Sublinear Approximate String Matching

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This is where you are now.

This is where you are now.

This is where you will end up.

What is that delicacy we want to prepare?

Definition Given a text string T of length n and a pattern string P of length m over a b-letter alphabet, the k-*differences approximate string matching problem* asks for all locations in T where P occurs with at most k differences (substitutions, insertions, deletions).

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   YELTSIN
   *   **
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- Genetics (e.g. GCACTT...) has conjured up new challenges in the field of string processing.
- Sequencing techniques are not perfect: experimental error up to 5–10%.
- Gene mutation (leading to polymorphism) is the mother of evolution. Thus matching a piece of DNA against a database of many individuals must allow a small but significant error.

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How will we cook the meal?

We will

- first gather the ingredients:
  suffix trees, matching statistics, lowest common ancestor retrieval, edit distance;
- then merge the ingredients and form the algorithm:
  linear expected time algorithm in detail, sublinear expected time after some modifications.

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Part I

Gathering the Ingredients

The Auxiliary Tools

Suffix trees

- Remember Olga: She told ya.
- Suffix tree of $P[1..m]\$$: $\mathfrak{S}_P$
- α branching word $\longleftrightarrow$ there are different letters x and y such that both αx and αy are substrings of $P\$$
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$$\begin{array}{rcl} \text{root} & \longleftrightarrow & \lambda \text{ (empty string)} \\ \{\text{internal nodes}\} & \longleftrightarrow & \{\text{branching words}\} \\ \{\text{leaves}\} & \longleftrightarrow & \{\text{suffixes}\} \end{array}$$

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- Label on edge (β, α): (x, l, r) such that
  $P\$[l] = x$; $\beta^{-1}\alpha = P\$[l..r]$
- $\mathrm{son}(\beta, x) := \alpha$
- $\mathrm{first}(\beta, x) := l$
- $\mathrm{len}(\beta, x) := r - l + 1$
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Matching statistics

Definition The *matching statistics* of text $T[1..n]$ with respect to pattern $P[1..m]$ is an integer vector $\mathfrak{M}_{T,P}$ together with a vector $\mathfrak{M}'_{T,P}$ of pointers to the nodes of $\mathfrak{S}_P$, where $\mathfrak{M}_{T,P}[i] = l$ if l is the length of the longest substring of $P\$$ (anywhere in $P\$$) matching exactly a prefix of $T[i..n]$ and where $\mathfrak{M}'_{T,P}[i]$ points to $\text{ceil}(T[i..i+l-1])$.
More shortly we will write $\mathfrak{M}$ and $\mathfrak{M}'$.

How do we compute the matching statistics?

- Goal: $\mathcal{O}(n+m)$ time algorithm for computing the matching statistics of T and P in a single left-to-right scan of T using just $\mathfrak{S}_P$
- Brief description: The longest match starting at position 1 in T is found by walking down the tree, matching one letter a time.
  Subsequent longest matches are found by following suffix links and carefully going down the tree. (cf. Ukkonen's construction of the suffix tree: "skip-and-count trick")

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- i, j, k are indices into T:
  - The i-th iteration computes $\mathfrak{M}[i]$ and $\mathfrak{M}'[i]$.
  - Position k of T has just been scanned.
  - j is some position between i and k.
- Invariants:
  - At all times true:
    (1) $T[i..k-1]$ is a substring of P; $T[i..j-1]$ is a branching word of P.
  - After step 3.1 the following becomes true:
    (2) $T[i..j-1] = \text{floor}(T[i..k-1])$ and corresponds to node α.
  - After step 3.2 the following becomes true as well:
    (3) $T[i..k]$ is not a word.

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- If $j < k$ after step 3.1, then $T[i..k-1]$ is not a branching word (2), so neither is $T[i-1..k-1]$.
  So, as substrings of P they must have the same single-letter extension.
  We know from iteration $i-1$ that $T[i-1..k-1]$ is a substring of P (1) but $T[i-1..k]$ is not (3), so $T[k]$ cannot be this letter. Hence the match cannot be extended.
- Together invariants (1) and (3) imply $\mathfrak{M}[i] = k - i$.
- i, j, k never decrease and are bounded by n: $i + j + k \leq 3n$.
  For every constant amount of work in step 3, at least one of i, j, k is increased. The running time is therefore $\mathcal{O}(n)$ for step 3, and of course $\mathcal{O}(m)$ for steps 1 and 2, yielding together the desired $\mathcal{O}(n+m)$.

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1 construct $\mathfrak{S}_P$ in $\mathcal{O}(m)$ time
2 $\alpha :=$ root; $j := k := 1$
3 **for** $i := 1$ to n **do**
3.1 **while** $(j < k) \wedge (j + \mathrm{len}(\alpha, T[j]) \leq k)$ **do** // *"skip and count"*
$\alpha := \mathrm{son}(\alpha, T[j])$;
$j := j + \mathrm{len}(\alpha, T[j])$
elihw
3.2 **if** $j = k$ **then** // *extend the match*
while $\mathrm{son}(\alpha, T[j])$ exists $\wedge\ T[k] = P\$[\mathrm{first}(\alpha, T[j]) + k - j]$ **do**
$k := k + 1$
if $k = j + \mathrm{len}(\alpha, T[j])$ **then**
$\alpha := \mathrm{son}(\alpha, T[j])$;
$j := k$ **fi**
elihw
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3.3 $\mathfrak{M}[i] := k - i$
if $j = k$ **then** $\mathfrak{M}'[i] := \alpha$
  else $\mathfrak{M}'[i] := \mathrm{son}(\alpha, T[j])$ **fi**
3.4 **if** (α is root) $\wedge$ $(j = k)$ **then**
  $j := j + 1$;
  $k := k + 1$ **fi**
if (α is root) $\wedge$ $(j < k)$ **then**
  $j := j + 1$ **fi**
if (α is not root) **then**
  $\alpha := \mathrm{shift}(\alpha)$ **fi**
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Lowest common ancestor (LCA) retrieval

Definition For nodes u, v of a rooted tree $\mathfrak{T}$, $\mathrm{LCA}(u, v)$ is the node furthest from the root that is an ancestor to both u and v.

- Goal: constant time LCA retrieval after some preprocessing
- Solution: Reduce the LCA problem to the *range minimum query (RMQ)* problem.

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If an algorithm has preprocessing time $p(n)$ and query time $q(n)$, we say it has complexity $\langle p(n), q(n)\rangle$.

Lemma If there is a $\langle p(n), q(n)\rangle$-time solution for RMQ on a length n array, then there is a $\langle \mathcal{O}(n) + p(2n-1), \mathcal{O}(1) + q(2n-1)\rangle$-time solution for LCA in a tree with n nodes.

The $\mathcal{O}(n)$ term will come from the time needed to create the soon-to-be-presented arrays.
The $\mathcal{O}(1)$ term will come from the time needed to convert the RMQ answer on one of these arrays to the LCA answer in the tree.

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Proof The LCA of nodes u and v is the shallowest (i.e. closest to the root) node between the visits to u and v encountered during a depth first search (DFS) traversal of $\mathfrak{T}$ (n nodes; labels: $1, \ldots, n$).
Therefore, the reduction proceeds as follows:

1. Let array $\mathfrak{D}[1..2n-1]$ store the nodes visited in a DFS of $\mathfrak{T}$. $\mathfrak{D}[i]$ is the label on the i-th node visited in the DFS.
2. Let the *level* of a node be its distance from the root. Compute the level array $\mathfrak{L}[1..2n-1]$, where $\mathfrak{L}[i]$ is the level of node $\mathfrak{D}[i]$.
3. Let the *representative* of a node be the index of its first occurrence in the DFS. Compute the representative array $\mathfrak{R}[1..n]$, where $\mathfrak{R}[w] = \min\{j \mid \mathfrak{D}[j] = w\}$.

Feasible during a single DFS; thus running time $\mathcal{O}(n)$.

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Proof The LCA of nodes u and v is the shallowest (i.e. closest to the root) node between the visits to u and v encountered during a depth first search (DFS) traversal of $\mathfrak{T}$ (n nodes; labels: $1, \ldots, n$). Therefore, the reduction proceeds as follows:

1. Let array $\mathfrak{D}[1..2n-1]$ store the nodes visited in a DFS of $\mathfrak{T}$. $\mathfrak{D}[i]$ is the label on the i-th node visited in the DFS.
2. Let the *level* of a node be its distance from the root. Compute the level array $\mathfrak{L}[1..2n-1]$, where $\mathfrak{L}[i]$ is the level of node $\mathfrak{D}[i]$.
3. Let the *representative* of a node be the index of its first occurrence in the DFS. Compute the representative array $\mathfrak{R}[1..n]$, where $\mathfrak{R}[w] = \min\{j \mid \mathfrak{D}[j] = w\}$.

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LCA computed as follows (suppose u is visited before v):

- Nodes between the first visits to u and v: $\mathfrak{D}[\mathfrak{R}[u]..\mathfrak{R}[v]]$
- Shallowest node in this subtour at index $\textsc{rmq}_{\mathfrak{L}}(\mathfrak{R}[u], \mathfrak{R}[v])$
- Node at this position and thus output of $\textsc{lca}(u, v)$: $\mathfrak{D}[\textsc{rmq}_{\mathfrak{L}}(\mathfrak{R}[u], \mathfrak{R}[v])]$

Time complexity as claimed in the lemma:

- Just $\mathfrak{L}$ (size $2n - 1$) must be proprocessed for RMQ. Total preprocessing: $\mathcal{O}(n) + p(2n - 1)$
- For the query: one RMQ in $\mathfrak{L}$ and three constant time array lookups. In total: $\mathcal{O}(1) + q(2n - 1)$. □

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What about RMQ's complexity?

- After procomputing (at least a crucial part of) all possible queries, lookup time $q(n) = \mathcal{O}(1)$.
- Preprocessing time $p(n) =$
  - $\mathcal{O}(n^3)$ – Brute force: For all possible index pairs, search the minimum.
  - $\mathcal{O}(n^2)$ – Still naive: Fill the table by dynamic programming.
  - $\mathcal{O}(n \log n)$ – Better: Precompute only queries for blocks of a power-of-two length; remaining answers may be inferred in constant time at the moment of query.
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Edit distance

Definition The *edit distance* (or Levenshtein distance) between two strings S_1 and S_2 is the minimum number of edit operations (insertions, deletions, substitutions) needed to transform S_1 into S_2.

Such a transformation may be coded in an *edit transcript*, i.e. a string over the alphabet $\{I, D, S, M\}$, meaning “insertion”, “deletion”, “substitution” or “match” respectively.

Example

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v intner   = S1
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Computing the edit distance

Lemma The edit distance is computable using dynamic programming:

- Build the table $\mathfrak{E}$ where $\mathfrak{E}[i,j]$ denotes the edit distance between $S_1[1..i]$ and $S_2[1..j]$.
- Base conditions: $\mathfrak{E}[i,0] = i$ (all deletions); $\mathfrak{E}[0,j] = j$ (all insertions)
- Recurrence: $\mathfrak{E}[i,j] = \min\{\mathfrak{E}[i,j-1]+1, \mathfrak{E}[i-1,j]+1, \mathfrak{E}[i-1,j-1]+I_{ij}\}$, where $I_{ij} = 0$, if $S_1[i] = S_2[j]$, and $I_{ij} = 1$ otherwise.

Proof The last letter of an optimal transcript is one of $\{I, D, S, M\}$. The recurrence selects the minimum of these possibilities. □

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Filling up the table row by row

$\mathfrak{E}[i,j]$	S_2		w	r	i	t	e	r	s
S_1		0	1	2	3	4	5	6	7
	0	0	$\leftarrow$ 1	$\leftarrow$ 2	$\leftarrow$ 3	$\leftarrow$ 4	$\leftarrow$ 5	$\leftarrow$ 6	$\leftarrow$ 7
v	1	$\uparrow$ 1	$\nwarrow$ 1	$\nwarrow\leftarrow$ 2	$\nwarrow\leftarrow$3	$\nwarrow\leftarrow$4	$\nwarrow\leftarrow$5	$\nwarrow\leftarrow$6	$\nwarrow\leftarrow$7
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- Complexity: $\mathcal{O}(|S_1| \cdot |S_2|)$
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We want some slightly different thing ...

- We need the minimum number of operations to transform $P[1..m]$ so that it *occurs* in $T[1..n]$, not that it actually *is* T; i.e. we want starting spaces to be "free".
- Compute table $\mathfrak{D}$, where

$$\mathfrak{D}[i,j] := \min_{1 \le l \le j} \{\text{edit distance between } P[1..i] \text{ and } T[l..j]\}$$

- Achieved by changing the base conditions: $\mathfrak{D}[i,0] = i$ (as before: all deletions); $\mathfrak{D}[0,j] = 0$ (λ ends anywhere)
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Reducing the complexity ...

- ... from $\mathcal{O}(mn)$ to $\mathcal{O}(kn)$ using the *Landau–Vishkin algorithm (LV)*
- Call cell $\mathfrak{D}[i,j]$ an entry of diagonal $j-i$ (range: $-m, ..., n$).
- Do not compute $\mathfrak{D}$ but, column by column, the $(k+1) \times (n+1)$ "meta table" $\mathfrak{L}$ where $\mathfrak{L}[x,y]$ is the row number of the last (i.e. deepest) x along diagonal $y-x$.
- $-k \le y-x \le n$, so all relevant diagonals and thus solutions represented because $\mathfrak{D}[k+1,0] = k+1 > k$ and diagonals are non-decreasing.
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How is $\mathfrak{L}$ computed?

- Define $\mathfrak{L}[x, -1] = \mathfrak{L}[x, -2] := -\infty$ because every cell of diagonal $-1 - x$ is at least $\mathfrak{D}[x+1, 0] = x + 1 > x$.
- Fill row 0: $\mathfrak{L}[0, y] = \mathrm{jump}(1, y+1)$, where $\mathrm{jump}(i, j)$ is the longest common prefix of $P[i..m]$ and $T[j..n]$, i.e. $\mathrm{jump}(i, j) = \min\{M_j, \text{length of word } \textsc{lca}(M'_j, \text{leaf } P\$[i..m])\}$

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Some part of $\mathfrak{L}$:

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- $\alpha := \mathfrak{L}[x-1, y-2]$ (last $x-1$ on diagonal $y-x-1$)
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- $\alpha := \mathfrak{L}[x-1, y-2]$ (last $x-1$ on diagonal $y-x-1$)
  $\leftarrow$ insert $T[\alpha + y - x]$ after $P[\alpha]$
- $\beta := \mathfrak{L}[x-1, y-1]$ (last $x-1$ on diagonal $y-x$)
  $\nwarrow$ substitute $T[\beta + 1 + y - x]$ after $P[\beta + 1]$
- $\gamma := \mathfrak{L}[x-1, y]$ (last $x-1$ on diagonal $y-x+1$)
  $\uparrow$ delete $P[\gamma + 1]$
- $t := \max\{\alpha, \beta + 1, \gamma + 1\}$
  $\mathfrak{L}[x,y] = t + \mathrm{jump}(t+1, t+1+y-x)$

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Now I'm hungry!
Let's go over to ...

Part II

Cooking the Meal

The Algorithm

Linear expected time

Conditions:

1. $T[1..n]$ is a uniformly random string over a b-letter alphabet.
2. Number of differences allowed in a match is

$$k < k^* = \frac{m}{\log_b m + c_1} - c_2.$$

(constants c_i to be specified later; m: pattern length)

Pattern P need not be random.

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The Chang–Lawler algorithm (CL)

$s_1 := 1;\ j := 1$

do

  $s_{j+1} := s_j + \mathfrak{M}[s_j] + 1;$ // *compute the start "positions"*

  $j := j + 1$

until $s_j > n$

$j_{max} := j - 1$

for $j := 1$ to j_{max} **do**

  if $(j + k + 2 \leq j_{max}) \wedge (s_{j+k+2} - s_j \leq m - k)$ **then**

    apply LV to $T[s_j..s_{j+k+2} - 1]$ **fi** // *"work at s_j"*

rof

Why does it work?

- If $T[p..p+d-1]$ matches P and $s_j \leq p \leq s_{j+1}$, then this string can be written in the form $\zeta_1 x_1 \zeta_2 x_2 ... \zeta_{k+1} x_{k+1}$, where each x_l is a letter or empty, and each ζ_l is a substring of P.
- Show by induction that, for every $0 \leq l \leq k+1$, $s_{j+l+1} \geq p + \text{length}(\zeta_1 x_1 ... \zeta_l x_l)$. (If you can't live without having seen it, tell me ...)
- So in particular $s_{j+k+2} \geq p + d$, which implies $s_{j+k+2} - s_j \geq d \geq m - k$.
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- $s_{k^*+3} - s_1 \geq s_{k+3} - s_1$; $m - k \geq m - k^*$
- Thus the event $s_{k+3} - s_1 \geq m - k$ implies the event $s_{k^*+3} - s_1 \geq m - k^*$.
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Lemma For suitably chosen constants c_1 and c_2, and $k^* = \frac{m}{\log_b m + c_1} - c_2$, $\Pr[s_{k^*+3} - s_1 \geq m - k^*] < 1/m^3$.

Proof For the sake of easiness, let us assume (i) $b = 2$ ($b > 2$ gives slightly smaller c_i's) and (ii) k^* and $\log m$ are integers ($\log m := \log_2 m$).

- Let X_j be the random variable $s_{j+1} - s_j$.
- Note that $s_{k^*+3} - s_1 = X_1 + ... + X_{k^*+2}$ (telescope sum).
- There are $m2^d$ different strings of length $\log m + d$, but at most m such substrings of P.
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$$\Pr[X_1 = \log m + d + 1] \leq 2^{-d} \quad \text{for all integer } d \geq 0 \qquad (1)$$

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- Let $Y_i := X_i - \frac{m-k^*}{k^*+2}$.
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- Inequality (1): $\Pr[X_1 = \log m + d + 1] < 2^{-d}$, is equivalent to

  $\Pr[Y_1 = \log m + d + 1 - \frac{m-k^*}{k^*+2}] < 2^{-d}$ for all integer $d \geq 0$

- So, the theorem of total expectation implies, for all $t > 0$ ($\alpha := \log m + 1 - \frac{m-k^*}{k^*+2}$),

$$\begin{aligned}
\mathbf{E}[e^{tY_1}] &= \mathbf{E}[e^{tY_1} | Y_1 \leq \alpha] \cdot \underbrace{\Pr[Y_1 \leq \alpha]}_{\leq 1} + \\
&\quad + \sum_{d=1}^{\infty} \mathbf{E}[e^{tY_1} | Y_1 = \alpha + d] \cdot \Pr[Y_1 = \alpha + d] \\
&\leq e^{t\alpha} + \sum_{d=1}^{\infty} e^{t(\alpha+d)} \cdot \Pr[Y_1 = \alpha + d] \\
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- So, the theorem of total expectation implies, for all $t > 0$ $(\alpha := \log m + 1 - \frac{m-k^*}{k^*+2})$,

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&\leq e^{t\alpha} + \sum_{d=1}^{\infty} e^{t(\alpha+d)} \cdot \Pr[Y_1 = \alpha + d] \\
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Homework Choose $t = \frac{\log_e 2}{2}$, do some algebra, and verify that the following is true for the probability to perform work at position s_1 and thus at each position:

$$\begin{aligned} \Pr[s_{k^*+3} - s_1 \geq m - k^*] &\leq \mathbf{E}[e^{tY_1}]^{k^*+2} \\ &< (\sum_{d=0}^{\infty} e^{t(\alpha+d)} \cdot 2^{-d})^{k^*+2} \\ &<^! 1/m^3, \end{aligned}$$

if $c_1 = 5.6$ and $c_2 = 8$.

So what time is it?

LV is applied with a probability of less than $1/m^3$, the text it is applied to is supposed to have length $(k+2)\mathbf{E}[X_1] < (k+2)(\log m + 3) = \mathcal{O}(k \log m)$, and LV has complexity $\mathcal{O}(kl)$, if l is the length of the input string.

Also recall that $k = \mathcal{O}(\frac{m}{\log m})$.

So the average expected work for any start position s_j is

$$\begin{aligned} m^{-3}\mathcal{O}(k^2 \log m) &= m^{-3}\mathcal{O}(\frac{m^2}{(\log m)^2} \log m) \\ &= \mathcal{O}(\frac{1}{m \log m}) \\ &= \mathcal{O}(\lambda n.\lambda m.1) \end{aligned}$$

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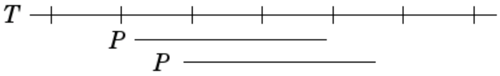
Let's go beneath the line: SET

Now an algorithm is derived from LET that is sublinear in n (when $k < k^*/2 - 3$; k^* as before).

The trick is:

- Partition T into regions of length $\frac{m-k}{2}$.
  Any substring of T that matches P must contain the whole of at least one region:



- Starting from the left end of each region R, compute $k+1$ "maximum jumps" (using $\mathfrak{M}$), say ending at position p.
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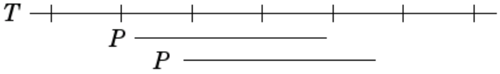

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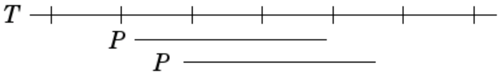

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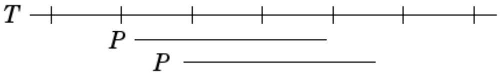

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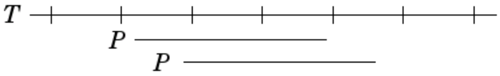

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$$\Pr[p \text{ is beyond } R] < 1/m^3$$

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- A combination of LET (for $k \geq k^*/2 - 3$) and SET (for $k < k^*/2 - 3$) runs in $\mathcal{O}(\frac{n}{m} k \log m)$ expected time.
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The moral

Mind the preprocessing!

“Gut gekaut ist halb verdaut.”
“A good chewing is half the digestion.”