THE RABIN-KARP ALGORITHM

LOUAY ELBICHE | SIDDHESH JETHE | ZUBIN KADVA
GROUP 2 | ALGORITHMICS 2017

ANALYSIS OF ALGORITHMS | SPRING 2017

STRING MATCHING

- Returns the position where a given pattern is found in a text

Pattern **P** of length **m**

String **S** of length **n**

$P \subseteq S$

S[i] = P[0]

S[i + 1] = P[1]

…

S[i + m + 1]= P[m - 1]

$\sum$ = alphabet

$\sum$ = {A, … , Z}

$\sum$ = {0, 1}

$\sum$ = {A, C, G, T}

EXAMPLE

- $\sum = \{X, Y, Z\}$
- S = X Y X Y X Y Z Y
- P = X Y X Y Z

Index	0	1	2	3	4	5	6	7
Text	X	Y	X	Y	X	Y	Z	Y

THE PROBLEM

Given a string $\boldsymbol{S} = \boldsymbol{s_1}, \boldsymbol{s_2}, \ldots, \boldsymbol{s_n}$ of characters in some alphabet $\boldsymbol{\Sigma} = \{\boldsymbol{a_1}, \boldsymbol{a_2} \ldots, \boldsymbol{a_K}\}$ and a pattern or query string $\boldsymbol{P} = \boldsymbol{p_1}, \boldsymbol{p_2} \ldots, \boldsymbol{p_m}; \ \boldsymbol{m} < \boldsymbol{n}$ in the same alphabet, find all occurrences of **P** in **S**.

ALGORITHMS

- Naïve string searching algorithm
- Rabin-Karp string searching algorithm
- Knuth-Morris-Pratt algorithm
- Boyer-Moore string search algorithm

BRUTE FORCE

- Naïve search algorithm

```
function NaiveSearch(string, pattern)
    n := length(string)
    m := length(pattern)
    for i = 0 to n - m + 1
        for j = 0 to m
                if string[i + j] != pattern[j]
                        break
        if j == m
                return i
    return not found
```

ALGORITHM TRACE

Text	F	I	N	D		M	E
Pattern	M	E					

ALGORITHM TRACE

Index	0	1	2	3	4	5	6
Text	F	I	N	D		M	E
Pattern	M	E					

ALGORITHM TRACE

Index	0	1	2	3	4	5	6
Text	F	I	N	D		M	E
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ALGORITHM TRACE

Index	0	1	2	3	4	5	6
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ALGORITHM TRACE

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ALGORITHM TRACE

Index	0	1	2	3	4	5	6
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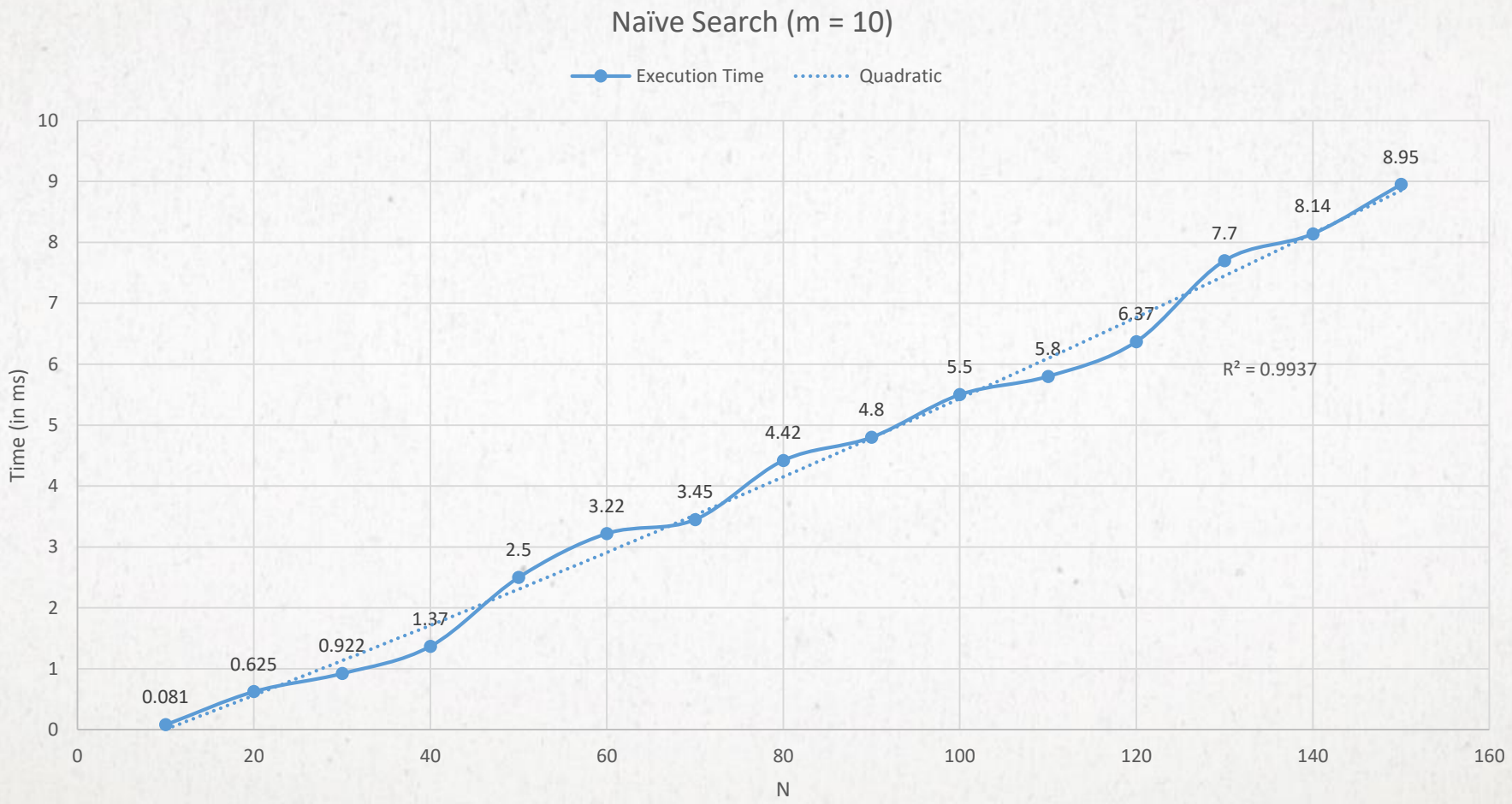
ANALYSIS

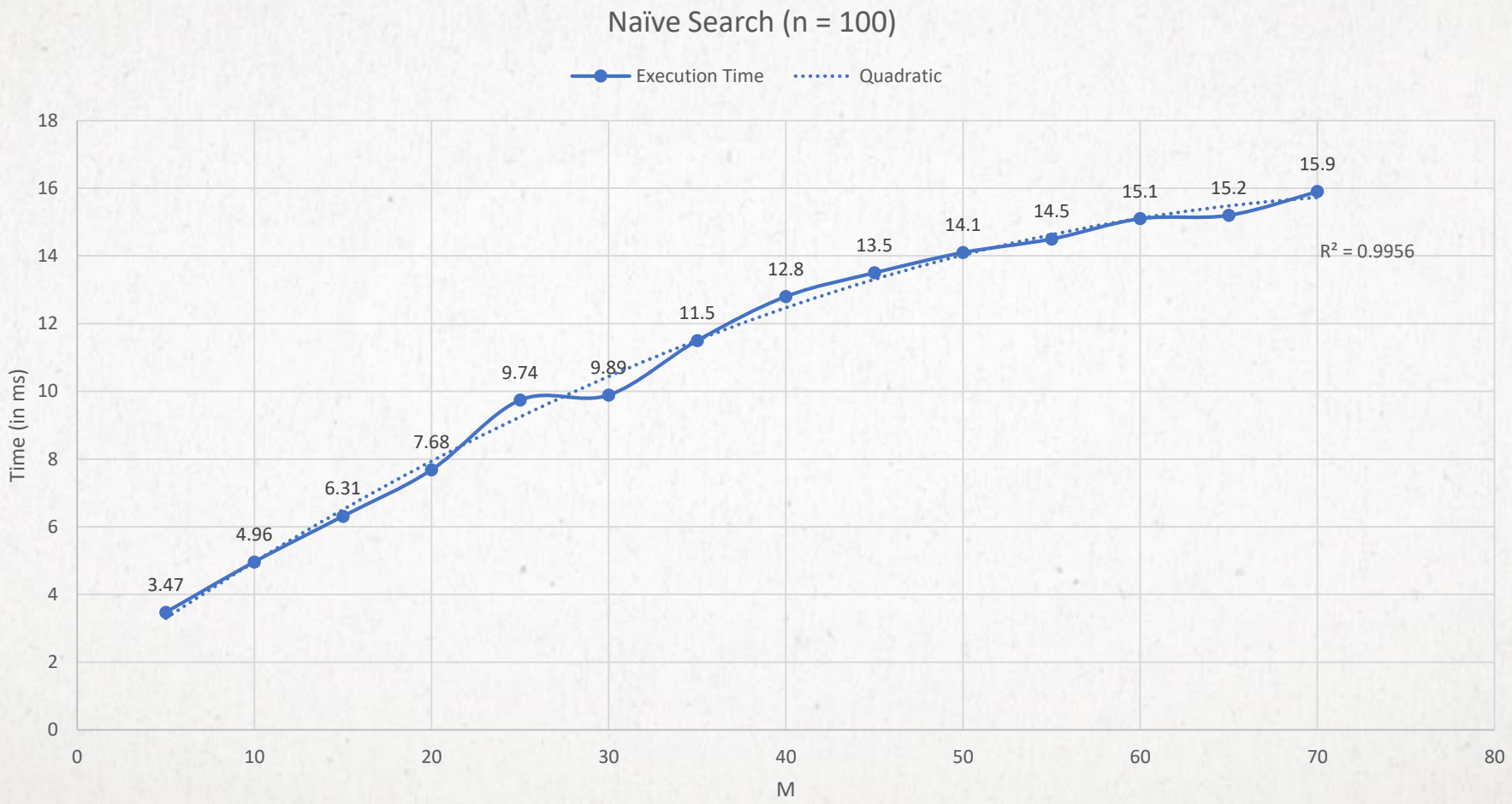
```
function NaiveSearch(string, pattern)
    for i = 0 to n - m + 1
        for j = 0 to m
            if string[i + j] != pattern[j]
                break
        if j == m
            return i
    return not found
```

Complexities		Naïve Search
Performance	Best	$\Omega\,(m)$
	Average	$\theta\,(m+n)$
	Worst	$O\,(mn)$
Space		$O\,(1)$

VISUAL PERFORMANCE



VISUAL PERFORMANCE



RABIN-KARP

- Based on computing hash of a pattern and then comparing it

```
function RabinKarp(string, pattern)
    hpattern := hash(pattern);
    hstring := hash(string)
    for i = 1 to n - m + 1
        if hstring = hpattern
            if string = pattern
                return i
        hstring:= reHash(i, i + m - 1)
    return not found
```

RABIN-KARP

- The hash is calculated as:

$$\sum_{i=0}^{length} val(string[i]) * prime^{i}$$

```
function hash(string, length)
    for i = 0 to length
        hash := hash + value(string[i]) * prime^i
    return hash
```

RABIN-KARP

- Updating the hash is done as:

$$new\_hash = old\_hash - val(string[old\_index])$$

$$new\_hash = new\_hash \,/\, prime$$

$$new\_hash = new\_hash + val(string[new]) * prime^{length-1}$$

```
function reHash(string, length, old, new, hash)
    newHash := hash - value(string[old])
    newHash := newHash / prime
    newHash := newHash + value(string[new]) * prime^(length - 1)
    return newHash
```

MODULAR RABIN-KARP

- To reduce:
  - Size of the hash result and
  - # of hash collisions

- Elements:
  - Radix **d**
  - Prime **q**

BASIS FOR RABIN-KARP

- q = 23

i	0	1	2	
	6	4	7	% 23 = 3

i	0	1	2	3	
	9	6	4	7	
0	9	6	4	% 23 = 21	
1		6	4	7	% 23 = 3

KEY COMPUTATION

- d = 10

i	0	1	2	3	4	...
current value	6	3	2	1	7	
new value		3	2	1	7	
		3	2	1	*current value*	
	-	3	0	0		
			2	1	*subtract leading digit*	
	*		1	0	*multiply by radix*	
		2	1	0		
	+			7	*add trailing digit*	
		2	1	7	*new value*	

HORNER'S METHOD

i	0	1	2	
	3	1	2	
0	3	% 23 = 3		
1	3	1	% 23 = (3 * 10 + 1) % 23 = 8	
2	3	1	2	% 23 = (8 * 10 + 2) % 23 = 13

MODULAR RABIN-KARP

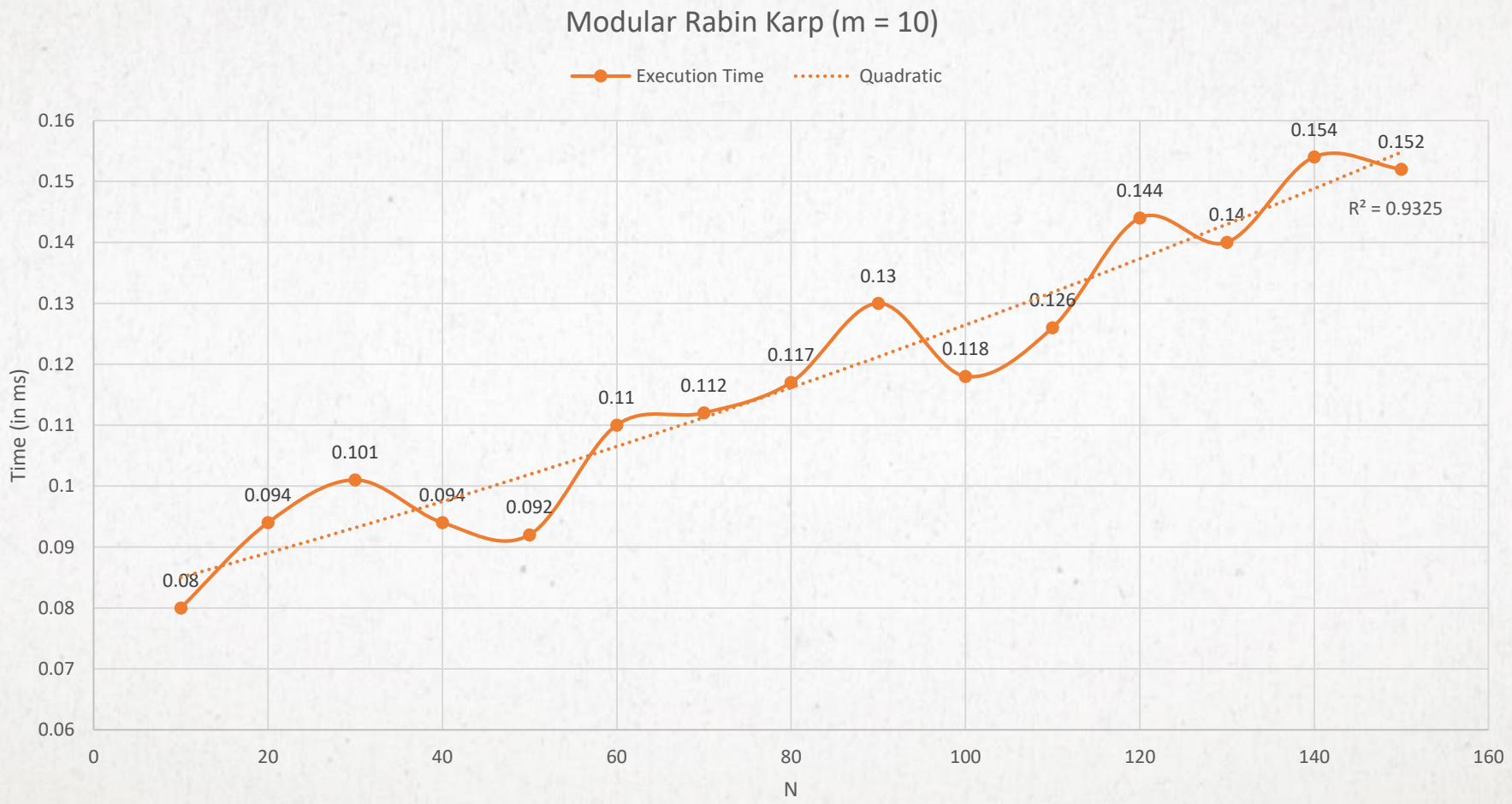
```
function rabin-karp-matcher(T, P, d, q)
    n := T.length
    m := P.length
    h := d^(m−1) mod q
    p := 0
    t_0 := 0
    for i = 1 to m
        p := (d * p + P[i]) mod q
        t_0 := (d * t_0 + T[i]) mod q
    for s = 0 to n - m
        if p == t_s
            if P[1 .. m] == T[s + 1 .. s + m]
                return s
        if s < n - m
            t_{s+1} = (d * (t_s − T[s + 1] * h) + T[s + m + 1]) mod q
    return not found
```

ANALYSIS

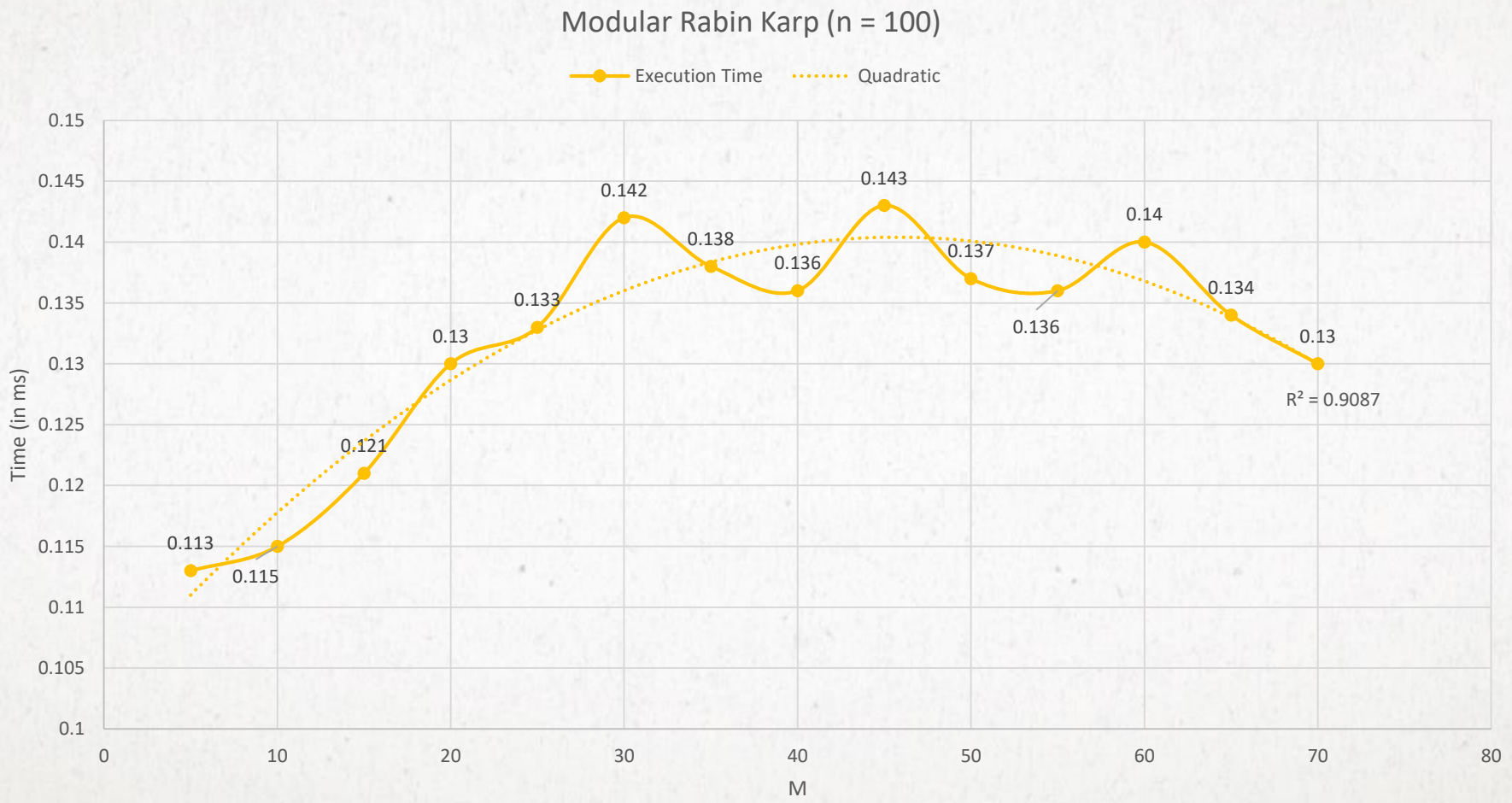
```
function rabin-karp-matcher(T, P, d, q)
    n := T.length
    m := P.length
    h := d^(m−1) mod q
    p := 0
    t_0 := 0
    for i = 1 to m
        p := (d * p + P[i]) mod q
        t_0 := (d * t_0 + T[i]) mod q
    for s = 0 to n - m
        if p == t_s
            if P[1 .. m] == T[s + 1 .. s + m]
                return s
        if s < n - m
            t_{s+1} = (d * (t_s − T[s + 1] * h) + T[s + m + 1]) mod q
    return not found
```

Complexities		Rabin Karp
Performance	Best	$\Omega\ (m+n)$
	Average	$\theta\ (m+n)$
	Worst	$O\ (mn)$
Space		$O\ (m)$

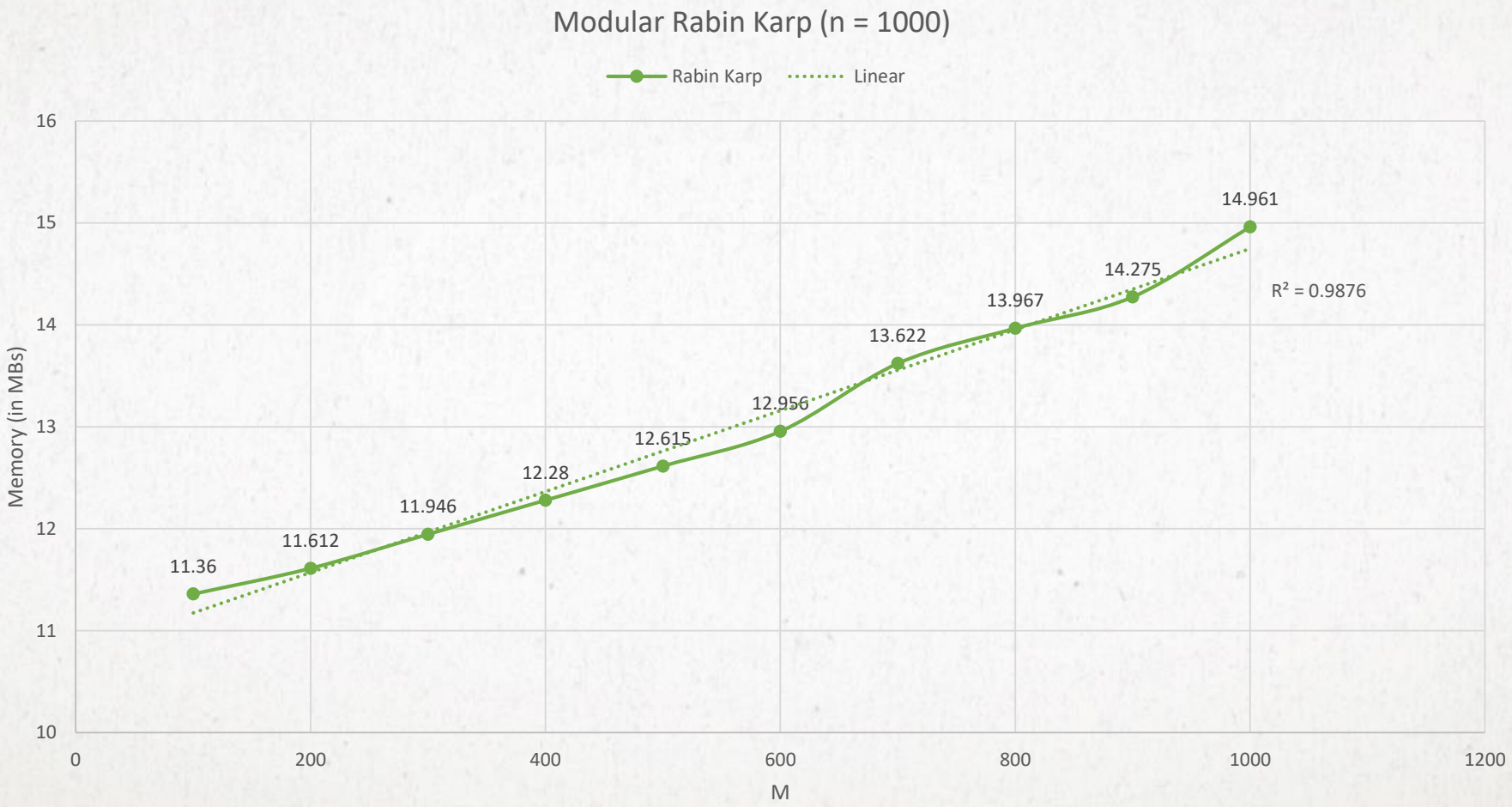
VISUAL PERFORMANCE



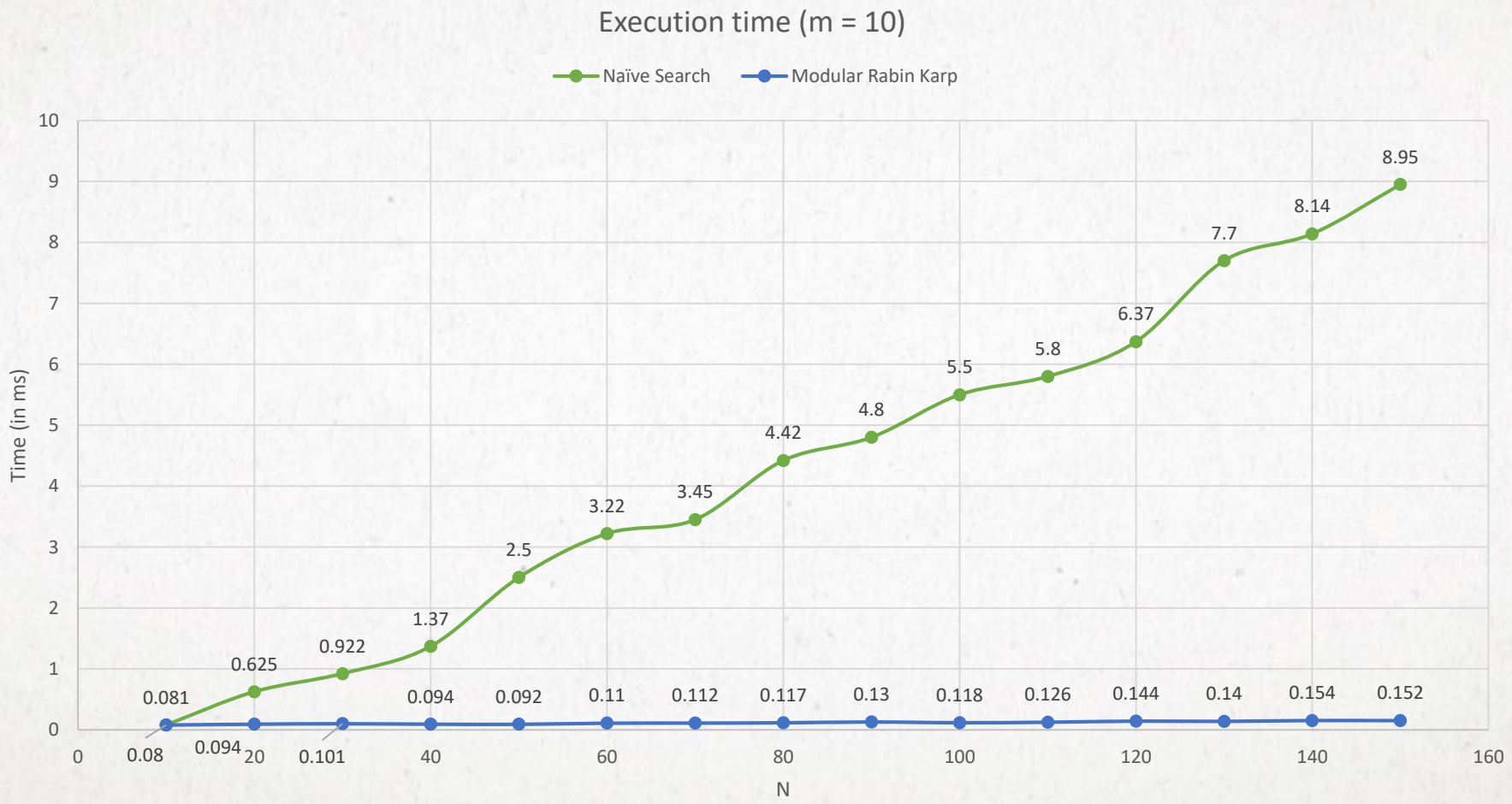
VISUAL PERFORMANCE



VISUAL SPACE



COMPARATIVE PERFORMANCE



COMPARATIVE PERFORMANCE

APPLICATION EXAMPLE: BIOINFORMATICS

- Certain known nucleotide and/or amino acid sequences have properties known to biologists
  - **ATG** is a string which must be present at the beginning of every protein (gene) a DNA sequence.

- A primer is a conserved DNA sequence used in the Polymerase Chain Reaction (PCR) to identify the location of the DNA sequence that will be amplified

- Genetic code is redundant. Consider the following sequence of nucleotides: **GCTACTATTTTTCAT**
  - When read in forward frame 0, this sequence encodes the following sequence of amino acids: **ATIFH**

APPLICATION EXAMPLE: BIOINFORMATICS

- Because of redundancy of the genetic code, the following sequences of nucleotides will produce the same sequence of amino acids

```
GCT ACT ATT TTT CAT
GCc ACc ATT TTa CAc
GCc ACc ATc TTg CAT
GCT ACT ATc TTa CAc
GCg ACc ATa TTc CAc

 A   T   I   F   H
```

Amino Acid	SLC	DNA codons
Isoleucine	I	ATT, ATC, ATA
Leucine	L	CTT, CTC, CTA, CTG, TTA, TTG
Valine	V	GTT, GTC, GTA, GTG
Phenylalanine	F	TTT, TTC
Methionine	M	ATG
Cysteine	C	TGT, TGC
Alanine	A	GCT, GCC, GCA, GCG
Glycine	G	GGT, GGC, GGA, GGG
Proline	P	CCT, CCC, CCA, CCG
Threonine	T	ACT, ACC, ACA, ACG
Serine	S	TCT, TCC, TCA, TCG, AGT, AGC
Tyrosine	Y	TAT, TAC
Tryptophan	W	TGG
Glutamine	Q	CAA, CAG
Asparagine	N	AAT, AAC
Histidine	H	CAT, CAC
Glutamic acid	E	GAA, GAG
Aspartic acid	D	GAT, GAC
Lysine	K	AAA, AAG
Arginine	R	CGT, CGC, CGA, CGG, AGA, AGG
Stop codons	Stop	TAA, TAG, TGA

http://www.cbs.dtu.dk/courses/27619/codon.html
http://users.csc.calpoly.edu/~dekhtyar/448-Spring2013/lectures/lec03.448.pdf

APPLICATION EXAMPLE: BIOINFORMATICS

- *Example*: Consider for following string S = "**ATTCCGT**".
  - Suppose we are looking for four-letter substrings.

```
function end-presentation()
    THANK YOU
    if questions?
        solve()
```