

Protein Sequence FASTA format

>MCHU - Calmodulin - Human, rabbit, bovine, rat, and chicken

MADQLTEEQIAEFKEAFSLFDKDGDGTITT KELGTVMRSLGQNPTEAELQDMINEVDAD GNGTID

FPEFLTMMARKMKDTDSEEEIREAFRVFDK DGNGYISAAELRHVMTNLGEKLTDEEVDE MIREA

DIDGDGQVNYEEFVQMMTAK*

DNA Sequence FASTA format

>OV986001.1 Pseudomonas fluorescens SBW25 genome assembly, chromosome: 1 GTGTCAGTGGAACTTTGGCCAGCAGTGCG TGGAGCTTTTTGCGCGATGAGCTGCCTGCC CAGCAATTCAACA CCTGGATCCGTCCACTACAGGTCGAAGCC GAAGGCGACGAGTTGCGTGTTTACGCGC CCAATCGTTTTGT TCTCGACTGGGTCAACGAGAAGTACCTGA GCCGCGTGCTCGAATTGCTCGATGAACAC GGCAACGGCCTC

DNA Sequence

GTGTCAGTGGAACTTTGGCAGCAGTGCG TGGAGCTTTTTGCGCGATGAGCTGCCC CAGCAATTCAACA CCTGGATCCGTCCACTACAGGTCGAAGCC GAAGGCGACGAGTTGCGTGTTTACGCGC CCAATCGTTTTGT TCTCGACTGGGTCAACGAGAAGTACCTGA GCCGCGTGCTCGAATTGCTCGATGAACAC GGCAACGGCCTC

Strings in Biology

Protein: Typical length in hundreds, many letters

DNA: Length in millions, 4 letters (A,C,G,T)

Algorithmic Problems with Strings

- 1. Sorting a collection of strings
- 2. Aligning two strings for similarity
- 3. Compressing one string for efficient storage

Sorting

0: TCAG

1: CGCCT

2: ATT

3: **GTA**

4: CATG

5: ACGC

6: CCG

7: ACGAT

8: TCAA

9: ATTC

ACGAT

ACGC

ATT

ATTC

CATG

CCG

CGCCT

GTA

TCAA

TCAG

0: TCAG

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7: ACGAT

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ATT

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CGCCT

ACGC

CATG

ATT

CCG

ATTC

GTA

TCAG

TCAA

ACGAT CATG

ACGC CCG

ATT CGCCT

ATTC

GTA

TCAG TCAA

ACGAT CATG

ACGC CCG

ATT CGCCT

ATTC

GTA TCAG
TCAA

ACGAT CATG

ACGC CCG

ATT CGCCT

ATTC

GTA TCAA TCAG

Algorithm:

RadixSortRecursive(Strings, position):

- 1. Create one table for each alphabet symbol.
- 2. For each string in Strings:
 Store string in Table[string[position]].
- 3. For each table T, T=RadixSortRecursive(T, position+1)
- 4. Strings=Concatenation of sorted tables. Return Strings.

Radix Sort: Analysis

Time Complexity:

O(Ln), where L=max length of strings, n=# strings

Space Complexity:

Above Description: O(Ln)

Review Exercise:

Sort the following strings:

CCGA

TT

AATC

GTATG

GGAT

TCCG

CACAGA

AACG

CCG

ACTAG

0: TCAG

1: CGCCT

2: ATT

3: GTA

4: CATG

5: ACGC

6: CCG

7: ACGAT

8: TCAA

9: ATTC

ATT

ACGC

ACGAT

ATTC

CGCCT

CATG

CCG

GTA

TCAG TCAA

0: TCAG

1: CGCCT

2: ATT

3: GTA

4: CATG

5: ACGC

6: CCG

7: ACGAT

8: TCAA

9: ATTC

0: TCAG	2	2	1
1: CGCCT	5	5	4
2: ATT	7	7	6
3: GTA	9	O	O
4: CATG	1		
5: ACGC	4		
6: CCG	6	2	0
7: ACGAT	3	3	8
8: TCAA	0		Ŏ
9: ATTC	8		

0: TCAG	2		5
1: CGCCT	5		7
2: ATT	7		,
3: GTA	9		
4: CATG	1		
5: ACGC	4		
6: CCG	6		2
7: ACGAT	3		2 9
8: TCAA	0		9
9: ATTC	8		

0: TCAG	5	 5
1: CGCCT	7	7
2: ATT	2	<i>1</i>
3: GTA	9	
4: CATG	1	
5: ACGC	4	
6: CCG	6	2
7: ACGAT	3	 9
8: TCAA	0	9
9: ATTC	8	

0: TCAG

1: CGCCT

2: ATT

3: GTA

4: CATG

5: ACGC

6: CCG

7: ACGAT

8: TCAA

9: ATTC

ATT

ACGC

ACGAT

ATTC

CGCCT

CATG

CCG

GTA

TCAG TCAA

0: ATT

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2: ACGAT

3: ATTC

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5: CATG

6: CCG

7: **GTA**

8: TCAG

9: TCAA

ATT

ACGC

ACGAT

ATTC

CGCCT

CATG

CCG

GTA

TCAG TCAA

0: ATT

1: ACGC

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3: ATTC

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5: CATG

6: CCG

7: **GTA**

8: TCAG

9: TCAA

ACGC ACGAT

ATT ATTC

0: ACGC

1: ACGAT

2: ATT

3: ATTC

4: CGCCT

5: CATG

6: CCG

7: **GTA**

8: TCAG

9: TCAA

--- ACGC ACGAT

-- ATT
ATTC

0: ACGC

CATG

 \overline{CCG}

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9: TCAG

TCAA

TCAG

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1: ACGC

2: ATT

3: ATTC

4: CATG

5: CCG

6: CGCCT

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8: TCAG

9: TCAA

Radix Sort: Analysis

Time Complexity:

O(Ln), where L=max length of strings, n=# strings Space Complexity With Optimization:

O(n+L)

Binary encoding: Zero Additional Space