

Computer Architecture HW3

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1 Critical Paper Reviews [500 points]

see here

2 Genome Analysis I [150 points]

2.1 Edit Distance

a) M O N - - - - T A G
s - - i i i i - - -
D O N N E R S T A G
Edit Distance: 5

b) F R E I T A G
s s s s - - -
S A M S T A G
Edit Distance: 4

c) D O N N E R S T A G
d d d d d d d d d
- - - - - - - - -
Edit Distance: 10

2.2 Read Mapping

a) read1: $6 + 3 + 3 = 12$
read2: $2 + 5 + 6 = 13$
read3: $2 + 0 + 0 = 2$
read4: $3 + 2 + 5 = 10$
read5: $6 + 5 + 3 = 14$
51 invocations

b) read1: 10, 15, 20 \rightarrow 1
read2: 50, 55, 60 & 615, 620, 625 \rightarrow 2
read3: - \rightarrow 0
read4: 610, 615, 620 \rightarrow 1
read5: 710, 715, 720 \rightarrow 1
5 invocations

c) AAAAA and GGCCT are above threshold.

read1: $0 + 3 + 3 = 6$

read2: $2 + 0 + 0 = 2$

read3: $2 + 0 + 0 = 2$

read4: $0 + 3 + 2 = 5$

read5: $0 + 0 + 3 = 3$

18 invocations

3 Genome Analysis II [150 points]

a) $\{AAAA\} \rightarrow \{1\}$

$\{ATAC\} \rightarrow \{5, 17, 41\}$

$\{TGAT\} \rightarrow \{9, 43\}$

$\{CCTT\} \rightarrow \{13\}$

$\{GTTG\} \rightarrow \{21, 37\}$

$\{TAAG\} \rightarrow \{25, 45\}$

$\{GTTT\} \rightarrow \{29\}$

$\{CAAA\} \rightarrow \{33\}$

b) $\{AAAA\} \rightarrow \{1\}$

$\{ATAC\} \rightarrow \{5, 17, 41\}$

$\{GTTG\} \rightarrow \{21\}$

$\{CAAA\} \rightarrow \{33\}$

c) non-overlapping 4-mers: $2^{\log_2(8)} + 13 = 21$ bytes

non-overlapping 4-mers minimizers: $2^{\log_2(2)} + 6 = 10$ bytes

d) **non-overlapping 4-mers**

3 cycles for hash table query

144 cycles for edit distance calculation

total cycles: $3 + 2 \times 144 = 291$ cycles

wasted cycles: $0.9 \times 291 = 262$ cycles

non-overlapping 4-mers minimizers

2 cycles for hash table query

144 cycles for edit distance calculation

total cycles: $2 + 144 = 146$ cycles

wasted cycles: $0.8 \times 146 = 117$ cycles

4 RowClone [150 points]

a) a

b) b

5 Tiered-difficulty [150 points]

- a) a
- b) b
- c) c
- d) d
- e) e

6 Low-Latency DRAM [150 points]

- a) a
- b) b
- c) c
- d) d
- e) e
- f) f
- g) g