

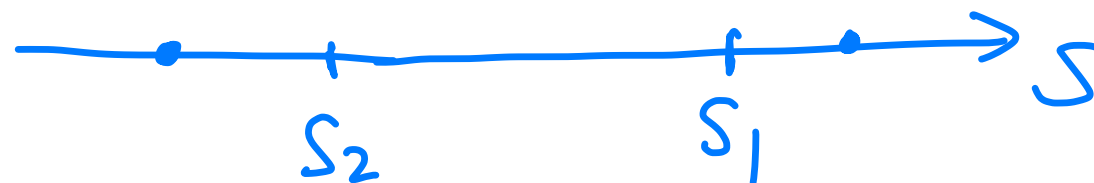
CSE 566 Spring 2023

Minimizers

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Gapped LSH Family

- A set of hash functions \mathcal{F} is said to be a (s_1, s_2, p_1, p_2) -gapped LSH family for similarity measure $s(\cdot, \cdot)$, where $s_1 \geq s_2$ and $p_1 \geq p_2$, if for any two x and y we have
 - If $s(x, y) \geq s_1$, then $\Pr_{f \in \mathcal{F}}(f(x) = f(y)) \geq p_1$;
 - If $s(x, y) \leq s_2$, then $\Pr_{f \in \mathcal{F}}(f(x) = f(y)) \leq p_2$.
- If \mathcal{F} is a (r, r, r, r) -gapped LSH family for measure $s(\cdot, \cdot)$ for every $0 < r < 1$, then \mathcal{F} is a LSH family for measure $s(\cdot, \cdot)$



Results for Edit Distance

$x = \text{A C G T G T A C}$
 $y = \text{A C T G T A C}$

- Define $es(x, y) := 1 - d(x, y)/n$ as the edit-similarity between strings x and y of length n , where $d(x, y)$ is the edit distance.
- Edit distance/similarity is fundamentally different from the distance/similarity on normed vector space.

$x = 0110$
 $y = 1011$

$x = \{1, 0, \dots, 1\}$
 $y = \{0, 1, \dots, 1\}$
 $U = \{x_1, \dots, x_n\}$

$x = (\dots) \in \mathbb{R}^d$
 $y = (\dots) \in \mathbb{R}^d$

- It remains open whether a LSH family exists for edit-similarity.
- A gapped LSH family for the edit distance exists!
 - OMH: <https://doi.org/10.1093/bioinformatics/btz354> (2019)

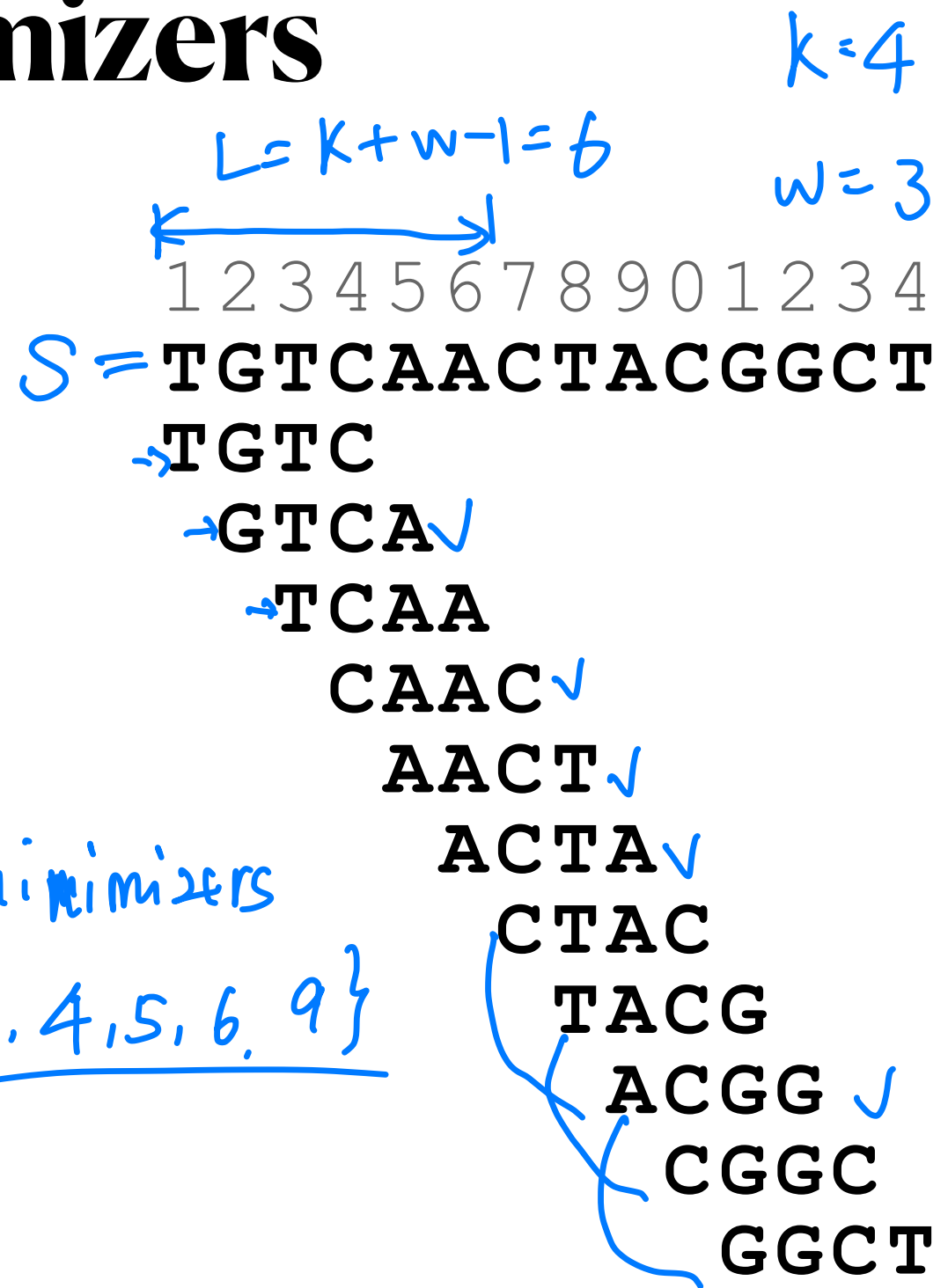
order min hash

Minimizers

- Given a string S , the **Minimizers** select the smallest kmer (according to order π) in each sliding window of w kmers.

- k : the length of kmer
- w : the window size
- π : an order over all kmers

AAAA, AAAC, ..., TTTT



naive algo: $O(|S| \cdot w)$ comparisons

Calculating Minimizers

Input: string S , k , w , order π

Output: array M to store the positions of minimizers

init an empty queue Q

for $i = 1$ **to** $(|S| - k + 1)$

let $m = S[i..i+k-1]$ be the current kmer

while $m < (\pi) \ S[\text{tail}(Q)..\text{tail}(Q)-k+1]$: pop-tail(Q)

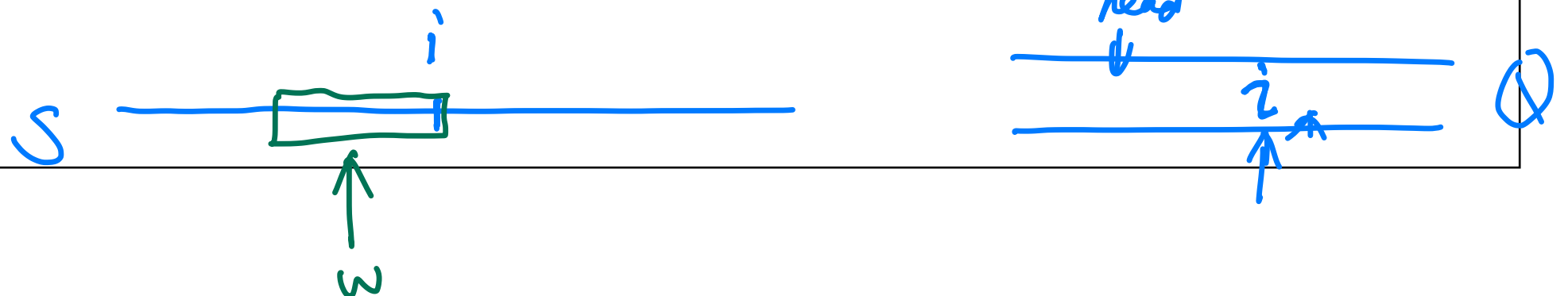
append i to the tail of Q

while $\text{head}(Q) \leq i - w$: pop-head(Q)

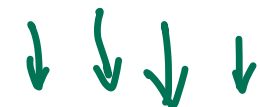
if $i \geq w \ \&\& \ \text{head}(Q) \neq \text{tail}(M)$: append $\text{head}(Q)$ to M

end for

return M ;



An Example



1 2 3 4 5 6 7 8 9 0 1 2 3 4

TGTCAACTACGGCT

TGTC

GTCA

TCAA

CAAC

AACT

ACTA

CTAC

TACG

ACGG

CGGC

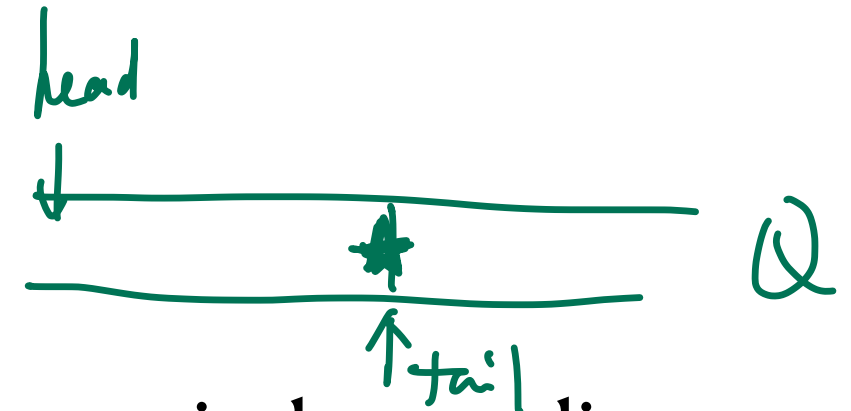
GGCT

Q: ≠ 4

M 12, 4 ..



Correctness



- Claim: head(Q) is the minimizer of the current window ending with the i-th kmer
 - Fact 1: it is safe to pop-tail(Q) when m is smaller than the kmer at tail(Q)
 - Fact 2: it is safe to pop-head(Q) when it is out of the current window
 - Fact 3: the kmers in Q are in increasing order
 - Fact 4: head(Q) is the smallest kmer in Q

Running Time

- The entire algorithm takes $O(|S|)$ comparisons
 - Each kmer gets added into Q once
 - Hence #pops is also bounded by $|S|$

$$\#pops \leq \underline{\#added-kmers}$$

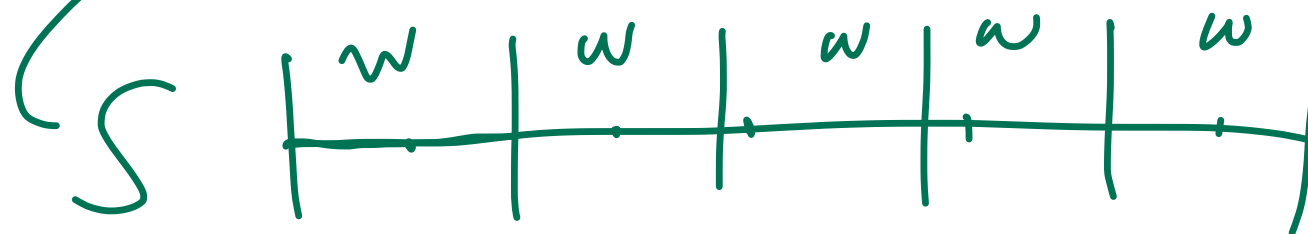


- Small gap: the distance between two selected positions is at most w , and hence provides a good “coverage”.
- Consistency: if two sequences share a substring of length $w + k - 1$, then they share a minimizer.
- Locality-sensitive: if two sequences share a “similar” substring of length $w + k - 1$, then with high probability that they also share a minimizer.

Density of Minimizers

- Given w , k , and order π , the particular density of a sequence S is defined as: $|M(S)| / (|S| - k + 1)$.
- Given w , k , and order π , the expected density is defined as the particular density over an infinity-length, random sequence (i.e., each base is sampled uniformly at random).
- Trivial bounds for expected density: $1/w \leq d \leq 1$.
- Proved lower bound for expected density: ~~$1/(w+1) \leq d$~~

$$d \geq \frac{1.5}{1+w}$$



Density with Random Order

- Order π is picked uniformed at random from all orderings.
- **Theorem:** the expected density wrt a random order π is $2/(1+w) + o(1/w)$.
- **Proof:** consider the probability that the next window uses a new minimizer.

$$P_V = \frac{2}{1+w}$$

