

Compressed Direct-Address Table - practical index for genomic sequences

Katarzyna Jabłonowska

Michał Sabaciński
Norbert Dojer



Segovia
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The problem

ATTATATAGTTGTAA

✓GTTGT

✓TAA

×CTA

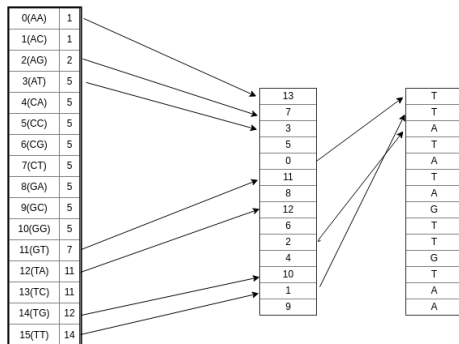
Our goal is to find an algorithm that:

- scans the whole text only once
- is flexible
- is fast and memory efficient

The basic idea

Two steps:

- 1 Building an index
- 2 Searching for patterns



Building an index

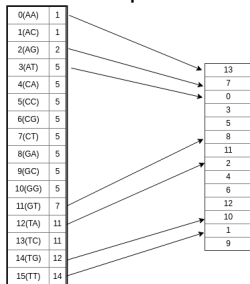
Step 1

0(AA)	1
1(AC)	0
2(AG)	1
3(AT)	3
4(CA)	0
5(CC)	0
6(CG)	0
7(CT)	0
8(GA)	0
9(GC)	0
10(GG)	0
11(GT)	2
12(TA)	4
13(TC)	0
14(TG)	1
15(TT)	2

Step 2

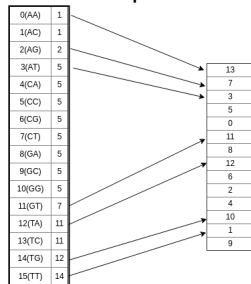
0(AA)	1
1(AC)	1
2(AG)	2
3(AT)	5
4(CA)	5
5(CC)	5
6(CG)	5
7(CT)	5
8(GA)	5
9(GC)	5
10(GG)	5
11(GT)	7
12(TA)	11
13(TC)	11
14(TG)	12
15(TT)	14

Step 3

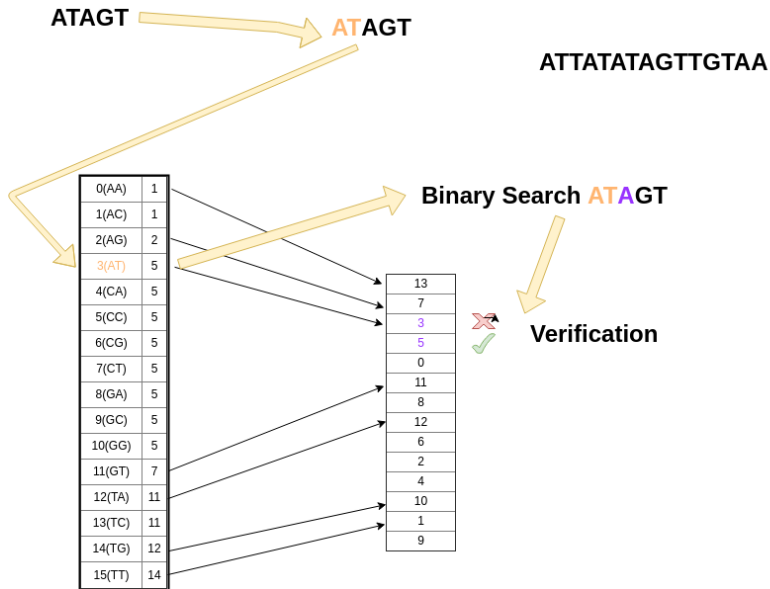


Prefix length = 2
Substring length = 3

Step 4



Searching for patterns

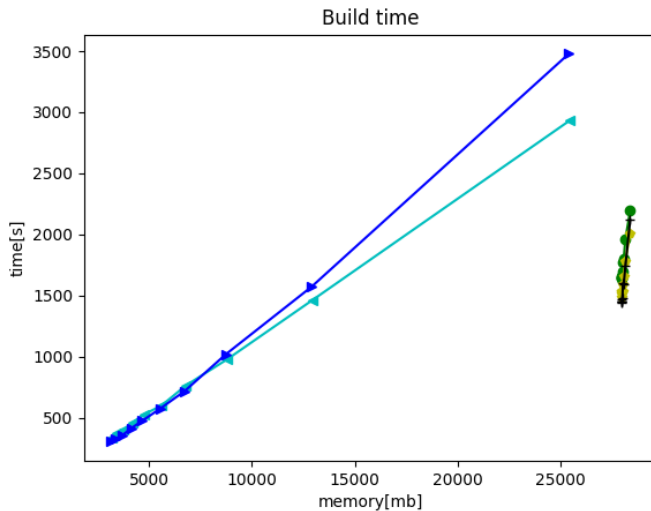


Compression

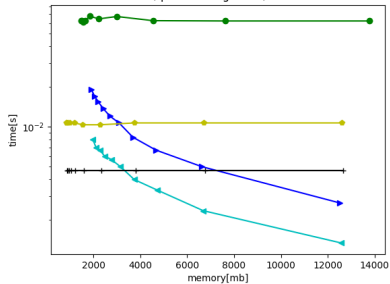
- 1 'GTCCAT'
- 2 'GTCCAT'
- 3 'GTCCAT*', $* \in \Sigma$
- 4 '*GTCCAT', $* \in \Sigma$
- 5 'GTCCAT**', $* \in \Sigma$

- human genome
- C++
- prefixLength = 10 and 12
- patterns of length 40 or 200. All or none of them appearing in the text

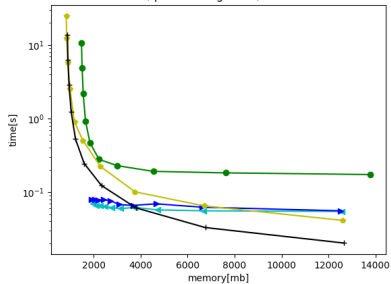
Results



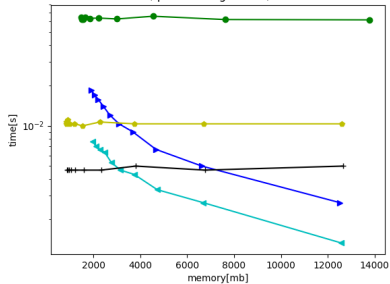
Location time, pattern length: 40, occurrences: 0%



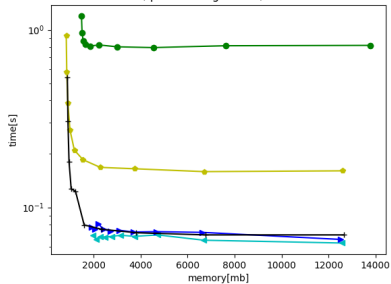
Location time, pattern length: 40, occurrences: 100%



Location time, pattern length: 200, occurrences: 0%



Location time, pattern length: 200, occurrences: 100%



Thank you