken as a means of comparison. The results are given in Figures 3.10 and 3.11, respectively. The experiments were carried out with a period equal to 15 with 1000 known ciphertext characters. The values in the graphs were obtained by averaging the results from 100 runs of each algorithm. These comparisons give a better indication of which method might be considered most efficient in searching for the solution of a transposition cipher.

Note that the curves in Figures 3.10 and 3.11 are not smooth, particularly for the case of simulated annealing. This can be explained by the fact that for some values on

Amount of	SA		GA		TS	
Ciphertext	$\bar{x}$	s	$\bar{x}$	s	$\bar{x}$	s
100	3.88	2.12	3.78	2.06	3.78	2.08
200	7.27	3.55	6.37	3.24	6.41	3.20
300	11.11	3.69	9.00	3.65	9.18	3.64
400	12.58	3.08	10.81	3.57	10.97	3.60
500	13.84	2.41	11.92	3.10	12.55	3.05
600	14.55	1.44	13.09	2.67	13.17	2.77
700	14.75	0.95	13.33	2.67	13.74	2.32
800	14.85	0.76	13.94	1.95	14.12	1.97
900	14.95	0.41	14.08	1.94	14.37	1.63
1000	14.96	0.38	14.14	1.75	14.51	1.49

Table 3.8: Mean and standard deviation statistics corresponding to the results in Figure 3.9.

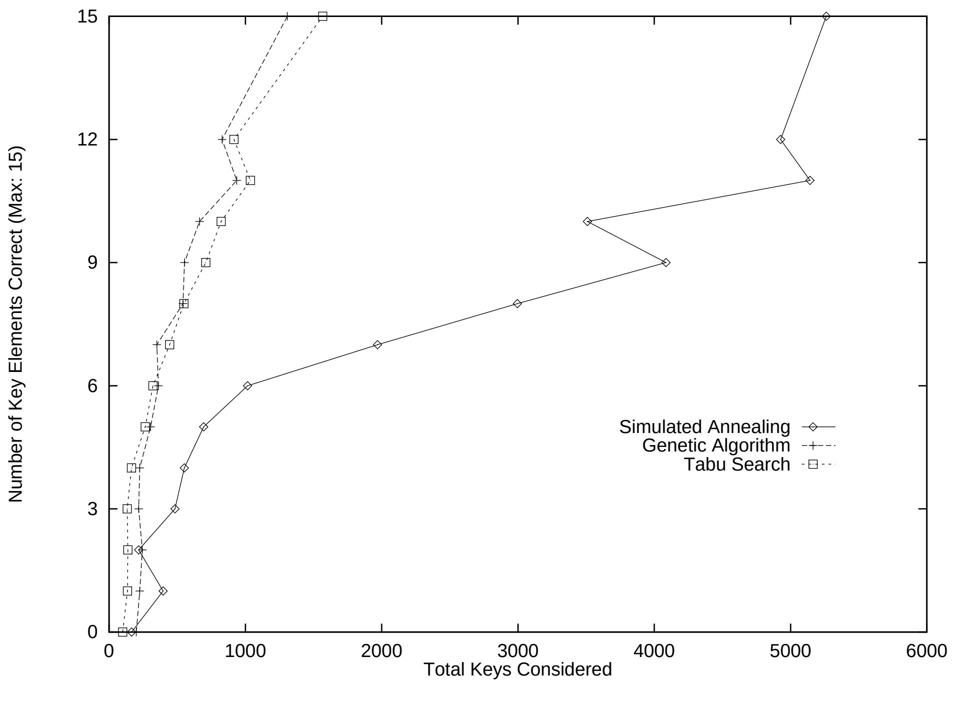


Figure 3.10: The amount of key recovered versus keys considered (transposition size 15).

the vertical axis, there were very few data points available in order to determine a good average for that position. The most noticeable instances are for simulated annealing when the number of correct key elements are 10 and 11. Despite this phenomenon it is still possible to make a direct comparison of the three techniques.

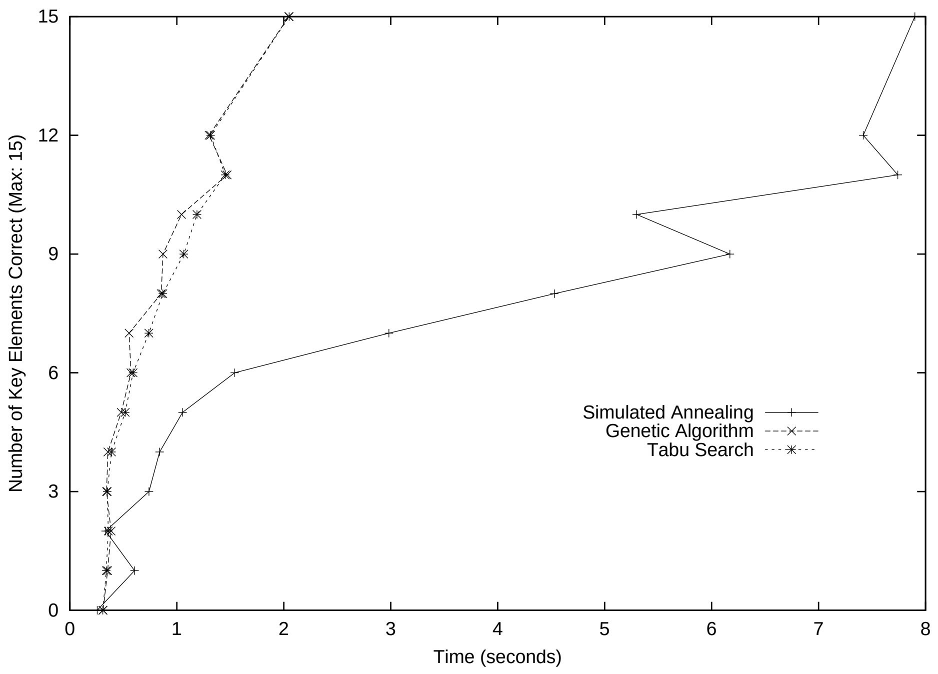


Figure 3.11: The amount of key recovered versus time taken (transposition size 15).

It can be seen that the genetic algorithm and the tabu search perform equally well in this case, however, the simulated annealing algorithm lags in both respects. The comparison based on the number of keys considered by each algorithm shows that the genetic algorithm out-performs even the tabu search. The time comparison, however, shows that the two algorithms required the same amount of time to find the correct solution. This indicates that the genetic algorithm is slower to process the keys than the tabu search. This is is expected since the tabu search does not include the mating process.

Figure 3.12 shows results for the transposition cipher based on the period. It should be noted that for periods less than fifteen, with one thousand available ciphertext characters, each of the algorithms could successfully recover the key all the time. The figure shows that the simulated annealing attack was the most powerful. For a transposition cipher of period 30 the simulated annealing attack was able to correctly place 26 of the key elements, on the average.

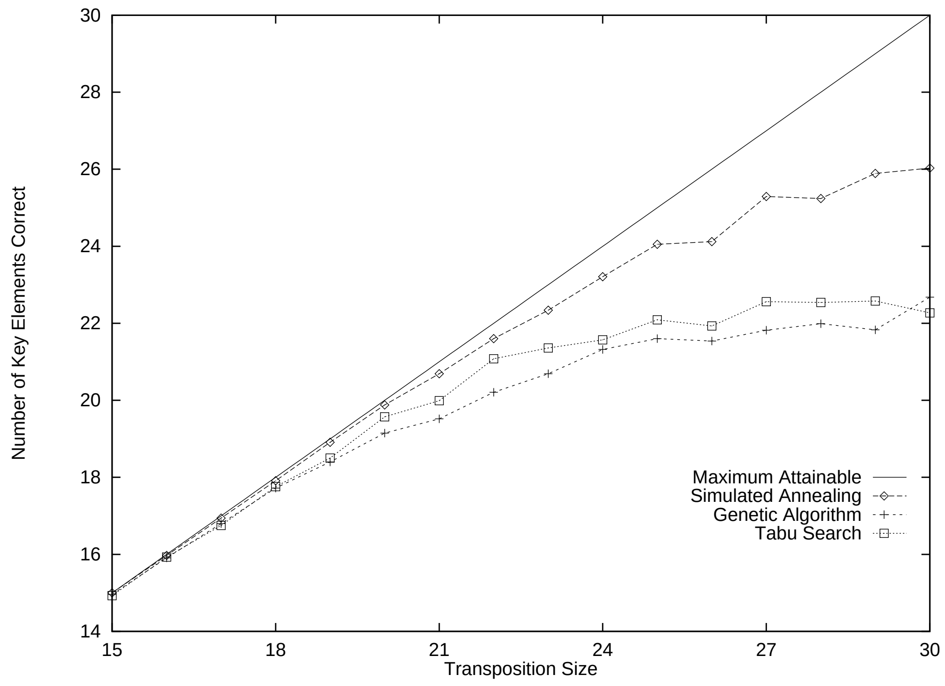


Figure 3.12: The amount of key recovered versus transposition size, 1000 known ciphertext characters.

3.4 Summary

This chapter has developed the theory and presented a number of automated attack methodologies against simple ciphers. In the first instance, properties of these ciphers which make them vulnerable were discussed. The common failing of each of the ciphers described (the simple and polyalphabetic substitution ciphers and the transposition cipher) is that none is sophisticated enough to hide the inherent properties or statistics of the language of the plaintext.

Examples of each of the simple ciphers are given in order to clarify their failings. Also the theory associated with determining the block length of both polyalphabetic substitution ciphers and transposition ciphers is given. These methods are sufficiently effective to allow the assumption that the block length is known in the attacks described for these ciphers.

For simple substitution ciphers and transposition ciphers attacks have been described and implemented using all three of the optimisation heuristics described in Chapter 2. In each case these techniques were found to provide effective automated techniques for the cryptanalysis of the ciphertext. Provided sufficient ciphertext is intercepted by an attacker, each of these algorithms will provide enough information to make the plaintext message understandable.

Comparisons of the three techniques were also made based on the number of keys considered and the time taken by the algorithm. It was found that for the simple substitution cipher the tabu search out-performed both simulated annealing and the genetic algorithm with simulated annealing taking roughly twice as long as the tabu search and the genetic algorithm taking roughly twice as long as simulated annealing. These results differed for the transposition cipher where the tabu search and the genetic algorithm performed equally well and roughly four times faster than the simulated annealing attack. However, the simulated annealing attack on the transposition cipher performed better than the other two techniques on large transposition sizes.

A parallel heuristic for the genetic algorithm is presented along with an associated algorithm for the cryptanalysis of the polyalphabetic substitution cipher. It is shown that this algorithm also gives an accurate indication of the block length used in the encryption process. A parallel technique is desirable considering the efficiency gains obtained from such an approach. The attack described in this chapter effectively reduces the complexity of a polyalphabetic substitution cipher attack to that of a monoalphabetic one (provided a computer with B processing nodes is available).

Overall, optimisation heuristics are ideally suited to implementations in attacks on the classic ciphers. This has been shown by the experimental results in the chapter. The remainder of this dissertation deals with different applications of optimisation heuristics in the fields of cryptanalysis and cryptography.

Chapter 4

Attacks on a Certain Class of Stream Ciphers

In this chapter a number of techniques for the cryptanalysis of a certain class of stream cipher are presented. In the most commonly used stream ciphers a pseudo-random sequence of bits is combined (using modulo 2 addition, or XOR) with the plaintext to produce the ciphertext. The class of stream ciphers being considered here produce a pseudo-random output sequence by the nonlinear combination of the output of a number of linear feedback shift register (LFSR) sequences. A general overview of the LFSR and LFSR-based stream ciphers is given in Appendix B.

Attacks on this class of stream cipher are well known. Meier and Staffelbach [48] and Zeng and Huang [78] are considered the pioneers of attacks on these ciphers. Subsequent to their research, a number of publications appeared which theoretically and experimentally analysed these and other similar attacks (for example, see [10, 54, 55]). All of these techniques have two features in common: an iterative error correction algorithm and a method of obtaining low density parity checks. The fast correlation attack (FCA) introduced by Meier and Staffelbach [48] uses a probability vector and Bayesian bit-by-bit error correction in order to recover the initial LFSR contents. All of the attacks considered in this chapter have as their goal the task of recovering the initial contents (or *seeds*) of the LFSR's using less effort than is required by an exhaustive search.

The fast correlation attack, as proposed by Meier and Staffelbach [48] is described in Section 4.1. This description includes discussion of the probabilistic model used by the attack as well as the concept of parity checks which are central to the algorithm.

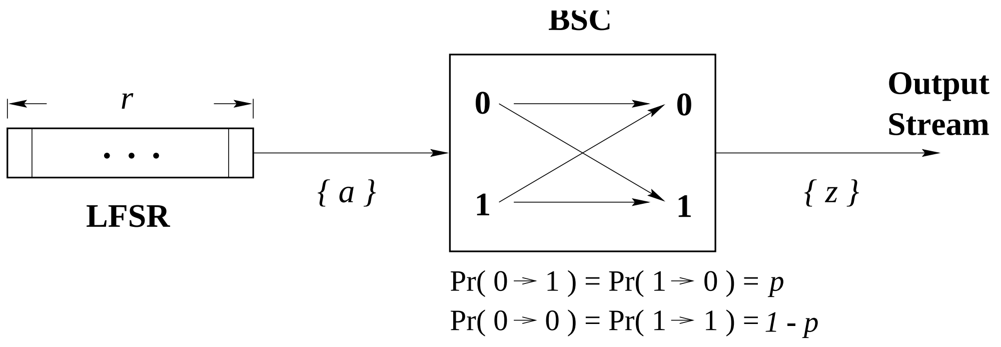

BSC
r
LFSR
{ a }
0
0
1
1
{ z }
Output Stream
Pr(0 -> 1) = Pr(1 -> 0) = p
Pr(0 -> 0) = Pr(1 -> 1) = 1 - p

Figure 4.1: Stream cipher model used by FCA.

In Section 4.2 a number of novel modifications are proposed with the aim of enhancing the fast correlation attack. These new techniques for modifying the basic FCA algorithm incorporate (separately) *resetting*, deterministic probability vector subset updates and probability vector subset updates based on simulated annealing.

The final technique considered in this chapter was proposed by MacKay [40] which uses an approach known as *free energy minimisation*. MacKay's technique, which is described in Section 4.3, was implemented in order that a comparison with the new techniques proposed in Section 4.2 could be made.

Experimental results for the newly proposed algorithms (based on the described modifications) are presented in Section 4.4. Also, a comparison with the free energy minimisation technique described in Section 4.3 is given.

4.1 The Fast Correlation Attack

This section will introduce the concepts associated with Meier and Staffelbach's fast correlation attack [48]. The attack uses a probabilistic model of the stream cipher which is described below. The fast correlation attack also requires a number of parity checks based on the feedback polynomial $f(x)$. Parity checks are also described below, before the overall algorithm description.

4.1.1 A Probabilistic Model

The fast correlation attack is based on the model shown in Figure 4.1 (from [69]), known as a Binary Symmetric (Memoryless) Channel (BSC). The figure shows the output key stream to be represented as a noise-corrupted version of the output of one of the LFSR's. The LFSR sequence is denoted $a = \{a_i\}_{i=1}^N$ and the output keystream sequence is denoted $z = \{z_i\}_{i=1}^N$. Thus $z_i = a_i \oplus e_i$, where $e = \{e_i\}_{i=1}^N$ is a binary noise sequence with the noise probability p defined by Pr$(e_i = 1) = p$ $(i = 1, \ldots, N)$. The LFSR is defined by the feedback polynomial $f(x)$ which is assumed known by the attacker. Let the length of the LFSR be denoted r. The aim of the attack is to reconstruct the LFSR output sequence, $a = \{a_i\}_{i=1}^N$, given the output keystream, $z = \{z_i\},_{i=1}^N$, with the restriction that N, the length of the keystream sequence, be as small as possible, but in the bounds $r < N < 2^r - 1$.

4.1.2 Parity Checks

Central to understanding the fast correlation attack is the concept of a parity check. In terms of a linear feedback shift register sequence, a parity check is any linear relationship which is satisfied by that LFSR sequence. Parity checks correspond to polynomial multiples of the LFSR feedback function $f(x)$ (see [10]). A simple method of generating parity checks is to repeatedly square the primitive feedback polynomial $f(x)$ (as suggested in [48]). However, each time $f(x)$ is squared the length of the required keystream, N, doubles. The keystream sequence can be used more efficiently by applying a polynomial residue method to generate parity checks (see [26]). To find all of the polynomial multiples of a certain weight W and of degree at most M, the residues of the power polynomials $x^m \bmod f(x)$, for all $r < m \leq M$ must first be determined. If the sum of any combination of $W - 1$ residues is equal to one, then the sum of the corresponding power polynomials plus one is a multiple of $f(x)$.

A set of parity checks, derived from polynomial multiples of the feedback function, is known as *orthogonal* if all of the exponents (greater than zero) from the parity checks occur only once. Such a set maximises the number of distinct bits involved in the parity check sums. The set of differences between all possible pairings of exponents of the parity checks is called a full positive difference set if each element of the set is unique. If the exponents form a full positive difference set it is possible to use the W phases of each of the parity check equations. A phase of a parity check is obtained by shifting the coefficients to coincide with the relevant bit (see example below). The number of phases which can be used is bounded by the weight of the parity check polynomial but may also be limited by the number of available bits (especially in the end-regions of the available keystream sequence). Consider the following example.

Example 4.1 *Let a be the output sequence from a LFSR defined by the feedback polynomial $f(x) = 1 + x^3 + x^{31}$. This LFSR has length $r = 31$. Assume that the first 63 bits of the LFSR sequence ($a_0, \ldots, a_{62}$) are known - bits $a_0, \ldots, a_{30}$ are the LFSR seed. Now consider the LFSR feedback polynomial, $f(x)$, to be a parity check polynomial. For bit 32 (a_{31}), it is possible to calculate a parity check sum for each of the three phases of the parity check polynomial. The first phase is realised by calculating $a_0 + a_3 + a_{31}$, the second from $a_{28} + a_{31} + a_{59}$ and the third from $a_{31} + a_{34} + a_{62}$. Each of these equations is obtained by shifting the parity check polynomial coefficients to align with the desired bit (a_{31} in this case) for each of the three possible alignments. Notice that it is not possible to calculate all phases of the parity check $f(x)$ for bits prior to a_{31}.*

The fast correlation attack, which makes use of the above probabilistic model as well as parity checks, is now described.

4.1.3 Attack Description

The technique used by the fast correlation attack is to iteratively update an error probability vector $\mathbf{p} = \{p_i\}_{i=1}^{N}$ based on a set of parity check calculations. Let $\Pi_i = \{\pi_k(i)\}_{k=1}^{|\Pi_i|}$ be a set of parity checks orthogonal on bit $i = 1, \ldots, N$ (where $|\Pi_i|$ denotes the cardinality of the set Π_i). Assume each parity check has the same weight W and let $w = W - 1$. The parity check value is defined as the modulo two sum of output stream bits: $c_k(i) = \sum_{l \in \pi_k(i)} z_l$. Since the noise sequence $e = \{e_i\}_{i=1}^{N}$ is random, so are the parity check values. It was shown by Mihaljević and Golić in [54] that, when the parity checks are orthogonal (as they are in Π_i), the posterior probability for noise bits, given the parity check values, is calculated by Equation 4.1. In Equation 4.1, p_i and q_i denote the posterior and prior probabilities, respectively, for the current iteration of the algorithm; $\overline{c}_l(i) = 1 - c_l(i)$, $q_l(i) = (1 - \prod_{t=1}^{w}(1 - 2q_{m_t}))/2$ and $\{m_t\}_{t=1}^{w}$ denote the set of indices of the bits involved in the parity check $\pi_l(i)$, for any $l = 1, \ldots, |\Pi_i|$ and $i = 1, \ldots, N$.

$$p_i \quad = \quad \Pr(e_i = 1 | \{c_k(i)\}_{k=1}^{|\Pi_i|})$$

$$= \frac{q_i \prod_{k=1}^{|\Pi_i|} q_k(i)^{\bar{c}_k(i)}(1-q_k(i))^{c_k(i)}}{q_i \prod_{k=1}^{|\Pi_i|} q_k(i)^{\bar{c}_k(i)}(1-q_k(i))^{c_k(i)} + (1-q_i)\prod_{k=1}^{|\Pi_i|}(1-q_k(i))^{\bar{c}_k(i)} q_k(i)^{c_k(i)}} \tag{4.1}$$

Initially, each of the p_i is set to the noise probability p, for $i = 1, \ldots, N$. Now, define the error rate $p_e = \sum_{i=1}^{N} p_i/N$. In the first iteration an optimal Bayesian decision is made which minimises the symbol error rate, p_e. In the following iterations the error rate almost always decreases for two reasons: the algorithm introduces error correction of the observed keystream sequence, and recycling of the probability vector (self-composition) causes the probabilities to decrease. Often, after a number of iterations, the algorithm becomes trapped in the region of a local minimum and the error correction of the keystream ceases. When this occurs it is possible to continue the algorithm by replacing the probability vector values with p, the noise probability (which it was initially). This process is called *resetting* which enhances the error correction capability of the algorithm and increases the overall number of satisfied parity checks. The set of iterations which occur between resets are referred to as a *round*. An algorithmic description of the fast correlation attack follows:

1. The inputs to the algorithm are the observed keystream sequence **z** $= \{z_i\}_{i=1}^{N}$, the noise probability p and a set of orthogonal parity checks $\Pi_i = \{\pi_k(i)\}$, $i = 1, \ldots, |\Pi_i|$.

2. Define j to be the number of iterations with no change in the number of satisfied parity checks and k to be the current round index. Initialise algorithm parameters: $j = 0$, $k = 0$, the maximum number of rounds k_{MAX}, the maximum number of iterations with no change in the number of satisfied parity checks j_{MAX}, and the minimum error rate ϵ.

3. Set the prior probabilities $q_i = p$, $i = 1, \ldots, N$ (**reset**). Increment k, the round index. If $k > k_{\text{MAX}}$ go to Step 5.

4. Repeat:

   (a) Calculate the parity checks $c_l(i)$ for each bit of the keystream sequence, i.e., z_i, $l \in \pi_k(i)$, $i = 1, \ldots, N$. If all parity checks are satisfied, go to Step 5. If the number of satisfied parity checks has not changed, increment j. If $j > j_{\text{MAX}}$, go to Step 3.

(b) Using Equation 4.1, calculate the posterior probabilities p_i, $i = 1, \ldots, N$.

(c) For $i = 1, \ldots, N$, if $p_i > 0.5$ then set $z_i = z_i \oplus 1$ and $p_i = 1 - p_i$.

(d) Make the posterior probabilities of the current iteration the prior probabilities for the next iteration. That is, $q_i = p_i$, $i = 1, \ldots, N$.

(e) Calculate $p_e = \sum_{i=1}^{N} p_i/N$. If $p_e < \epsilon$ go to Step 3.

5. Set $a_i = z_i$, $i = 1, \ldots, N$. Output $\{a_i\}_{i=1}^{N}$ which represents the reconstructed LFSR sequence and stop.

Notice that the algorithm incorporates two stopping conditions to prevent it from iterating infinitely. One of the stopping conditions is that all the parity checks are satisfied. This is the desired result from the algorithm although having all parity checks satisfied does not necessarily imply that the correct LFSR sequence will be obtained. The second stopping condition limits the number of rounds that the algorithm will perform. If the algorithm converges to a non-optimal solution (i.e., not all parity checks are satisfied), it will reset forever. To prevent this a maximum number of resets is imposed.

4.2 Modifications to the FCA Providing Enhancement

In this section a number of modifications are made to the basic fast correlation attack algorithm (as described in the previous section) in order to gain some improvement. These techniques are new and have not previously been recorded in the literature. Three different types of modifications were made which are described in detail in the following sections. The first technique, called *fast resetting* operates by forcing a reset when a certain number of bits in the output sequence (**z**) have been complemented. The second and third techniques are similar and involve updating subsets of the probability vector (**p**) in each iteration - rather than all N values. The first of the subset update techniques makes a deterministic choice based on certain conditions. The second utilised simulated annealing to make random and deterministic probability updates.

4.2.1 Fast Resetting

It was found that by increasing the rate at which a reset occurs the number of satisfied parity checks can be improved further. This technique, which is termed *fast resetting*, requires that a reset occur after a certain number of complementations to the output keystream have occurred. Note that complementations occur in the algorithm of Section 4.1 above, when any of the posterior probabilities exceed one half (0.5). By keeping track of the number of complementations that have occurred, and forcing a reset when this number exceeds some threshold, C, the effectiveness of the algorithm is improved. The value of C depends on a number of factors, namely the noise probability, p, the keystream sequence, **z**, and the set of parity checks being used, Π.

Complementations occur in Step 4c of the fast correlation attack algorithm description above. However, as was shown in [75], these complementations are ineffective due to the transformation $p_i \to 1 - p_i$. The complementations become effective only after resetting, where such a transformation does not take place. This is less likely to occur if the error rate approaches zero. Accordingly, it is expected that the performance will improve if the resetting is performed before the error rate falls below a threshold, or, similarly, when the cumulative number of complementations in a round exceeds some threshold.

It should be noted that not all of the complementations may be correct and the algorithm may introduce new errors to the keystream sequence **z**.

The algorithm described above can be modified to include fast resetting by making an additional check in Step 4e. Step 4e checks to see if the error rate has dropped below a certain bound and, if so, the algorithm resets. For the case of fast resetting, the algorithm should also reset if the cumulative number of complementations in the current round exceeds a predefined threshold, C. In other words, Step 4e should now read:

4(e) Calculate $p_e = \sum_{i=1}^{N} p_i/N$. If $p_e < \epsilon$ or the cumulative number of complementations $> C$, go to Step 3.

4.2.2 Deterministic Subset Selection

When considering methods of modifying the fast correlation attack in order to make it more effective, the cases which fail for the unmodified attack are of most interest. The fast correlation attack in its original state usually fails due to a high noise probability combined with the limited availability of suitable parity checks. The updates to the error probability vector, **p** (Step 4b), and the consequent keystream bit complementations (Step 4c) in the fast correlation attack described above tend to reduce the overall error probability, p_e. However, if the initial noise probability, p, is high, the reduction in the error rate is mostly due to the self-composition property of the probability update equation, and not the increase in the number of satisfied parity checks.

It is hypothesised that this problem can be avoided by selecting a subset of the N probabilities in **p**, of size L, and only updating those probabilities for the given iteration. This will tend to make the complementations more reliable in increasing the number of satisfied parity checks. The criteria used to select the L positions which will be updated may be based upon a variety of factors. The $N - L$ positions which are not updated in the given iteration may either remain unchanged (called a *partial update*) or they may be reset to the initial noise probability, p (referred to as a *partial reset*).

In the experiments performed three different criteria were tested for the selection of the L update positions. They are:

1. Calculate $|p_i - q_i|$, $i = 1, \ldots, N$, in each iteration and select the L positions with the highest absolute difference.

2. Choose the L positions with the lowest posterior probabilities, p_i, $i = 1, \ldots, N$.

3. Choose the L positions with the highest number of satisfied parity checks.

Each of these techniques is designed to accentuate the aim of increasing the number of satisfied parity checks rather than minimising the error rate which does not always guarantee that the number of satisfied parity checks will increase.

The necessary modifications to the algorithm are now detailed. The modifications involve an additional step of determining which of the L probabilities will be updated. Also, depending on whether a partial update or partial reset is being performed, the updating of the posterior probabilities will be affected as follows:

4(d) According to the chosen criterion, select L positions for update. For those L positions, make the posterior probabilities of the current iteration the prior probabilities for the next iteration. Depending upon whether partial updates or partial resetting is being used, the remaining $N - L$ probabilities will remain unchanged or be set to p.

4.2.3 Probability Updates Chosen Using Simulated Annealing

Another alternative when considering modifications to the fast correlation attack is the use of a pseudorandom search heuristic (such as the ones introduced in Chapter 2 of this thesis) instead of the deterministic approach outlined in the section above. It has been shown, in Chapter 3, that such techniques may provide an effective method of automating the cryptanalysis task. In this section a number of techniques based on random changes to the probability vector, **p**, and the output keystream, **z**, are considered.

Simulated annealing is the most appropriate algorithm for testing modifications to the fast correlation attack because the technique maintains only a single solution at any one time - and not a pool of solutions as in the genetic algorithm, or a tabu list as in the tabu search. The objects which are to be manipulated in the case of the fast correlation attack are the probability vector and the reconstructed keystream sequence. In general these vectors are large (10000 for experiments here), so maintaining and manipulating lists of these vectors is impractical and leads to prohibitive computational complexity of the attack.

As is always the case for simulated annealing, a cost function is required. The aim of this attack is to minimise the Hamming distance between the reconstructed LFSR output sequence and the actual LFSR sequence. Since the actual LFSR sequence is unknown a cost function which closely mimics this relationship is desired. There are two obvious possibilities for a cost function - the error rate, p_e, and the number of unsatisfied parity checks. The error rate tends to be minimised by the fast correlation attack algorithm due to its self-composition property. When the algorithm can correct almost all of the errors, the error rate gives an indication of the relative number of errors in the reconstructed keystream sequence. The error rate gives an error prediction based on the probability that each bit in the reconstructed sequence is correct. The second choice of cost function, i.e., the number of unsatisfied parity checks was found, experimentally, to be less effective due to its poor correlation with the Hamming distance measure described above.

Three possibilities for random modifications to the fast correlation attack algorithm were considered:

1. **Random Subset Selection:** The justification for this technique is the same as that proposed for deterministic subset selection in the previous section. That is, when the noise probability, p, is high the algorithm is more likely to become trapped in the region of a local minimum. Similar to the deterministic subset selection technique, this method involves updating a subset of the probability vector in each iteration. However, in this case, the subset is randomly chosen. The Metropolis criterion of the simulated annealing algorithm is used to decide if a proposed probability value should be updated. Recall that the Metropolis criterion accepts updates which lead to a poorer value of the cost function, based on the temperature parameter, T, which reduces over time. The expected effect of this on the fast correlation attack is that probability updates which cause the cost function to increase (worsen) are allowed with probability which decreases as the algorithm progresses. For this particular technique, it is worthwhile to note that when the number of unsatisfied parity checks is used as a cost function, the cost value will only change if the corresponding probability update forces the probability to exceed one half (0.5). In this case the corresponding bit in the keystream sequence will be complemented causing a change in the number of unsatisfied parity checks.

2. **Random Subset Complementation:** The problem present in random probability updates - that the parity checks only change when an updated element of the probability vector causes a complementation in the keystream sequence - can be avoided by bypassing the probability vector and simply complementing random elements of the keystream sequence, regardless of whether or not the corresponding probability was forced over one half in the probability update phase. If only a small number of positions in the keystream vector are complemented, then this technique has the potential to be powerful. The number of errors introduced is kept to a minimum by using the Metropolis criterion to ensure that the cost function is usually decreasing.

3. **Combined Deterministic Subset Selection and Random Subset Complemen-**

tation: As a final alternative, a method involving deterministic subset selection (as described in the previous section) and random keystream complementation is proposed. This technique involves the update of elements of the probability vector using one of the three criteria described previously, followed by the complementation of a small number of elements in the keystream sequence. The probability with which bits are complemented reduces over time - due to the annealing temperature in the Metropolis criterion. The desired effect of this is to reduce the number of incorrect complementations as the algorithm progresses towards an optimal solution.

Results for the algorithm modified using simulated annealing are given in Section 4.4 of this chapter.

4.3 Free Energy Minimisation

In this section an alternate algorithm - which is closely related to the fast correlation attack - called *free energy minimisation* (FEM) is introduced. MacKay, in [40], has proposed this technique for the cryptanalysis of the types of cipher being considered in the chapter - namely the LFSR based stream cipher with a nonlinear combiner. In the results section of this chapter a comparison of MacKay's free energy minimisation technique with the modified Meier-Staffelbach algorithms described above, is given.

MacKay presents an algorithm for solving a class of problems which can be represented in the form $(As + n) \bmod 2 = r$, where s is a binary vector of length N, n and r are binary vectors of length M and A is a binary matrix. The problem, then, is to solve for s given A and r. The algorithm is based on the "variational free energy minimisation method". Only an overview of this method will be included. For a more thorough discussion of this method the reader is referred to MacKay's paper. When applied to a fast correlation attack, s denotes the unknown LFSR output sequence, r contains M parity check values and n is essentially ignored (let it gradually approach 0). The matrix A has as its rows all the parity checks for each bit position.

The problem is parameterised by a real valued vector θ of length N. Then q_n^1 and q_n^0 are defined as follows:

$$q_n^1 = \frac{1}{1+e^{-\theta_n}} \tag{4.2}$$

$$q_n^0 = \frac{1}{1+e^{+\theta_n}} \tag{4.3}$$

for $n = 1, \ldots, N$. It follows that q_n^1 and q_n^0 are related so that $\theta_n = \log(q_n^1/q_n^0)$. A constant

$$b = \log\left(\frac{p}{1-p}\right) \tag{4.4}$$

is called the *bias* constant, where p is the noise probability. Let g be a $(1, -1)$ binary encoding of the parity check vector (or syndrome vector) $r = Az$, obtained from the observed keystream sequence. Probabilities $p_{m,\nu}^1$ and $p_{m,\nu}^0$ are defined as the probability that the partial sum $\sum_{n=1}^{\nu} A_{m,n}s_n \bmod 2$ is equal to 1 and 0, respectively. These probabilities

$$\begin{aligned}
&\left.\begin{aligned} p_{m,\nu}^1 &= q_\nu^0 p_{m,\nu-1}^1 + q_\nu^1 p_{m,\nu-1}^0 \\ p_{m,\nu}^0 &= q_\nu^0 p_{m,\nu-1}^0 + q_\nu^1 p_{m,\nu-1}^1 \end{aligned}\right\} \quad \text{if } A_{m,\nu} = 1 \\
&\left.\begin{aligned} p_{m,\nu}^1 &= p_{m,\nu-1}^1 \\ p_{m,\nu}^0 &= p_{m,\nu-1}^0 \end{aligned}\right\} \quad \text{if } A_{m,\nu} = 0
\end{aligned} \tag{4.5}$$

have the initial condition $p_{m,0}^1 = 0$ and $p_{m,0}^0 = 1$. Similarly, let $r_{m,\nu}^1$ and $r_{m,\nu}^0$ be the probabilities that the partial sum $\sum_{n=\nu}^{N} A_{m,n}s_n \bmod 2$ is equal to 1 and 0, respectively. They are obtained by an analogous reverse recursion of (4.5).

The free energy is broken into three terms: *likelihood energy*, *prior energy* and *entropy*:

$$F(\theta) = E_L(\theta) + E_P(\theta) - S(\theta) \tag{4.6}$$

where

$$E_L(\theta) = -\sum_m g_m p_{m,N}^1 \tag{4.7}$$

$$E_P(\theta) = -\sum_n b q_n^1 \tag{4.8}$$

$$S(\theta) = -\sum_n \left(q_n^0 \log q_n^0 + q_n^1 \log q_n^1\right). \tag{4.9}$$

It can be shown that the derivative of the free energy is given by:

$$\frac{\partial F}{\partial \theta_n} = q_n^1 q_n^0 \left(\theta_n - b - \sum_m g_m d_{m,n}\right) \tag{4.10}$$

where

$$\begin{aligned} d_{m,n} &= (p^1_{m,n-1}r^1_{m,n+1} + p^0_{m,n-1}r^0_{m,n+1}) - \\ &\quad (p^1_{m,n-1}r^0_{m,n+1} + p^0_{m,n-1}r^1_{m,n+1}). \end{aligned} \tag{4.11}$$

By setting the derivative to zero a "re-estimation optimiser" is obtained which defines a recursive update procedure for the θ parameter. MacKay introduces an "annealing" parameter β which gradually increases as the algorithm progresses. Its purpose is to prevent the search from heading too quickly into a local minimum. It should be noted that the annealing procedure is deterministic unlike some other annealing procedures (such as the simulated annealing approach). The θ vector is then updated according to

$$\theta_n = b + \beta \sum_m g_m d_{m,n}, \quad n = 1, \ldots, N. \tag{4.12}$$

The free energy minimisation algorithm, as implemented, is now described in detail:

1. Algorithm inputs are: syndrome vector r, parity check matrix A, the noise probability p, the initial value for β (β_0), the scaling factor for β (β_f), the maximum value for β (β_{MAX}) and the maximum number of iterations.

2. Set number of iterations = 0, $\beta = \beta_0$,

$$g_m = \begin{cases} +1 \text{ if } r_m = 1 \\ -1 \text{ if } r_m = 0 \end{cases}, \quad m = 1, \ldots, M$$
$$b = \theta_n = \log\left(\frac{p}{1-p}\right), \quad n = 1, \ldots, N$$
$$\left.\begin{array}{l} p^1_{m,0} = r^1_{m,0} = 0 \\ p^0_{m,0} = r^0_{m,0} = 1 \end{array}\right\}, \quad m = 1, \ldots, M.$$

3. Update q^1_n, q^0_n, $n = 1, \ldots, N$, by using (4.2) and (4.3).

4. (Forward Pass) Update $p^1_{m,n}$ and $p^0_{m,n}$, $m = 1, \ldots, M$, and $n = 1, \ldots, N$, according to the recursion (4.5).

5. (Reverse Pass) Update $r^1_{m,n}$ and $r^0_{m,n}$ this time using (4.5) in the reverse order, i.e., $m = M, \ldots, 1$ and $n = N, \ldots, 1$.

6. Update each $\theta_n, n = 1, \ldots, N$, by calculating the gradient and using equation (4.12).
7. Increment the number of iterations.
8. Calculate the free energy using (4.6). If the energy has decreased since the previous iteration return to Step 3.
9. Scale β by β_f, i.e., let $\beta = \beta \times \beta_f$. If $\beta < \beta_{max}$ and the number of iterations is less than the maximum, return to Step 3.
10. Output the noise sequence as determined from θ as follows: if $\theta_n > 0$ output 1, otherwise output 0, for $n = 1, \ldots, N$. The LFSR sequence can be obtained as the modulo 2 sum of the output noise sequence and the observed keystream sequence.

The free energy minimisation technique was compared with the fast resetting algorithm described in Section 4.2.1 of this chapter. The results are given below.

4.4 Experimental Results

In this section a number of experimental results are presented. The results can be broken into two sections. The first section deals with the modifications to the fast correlation attack proposed by Meier and Staffelbach in [48]. These results show the differing levels of improvement obtained by these modifications. The second results section presents a comparison of the fast correlation attack, modified with fast resetting, with the free energy minimisation technique.

4.4.1 Modifications to FCA

Many of the parameters for tests on the modified fast correlation attack were fixed. The shift register length was chosen to be 31 with the defining LFSR polynomial $f(x) = 1 + x^3 + x^{31}$ (weight 3). The length of known keystream was set to 10000 bits and five orthogonal parity check equations corresponding to a full positive difference set were obtained by repeated squaring of the feedback polynomial $f(x)$. Thus, the maximum degree of the parity checks was 496. For as many bits of the keystream as possible (approximately 90%), all three phases of the parity checks were used. For the remaining bits as many phases as possible were utilised.

Results of the modified algorithm with fast resetting show a considerable improvement over the basic algorithm with slow resetting for relatively high initial error probabilities. It was also found that partial resetting with deterministic subset selection out-performed the fast resetting technique. These results can be observed in Figure 4.2.

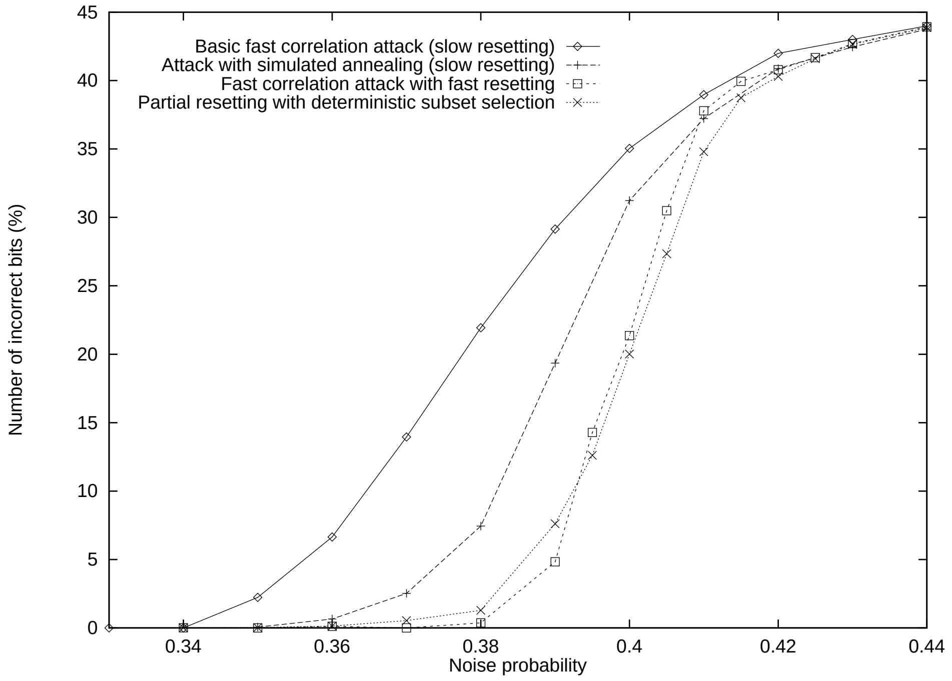


Figure 4.2: Comparative results for the fast correlation attack.

Results for the algorithm adapted for simulated annealing were varied. It was found that a cost function based on the error rate, rather than the number of satisfied parity checks was far more effective. This is because the number of unsatisfied parity checks does not correlate very well with the Hamming distance from the LFSR sequence. Also, the algorithm which updates probabilities at random outperforms the algorithm which complements bits at random.

Figure 4.2 shows how the attack combined with simulated annealing and slow resetting compared with the other modified algorithms. It can be seen that the simulated annealing technique significantly out-performed the basic fast correlation attack. Since the attacks modified with fast resetting and partial resetting each performed better than the simulated annealing algorithm with slow resetting, it is interesting to observe the performance of the attack modified with simulated annealing when combined with the fast resetting technique.

The results in Figure 4.3 give a comparison of the basic fast correlation attack with fast resetting and the two algorithms modified with simulated annealing. It can be seen that for noise probabilities greater than 0.4 the fast correlation attack with simulated annealing and fast resetting performed slightly better that the fast correlation attack alone. However for the lower noise probabilities the addition of the simulated annealing to the attack was less beneficial.

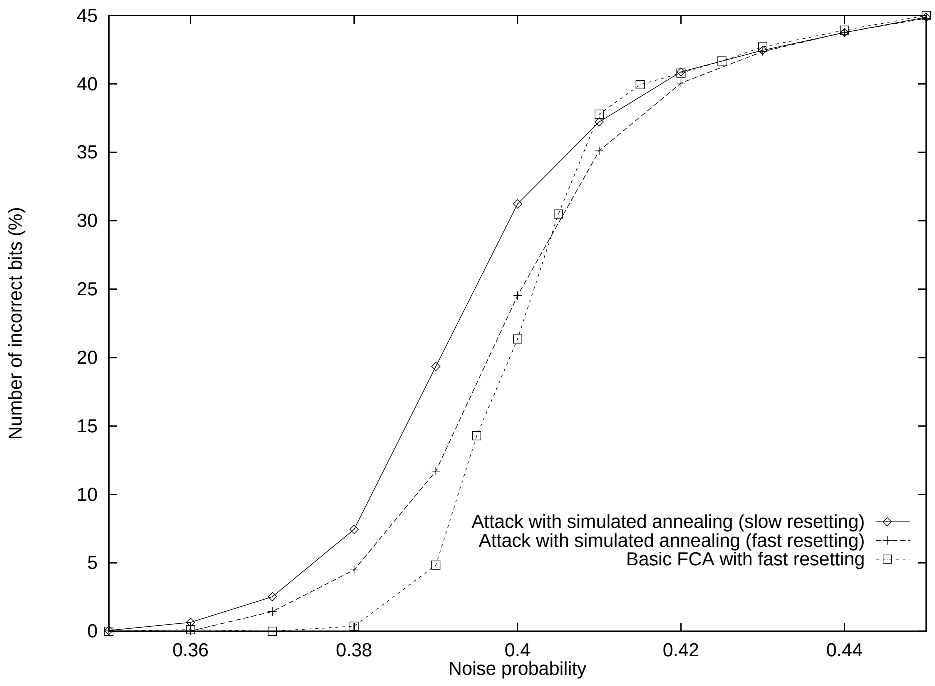


Figure 4.3: Comparative results for fast correlation attack modified with simulated annealing.

Because of the complexity added by the annealing algorithm, combined with the limited improvement that it gained over the fast resetting technique, the annealing approach is not considered in the following section which compares the fast resetting technique with a technique which was proposed by MacKay, namely free energy minimisation, which was described above in Section 4.3.

4.4.2 FCA versus FEM

In this section experimental results are presented for the fast correlation attacks based on the basic fast correlation attack, the attack modified with fast resetting and a free energy minimisation algorithm. All results are averaged over 50 different noise samples. Shift registers using three different characteristic polynomials are used. In each case the number of taps is different (two, four and six). The chosen polynomials are all primitive and are given in Table 4.1.

Number of taps	LFSR length	Primitive characteristic polynomial
2	31	$1 + x^3 + x^{31}$
4	50	$1 + x^2 + x^3 + x^4 + x^{50}$
6	72	$1 + x + x^2 + x^3 + x^4 + x^6 + x^{72}$

Table 4.1: Characteristics of shift registers used in experiments.

For each trial, 10000 bits of observed keystream sequence are used. The characteristic polynomials were deliberately chosen to produce a set of non-orthogonal parity checks (different phases are not orthogonal) to test the robustness of the attacks, since the fast correlation attack requires that the parity checks be orthogonal while the free energy minimisation algorithm does not.

The best value for the variable threshold C in the fast resetting algorithm was determined experimentally. In the case of two taps, C was chosen to be 10. For the shift registers with four and six taps a value of 100 was used for C. For the free energy minimisation algorithm the values suggested in [40] were used: $\beta_0 = 0.25$, $\beta_f = 1.4$ and $\beta_{max} = 4$. Both algorithms used the same set of parity checks for each of the respective characteristic polynomials. The parity checks were obtained simply by repeated squaring of $f(x)$ until a polynomial with the maximum degree not exceeding $N - 1$ (in this case 9999) is found. The number of parity checks in each case is equal to $\lfloor \log_2(N-1)/r \rfloor + 1$ where r is the degree of $f(x)$. For shift registers of lengths 31, 50 and 72 the numbers of parity checks are 9, 8 and 8, respectively. As suggested in [48], all the phases of the parity checks are utilised. However, in the end regions only some of the phases can be used. In this case as many phases of the parity checks as possible were used.

For each test, two sets of results were obtained. The first involved finding the minimum Hamming distance between the actual LFSR output and the solution that each algorithm found. This gives an indication of how close the algorithm is getting to the actual solution. The second test makes use of error free information sets. A sliding window technique [53] is used in which a search for r consecutive bits satisfying the characteristic polynomial is made (r is the shift register length). If r such bits can be found, then the attack is deemed successful.

It is clear from each of Figures 4.4 to 4.6 that the fast resetting algorithm outperforms MacKay's free energy minimisation algorithm for each considered number of taps. It can also be seen that the free energy minimisation algorithm performs better than the basic correlation attack algorithm if the number of taps increases. The two testing techniques, minimum Hamming distance and error free information sets, appear to correlate well with the results being consistent in all the cases except when the number of taps is six and the probability is 0.26. Here the Hamming distance result shows fast resetting to be superior but the result obtained using the information set technique shows the free energy minimisation algorithm to be (just slightly) better.

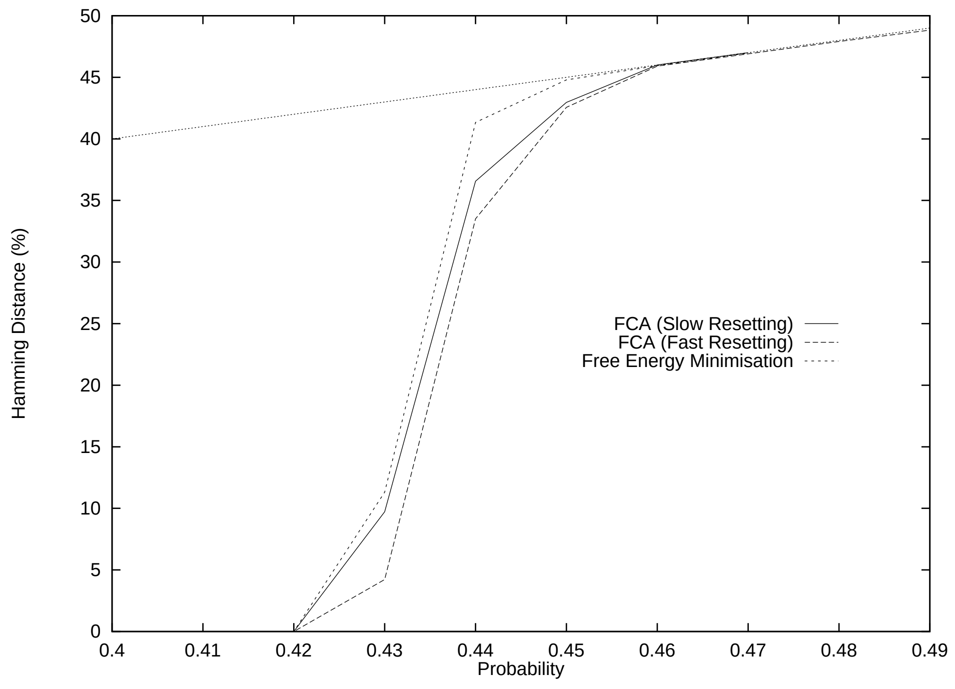
According to [55], the critical noise probability beyond which successful iterative error correction is not possible can be approximated (the exact expression can be found in [55]) as

$$p_{\mathrm{cr}} = \frac{1 - M_w^{\frac{1}{w-1}}}{2} \tag{4.13}$$

where M_w is the average number of parity checks (of weight $w+1$) per bit used in the algorithm. This is of particular interest for the original fast correlation attack with slow resetting and orthogonal parity checks. In the three cases examined, $M_2 = 22.248$, $M_4 = 33.625$ and $M_6 = 43.148$, so that p_{cr} is then given as 0.477, 0.345 and 0.265, respectively. These noise probabilities are in accordance with the experimental results shown in Figures 4.4 to 4.6. So, if $p > p_{\mathrm{cr}}$, then the fast correlation attacks are bound to fail on the average. However, it may be possible to extend the set of low weight parity checks by using techniques other than repeated squaring (see [26]) which in turn increases the critical noise probability.

4.5 Summary

In this chapter a number of approaches for attacking a certain stream cipher model, namely the one in Figure 4.1, have been considered. In the introduction an overview of these ciphers was given, along with a description of the fast correlation attack as proposed by Meier and Staffelbach [48].



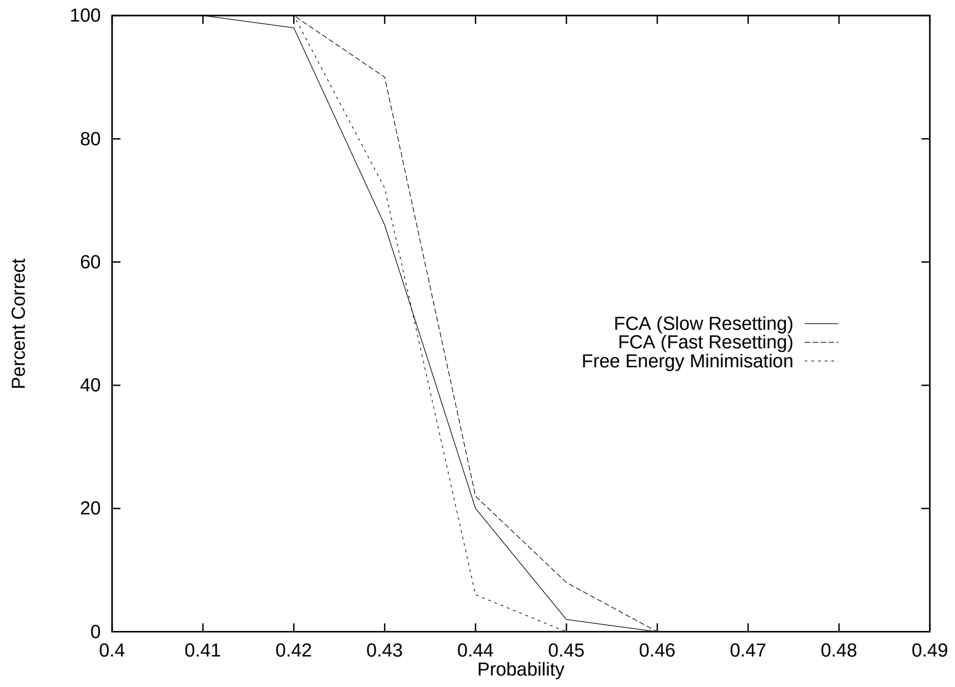


Figure 4.4: Results for a shift register with 2 taps.

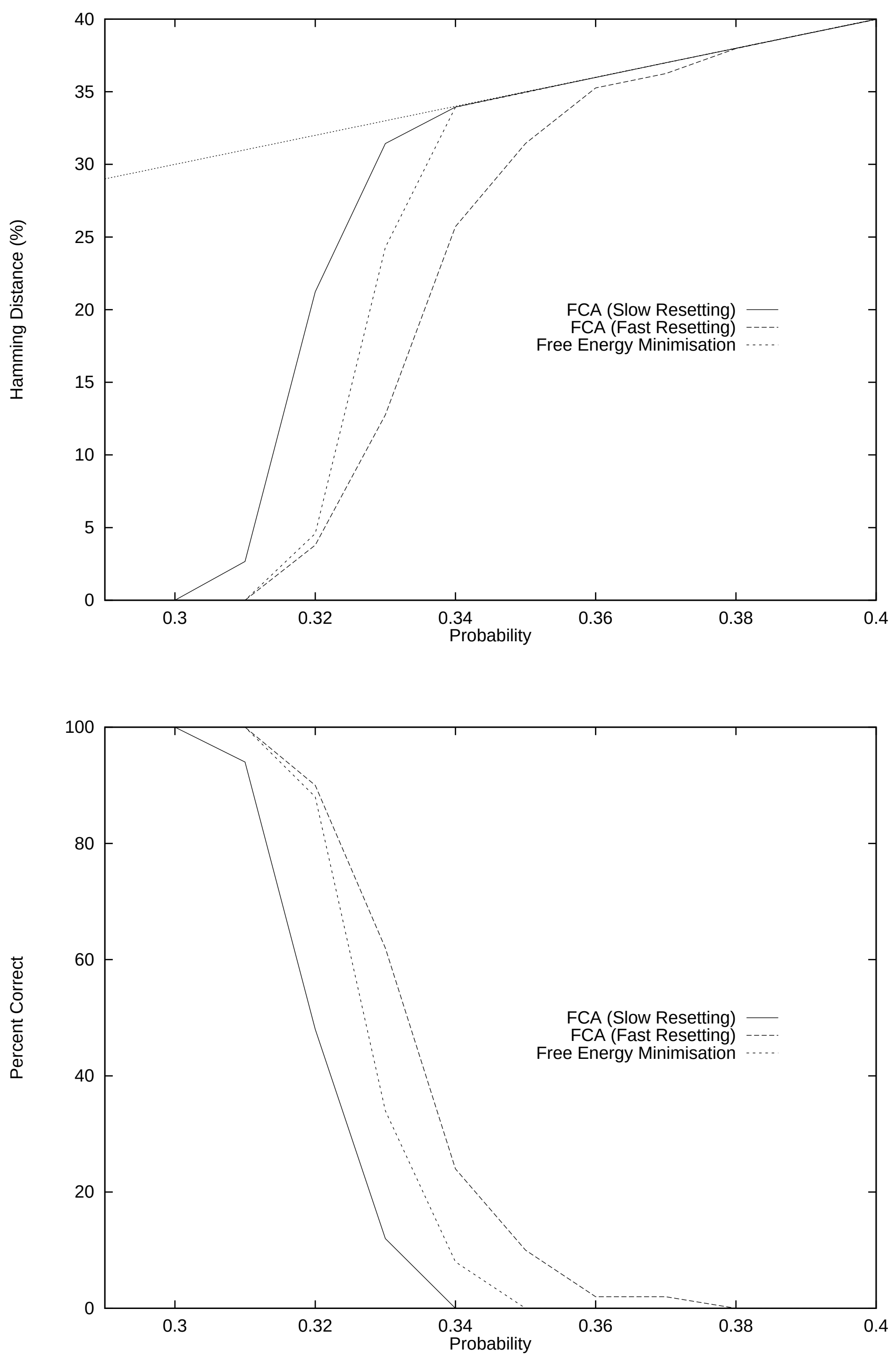
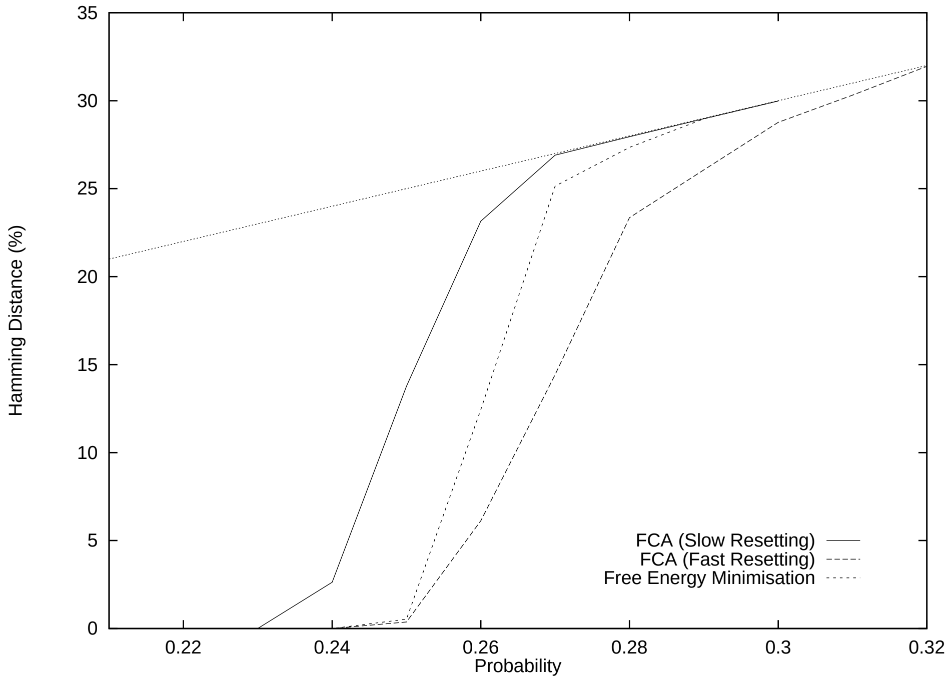


Figure 4.5: Results for a shift register with 4 taps.



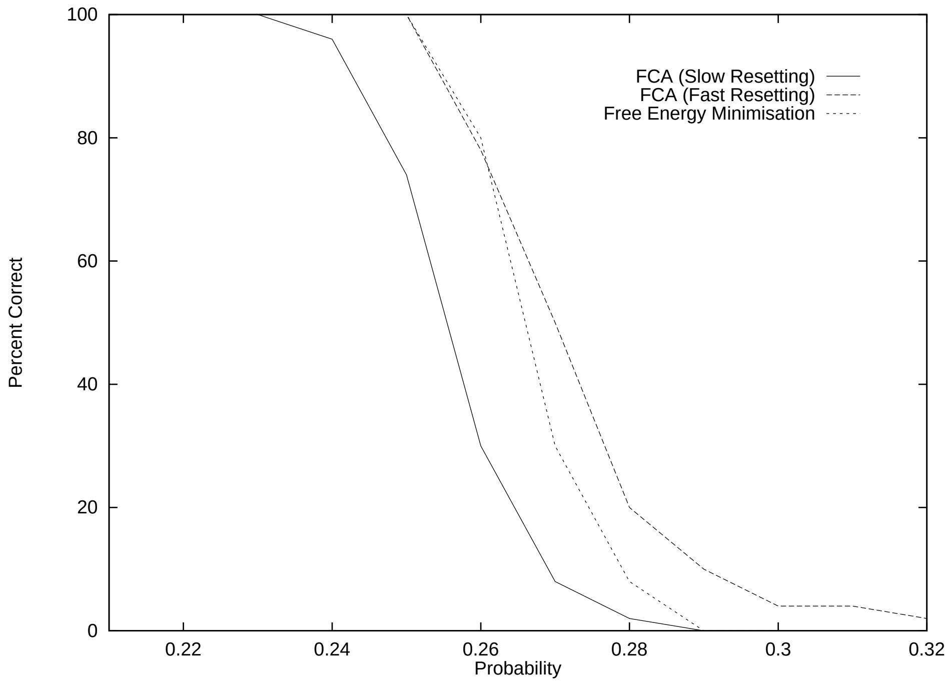


Figure 4.6: Results for a shift register with 6 taps.

Several modifications were suggested which allows the fast correlation attack to recover initial LFSR contents for ciphers with a higher noise probability than the original search allowed. This has been shown in the experimental results. The fast resetting technique provides significant improvement by preventing the algorithm from arriving at a locally minimum solution. Similarly, by updating a subset of the probability vector in any iteration, using either deterministic techniques or a random selection, it was found that higher noise probabilities could be compromised.

In a further experiment, simulated annealing was used in combination with the fast correlation attack in an attempt to attack even greater noise probabilities. While this technique provided a significant improvement of the basic algorithm as published by Meier and Staffelbach, it was found to not significantly improve the other modifications outlined - that is, fast resetting alone and deterministic and random probability updates.

Chapter 5

The Knapsack Cipher: What Not To Do

The success of the approximate algorithms which were presented in Chapter 2 is dependent upon the availability of a suitable solution evaluation mechanism. Such a mechanism (a fitness function or a cost function) must accurately assess every feasible solution giving an indication of its optimality - i.e., how close it is to the optimal solution. In this chapter an example of a problem for which no suitable solution assessment exists is presented. The problem in question is the *knapsack* problem. Spillman [71] presented a genetic algorithm which he claimed could solve large instances of the knapsack problem. This chapter shows that such an approach has little merit, due to the lack of a suitable fitness function.

A description of the Merkle-Hellman cryptosystem is given in Appendix C. The processes of encryption and decryption are outlined, along with the method used to generate the public/private key pair. The Merkle-Hellman cryptosystem was shown to be insecure in the early 1980's by Shamir [68]. Details of Shamir's attack which is based upon the structure of the secret key is given in Appendix C.

The attack proposed by Spillman uses an entirely different approach. Rather than attacking the structure of the secret key, Spillman's approach was to determine the original message by finding the elements of the public key which were added together to obtain the ciphertext. In Section 5.1 the fitness function which was suggested by Spillman [73] is analysed and an alternative proposed. It will be shown that there is no truly suitable fitness function for attacks on the knapsack cipher using the technique discussed in this chapter. Section 5.2 presents an algorithm similar to the one proposed by Spillman [73] for attacking the knapsack cipher using the genetic algorithm. This attack was implemented in order to obtain some experimental results which provide evidence for the argument presented in this chapter. Section 5.3 provides some results of the attacks. The results highlight the futility of approximate algorithms in attacks on the knapsack cipher.

5.1 A Fitness Function for the Knapsack Cipher

To solve NP-complete problems such as the subset sum problem using genetic algorithms, it is important to be able to accurately assess any feasible solution. To determine the suitability of a given solution we use what is known as a *fitness function*. In this section the fitness function suggested from [71] is described. It is shown how to adapt this to a more suitable fitness function.

If we think of a solution to the knapsack cipher as being represented by a binary string of length n, then the ideal way of assigning a "fitness" to a solution would be to determine the Hamming distance between a proposed solution and the known solution. However, this is not possible since the solution (A') is not known - just the sum of the elements of A'. Thus one way of assigning a fitness to an arbitrary solution is to measure how close the sum of the elements of the proposed solution is to that of the known solution. It should be apparent to a reader that for a large public key set A such a measure will not be very reliable, given the random distribution of the elements of the set. To clarify these points we provide the following example. Let $n = 5$ and $A = \{$ 5457, 1663, 216, 6013, 7439 $\}$. Consider a plaintext message block $M = \{$ 1, 0, 1, 1, 0 $\}$ which gives a target sum of $B = 5457 + 216 + 6013 = 11686$. A guess of $M_1 = \{$ 1, 1, 1, 1, 0 $\}$ is very close to the original message (the Hamming distance between them is one). The corresponding sum is $5457 + 1663 + 216 + 6013 = 13349$. A second guess $M_2 = \{$ 1, 0, 0, 0, 1 $\}$ which has a Hamming distance of 3 from the correct solution, gives a sum of $5457 + 7439 = 12896$ which is closer to the required sum than the first guess which was only incorrect in one bit position. It is shown in Section 5.4 that this property is the norm rather than an exception and in general comparing sums is a poor technique for finding the solution to the knapsack problem.

With this problem in mind the fitness function proposed by Spillman in [71] is presented (Equation 5.1).

$$\text{Fitness}(M) = \begin{cases} 1 - (|\text{Target} - \text{Sum}|/\text{Target})^{1/2} & \text{if Sum} < \text{Target} \\ 1 - (|\text{Target} - \text{Sum}|/\text{MaxDiff})^{1/6} & \text{if Sum} \geq \text{Target} \end{cases} \tag{5.1}$$

where (let $M = \{m_1, m_2, \ldots, m_n\}, m_i \in \{0, 1\}$ be an arbitrary solution and the public key $A = \{a_1, a_2, \ldots a_n\}$)

$$\text{Sum} = \sum_{j=1}^{n} a_j m_j, \tag{5.2}$$

$$\text{Target} = \sum_{j} a'_j, \tag{5.3}$$

$$\text{FullSum} = \sum_{j=1}^{n} a_j, \tag{5.4}$$

$$\text{MaxDiff} = \max\{\text{Target}, \text{FullSum} - \text{Target}\}. \tag{5.5}$$

This fitness function penalises solutions which have a sum greater than the target sum. The reason for this is not clear. There is no reason why a solution which has a sum greater than the target sum is any better than one which is less than the target sum. Since we are only interested in solutions which are exactly equal to the target sum, the fitness in (5.6) is suggested as being more appropriate.

$$\text{Fitness} = 1 - (|\text{Sum} - \text{Target}|/\text{MaxDiff})^{1/2}. \tag{5.6}$$

An analysis of the two fitness functions in Equations 5.1 and 5.6 indicates that the modified fitness function - Equation 5.6 - will find the solution more quickly since solutions with their sum greater than the target are not being unfairly penalised. In order to investigate this hypothesis 100 different knapsack sums were formed from the same knapsack of size fifteen as used by Spillman in [71] - $A = \{$ 21031, 63093, 16371, 11711, 23422, 58555, 16615, 54322, 1098, 46588, 6722, 34475, 47919, 51446, 16438 $\}$. These knapsack sums were then attacked using the genetic algorithm as described in Section 5.2 using separately the fitness functions in Equations 5.1 and 5.6. The results of these attacks are given in Table 5.1 which clearly demonstrates that the fitness function in Equation 5.6 is more efficient.

Hence, for the remaining discussion in this paper the fitness function of Equation 5.6 is used.

Fitness Function	Number of Generations		Key Space Searched	
	Mean ($\bar{x}$)	Std Dev. (s)	Mean ($\bar{x}$)	Std Dev. (s)
Equation 5.1	1647	2038	24.4%	24
Equation 5.6	937	873	20.7%	21

Table 5.1: A comparison of two fitness functions.

5.2 The Genetic Algorithm Applied to the Knapsack Cipher

Here the algorithm presented by Spillman in [71] is interpreted. As indicated previously, a solution (or key) is represented as a binary string of length n. The mating operation is a simple crossover which is very commonly used in genetic algorithms. Two parents are chosen at random from the current gene pool. The first r, $(1 \leq r \leq n)$ bits of the two keys are then swapped (r is randomly generated). For example, $(n = 8, r = 3)$,

Parents	Children
01000101	11100101
11100110	01000110

Spillman describes three mutation operators. They are:

1. Each bit in the key is complemented with low probability.
2. Each bit has a low probability of being swapped with its neighbour.
3. A random section of the bit string is reversed. Once again this mutation occurs with low probability.

Putting these steps together, the following algorithm is obtained:

1. Generate a random initial gene pool and calculate the fitness of each of its elements (using (5.6)).
2. For G generations do
   (a) Select $G/2$ pairings from the current gene pool. These will become the parents of the new generation. The selection of parents, although random, is biased towards the fittest genes in the pool.

Knapsack	Number of Generations		Key Space Searched	
Size	Mean ($\bar{x}$)	Std Dev. (s)	Mean ($\bar{x}$)	Std Dev. (s)
15	1462	1470	23.40%	23.5
20	55220	55317	24.13%	24.1
25	1581735	1596872	23.60%	23.9

Table 5.2: Results for the Genetic Algorithm

(b) The parents mate (as described above) to produce the new gene pool.

(c) Each member of the new gene pool is mutated in the following manner.
Toss a coin

i. if heads apply mutation (1) described above,
ii. if tails, apply mutation (2).

Apply mutation (3), from above.

(d) It is desirable to retain some of the keys from the previous generation for the new generation. One way of doing this is to discard the x most unfit keys from the new generation and replace them with the x fittest from the old generation.

3. The fittest gene from the current gene pool is taken as the solution.

For the knapsack cipher we are only interested in the exact solution. For this reason we check each gene pool for a solution which has a fitness of 1.0. If one is found then the algorithm stops immediately, since the solution has been found. (There is only one solution - the uniqueness of the solution is ensured by the parameters on the knapsack.)

5.3 Results of Attacks on the Knapsack Cipher

For each of three different knapsack sizes (15, 20 and 25), 100 different knapsack sums were formed, and each time the algorithm was run until the solution was found. The results are given in Table 5.2.

Table 5.2 indicates that the amount of key space searched is about half that of an exhaustive attack. It can also be seen that the variation in the percentage of the key space searched, as well as the number of generations required by the algorithm, is large.

It is worth noting that although the methods discussed in this chapter do provide some improvement over an exhaustive search in terms of the amount of key space searched (on the average an exhaustive search would traverse 50% of the key space before finding the correct solution), in practice an exhaustive search will complete more quickly than a genetic algorithm search due to the large decrease in the complexity. It is very quick to test an arbitrary solution without determining its fitness, mutating it and combining it with other solutions - as happens in the genetic algorithm. This point further highlights the unsuitability of combinatorial optimisation in solving the subset sum problem in this manner.

5.4 Correlation Between Hamming Distance and Fitness

The reason for this attack being poor lies with the fact that the fitness function does not accurately describe the suitability of a given solution. This is because the fitness function does not always give a true indication of the Hamming distance between the proposed solution and the solution sought. To show this we investigate the distribution of Hamming distances for particular regions of fitness values. We are particularly interested in possible solutions which have a high fitness value. The results (shown in Table 5.3) were obtained using a randomly generated knapsack of size 30. The fitness of all possible (i.e. 2^{30}) solutions was calculated, along with the Hamming distance of each solution from the desired solution. Table 5.3 clearly shows that a high fitness value does not necessarily mean a low Hamming distance. In fact the distribution of Hamming distances for a given range of fitness values appears to be ‘binomial’-like. It can also be seen from Table 5.3 that the fitness values very close to 1.0 the distribution remains very spread. That is, there are solutions with a very high fitness value which have Hamming distances that are by no means close to that of the required solution.

In a recent paper by Spillman [72] addressing the use of genetic algorithms in solving the knapsack problem it was suggested that a “local search” routine would speed up the search. This routine involved taking solutions with a high fitness (greater

Hamming Distance	Fitness Value				
	> 0.9	> 0.95	> 0.99	> 0.999	> 0.9999
30	0	0	0	0	0
29	1	0	0	0	0
28	15	7	0	0	0
27	131	31	2	0	0
26	932	223	8	0	0
25	4937	1208	51	0	0
24	20318	5080	188	3	0
23	69048	17289	654	6	0
22	196683	49186	1985	16	0
21	477337	119098	4720	50	1
20	996841	248696	9789	82	1
19	1806512	451327	18176	182	2
18	2858033	714445	28630	275	2
17	3963985	989898	39301	395	3
16	4835383	1207311	47986	500	5
15	5196364	1298561	52285	515	3
14	4923282	1230811	49383	513	4
13	4111416	1027101	40613	395	7
12	3022419	755006	30014	295	1
11	1950970	487647	19785	203	0
10	1101829	275545	10988	113	2
9	541506	135305	5214	58	2
8	230325	57498	2298	26	1
7	83872	20973	911	14	0
6	25882	6446	247	0	0
5	6664	1692	57	2	0
4	1384	366	14	0	0
3	243	48	3	0	0
2	25	6	0	0	0
1	3	0	0	0	0
0	1	1	1	1	1

Table 5.3: Typical hamming distance distribution for high fitness values.

than 0.95) and complementing each bit of the solution, one by one. If the fitness improved then the adjusted solution was accepted. Table 5.3 indicates that such a routine will have very little affect on the efficiency of the algorithm since the fitness equation is not representative of the Hamming distance. In fact for the example in Table 5.3 this method would never have found the optimum since there were no solutions with a fitness greater than 0.95 and a Hamming distance of 1 from the solution sought.

5.5 Summary

The purpose of this chapter was to highlight the fact that combinatorial optimisation techniques rely heavily upon the suitability of the solution evaluation technique (fitness or cost). It has been shown, that for the subset sum problem, there is no (known) suitable evaluation technique when solving based on the subset sum. This is why the Merkle-Hellman cryptosystem is so elegant - a known NP-complete problem has been converted to an NP-hard problem and utilised as a cryptosystem. Of course the weakness with the cryptosystem is in the structure of the secret key rather than the actual encryption process (which Spillman has attempted to attack).

Spillman's fitness is based on the difference between the sum of a proposed solution and the known target sum. As Table 5.3 shows, such an approach gives no indication of the Hamming distance between the proposed solution and the binary representation of the target solution which is sought. Thus basing an genetic algorithm upon such a fitness function is inappropriate. This is further illustrated by the results in Table 5.2 which indicate that approximately one quarter of the solution space is searched, on the average, before the correct solution is found. This is not significantly better than an exhaustive search and, in fact, when complexity is considered, is worse due to the simplicity of an exhaustive search compared to the genetic algorithm search.

Chapter 6

Finding Cryptographically Sound Boolean Functions

The previous three chapters of this thesis have looked at the use of optimisation heuristics in the field of *cryptanalysis*. In this chapter a useful application of the genetic algorithm to the field of *cryptography* is presented. The genetic algorithm is used to search for cryptographically sound Boolean functions. Most block and stream ciphers incorporate Boolean functions which are chosen, in general, to satisfy a number of cryptographic criteria. Because many cryptographic properties of Boolean functions conflict with each other, the final choice of functions is usually a compromise between the desired properties of the functions.

An introduction to the theory and cryptographic properties of Boolean functions is given in Appendix D. In this chapter the property of nonlinearity is considered, although the work could be extended to include other cryptographic properties. When designing cryptosystems (ciphers) careful consideration must be given to the choice of functions used. High nonlinearity is an extremely important property required in order to reduce the effectiveness of attacks such as linear cryptanalysis – recently proposed by Matsui [45].

In this chapter a number of algorithms are introduced which assist with finding Boolean functions with good cryptographic properties. A new approach is used to determining bit positions in a function's truth table which, when complemented, will improve the nonlinearity of the function. The theory behind this principle, which is based on the coefficients of the Walsh-Hadamard transform (WHT – see Appendix D), is described in Section 6.1. It is also shown in this section that the balance of the function can either be improved or maintained as required.

A basic hill climbing technique which makes use of this new approach is described in Section 6.2. This technique is modified to incorporate a genetic algorithm in Section 6.3. It is shown that these new search techniques are extremely powerful when compared to traditional random search techniques. Experimental results reinforcing the techniques' usefulness are given in Section 6.4. These techniques represent novel methods of systematically generating highly nonlinear Boolean functions.

6.1 Improving Nonlinearity

Consider altering a Boolean function by complementing its binary truth table in a single position such that the nonlinearity is improved. Each truth table position corresponds to a unique function input. A technique is now introduced which enables the creation of a complete list of Boolean function inputs such that complementing any one of the corresponding truth table positions will increase the nonlinearity of the function. This list of truth table positions is referred to as the 1-Improvement Set of $f(x)$, or 1-IS$_f$ for short. A formal definition of the 1-IS$_f$ is now given.

Definition 1 *Let $g(x) = f(x) \oplus 1$ for $x = x_a$ and $g(x) = f(x)$ for all other x. If $N_g > N_f$ then $x_a \in$ 1-IS$_f$.*

Of course the set may be empty in which case $f(x)$ is referred to as 1-locally maximum for nonlinearity and cannot be improved using the technique described below. Since all Bent functions (see Appendix D) are globally maximum, their 1-Improvement Sets must be empty. There also exist sub-optimum local maxima that will be found by hill climbing algorithms. It is computationally intensive to exhaustively alter truth table positions, find new WHTs and determine the set 1-IS$_f$. Thus, a fast, systematic method of determining the 1-Improvement Set of a given Boolean function from its truth table and Walsh-Hadamard transform is sought. In this section a set of conditions are presented which provide a method of determining whether or not an input x is in the 1-Improvement Set.

In order to find the 1-IS$_f$ of a Boolean function it is first necessary to find values of the Walsh-Hadamard transform coefficients which correspond to values close in absolute value to the maximum coefficient value, WH$_{\text{MAX}}$.

Definition 2 *Let $f(x)$ be a Boolean function with Walsh-Hadamard transform $\hat{F}(\omega)$ where WH$_{MAX}$ denotes the maximum absolute value of $\hat{F}(\omega)$. There will exist one or more linear functions $L_\omega(x)$ that have minimum distance to $f(x)$, and $|\hat{F}(\omega)| = \text{WH}_{MAX}$ for these ω. The following sets are defined:*

$$\begin{aligned} W_1^+ &= \{\omega : \hat{F}(\omega) = \text{WH}_{MAX}\} \text{ and} \\ W_1^- &= \{\omega : \hat{F}(\omega) = -\text{WH}_{MAX}\}. \end{aligned}$$

Also needed are the sets of ω for which the WHT magnitude is close to the maximum:

$$\begin{aligned} W_2^+ &= \{\omega : \hat{F}(\omega) = \text{WH}_{MAX} - 2\}, \\ W_2^- &= \{\omega : \hat{F}(\omega) = -(\text{WH}_{MAX} - 2)\}, \\ W_3^+ &= \{\omega : \hat{F}(\omega) = \text{WH}_{MAX} - 4\}, \text{ and} \\ W_3^- &= \{\omega : \hat{F}(\omega) = -(\text{WH}_{MAX} - 4)\}. \end{aligned}$$

When a truth table is changed in exactly one place, all WHT values are changed by +2 or -2. It follows that in order to increase the nonlinearity the WHT values in set W_1^+ must change by -2, the WHT values in set W_1^- must change by +2, and also the WHT values in set W_2^+ must change by -2 and the WHT values in set W_2^- must change by +2. The first two conditions are obvious, and the second two conditions are required so that all other $|\hat{F}(\omega)|$ remain less than WH$_{\text{MAX}}$. These conditions can be translated into simple tests.

Theorem 1 *Given a Boolean function $f(x)$ with WHT $\hat{F}(\omega)$, define sets $W^+ = W_1^+ \cup W_2^+$ and $W^- = W_1^- \cup W_2^-$. For an input x to be an element of the Improvement Set, the following two conditions must be satisfied.*

(i) $f(x) = L_\omega(x)$ *for all* $\omega \in W^+$, *and*

(ii) $f(x) \neq L_\omega(x)$ *for all* $\omega \in W^-$.

If the function $f(x)$ is not balanced, a reduction in the imbalance can be achieved by imposing the additional restriction that

(iii) when $\hat{F}(0) > 0$, $f(x) = 0$, *else* $f(x) = 1$.

Proof: Start by considering the conditions to make WHT values change by a desired amount. When $\hat{F}(\omega)$ is positive, there are more 1 than -1 in the polarity truth table, and more 0 than 1 in the binary truth table of $f(x) \oplus L_\omega(x)$. Thus changing a single 0, in the truth table of $f(x) \oplus L_\omega(x)$, to a 1 will make $\Delta\hat{F}(\omega) = -2$. This means that an input, x, is selected such that $f(x) = L_\omega(x)$. A change of -2 is desired for all WHT values with $\omega \in W^+$, so this proves condition (i). A similar argument proves condition (ii). A function is balanced when $\hat{F}(0) = 0$, so to reduce the imbalance x must be selected according to condition (iii). □

To further clarify the task of determining the 1-Improvement Set of a given Boolean function, $f(x)$, consider the following example.

Example 6.1 *Consider the function described by the truth table given in Table 6.1. The corresponding Walsh-Hadamard transform is also given. Observe that WH*$_{MAX} = 8$ *is attained for* $\omega = 0101$ *and* $\omega = 1110$*. There are no transform values equal to WH*$_{MAX} - 2 = 6$*, so* $W_1^+ = \{0101, 1110\}$ *and* $W_1^- = W_2^+ = W_2^- = \phi$*. Thus, from Theorem 1, candidate values for the 1-IS*$_f$ *occur when* $L_{0101}(x) = L_{1110}(x) = f(x)$*. Thus 1-IS*$_f$ $= \{0000, 0011, 0100, 0111, 1001, 1010, 1101, 1110\}$ *and complementing any one of the corresponding truth table bits (the* $f(x)$ *column) will increase the nonlinearity from* $N_f = \frac{1}{2}(2^n - WH_{MAX}) = 4$ *to* $N_f = 5$*.*

It is often desirable to improve the nonlinearity of balanced Boolean functions, while retaining balance. Clearly this requires an even number of truth table changes. A set of conditions are now presented which define a pair of inputs x_a, x_b so that complementing both their function values causes an increase in nonlinearity, without changing the Hamming weight. The 2-Improvement Set, 2-IS$_f$, is defined as the set of all such input pairs. A function for which no pair satisfies these conditions is said to be 2-locally maximum.

Theorem 2 *Given a Boolean function* $f(x)$ *with WHT* $\hat{F}(\omega)$*, define sets* $W_1 = W_1^+ \cup W_1^-$, $W_{2,3}^+ = W_2^+ \cup W_3^+$ *and* $W_{2,3}^- = W_2^- \cup W_3^-$*. A pair of inputs* (x_a, x_b) *is in the 2-Improvement Set of* $f(x)$ *if and only if all of the following conditions are satisfied:*

(i) $f(x_a) \neq f(x_b)$,

(ii) $L_\omega(x_a) \neq L_\omega(x_b)$ *for all* $\omega \in W_1$,

x/ω	$f(x)$	$\hat{F}(\omega)$	$L_{0101}(x)$	$L_{1110}(x)$	$x \in$ 1-IS$_f$?
0000	0	0	0	0	$\surd$
0001	1	4	1	0	
0010	0	0	0	1	
0011	1	4	1	1	$\surd$
0100	1	4	1	1	$\surd$
0101	1	8	0	1	
0110	1	-4	1	0	
0111	0	0	0	0	$\surd$
1000	0	-4	0	1	
1001	1	0	1	1	$\surd$
1010	0	-4	0	0	$\surd$
1011	0	0	1	0	
1100	0	0	1	0	
1101	0	4	0	0	$\surd$
1110	1	8	1	1	$\surd$
1111	1	-4	0	1	

Table 6.1: Table for Example 6.1.

(iii) $f(x_i) = L_\omega(x_i)$, $i \in \{1, 2\}$, *for all* $\omega \in W_1^+$,

(iv) $f(x_i) \neq L_\omega(x_i)$, $i \in \{1, 2\}$, *for all* $\omega \in W_1^-$,

(v) *for all* $\omega \in W_{2,3}^+$, *if* $L_\omega(x_a) \neq L_\omega(x_b)$ *then* $f(x_i) = L_\omega(x_i)$, $i \in \{1, 2\}$, *and*

(vi) *for all* $\omega \in W_{2,3}^-$, *if* $L_\omega(x_a) \neq L_\omega(x_b)$ *then* $f(x_i) \neq L_\omega(x_i)$, $i \in \{1, 2\}$.

Proof: Condition (i) is required to maintain the Hamming weight. Conditions (iii) and (iv) are proven similarly to Theorem 1 (condition (ii) follows from (iii) and (iv)). In order to stop the correlation to other linear functions increasing too much, it is required that $\Delta\hat{F}(\omega) \neq +4$, for all $\omega \in W_{2,3}^+$, and it follows that not both of $f(x_i) \oplus L_\omega(x_i) = 1$, or equivalently that at least one of $f(x_i) \oplus L_\omega(x_i) = 0$. Consequently,

$$[f(x_a) \oplus L_\omega(x_a)][f(x_b) \oplus L_\omega(x_b)] = 0,$$

and expanding this, noting from (i) that $f(x_a)f(x_b) = 0$, it follows that

$$f(x_a)L_\omega(x_b) \oplus f(x_b)L_\omega(x_a) \oplus L_\omega(x_a)L_\omega(x_b) = 0.$$

Four cases need to be considered in order to find the exact conditions under which this expression will be satisfied:

(a) When $L_\omega(x_a) = L_\omega(x_b) = 0$ the expression is satisfied and no further conditions on (x_a, x_b) are required.

(b) When $L_\omega(x_a) = L_\omega(x_b) = 1$ the expression becomes $f(x_a) \oplus f(x_b) = 1$ which is equivalent to condition (i).

(c) When $L_\omega(x_a) = 0$ and $L_\omega(x_b) = 1$ the expression becomes $f(x_a) = 0$.

(d) When $L_\omega(x_a) = 1$ and $L_\omega(x_b) = 0$ the expression becomes $f(x_b) = 0$.

Combining (a)-(d) it can be seen that when $L_\omega(x_a) \neq L_\omega(x_b)$ for $\omega \in W^+_{2,3}$ it is required that $f(x_i) = L_\omega(x_i)$, $i = 1, 2$, thus proving condition (v). The Proof of (vi) is similar. □

The following theorem shows how to modify the WHT of a Boolean function that has been altered in a single truth table position, with complexity $O(2^n)$. It is noted that the algorithm for incremental improvement of Boolean functions suggested in [17] recomputes the WHT after every single bit change regardless of whether that change improves the nonlinearity. Therefore the algorithms presented here are superior on two counts - every change is an improvement and the new WHT is found n times faster.

Theorem 3 *Let $g(x)$ be obtained from $f(x)$ by complementing the output for a single input, x_a. Then each component of the WHT of $g(x)$, $\hat{G}(\omega) = \hat{F}(\omega) + \Delta(\omega)$, can be obtained as follows: If $f(x_a) = L_\omega(x_a)$, then $\Delta(\omega) = -2$, else $\Delta(\omega) = +2$.*

Proof: When $f(x_a) = L_\omega(x)$, it follows that $(-1)^{f(x_a) \oplus L_\omega(x_a)} = 1$, which contributes to the sum in $\hat{F}(x_a)$. Changing the value of $f(x_a)$ changes this contribution to -1, so $\Delta\hat{F}(\omega) = -2$. Similarly when $f(x_a) \neq L_\omega(x)$, $\Delta\hat{F}(\omega) = +2$. □

This idea is further clarified by continuing Example 6.1 so that a particular position is complemented and the new Walsh-Hadamard transform calculated. Consider Example 6.2.

Example 6.2 *Consider the function $f(x)$ which was presented in Example 6.1. It was shown that the 1-IS$_f$ $= \{0000, 0011, 0100, 0111, 1001, 1010, 1101, 1110\}$. Suppose the truth table bit corresponding to input $x_a = 0100$ is complemented to give a new function $g(x)$. Theorem 3 states that the change in the Walsh-Hadamard transform*

x/ω	$f(x)$	$\hat{F}(\omega)$	$L_{0100}(x)$	$\Delta(\omega)$	$\hat{G}(\omega)$
0000	0	0	0	2	2
0001	1	4	0	2	6
0010	0	0	0	2	2
0011	1	4	0	2	6
0100	1	4	1	-2	2
0101	1	8	1	-2	6
0110	1	-4	1	-2	-6
0111	0	0	1	-2	-2
1000	0	-4	0	2	-2
1001	1	0	0	2	2
1010	0	-4	0	2	-2
1011	0	0	0	2	2
1100	0	0	1	-2	-2
1101	0	4	1	-2	2
1110	1	8	1	-2	6
1111	1	-4	1	-2	-6

Table 6.2: Table accompanying Example 6.2.

coefficients, $\Delta(\omega) = -2$ when $f(x_a) = L_\omega(x)$, and $\Delta(\omega) = +2$, otherwise. Table 6.2 illustrates this process of computing the Walsh-Hadamard transform for $g(x)$, i.e., $\hat{G}(\omega)$.

6.2 Hill Climbing Algorithms

In this section the implementation details for the one step improvement and two step improvement algorithms - **HillClimb1** and **HillClimb2** - are given. It should be noted that condition (ii) of Theorem 2 is redundant, and is not referred to in the implementation of that algorithm.

The one step improvement algorithm, **HillClimb1**, takes as its input a Boolean functions binary truth table and the corresponding Walsh-Hadamard transform, and recursively improves the Boolean function's nonlinearity until the function is 1-locally maximum. The **HillClimb1** algorithm tries each bit in the truth table successively in an attempt to find a candidate bit which, upon complementation, will improve the function's nonlinearity by one. The algorithm terminates when no improvement in nonlinearity can be obtained by complementing any one of the bits in the function's truth table.

- **HillClimb1(BF, WHT)**

  1. Determine the maximum value of the Walsh-Hadamard transform - WH_{MAX}.
  2. By parsing the WHT find the values of ω which correspond to transform values equal to $|\text{WH}_{\text{MAX}}|$ and $|\text{WH}_{\text{MAX}} - 2|$. In this manner create the two sets: $W^+ = W_1^+ \cup W_2^+$ and $W^- = W_1^- \cup W_2^-$.
  3. For $i = 1, \ldots, 2^n$, do
     (a) Complement the i^{th} bit in the truth table of **BF** to produce the new Boolean function **BF′**.
     (b) By parsing the sets W^+ and W^- check that conditions (iii) and (iv) of Theorem 2 above are satisfied for **BF**. If they are, calculate the updated Walsh-Hadamard transform - **WHT′** - using Theorem 3 above, and restart the algorithm - i.e., call **HillClimb1(BF′, WHT′)**.
  4. BF represents a 1-locally maximum Boolean function - terminate processing.

The second algorithm described here - **HillClimb2** - is an implementation of the steps required to find a 2-locally maximum Boolean function, given a random Boolean function as a starting point. The algorithm maintains the balance of the original function whilst improving the nonlinearity each time two candidate bits can be found for complementation. This algorithm must generate two candidate lists of possible bit positions in the truth table for complementation. These two lists - called C_0 and C_1 - contain candidate positions in the truth table with corresponding values of zero and one, respectively. When one position from each of the sets C_0 and C_1 is found which satisfy the required conditions of Theorem 2, the corresponding bits are complemented. The new function's Walsh-Hadamard transform is computed efficiently by two successive calls to the operation described in Theorem 3. The function calls itself in a recursive manner in an attempt to further improve the new function.

- **HillClimb2(BF, WHT)**

1. Determine the maximum value of the WHT - WH_{MAX}.
2. By parsing the WHT obtain the values of ω which correspond to transform values of $|\text{WH}_{\text{MAX}}|$, $|\text{WH}_{\text{MAX}} - 2|$ and $|\text{WH}_{\text{MAX}} - 4|$ and hence create the sets W_1^+, W_1^-, $W_{2,3}^+ = W_2^+ \cup W_3^+$ and $W_{2,3}^- = W_2^- \cup W_3^-$.
3. For $i = 1, \ldots, 2^n$, do
   (a) By parsing the sets W_1^+ and W_1^- ensure that conditions (iii) and (iv) in Theorem 2 are satisfied for **BF**. If they are, depending on the value of the i^{th} bit in the truth table, add i to C_0 or C_1.
4. For each element of C_0, do
   (a) For each element of C_1, do
      i. Check conditions (v) and (vi) of Theorem 2. If they are satisfied for **BF**, complement the corresponding bits in the truth table of **BF** - call the resulting Boolean function **BF**$'$, find the adjusted Walsh-Hadamard transform - **WHT**$'$ by applying Theorem 3 twice and call **HillClimb2(BF$'$, WHT$'$)**.
5. **BF** represents a 2-locally maximum Boolean function - terminate processing.

6.3 Using a Genetic Algorithm to Improve the Search

The genetic algorithm was described in detail in Chapter 2 and has been used extensively in various cryptanalytic algorithms in the previous chapters. In this chapter the genetic algorithm is used to improve the hill climbing algorithms described above. In the classical genetic algorithm the solution is represented as a binary string. The same representation is utilised here for the Boolean function - in this case the binary string represents the binary truth table of the function. Given a solution representation, there are three other requirements of the genetic algorithm, namely a solution evaluation technique, a mating function and a mutation function. The mating function allows the combining of solutions, hopefully, in a meaningful manner. Mutation is performed on a single solution in order to introduce a degree of randomness to the solution pool. These three genetic algorithm requirements are now discussed individually.

The genetic algorithm requires a method of assessing and comparing solutions. Typically this measure is referred to as the "fitness". The fitness which is used here is simply the nonlinearity (N_f) of the Boolean function $f(x)$. This is suitable for a genetic algorithm, since $|N_f - N_g| \leq dist(f(x), g(x))$. In other words nonlinearity is a locally smooth fitness function. With Boolean functions there are also numerous other fitness functions possible (for example, the maximum value taken by the auto-correlation function could be minimised).

The genetic algorithm also requires a method for combining two (possibly more) solutions in order to obtain offspring. The usual mating process utilised in classical genetic algorithm is often referred to as "crossover". The crossover operation involves selecting two "parents" from the current solution pool, picking a random point in the binary string representing each of the parents and swapping the values beyond that point between the two parents. This process results in two "children" with some characteristics of each of the parents. Here a slightly different breeding process is used, namely "merging", which is described below. Notice that this mating operation is different from ones in previous chapters by the fact that only a single child function is produced.

Definition 3 *Given the binary truth tables of two Boolean functions $f_1(x)$, $f_2(x)$ of n variables at Hamming distance d, the merge operation is defined as:*

- *If $d \leq 2^{n-1}$*

$$\mathit{MERGE}_{f_1,f_2}(x) = \begin{cases} f_1(x) \text{ if } f_1(x) = f_2(x) \\ \text{a random bit, otherwise.} \end{cases}$$

- *else*

$$\mathit{MERGE}_{f_1,f_2}(x) = \begin{cases} f_1(x) \text{ if } f_1(x) \neq f_2(x) \\ \text{a random bit, otherwise.} \end{cases}$$

Note that this merging operation is partly deterministic and partly probabilistic, and that it takes the fact that complementation does not change nonlinearity into account. The number of distinct children that can result from a merge is given by $2^{dist(f_1,f_2)}$, and all are equally probable. Thus the use of MERGE as a breeding scheme includes implicit mutation. Since random mutation of a highly nonlinear function is likely to reduce the nonlinearity, additional random mutations are avoided and instead the merge is relied upon to direct the pool into new areas of the search space. The motivation for this operation is that two functions that are highly nonlinear and close to each other will be close to some local maximum, and the merging operation produces a function also in the same region, hopefully close to that maximum. Also when applied to uncorrelated functions, the merge operation produces children spread over a large area, thus allowing the genetic algorithm to search the space more fully. At the start of the genetic algorithm, the children are scattered widely, then as the pool begins to consist of good functions, the merging assists convergence to local maxima. The experiments have shown that other simple combining methods, such as XOR and crossover, do not assist convergence to good solutions. It is the use of merging that allows the genetic algorithm to be effective.

The mutation operation simply introduces randomness to the solution pool. Mutation is generally applied to the children which result from the breeding process. In some cases the breeding step is ignored and mutation is applied to the selected parents in order to produce children. Such an option is not considered here. It is usual to mutate a child by complementing a random subset of the binary string representing the child. The number of values complemented is a parameter of the algorithm - sometimes referred to as the “mutation factor”.

Combining each of the genetic algorithm operations described above the overall algorithm is obtained. Generally the initial solution pool is generated randomly or using some “smart” technique specific to the type of optimisation problem being tackled. In this case a random initial pool is suitable since very few randomly generated functions have low nonlinearity. The problem with random generation is that very highly nonlinear functions are difficult to find. The algorithm then updates the solution pool over a number of iterations (or *generations*). The maximum number of iterations is fixed, although additional stopping criteria may be specified. In each iteration a number of steps are involved: selection of parents from the current solution pool, mating of parents to produce offspring, mutation of the offspring, and selection from the mutated offspring and the current solution pool to determine the solution pool for the next iteration.

Much of the implementation detail of the genetic algorithm is specific to the problem being solved. In this case mating and mutation are combined in the merge operation, which allows two good parents that are close together in Hamming distance to produce a child close to both parents. It follows that the child is expected to have a good fitness.

In the algorithm described below all possible combinations of parents undergo the breeding process. The number of such pairings is dependent upon the pool size P - there are $\frac{P(P-1)}{2}$ such pairings. After initial experiments a pool size of 10 was chosen as a compromise between efficiency and convergence. Another parameter of the genetic algorithm is the "breed factor": the number of children produced by each parent pair. Experimental results show that for a small, fast genetic algorithm, the most efficient breed factor is 1, when efficiency is taken to mean the fitness of the best functions found as compared with the number of functions evaluated. However using larger values may be useful in gaining quick access to the entire search space. The following algorithm describes the genetic algorithm as used in experiments. There are four inputs to the algorithm - **MaxIter**, which defines the maximum number of iterations that the algorithm should perform, **P**, the size of the solution pool, **BreedFactor**, the number of offspring produced by the MERGE operation, and **HC** a Boolean value indication whether or not the algorithm should incorporate one of the Hill climbing algorithms described above (i.e., **HillClimb1** or **HillClimb2**).

- **GeneticAlgorithm(MaxIter, P, BreedFactor, HC)**

```
1. Generate a pool of $P$ random Boolean functions and calculate their corresponding Walsh-Hadamard transforms.
2. For $i = 1, \ldots,$ MaxIter, do
   (a) For each possible pairing of the functions in the solution pool, do
       i. Perform the MERGE operation on the two parents to produce a number of offspring equal to the "breed factor" (BreedFactor).
       ii. For each child, do
           A. If hill climbing is desired (i.e., if HC=1) call the HillClimb1 function.
           B. Provided the resulting offspring is not already in the list of children, add the new child to the list of children.
```

   (b) Select the best solutions from the list of children and the current pool of solutions. In the case where a child has equal fitness (nonlinearity) to a solution in the current solution pool, preference is given to the child.

3. Report the best solution(s) from the current solution pool.

6.4 Experimental Results

The experimental results for the algorithms described above are presented in two stages. In the first instance the effectiveness of the two hill climbing algorithms is explored, when compared with a pure random search for Boolean functions with high nonlinearity. As the two hill climbing algorithms suggest, there are two cases here - the first is where functions have no requirement on their balance, and in the second case only balanced functions are considered since balance is maintained by the **HillClimb2** algorithm. The second stage of experiments is designed to illustrate the improvement gained by adding the genetic algorithm to the Boolean function search mechanism.

6.4.1 Random Generation versus Hill Climbing

The first set of results are now presented. In the first instance the nonlinearity of randomly generated Boolean functions is compared with the nonlinearity of 1-locally maximum Boolean functions obtained using the **HillClimb1** algorithm detailed above. This comparison was performed for eight ($n = 8$) and twelve ($n = 12$) input functions. The results are given in Figures 6.1 and 6.2. The first observation to be made from these figures is that the distribution of nonlinearity for randomly generated Boolean functions is a roughly bell-shaped one. The second point of interest is that the distribution of nonlinearities for functions discovered using the **HillClimb1** algorithm is spiky. In fact the likelihood of finding a function with even nonlinearity is much greater than that of finding an odd one when the hill climbing algorithm is used. This seems to indicate that most functions with odd linearity are not 1-locally maximum. Of course the most important result which is evident upon observation of Figures 6.1 and 6.2 is the improvement achieved through the use of the hill climbing algorithm. The most nonlinear functions obtained using the hill climbing algorithm are significantly closer

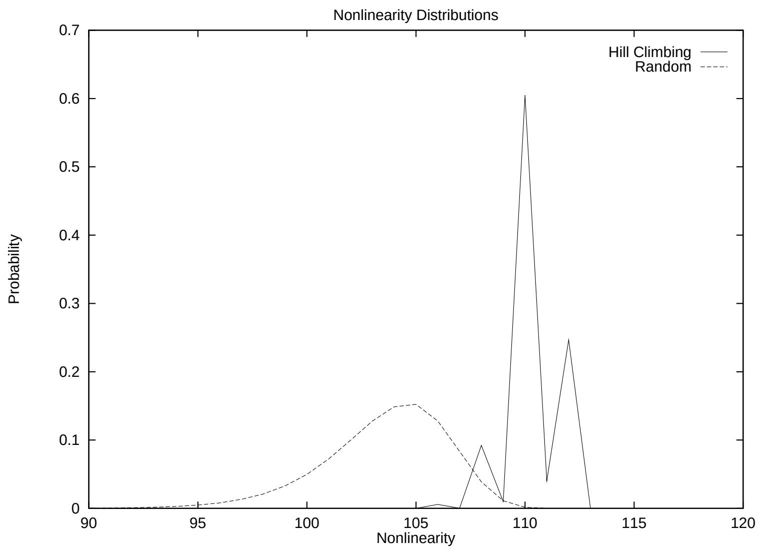


Figure 6.1: A comparison of hill climbing with random generation, n=8.

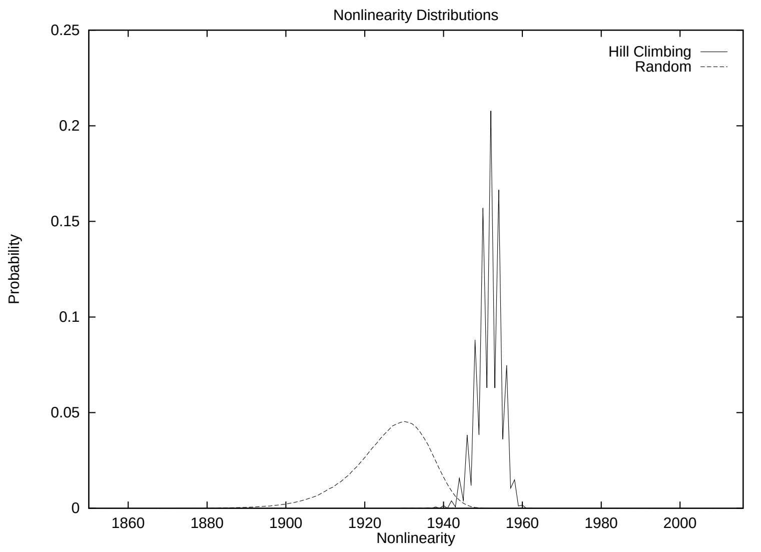


Figure 6.2: A Comparison of hill climbing with random generation, n=12.

to the maximum attainable than those found by random search. Note that for $n = 8$ and $n = 12$ the highest attainable nonlinearities are $N_f = 120$ and $N_f = 2016$, respectively - i.e., the nonlinearity of Bent functions for $n = 8$ and $n = 12$.

A similar comparison was performed using the **HillClimb2** algorithm on balanced functions only. In this case the randomly generated functions were restricted to the balanced functions. It is known that balanced functions always have even nonlinearity. The results for these experiments appear in Figures 6.3 and 6.4. Once again,

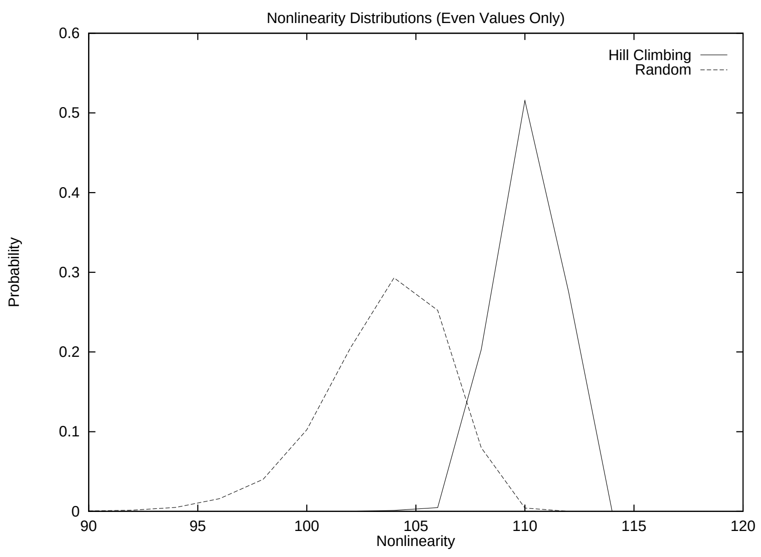


Figure 6.3: A comparison of hill climbing with random balanced generation, n=8.

the experiments were performed for $n = 8$ and $n = 12$. Observe that the randomly generated functions still have the bell-shaped distribution. The hill climbing algorithm - **HillClimb2** - was initialised with balanced functions, in this case, so that the 2-locally maximum function obtained by the search were also balanced (since **HillClimb2** maintains the balance of the function being optimised). It can be seen that the functions obtained using the hill climbing algorithm, on average, were superior to the ones obtained by random search.

It is also interesting to observe the amount of improvement which can be expected from the hill climbing algorithms. As a measure of the worth of the hill climbing algorithm experiments were performed to determine the average number of steps to find a 1-locally maximum function from a random starting function. This experiment was performed for values of n ranging from six to twelve. The results are presented in Figure 6.5. For example, the results indicate that for a randomly generated Boolean function of twelve inputs ($n = 12$), the expected improvement in nonlinearity obtained from the hill climbing algorithm is 25 on the average. It can be seen from Figure 6.5 that as n increases the relative gain obtained from hill climbing increases also. Or, in other words, as n increases the distance from a randomly generated function to a local maximum is also increasing. Another point to be aware of is the efficiency of the hill climbing algorithm in recomputing the next function's Walsh-Hadamard trans-

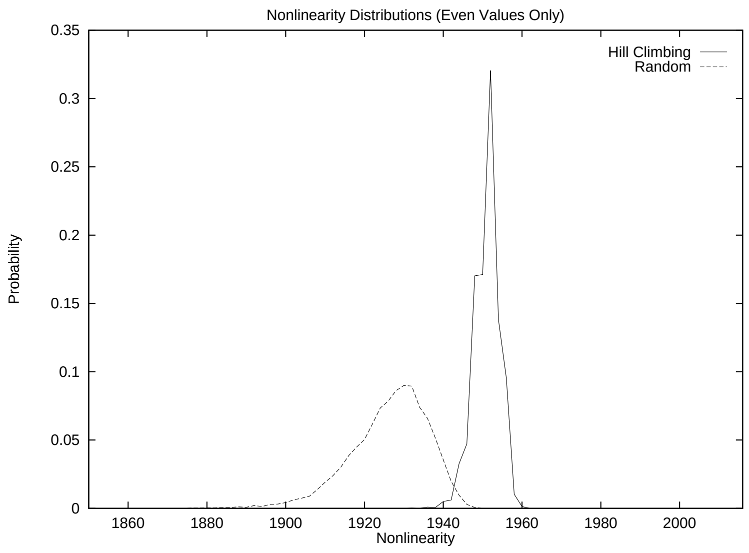


Figure 6.4: A comparison of hill climbing with random balanced generation, n=12.

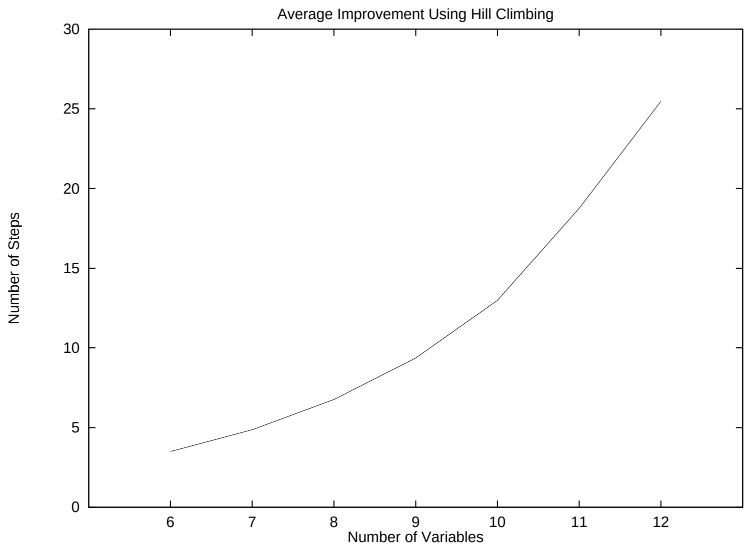


Figure 6.5: Average number of improvement steps by the hill climbing algorithm for various n.

form. From Theorem 3 it is evident that the complexity required by the hill climbing algorithm in order to improve the nonlinearity by n is equivalent to the generation of a random Boolean function and the calculation of its Walsh-Hadamard transform.

6.4.2 Genetic Algorithms with and without Hill Climbing

The second stage of experiments involve the genetic algorithm technique for finding Boolean functions as described above. The experiments have shown that a genetic algorithm with a pool size of less than 10 tends to converge too quickly, since a single good solution comes to dominate the pool: it is the parent of many children that survive into subsequent generations. When both parent and offspring survive and breed, their progeny tend to survive also, and that “family” soon dominates the gene pool, producing convergence. A policy precluding “incest” counters this effect. This policy may take the form of forbidding a parent pair from breeding if their Hamming distance is too small, as set by some threshold parameter. However, when this parameter is set too large, it prevents breeding by the best pairs, thus undermining the motivation for the merge operation. Further experiments will be required to determine optimum sets of genetic algorithm parameters. It is clear that to find very highly nonlinear functions, larger pools are useful, since they converge less rapidly.

As an example of how the genetic algorithm performs, a single genetic algorithm search was performed for $n = 14$ and the nonlinearity of the best function recorded at the end of each iteration. Figure 6.6 is a plot of the results obtained for this particular case, which compares the number of iterations against the best nonlinearity found thus far. It can be seen that the most dramatic improvement in the nonlinearity occurs in the early stages of the algorithm. After a certain number of iterations (approximately 40 in this case) the rate of improvement in the nonlinearity decreases rapidly. In Figure 6.6 the solid line represents the nonlinearity of the best solution in the current pool and the dotted line presents the average nonlinearity of all the functions currently in the solution pool. After a while nearly all functions in the solution pool have the same nonlinearity, indicating that the GA usually finds more than one function with the highest nonlinearity.

The remaining results presented in this section are designed to illustrate the merits of the genetic algorithm search over both random Boolean function generation and the hill climbing algorithm, **HillClimb1**. Note that in this section there is no requirement of balance on the functions being generated.

As a benchmark the best results obtained from random search for functions with inputs ranging from eight ($n = 8$) to sixteen ($n = 16$) were obtained for various search

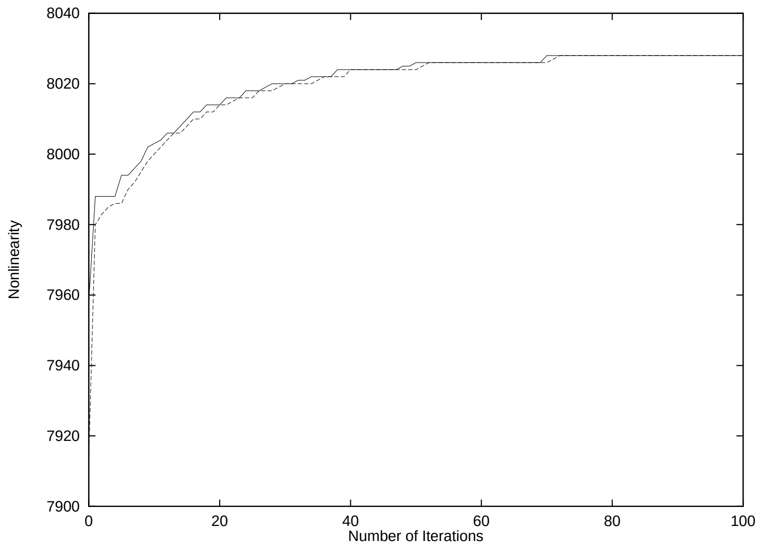


Figure 6.6: Performance of a typical genetic algorithm, $n = 14$, $P = 10$.

Sample Size	8	9	10	11	12	13	14	15	16
1000	110	228	468	958	1947	3946	7966	16048	32273
10000	111	229	469	959	1949	3950	7971	16054	32280
100000	112	230	470	961	1952	3952	7975	16058	32288
1000000	112	230	472	962	1955	3954	7978	16065	n/a

Table 6.3: Best nonlinearity achieved by random search - typical results.

sizes ranging from 1000 to 1000000. The results (for nonlinearity) of this extensive search are given in Table 6.3. The table clearly shows that increasing the sample size ten times only marginally increases the nonlinearity obtained. This results from the shape of the probability distribution of nonlinearity of Boolean functions: most functions do not have low nonlinearity, but very highly nonlinear functions are extremely rare. This is evident from Figures 6.1 to 6.4 in the previous section. These graphs show that functions approaching the maximum nonlinearity are very rare.

Table 6.4 shows typical values for the number of functions that need to be tested before an example with nonlinearity equal to or exceeding the benchmark is obtained. In Table 6.4 (and the following two tables - Tables 6.5 and 6.6), the acronyms have the following meanings: “R HC” means a random search utilising a hill climbing routine; “GA” means a basic genetic algorithm with no hill climbing; and “GA HC” means a genetic algorithm which incorporates a hill climbing routine.

n	8	9	10	11	12	13	14	15	16
Benchmark	112	230	472	962	1955	3954	7978	16065	32288*
R HC	4	3	2	8	3	2	2	2	1
GA	591	422	767	588	639	721	722	1108	588
GA HC	2	4	4	5	9	3	2	2	1

Table 6.4: Number of functions considered before achieving benchmark results - typical results.

Method	8	9	10	11	12	13	14	15	16
Random	110	228	468	958	1947	3946	7966	16048	32276
R HC	112	232	474	966	1960	3962	7991	16080	32319
GA	111	232	473	964	1955	3962	7982	16076	32289
GA HC	114	236	478	974	1972	3978	8014	16114	32366

Table 6.5: Best nonlinearity achieved after testing 1000 functions - typical results.

Method	8	9	10	11	12	13	14	15	16
Random	111	229	469	959	1949	3950	7971	16054	32280
R HC	114	232	476	968	1961	3964	7995	16090	32332
GA	113	232	475	968	1964	3968	7996	16085	32329
GA HC	114	236	482	980	1980	3994	8036	16144	32405

Table 6.6: Best nonlinearity achieved after testing 10000 functions - typical results.

The benchmark being used is the highest nonlinearity found in a random sample of 1000000 functions. In most cases a simple genetic algorithm needs less than 1000 functions to get a benchmark result, indicating that the genetic algorithm is far more efficient than random search in finding highly nonlinear Boolean functions even when the overhead involved with the genetic algorithm is taken into account. The results for hill climbing algorithms are even better than the genetic algorithm alone (see later), indicating that hill climbing is a very effective technique for finding strong functions quickly. Note that the benchmark used for $n = 16$ is the highest obtained in 100000 random generations, since a complete search of a million functions for this number of inputs has not yet been obtained.

Tables 6.5 and 6.6 indicate the best results achieved by the algorithms when they are forced to terminate after a specific number of functions have been tested. A direct comparison between random generation with hill climbing, and a simple genetic algorithm without hill climbing shows that these algorithms are about equally effective for 1000 or 10000 function tests. Other experiments have suggested that as the computation bound is increased, the performance of the genetic algorithm will eventually exceed that of hill climbing. It is interesting to note that the best algorithm is clearly a genetic algorithm with hill climbing. This hybrid algorithm is able to quickly obtain functions far better than the benchmarks.

6.5 Summary

A cryptographic application of combinatorial optimisation has been proposed. It has been shown in this chapter that the genetic algorithm is a powerful tool, when used in combination with a simple hill climbing heuristic, for finding highly nonlinear Boolean functions suitable for cryptographic applications. It is suggested that a similar technique could be used to find functions with other properties, or even a combination of properties. Also, the technique could be extended to finding highly nonlinear substitution boxes.

The hill climbing technique exploits the properties of the Walsh-Hadamard transform of the Boolean function in order to determine which bits of its truth table may be complemented to improve the nonlinearity of the function. It is shown that the technique can be used to choose two different-valued bits to complement to improve the nonlinearity while at the same time maintaining the function's balance properties.

This technique is shown to be significantly superior to a random search. The genetic algorithm can be seen to further improve the hill climbing technique allowing functions which are even more nonlinear to be found.

This work could be extended to include an analysis of the algorithm to determine if the bits selected for complementation can be chosen more carefully in order to extend the number of steps the nonlinearity can take before a local maximum is achieved.

Chapter 7

Conclusions

This thesis has investigated the use of three well-studied optimisation heuristics - simulated annealing, the genetic algorithm and the tabu search - in the fields of automated cryptanalysis of ciphers and automated Boolean function design. These fields are important to cryptologists since, for example, cryptographers designing ciphers need access to Boolean functions satisfying an ever-growing list of criteria, while, on the other hand, cryptanalysts need to process vast amounts of information in order to discover and exploit the weaknesses in ciphers. As was demonstrated in the thesis, these three techniques provide cryptographers and cryptanalysts with a tool which meets both of these requirements.

There are two key issues to consider when considering the use of optimisation heuristics. The first is to consider if a suitable solution evaluation mechanism exists. As has been illustrated in this thesis, it is clear that a reliable and accurate assessment technique must exist if the types of search heuristics used are to be of practical use. The second issue to consider is to determine which technique is going to be most suitable. This decision will be based upon the characteristics of the problem being solved and the characteristics of each of the heuristics. For example, if a genetic algorithm is being considered a suitable mating operation must be defined.

Understanding the limitations of optimisation techniques requires knowledge of the characteristics associated with the problems which are typically being solved. The theory of NP-completeness, which was discussed in Chapter 2 defines a class of problems which are known to be difficult to solve. Once convinced that large instances of such problems are impossible to solve *exactly*, one quickly comes to realise the importance of approximate techniques such as the ones presented here. The large amount of research which has been, and still is being, carried out emphasises the power of these techniques. The different characteristics of each of the optimisation techniques considered in this work makes them suitable for different applications.

The classical ciphers generally have a very large number of possible keys and yet they are relatively simple to cryptanalyse. This is because the encryption process does not hide the statistics of the plaintext language. Knowledge of the n-gram statistics for the language (in this case English) allows the definition of a key assessment method based upon the n-gram statistics of the message decrypted with a proposed key. Once a key assessment method is defined it is possible to implement a search algorithm based on an optimisation heuristic. As was shown, these ciphers are especially vulnerable to automated attacks based on such techniques. This is the case since an attacker can use these automated techniques to find a "close" approximation to the actual key which may render the cryptogram readable, or, if not, partly readable. Heuristics which utilised, separately, simulated annealing, the genetic algorithm and the tabu search were designed and implemented in attacks on both the simple substitution cipher and the transposition cipher. Overall, the tabu search was found to be the most effective search heuristic when applied to the substitution and transposition ciphers. The success of the tabu search can be attributed to its "memory" features which force the search away from regions of the search space that have already been considered. Simulated annealing and the genetic algorithm, which do not possess this feature, are less efficient in their search of the key space. While all three techniques were found to successfully cryptanalyse simple substitution ciphers and transposition ciphers, the genetic algorithm is best suited to parallel implementations and because of the structure of the polyalphabetic substitution cipher was the only technique applied to this cipher.

The parallel genetic algorithm approach to cryptanalysis of the polyalphabetic substitution cipher provides a linear improvement in complexity over traditional sequential-type attacks since it can solve each of the separate keys simultaneously. Processing nodes are able to share information about their keys so that any node can determine a set of statistics based on how the message decrypts using those keys. This technique was shown to work equally well for all polyalphabetic block sizes up to nine characters. It is suggested that, provided sufficient computing processors and ciphertext are available, this attack would be successful on much larger block sizes as well.

A number of modifications to the fast correlation attack were proposed. Although incorporating an optimisation heuristic (in this case simulated annealing) in the probability update stage does lead to some improvement over the original algorithm, it is found that the fast resetting technique leads to even greater improvement. By resetting the error probability vector after a fixed number of complementations of the recovered keystream, a marked improvement in the attack is obtained. The fast resetting technique is shown to be superior to MacKay's free energy minimisation method. This result is based on extensive experiments with shift registers of various lengths.

This work could possibly be extended to include other types of stream ciphers. Fast correlation attacks have been proposed on a large number of stream ciphers including clock-controlled shift register based stream ciphers [29], the multiplexed generator [34] and the summation generator [66] (which incorporates memory - see Appendix B). Techniques similar to the ones discussed in this thesis could be modified to possibly enhance the existing attacks.

The Merkle-Hellman public key cryptosystem utilises an NP-hard relative of the NP-complete subset sum problem. Spillman's method for attacking the Merkle-Hellman system is shown to be flawed. The fitness function proposed by Spillman does not accurately reflect how close a solution is to the correct one. An example is used to show that it is possible to find a candidate solution whose fitness is within 0.01% of the fitness of the correct solution and yet the candidate solution is different from the correct solution in more than half of its bit positions. An additional problem with Spillman's approach is that the knapsack cryptosystem has only one solution. Traditionally, optimisation heuristics are applied when we are satisfied that the optimum solution cannot be found but, instead, a "good" solution is sought. Applying a genetic algorithm to a problem which is known to be NP-hard and which has only one correct solution (among 2^n) can only be futile.

Based on the research presented in this thesis it could be concluded that optimisation heuristics show potential for use in the field of automated cryptanalysis. Although rarely useful for completely cryptanalysing a cipher (except in the case of the classical ciphers), these techniques have shown some promise when used to optimise existing methods for attacking certain ciphers. Optimisation heuristics are proven performers for problems which require searching a large solution space for solutions with "good" characteristics (rather than the “best” solution). One possible example for further research in this area is searching for *characteristics* for use in differential, or linear cryptanalysis. Matsui has proposed a branch-and-bound search for this purpose, and it is possible that another optimisation heuristic may be more efficient for such a purpose. The branch-and-bound approach is sufficient to find characteristics for DES; however, characteristics for ciphers which utilise larger S-boxes (such as CAST – [1]) may be better determined using an optimisation technique such as the ones discussed in this thesis.

In addition to their application to the field of cryptanalysis, optimisation heuristics have also proven to be useful for cryptographic applications.

A technique for determining “neighbours” of a given function which have higher nonlinearity is introduced. This approach can be used iteratively in order to find a Boolean function which is locally maximum in nonlinearity, in the sense that complementing any one of the bits in its truth table will not lead to a function with higher nonlinearity. In addition to nonlinearity, balance is one of the fundamental properties required of cryptographically sound Boolean functions. A technique is presented which allows the search to determine two differently-valued truth table positions such that complementing each of these (binary) values increases the overall nonlinearity of the function and at the same time maintains its balance. Thus, the techniques can be used to either improve both nonlinearity and balance of a non-balanced function, or to improve nonlinearity while maintaining the balance of a function. Incorporating this technique in a genetic algorithm is shown to produce a search which reliably finds functions with higher nonlinearity than other techniques.

This cryptographic application for optimisation heuristics is open to a number of extensions in future work. Similar techniques could be used to determine highly nonlinear S-boxes. Also, many other cryptographically desirable properties of Boolean functions are known. These techniques, or similar ones, could be used to find functions satisfying other cryptographic criteria, or (ideally) a combination of a number of criteria. This would be an especially useful extension since several cryptographic properties are known to conflict so that the “best” function is based on a trade-off between a number of properties.

A number of applications of optimisation heuristics to the field of cryptology have been presented. The optimisation heuristics do not work for all applications and it is important to be aware of this. Once the limitations of these techniques are understood it becomes clear which applications will gain the most benefit from an approach based on them. The examples provided in this thesis, along with suggestions of further applications, are intended to increase others' awareness of optimisation heuristics as a useful tool in cryptology, and to assist in understanding when and when not they are best utilised.

Appendix A

Classical Ciphers

In this appendix three different classical ciphers - the simple substitution cipher, the polyalphabetic substitution cipher and the transposition cipher - are described. In each case an example is given to illustrate the usage of the cipher. Properties of each of the ciphers which are utilised in their cryptanalysis are also discussed.

Several variations of substitution and transposition ciphers exist. The ones presented here are the most general. Most historical cases of the substitution cipher are just specific instances of the general cases described in the following two sections (examples are the Caesar, Vigenére and Beaufort ciphers - see [35] or [4]).

A.1 Simple Substitution Ciphers

The simple substitution cipher (sometimes referred to as the monoalphabetic substitution cipher to distinguish it from the polyalphabetic substitution cipher which is presented in Section A.2) is the most simple of substitution ciphers. Each symbol in the plaintext maps to a (usually different) symbol in the ciphertext. The processes of encryption and decryption are best described with an example, such as the one following.

Example A.1 *A simple substitution cipher key can be represented as a permutation of the plaintext alphabet. Table A.1 gives a sample key. Using this representation the i^{th} letter in the plaintext alphabet is encrypted to the i^{th} element of the key. The string "…the money is in a locker at the airport…" is encrypted using the key in the table (see Table A.1).*

Using the key representation in Table A.1, the original message can be discovered

KEY:

Plaintext:	`ABCDEFGHIJKLMNOPQRSTUVWXYZ_`
Ciphertext:	`PQOWIEURYTLAKSJDHFGMZNX_BCV`

ENCRYPTION:

Plaintext:	`THE_MONEY_IS_IN_A_LOCKER_AT_THE_AIRPORT`
Ciphertext:	`MRIVKJSIBVYGVYSVPVAJOLIFVPMVMRIVPYFDJFM`

Table A.1: Example simple substitution cipher key and encryption.

by reversing the encryption procedure. That is, the ciphertext character at position i in the key decrypts to the i^{th} character in the plaintext alphabet.

For an alphabet of 27 characters there are 27! ($\approx 1.09 \times 10^{28} \approx 2^{93}$) possible keys for a simple substitution cipher. This number is far too large to allow a brute force attack - even on the fastest of todays computers. However, because of the properties of the simple substitution cipher they are relatively easy to cryptanalyse.

One property of the simple substitution cipher is that n-gram statistics are unchanged by the encryption process. Notice in Example A.1 how the most frequent 2-gram (or *bigram*) in the message (_A) becomes VP each time it is encrypted (three times in the message in Table A.1). So, for every grouping of letters in the plaintext there is a distinct and corresponding grouping of characters in the ciphertext. In a message of sufficient length, the most frequent n-grams in the English language will, with high probability, correspond to the most frequent n-grams in the encrypted message (provided, of course, that the plaintext is from the English language). This fact is used frequently as the basis of attacks on the simple substitution cipher.

The Caesar cipher is an example of a simple substitution cipher in which the key is simply the rotation of the plaintext alphabet by j places (see [4] or [74]).

A.2 Polyalphabetic Substitution Ciphers

The polyalphabetic substitution cipher is a simple extension of the monoalphabetic one. The difference is that the message is broken into blocks of equal length, say B, and then each position in the block $(1, \ldots, B)$ is encrypted (or decrypted) using a different simple substitution cipher key. The block size B is often referred to as the period of the cipher. The following example is utilised to illustrate the encryption process using a polyalphabetic substitution cipher.

Example A.2 *In this example the same message as in Example A.1 is used. The block size (i.e., B) is chosen to be three. Table A.2 gives an example key and shows the corresponding encryption.*

KEY:

Plaintext:	`ABCDEFGHIJKLMNOPQRSTUVWXYZ_`	
Ciphertext:	`LP_MKONJIBHUVGYCFTXDRZSEAWQ`	(Position 1)
	`GFTYHBVCDRUJNXSEIKM_ZAWOLQP`	(Position 2)
	`ZQSCEFBTHUMKO_PLIJYNGRVDWXA`	(Position 3)

ENCRYPTION:

Position:	`123123123123123123123123123123123123123`
Plaintext:	`THE_MONEY_IS_IN_A_LOCKER_AT_THE_AIRPORT`
Ciphertext:	`DCEQNPGHWQDYQD_QGAUSSHHJQGNQ_TKPZIKLYKN`

Table A.2: Example polyalphabetic substitution cipher key and encryption.

The decryption process is an intuitive reversal of the encryption.

The number of possible keys for a polyalphabetic substitution cipher using an alphabet size of 27 and a block size of B is $27!^B$. This is significantly greater than the simple substitution cipher with 27! possible keys (especially for large B). The polyalphabetic substitution cipher is somewhat more difficult to cryptanalyse than the simple substitution cipher because of the independent keys used to encrypt successive characters in the plaintext. Despite this, it is still relatively simple to cryptanalyse the polyalphabetic substitution cipher based on the n-gram statistics of the plaintext language.

In Example A.1 which describes the monoalphabetic substitution cipher the most common bigram (`_A`) is mapped to the same encrypted bigram each time. This is not the case for the polyalphabetic substitution cipher. From Example A.2, it can be seen that `_A` is twice encrypted to `QG` and once to `PZ`. The encrypted value is dependent upon two factors: the individual key values and the position of the characters within the block (the two times `_A` is encrypted to `QG` the letters "`_`" and "`A`" are located in positions `1` and `2`, respectively).

The Vigenére and Beaufort ciphers are examples of polyalphabetic substitution ciphers (see [4] for descriptions).

Any attack on the polyalphabetic substitution cipher must involve determining the period as well as decrypting the ciphertext. Usually the task of determining the period is performed separately and prior to the message recovery phase. Methods for determining the period are now discussed.

A.2.1 Determining the Period of a Polyalphabetic Cipher

A number of methods for determining the block length (or period) have been reported in the literature. Two such methods are now described briefly.

Friedman [19] discovered that the *Index of Coincidence* (IC) (see also [4]) can be used to give a general indication of the period of a polyalphabetic substitution cipher. Given an intercepted ciphertext message of length K, the index of coincidence is given by Equation A.1 where f_λ denotes the frequency of character λ in the ciphertext.

$$\text{IC} = \frac{\sum_{\lambda \in \mathcal{C}} f_\lambda (f_\lambda - 1)}{K(K-1)} \tag{A.1}$$

A discussion of the theory of the IC is given in [19] and does not fall into the scope of this work. However, it can be shown that the IC and the period of a cipher are related and, providing K is sufficiently large, the IC can be used to give a reasonable indication of the block length, B. The IC can also be used to support the findings of another method, especially when more than one period is indicated by that method.

The second technique discussed here is the *Kasiski* test devised by Kasiski in 1863 (see [4]). In an encrypted message produced by a polyalphabetic substitution cipher, a particular sequence of characters may be repeated a number of times. It is highly likely (although not certain) that the repeated sequence will represent the same plaintext. In the case that the repeated sequence does represent the same plaintext, the distance between the two instances of the sequence will give an indication of the period of the cipher. All of the prime factors of the distance between the two instance are possibilities for the period of the cipher. If there are a number of different sequences in the cryptogram which are repeated, or if a particular sequence is repeated many times, then by finding the factors of all the distances between them, a good indication of the period can be obtained.

In some cases the period may actually be a multiple of one indicated by the Kasiski test. For this reason it is wise to use the Index of Coincidence to increase the certainty of the chosen period being correct. For example, to test whether or not a period of b is likely divide the cryptogram into blocks of length b and calculate the IC for each position in the block.

A.3 Transposition Ciphers

Another common technique often used in cryptographic algorithms is the permutation or transposition. In this section a simple transposition cipher is introduced. A transposition cipher works by breaking a message into fixed size blocks, and then permuting the characters within each block according to a fixed permutation, say Π. The key to the transposition cipher is simply the permutation Π. In contrast to the substitution ciphers described in the previous sections, the transposition cipher has the property that the encrypted message (i.e., the ciphertext) contains all the characters that were in the plaintext message, albeit in a different (and hopefully meaningless) order. In other words, the unigram statistics for the message are unchanged by the encryption process.

To further illustrate the concept of the transposition cipher Example A.3 is presented.

Example A.3 *The size of the permutation is known as the period. For this example a transposition cipher with a period of six is used. Let* $\Pi = \{4, 2, 1, 5, 6, 3\}$. *Then the message is broken into blocks of six characters. Upon encryption the fourth character in the block will be moved to position 1, the second remains in position 2, the first is moved to position 3, the fifth to position 4, the sixth to position 5 and the third to position 6. The message used in the previous two examples is now used to illustrate this process on a number of blocks.*

Notice that the random string "XLS" was appended to the end of the message to enforce a message length which is a multiple of the block size. Notice also that decryption can be achieved by following the same process as encryption using the "inverse" of the encryption permutation. In this case the decryption key, Π^{-1} *is equal to* $\{3, 2, 6, 1, 4, 5\}$.

From Example A.3 it can be seen that the bigram and trigram statistics are lost

KEY:

Plaintext:	123456
Ciphertext:	421563

ENCRYPTION:

Position:	123456123456123456123456123456123456123456
Plaintext:	THE_MONEY_IS_IN_A_LOCKER_AT_THE_AIRPORTXLS
Ciphertext:	_HTMOE_ENISY_I_A_NKOLERC_A_THTI_ERPAXROLST

Table A.3: Example transposition cipher key and encryption.

upon encryption. That is, there is no direct correspondence between the frequency of certain bigrams (or trigrams) in the plaintext with certain other bigrams (or trigrams) in the ciphertext. This property was not true for the substitution ciphers described above. This does not, however, imply that a suitability assessment method cannot be based on these statistics, as will be shown.

Appendix B

LFSR Based Stream Ciphers

A stream cipher produces a pseudo-random sequence of bits which are exclusive-or'ed with the plaintext to produce the ciphertext. Many stream ciphers make use of the linear feedback shift register (LFSR).

Figure B.1 illustrates a linear feedback shift register. A periodic LFSR is defined by a (primitive) feedback polynomial of degree L, the length of the LFSR. When the feedback polynomial is primitive and of degree L the shift register is known as a *maximum-length* LFSR [50]. The output sequence of a maximum length LFSR is periodic with period $2^L - 1$ and is called a m*-sequence*. Many properties of m-sequences are known.

One particular example of a LFSR-based stream cipher is the *nonlinear combiner* (see Figure B.2) which combines the output of k LFSR's using a nonlinear Boolean function to obtain the keystream. The combiner may include the previous output bit as one of its inputs, in which case the combiner is said to contain *memory*. Thus, the combiner with memory requires a nonlinear Boolean function of $k + 1$ variables and a memoryless combiner requires a nonlinear Boolean function of k inputs. The dashed line in Figure B.2 is used to represent the inclusion of memory in the combiner. The keying material for this cipher is generally the initial contents of the LFSR's. In some

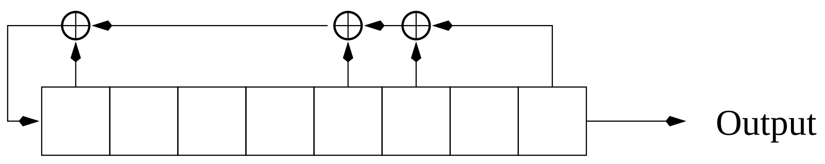


Figure B.1: A linear feedback shift register, defined by the primitive polynomial $f(x) = x^8 + x^6 + x^5 + x + 1$, with length $L = 8$.

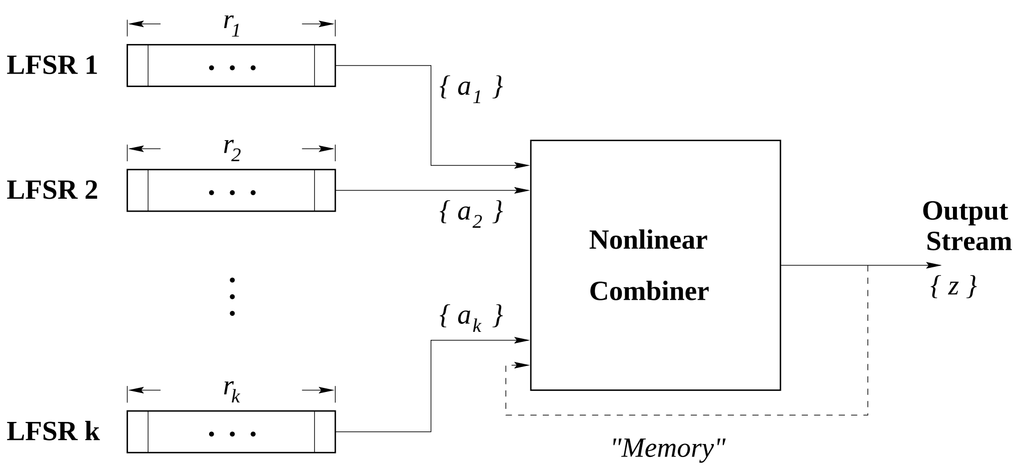


Figure B.2: A nonlinear combiner type stream cipher.

cases the feedback polynomials are assumed to be public knowledge, along with the combining function.

A cryptographic weakness with some LFSR-based stream ciphers is that the output sequence from the LFSR is correlated to the output keystream sequence of the generator. An attacker may be able reconstruct the keystream sequence if they possess some known plaintext (i.e., plaintext and its corresponding ciphertext). Given a sufficient length of the keystream sequence and knowledge of the feedback polynomial for one of the LFSR's, it is possible to reconstruct the initial contents of the shift register. Attacks using this strategy were proposed by Meier and Staffelbach [48], and Zeng and Huang [78].

Appendix C

The Merkle-Hellman Public Key Cryptosystem

Merkle and Hellman (in [51]) proposed their "knapsack" cipher in 1978. The term "knapsack" is a misnomer because the security of the cryptosystem is based on the difficulty of solving the subset sum problem, rather than the closely related knapsack problem. Since their pioneering work, many cryptosystems based on the difficulty of solving the same problem have been proposed.

The *subset sum* problem (which is defined in [22] and known to be NP-complete) can be expressed as follows: "Given $A = \{a_1, a_2, \ldots, a_n\}$ a finite set of positive integers, and B a positive integer, is there a subset $A' \subseteq A$ such that the sum of the sizes of the elements in A' is exactly B?" To break the Merkle-Hellman cryptosystem by attacking the encryption process rather than the structure of the secret key, one has to solve the following related NP-hard problem: "Given $A = \{a_1, a_2, \ldots, a_n\}$ a finite set of positive integers, and B a positive integer, find the subset $A' \subseteq A$ such that the sum of the sizes of the elements in A' is exactly B (given that A' exists)."

In the Merkle-Hellman cipher the public key is the set A and the finite field modulus, p. The public key A is formed by multiplying each element of a super-increasing sequence by a secret multiplier, w, and reducing modulo p, where gcd$(w, p) = 1$. The secret key is the super-increasing sequence and the secret multiplier, w. In general the public key A will be randomly distributed elements. Encryption is performed on n bit binary blocks by summing the elements in A which correspond to a `1` in the plaintext block. Typically w and p would be very large numbers and n should be sufficiently large to prevent an exhaustive search of the solution space. The following example describes the operations of generating a public/private key pair for a knapsack cipher and gives an example of the encryption and decryption processes.

Example C.1 *Suppose Alice wishes to establish a knapsack public/private key pair. The key pair is generated using, in this case, the parameters* $n = 8$*, the knapsack size,* $w = 500$*, the secret multiplier and* $p = 711$ *the public modulus. A super-increasing sequence* $S = \{$ *2, 5, 11, 20, 41, 85, 211, 463* $\}$ *is chosen to form part of the secret key (*S *and* w *together constitute the secret key). The public part of the key is made up of* p*, the modulus, and the set* A *obtained by multiplying the elements of* S *with* w *modulo* p*. In this instance* $A = \{$ *289, 367, 523, 46, 592, 551, 272, 425* $\}$*.* A *and* p *are published as the public key for Alice.*

Now suppose Bob wishes to send Alice an encrypted message. Binary messages are encoded in n *bit blocks. A block of Bob's message is as follows:* $M = \{$ *0, 1, 0, 1, 1, 1, 0, 1* $\}$*. The ciphertext,* C*, is computed from* A *and* p *as follows:* $C = (\sum_{i=1}^{n} a_i m_i) \bmod p$ *where* $A = \{a_1, a_2, \ldots, a_n\}$ *and* $M = \{m_1, m_2, \ldots, m_n\}$*. Thus Bob's ciphertext will be:* $C = 367 + 46 + 592 + 551 + 425 \bmod 711 = 1981 \bmod 711 = 559$*. Bob sends* $C = 559$ *to Alice.*

Alice wishes to decode Bob's message. Alice's first step is to multiply the ciphertext by the inverse of the secret multiplier (w^{-1}*) modulo* p*. Here* $w^{-1} = 155$ *and* $Cw^{-1} \bmod p = 559 \times 155 \bmod 711 = 614$*. It is then trivial for Alice to decode the message by determining the elements of* S *which add to give 614. For example, Alice can repeatedly subtract the largest possible value of* S *from the ciphertext until a value of zero results. The values from* S *used in the subtraction will correspond to 1's in the decrypted message block.*

The Merkle-Hellman cryptosystem was broken by Shamir [68] (and others) in the early 1980's. Details of the attack are given below. The problem with most knapsack-type cryptosystems is that the public key does not properly hide the structure of the secret key.

C.1 A review of Attacks on the Merkle-Hellman Cryptosystem

In this section some of the theoretical aspects of attacks on knapsack-type ciphers are presented. The analysis given here follows the description given in [70], however several attacks were presented around 1982 by Brickell [7], Shamir [68] and Desmedt et al [15].

In accordance with the notation above, $S = \{s_1, s_2, \ldots, s_n\}$ represents the super-increasing sequence which, together with the secret multiplier, w, comprises the secret portion of the public key cryptosystem.

Recall that the public key portion comprises the set $A = \{a_1, a_2, \ldots, a_n\}$ and the modulus, p. Each element of A is obtained using the relation

$$a_i = w \times s_i \bmod p.$$

Then, if w^{-1} is the modular inverse of w,

$$s_i = w^{-1} \times a_i - p \times k_i,$$

and when $i = 1$

$$s_1 = w^{-1} \times a_1 - p \times k_1.$$

Multiplying the first of these by b_1 and the second by b_i and subtracting one from the other gives

$$a_i \times k_1 - a_1 \times k_i = (a_1 \times s_i - a_i \times s_1)/p$$

Now, since $p > s_1 + s_2 + \ldots s_n$, $a_i < p$ and $s_1 < s_i$, we have

$$\begin{aligned} a_1 \times s_i - a_i \times s_1 &> a_1 \times s_i - p \times s_1 \\ &> a_1 \times s_i - p \times s_i \\ &> (a_1 - p) \times s_i \\ &> -p \times s_i \end{aligned}$$

and hence

$$|a_i \times k_1 - a_1 \times k_i| < p \times s_i/(a_1 + a_2 + \ldots + a_n).$$

A property of the super-increasing sequence is that

$$s_{i+j} \geq 2^{j-1} \times (s_i + 1),$$

or, expressed differently,

$$(s_i + 1)/s_{i+j} \leq 2^{1-j}.$$

When $j = n - i$ it follows that

$$(s_i + 1)/s_n \leq 2^{i+1-n}$$

and thus

$$s_i/(s_1 + s_2 + \ldots + s_n) < (s_i + 1)/s_n \leq 2^{i+1-n}.$$

Therefore

$$|a_i \times k_1 - a_1 \times k_i| < p \times 2^{i+1-n}$$

and, dividing by $k_i \times a_i$,

$$\begin{aligned} |k_1/k_i - a_1/a_1| &< p \times 2^{i+1-n}/(k_i \times a_i) \\ &< p \times 2^{i+1-n}/a_i. \end{aligned}$$

This results shows that the k_i are not random and can be determined using the above inequalities if p is known. Shamir showed that the final inequality can be solved using an algorithm proposed by Lenstra [39]. This attack can be used to determine the k_i in polynomial time and hence the Merkle-Hellman cryptosystem is broken easily. This attack can be used on all similar cryptosystems based on disguising a secret trapdoor sequence (in the case of the Merkle-Hellman cryptosystem, the super-increasing sequence S is the trapdoor).

Appendix D

Boolean Functions and their Cryptographic Properties

This appendix provides an introduction to Boolean functions: their representation, operators and properties.

The most basic representation of a Boolean function is by its binary truth table. The *binary truth table* of a Boolean function of n variables is denoted $f(x)$ where $f(x) \in \{0, 1\}$ and $x = \{x_1, x_2, \ldots, x_n\}, x_i \in \{0, 1\}, i = 1, \ldots, n$. The truth table contains 2^n elements corresponding to all possible combinations of the n binary inputs.

Sometimes it is desirable to consider a Boolean function over the set $\{1, -1\}$ rather than $\{0, 1\}$. The *polarity truth table* of a Boolean function is denoted $\hat{f}(x)$ where $\hat{f}(x) \in \{1, -1\}$ and $\hat{f}(x) = (-1)^{f(x)} = 1 - 2f(x)$. Thus when $f(x) = 1$ it follows that $\hat{f}(x) = -1$. It is also important to note that XOR (exclusive or) over $\{0, 1\}$ is equivalent to real multiplication over $\{1, -1\}$. Thus,

$$\begin{aligned} h(x) &= f(x) \oplus g(x) \\ \Rightarrow \hat{h}(x) &= \hat{f}(x)\hat{g}(x). \end{aligned}$$

Two fundamental properties of Boolean functions are Hamming weight and Hamming distance. The *Hamming weight* of a Boolean function is the number of ones in the binary truth table, or equivalently the number of -1s in the polarity truth table. That is, the Hamming weight of a Boolean function, hwt(f), is given by:

$$\begin{aligned} \text{hwt}(f) &= \sum_x f(x) \\ &= \frac{1}{2}\left(2^n - \sum_x \hat{f}(x)\right). \end{aligned}$$

The *Hamming distance* between two Boolean functions is the number of positions in which their truth tables differ. The Hamming distance between two Boolean functions, dist(f, g), can be calculated from either the binary truth table or the polarity truth table as follows:

$$\begin{aligned}\text{dist}(f,g) &= \sum_x (f(x) \oplus g(x)) \\ &= \frac{1}{2}\left(2^n - \sum_x (\hat{f}(x)\hat{g}(x))\right).\end{aligned}$$

How well two Boolean functions correlate is also of interest. The correlation between two Boolean functions, $c(f, g)$, gives an indication of the extent to which two functions approximate each other. The correlation is a real number in the range [-1,1] and is given by:

$$\begin{aligned}c(f,g) &= 1 - \frac{\text{dist}(f,g)}{2^{n-1}} \\ &= 2^{-n}\sum_x \hat{f}(x)\hat{g}(x).\end{aligned}$$

Complementing one of the Boolean functions truth tables does not alter the magnitude of the correlation between the two functions.

For cryptographic Boolean functions it is usually desired that there are an equal number of 0's and 1's in the binary truth table. When this is the case the function is said to be *balanced*. Balance is a primary cryptographic criterion: an imbalanced function has sub-optimum unconditional entropy (i.e., it is correlated to a constant function). The imbalance of a Boolean function is defined as:

$$\begin{aligned}I_f &= \frac{1}{2}|\sum_x \hat{f}(x)| \\ &= 2^{n-1}|c(f, \mathbf{0})|,\end{aligned}$$

where **0** denotes the constant zero Boolean function. The magnitude of the correlation between a function and the constant zero function is simply $\frac{I_f}{2^{n-1}}$. A function with zero imbalance is balanced and has no correlation to the constant functions.

A *linear* function, $L_\omega(x)$, selected by $\omega \in Z_2^n$ is defined:

$$\begin{aligned}L_\omega(x) &= \omega \cdot x \\ &= \omega_1 x_1 \oplus \omega_2 x_2 \oplus \cdots \oplus \omega_n x_n.\end{aligned}$$

An *affine* function is one of the form

$$A_\omega(x) = \omega \cdot x \oplus c,$$

where $c \in Z_2$.

The Hamming distance to linear functions is an important cryptographic property, since ciphers that employ nearly linear functions can be broken easily by a variety of methods (for example see [43, 27]). In particular, both differential and linear cryptanalysis techniques [5, 44] are resisted by highly nonlinear functions. Thus the minimum distance to any affine function is an important indicator of the cryptographic strength of a Boolean function.

The *nonlinearity* of a Boolean function is this minimum distance, or the distance to the set of affine functions. Note that complementing a Boolean function's binary truth table will not change the nonlinearity, so the magnitude of the correlation to all linear functions, of which there are 2^n, must be considered.

The Hamming distance between a pair of functions can be determined by evaluating both functions for all inputs and counting the disagreements. This process has complexity $O(2^n)$. It follows that determining the nonlinearity in this naive fashion will require $O(2^{2n})$ function evaluations, which is infeasible even for small n. However, a tool exists that enables the calculation of all linear correlation coefficients in $O(n2^n)$ operations. This is the fast Walsh-Hadamard Transform (denoted $\hat{F}(\omega)$), and its uses in cryptography and elsewhere are well known [3, 77]. The Walsh-Hadamard Transform (WHT) of a Boolean function is defined as:

$$\hat{F}(\omega) = \sum_x \hat{f}(x)\hat{L}_\omega(x).$$

It is clear from this definition that the value of $\hat{F}(\omega)$ is closely related to the Hamming distance between $f(x)$ and the linear function $L_\omega(x)$. In fact the correlation to the linear function is given by $c(f, L_\omega) = \frac{\hat{F}(\omega)}{2^n}$.

The nonlinearity, N_f, of $f(x)$ is related to the maximum magnitude of WHT values WH_{MAX} and is given by:

$$N_f = \frac{1}{2} * (2^n - \text{WH}_{\text{MAX}}).$$

Clearly in order to increase the nonlinearity, WH_{MAX} must be decreased. A function is uncorrelated with linear function $L_\omega(x)$ when $\hat{F}(\omega) = 0$. Cryptographically, it would be desirable to find Boolean functions which have all WHT values equal to zero, since such functions have no correlation to any affine functions. However, it is known [49] that such functions do not exist. A well known theorem, widely attributed to Parseval [41], states that the sum of the squares of the WHT values is the same constant for every Boolean function: $\sum_\omega \hat{F}^2(\omega) = 2^{2n}$. Thus a tradeoff exists in minimising affine correlation. When a function is altered so that its correlation to some affine function is reduced, the correlation to some other affine function is increased.

It is known that the Bent functions [65] satisfy the property that $|\hat{F}(\omega)| = 2^{\frac{n}{2}}$ for all ω. Bent functions exist only for even n, and they attain the maximum possible nonlinearity of $N_{\text{BENT}} = 2^{n-1} - 2^{\frac{n}{2}-1}$. Note, however, that Bent functions are not balanced. It is an open problem to determine an expression for the maximum nonlinearity of functions with an odd number of inputs. It is known that, for n odd, it is possible to construct a function with nonlinearity $2^{n-1} - 2^{\frac{n-1}{2}}$ by concatenating Bent functions. It is known that for $n = 3, 5, 7$ that this is in fact the upper bound of nonlinearity. The only value of n for which it is known that this value is not the upper bound is $n = 15$ [58, 59].

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