Similarity Tests for Metamorphic Virus Detection

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A metamorphic computer virus generates copies of itself using code morphing techniques. A new virus has the same functionality as the parent but it has a different internal structure. The goal of the metamorphic virus writer is to produce viral copies that have no common signature. If the viral copies are sufficiently different, they can evade signature detection, which is the most widely-used anti-virus technique.

In previous research, hidden Markov models (HMMs) have been used to detect some metamorphic viruses. However, recent research has shown that it is possible for carefully designed metamorphic viruses to evade HMM-based detection.

In this project, we analyze similarity-based techniques for detecting metamorphic viruses. We first consider a similarity index technique that was previously studied. We then consider new similarity techniques based on edit distance and pairwise sequence alignment. We test these similarity measures on the challenging problem of metamorphic virus detection. We compare our detection results with those obtained using an HMM-based detection method.

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1. INTRODUCTION

A computer virus is a program that, when executed, replicates itself without the user's permission or knowledge [13]. A virus spreads its infection by attaching itself to other executable code. The infected program, when launched, can then replicate itself to infect other executables and change their behavior [8]. Note that a virus relies in some way on other executable code to spread its infection.

A virus might perform malicious activities such as corrupting the file system by infecting batch files, macros, shell script, system sectors, companion and binary executable. Modern viruses also called worms take advantage of the Internet to propagate over the network and spread their infection globally.

Virus construction kits are available, which makes virus creation extremely simple [19]. Consequently, users who have minimal knowledge can create potential viruses. There are several antivirus programs available that can be used to detect malware [16]. The most commonly used antivirus detection technique is signature detection, which consists of searching the content of the files in file for "signatures" stored in antivirus database. A signature consists of a string of bits found in a particular virus. Another detection approach is code emulation, where code is executed in a virtual environment and its actions are recorded in log file. Based on logged action, the antivirus determines whether the program is a virus or not [16].

To evade signature-based detection, virus writers sometimes use code obfuscation techniques which alter the structure of the code. The techniques used to obfuscate code include reordering assembly instructions, dead code insertion, and equivalent instruction substitution [3]. The result is a morphed virus that has the same functionality as the original. However, if the morphing is sufficient, no common signature will exist. These metamorphic viruses generate different copies of it using code morphing techniques.

To contend with metamorphic viruses, a detection tool based on hidden Markov models (HMMs) was developed [2]. This virus detection tool is initially trained on metamorphic variants belonging to the same family. Then the trained model can be used to detect new metamorphic variants from the same family. This technique was successful at detecting all hacker-generated metamorphic viruses tested [2]. Several of the metamorphic viruses studied in [2] were not

detected by commercial virus scanners. Subsequent work has shown that it is possible to produce a metamorphic generator that can evade signature detection and HMM-based detection [3].

The goal of the research presented here is to test similarity-based approaches to see if we can detect the metamorphic viruses in [3]. Similarity index techniques classify a program as belong to virus family provided that it is sufficiently similar to a given member of the family.

This paper is organized as follows. Section 2 contains background information on computer viruses. In Section 3, we discuss antivirus techniques. Then in Section 4, we detail various code obfuscation techniques that can be used to generate highly morphed viruses. Section 5 presents the design and implementation of our several similarity-based techniques. Section 6 covers experimental results obtained from our similarity-based method experiments involving metamorphic viruses. Section 7 presents our conclusions. Finally, Section 8 presents possible future work.

2. COMPUTER VIRUS

Computer virus is self-replicating program that performs malicious activities by infecting other host files. The host files, when executed, can infect other files in turn. For example, the file infector virus, which embeds itself in the code of other host programs. The infected file can be any executable application. On execution of the infected program, virus loads itself into the computer's memory and continues to run even after the host files shut down its execution. "Before the initiation of the internet, file infector viruses accounted for probably 85% of all virus infections [11]."

A typical virus comprises of three modules [8] which are infect, trigger and payload. The method *infect* defines the process of spreading viruses by changing the host to contain a copy of the virus code. *Trigger* is a test condition, which decides to load payload or not. *Payload* defines the damage by the virus. Figure 2 shows the pseudo code which will infect the target.

```
def virus() :
        infect ()
        if trigger () is true then
                payload ()
```

```
def infect() :
        repeat k times:
                target = select_target()
                if no target then
                        return
                infect_code (target)
```

Figure 1 Pseudo Code of Virus and Infect Module [8]

3. VIRUS PREVENTION TECHNIQUES

This section outlines some of the most commonly used techniques to detect computer viruses.

3.1 Signature Detection

Signature detection technique is widely used to detect viruses. Signature is a pattern of bits found in a virus [1]. These string of bits, which are found in a virus file are stored in the antivirus databases. The virus scanner searches the entire file system for known signatures. If the known signature is found then the file is marked as infected. For example, executable file infected by "W32.Sample.A" virus comprises of the following pattern of bits as signature [12].

Virus Name : **W32.Sample.A**

Byte Signature: **0A 8E 91 82 86 4C D2**

The virus scanner searches the entire file system for this signature and if found, it declares the file to be the Beast virus.

Some virus scanners support wildcard search strings, such as "??02 34C9 8CD1 429C" where '?' indicates the wildcard. These wildcard strings permit skipped bytes and regular expressions, which also helps in detecting encrypted viruses in some cases [17].

3.2 Heuristic Analysis

Heuristic analysis is a method used by the antivirus software's to detect new or unknown computer viruses. There are two types of heuristic scanning techniques. The difference between the two approaches is whether the heuristic scanner makes use of CPU emulation to scan for virus like behavior or not. A heuristic scanner has two phases of operation when scanning files for viruses. In the first phase of the operation, the scanner observes the behavior of the program and looks for a specific area in the file where the virus would attach itself. In the second phase, it determines the program logic which can be executed by computer instructions in the specific areas identified in the first phase [10]. The program is flagged as a virus, if it contains a certain percentage of the computer instructions similar to the viral instructions.

The Heuristic analysis results in many false positives as it mostly operates on the basis of past experience [20]. This might not detect new viruses that contain code different from a previously known virus program. The heuristic scanner creates many false positives which can lose users' trust and interest.

4 VIRUS EVOLUTION

The following techniques are different strategies used by virus writers to make their viruses more difficult to detect.

4.1 Encrypted Viruses

Encryption is the simplest way to conceal a virus from the antivirus program. The encrypted virus contains an encrypted body and a decryptor module. Most of the antivirus programs attempt to find the virus by looking for a specific string of bits in a program. To avoid detection, viruses encrypt the body using the encryption key to conceal the pattern of code. Different encryption key generates a different encrypted virus body. The logic of encryption is kept simple, such as XOR, the key for encrypting the virus body [3]. The encrypted virus body is

different in all infections, but the decryptor module is similar in all infected copies. The antivirus program can detect the decryptor by its code pattern even if it cannot decrypt the virus body.

4.2 Polymorphic Viruses

Polymorphic viruses are one of the more complex techniques implemented by virus coders to overcome the disadvantage of the encrypted viruses [19]. To make it more effective than the encrypted viruses, polymorphic viruses have different methods of decryption by mutating the decryptor logic. More advanced versions of the polymorphic virus substitutes the mutually independent instructions, such as moving "0" to B or adding "0" to A, resulting in inexact values. This evades the antivirus program looking for a specific code of pattern in the virus [16]. To detect polymorphic viruses, virus scanners based on signature detection method have to search different string of bits for each likely decryption methods.

Anti-virus software even uses code emulation to detect the polymorphic virus. The code emulator lets the virus execute and observe its behavior. It emulates the decryption process and detects the decrypted virus body.

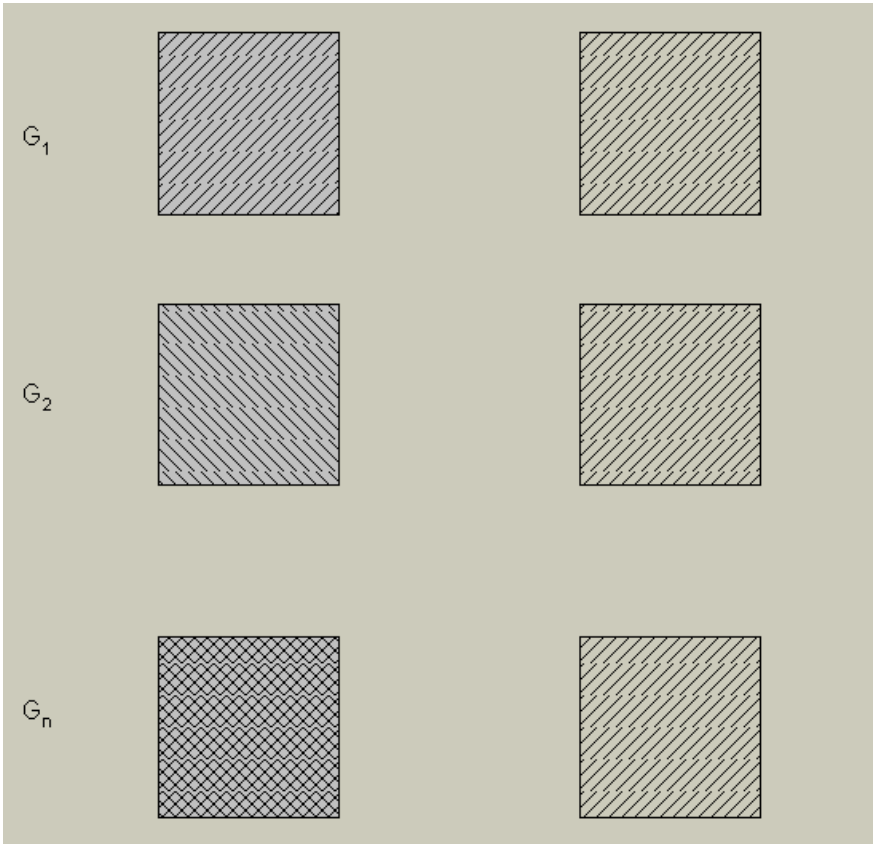


Figure 2 Polymorphic Virus Generations [18]

4.3 Metamorphic Viruses

Virus writers have developed metamorphic viruses which do not carry any decryptor or constant virus body like polymorphic viruses. A metamorphic virus changes its code at each infection by using various code obfuscation techniques. Code obfuscation techniques are performed on both the data section and the control flow of an assembly program [15]. Control flow obfuscation technique involves unconditional jump instructions and instruction reordering. Data flow obfuscation is achieved by transposition, junk code insertion, equivalent instruction substitution, register renaming, and subroutine permutation. This makes it more resistant to code emulation detection technique. Unlike polymorphic viruses, encryption is not used in metamorphic viruses. The virus body has different structures with same functional behavior. Figure 3 shows a metamorphic virus with different body structures.

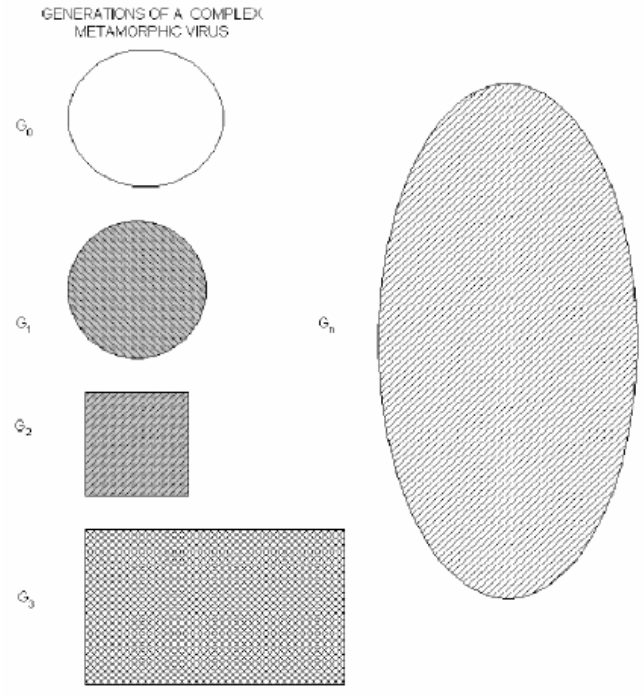
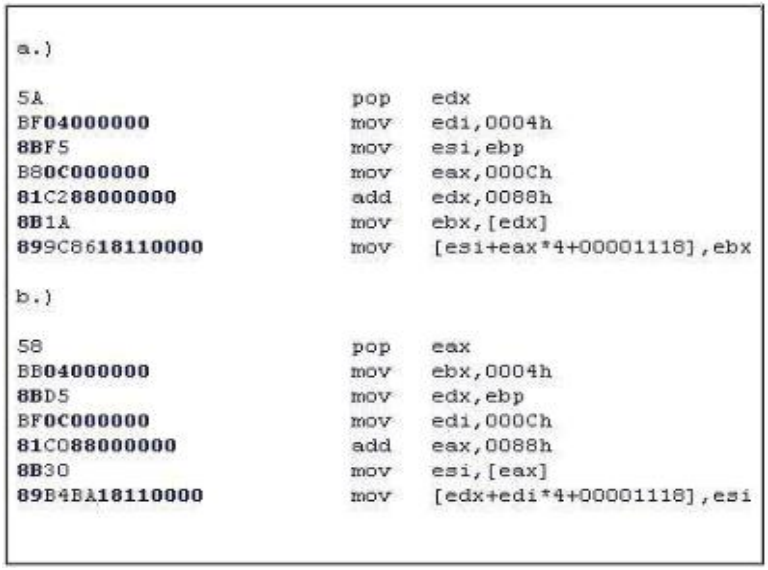


Figure 3 Metamorphic Virus Generations [18]

4.3.1 Register Swap (Register Usage Exchange)

Register swapping is one of the simplest metamorphic techniques. This technique changes register operands in the virus body with different equivalent registers. Instructions remains

constant for all virus generation, only register changes. For example, instruction “mov edi, 0004h” can be substituted with “mov ebx, 0004h.” The W95/RegSwap virus [7] is an example of metamorphic virus that uses the register swap technique. Figure 4 shows a sample code snippet from RegSwap, which follows register swapping technique. Wildcard string can usually detect such metamorphic viruses [17].



```
a.)

5A                      pop   edx
BF04000000              mov   edi,0004h
8BF5                    mov   esi,ebp
B80C000000              mov   eax,000Ch
81C288000000            add   edx,0088h
8B1A                    mov   ebx,[edx]
899C8618110000          mov   [esi+eax*4+00001118],ebx

b.)

58                      pop   eax
BB04000000              mov   ebx,0004h
8BD5                    mov   edx,ebp
BF0C000000              mov   edi,000Ch
81C088000000            add   eax,0088h
8B30                    mov   esi,[eax]
89B4BA18110000          mov   [edx+edi*4+00001118],esi
```

Figure 4 Two Different Generations of RegSwap [9]

4.3.2 Junk Instruction Insertion

Junk code insertion is an effective technique employed by metamorphic viruses to change the appearance of the virus body. Junk instructions do not have an effect on the program outcome and it may not even execute [13]. Examples of do-nothing instructions are “mov edx, edx”, “add R1, 0”, “sub R1, 0” or “nop.”

Dead code insertion can be done as a single instruction or a block of instructions between the core instructions. Figure 5 shows the example of the Evol virus which implemented the junk code insertion technique by adding a block of dead code.

```
C7060F000055    mov [esi], 5500000Fh
C746048BEC5151  mov [esi+0004], 5151EC8Bh
```

```
BF0F00055     mov edi, 5500000Fh
893E          mov [esi], edi
5F            pop edi              ; garbage
52            push edx             ; garbage
B640          mov dh, 40           ; garbage
BA8BEC5151    mov edx, 5151EC8Bh
53            push ebx             ; garbage
8BDA          mov ebx, edx
895E04        mov [esi+0004}, ebx
```

Figure 5 Dead Code Insertion in Evol Virus [14]

4.3.3 Equivalent Instruction Substitution

Equivalent instruction substitution is another useful technique used to substitute an instruction or a block of instructions with an equivalent instruction or an equivalent block of instructions. For example, "push edx," "pop eax" can be substituted by "add eax,1" followed by "mov eax,edx." Table 1 shows the W32/MetaPhor virus [15] implementing instruction substitution. The "mov reg,imm" operation is equivalent to "mov mem,reg" followed by "op mem,reg2" and "mov reg,mem."

Single Instruction	Instruction block
XOR Reg,Reg	MOV Reg,0
MOV Reg,Imm	PUSH Imm POP Reg

OP Reg,Reg2	MOV Mem,Reg
	OP Mem,Reg2
	MOV Reg,Mem

Table 1 W32.MetaPhor Instruction Substitution [15]

4.3.4 Instruction Transposition

Transposition is a method to change the order of execution of the instructions. Instruction permutation between the instructions does not affect the program outcome and it can be applied only if there is no mutual dependency between the instructions. Consider the following instruction set:

(op1 r1, r2)
(op2 r3, r4) // r1 and/or r3 register are to be modified

The instructions can be reordered only if following conditions are satisfied:

i) r1 is not equal to r4,
ii) r2 is not equal to r3,
iii) r1 is not equal to r3,

For example, instructions “mov edx,eax” and “add ecx,3” can be swapped as they satisfy the transpose criteria.

…		…
mov edx,eax	⟺	add ecx,3
add ecx,3		mov edx,eax

4.3.5 Subroutine Transposition

Subroutine transposition is an effective technique that changes the appearance of a virus by reordering the subroutines. There can be n! different generation of subroutines for n different subroutines. The W32/Ghost virus [15] implements the subroutine transposition technique. This virus contains 10 subroutines generating 10! distinct copies. Detection of such virus can be accomplished by the string driven pattern detection technique.

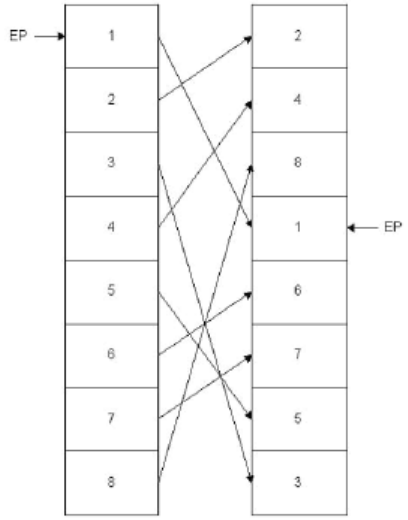


Figure 6 Subroutine Transposition

5 SIMILARITY-BASED TECHNIQUES

To evade the signature based detection and HMM-based detection, the metamorphic generator produces highly morphed copies of itself [3]. Each generation of viruses is different in structure. We consider different similarity-based approaches to see if we can detect the highly morphed viruses [3]. The similarity-based methods measure the similarity between the dissimilar virus copies. It classifies a program as belonging to a virus family or non-virus family based on the similarity results obtained by comparisons between several virus and non-virus programs; between virus programs; and between non-virus programs. We first considered a similarity index technique that was previously studied [4]. We then considered new similarity techniques based on edit distance and pairwise sequence alignment methods.

5.1 Similarity Index Test Method

To measure the similarity between the virus copies, two assembly files are compared based on the op-code sequence presented in them. The following steps are followed to compute the similarity between two files and are graphically illustrated in Figure 7.

1. Given two assembly files, file1.asm and file2.asm, we extract the sequence of op-codes from both the files, excluding labels, comments, blank lines and other directives. Let's call these resulting op-code sequences F1 and F2 for file1.asm and file2.asm, respectively. Let m and n represent the number of op-codes in F1 and F2, respectively. A number is assigned to each of the op-code in the resulting op-code sequence: 1 for the first op-code, 2 for the second, and so on.

2. Op-code sequence is divided into subsequences of three consecutive op-codes as shown in Figure 8. We compare the op-code sequences, F1 and F2, considering all the subsequences of three consecutive op-codes from each sequence. We considered a match, if three op-codes are the same in any order. For example F1 is (add, call, test, sub, mov) and F2 is (mov, add, call, sub, test). The sequence (call, test, sub) in F1 matches with (call, sub, test) of F2. The process is repeated for all the op-codes in F1 and F2.

   For example:

Opcode	Op-code sequence

Index	F1	F2
0	add	mov
1	call	add
2	test	call
3	sub	sub
4	mov	test

Table 2 File Op-code Sequences

3. As shown in Figure 7, m and n represents total number of op-code in F1 and F2 respectively. To find the total number of matches in F1, all matches are computed and added together. The total number of match is divided by m to get the similarity score of F1. Similarly, similarity score for F2 is computed.
   Similarity score for F1: S1= (total number of matches in F1) / m
   Similarity score for F2: S2= (total number of matches in F2) / n

4. The similarity score between the files, file1.asm and file2.asm is obtained by taking the average of F1 and F2.
   Total Similarity Score: (S1+S2)/2

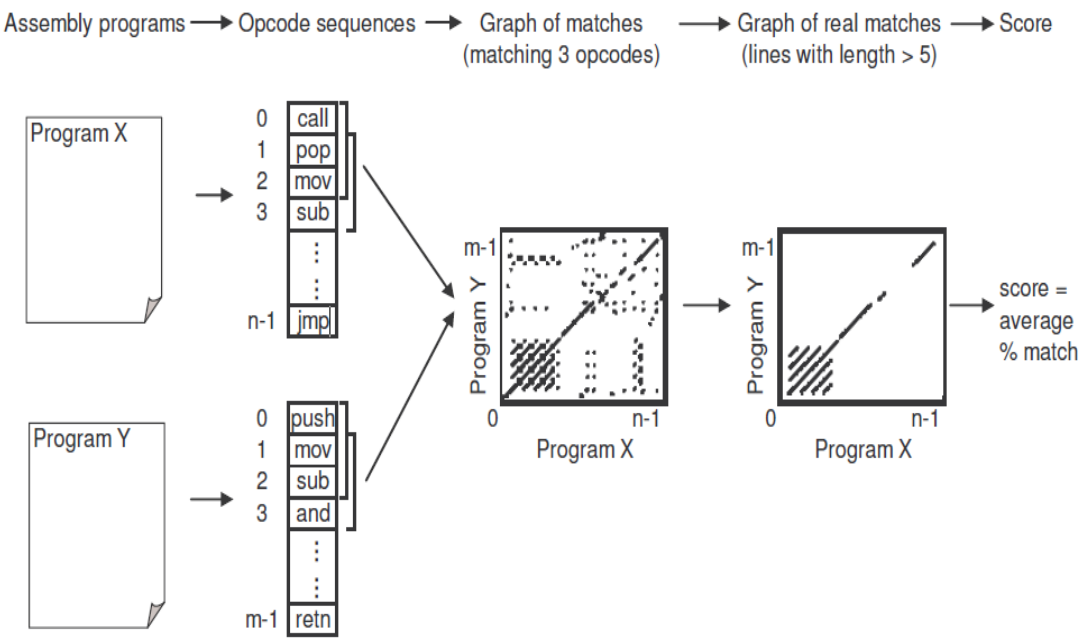


Figure 7 Similarity between Two Assembly Programs

A graph is generated to show the similarity of the assembly files. The following steps are followed to generate the graph:

1 We mark the match on the graph coordinate(X,Y) where X represents the op-code number of the first op-code of the three op-code subsequence in file F1, and Y represents the op-code number of the op-code subsequence in file F2.

2 A graph can plot a grid of dimension n × m to visualize the similarity of both files by marking all the matched coordinates. The x-axis represents the op-code numbers of file F1 and the y-axis represents the op-code numbers of file F2.

3 The graph in Figure 7 is very populated with the matches. This makes it difficult to understand the similarity. So to remove noise and to make similarity index technique more efficient, we determine a window size (i.e. threshold). The similarity score match below the window size is dropped. In Figure 7, the window size forms the line segments having the length greater than 5.

5.2 Edit Distance

Levenshtein distance (i.e. an edit distance) is an algorithm to measure the number of edit operations needed to transform one string into another [23]. For given string s1 and s2, the edit distance is calculated based on the amount of difference between the two sequences of the strings. The difference in the strings is based on the sequence of characters each string contains. Allowable edit operation to transform one into another are insertion, deletion and substitution.

For example, the edit distance between "meeting" and "readings" is 4, as the following four edits are required to change one string into the other, and there is no alternate way to get the same result in fewer than four edits [23]:

1. meeting → reeting (substitution of 'r' for 'm')
2. reeting →reating (substitution of 'a' for 'e')
3. reating → reading (substitution of 'd' for 't')
4. reading → readings (insertion of 's' at the end)

5.2.1 Computing Edit Distance

For a given two sequence s1 and s2 and three edit operations, the edit distance for the sequences is valued to transform sequence s1 to sequence s2. We use dynamic programming to find the edit distance from s1 to s2.

If s1 has n characters and s2 has m characters, D(i,j) is the least distance between the first i characters of s1 and the first j characters of s2. So the edit distance between s1 and s2 is given by D(n,m) .

D(i,0) = i , as i deletions are required to transform a string with i characters to the empty string

D(0,j) = j, as j insertions are required to transform an empty string into a j character string

In general

D(i,j) = min {[D(i-1,j)+1], [D(i,j-1)+1], [D(i-1,j-1)+ (0, if s1[i])=s2[j] or 1, if s1[i] != s2[j])] }

The psuedocode is pointed directly ahead as shown in Figure 8.

```
int LevenshteinDistance(char s[1..m], char t[1..n])
{
  // for all i and j, d[i,j] will hold the Levenshtein distance between
  // the first i characters of s and the first j characters of t;
  // note that d has (m+1)x(n+1) values
  declare int d[0..m, 0..n]

  for i from 0 to m
    d[i, 0] := i // the distance of any first string to an empty second string
  for j from 0 to n
    d[0, j] := j // the distance of any second string to an empty first string

  for j from 1 to n
  {
    for i from 1 to m
    {
      if s[i] = t[j] then
        d[i, j] := d[i-1, j-1]       // no operation required
      else
        d[i, j] := minimum
                   (
                     d[i-1, j] + 1,  // a deletion
                     d[i, j-1] + 1,  // an insertion
                     d[i-1, j-1] + 1 // a substitution
                   )
    }
  }

  return d[m,n]
}
```

Figure 8 Pseudo code for Levenshtein Distance [23]

We can draw an (n+1)*(m+1) matrix, following the pseudocode by filling it, top to bottom, left to right. The initial row and column can be filled as mentioned above, proceeding row by row to fill the remaning entries in the matrix. The matrix shown in Figure 9, gives the edit distance between MEETING and READINGS. The total entries in the matrix is O(mn) and each computation takes O(1) constant time. The total running time is O(mn).

		m	e	e	t	i	n	g
	0	1	2	3	4	5	6	7
r	1	1	2	3	4	5	6	7
e	2	2	1	2	3	4	5	6
a	3	3	2	2	3	4	5	6
d	4	4	3	3	3	4	5	6
i	5	5	4	4	4	3	4	5
n	6	6	5	5	5	4	3	4
g	7	7	6	6	6	5	4	3
s	8	8	7	7	7	6	5	4

```
meeting-
 |  |||
readings
d(s1,s2)=4
```

Figure 9 Edit Distance between String s1 and s2

5.2.2 Edit Distance for Op-code Sequences

To find similarity between two virus files, all the op-codes from each assembly file were extracted and the comparison between the op-codes present in both the virus files were done. The edit distance technique deals with the sequence of the characters and finds the edit score. To use the edit distance technique for finding the similarity between virus copies, we assigned unique symbols to each op-code. For scoring edit distance, we have only considered the op-codes that appear in the Table 3.

OP-CODE	SYMBOL	OP-CODE	SYMBOL
xchg	a	**lea**	v
jmp	b	**popad**	w
mov	c	**pushad**	x
adc	d	**pop**	y
add	e	**push**	z
and	f	**jnz**	A
cmp	g	**jz**	B
sbb	h	**nop**	C
sub	i	**rep**	D
xor	j	**retn**	E
div	k	**ret**	F

mul	l	**movzx**	1
neg	m	**movsd**	2
not	n	**movsb**	3
shl	o	**stosb**	4
shr	p	**stosd**	5
test	q	**Lodsb**	6
inc	r	**Lodsd**	7
call	s	**invoke**	8
dec	t	**stdcall**	9
or	u		

Table 3 Op-code to Symbol Conversion

The following steps are followed to compute the similarity between two files:

1. Given two assembly files, file1.asm and file2.asm, op-code sequence are extracted from both the files as described in Section 5.1. Let's give names to the resulting op-code sequence from file1.asm and file2.asm as F1 and F2.

2. Replace each op-code with their respective symbol as shown in Table 3. As a result, the sequence of symbols F1 and F2 is formed from sequence of op-codes F1 and F2.

3. The above steps allow the edit distance technique to calculate the number of edit operations required to convert the sequence of symbols from F1 to F2. The length, x and y is number of symbols in F1 and F2 respectively. ed(x,y) is the edit distance score for F1 and F2.

4. Similarity between two programs of length x and y respectively is:

   [1 - ed(x, y) / max(x, y)]

5.3 Pairwise Sequence Alignment Method

The sequence alignment is a method which arranges different sequences of DNA, or protein to determine the region of similarity due to structural, or functional relationships between the

sequences. Aligned sequences of nucleotide or amino acid are represented as rows in matrix, and symbols as individual columns [25].

5.3.2 Op-code Conversion

A disassembled virus program is sequence of op-codes. Previous studies in [26] have showed that instead of considering all the instructions, only 36 high level op-code instructions are taken into account while aligning pairs of op-code sequences. The most frequently used op-codes will be considered and each of them is assigned with a single character as a symbol. The symbols are the letters from the English alphabet and single numerical digits. The rest of the op-codes are assigned with an asterisk '*' [26].

By this approach, less number of unique op-codes are aligned in an op-code sequence. The top 14 op-codes account for approximately 90% of all the instructions used in any typical program [27]. In this research, the 36 most frequently used op-codes accounted for approximately 99.3% of all op-codes found in sequences [26].

Op-Code	Rep
ÄÄÄÄ	;
ÛÛÛÛ	|
mov	A
add	B
push	C
pop	D
call	E
sub	F
cmp	G
jz	H
retn	I
jnz	J
jmp	K
dec	L
xor	M
inc	N
lea	O
and	P

Op-Code	Rep
jb	Q
or	R
shl	S
clc	T
test	U
stc	V
not	W
adc	X
rcl	Y
cld	Z
neg	0
ror	1
shr	2
rol	3
imul	4
div	5
jnb	6

Op-Code	Rep
xchg	7
ja	8
sbb	9
sar	*
stosd	*
rcr	*
rep	*
lodsw	*
stosw	*
lodsd	*
stosb	*
lodsb	*
loop	*
in	*
retf	*
std	*
jnp	*

Op-Code	Rep
Bound	*
js	*
jp	*
fild	*
fld	*
scasb	*
aad	*
enter	*
cmc	*
jns	*
jno	*
jecxz	*
hlt	*
icebp	*
jle	*
fnstenv	*
out	*

Figure 10 Op-code to Symbol Lookup Mapping [26]

The representation of unique op-codes and their symbols is shown in Figure 10. The op-codes are shown by the frequency, where op-code ‘mov’ assigned with symbol ‘A’ is most frequent and least frequent op-code ‘sbb’ with symbol ‘9’ [26]. The op-codes with the asterisk ‘*’ symbol rarely appears.

5.3.3 Pairwise Alignment Scoring

The op-code conversion is done as described in Section 5.3.1. To detect the metamorphic viruses, a proper alignment approach needs to be defined. For the same pair of sequences, no alignment is required. In pairwise alignment, sequences are represented as rows in matrix, and symbols as individual columns. All the symbols in sequence 1 are aligned with the symbols in sequence 2 to get related symbols aligned in the same column [26]. A special character dash ‘-’ is inserted into either sequence to achieve the expected result.

In Figure 11, an alignment of two op-code sequences from NGVCK virus is shown. There are several matched sequences of small lengths from 3 to 10.

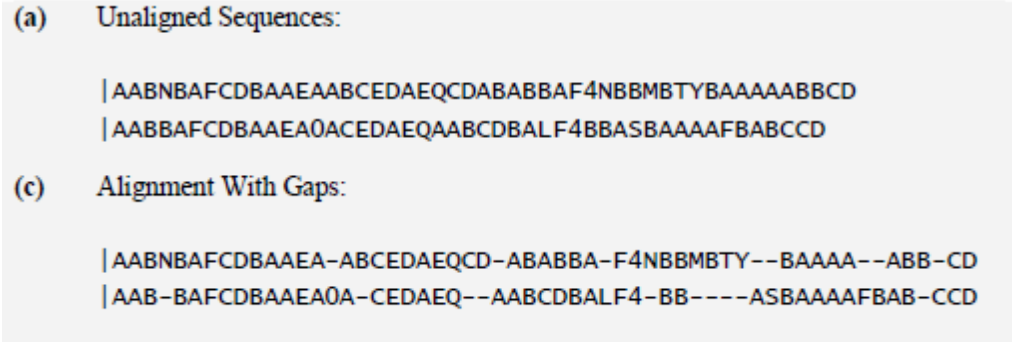


Figure 11 Alignment of two Op-code Sequences from NGVCK Virus [26]

5.3.4 Substitution Matrices and Gap Penalties

The decision of scoring the alignment is very important. The score indicates the similarity of the sequences. In the substitution matrices, the scoring matrix for sequence having 50 symbols will be 50*50 in size. The alignment function rewards matches and penalizes mismatches and spaces [24].

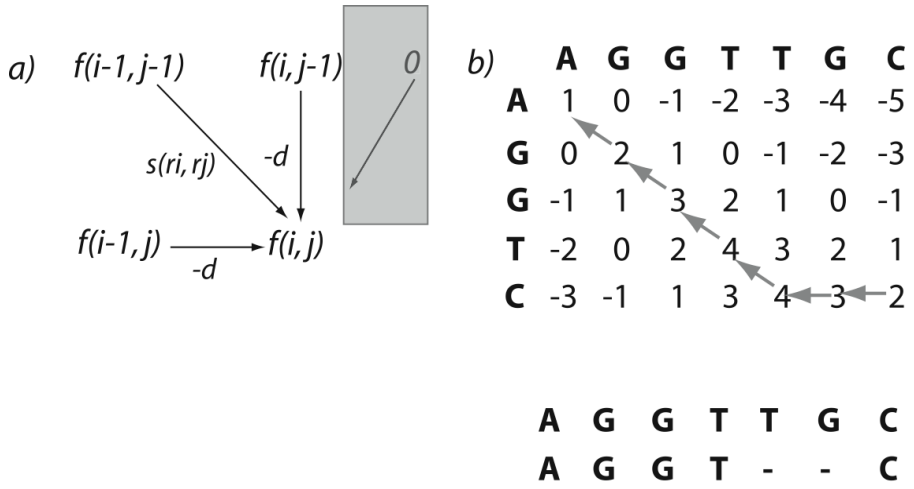


Figure 12 Substitution Matrix for AGGTTGC and AGGTC [28]

As shown in Figure 12, substituting 'G' with 'A' will be penalized by the alignment function with score -1, whereas for a match of symbol 'A' with 'A' will have score of +1.

We need to find a similar scoring model which can be applied to the op-codes. After careful research for scoring values, the scoring matrix used in this paper is shown in Figure 13 [26].

	;	|	A	B	C	...	9	*
;	1	1	-20	-20	-20	...	-20	-20
|	1	1	-20	-20	-20	...	-20	-20
A	-20	-20	2	-1	-1	...	-1	-1
B	-20	-20	-1	2	-1	...	-1	-1
C	-20	-20	-1	-1	2	...	-1	-1
...	...	...	...	...	...	...	...	...
9	-20	-20	-1	-1	-1	...	2	-1
*	-20	-20	-1	-1	-1	...	-1	1

Figure 13 Substitution Matrix for Op-codes with Values for Relative Scores

In Figure 13, the high positive score(+2) is given for two exact same symbols, a medium positive score(+1) for two rare symbols, low negative score for two different symbols(-1), low positive score(+1) for aligning two "markers" and high negative score(-20) for a marker matching with non marker.

The gap penalties are defined in two ways:

1. Linear gap penalty – The penalty is defined as a product of gap determined by the size of gap : f(g) = c.g where c represents gap cost and g represents gap size.

2. Affine gap penalty – The initial gap cost is taken for the first gap and the varying cost for every subsequent gap. f(g) = c + e.(g-1), where c represents the initial gap cost, and e represents the gap extension cost [26].

In this paper, affine gap penalty values from [26] is taken into consideration. The algorithmn description shown below is taken from [26][29].

Pairwise Alignment Algorithm Specification

Definitions

x = first sequence

y = second sequence

$|a|$ = length of sequence a

a_i = indicates the ith symbol of sequence a

$a_{i...j}$ = subsequence of a with indices i to j, where $a \equiv a_{1...|a|}$

$s(a, b)$ = score assigned to substituting symbols a with b

$g(n)$ = cost of adding one gap to a sequence with n-1 gaps

F and G = matrix of size $|x|+1 \times |y|+1$ (indices will be 0 based)

$F(i, j)$ = optimal score for aligning $x_{1...i}$ with $y_{1...j}$

$G(i, j)$ = number of subsequent gaps used to generate $F(i, j)$

Recursive definition of F and G for i, j ≥ 0

$G(i, 0) = F(i, 0) = 0$

$G(0, j) = j$

$F(0, j) = \sum_{n=1}^{j} g(n)$ (the cost of aligning j gaps)

$$F(i,j) = \max \begin{cases} F(i-1, j-1) + s(x_i, y_i), & \text{(case 1)} \\ F(i-1, j) - g(G(i-1, j)), & \text{(case 2)} \\ F(i, j-1) - g(G(i, j-1)). & \text{(case 3)} \end{cases}$$

if (case 1) $G(i, j) = 0$
if (case 2) $G(i, j) = G(i-1, j)+1$
if (case 3) $G(i, j) = G(i, j-1)+1$

Pseudo code:

Initialize the first row in F and G : $G(0, j) = j$ and $F(0, j) = \sum_{n=1}^{j} g(n)$

For each row i, 1…|x|

Initialize $F(i, 0) = 0$ and $G(i, 0) = 0$

For each column j, 1…|y|

(i - 1, j - 1), (i - 1, j) and (i, j - 1) for F and G are all known

Calculate $F(i, j)$ and $G(i, j)$ using the recursive definition

5.3.5 Scoring Pairwise Op-code Sequence Alignment

The following steps were performed to test the similarity between op-code sequences from NGVCK generated viruses and various normal files [2]:

1. Several base viruses (NGVCK) and non virus files from [2] were taken to test this technique. Op-codes from each program were extracted and assigned with their respective symbols as described in Section 5.3.1.
2. The conversion of op-code to symbols was done based on Figure 10. The Scoring substitution matrix used for aligning the sequences was based on Figure 13. The affine gap scoring mechanism is used to penalize spaces in the sequences. After several trials, the gap open cost taken is 10 and gap extension cost is 1.
3. Tests were conducted based on different set of programs. To get the similarity score between two sequences, the alignment score S is computed as described in Section 5.3.2. Let X be the resultant length of one of the sequences after being aligned.
4. After that, the similarity between the two sequences was computed using an alignment score S and the resultant length X of one of the sequences. The similarity score between the sequences is equal to alignment score divided by the total length of the either of the sequences i.e. Score = (S / X).

6 EXPERIMENTS AND RESULTS

6.1 Similarity Index

Analyses of different programs are made to determine the results of the similarity score by the similarity index technique. Comparison is done between 40 randomly selected utility files from the Cygwin DLL [22] and 40 viruses generated from NGVCK metamorphic engine [2].

Virus executables and random cygwin executables were disassembled using IDA Pro generating disassembled virus ASM files and disassembled random ASM files. Analyzing the similarity score of these assembly files is required.

6.1.1 Base Virus

The straightforward way to detect virus file would work as follows. To distinguish whether a file belongs to the base viruses generated by NGVCK engine [2] or the morphed copies of base

viruses generated by the improved metamorphic engine [3], we compute the similarity score between the virus file and the normal file. If the score falls below the "threshold value" then the program is classified as a family virus (i.e. belonging to the NGVCK virus family). A threshold value is the least similar score determined between normal files. We compare similarity scores between normal files, between normal and base virus files, and between normal and morphed copies of base virus with different percentages of subroutine and dead code insertion. If the similarity of an unknown file with non-virus file is lower than the threshold value, then the unknown file is classified as family virus. If the similarity score of any file with non-virus file is greater than the threshold value, then it belongs to the non-virus family.

We compared each of the normal files with all the other normal files; and in the same way each of the virus files with all other virus files. The similarity score was computed for each pair of virus variants and normal files using the similarity method described above in Section 5.1. The similarity score of all comparisons is listed in Table A-1 and Table A-2 in Appendix A. Figure 14 shows the similarity score of 120 pair-wise comparisons between 16 normal files and the 120 pair wise comparisons among 16 Normal files and 16 NGVCK base virus files. Apparently, the similarities between normal files are higher than those between normal files and virus files. At no point, does the similarity score between the normal files falls in region of similarity score of normal and virus files. Therefore, any file, when compared to a normal file, which has a similarity score less than 3%, belongs to a virus family; and furthermore identifies that the program belongs to normal file family or virus family.

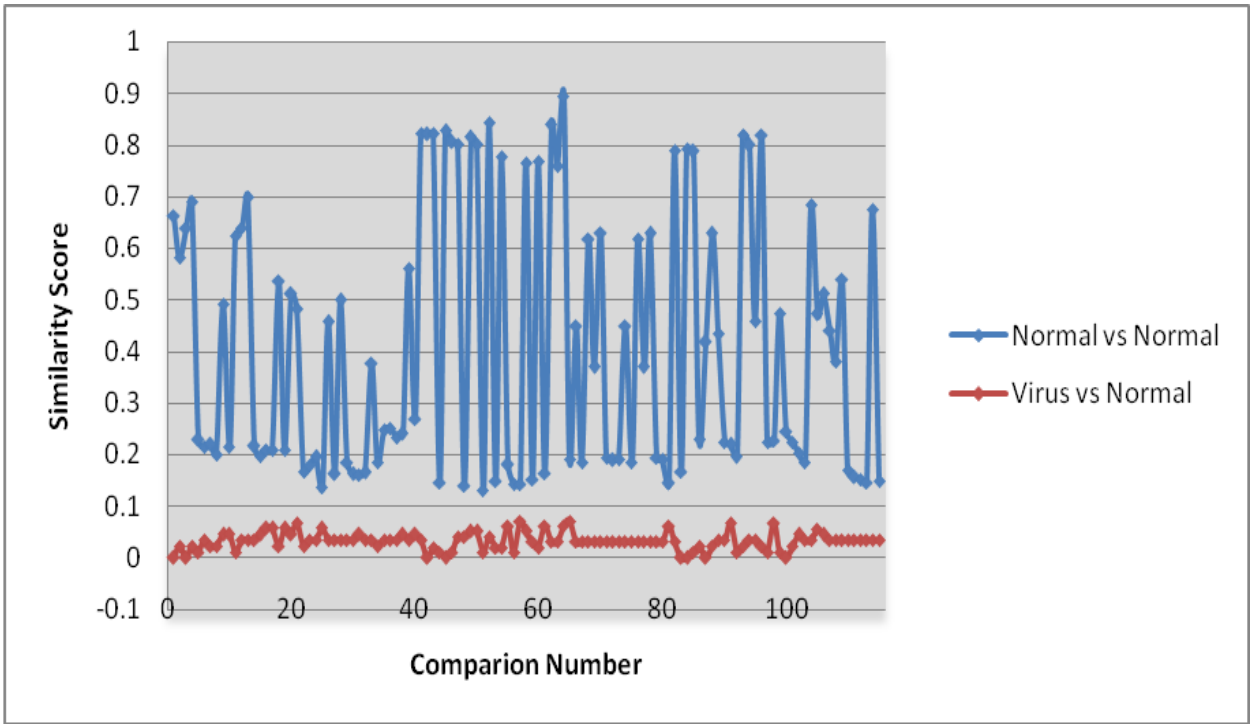


Figure 14 Similarity Scores between Normal Files and between Virus and Normal files.

The minimum, maximum and average similarity scores from Figure 14 are summarized in Table 4. The minimum similarity score between normal file is taken as a threshold value, which is 13.6%. The viruses generated by NGVCK engine in [2] have the maximum similarity score of 5% with non-virus files, which is less then the threshold value of 13.06%. As discussed above, using the threshold value of 13.06%, all the base viruses(NGVCK) are completely detected using similarity index technique with no false positives and no false negatives.

	Base Virus vs. Normal	Normal vs. Normal
Min	0	0.1306
Max	0.05	0.8936
Average	0.02	0.3865

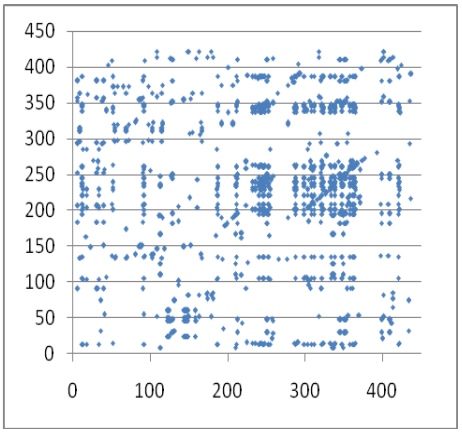
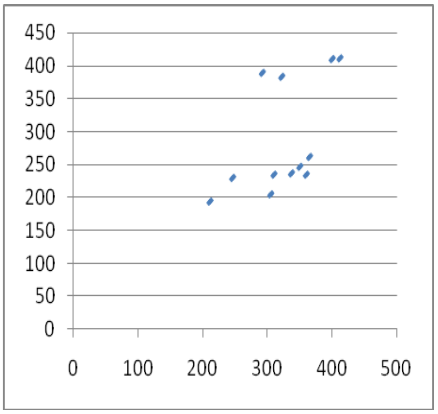
Table 4 Similarity Scores between Virus and Normal Files, and between Normal Files.

Table 5 shows the similarity graphs of NGVCK virus pair, other family viruses and one normal file pair. To show how different the virus pairs are, the first column represents the type of virus

and its similarity score. The second column shows the graph representing the similarity scores for all the matches as described in Section 5.1. The third column represents the graph after removing noise by considering a match only when the line length is greater then 5. NGVCK virus pairs are denoted by IDAN. Comparing IDAN1 with IDAN2 gives a similarity score of 13.9%.

IDAV1 is the other family virus file than NGVCK which has a similarity score of 67.7% when compared to IDAV2. The IDAR denotes the normal file having a similarity score of 39.2%. Clearly, NGVCK has less similarity then the other virus pairs and they are dissimilar from the other viruses. Normal file pairs have more similarity than the NGVCK virus pair but has a lower similarity than other family virus pair.

All the matches in the IDAV virus pair forms the diagonal line in the graph which indicates that both the virus variants have identical op-codes at an identical position. This kind of similarity match represents poor metamorphism. On the other hand, NGVCK virus pair has a better metamorphism power, as all the similarity matches are scattered in the graph and falls far away from the diagonal line.

Virus Pair (Similarity score)	Graph (all matches)	Optimized Graph (removing noise by match of length > 5)
IDAN1_IDAN2 (13.9%)		

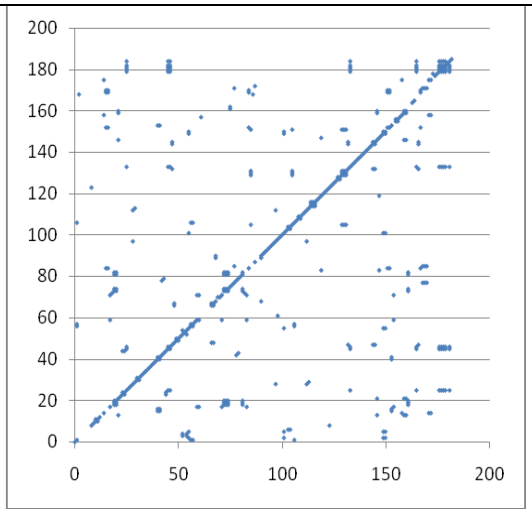
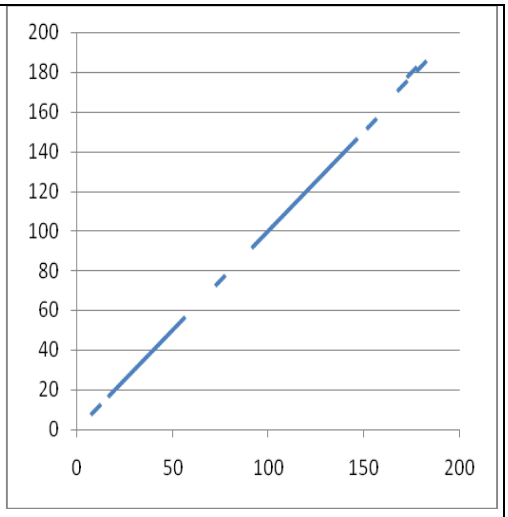
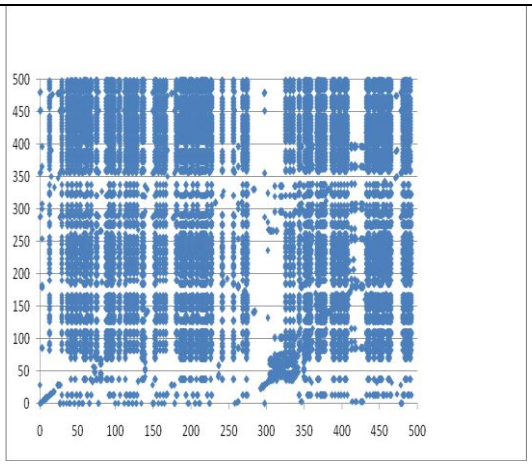
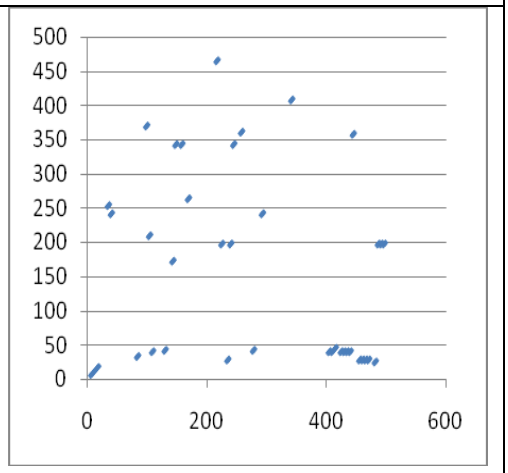
IDAV1_IDAV2 (67.7%)		
IDAR1_IDAR2 (39.2%)		

Table 5 Similarity Graphs for Two Chosen Virus Pair and One Normal File Pair

6.1.2 Morphed Virus

We repeated our test for morphed viruses generated with different engine settings in [3] (i.e., morphed copies of viruses were generated by varying the number of subroutines and junk codes copied from the normal file to the base NGVCK generated virus file). Several morphed virus comparisons were made with the normal file to find the threshold at which the similarity index classified the morphed virus file from the normal file. We started with insertion of 5% junk code, which included the subroutine insertion and junk instruction insertions. With an increase in the percentage of dead code insertion from normal file to virus file, the similarity score increases as we expected. This also results in increase in size of the morphed virus file. The 5% junk code

insertion was followed by 10%, 15%, 25%, and 30% junk code insertion from normal file to the virus file. Table 6 shows the similarity between the non-virus files and the morphed virus files with an increase in the percentage of dead code insertion.

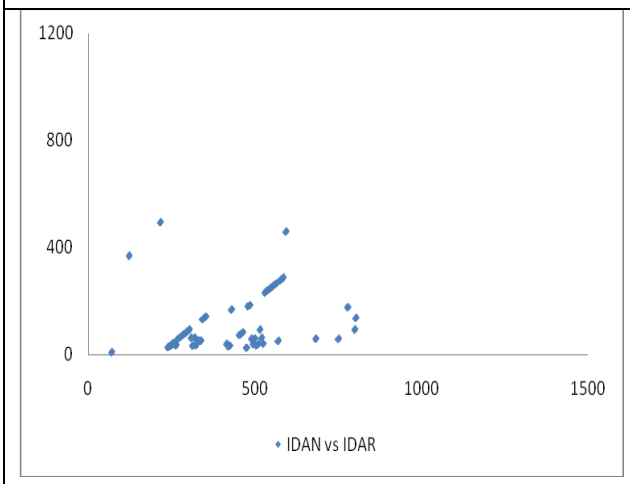
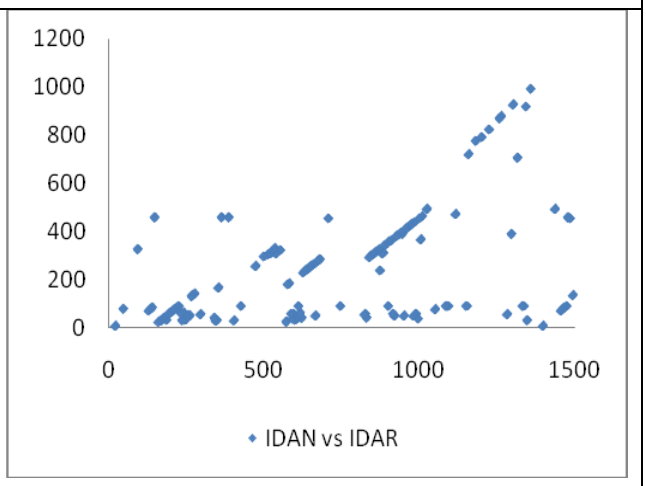
Morphed virus file with 5% of junk code insertion (Window size 5)	Morphed virus file with 30% of junk code insertion (Window size 5)
	

Table 6 Similarity Graphs between the Morphed Virus and the Normal File

Large amount of junk code insertion, results in a greater similarity score. That in turn, destroys the feature of the IDAN virus files as it has less similarity than the other virus pairs (like IDAV) as shown in Table 5. Since the junk code blocks copied from a normal file were of different sizes, we will use the increase in file size percentages as y-axis for our graph. Figure 15 shows an increase in percentage of file size with an increase in the percentage of dead code insertions from normal file to virus file.

Figure 15 Graph of File Size and different Percentage of Junk Code Insertion

6.1.3 Similarity Among Same Family Viruses

We performed several tests to score the similarities between base virus pairs, and between morphed virus pairs. NGVCK (Next Generation Virus Creation Kit) base viruses were compared with each other using the similarity index. Initially, base viruses were compared with each other, followed by comparisons between morphed viruses with different percentages of dead code insertion. The results were gathered and all the matches were plotted on graph. The base viruses were about 10.86% similar among themselves. These viruses gave a lower similarity when compared with normal files (0 to 3%). The morphed viruses with 5% of junk code insertion have about 17% of similarity among themselves. The similarity score increases to 40% with 15% of junk code insertion. All the similarity score matches are plotted on graph as shown in Figure 16 and listed in Table B-1 in Appendix B.

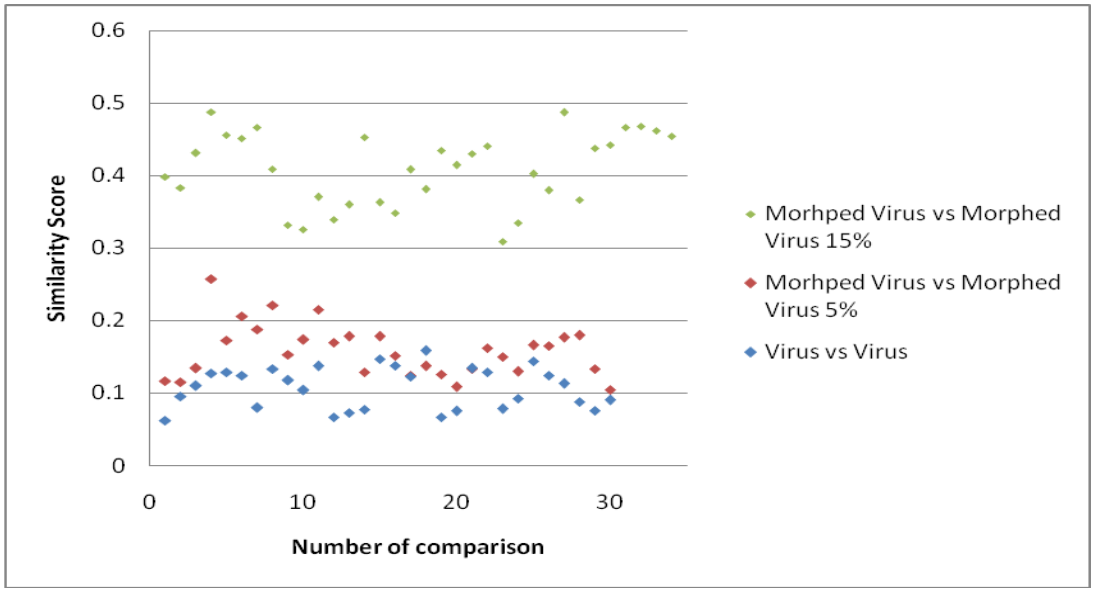


Figure 16 Similarity Graph of Scores for Base Viruses, and Morphed Viruses

6.1.4 Morphed Virus Detection using a Default Window Size

We carried out several similarity tests for a default window size of 5 (i.e. only matches having line of length greater than 5 were consider as described in Section 5.1) for morphed viruses generated by metamorphic engine in [3]. The amount of dead code insertion was varied every time and similarity score results were plotted on graph. Figure 17 shows the similarity between various morphed virus files (i.e., formed by different percentage of dead code insertion from normal file) and normal files, between normal files, and between base viruses and normal files.

The increase in percentage of dead code blocks and subroutine blocks to a virus file from normal files results in a higher similarity between generated morphed files by metamorphic engine in [3] and normal files. We inserted junk code of various percentages starting from 5%, 15%, 25%, and 30% into the virus file, which resulted with the generated morphed virus file looking more similar to normal file.

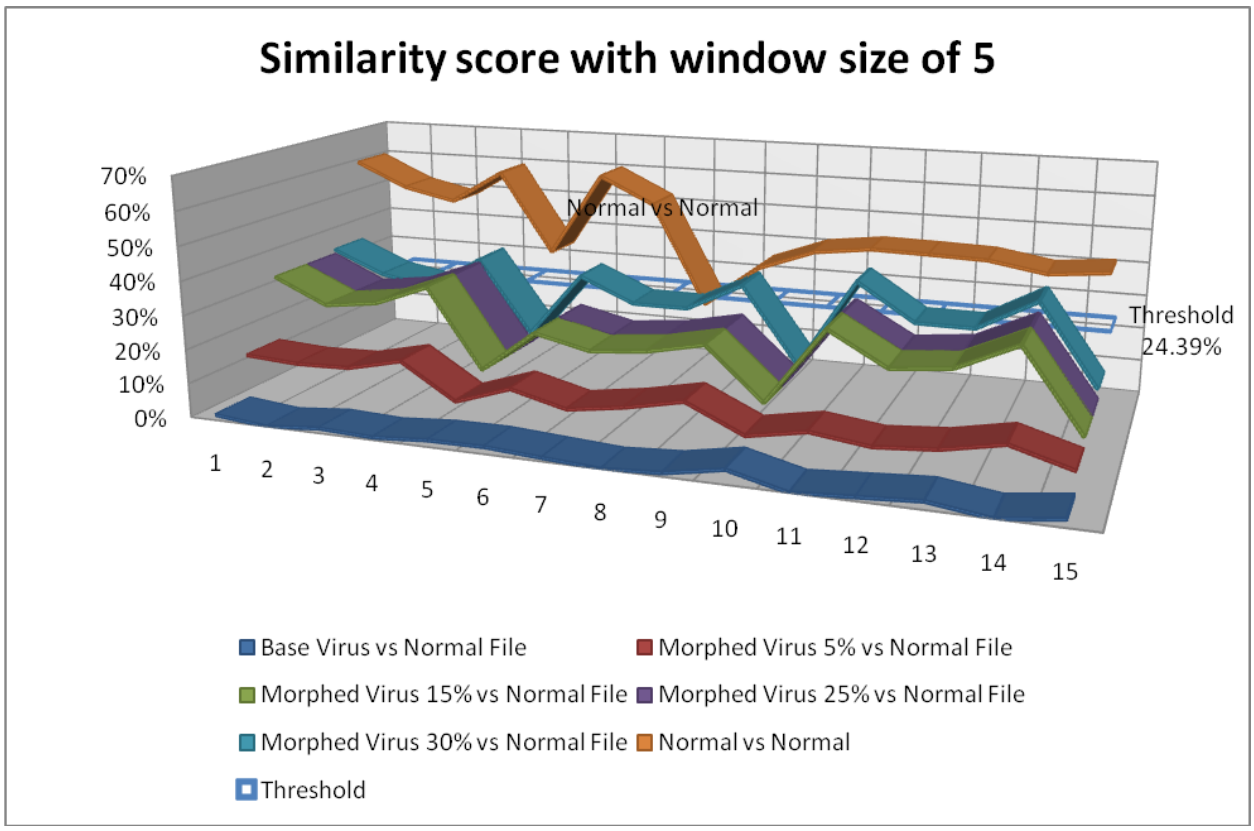


Figure 17 Similarity Graph for Morphed Viruses and Normal Files

Using the approach as discussed in Section 6.1.1, we determined the threshold value as 24.39% from the results obtained from Figure 17. A threshold is the minimum similarity score for various pair wise comparisons between normal files. The window size of 5 was only able to detect the morphed viruses with 5% of junk code insertion. The morphed viruses with 15%, and 25% remain undetected as the similarity between normal and morphed viruses with 15% and 25% were higher than virus threshold value (i.e. 24.39%). The undetected viruses are referred as false positives, as some higher similarity scores of morphed viruses crossed the threshold value. Error rates produced while detecting morphed viruses is shown in Table 7. The similarity score for different file comparisons with various window sizes is listed in Table C-1 to Table C-3 in Appendix C.

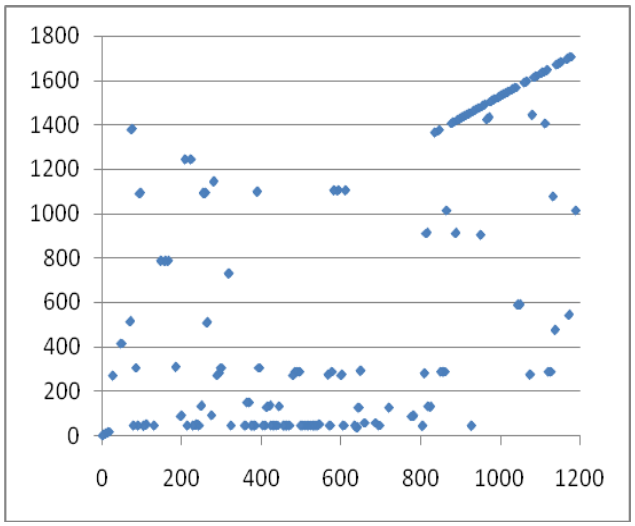
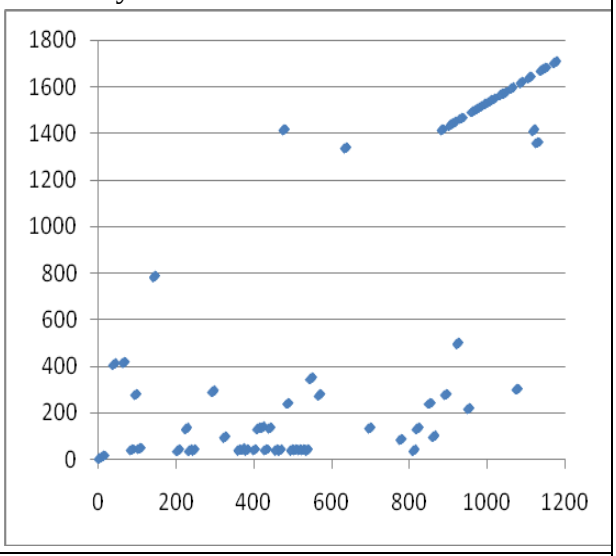
Window Size = 5	
Morphed virus with X% dead	Error rate %

code and subroutine insertion	
Base Virus	0%
Morphed Virus 5%	0%
Morphed Virus 15%	13.33%
Morphed Virus 25%	66.67%
Morphed Virus 30%	80%

Table 7 Error Rate for Morphed Viruses having Window Size of 5

6.1.5 Morphed Virus Detection by Varying Window size

Window is the size limit where all the matches below that size is not considered as a match for computing the similarity score between the files. We assumed window size to be 5 until now. Variation in window size results in different similarity scores. We varied the window size to 10, 15, 20, 25, and 30 calculated the score. In Table 8, a different window is applied while computing the similarity between IDAR1 and IDAR2 normal files. We started with window size of 5 and went up to 30. It showed that the similarity score decreases with the increase in the window size.

Window Size = 5 Similarity Score = 54.16% 	Window Size = 10 Similarity Score = 44.44% 
Window Size = 15 Similarity Score = 38.53%	Window Size = 20 Similarity Score = 34.71%

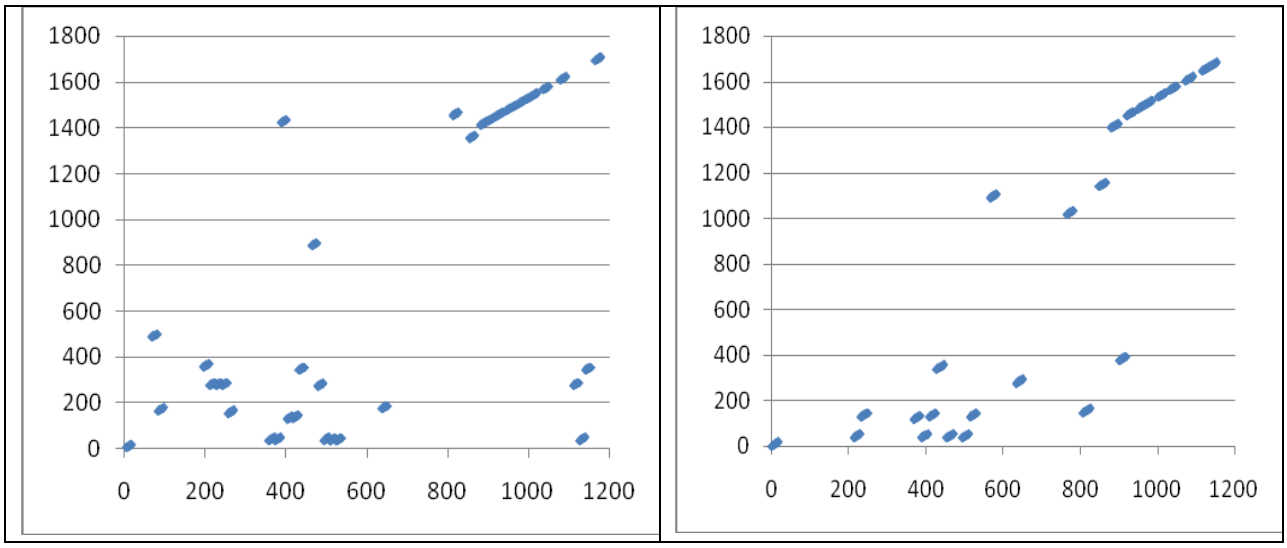
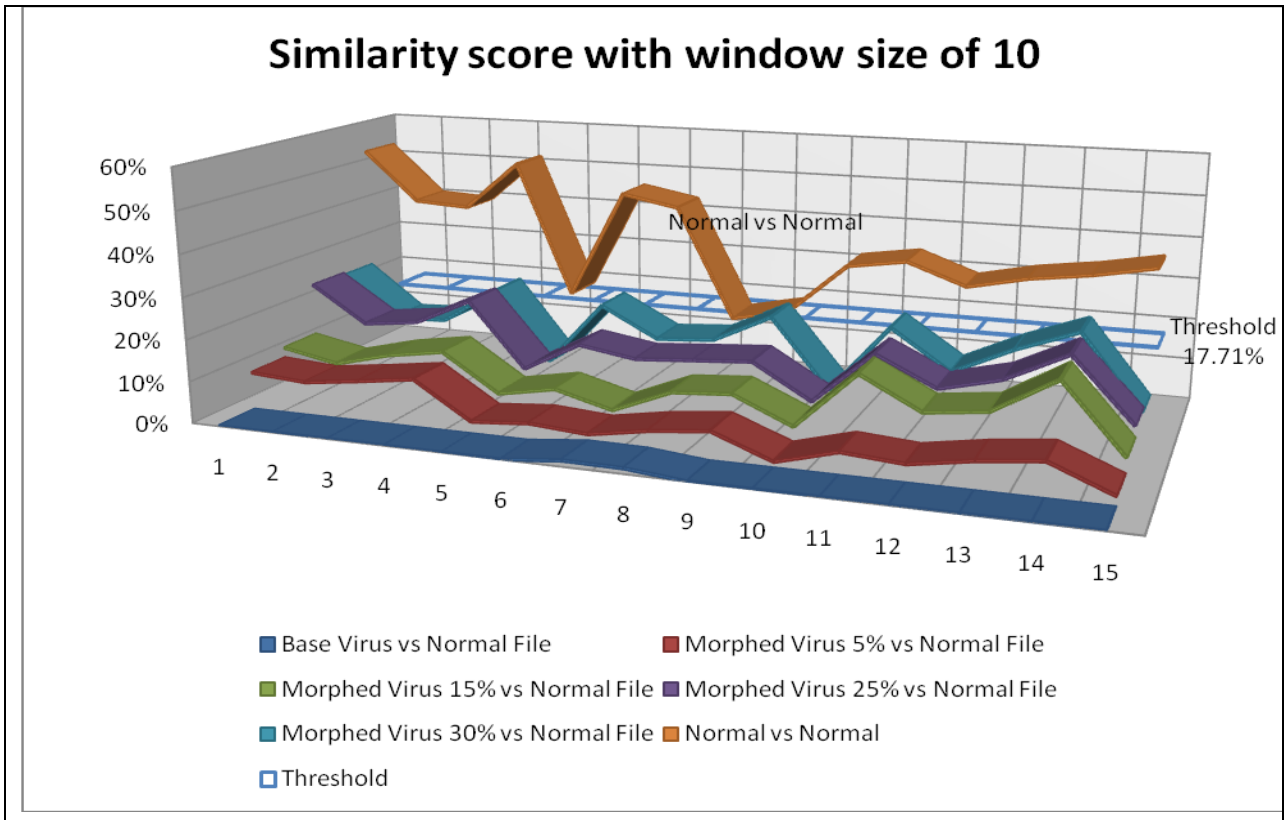
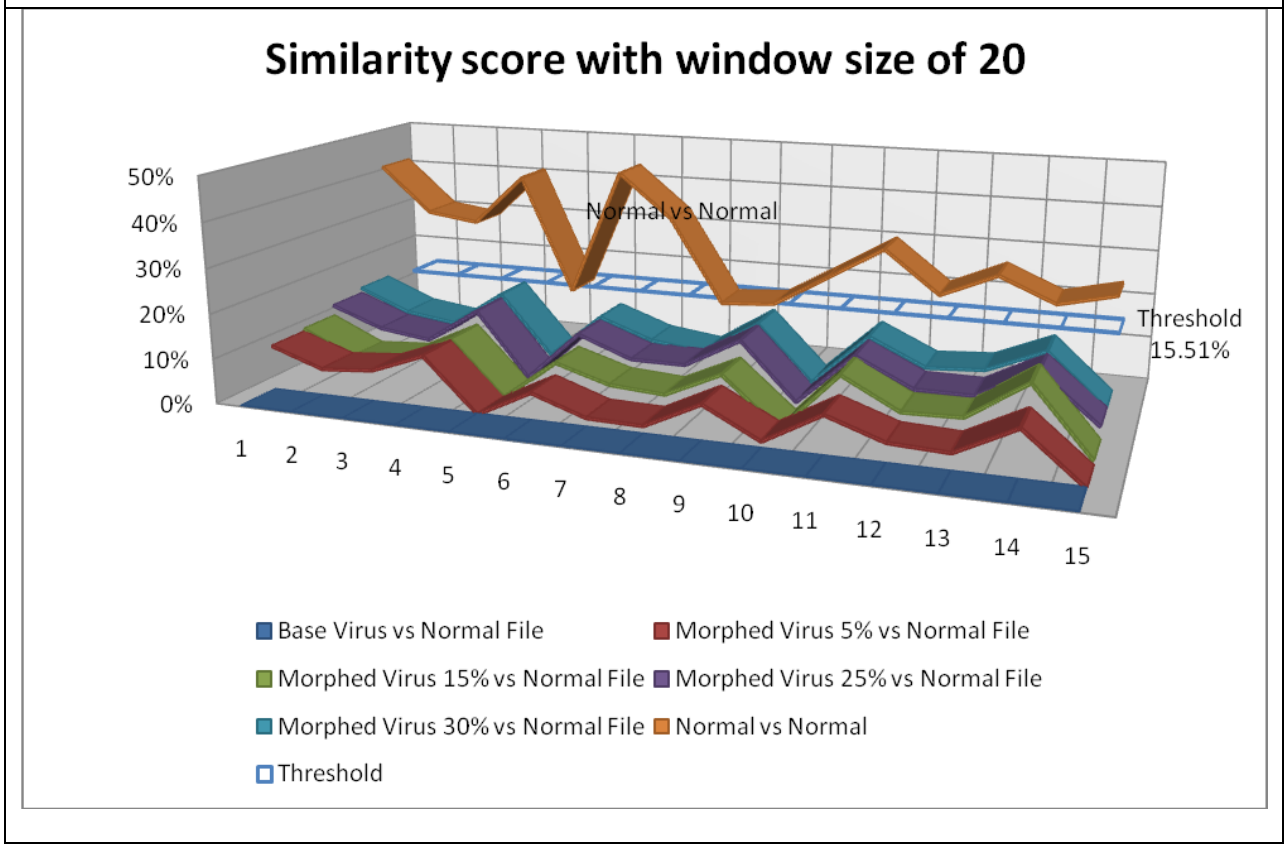


Table 8 Similarity Scores between Normal Files for different Window Size

Varying window size changes the similarity score between the files. However, this does not help in determining whether detection of morphed viruses is possible or not. To determine the results of how the variation in window size helps in detecting the morphed virus, we applied similarity tests with varying window size between morphed virus and normal files; between normal and normal files; and between base virus and normal files. We generated graphs, as shown in Figure 18, for the results.


Similarity score with window size of 10
60%
50%
40%
30%
20%
10%
0%
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
Normal vs Normal
Threshold
17.71%
Base Virus vs Normal File
Morphed Virus 5% vs Normal File
Morphed Virus 15% vs Normal File
Morphed Virus 25% vs Normal File
Morphed Virus 30% vs Normal File
Normal vs Normal
Threshold


Similarity score with window size of 20
50%
40%
30%
20%
10%
0%
1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
Normal vs Normal
Threshold
15.51%
Base Virus vs Normal File
Morphed Virus 5% vs Normal File
Morphed Virus 15% vs Normal File
Morphed Virus 25% vs Normal File
Morphed Virus 30% vs Normal File
Normal vs Normal
Threshold

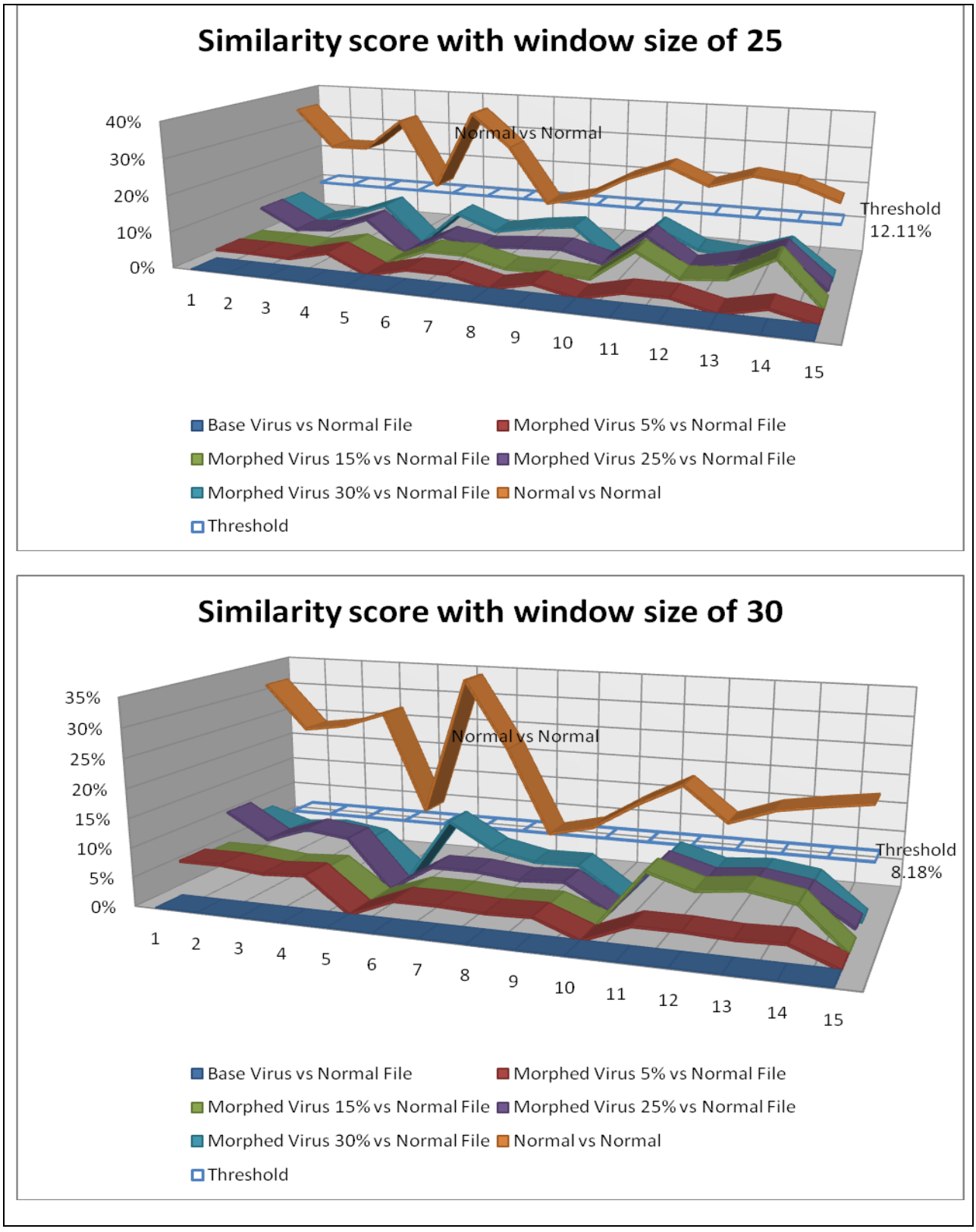


Figure 18 Similarity Graph of Scores for different Window Size

It is possible to distinguish the NGVCK base virus and its morphed copies from normal files using the similarity index with a proper window size.

To overcome the problem of detecting morphed copies with 15%, 25%, and 30% subroutine and junk instruction insertions, we varied the window size from 5 to 10, 20, 25 and 30. The increase in the window size resulted in reducing the false positives. As shown in Figure 18, the graph with the window size of 10, decreases the similarity score of every computation that we had in the graph with window size of 5. But still, there were some false positives. The graph with window size of 20 and 25 does the job of eliminating almost all the false positives. All of the morphed virus similarity scores, other than the morphed virus with 30% of dead code insertion, were below the threshold value. It completely removed all the false positives for the morphed viruses up to 25% junk instruction insertion, which were not detected by the similarity method with the window size of 5 and 10.

The similarity score with a different threshold value of Figure 17 and 19 is summarized in Table 9. The minimum similarity score of normal files represents the threshold value. Keeping window size of 5 gives a threshold value 24.39%. The only virus whose similarity score falls below the threshold is the morphed virus with a 5% dead code insertion having a maximum similarity score of 17.97%, which is less then threshold value (i.e. 24.39%). The other morphed virus copies greater than 5% junk insertion, as shown in Figure 17, were undetected as their similarity scores were higher than the threshold value.

We increased the window size and computed the similarity again. With the window size of 20, we found that the threshold value 15.61% detected all the morphed copies upto 25% junk code insertion. As shown in Table 9, the maximum similarity score of morphed virus 25% is 15.32% which is less than the threshold value. As a result, any file whose similarity with a normal file is less than the threshold value belongs to the virus family. The increase of the window size to 25; morphed copies up to 25% were completely detected as with the window size of 20.

Maximum,minimum, and average similarity score for different threshold values Comparing normal file to:					
Window Size	Normal - Min. Similarity Score	Morphed 5% - Max. Similarity Score	Morphed 15% - Max. Similarity Score	Morphed 25% - Max. Similarity Score	Morphed 30% - Max. Similarity Score
5	0.2439	0.1797	0.2930	0.3553	0.3929
10	0.1771	0.1165	0.2158	0.2447	0.2501
20	0.1561	0.1026	0.1542	0.1532	0.1628
25	0.1211	0.0485	0.1156	0.1131	0.1281
30	0.0818	0.0613	0.0979	0.1112	0.1173

Table 9 Similarity Score of Files having different Window Size

Increase in window size helps in determining threshold properly, but at one stage it stops detecting the morphed viruses and results again with some false positives. This is shown in Figure 19, graph with window size of 30. The threshold value with window size 30 is 8.18% as shown in Table 9. Although the window size is high, it just detects morphed virus until 5% of junk instruction insertion. Therefore, too much increase in window size deteriorates the similarity index method performance and the decision for window size is typical for detecting morphed viruses.By performing several test cases and their results shown in Table 9, we concluded an optimal window size to be between 20 to 25 for detecting a morphed virus with up to 25% of dead code and subroutine insertion. The error rate for various morphed viruses keeping a different window size is shown in form of graph in Figure 19.

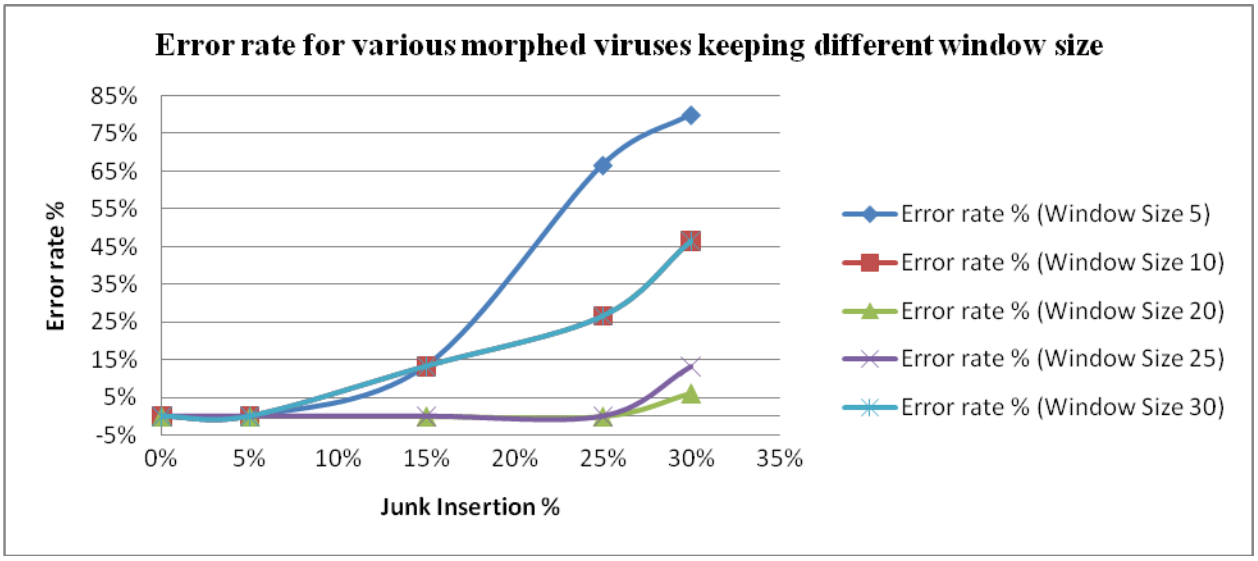


Figure 19 Graph of Error Rate for different Window Size

6.2 Edit Distance

We started comparing programs from the 40 base viruses (NGVCK), and 40 normal files using the approach described in Section 5.2.2. We computed the edit distance score between various normal files; between normal files and base virus files; and between normal files and morphed viruses which are produced by different percentage of dead code insertion from normal files. The similarity between files was obtained by using the edit score from the above comparison and putting it into the formula mentioned in Section 5.2.2. The similarity scores were plotted on the graph as shown in Figure 20.

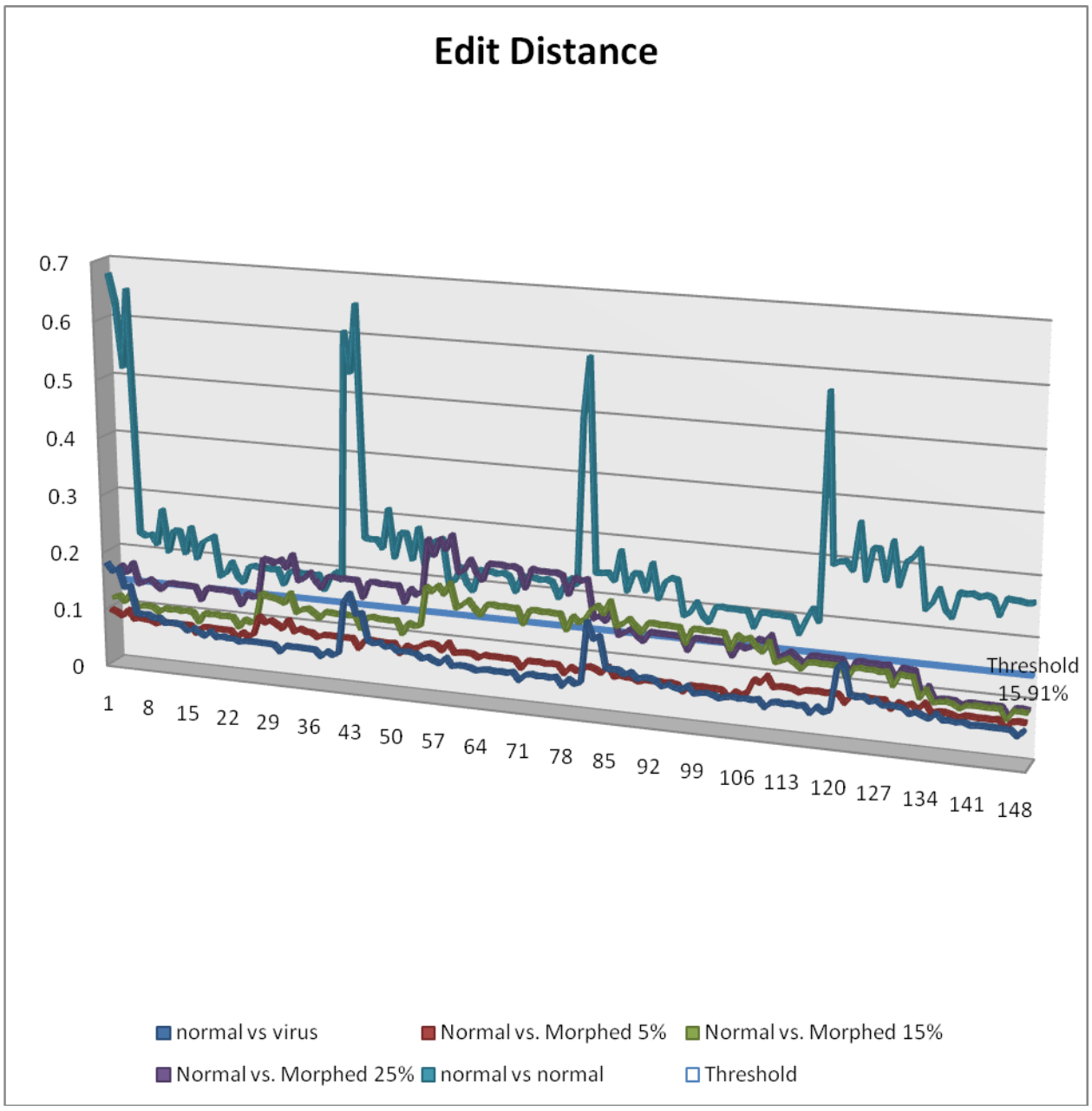


Figure 20 Similarity Graph for Morphed Viruses and Normal Files

In Figure 20, x-axis represents the number of comparisons made between files and y-axis represents the similarity between those files. It is clear from the graph that similarity score between normal files is higher than between normal files and base viruses/morphed viruses. The percentage of minimum, maximum and average similarity scores for various programs is shown

in Table 10. The raw similarity scores for the first 40 comparisons between various files in Figure 20 is listed in Table D-1 in Appendix D.

	Base Virus vs. Normal	Morphed 5% vs. Normal	Morphed 15% vs. Normal	Morphed 25% vs. Normal	Normal vs. Normal
Min	0.0535	0.0617	0.0739	0.0748	0.1591
Max	0.1818	0.1934	0.2024	0.2816	0.7893

Table 10 Similarity Scores for Various Programs using Edit Distance Technique

To determine whether the file belongs to virus family or non-virus family, we kept the minimum similarity score between normal files as a threshold value (15.91%). The threshold value is smaller than the maximum similarity score between normal and base virus files; between normal and viruses morphed with 5% dead code insertion; between normal and morphed virus with 15% dead code insertion; and between normal and morphed virus with 25% dead code insertion.

The scores obtained using edit distance techniques generated a false positive rate. We defined the false positive as an error rate. The error rate obtained using the edit distance method for various base viruses and morphed viruses is shown in form of graph in Figure 21. Figure 21 shows that the edit distance method detects a base virus with a 1.16% error rate; viruses morphed with 5%, 15% and 25% with 14.84%, 40.31%, and 45.70% error rate. This technique gives a high error rate with low percentage of morphing.

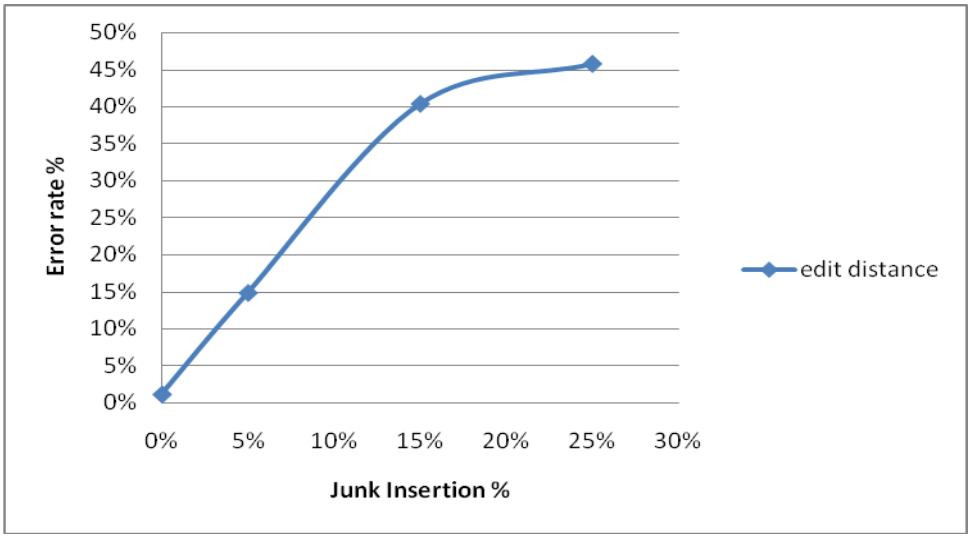


Figure 21 Graph of Error Rates for Various Morphed Virus Copies

6.3 Pairwise Sequence Alignment

6.3.1 Base Virus and Non-Virus Op-code Sequence Alignment

The test sets were made up of 20 base viruses (NGVCK) and 20 non-virus files. The number of alignments possible for 20 base viruses = 190 alignments. Similarly, non-virus files have 190 alignments between them.

In Figure 22, scores between normal op-code sequences; between virus op-code sequences; and between virus and normal file op-code sequences are plotted on the graph. We classify a program from the virus family by determining a threshold value. This means that if the score between the unknown file op-code sequence when aligned with normal file op-code sequence is lower than the threshold, then that unknown file belongs to the virus family.

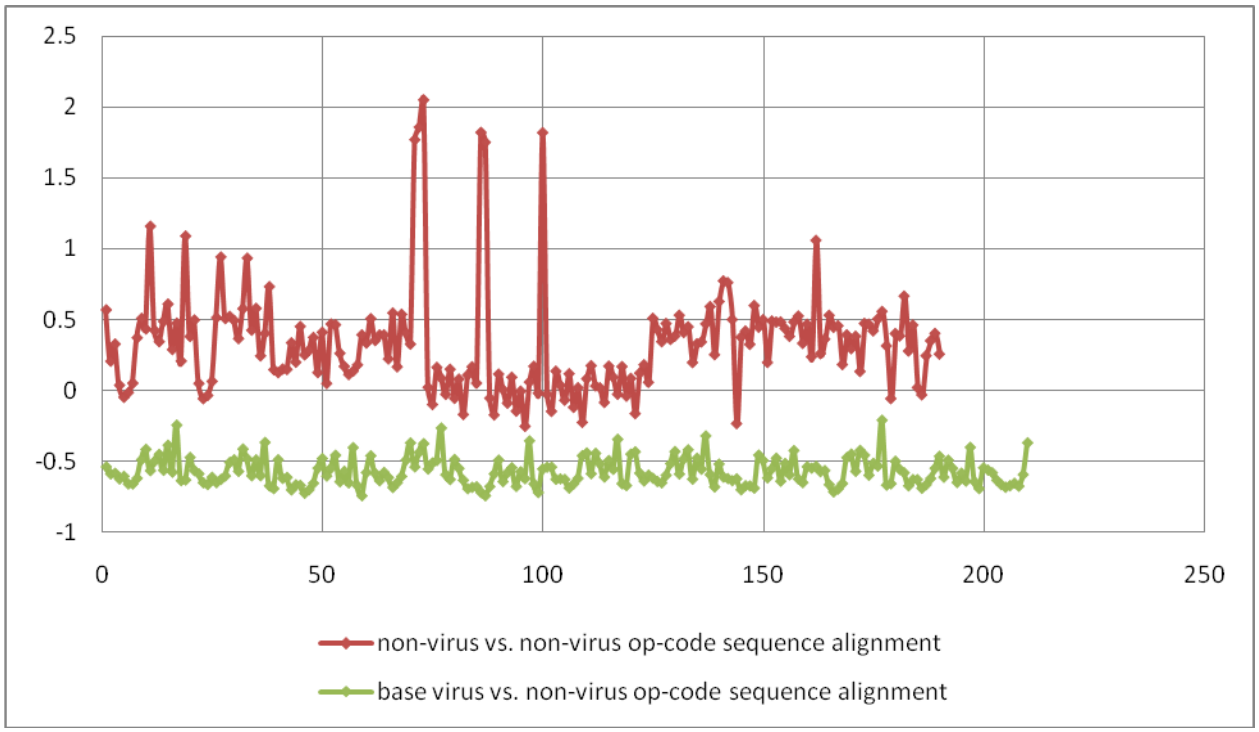


Figure 22 Alignment Scores for Non-Virus and Virus Op-code Sequences

The results displayed in Figure 22, detects virus from normal files with a zero error rate having 0% false positive rate, and 0% false negative rate. Table 11 shows the minimum, maximum and average score for the various program comparisons displayed in Figure 22. All of the similarity alignment scores are listed in Table E-1 in Appendix E.

	Normal vs. Normal	Base Virus vs. Normal
Min.	-0.3445	-0.7459
Max.	2.0496	-0.2063
Avg.	0.2566	-0.5721

Table 11 Sequence Alignment Scores between Various Programs

6.3.2 Morphed Virus and Non Virus Op-code Sequence Alignment

Morphed viruses were generated by inserting dead code instructions and subroutines from normal file. The sets of 10 morphed virus files were generated using [3] with 30% of junk block

insertions from normal files. The morphed file op-code sequence is aligned with normal file op-code sequence and the scores were computed as described in Section 5.3.4.

The total alignments possible for 10 morphed viruses = 45 alignments. Figure 23 shows the graph with different similarity scores for various morphed virus and normal file alignments.

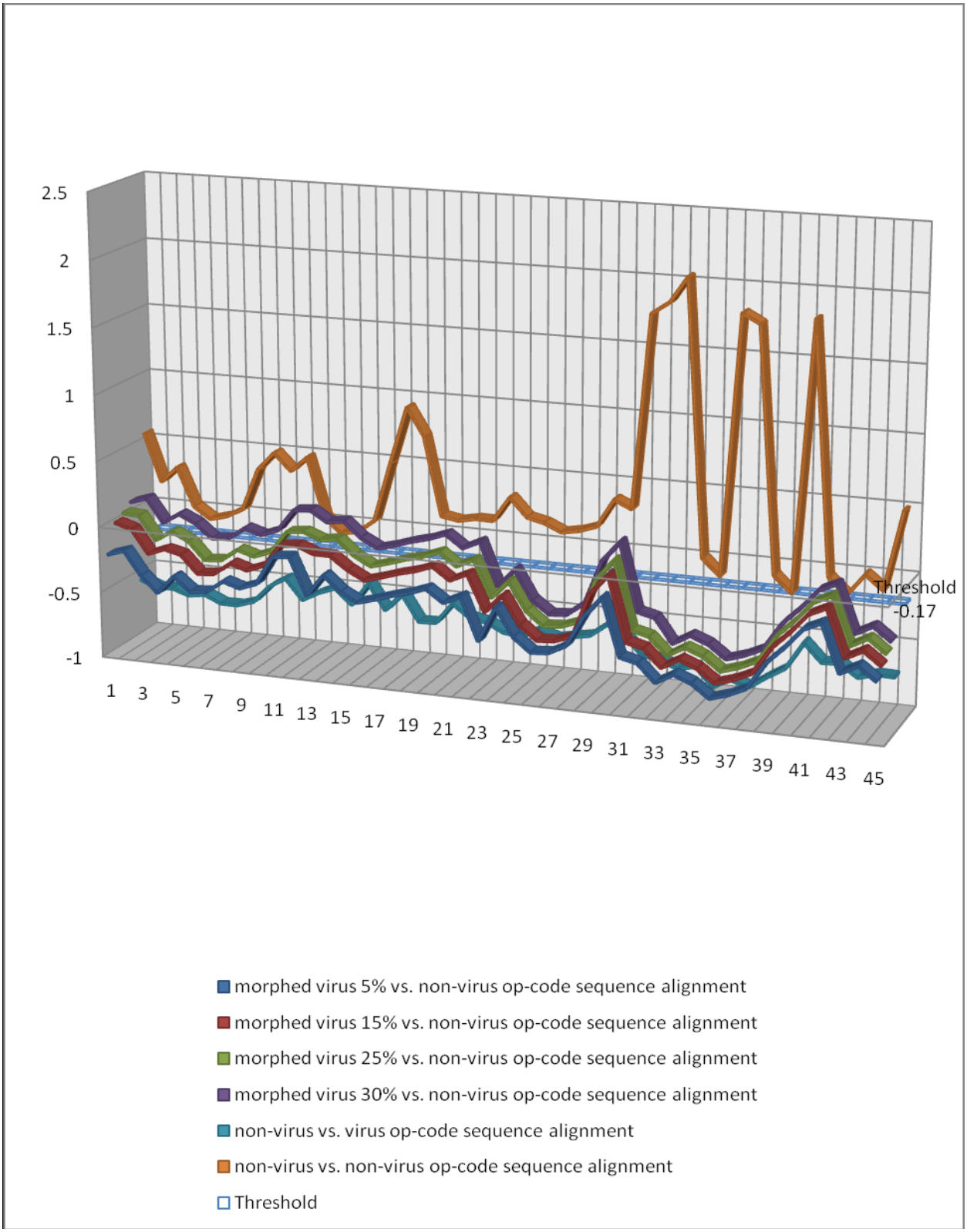


Figure 23 Alignment Scores for Non-Virus, and Various Morphed Virus Op-code Sequences

The results from Figure 23 indicates that for morphed viruses, the alignment score between normal files and between normal and morphed virus with 30% dead code insertion are overlapping a lot. Using the approach to find the threshold described in Section 6.3.1, the alignment score results in false postive rate greater than 0%. All of the similarity scores plotted in Figure 23 is listed in Table E-2 in Appendix E.

The results from the Figure 23 show that the threshold -0.17, gives 21% false positive rate. We defined the false positive as an error rate. These results shows that viruses morphed with 30% subroutine and dead code insertions are not completely detected using the sequence alignment technique as it an give error rate of 21%. This technique gives 100% detection for base viruses, but morphed viruses remain undetected. Some alteration for the sequence alignment algorithm is required to detect the morphed viruses, which can reduce false positive rate.

The error rate obtained using a pairwise sequence alignment for various base viruses and morphed viruses is shown in form of graph in Figure 24. This method detects base viruses with a 0% error rate; viruses morphed with 5%, 15%, 25% and 30% with 4%, 8%, 15%, and 21% error rates respectively. This technique gives a high error rate with high percentage morphing.

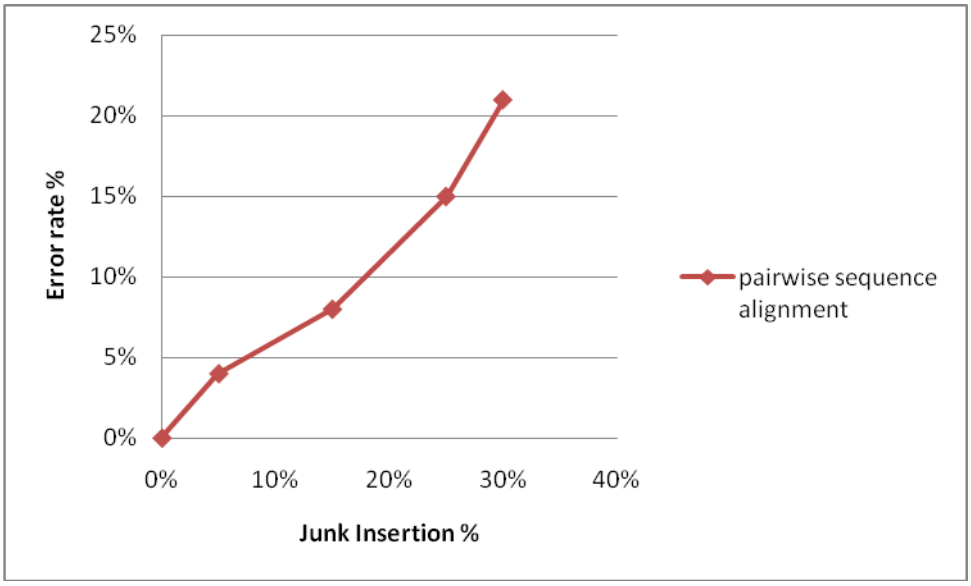


Figure 24 Graph of Error Rates for Various Morphed Virus Copies

7 CONCLUSION

The results from the edit distance and pairwise sequence alignment methods used in this paper shows that the morphed viruses having random percentages of dead code and subroutine insertions (i.e., 5%, 15%, 25% and 30%) are still detectable within a certain error rate. The similarity index method detects the morphed viruses up to 25% of dead code and subroutine insertion with 0% error rate- unlike edit distance and pairwise alignment method. We analyzed the results of different similarity-based techniques. Figure 25 shows the error rate produced by different similarity-based techniques for various morphed viruses having random percentages of dead code and subroutine insertion from normal files. From Figure 25, we conclude that the similarity index technique mentioned in this paper gives the best results for the morphed viruses. The similarity index technique detects all the viruses morphed with different percentages of dead code and subroutine insertion (i.e., 5%, 15%, and 25%) with 0% error rate by keeping an optimum window size from 20 to 25. It gives 6%, and 13.33% error rate for 30% morphed viruses with a window size of 20, and 25 respectively.

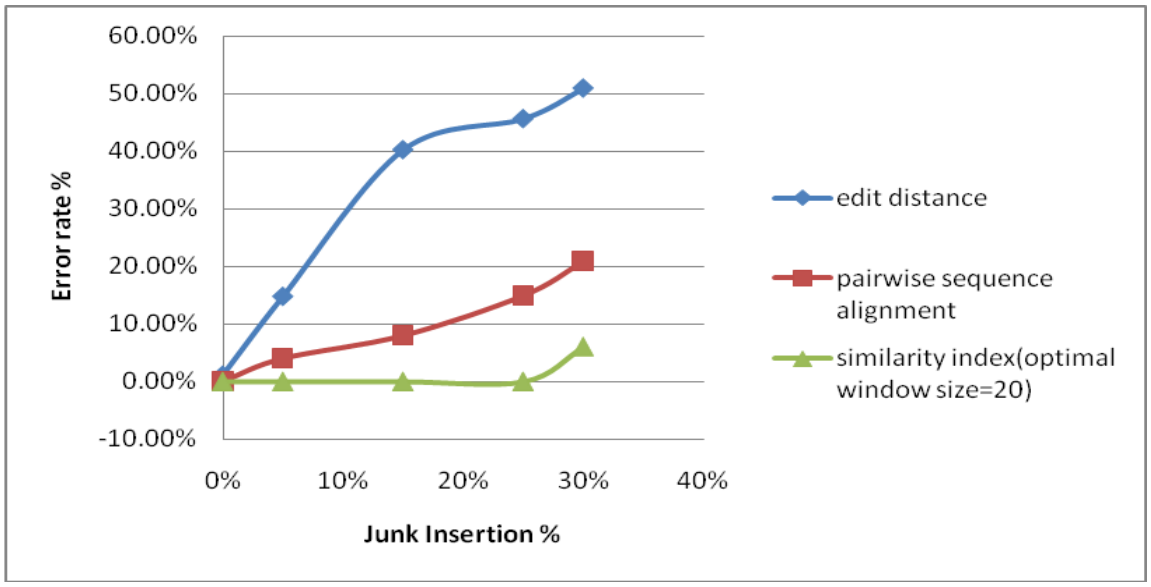


Figure 25 Graph of Error Rates produced by different Similarity-Based Methods

The edit distance method distinguished the base viruses with an error rate of 1.16%. It gives a higher error rate while detecting morphed viruses with a different percentage of subroutine and

dead code insertions. The pairwise sequence alignment technique does give the results better than the edit distance. It detects the base viruses with 0% error rate. For morphed virus copies of 5% and 15% it gives a low error rate of 4% and 8%, respectively. This error rate increases with the increase in morphing viruses with higher percentage of dead code and subroutine insertions. As shown in previous studies [3], by making viruses closer to normal files, the HMM-based detector began to fail to detect the morphed viruses with 5% of subroutine and dead code insertion from normal files. When we compared it with the similarity-index technique for detecting morphed viruses, similarity index technique detects the morphed virus copies up to 25% of subroutine and dead code insertions.

8 FUTURE WORK

For future work, we are interested in exploring enhancements to the proposed algorithms presented in this report to improve the accuracy of similarity index technique. Furthermore, research is required to expand on the findings to decide if the similarity index can be used to detect more advanced metamorphic viruses with 30% of dead code and subroutine insertions by creating more intelligent threshold.. The next step for the sequence alignment technique would be to analyze the viruses and their subroutines to remove the dead code inserted and giving same scores for exchangeable instructions before computing the virus' similarity score.

The similarity-index method which gave the best results so far might be more efficient compared to the other similarity-based techniques used in this paper, if we preprocess all the morphed viruses by removing dead code and subroutine insertions. We can then analyze the similarity score for resultant viruses and define some optimum threshold to classify these viruses from normal files.

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Appendix A: Similarity test results for base virus variants (IDAN) and normal files (IDAR)

Table A- 1 Scores for various NGVCK virus variants and normal files

Similarity scores between various NGVCK virus variants and normal files					
IDAN101 vs. IDAR0	0	IDAN141 vs. IDAR0	0	IDAN191 vs. IDAR0	0
IDAN101 vs. IDAR1	0.0227	IDAN141 vs. IDAR1	0.0204	IDAN191 vs. IDAR1	0
IDAN101 vs. IDAR2	0	IDAN141 vs. IDAR2	0.0102	IDAN191 vs. IDAR2	0.0112
IDAN101 vs. IDAR3	0.0227	IDAN141 vs. IDAR3	0	IDAN191 vs. IDAR3	0.022
IDAN101 vs. IDAR4	0.0113	IDAN141 vs. IDAR4	0.0102	IDAN191 vs. IDAR5	0.022
IDAN101 vs. IDAR5	0.0340	IDAN141 vs. IDAR5	0.0408	IDAN191 vs. IDAR6	0.0337
IDAN101 vs. IDAR6	0.0227	IDAN141 vs. IDAR6	0.0408	IDAN191 vs. IDAR7	0.0337
IDAN101 vs. IDAR7	0.0227	IDAN141 vs. IDAR7	0.0510	IDAN191 vs. IDAR8	0.067
IDAN101 vs. IDAR8	0.0454	IDAN141 vs. IDAR8	0.0510	IDAN191 vs. IDAR9	0.0112
IDAN101 vs. IDAR9	0.0454	IDAN141 vs. IDAR9	0.0102	IDAN191 vs. IDAR10	0.022
IDAN101 vs. IDAR10	0.0113	IDAN141 vs. IDAR10	0.0408	IDAN191 vs. IDAR11	0.0337
IDAN101 vs. IDAR11	0.0340	IDAN141 vs. IDAR11	0.0204	IDAN191 vs. IDAR12	0.0337
IDAN101 vs. IDAR12	0.0340	IDAN141 vs. IDAR12	0.0204	IDAN191 vs. IDAR13	0.022
IDAN101 vs. IDAR13	0.0340	IDAN141 vs. IDAR13	0.061	IDAN191 vs. IDAR14	0.0112
IDAN101 vs. IDAR14	0.0454	IDAN141 vs. IDAR14	0.0102	IDAN191 vs. IDAR15	0.067
IDAN101 vs. IDAR15	0.0568	IDAN141 vs. IDAR15	0.0714	IDAN191 vs. IDAR16	0.0112
IDAN101 vs. IDAR16	0.0568	IDAN141 vs. IDAR16	0.0510	IDAN191 vs. IDAR17	0
IDAN101 vs. IDAR17	0.0227	IDAN141 vs. IDAR17	0.0306	IDAN191 vs. IDAR18	0.022
IDAN101 vs. IDAR18	0.0568	IDAN141 vs. IDAR18	0.0204	IDAN191 vs. IDAR19	0.044
IDAN101 vs. IDAR19	0.0454	IDAN141 vs. IDAR19	0.061	IDAN191 vs. IDAR20	0.0337
IDAN101 vs. IDAR20	0.0681	IDAN141 vs. IDAR20	0.0306	IDAN191 vs. IDAR21	0.0337
IDAN101 vs. IDAR21	0.0227	IDAN141 vs. IDAR21	0.0306	IDAN191 vs. IDAR22	0.0561
IDAN101 vs. IDAR22	0.0340	IDAN141 vs. IDAR22	0.061	IDAN191 vs. IDAR23	0.044
IDAN101 vs. IDAR23	0.0340	IDAN141 vs. IDAR23	0.0714	IDAN191 vs. IDAR24	0.0337
IDAN101 vs. IDAR24	0.0568	IDAN141 vs. IDAR24	0.0306	IDAN191 vs. IDAR25	0.0337
IDAN101 vs. IDAR25	0.0340	IDAN141 vs. IDAR25	0.0306	IDAN191 vs. IDAR26	0.0337
IDAN101 vs. IDAR26	0.0340	IDAN141 vs. IDAR26	0.0306	IDAN191 vs. IDAR27	0.0337
IDAN101 vs. IDAR27	0.0340	IDAN141 vs. IDAR27	0.0306	IDAN191 vs. IDAR28	0.0337
IDAN101 vs. IDAR28	0.0340	IDAN141 vs. IDAR28	0.0306	IDAN191 vs. IDAR29	0.0337
IDAN101 vs. IDAR29	0.0340	IDAN141 vs. IDAR29	0.0306	IDAN191 vs. IDAR30	0.0337
IDAN101 vs. IDAR30	0.0454	IDAN141 vs. IDAR30	0.0306	IDAN191 vs. IDAR31	0.0337
IDAN101 vs. IDAR31	0.0340	IDAN141 vs. IDAR31	0.0306	IDAN191 vs. IDAR32	0.0337
IDAN101 vs. IDAR32	0.0340	IDAN141 vs. IDAR32	0.0306	IDAN191 vs. IDAR33	0.0337
IDAN101 vs. IDAR33	0.0227	IDAN141 vs. IDAR33	0.0306	IDAN191 vs. IDAR34	0.0337
IDAN101 vs. IDAR34	0.0340	IDAN141 vs. IDAR34	0.0306	IDAN191 vs. IDAR35	0.0337
IDAN101 vs. IDAR35	0.0340	IDAN141 vs. IDAR35	0.0306	IDAN191 vs. IDAR36	0.0337
IDAN101 vs. IDAR36	0.0340	IDAN141 vs. IDAR36	0.0306	IDAN191 vs. IDAR37	0.0337
IDAN101 vs. IDAR37	0.0454	IDAN141 vs. IDAR37	0.0306	IDAN191 vs. IDAR38	0.0337
IDAN101 vs. IDAR38	0.0340	IDAN141 vs. IDAR38	0.0306	IDAN191 vs. IDAR39	0.0337
IDAN101 vs. IDAR39	0.0454	IDAN141 vs. IDAR39	0.061	IDAN191 vs. IDAR40	0.0337
IDAN101 vs. IDAR40	0.0340	IDAN141 vs. IDAR40	0.0306		

Min score:	0.00
Max score:	0.05
Average:	0. 02

Table A- 2 Similarity scores between normal files

IDAR0 vs. IDAR1	0.6150	IDAR4 vs. IDAR10	0.2692	IDAR12 vs. IDAR19	0.1940
IDAR0 vs. IDAR2	0.5440	IDAR5 vs. IDAR6	0.8223	IDAR12 vs. IDAR20	0.1898
IDAR0 vs. IDAR3	0.5103	IDAR5 vs. IDAR7	0.8209	IDAR13 vs. IDAR14	0.1447
IDAR0 vs. IDAR4	0.6090	IDAR5 vs. IDAR8	0.8223	IDAR13 vs. IDAR15	0.7890
IDAR0 vs. IDAR5	0.2285	IDAR5 vs. IDAR9	0.1449	IDAR13 vs. IDAR18	0.1660
IDAR0 vs. IDAR6	0.2142	IDAR5 vs. IDAR10	0.8267	IDAR13 vs. IDAR19	0.7926
IDAR0 vs. IDAR7	0.2190	IDAR6 vs. IDAR7	0.8059	IDAR13 vs. IDAR20	0.7877
IDAR0 vs. IDAR8	0.2	IDAR6 vs. IDAR8	0.8004	IDAR14 vs. IDAR15	0.2285
IDAR0 vs. IDAR9	0.4904	IDAR6 vs. IDAR9	0.1401	IDAR14 vs. IDAR16	0.4179
IDAR0 vs. IDAR10	0.2142	IDAR6 vs. IDAR10	0.8147	IDAR14 vs. IDAR17	0.628
IDAR1 vs. IDAR2	0.6183	IDAR7 vs. IDAR8	0.8001	IDAR14 vs. IDAR18	0.4344
IDAR1 vs. IDAR3	0.5416	IDAR7 vs. IDAR9	0.1306	IDAR14 vs. IDAR19	0.2247
IDAR1 vs. IDAR4	0.6991	IDAR7 vs. IDAR10	0.8422	IDAR14 vs. IDAR20	0.2196
IDAR1 vs. IDAR5	0.2166	IDAR8 vs. IDAR9	0.1481	IDAR15 vs. IDAR18	0.1953
IDAR1 vs. IDAR6	0.1962	IDAR8 vs. IDAR10	0.7765	IDAR15 vs. IDAR19	0.8189
IDAR1 vs. IDAR7	0.2085	IDAR9 vs. IDAR10	0.1799	IDAR15 vs. IDAR20	0.7992
IDAR1 vs. IDAR8	0.2085	IDAR10 vs. IDAR11	0.1423	IDAR16 vs. IDAR17	0.457
IDAR1 vs. IDAR9	0.5355	IDAR10 vs. IDAR12	0.1424	IDAR16 vs. IDAR18	0.8184
IDAR1 vs. IDAR10	0.2085	IDAR10 vs. IDAR13	0.7657	IDAR16 vs. IDAR19	0.2237
IDAR2 vs. IDAR3	0.4312	IDAR10 vs. IDAR14	0.1523	IDAR16 vs. IDAR20	0.2263
IDAR2 vs. IDAR4	0.4521	IDAR10 vs. IDAR15	0.7682	IDAR17 vs. IDAR18	0.473
IDAR2 vs. IDAR5	0.1662	IDAR10 vs. IDAR18	0.1634	IDAR17 vs. IDAR19	0.2439
IDAR2 vs. IDAR6	0.1787	IDAR10 vs. IDAR19	0.8389	IDAR17 vs. IDAR20	0.2237
IDAR2 vs. IDAR7	0.1953	IDAR10 vs. IDAR20	0.7583	IDAR18 vs. IDAR19	0.2019
IDAR2 vs. IDAR8	0.1371	IDAR11 vs. IDAR12	0.8936	IDAR18 vs. IDAR20	0.1846
IDAR2 vs. IDAR9	0.4571	IDAR11 vs. IDAR13	0.1911	IDAR19 vs. IDAR20	0.6831
IDAR2 vs. IDAR10	0.1620	IDAR11 vs. IDAR14	0.4493	IDAR0 vs. IDAR21	0.4714
IDAR3 vs. IDAR4	0.4448	IDAR11 vs. IDAR15	0.185	IDAR1 vs. IDAR21	0.511
IDAR3 vs. IDAR5	0.1856	IDAR11 vs. IDAR16	0.4179	IDAR2 vs. IDAR21	0.4405
IDAR3 vs. IDAR6	0.1627	IDAR11 vs. IDAR17	0.3698	IDAR3 vs. IDAR21	0.3797
IDAR3 vs. IDAR7	0.1599	IDAR11 vs. IDAR18	0.6293	IDAR4 vs. IDAR21	0.5385
IDAR3 vs. IDAR8	0.1656	IDAR11 vs. IDAR19	0.1939	IDAR5 vs. IDAR21	0.1691
IDAR3 vs. IDAR9	0.3769	IDAR11 vs. IDAR20	0.1897	IDAR6 vs. IDAR21	0.1560
IDAR3 vs. IDAR10	0.1856	IDAR12 vs. IDAR13	0.191	IDAR7 vs. IDAR21	0.1524
IDAR4 vs. IDAR5	0.2474	IDAR12 vs. IDAR14	0.4495	IDAR8 vs. IDAR21	0.1451
IDAR4 vs. IDAR6	0.2510	IDAR12 vs. IDAR15	0.1857	IDAR9 vs. IDAR21	0.6753
IDAR4 vs. IDAR7	0.2328	IDAR12 vs. IDAR16	0.6185	IDAR10 vs. IDAR21	0.1486
IDAR4 vs. IDAR8	0.2401	IDAR12 vs. IDAR17	0.3700		
IDAR4 vs. IDAR9	0.5604	IDAR12 vs. IDAR18	0.6283		

Min score:	0.1306
Max score:	0.8936
Average:	0.3865

Appendix B: Similarity between morphed viruses

Table B- 1 Scores for morphed viruses and normal files

Similarity scores between morphed viruses (IDAN) with different percentage of subroutine and dead code insertion from non-virus files **Window Size 5:**				
IDAN vs. IDAN	Base viruses : scores	Morphed Virus 5% : scores	IDAN vs. IDAN	Morphed Virus 15% : scores
IDAN5 vs. IDAN6	0.1044	0.3159	IDAN2 vs. IDAN17	0.398
IDAN5 vs. IDAN7	0.1091	0.2567	IDAN2 vs. IDAN18	0.3825
IDAN5 vs. IDAN8	0.1584	0.3025	IDAN3 vs. IDAN8	0.4309
IDAN5 vs. IDAN9	0.1115	0.3240	IDAN3 vs. IDAN11	0.4875
IDAN5 vs. IDAN13	0.0626	0.1169	IDAN3 vs. IDAN13	0.4558
IDAN5 vs. IDAN14	0.0954	0.115	IDAN3 vs. IDAN14	0.4510
IDAN5 vs. IDAN17	0.1098	0.1339	IDAN3 vs. IDAN15	0.4668
IDAN7 vs. IDAN8	0.1269	0.2575	IDAN3 vs. IDAN16	0.4089
IDAN7 vs. IDAN9	0.1289	0.1723	IDAN3 vs. IDAN17	0.3320
IDAN7 vs. IDAN10	0.1241	0.2056	IDAN3 vs. IDAN18	0.3261
IDAN7 vs. IDAN11	0.0794	0.1876	IDAN4 vs. IDAN5	0.3704
IDAN7 vs. IDAN12	0.1331	0.2210	IDAN4 vs. IDAN6	0.3397
IDAN7 vs. IDAN13	0.1173	0.1528	IDAN4 vs. IDAN7	0.3596
IDAN8 vs. IDAN9	0.1036	0.1735	IDAN4 vs. IDAN8	0.4527
IDAN8 vs. IDAN10	0.1372	0.2153	IDAN4 vs. IDAN9	0.3624
IDAN8 vs. IDAN11	0.0665	0.1696	IDAN4 vs. IDAN10	0.3488
IDAN8 vs. IDAN12	0.0729	0.1777	IDAN4 vs. IDAN11	0.4080
IDAN10 vs. IDAN13	0.0769	0.1291	IDAN4 vs. IDAN12	0.380
IDAN10 vs. IDAN14	0.1465	0.1779	IDAN4 vs. IDAN13	0.4348
IDAN10 vs. IDAN17	0.1374	0.1519	IDAN4 vs. IDAN14	0.4143
IDAN11 vs. IDAN13	0.1228	0.1243	IDAN4 vs. IDAN15	0.4295
IDAN11 vs. IDAN15	0.1582	0.1370	IDAN4 vs. IDAN16	0.440
IDAN11 vs. IDAN17	0.0665	0.1261	IDAN4 vs. IDAN17	0.3087
IDAN12 vs. IDAN13	0.0750	0.1085	IDAN4 vs. IDAN18	0.3349
IDAN12 vs. IDAN17	0.1339	0.1338	IDAN4 vs. IDAN19	0.4022
IDAN13 vs. IDAN14	0.1283	0.1625	IDAN4 vs. IDAN20	0.3792
IDAN13 vs. IDAN15	0.0779	0.1499	IDAN5 vs. IDAN15	0.4868
IDAN13 vs. IDAN16	0.0922	0.1294	IDAN5 vs. IDAN17	0.3662
IDAN13 vs. IDAN17	0.1442	0.1658	IDAN5 vs. IDAN18	0.4378
IDAN14 vs. IDAN15	0.1237	0.1656	IDAN6 vs. IDAN8	0.4421
IDAN14 vs. IDAN16	0.113	0.1767	IDAN6 vs. IDAN13	0.466
IDAN14 vs. IDAN17	0.0875	0.1797	IDAN6 vs. IDAN14	0.4674
IDAN15 vs. IDAN17	0.0759	0.1334	IDAN6 vs. IDAN15	0.4616
IDAN16 vs. IDAN17	0.0899	0.1043	IDAN6 vs. IDAN16	0.4538

	Base Virus	Morphed Virus 5%	Morphed Virus 15%
Min.	0.0626	0.1043	0.3087
Max.	0.1584	0.3241	0.4875
Avg.	0.1086	0.1751	0.4085

Appendix C: Detection using similarity index test

Similarity scores between morphed viruses and normal file (IDAN vs. IDAR), between base viruses and normal files, and between normal files

Table C- 1 Similarity scores for Window size = 5

Similarity scores between various normal (IDAR) and morphed viruses (IDAN):					
	Base NGVCK viruses : scores	Morphed Virus 5% : scores	Morphed Virus 15% : scores	Morphed Virus 25% : scores	Morphed Virus 30% : scores
IDAN101 vs. IDAR1	0.0154	0.1473	0.1850	0.3448	0.3601
IDAN101 vs. IDAR2	0	0.1381	0.1546	0.2732	0.2937
IDAN101 vs. IDAR3	0.0142	0.1428	0.1871	0.2937	0.2658
IDAN101 vs. IDAR4	0.0075	0.179	0.2144	0.3553	0.3651
IDAN101 vs. IDAR5	0.0192	0.0791	0.0927	0.1244	0.1486
IDAN141 vs. IDAR1	0.0204	0.1336	0.1835	0.2496	0.3405
IDAN141 vs. IDAR2	0.0102	0.0931	0.1340	0.2131	0.270
IDAN141 vs. IDAR3	0	0.1176	0.1827	0.2289	0.2705
IDAN141 vs. IDAR4	0.0102	0.1524	0.2095	0.2640	0.3533
IDAN141 vs. IDAR5	0.0408	0.0765	0.085	0.1162	0.1315
IDAN191 vs. IDAR1	0	0.107	0.2815	0.3395	0.3929
IDAN191 vs. IDAR2	0.0112	0.086	0.1974	0.2474	0.2874
IDAN191 vs. IDAR3	0.022	0.0995	0.2147	0.2651	0.2868
IDAN191 vs. IDAR4	0	0.1333	0.2930	0.3441	0.3785
IDAN191 vs. IDAR5	0.022	0.084	0.1161	0.1179	0.146
Similarity scores between various normal files					
IDAR0 vs. IDAR1	0.6150				
IDAR0 vs. IDAR2	0.5440				
IDAR0 vs. IDAR3	0.5103				
IDAR0 vs. IDAR4	0.6090				
IDAR11 vs. IDAR17	0.3698				
IDAR1 vs. IDAR2	0.6183				
IDAR1 vs. IDAR3	0.5416				
IDAR17 vs. IDAR19	0.2439				
IDAR12 vs. IDAR17	0.3700				
IDAR2 vs. IDAR3	0.4312				
IDAR2 vs. IDAR4	0.4521				
IDAR11 vs. IDAR14	0.4493				
IDAR3 vs. IDAR4	0.4448				
IDAR14 vs. IDAR16	0.4179				
IDAR14 vs. IDAR18	0.4344				
Threshold determination:					
Min score between normal file:	0.2439 (threshold)				
Max score between normal file and morphed virus 5%:	0.1797 (< threshold)				
Max score between normal file and morphed virus 15%:	0.2930 (> threshold)				
Max score between normal file and morphed virus 25%:	0.3553 (> threshold)				
Max score between normal file and morphed virus 30%:	0.3929 (> threshold)				

Table C- 2 Similarity scores for Window size = 10

Window Size 10: Similarity scores between various normal (IDAR) and morphed viruses (IDAN):					
	Base NGVCK viruses : scores	Morphed Virus 5% : scores	Morphed Virus 15% : scores	Morphed Virus 25% : scores	Morphed Virus 30% : scores
IDAN101 vs. IDAR1	0	0.0914	0.1173	0.2447	0.2490
IDAN101 vs. IDAR2	0	0.0818	0.0909	0.1571	0.1695
IDAN101 vs. IDAR3	0	0.0982	0.1247	0.1731	0.1950
IDAN101 vs. IDAR4	0	0.1165	0.1458	0.236	0.2420
IDAN101 vs. IDAR5	0	0.0301	0.0575	0.081	0.0950
IDAN141 vs. IDAR1	0	0.0411	0.0826	0.1536	0.2173
IDAN141 vs. IDAR2	0.0143	0.0310	0.0462	0.1317	0.1462
IDAN141 vs. IDAR3	0.0130	0.0543	0.1033	0.1419	0.1563
IDAN141 vs. IDAR4	0	0.0688	0.1134	0.1519	0.2242
IDAN141 vs. IDAR5	0	0.0153	0.0523	0.0707	0.0899
IDAN191 vs. IDAR1	0	0.053	0.187	0.1961	0.2234
IDAN191 vs. IDAR2	0	0.043	0.1151	0.1294	0.1309
IDAN191 vs. IDAR3	0	0.0663	0.1316	0.1641	0.1972
IDAN191 vs. IDAR4	0	0.0820	0.21	0.234	0.2501
IDAN191 vs. IDAR5	0	0.0242	0.0608	0.0884	0.0978

Similarity scores between various normal files	
IDAR0 vs. IDAR1	0.5398
IDAR0 vs. IDAR2	0.4191
IDAR0 vs. IDAR3	0.4113
IDAR0 vs. IDAR4	0.5292
IDAR11 vs. IDAR17	0.2068
IDAR1 vs. IDAR2	0.4699
IDAR1 vs. IDAR3	0.4444
IDAR17 vs. IDAR19	0.1771
IDAR12 vs. IDAR17	0.2069
IDAR2 vs. IDAR3	0.3295
IDAR2 vs. IDAR4	0.3507
IDAR11 vs. IDAR14	0.3011
IDAR3 vs. IDAR4	0.3312
IDAR14 vs. IDAR16	0.3501
IDAR14 vs. IDAR18	0.3767

Threshold determination:	
Min score between normal file:	0.1771 (threshold)
Max score between normal file and morphed virus 5%:	0.1165 (< threshold)
Max score between normal file and morphed virus 15%:	0.2158 (> threshold)
Max score between normal file and morphed virus 25%:	0.2447 (> threshold)
Max score between normal file and morphed virus 30%:	0.2501 (> threshold)

Table C- 3 Similarity scores for Window size = 20

Similarity scores between various normal (IDAR) and morphed viruses (IDAN):					
	Base NGVCK viruses : scores	Morphed Virus 5% : scores	Morphed Virus 15% : scores	Morphed Virus 25% : scores	Morphed Virus 30% : scores
IDAN101 vs. IDAR1	0	0.1016	0.1083	0.133	0.1464
IDAN101 vs. IDAR2	0	0.0613	0.0545	0.0898	0.0987
IDAN101 vs. IDAR3	0	0.0714	0.0623	0.0742	0.0825
IDAN101 vs. IDAR4	0	0.1165	0.1201	0.153	0.1628
IDAN101 vs. IDAR5	0	0	0	0.0095	0.0278
IDAN141 vs. IDAR1	0	0.0617	0.0917	0.12	0.1304
IDAN141 vs. IDAR2	0	0.0207	0.0554	0.0775	0.0877
IDAN141 vs. IDAR3	0	0.0181	0.0476	0.0774	0.0721
IDAN141 vs. IDAR4	0	0.0786	0.1047	0.144	0.1495
IDAN141 vs. IDAR5	0	0.0153	0	0.0202	0.0276
IDAN191 vs. IDAR1	0	0.0856	0.1305	0.1358	0.1441
IDAN191 vs. IDAR2	0	0.043	0.0658	0.0761	0.0873
IDAN191 vs. IDAR3	0	0.0379	0.0692	0.075	0.0956
IDAN191 vs. IDAR4	0	0.1026	0.1542	0.1419	0.1487
IDAN191 vs. IDAR5	0	0	0.0110	0.0393	0.0383

Similarity scores between various normal files	
IDAR0 vs. IDAR1	0.4248
IDAR0 vs. IDAR2	0.3210
IDAR0 vs. IDAR3	0.3046
IDAR0 vs. IDAR4	0.4200
IDAR11 vs. IDAR17	0.1551
IDAR1 vs. IDAR2	0.4452
IDAR1 vs. IDAR3	0.3471
IDAR17 vs. IDAR19	0.1561
IDAR12 vs. IDAR17	0.1651
IDAR2 vs. IDAR3	0.2384
IDAR2 vs. IDAR4	0.3118
IDAR11 vs. IDAR14	0.2185
IDAR3 vs. IDAR4	0.2727
IDAR14 vs. IDAR16	0.2197
IDAR14 vs. IDAR18	0.2494

Threshold determination:	
Min score between normal file:	0.1551 (threshold)
Max score between normal file and morphed virus 5%:	0.1026 (< threshold)
Max score between normal file and morphed virus 15%:	0.1542 (< threshold)
Max score between normal file and morphed virus 25%:	0.1532 (< threshold)
Max score between normal file and morphed virus 30%:	0.1628 (> threshold)

Appendix D: Detection using Edit Distance technique

Table D- 1 Scores for base viruses, morphed viruses and normal files using edit distance technique

Similarity scores between normal files (IDAR), and between morphed viruses and normal files (IDAN vs. IDAR):				
	Base NGVCK viruses : scores	Morphed Virus 5% : scores	Morphed Virus 15% : scores	Morphed Virus 25% : scores
IDAR0 vs. IDAR1	0.1818	0.097	0.1162	0.1610
IDAR0 vs. IDAR2	0.1687	0.0931	0.1195	0.1705
IDAR0 vs. IDAR3	0.174	0.08	0.1099	0.1586
IDAR0 vs. IDAR4	0.1426	0.100	0.126	0.1775
IDAR0 vs. IDAR5	0.1455	0.0843	0.102	0.1407
IDAR0 vs. IDAR6	0.0988	0.0868	0.1053	0.1451
IDAR0 vs. IDAR7	0.0976	0.0858	0.1069	0.1512
IDAR0 vs. IDAR8	0.0984	0.0848	0.105	0.1425
IDAR0 vs. IDAR9	0.0932	0.0802	0.0975	0.1347
IDAR0 vs. IDAR10	0.094	0.084	0.1061	0.1465
IDAR0 vs. IDAR11	0.0864	0.0841	0.1040	0.1481
IDAR0 vs. IDAR12	0.0882	0.0840	0.1060	0.1468
IDAR0 vs. IDAR13	0.0882	0.0837	0.1036	0.1473
IDAR0 vs. IDAR14	0.0862	0.0838	0.1060	0.1464
IDAR0 vs. IDAR15	0.0772	0.0838	0.1034	0.1460
IDAR0 vs. IDAR16	0.0829	0.0705	0.0877	0.1238
IDAR0 vs. IDAR17	0.0768	0.0831	0.104	0.1460
IDAR0 vs. IDAR18	0.0712	0.0837	0.1034	0.146
IDAR0 vs. IDAR19	0.0816	0.0829	0.1050	0.1450
IDAR0 vs. IDAR20	0.0713	0.0827	0.1028	0.146
IDAR0 vs. IDAR21	0.0737	0.0825	0.1040	0.1443
IDAR0 vs. IDAR22	0.0719	0.0827	0.1026	0.1445
IDAR0 vs. IDAR23	0.0726	0.0695	0.0863	0.1223
IDAR0 vs. IDAR24	0.067	0.0817	0.1011	0.1435
IDAR0 vs. IDAR25	0.0705	0.075	0.0969	0.1387
IDAR0 vs. IDAR26	0.0706	0.0808	0.1019	0.1415
IDAR0 vs. IDAR27	0.0706	0.1134	0.1503	0.2078
IDAR0 vs. IDAR28	0.0701	0.1025	0.1465	0.2057
IDAR0 vs. IDAR29	0.0704	0.1080	0.1445	0.2017
IDAR0 vs. IDAR30	0.0694	0.1024	0.1425	0.2098
IDAR0 vs. IDAR31	0.0581	0.0957	0.1373	0.195
IDAR0 vs. IDAR32	0.0703	0.112	0.1564	0.2202
IDAR0 vs. IDAR33	0.0693	0.0926	0.1231	0.1757
IDAR0 vs. IDAR34	0.0699	0.0989	0.1295	0.1807
IDAR0 vs. IDAR35	0.0693	0.0949	0.1323	0.1927
IDAR0 vs. IDAR36	0.0691	0.0945	0.1256	0.1772
IDAR0 vs. IDAR37	0.0685	0.0873	0.1177	0.1672
IDAR0 vs. IDAR38	0.0579	0.0926	0.1297	0.1878
IDAR0 vs. IDAR39	0.0683	0.0930	0.1293	0.1891
IDAR0 vs. IDAR40	0.0624	0.0926	0.1281	0.1873

Similarity scores between various normal files	
IDAR5 vs. IDAR10	0.6726
IDAR5 vs. IDAR11	0.6253
IDAR5 vs. IDAR12	0.5148
IDAR5 vs. IDAR13	0.6485
IDAR5 vs. IDAR14	0.2291
IDAR5 vs. IDAR15	0.2238
IDAR5 vs. IDAR16	0.2274
IDAR5 vs. IDAR17	0.211
IDAR5 vs. IDAR18	0.2726
IDAR5 vs. IDAR19	0.1999
IDAR5 vs. IDAR20	0.2382
IDAR5 vs. IDAR21	0.2382
IDAR5 vs. IDAR22	0.2000
IDAR5 vs. IDAR23	0.2470
IDAR5 vs. IDAR24	0.1931
IDAR5 vs. IDAR25	0.222
IDAR5 vs. IDAR26	0.2289
IDAR5 vs. IDAR27	0.2347
IDAR5 vs. IDAR28	0.1660
IDAR5 vs. IDAR29	0.172
IDAR5 vs. IDAR30	0.1932
IDAR5 vs. IDAR31	0.1681
IDAR5 vs. IDAR32	0.1591
IDAR5 vs. IDAR33	0.1876
IDAR5 vs. IDAR34	0.1902
IDAR5 vs. IDAR35	0.187
IDAR5 vs. IDAR36	0.1887
IDAR5 vs. IDAR37	0.1874
IDAR5 vs. IDAR38	0.1888
IDAR5 vs. IDAR39	0.1631
IDAR5 vs. IDAR40	0.186
IDAR6 vs. IDAR7	0.1887
IDAR6 vs. IDAR8	0.1857
IDAR6 vs. IDAR9	0.1861
IDAR6 vs. IDAR10	0.1848
IDAR6 vs. IDAR11	0.1866
IDAR6 vs. IDAR12	0.1611
IDAR6 vs. IDAR13	0.1841
IDAR6 vs. IDAR14	0.1945
IDAR6 vs. IDAR15	0.1809

Threshold determination:	
Min score between normal file:	0.1591 (threshold)
Max score between normal file and morphed virus 5%:	0.1934 (> threshold)
Max score between normal file and morphed virus 15%:	0.2024 (> threshold)
Max score between normal file and morphed virus 25%:	0.2816 (> threshold)

Appendix E: Detection using Sequence Alignment technique

Table E- 1 Scores for base viruses, and normal files using pairwise sequence alignment technique

Alignment scores between base viruses and normal files (IDAR vs. IDAN), between normal files (IDAR), between base viruses (IDAN)		
Base Virus vs. Normal File :Scores (IDAN,IDAR) : Scores	Normal vs. Normal File : Scores (IDAR,IDAR) : Scores	Base Virus vs. Base Virus : Scores (IDAN,IDAN) : Scores
(0,20) Score = -456.0	(0,1) Score = 513.0	(0,1) Score = -1.0
(0,21) Score = -506.0	(0,2) Score = 263.0	(0,2) Score = -99.0
(0,22) Score = -750.0	(0,3) Score = 382.0	(0,3) Score = -43.0
(0,23) Score = -725.0	(0,4) Score = 44.0	(0,4) Score = 50.0
(0,24) Score = -758.0	(0,5) Score = -74.0	(0,5) Score = 8.0
(0,25) Score = -931.0	(0,6) Score = -25.0	(0,6) Score = 15.0
(0,26) Score = -905.0	(0,7) Score = 62.0	(0,7) Score = 47.0
(0,27) Score = -774.0	(0,8) Score = 349.0	(0,8) Score = 27.0
(0,28) Score = -435.0	(0,9) Score = 430.0	(0,9) Score = 154.0
(0,29) Score = -275.0	(0,10) Score = 446.0	(0,10) Score = -26.0
(0,30) Score = -574.0	(0,11) Score = 1038.0	(0,11) Score = 44.0
(0,31) Score = -429.0	(0,12) Score = 391.0	(0,12) Score = 30.0
(0,32) Score = -379.0	(0,13) Score = 371.0	(0,13) Score = -14.0
(0,33) Score = -604.0	(0,14) Score = 412.0	(0,14) Score = 83.0
(0,34) Score = -263.0	(0,15) Score = 587.0	(0,15) Score = -30.0
(0,35) Score = -530.0	(0,16) Score = 243.0	(0,16) Score = 41.0
(0,36) Score = -145.0	(0,17) Score = 504.0	(0,17) Score = 4.0
(0,37) Score = -667.0	(0,18) Score = 285.0	(0,18) Score = 63.0
(0,38) Score = -871.0	(0,19) Score = 966.0	(0,19) Score = -25.0
(0,39) Score = -416.0	(1,2) Score = 484.0	(0,20) Score = -74.0
(1,20) Score = -481.0	(1,3) Score = 589.0	(1,2) Score = -73.0
(1,21) Score = -501.0	(1,4) Score = 59.0	(1,3) Score = 15.0
(1,22) Score = -842.0	(1,5) Score = -86.0	(1,4) Score = -16.0
(1,23) Score = -784.0	(1,6) Score = -52.0	(1,5) Score = -71.0
(1,24) Score = -771.0	(1,7) Score = 78.0	(1,6) Score = 149.0
(1,25) Score = -919.0	(1,8) Score = 474.0	(1,7) Score = -33.0
(1,26) Score = -847.0	(1,9) Score = 810.0	(1,8) Score = 4.0
(1,27) Score = -750.0	(1,10) Score = 530.0	(1,9) Score = 17.0
(1,28) Score = -442.0	(1,11) Score = 482.0	(1,10) Score = -47.0
(1,29) Score = -335.0	(1,12) Score = 460.0	(1,11) Score = 82.0
(1,30) Score = -580.0	(1,13) Score = 391.0	(1,12) Score = -14.0
(1,31) Score = -349.0	(1,14) Score = 495.0	(1,13) Score = -122.0
(1,32) Score = -406.0	(1,15) Score = 872.0	(1,14) Score = -50.0
(1,33) Score = -652.0	(1,16) Score = 361.0	(1,15) Score = -62.0
(1,34) Score = -339.0	(1,17) Score = 604.0	(1,16) Score = -15.0
(1,35) Score = -536.0	(1,18) Score = 334.0	(1,17) Score = 50.0
(1,36) Score = -226.0	(1,19) Score = 377.0	(1,18) Score = -63.0
(1,37) Score = -691.0	(2,3) Score = 978.0	(1,19) Score = 123.0
(1,38) Score = -974.0	(2,4) Score = 208.0	(1,20) Score = -44.0
(1,39) Score = -428.0	(2,5) Score = 187.0	(2,3) Score = 61.0

Table E- 2 Scores for morphed viruses, and normal files using pairwise sequence alignment technique

Alignment scores between morphed viruses 30% and normal files (IDAR vs. IDAN), between normal files (IDAR), between morphed viruses 30% (IDAN)		
Morphed Virus 30% vs. Normal File : Scores (IDAN,IDAR) : Scores	Normal vs. Normal File : Scores (IDAR,IDAR) : Scores	Morphed Virus 30% vs. Morphed Virus 30% :Scores (IDAN,IDAN) : Scores
(0,10) Score = 103.0	(0,1) Score = 513.0	(1,2) Score = -73.0
(0,11) Score = 147.0	(0,2) Score = 263.0	(1,3) Score = 15.0
(0,12) Score = -49.0	(0,3) Score = 382.0	(1,4) Score = -16.0
(0,13) Score = 50.0	(0,4) Score = 44.0	(1,5) Score = -71.0
(0,14) Score = -24.0	(0,5) Score = -74.0	(1,6) Score = 149.0
(0,15) Score = -171.0	(0,6) Score = -25.0	(1,7) Score = -33.0
(0,16) Score = -156.0	(0,7) Score = 62.0	(1,8) Score = 4.0
(0,17) Score = -22.0	(0,8) Score = 349.0	(1,9) Score = 17.0
(0,18) Score = -60.0	(0,9) Score = 430.0	(1,10) Score = -47.0
(0,19) Score = -9.0	(0,10) Score = 446.0	(2,3) Score = 61.0
(1,10) Score = 164.0	(0,11) Score = 1038.0	(2,4) Score = -80.0
(1,11) Score = 183.0	(0,12) Score = 391.0	(2,5) Score = 83.0
(1,12) Score = 123.0	(0,13) Score = 371.0	(2,6) Score = 60.0
(1,13) Score = 135.0	(0,14) Score = 412.0	(2,7) Score = -7.0
(1,14) Score = -3.0	(0,15) Score = 587.0	(2,8) Score = 96.0
(1,15) Score = -99.0	(0,16) Score = 243.0	(2,9) Score = -73.0
(1,16) Score = -46.0	(0,17) Score = 504.0	(2,10) Score = 55.0
(1,17) Score = 10.0	(0,18) Score = 285.0	(3,4) Score = 3.0
(1,18) Score = 44.0	(0,19) Score = 966.0	(3,5) Score = -8.0
(1,19) Score = 89.0	(1,2) Score = 484.0	(3,6) Score = 55.0
(2,10) Score = -3.0	(1,3) Score = 589.0	(3,7) Score = -73.0
(2,11) Score = 49.0	(1,4) Score = 59.0	(3,8) Score = -51.0
(2,12) Score = -336.0	(1,5) Score = -86.0	(3,9) Score = 82.0
(2,13) Score = -145.0	(1,6) Score = -52.0	(3,10) Score = 55.0
(2,14) Score = -434.0	(1,7) Score = 78.0	(4,5) Score = -105.0
(2,15) Score = -612.0	(1,8) Score = 474.0	(4,6) Score = 55.0
(2,16) Score = -581.0	(1,9) Score = 810.0	(4,7) Score = -60.0
(2,17) Score = -409.0	(1,10) Score = 530.0	(4,8) Score = -85.0
(2,18) Score = 7.0	(1,11) Score = 482.0	(4,9) Score = 41.0
(2,19) Score = 119.0	(1,12) Score = 460.0	(4,10) Score = -72.0
(3,10) Score = -288.0	(1,13) Score = 391.0	(5,6) Score = -62.0
(3,11) Score = -324.0	(1,14) Score = 495.0	(5,7) Score = 155.0
(3,12) Score = -715.0	(1,15) Score = 872.0	(5,8) Score = 60.0
(3,13) Score = -558.0	(1,16) Score = 361.0	(5,9) Score = -76.0
(3,14) Score = -666.0	(1,17) Score = 604.0	(5,10) Score = 20.0
(3,15) Score = -890.0	(1,18) Score = 334.0	(6,7) Score = -58.0
(3,16) Score = -800.0	(1,19) Score = 377.0	(6,8) Score = 30.0
(3,17) Score = -652.0	(2,3) Score = 978.0	(6,9) Score = -4.0
(3,18) Score = -285.0	(2,4) Score = 208.0	(6,10) Score = 41.0
(3,19) Score = -135.0	(2,5) Score = 187.0	(7,8) Score = 22.0
(4,10) Score = -46.0	(2,6) Score = 218.0	(7,9) Score = -106.0
(4,11) Score = 6.0	(2,7) Score = 206.0	(7,10) Score = -9.0
(4,12) Score = -444.0	(2,8) Score = 434.0	(8,9) Score = -19.0
(4,13) Score = -321.0	(2,9) Score = 251.0	(8,10) Score = -72.0
(4,14) Score = -475.0	(2,10) Score = 587.0	(9,10) Score = -53.0