Approximate String Search in Spatial Databases

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Introduction

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  - data cleaning
  - data integration
  - online search engine

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- Also, spatial database
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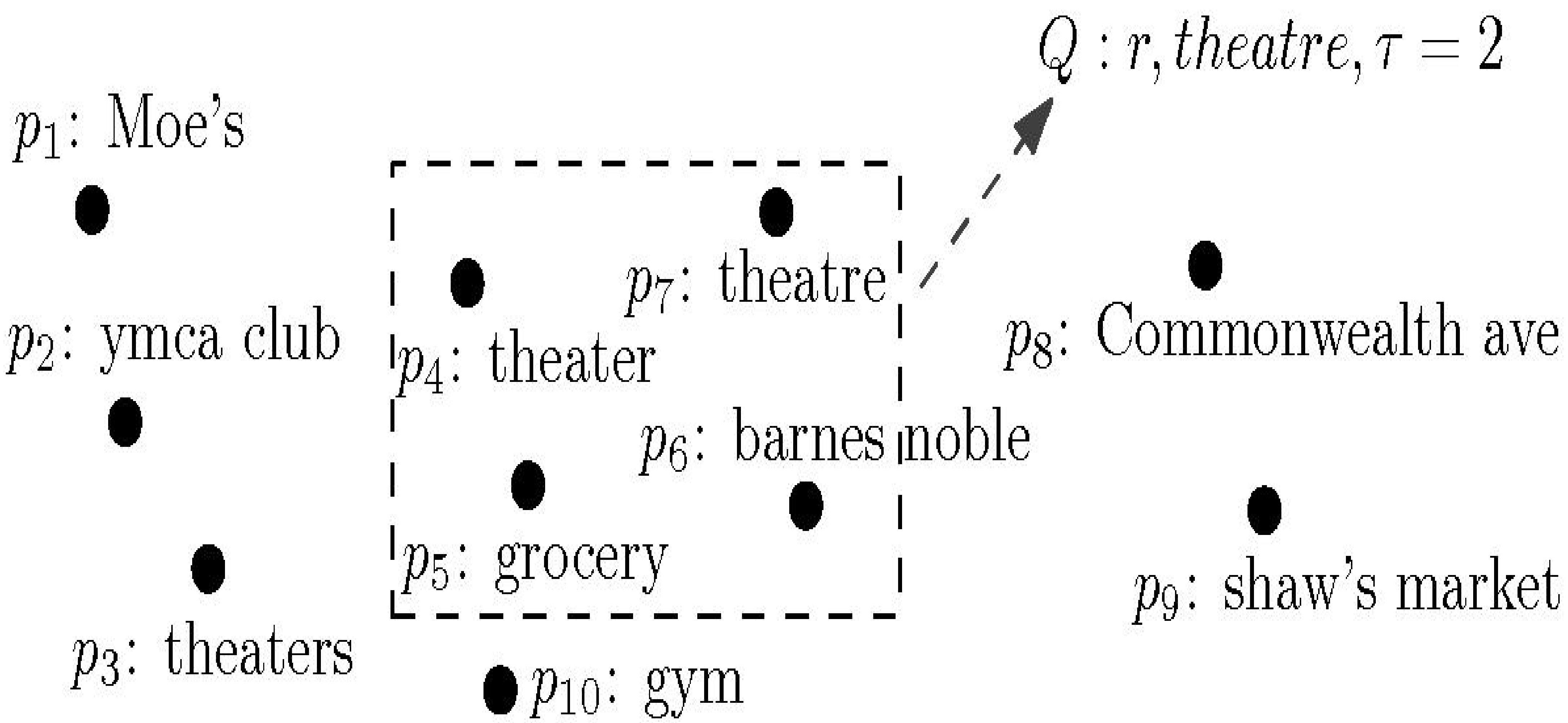
  - strategic planning of resources
- Our work: the approximate string search in spatial database (*Spatial Approximate String* (SAS) queries).

Example of a SAS range query



String similarity metric: edit distance with threshold τ.

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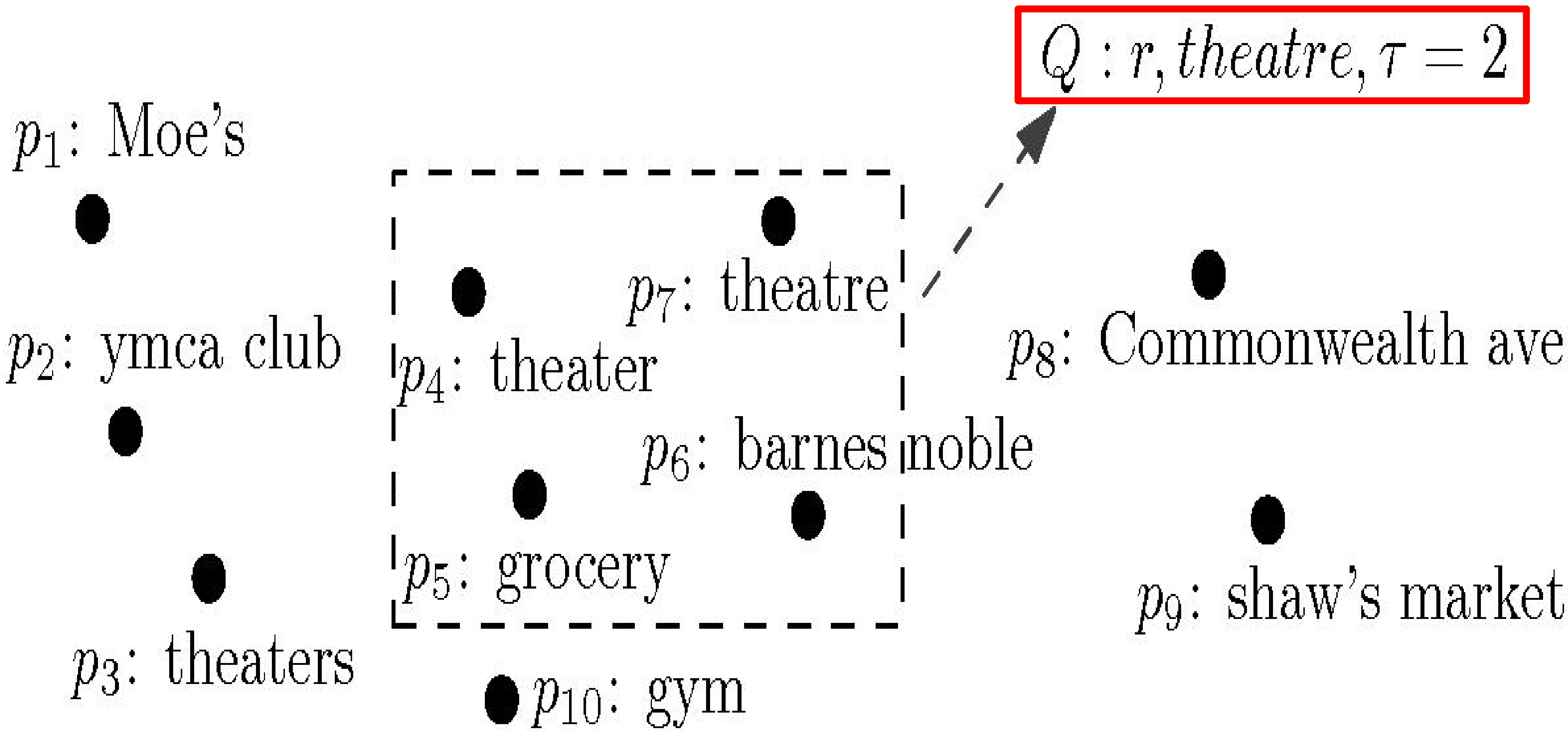

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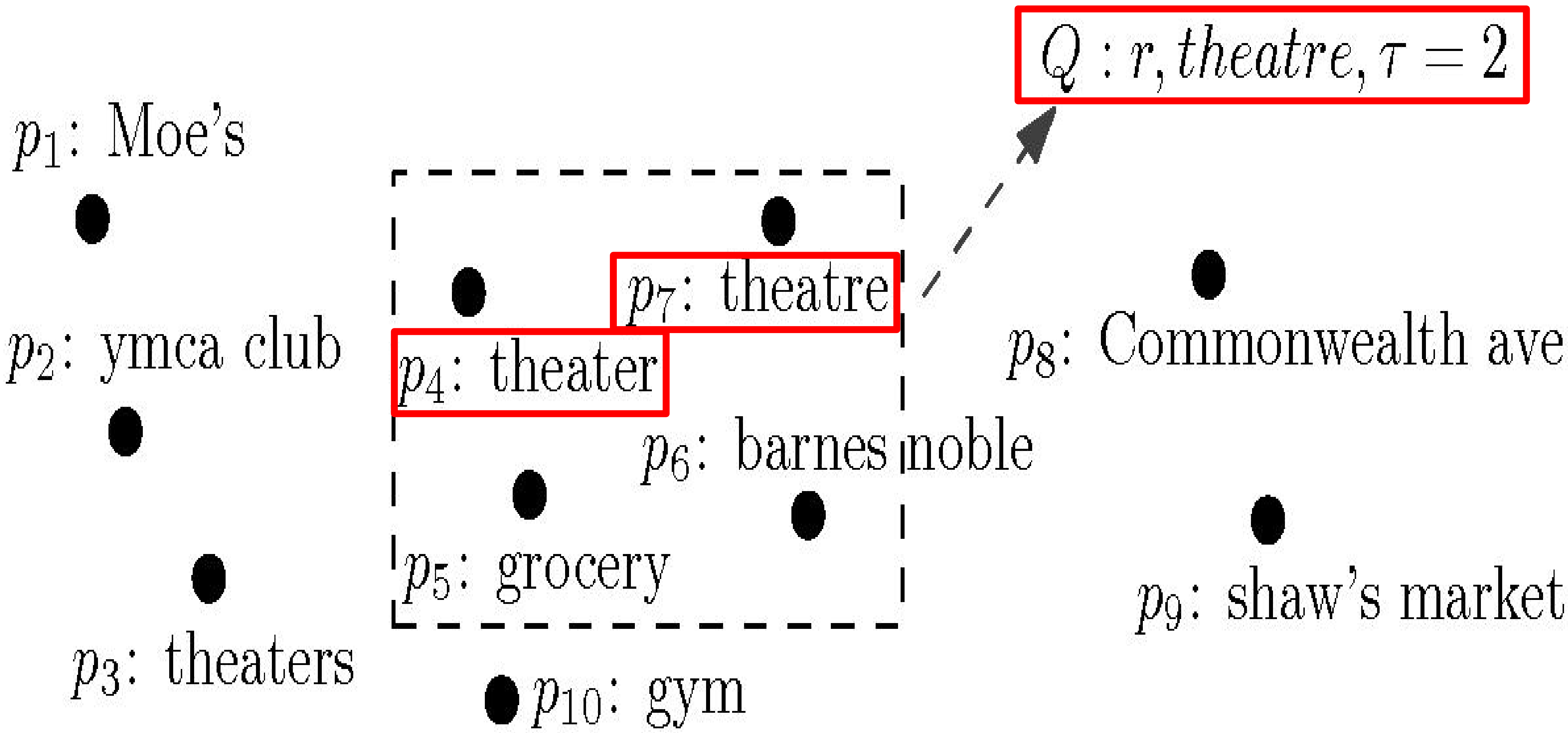

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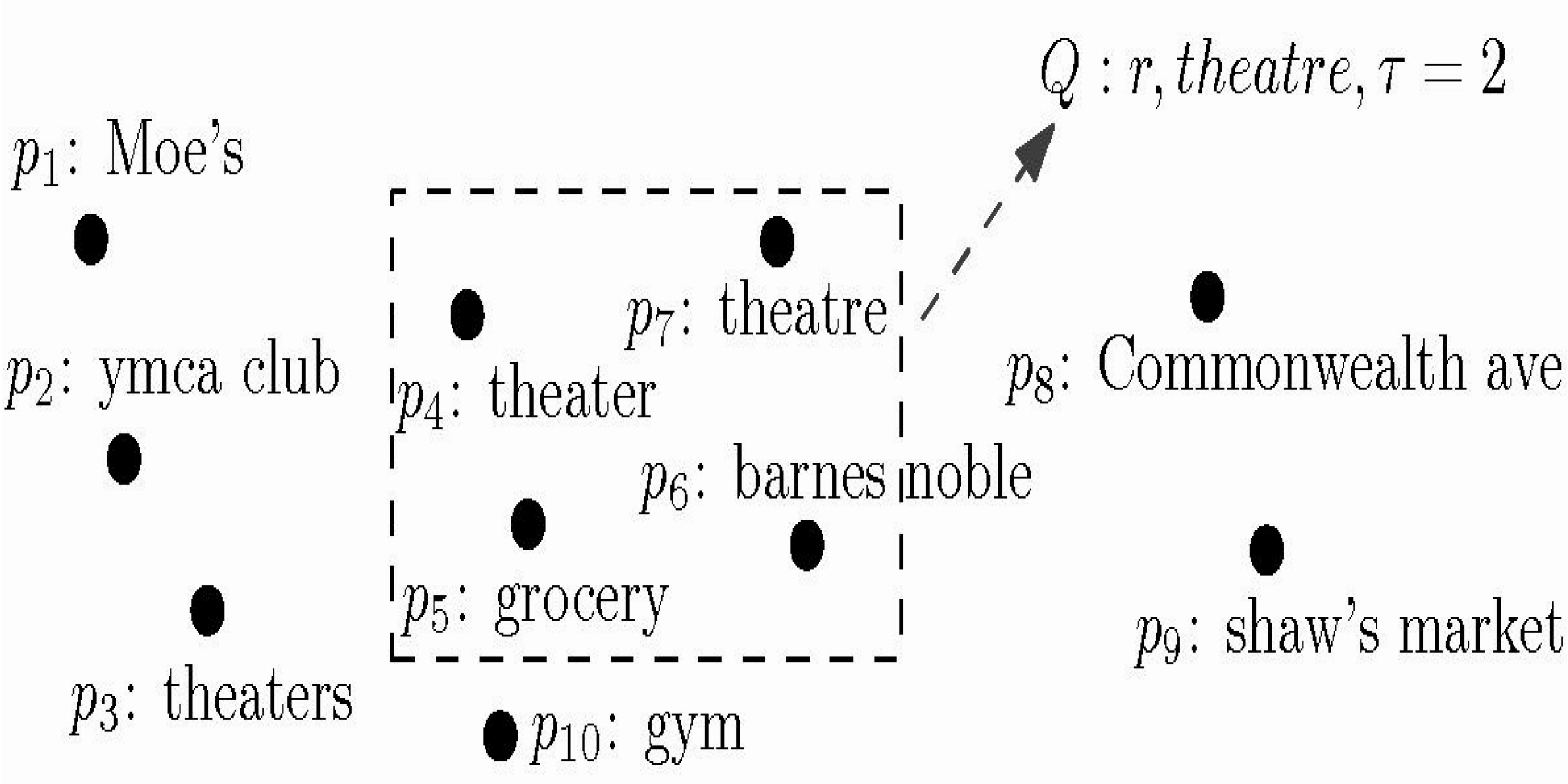
A straightforward solution

R-tree solution:



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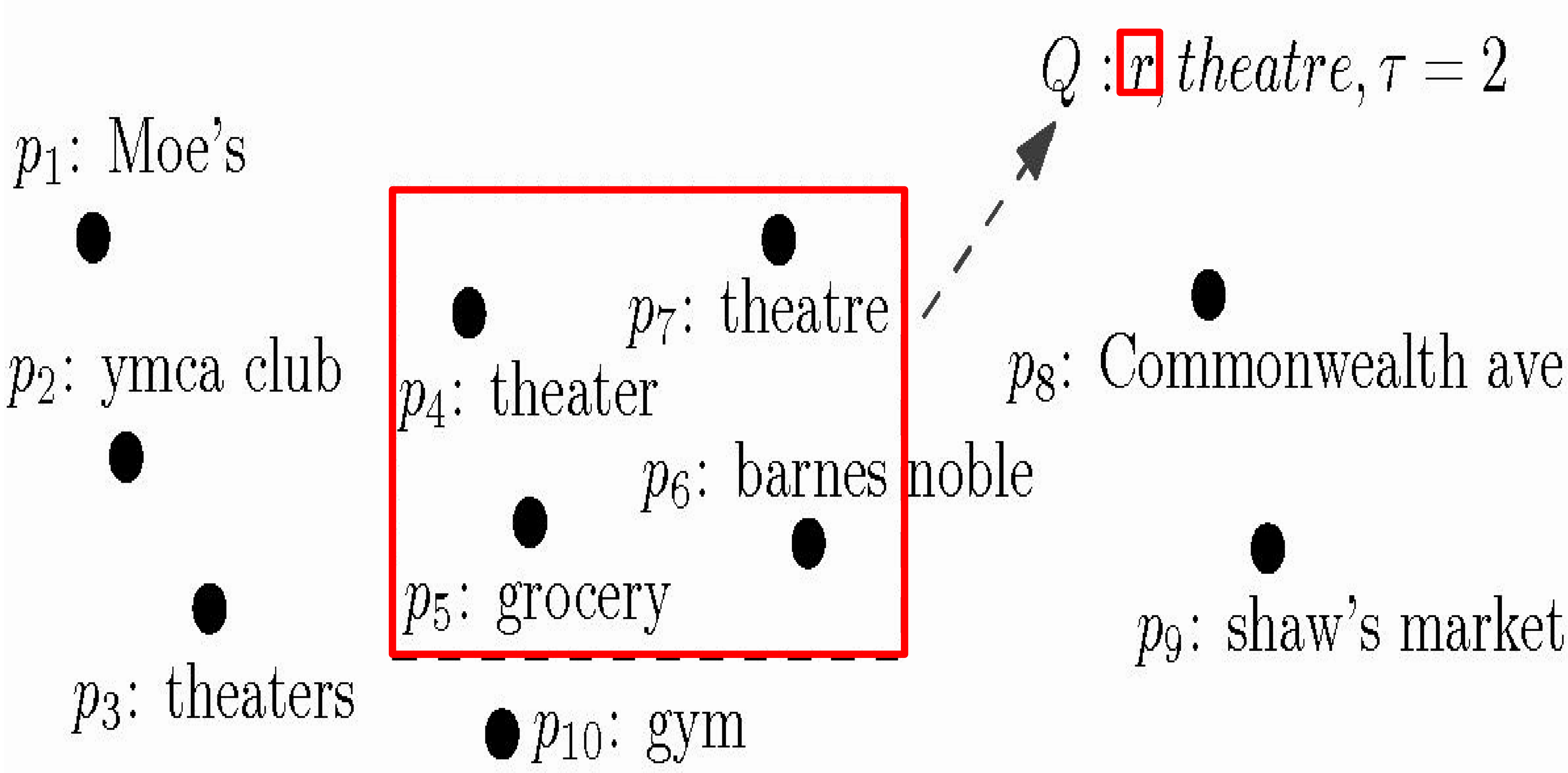

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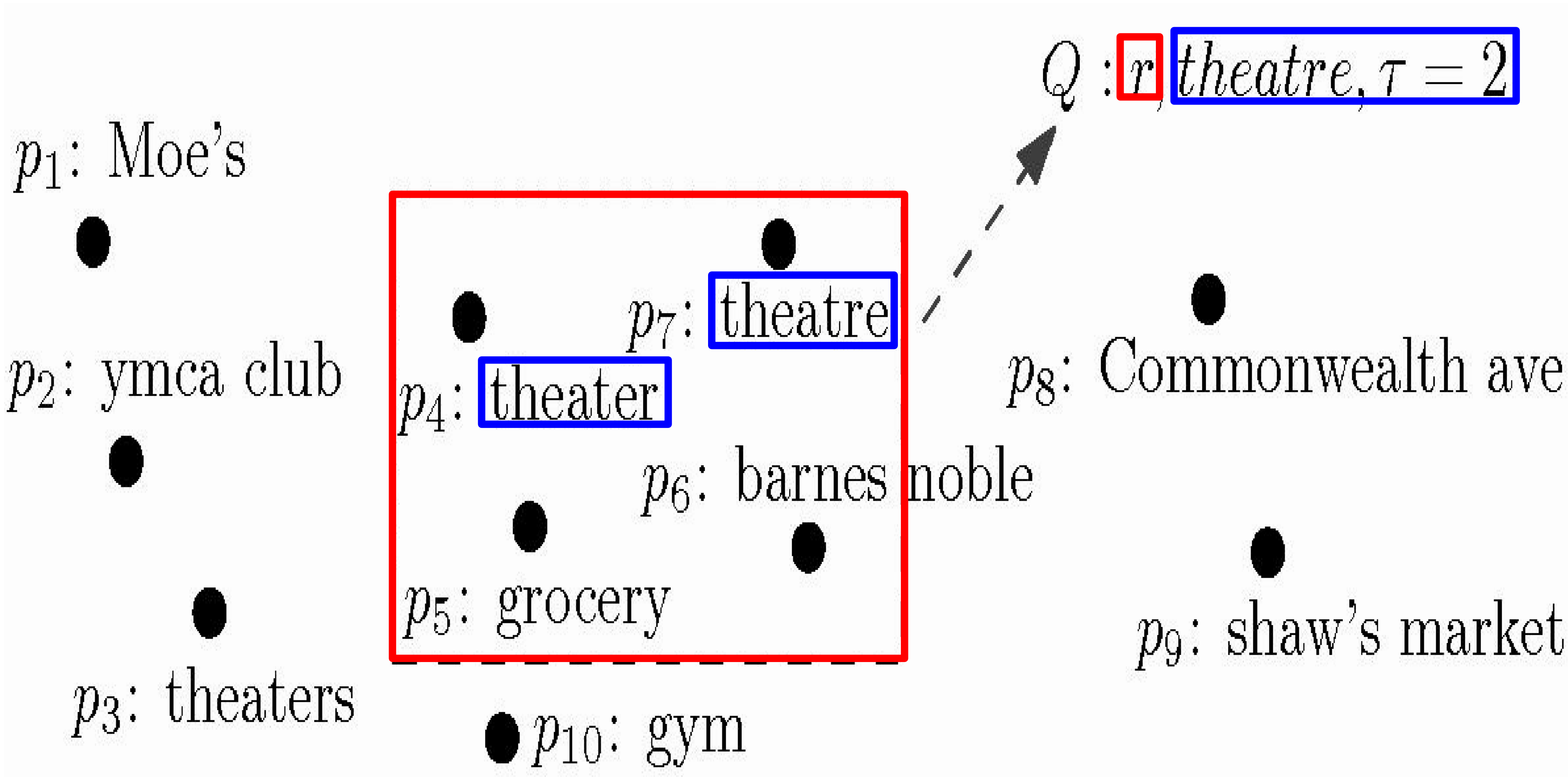

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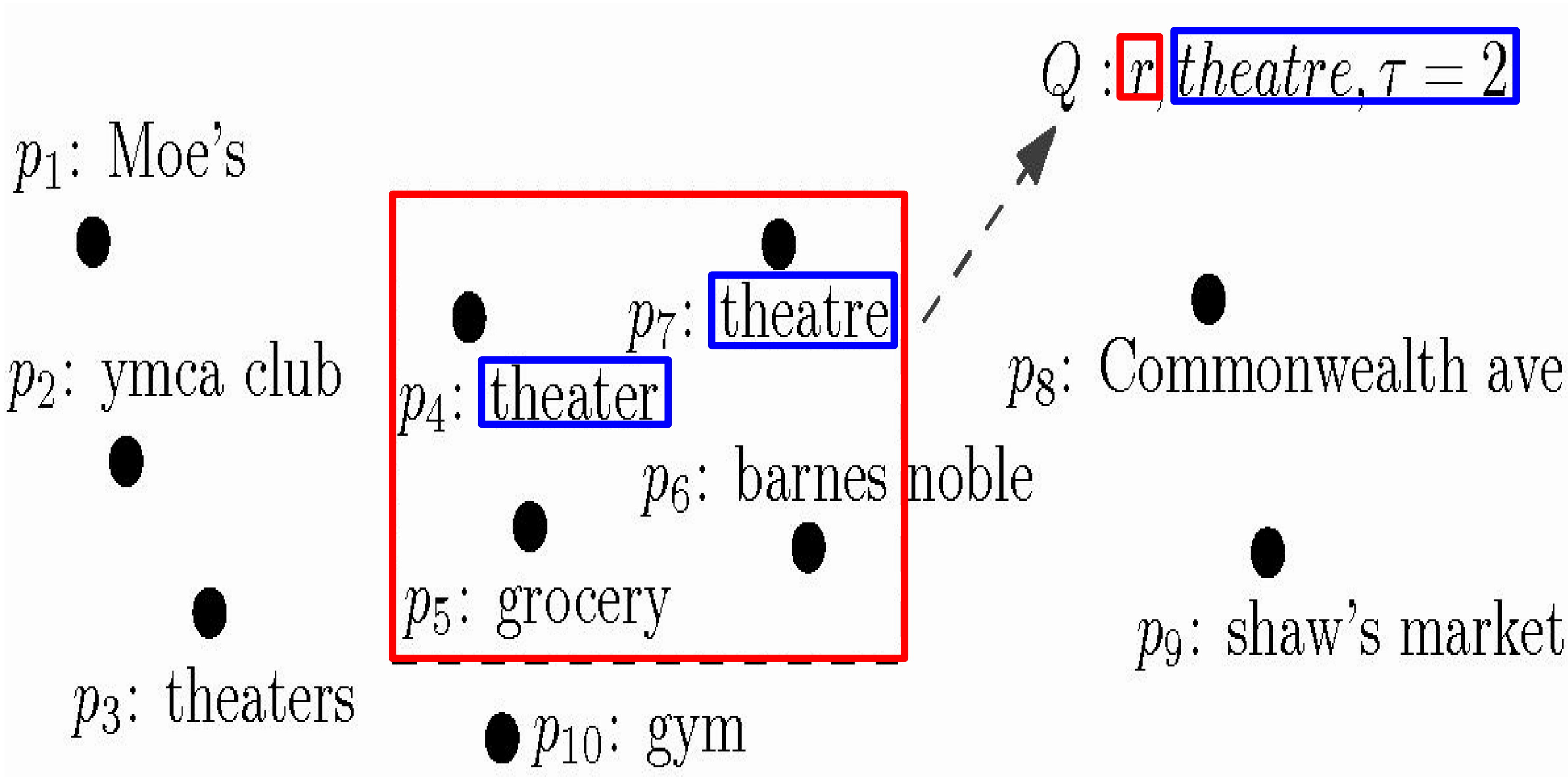

Problem: only utilize the spatial dimension for the pruning.

Background: q-grams based edit distance pruning

- Lemma: For strings σ_1 and σ_2 of length $|\sigma_1|$ and $|\sigma_2|$, if $\varepsilon(\sigma_1, \sigma_2) = \tau$, then $|G_{\sigma_1} \cap G_{\sigma_2}| \geq \max(|\sigma_1|, |\sigma_2|) - 1 - (\tau - 1) * q$.

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Set $A = \{1, 2, 4\}$

hashes	1	2	4
h_1	1	3	4
h_2	3	1	2
h_3	2	4	3
h_4	4	2	1

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Set $B = \{2, 3\}$

hashes	2	3
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h_3	4	(1)
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signature of B
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1
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signature of A		signature of B
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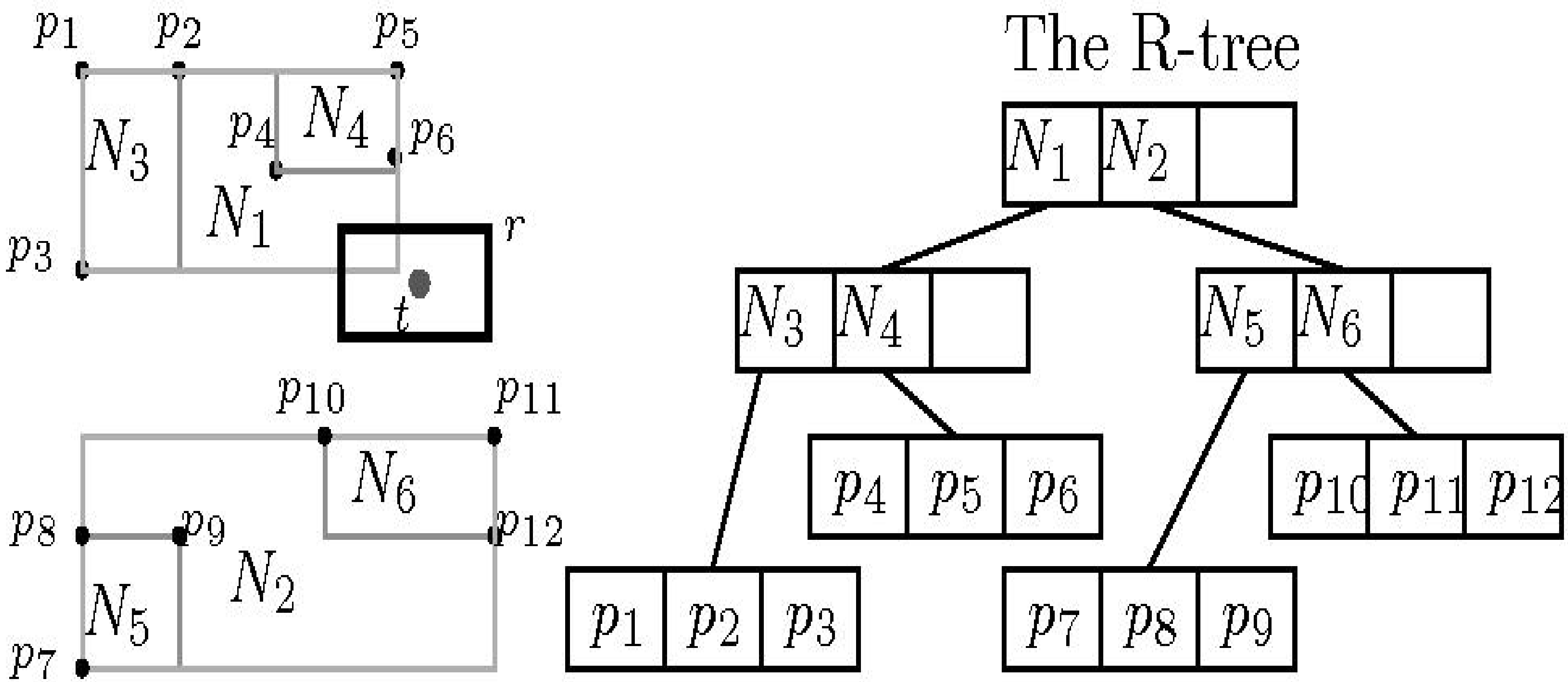
1	⟷	1
2		1
1		2

$$\widehat{\rho}(A, B) = 1/4$$

The MHR-tree: basic idea



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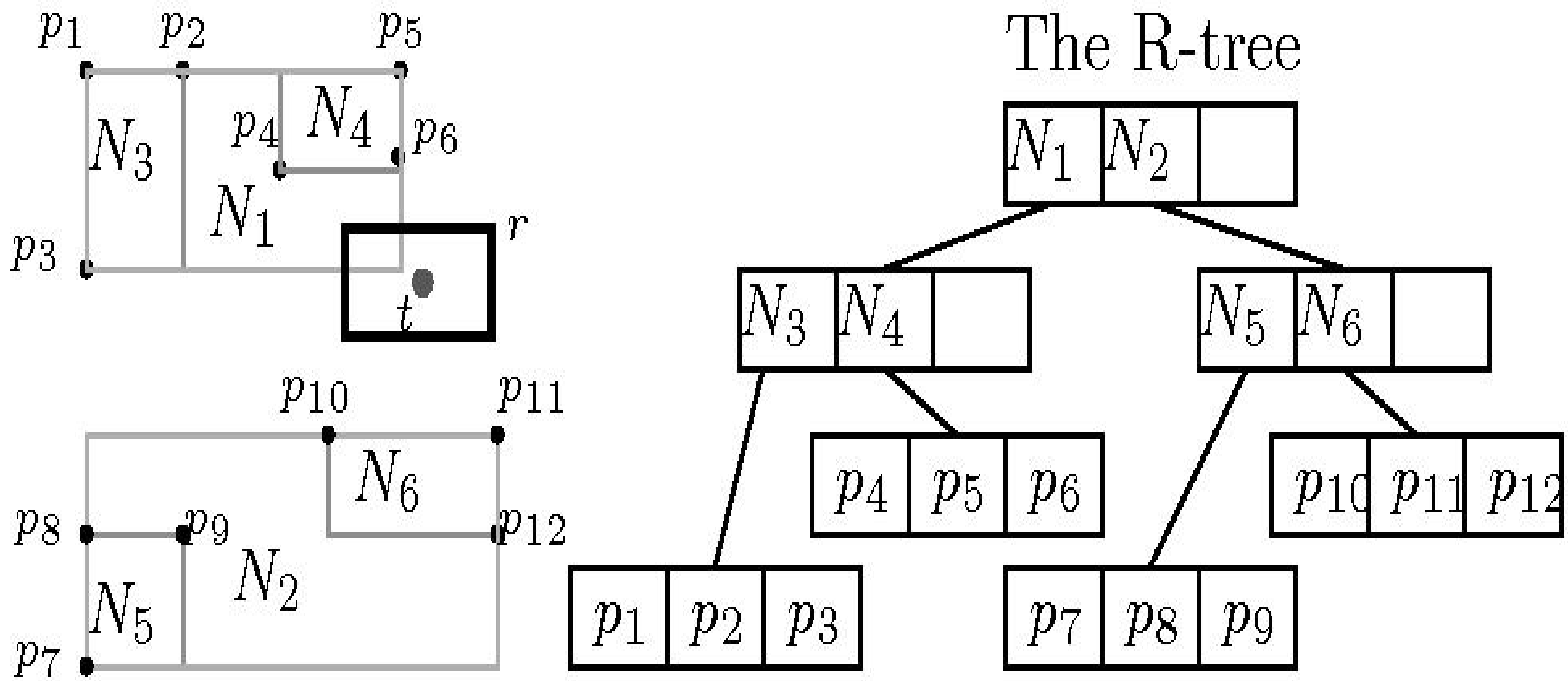
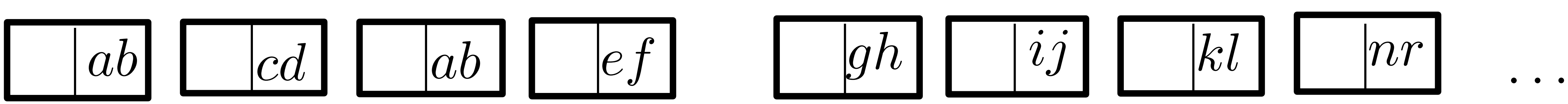


Lemma 2 Let G_u be the set for the union of q-grams of strings in the subtree of node u. For a SAS query (r, σ, τ), if $|G_u \cap G_\sigma| < |\sigma| - 1 - (\tau - 1) * q$, then the subtree of node u does not contain any element from A_s.

The MHR-tree: union of q-grams ($q = 2$)



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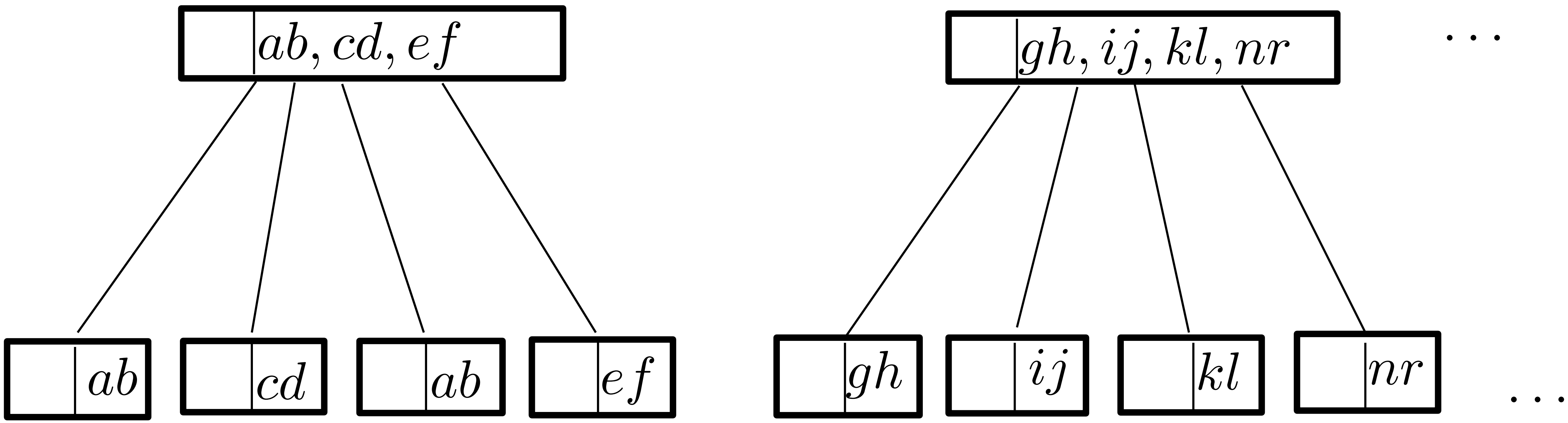

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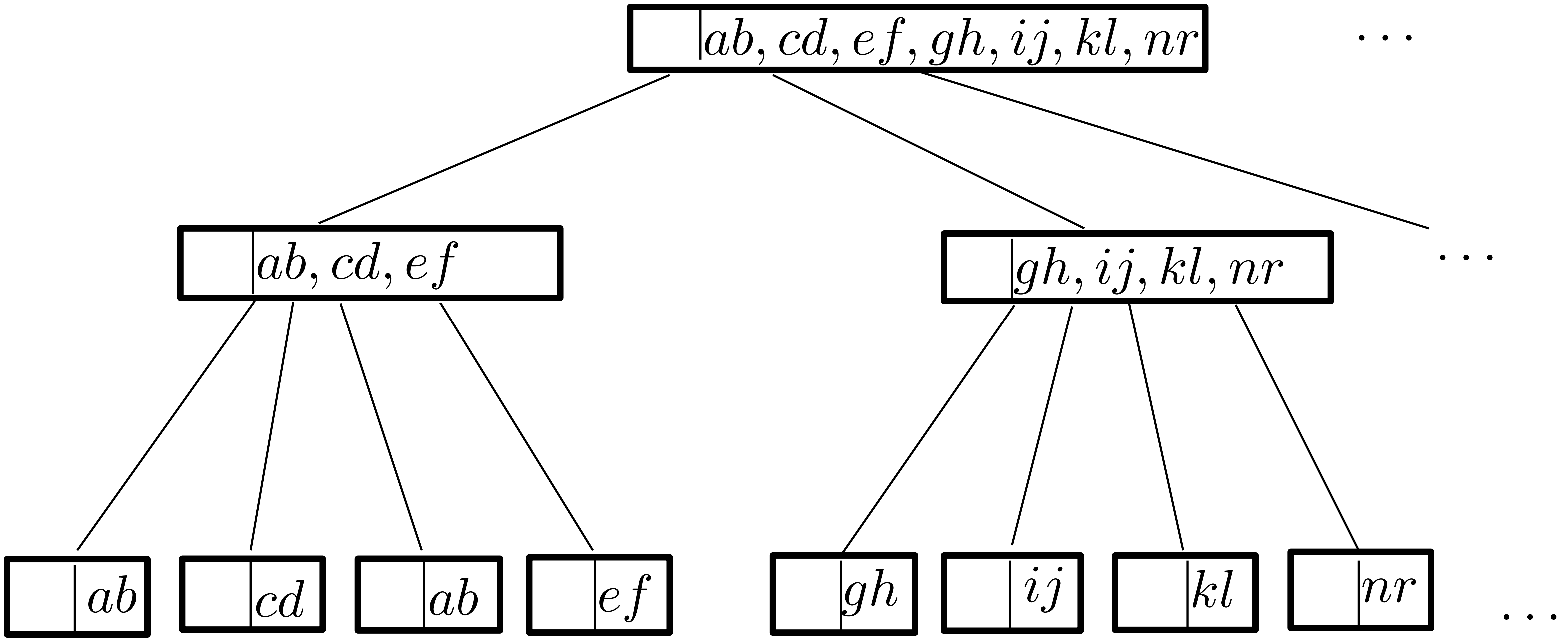

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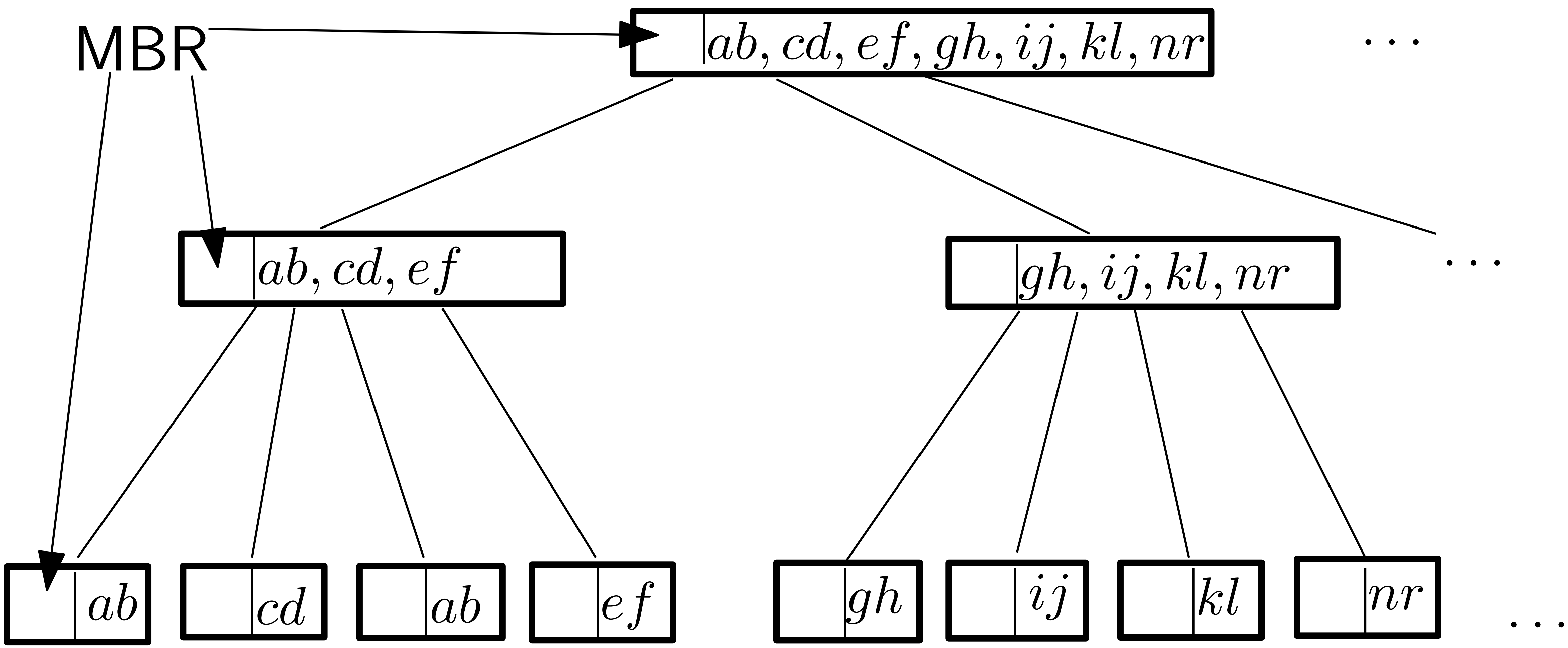

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Min-wise signature with linear hashing R-tree (MHR-tree)

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$2,1,3$ | $4,1,2$ | $5,2,1$ | $7,2,5$ | $6,2,1$ | $1,6,3$ | $2,7,4$ | $8,3,2$ | $\cdots$

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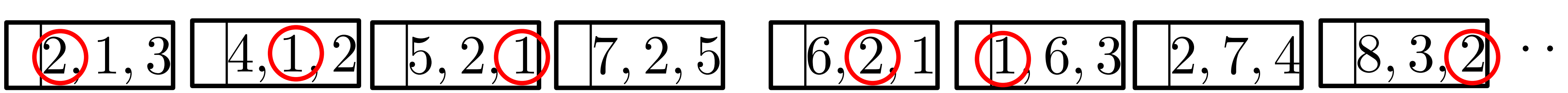

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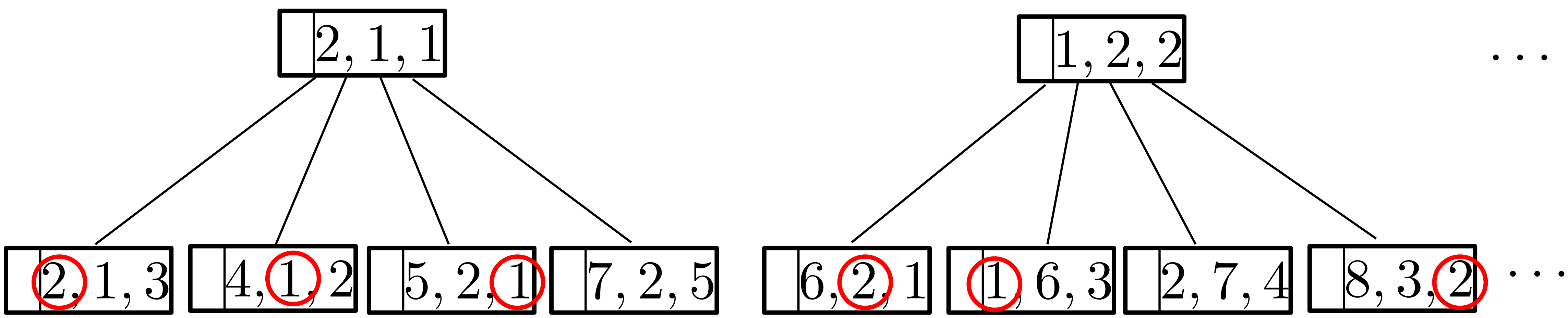

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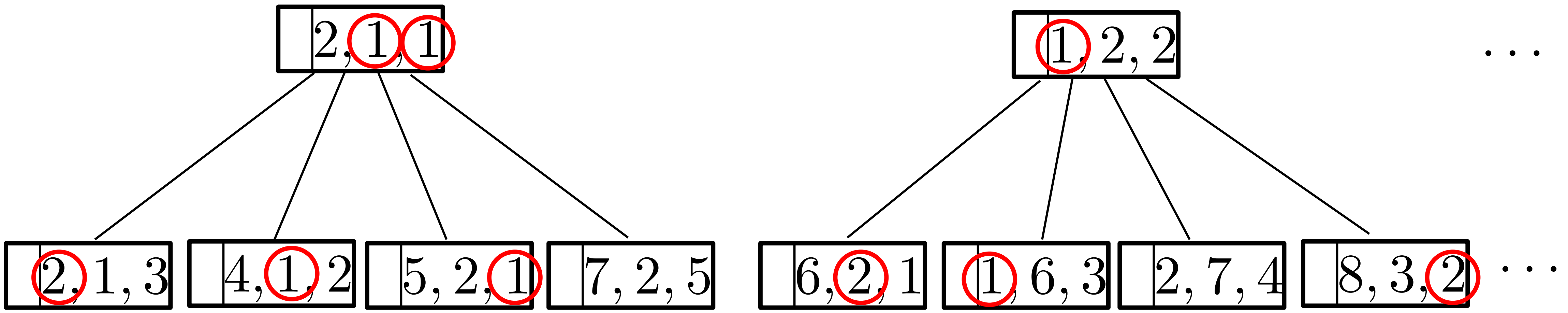

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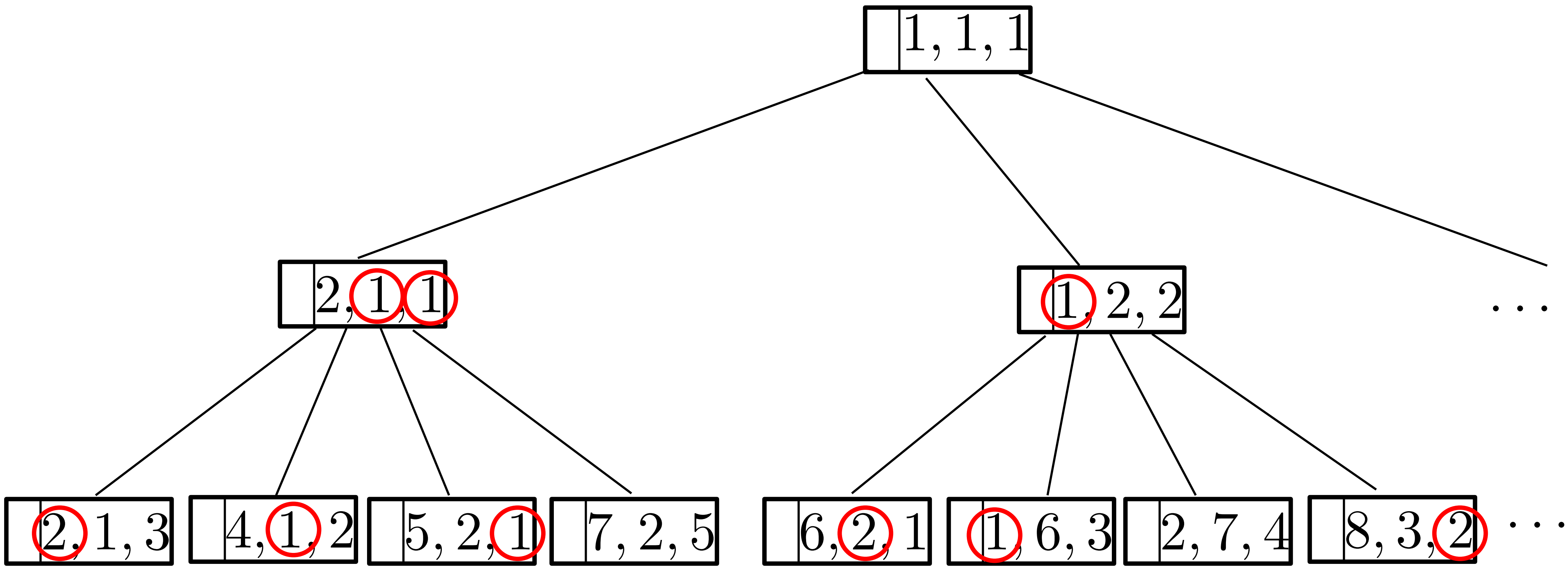

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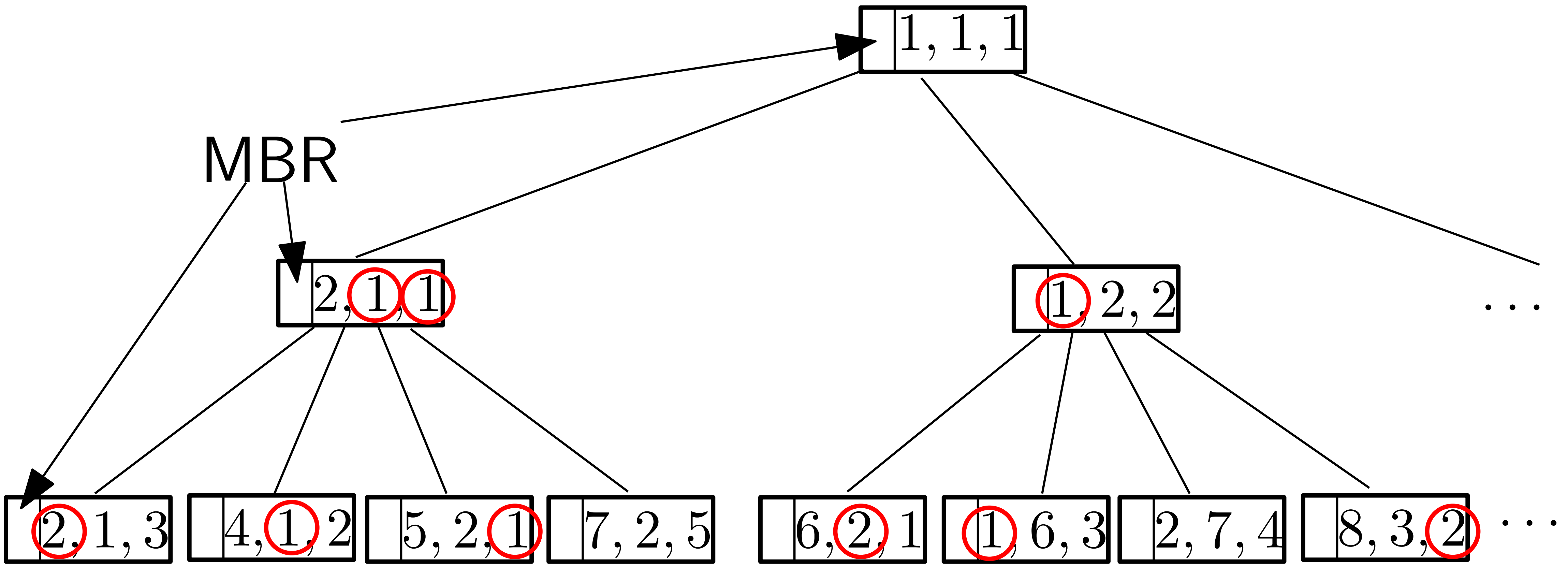

Query algorithms for the MHR-tree

RANGE-MHR(MHR-tree R, Range r, String σ, int τ)

Follow the range query algorithm on R-tree,

If u is a leaf node

For every point $p \in \mathbf{u}_p$

If p is contained in r and $|G_p \cap G_\sigma| \geq \max(|\sigma_p|, |\sigma|) - 1 - (\tau - 1) * q$ and $\varepsilon(\sigma_p, \sigma) < \tau$ then Insert p in A;

Else

For every child node w_i of u

If r and MBR(w_i) intersect, and $|\widehat{G_{w_i} \cap G_\sigma}| \geq |\sigma| - 1 - (\tau - 1) * q$

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$$|\widehat{G_u \cap G_\sigma}| = \widehat{\rho}(G_u, G_\sigma) * |\widehat{G_u \cup G_\sigma}| = 3/4 * 20/3 = 5.$$

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  example:

  s: aabbaabb, {1#a,1aa, 1ab, 1bb, 1ba, 2aa, 2ab, 2bb, 1b$}

  q: aabcaa, {1#a, 1aa, 1ab, 1bc, 1ca, 2aa, 1a$}

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- Issue 2: duplicate q-grams between strings.

  Do not distinguish q-grams from different nodes.
  node 1: pizz (#p, pi, iz, zz, z$);
  node 2: zza (#z, zz, za, a$)
  parent node 3:
  union of signatures corresponding to (#p, pi, iz, zz, z$, #z, za, a$)

Selectivity estimation for SAS range queries

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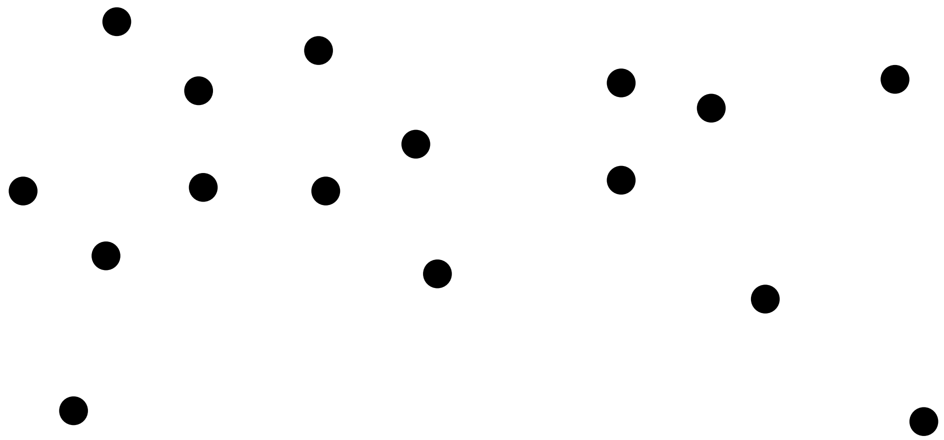

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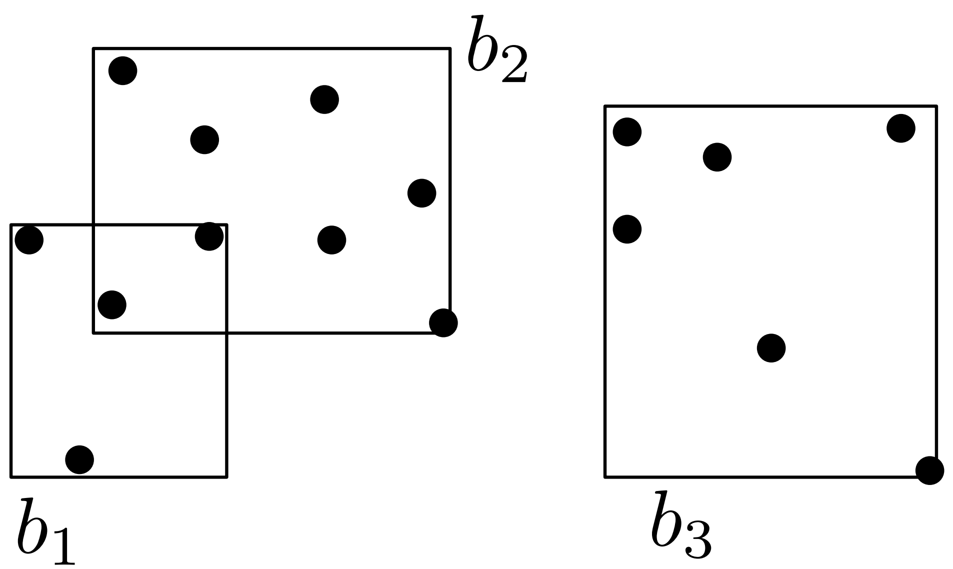

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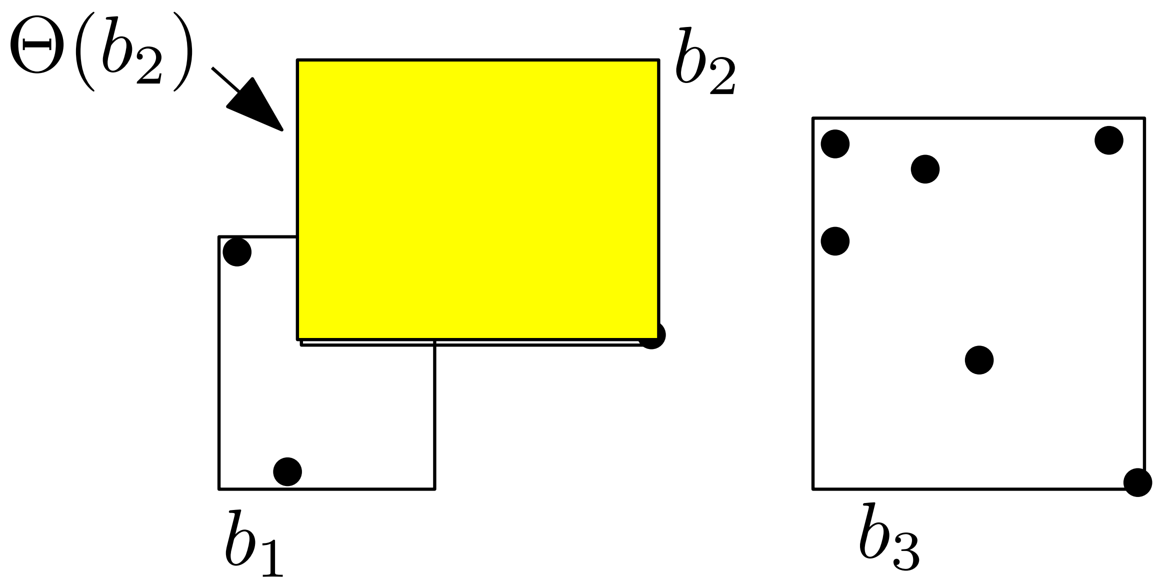

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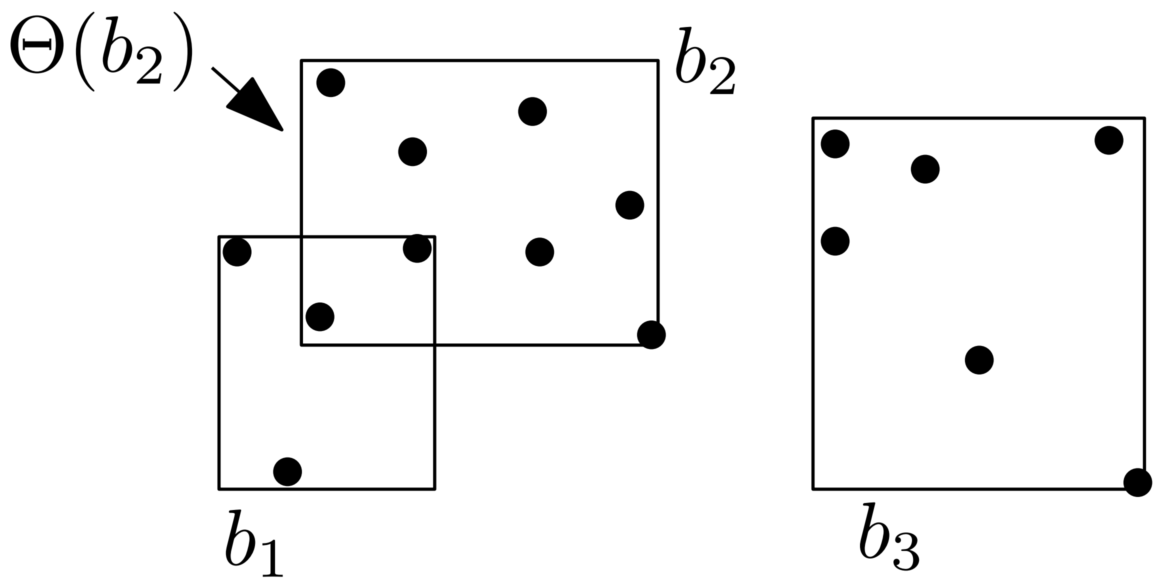

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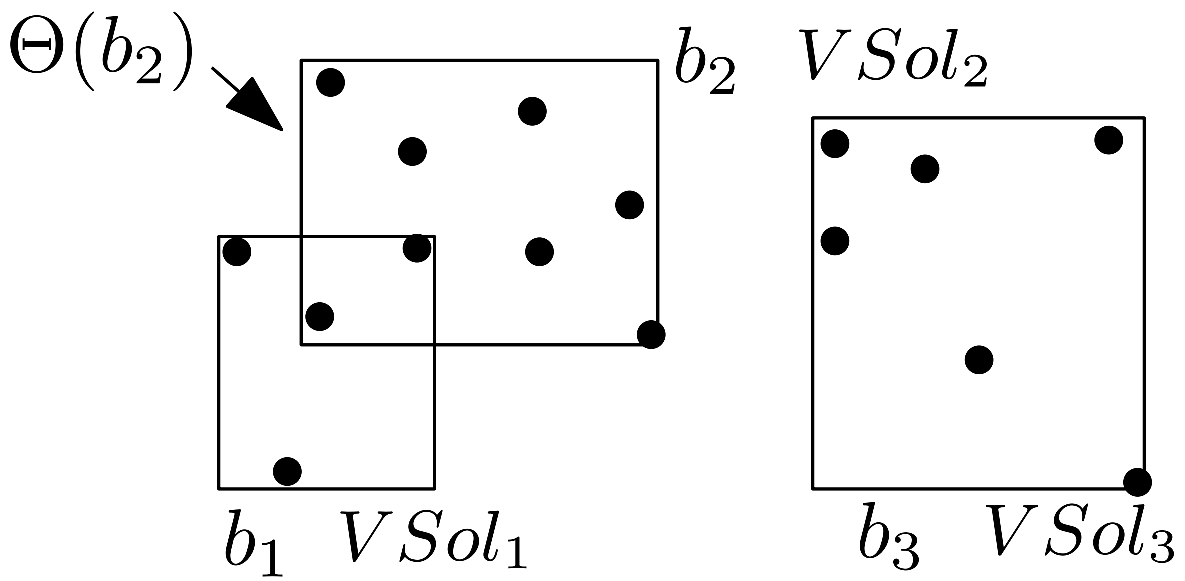

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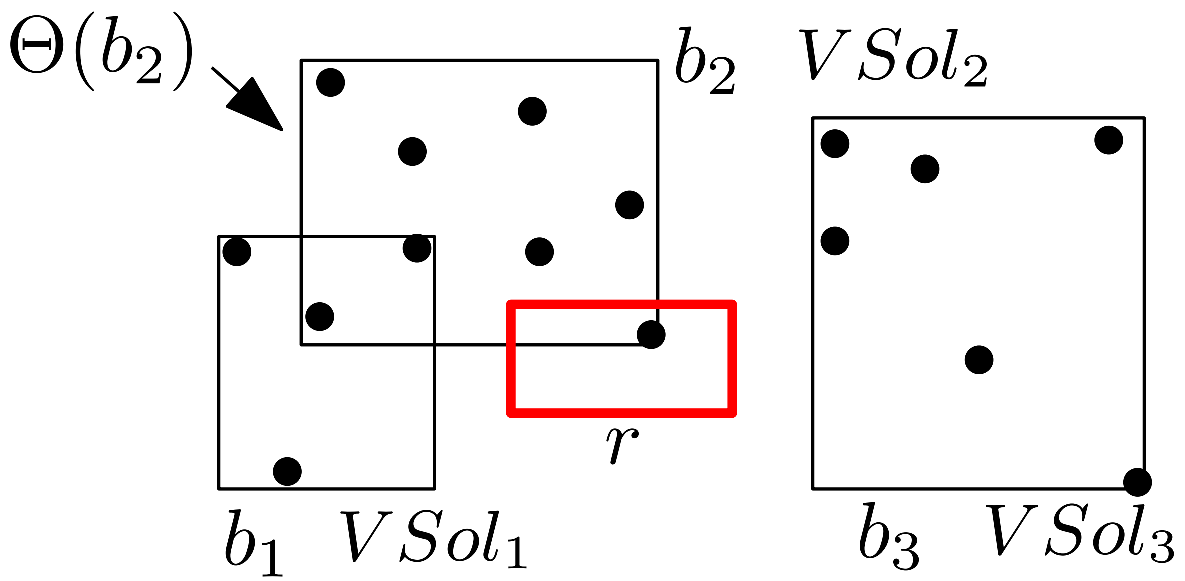

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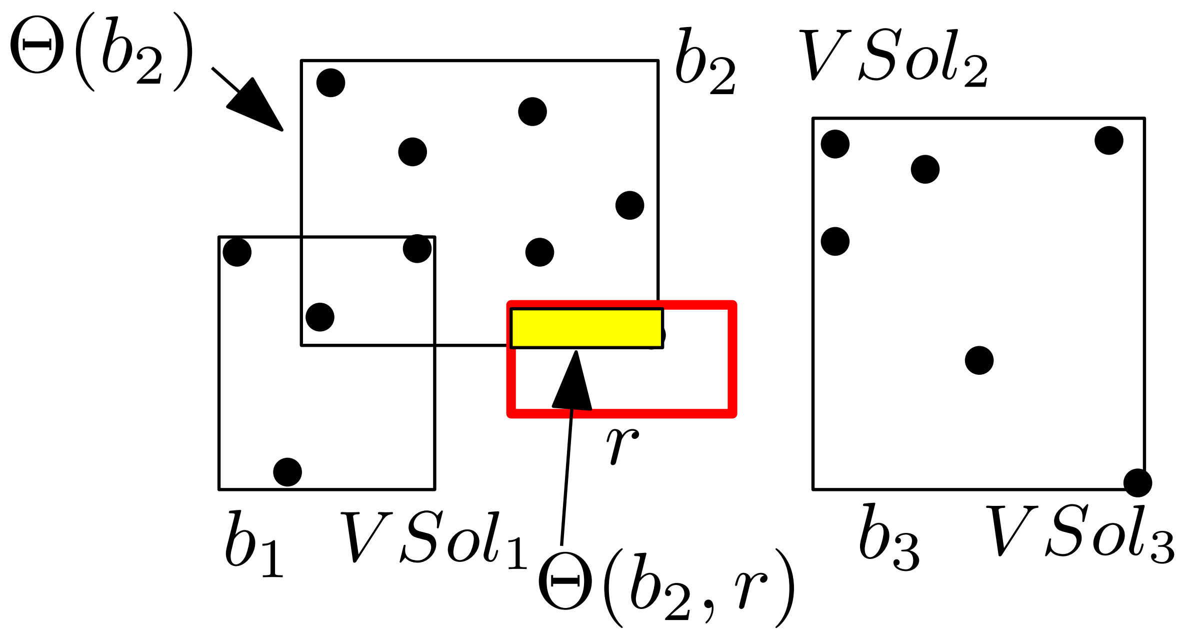

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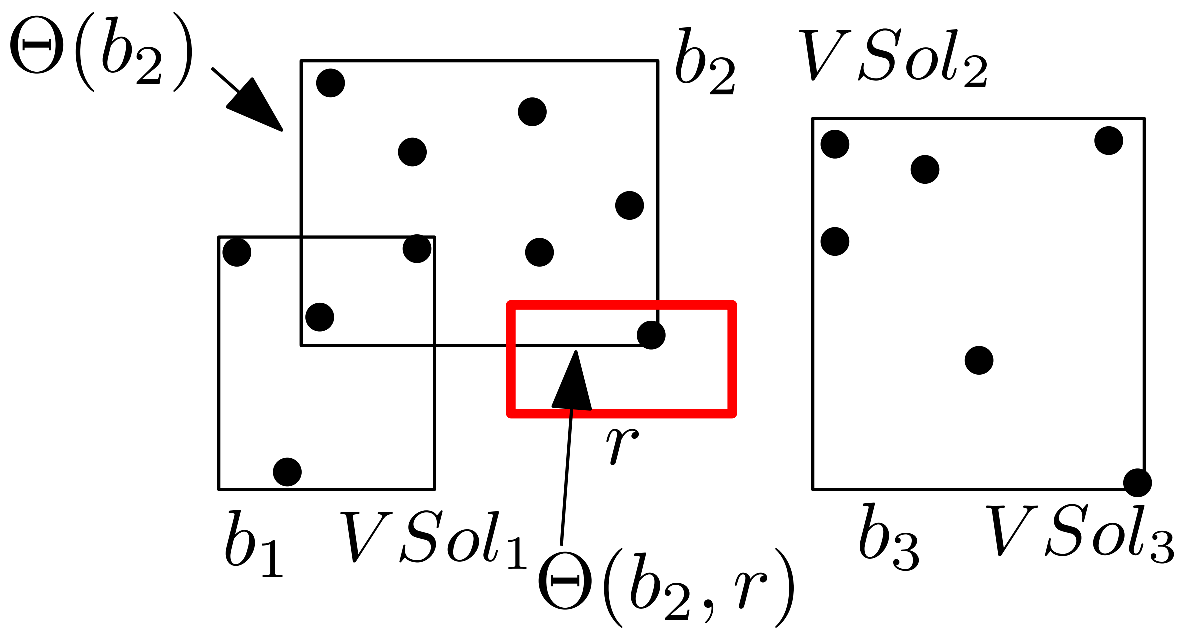

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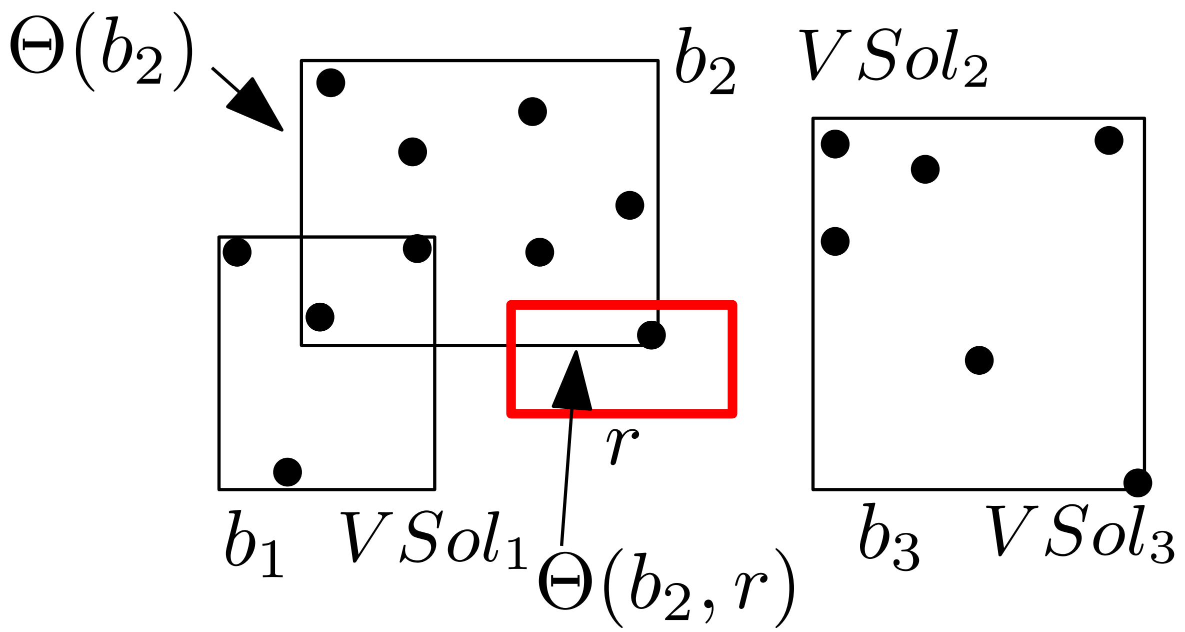

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- Improvements:
  Minimum number of neighborhoods principle,
  Spatial uniformity principle.

Two improvements for selectivity estimation

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too men

toy min

boy

coy mine

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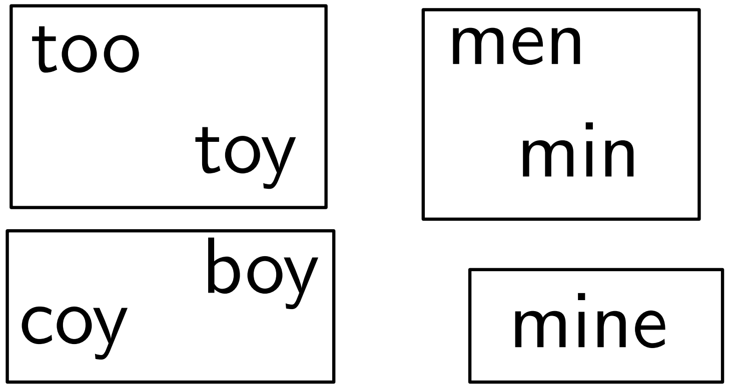

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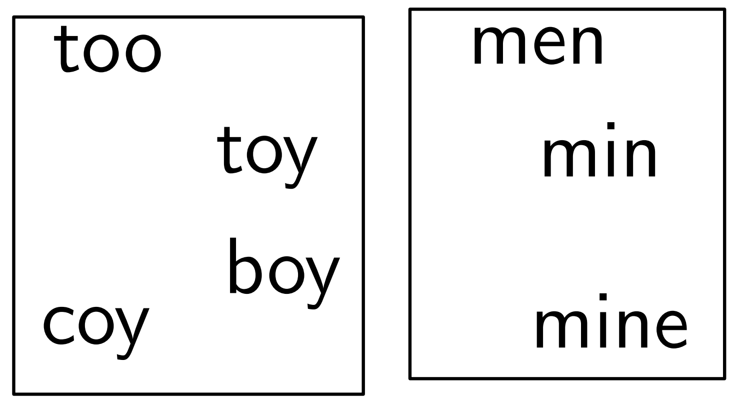

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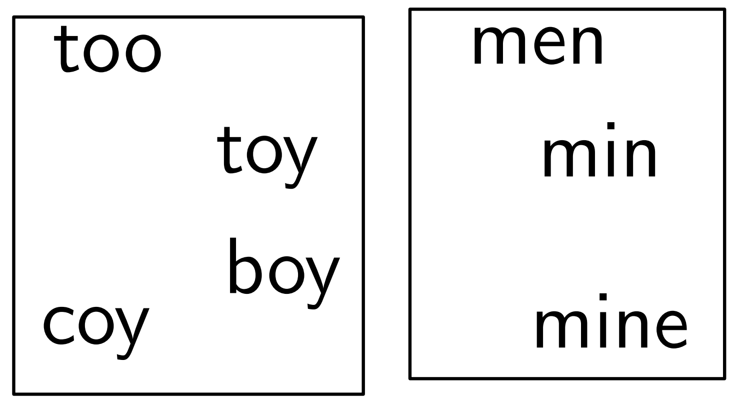

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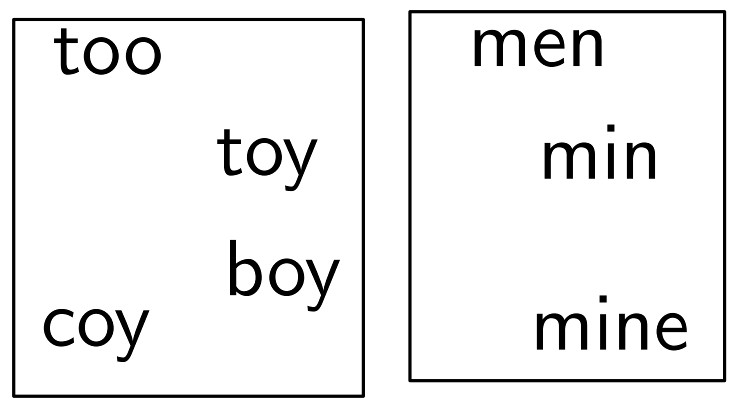

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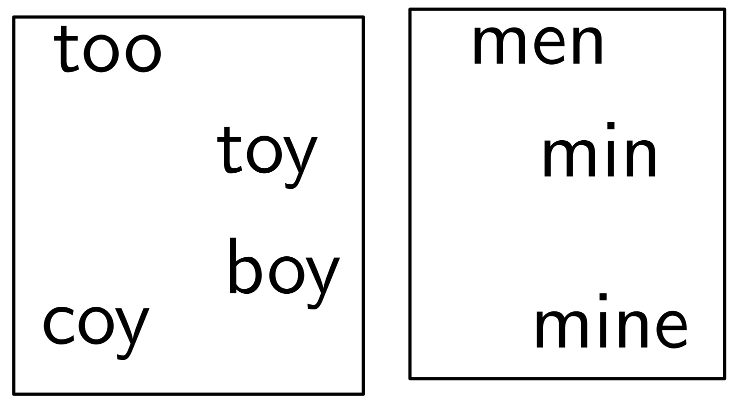

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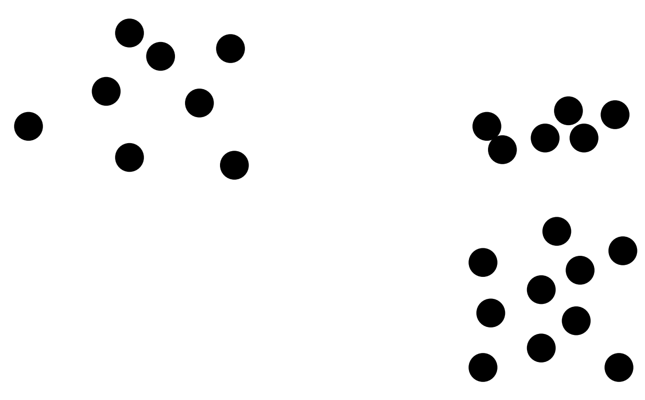

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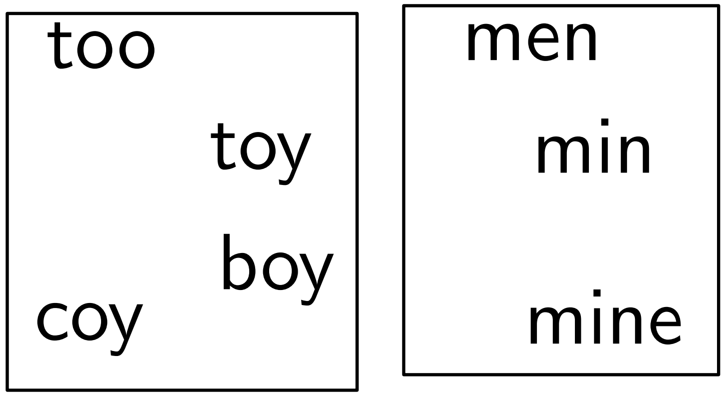

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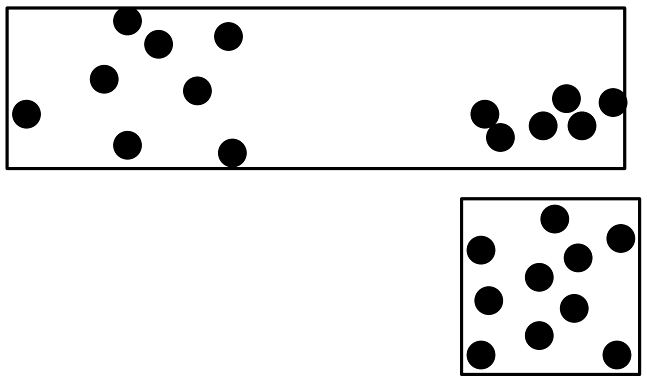

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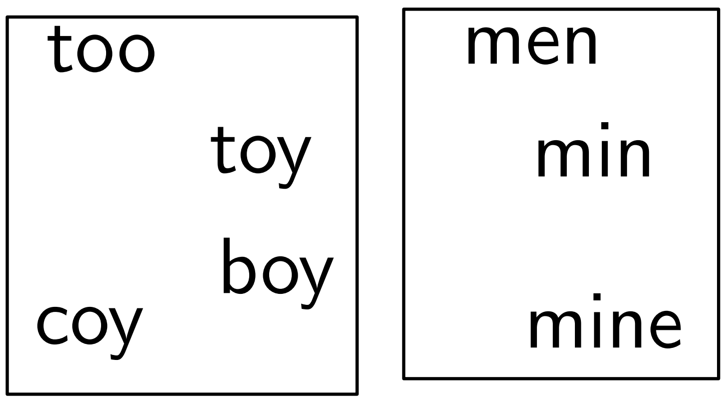

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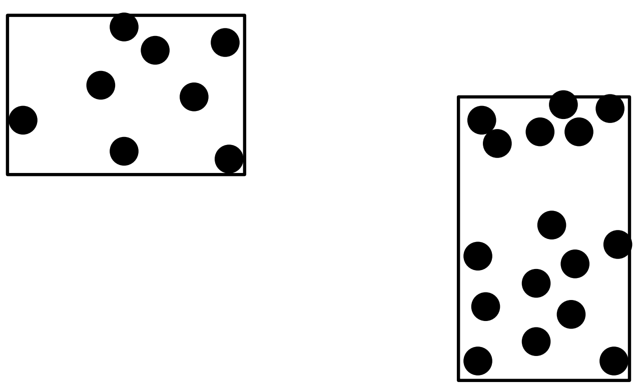

The partitioning metric

- Neighborhood and uniformity quality of b:
  $\Delta(b) = \eta_b n_b \sum_{1,\ldots,d} X_i$,
  $\{X_1, \ldots, X_d\}$: the side lengths of b in each dimension.

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- The greedy algorithm;
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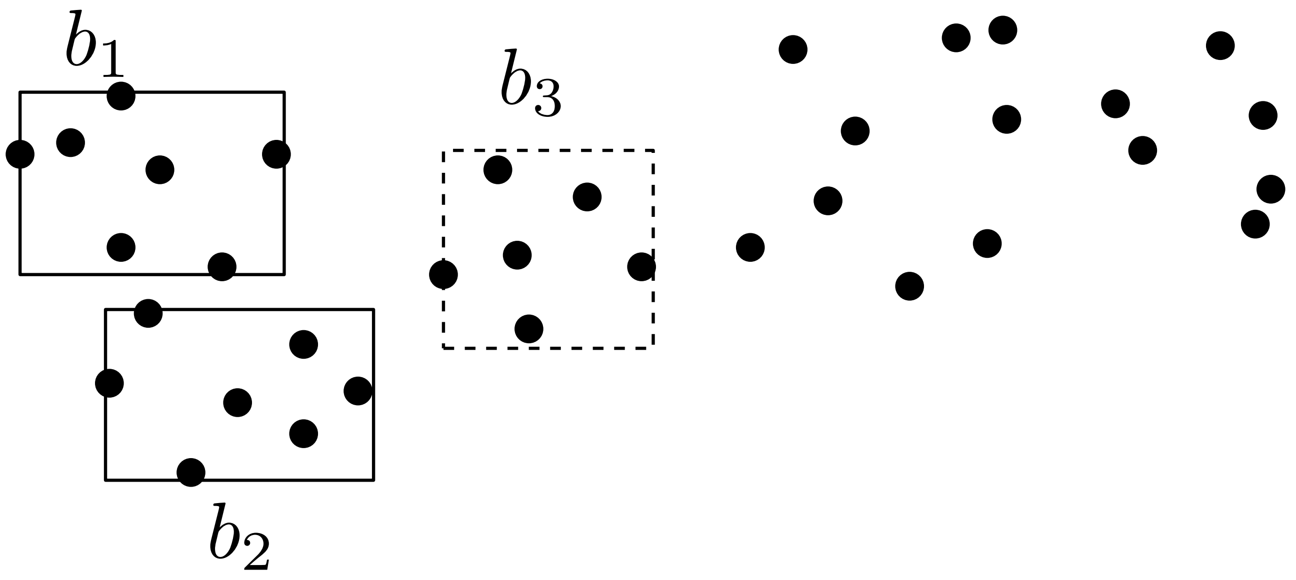
The greedy algorithm



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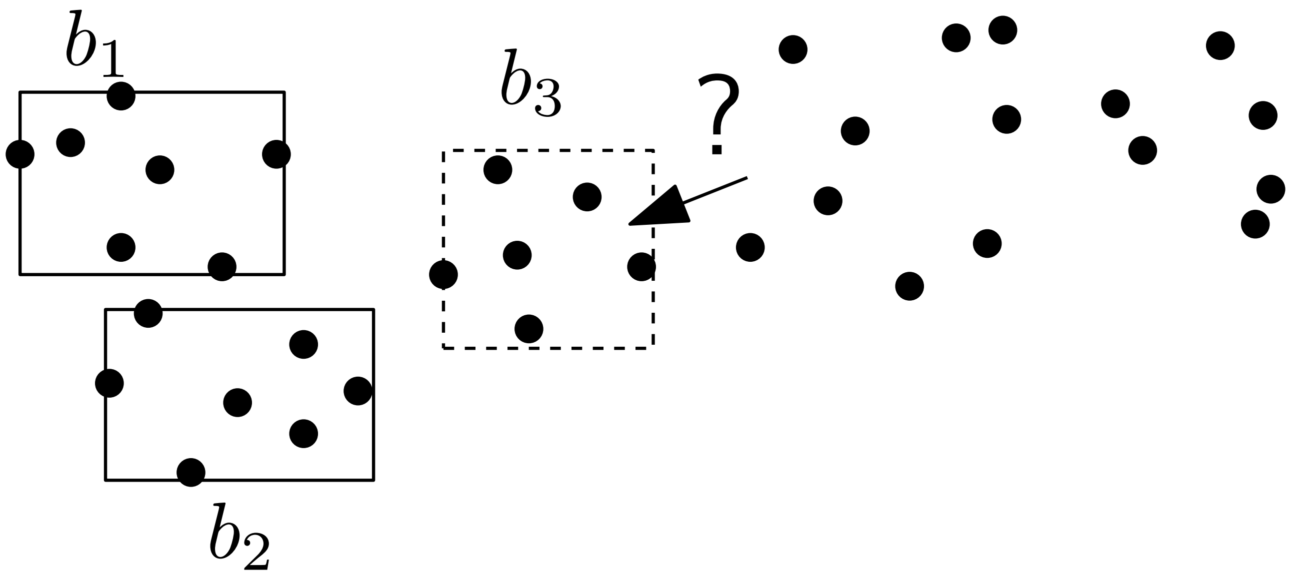

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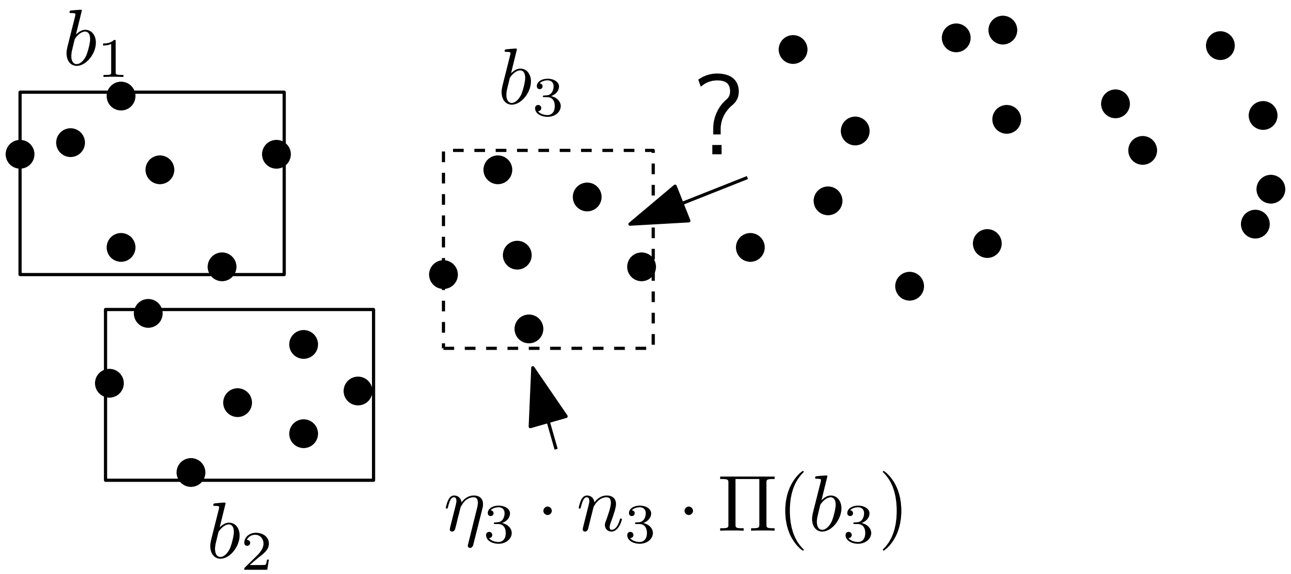

$\Pi(b_i)$: the perimeter of b_i.

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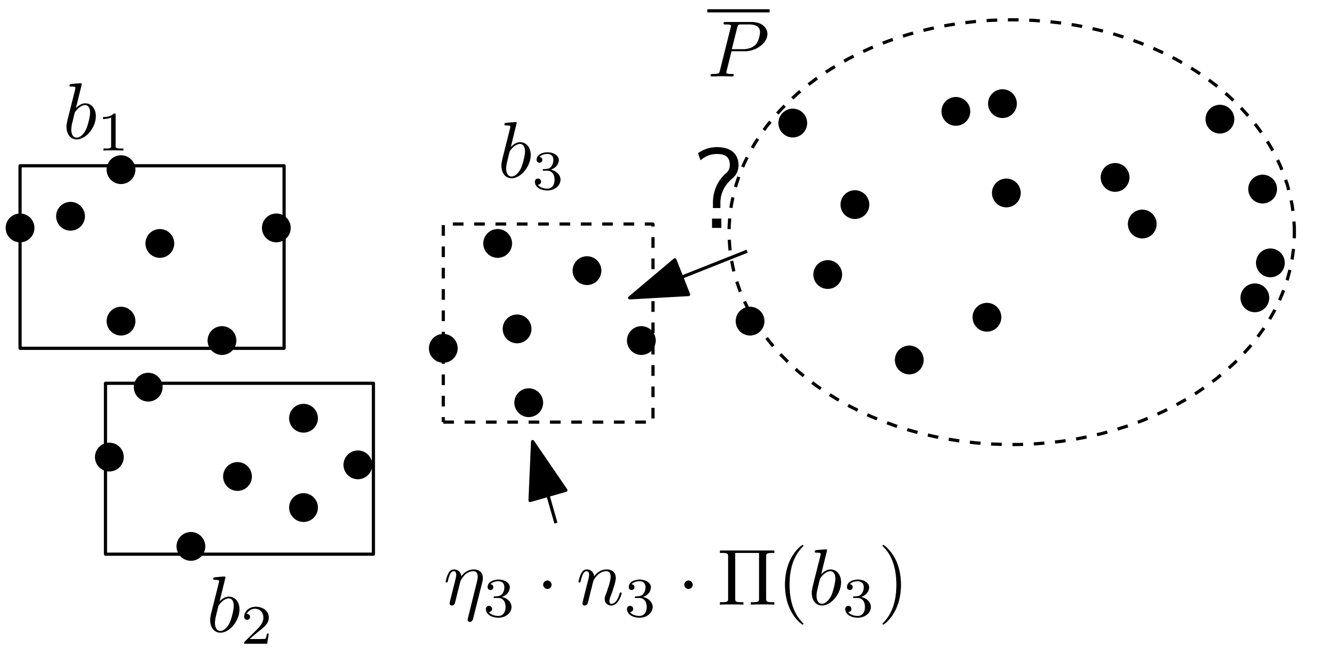

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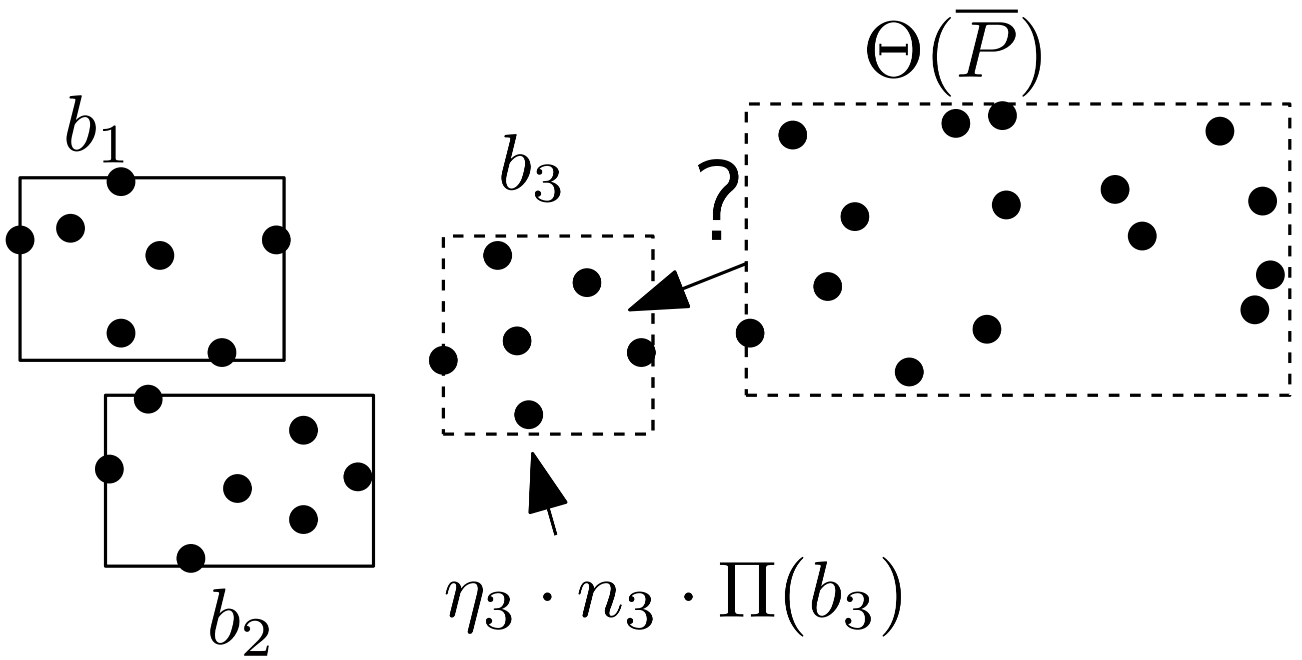

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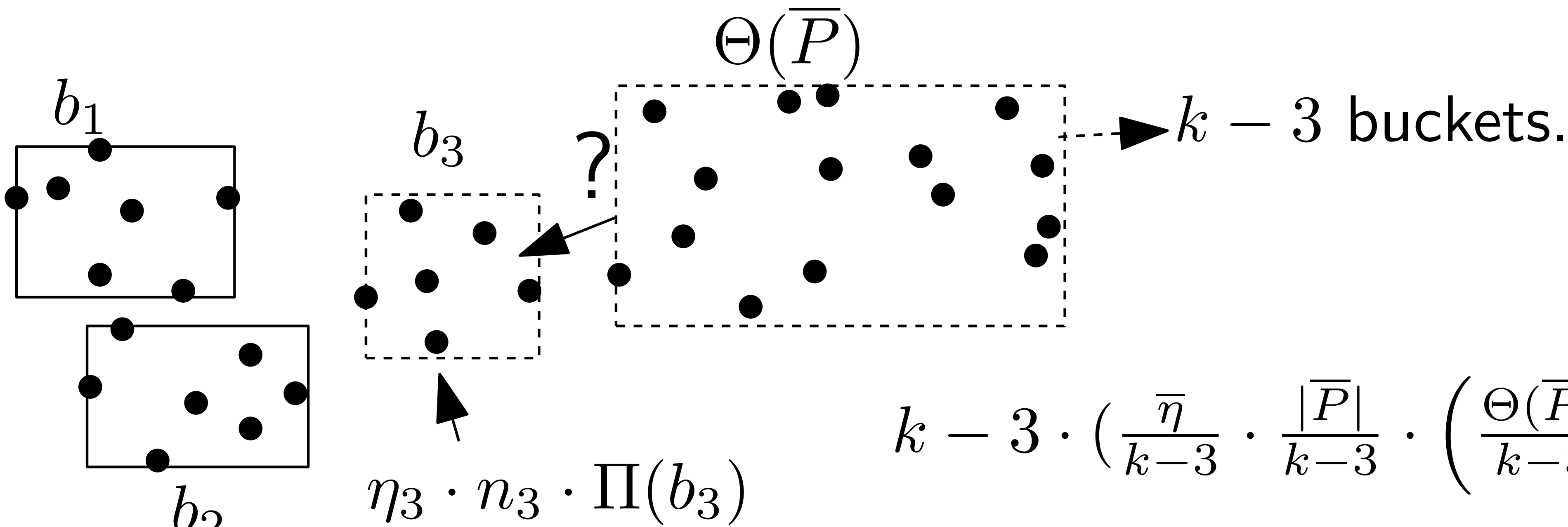

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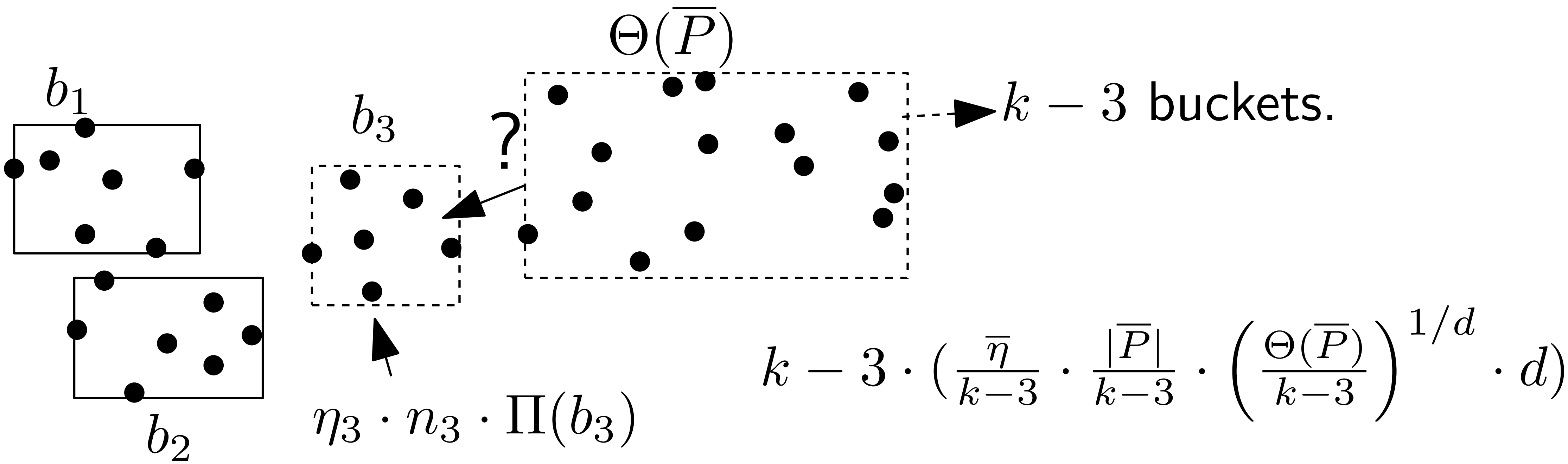

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($\Pi(b_i)$ is the perimeter of bucket b_i)

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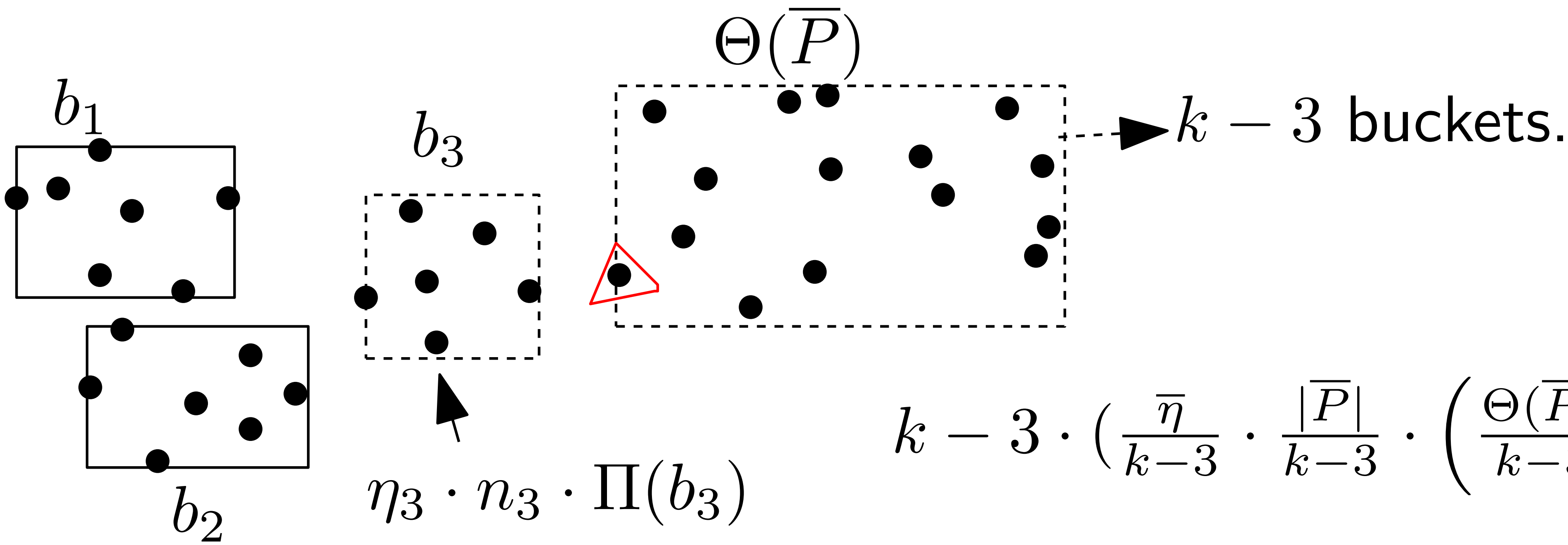

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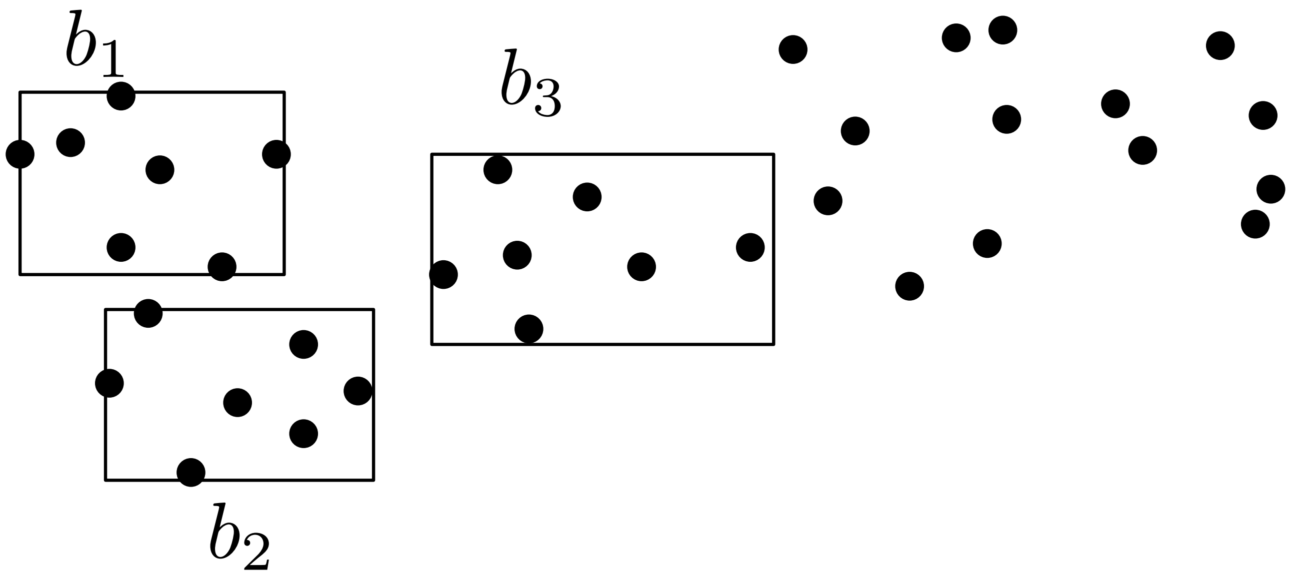

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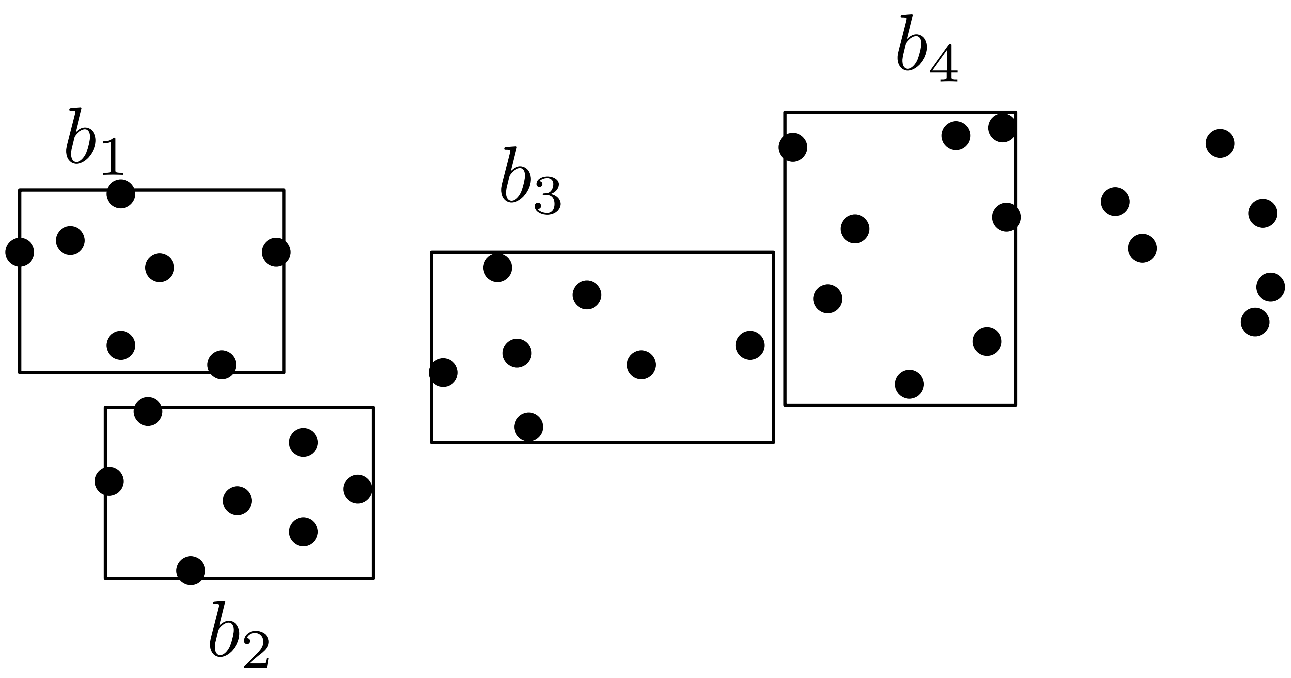

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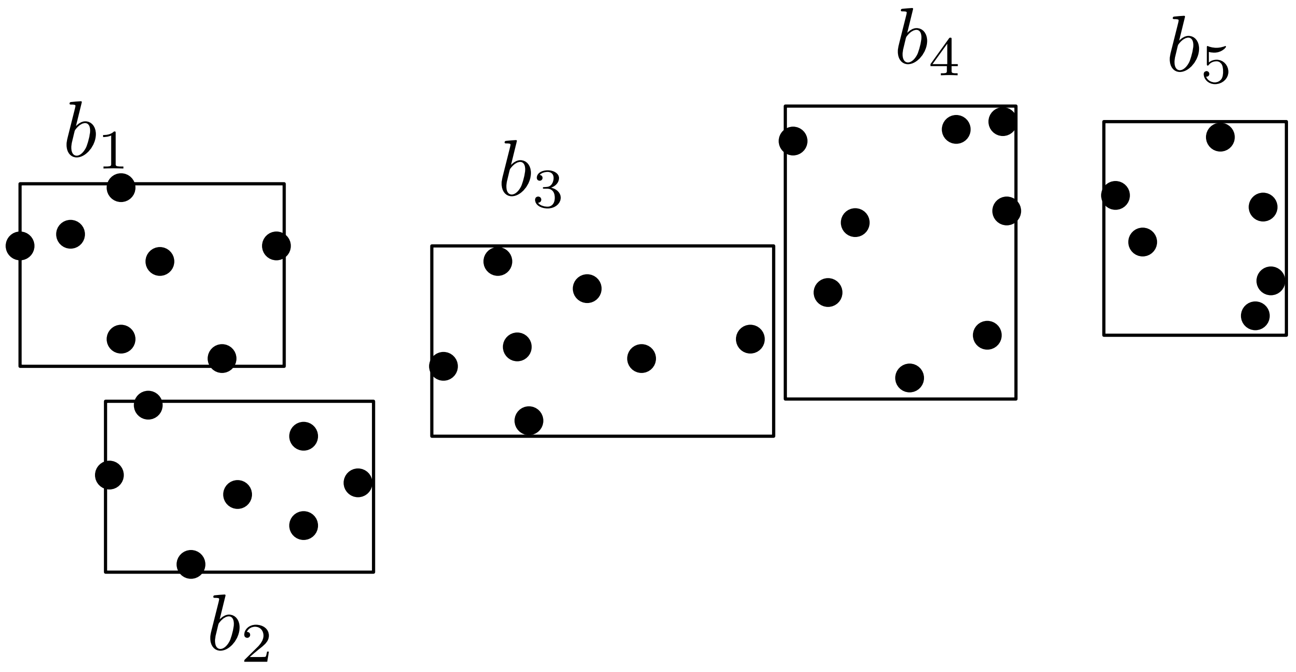
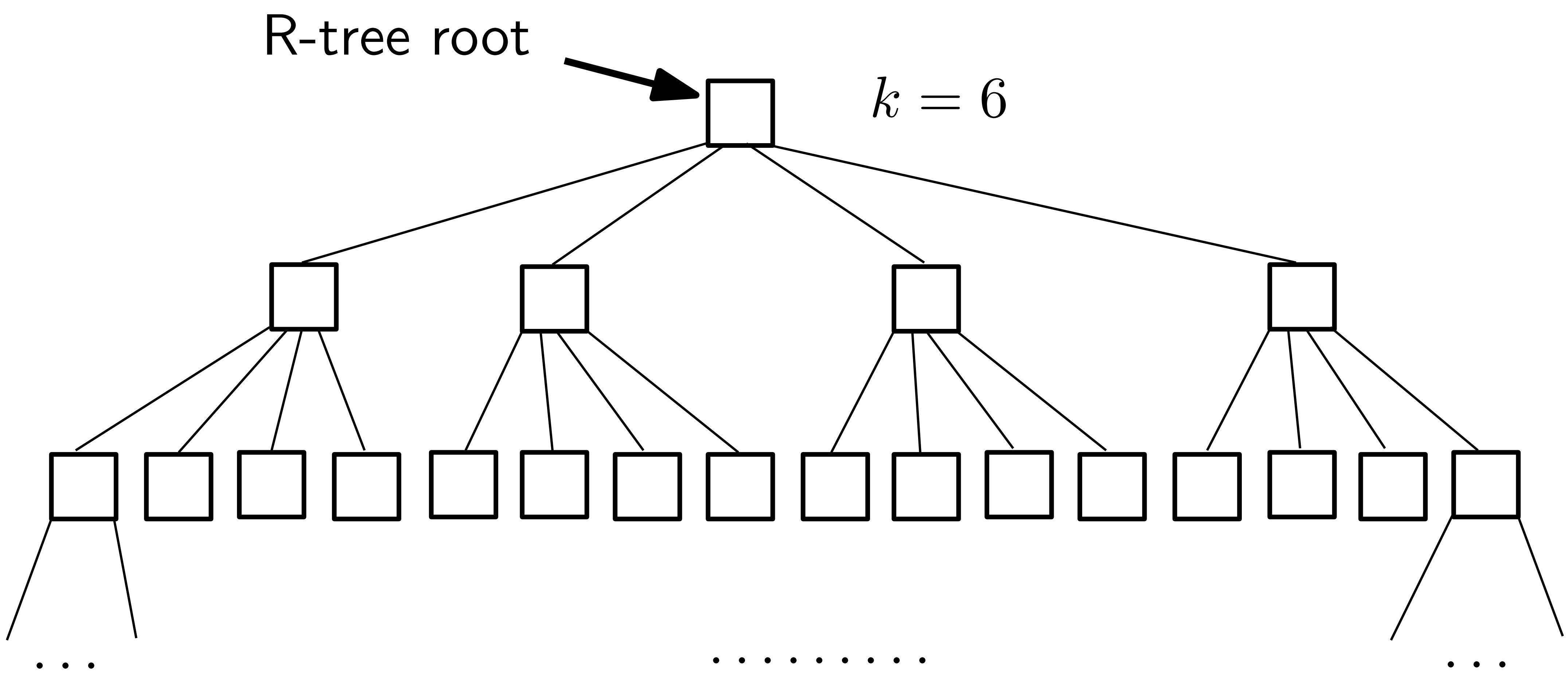


The adaptive R-tree algorithm



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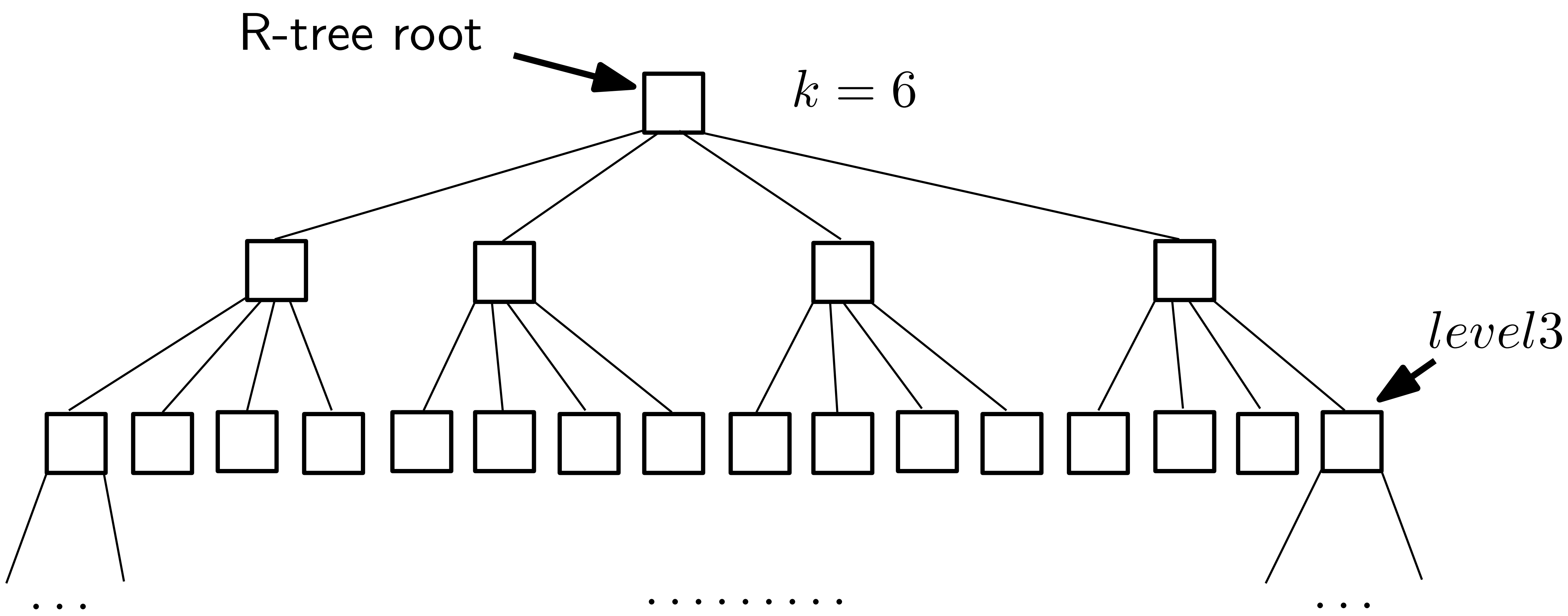

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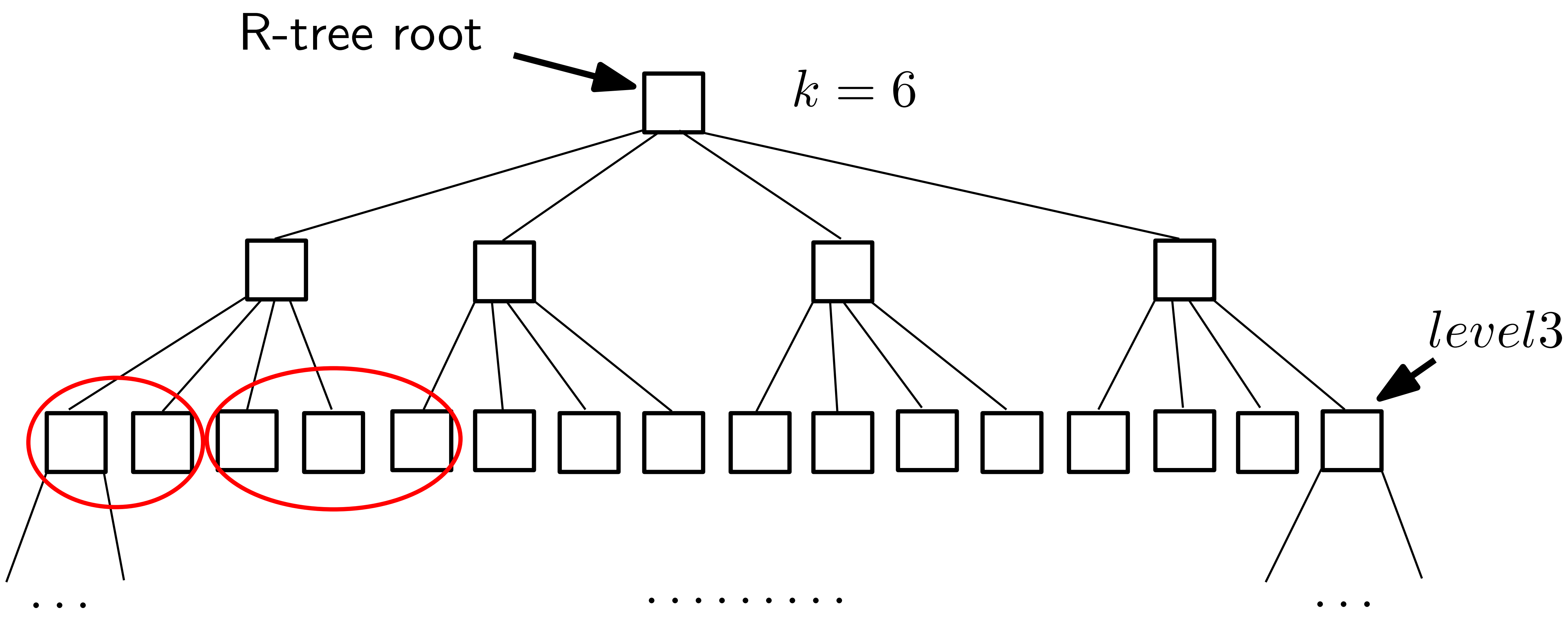

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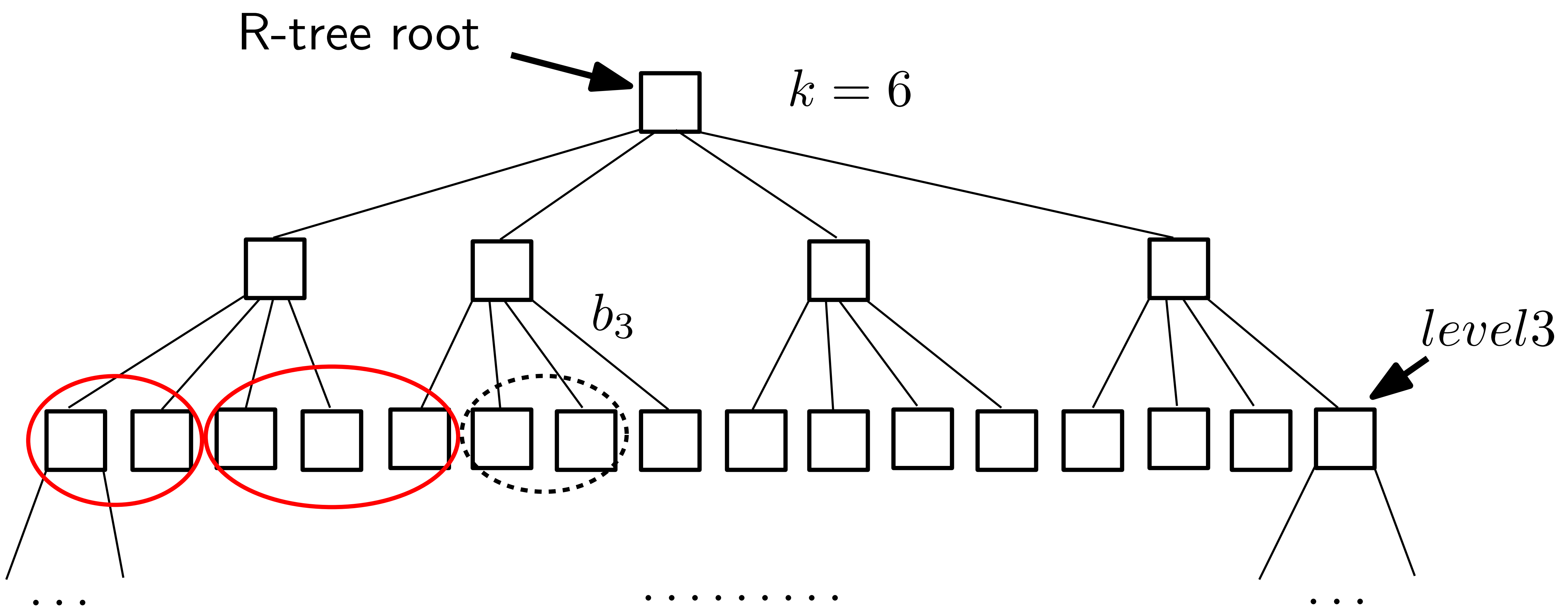

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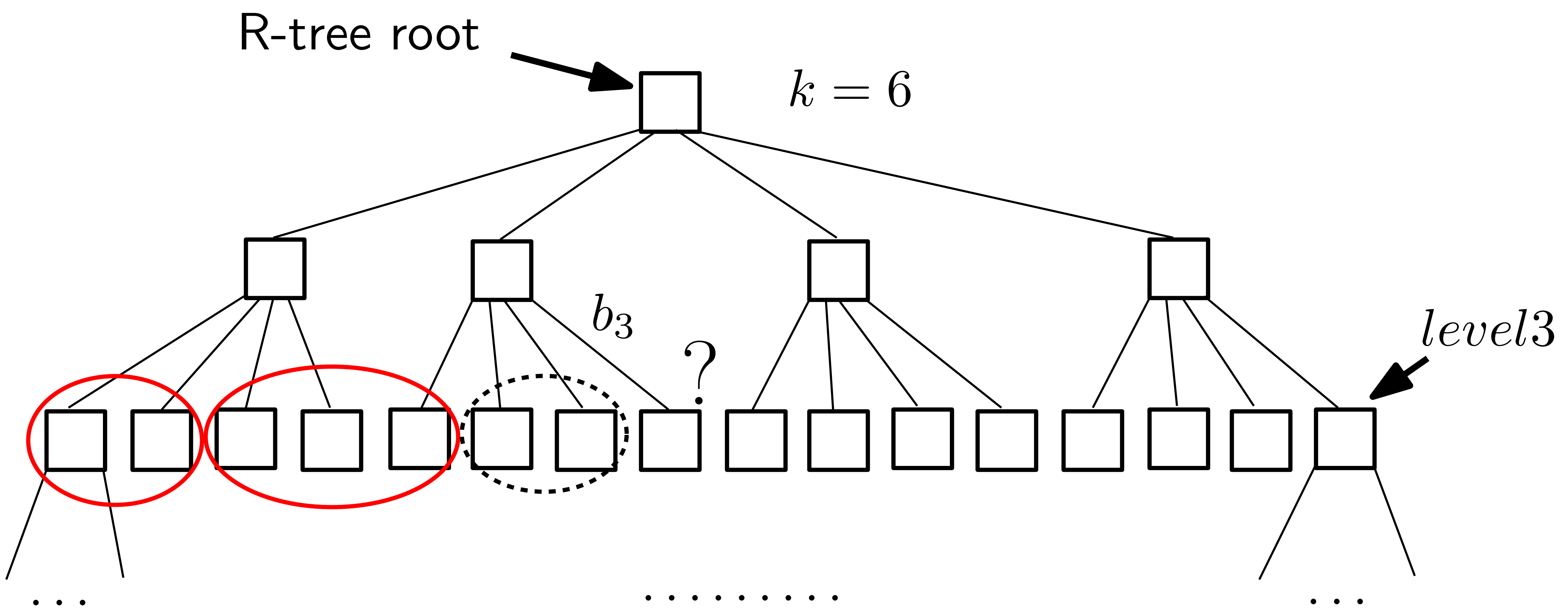

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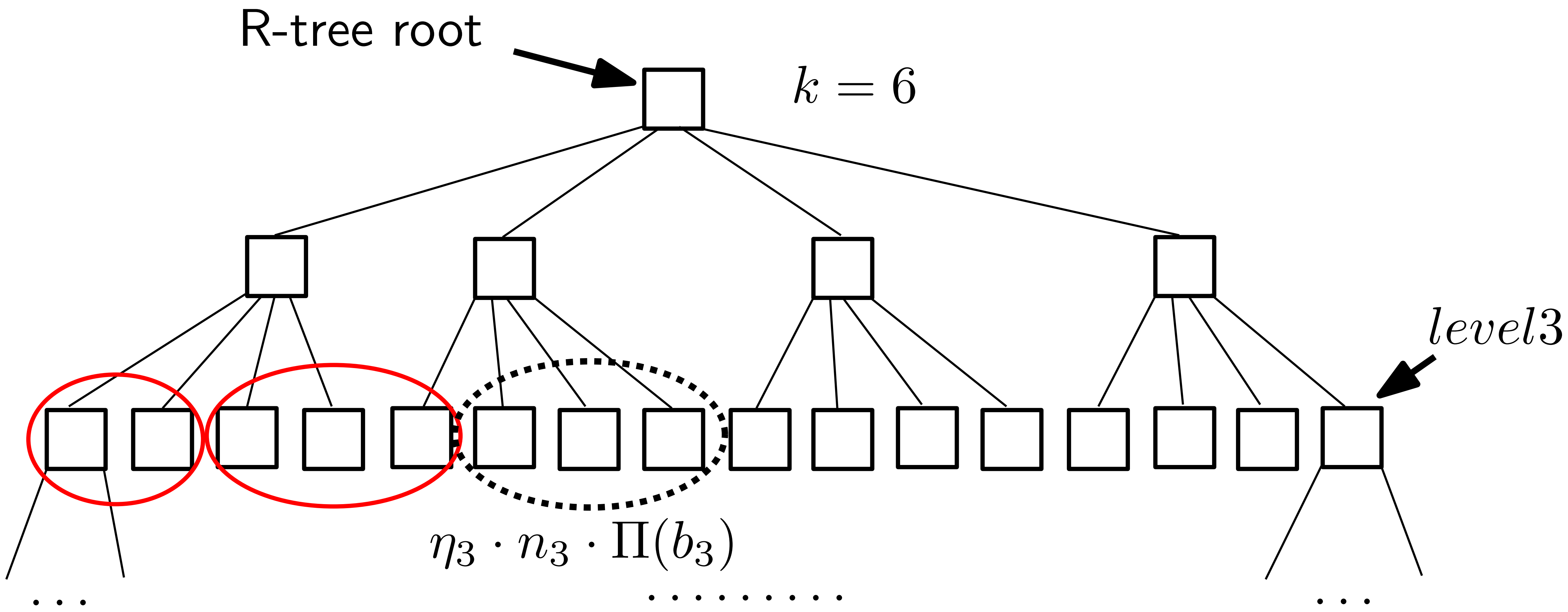

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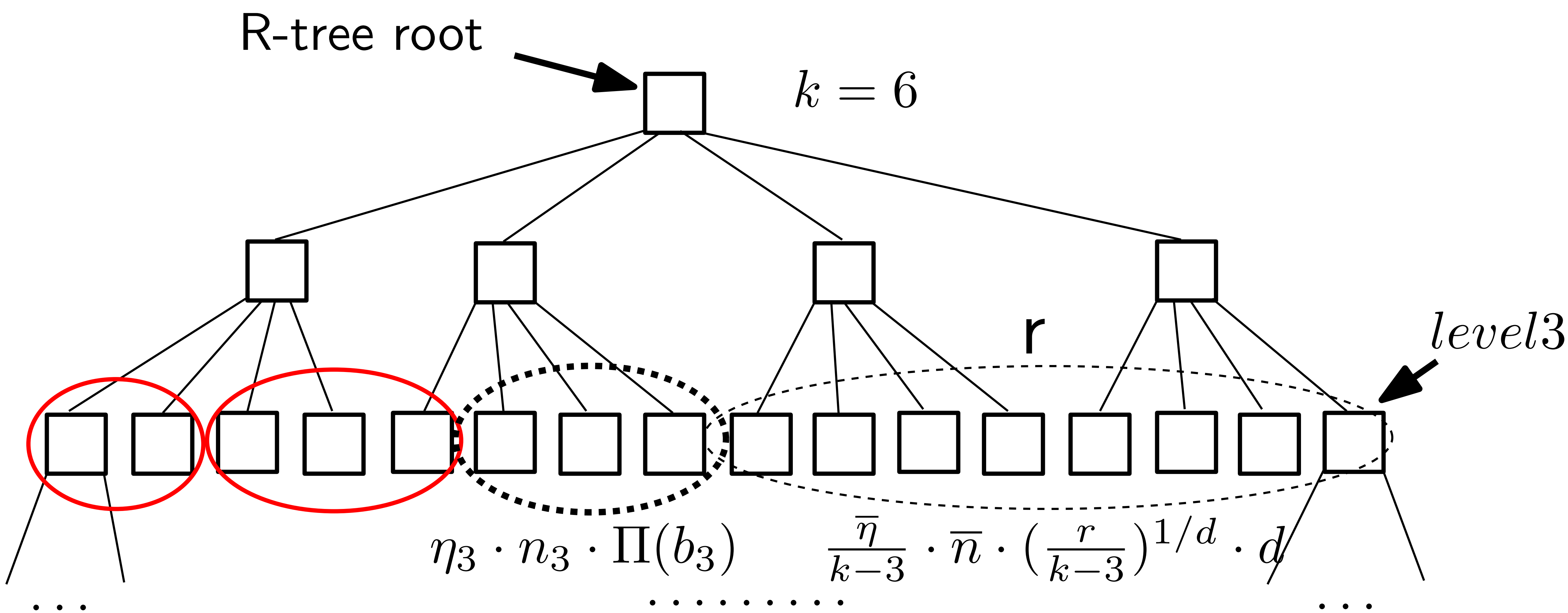

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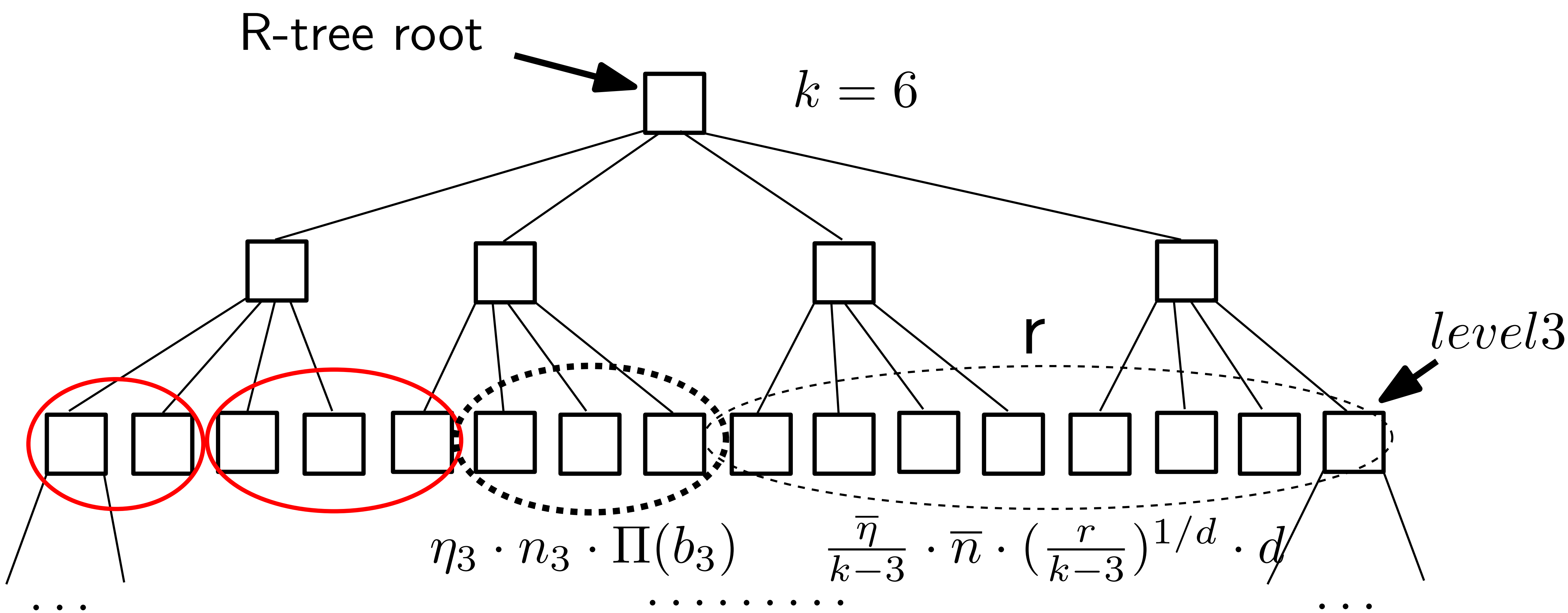

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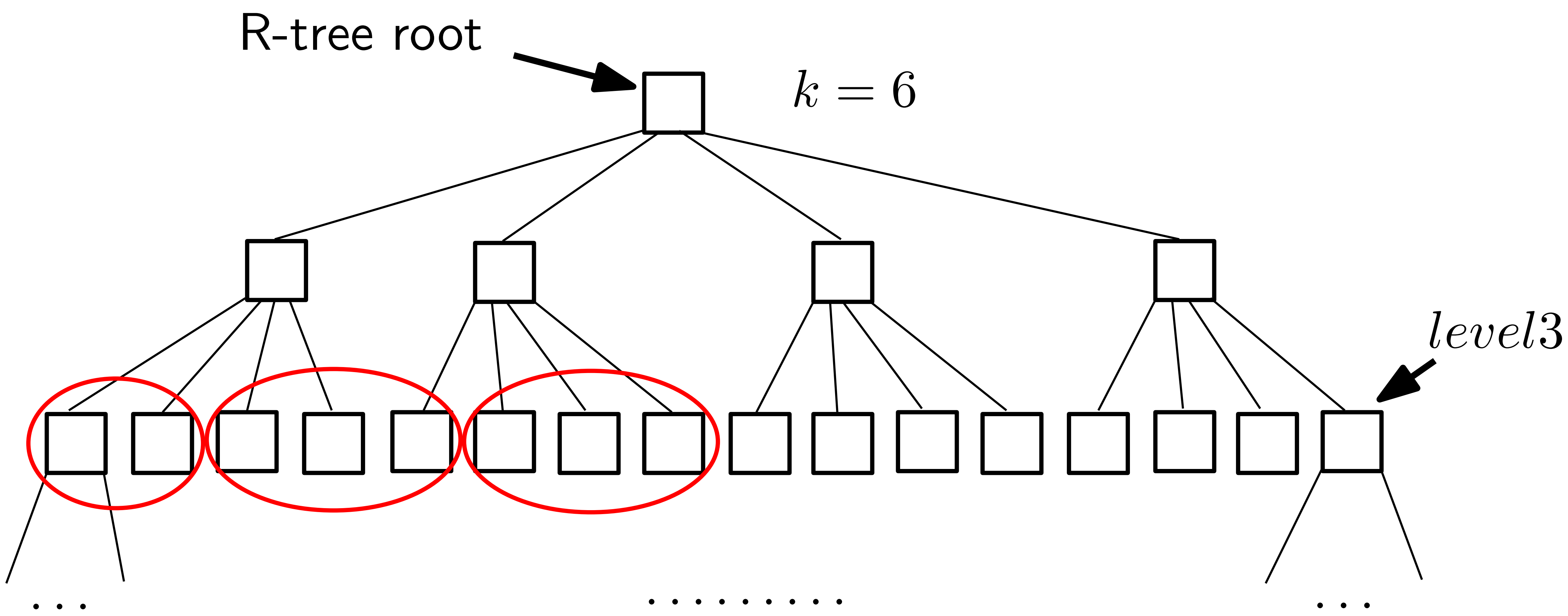

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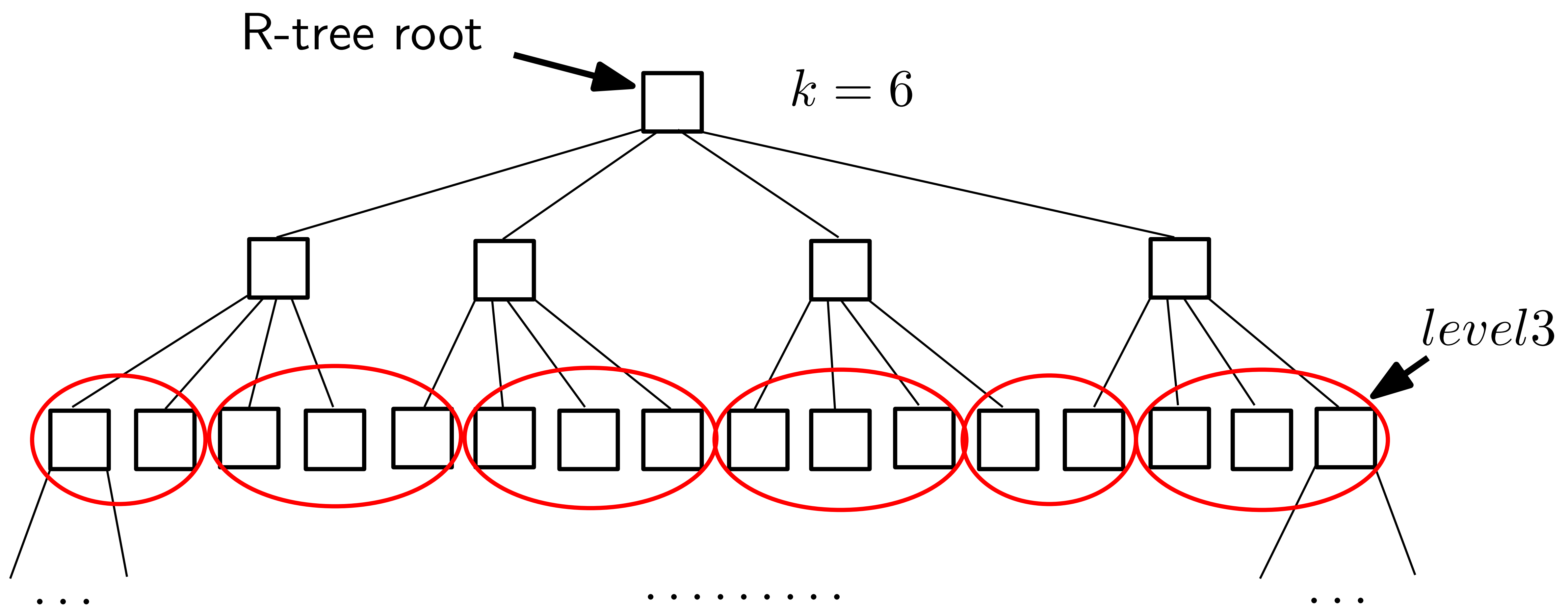

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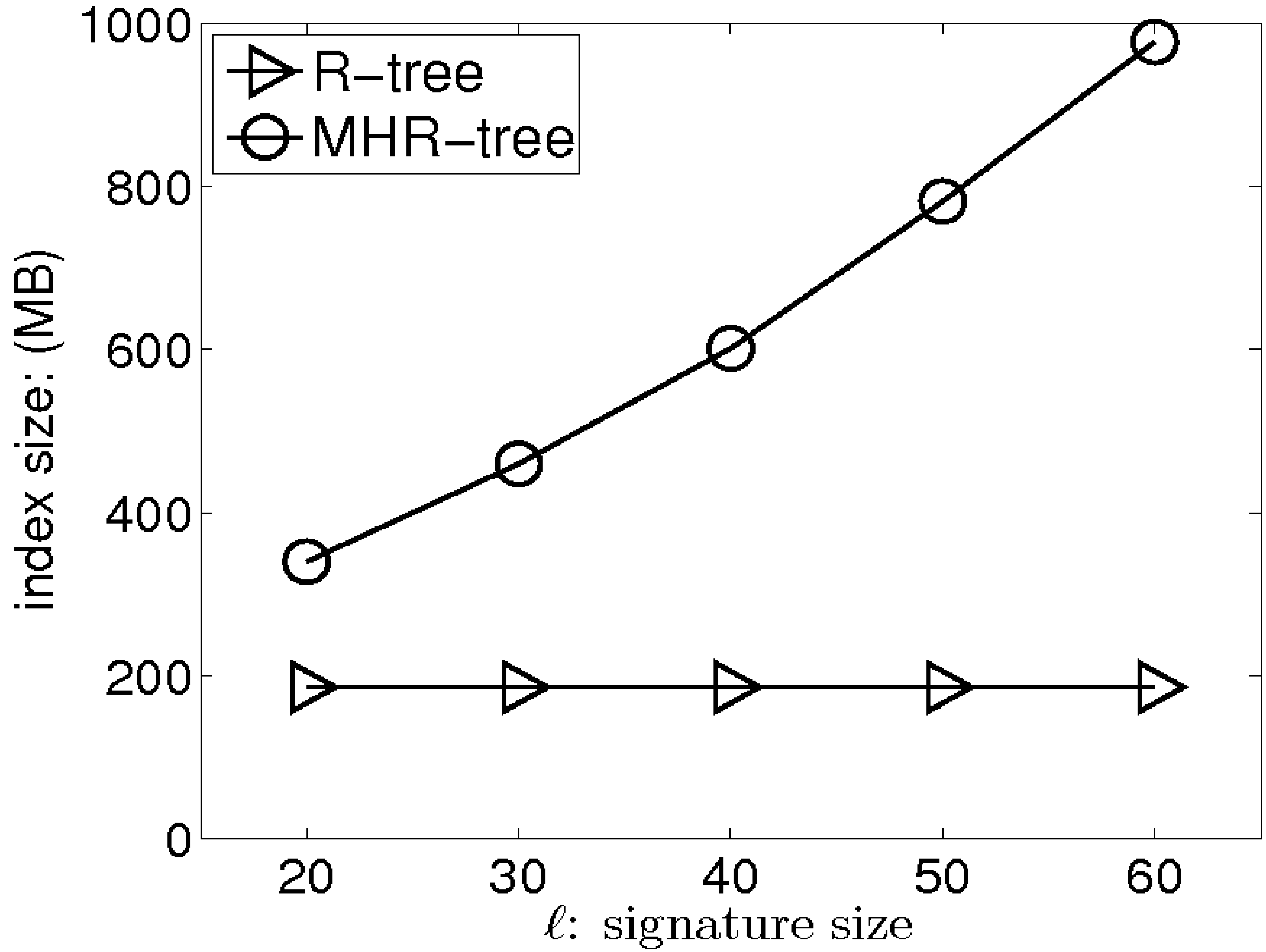
- The default experimental parameters are summarized below.

Symbol	Definition	Default Value
θ	query area percentage of data space	3%
N	size of points set	2,000,000
l	signature length	50
τ	edit distance threshold	2
d	dimensionality	2

SAS range queries: impact of the signature size



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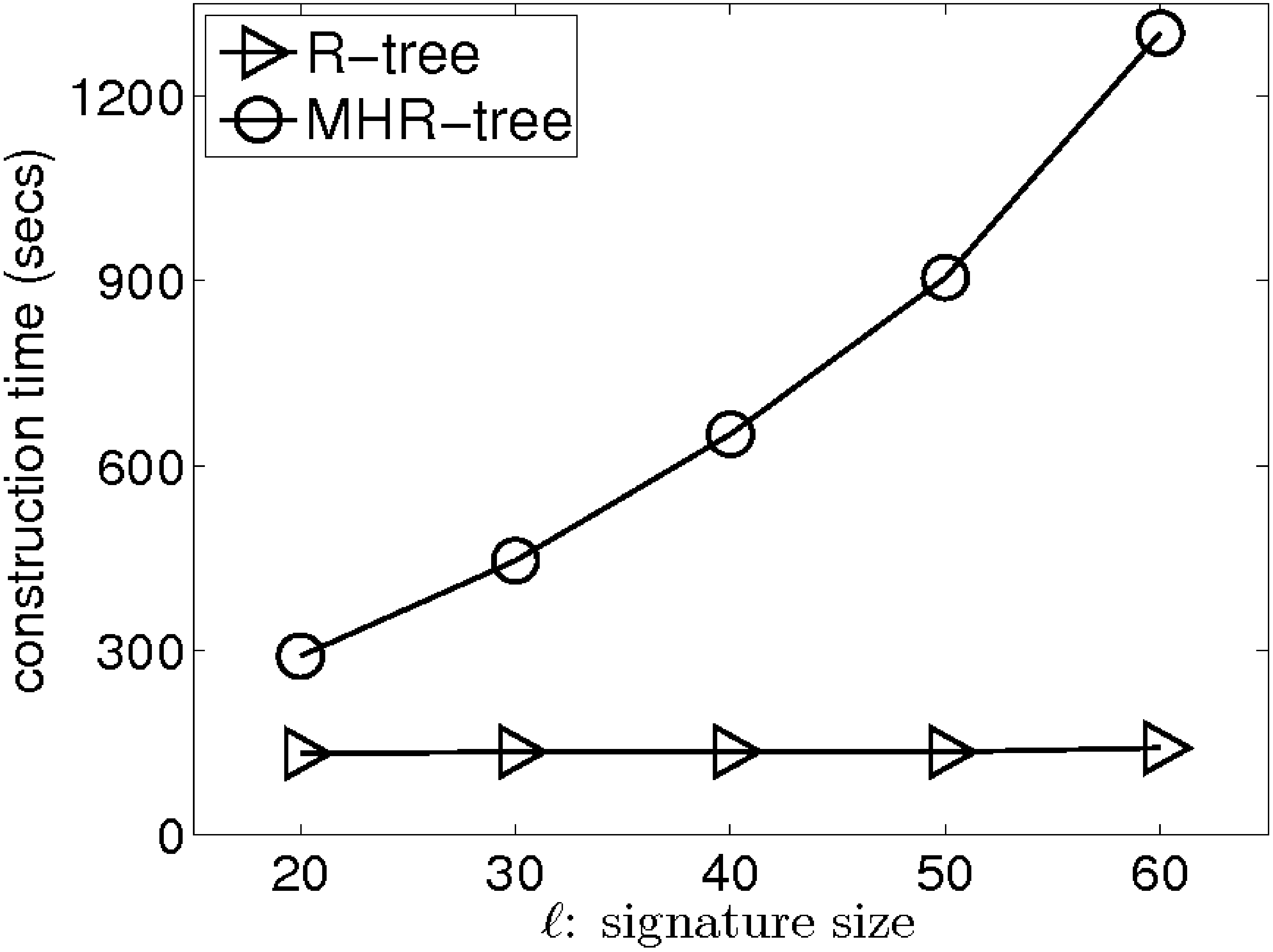

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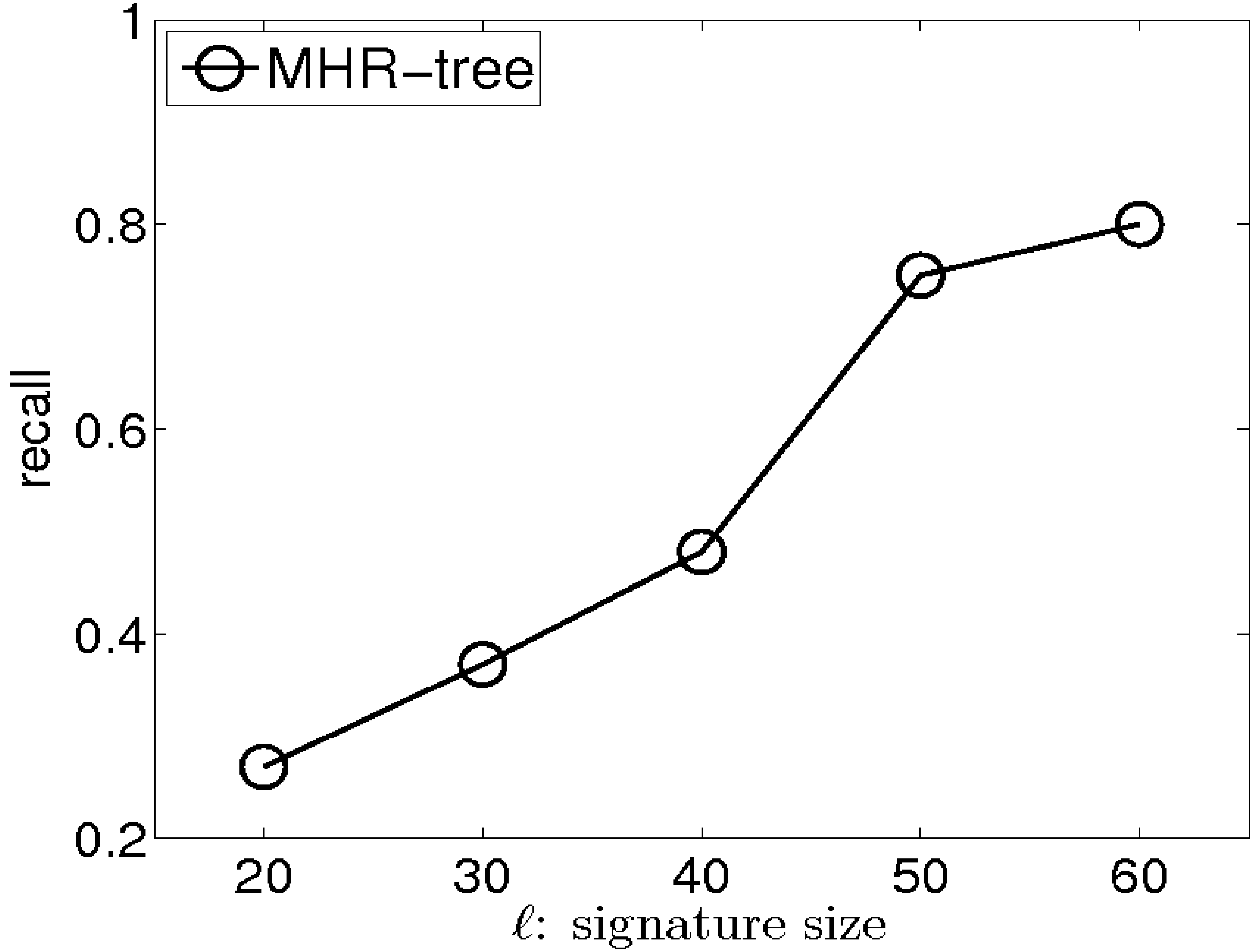

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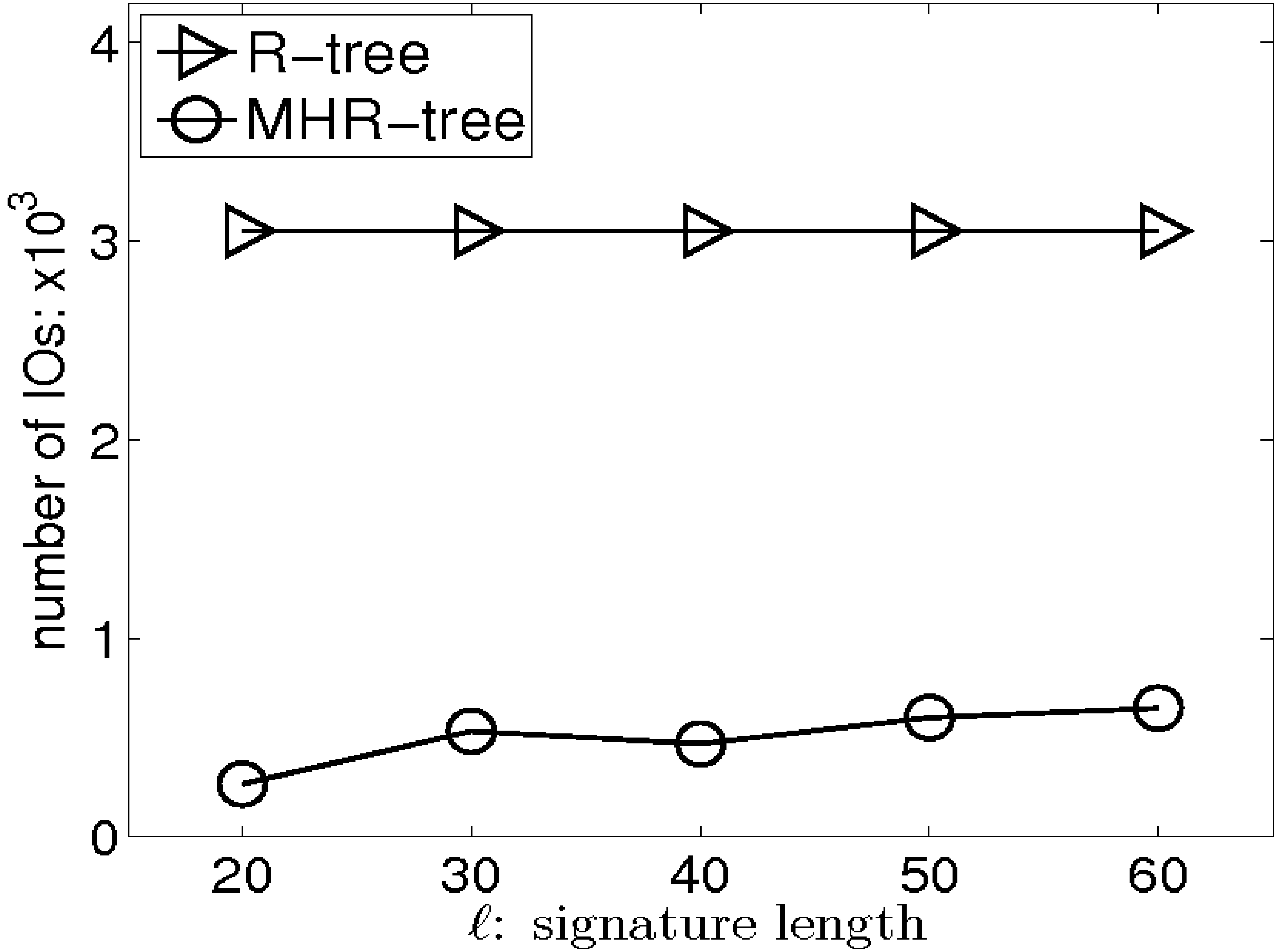
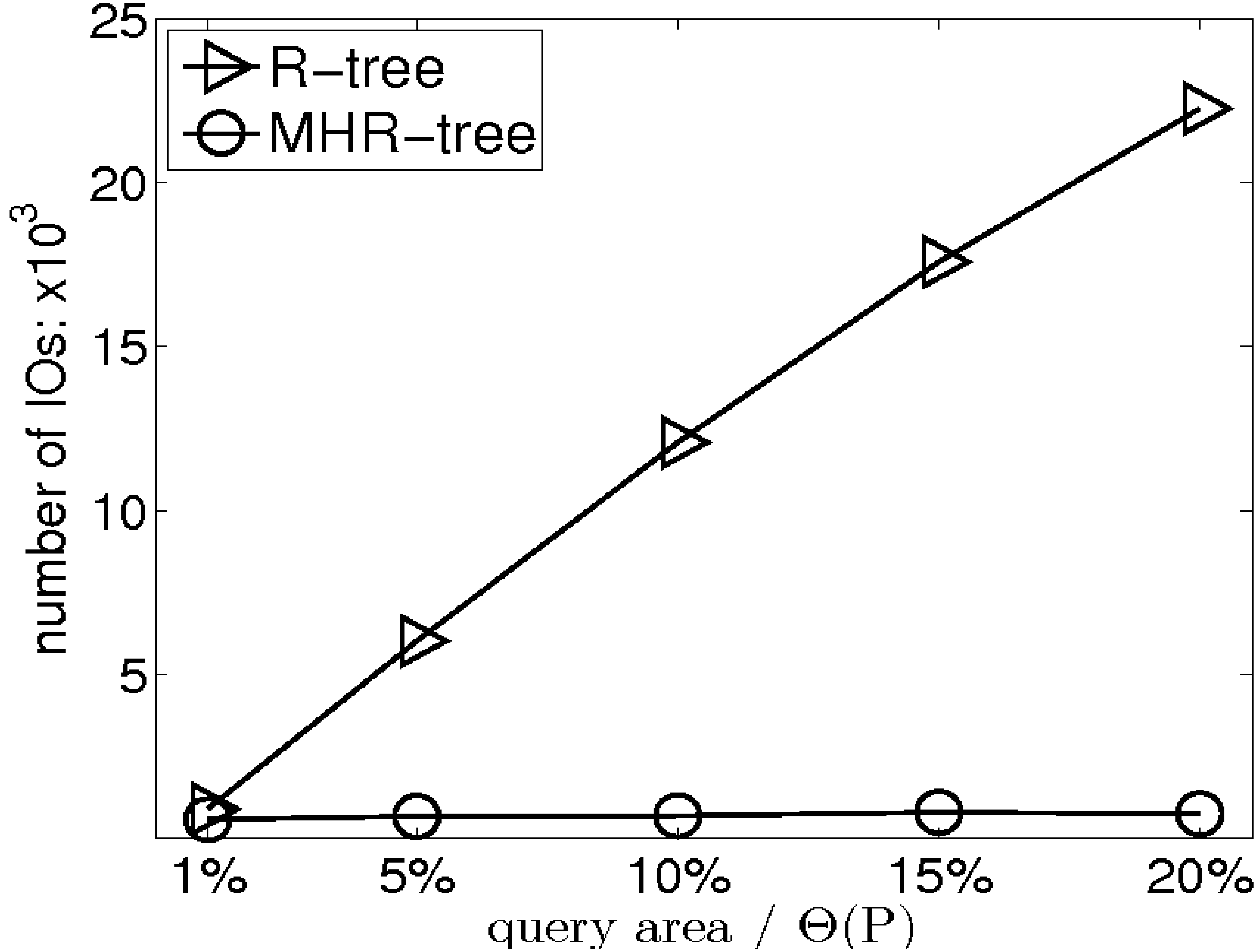


SAS range queries: query performance



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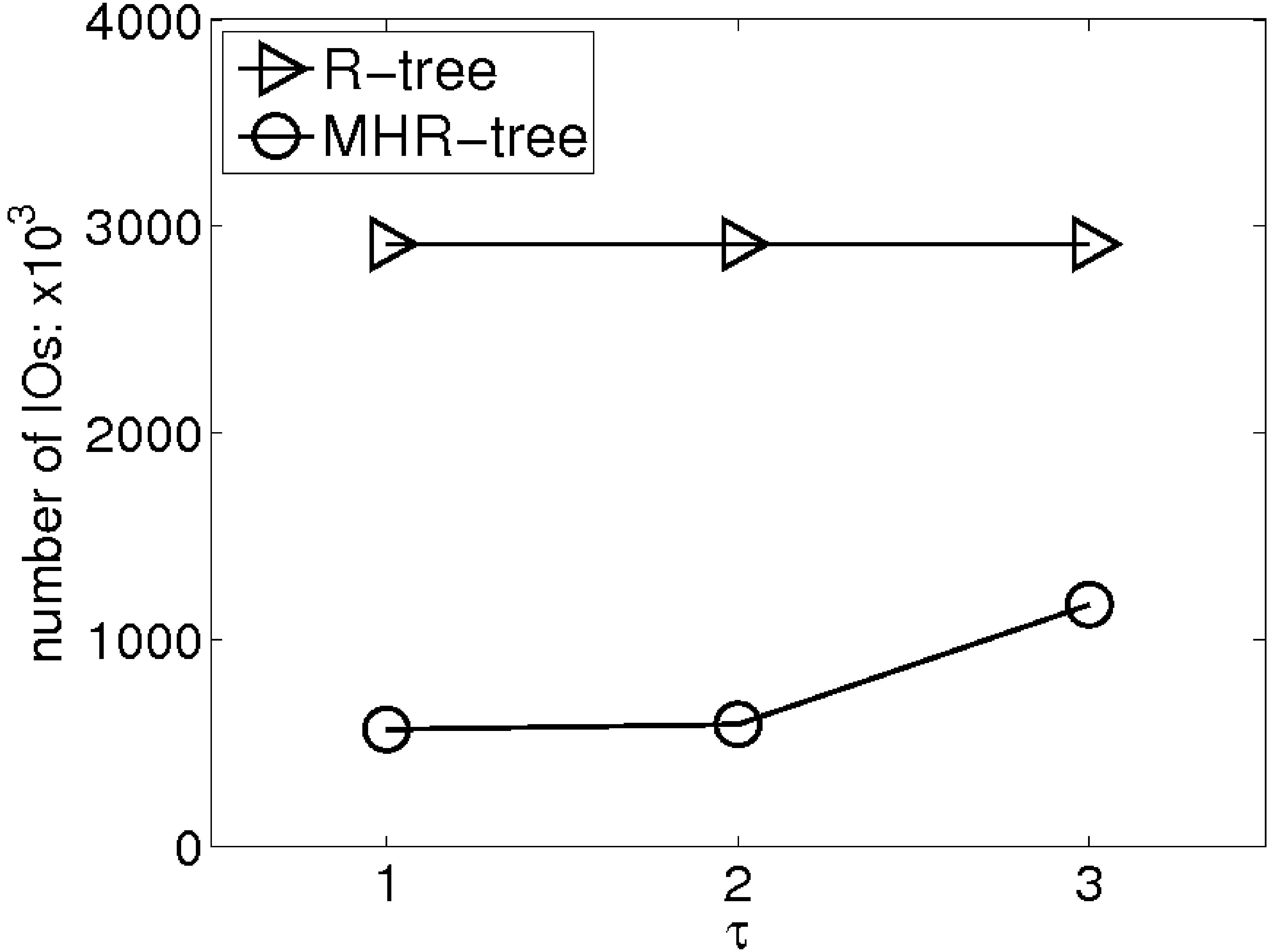
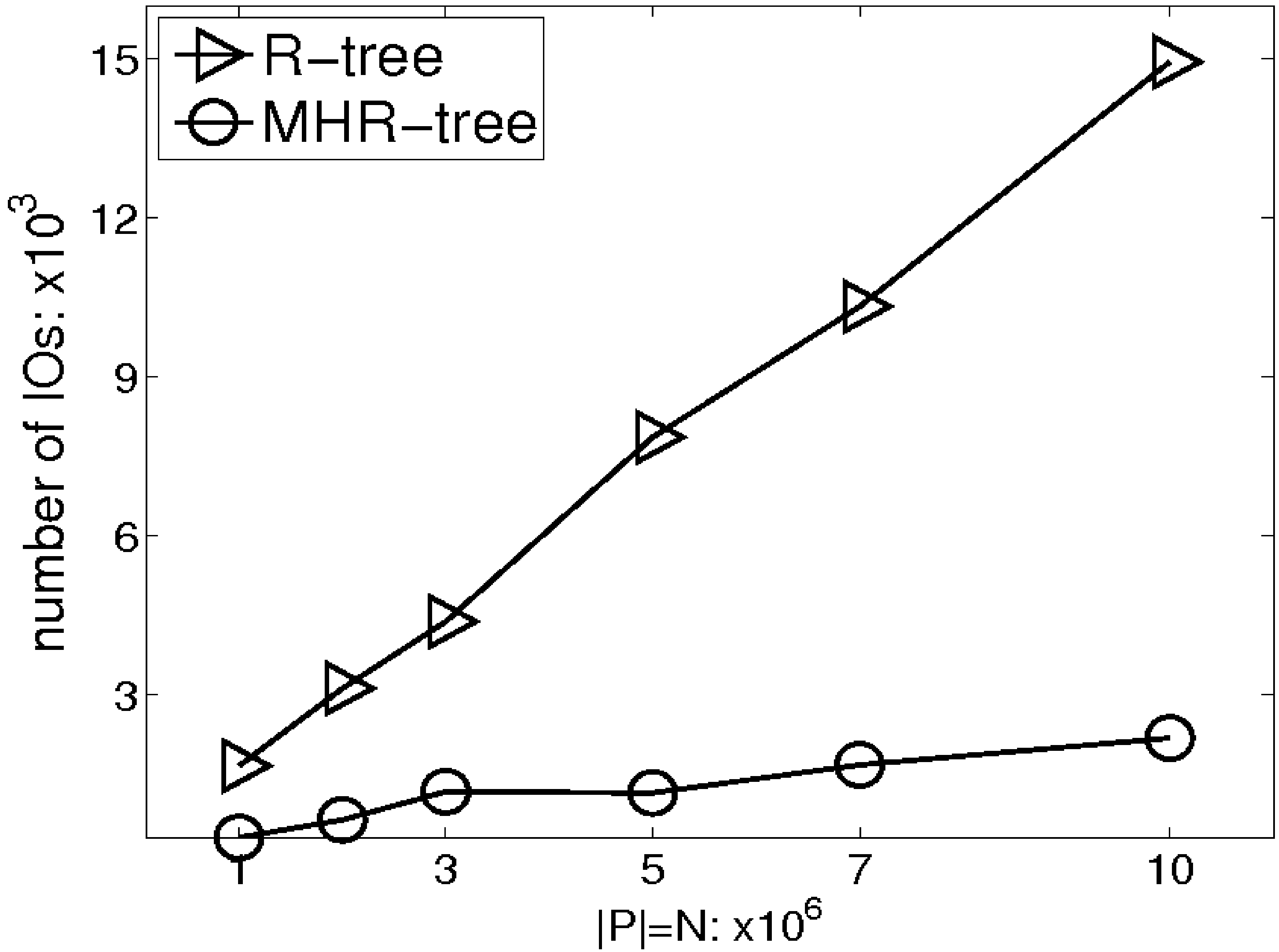


SAS range queries: query performance



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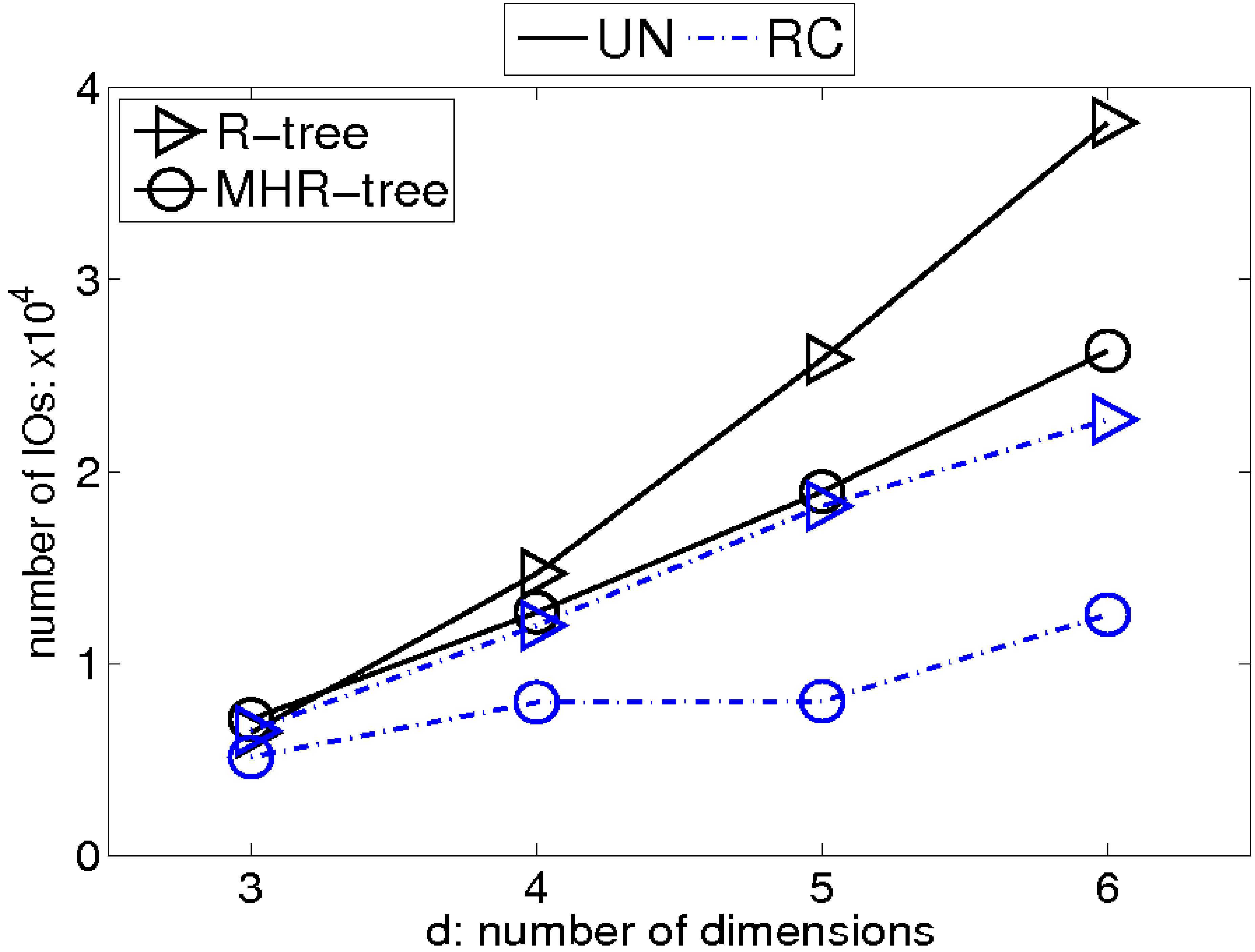
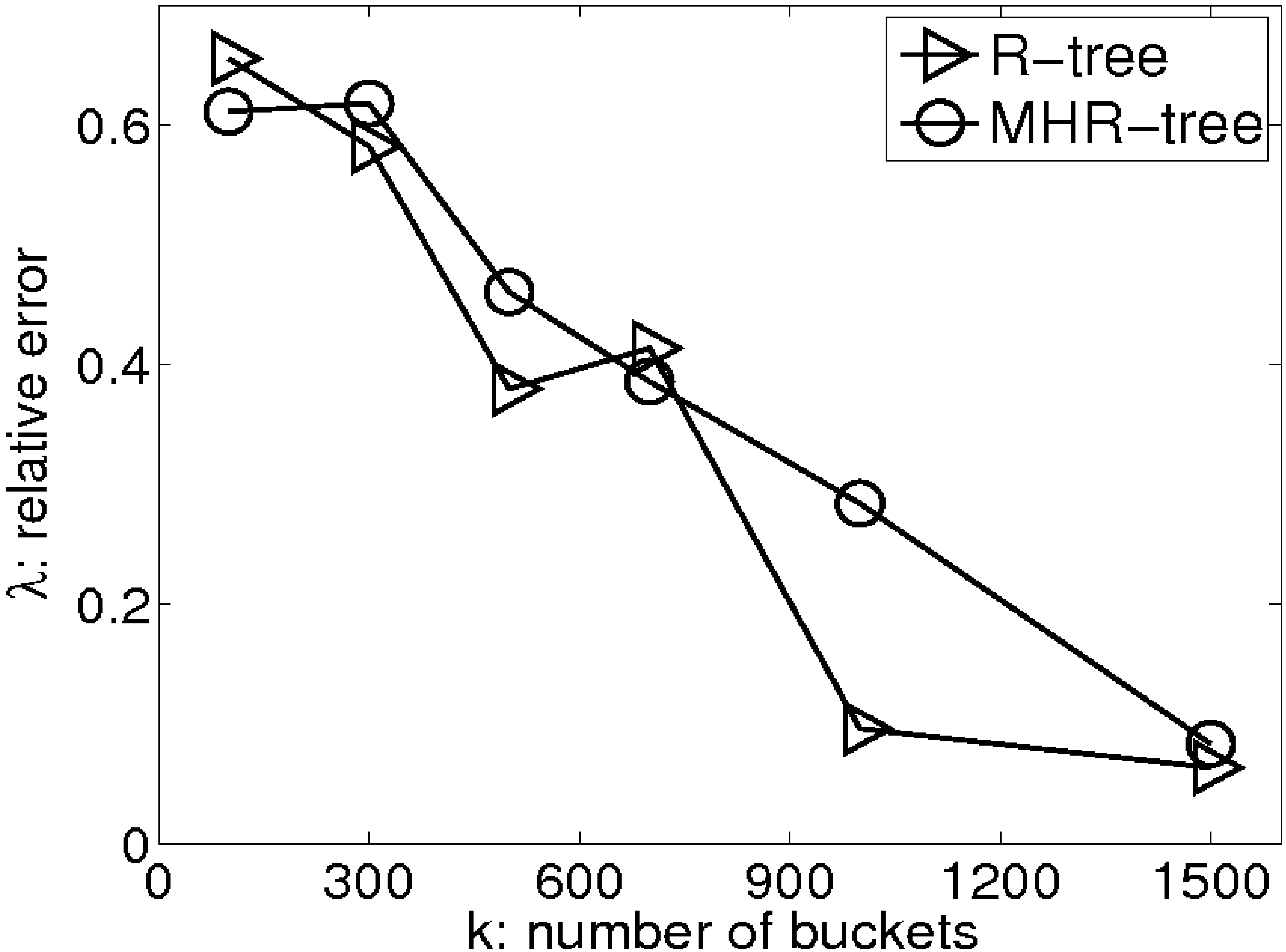
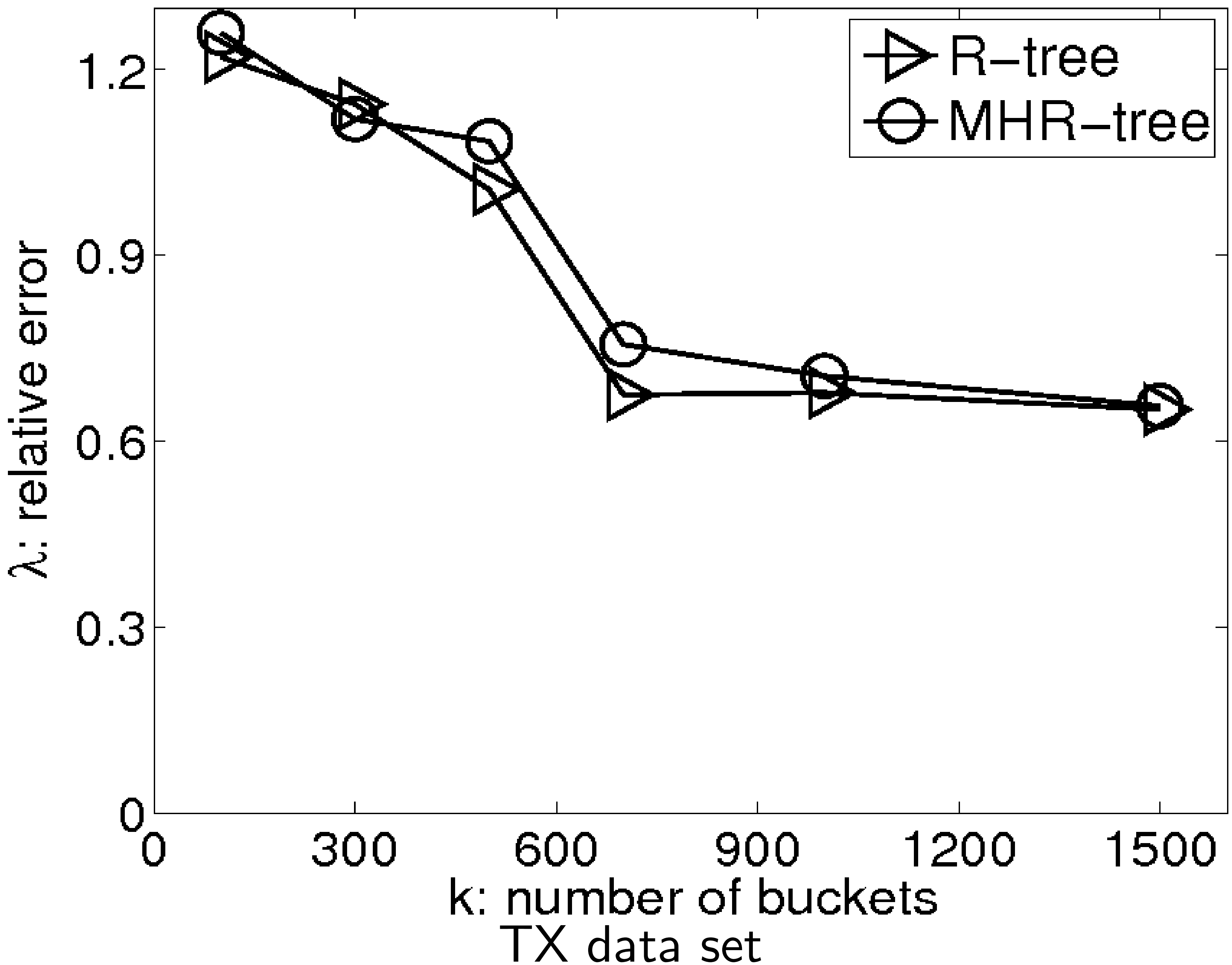


Selectivity estimation: relative errors

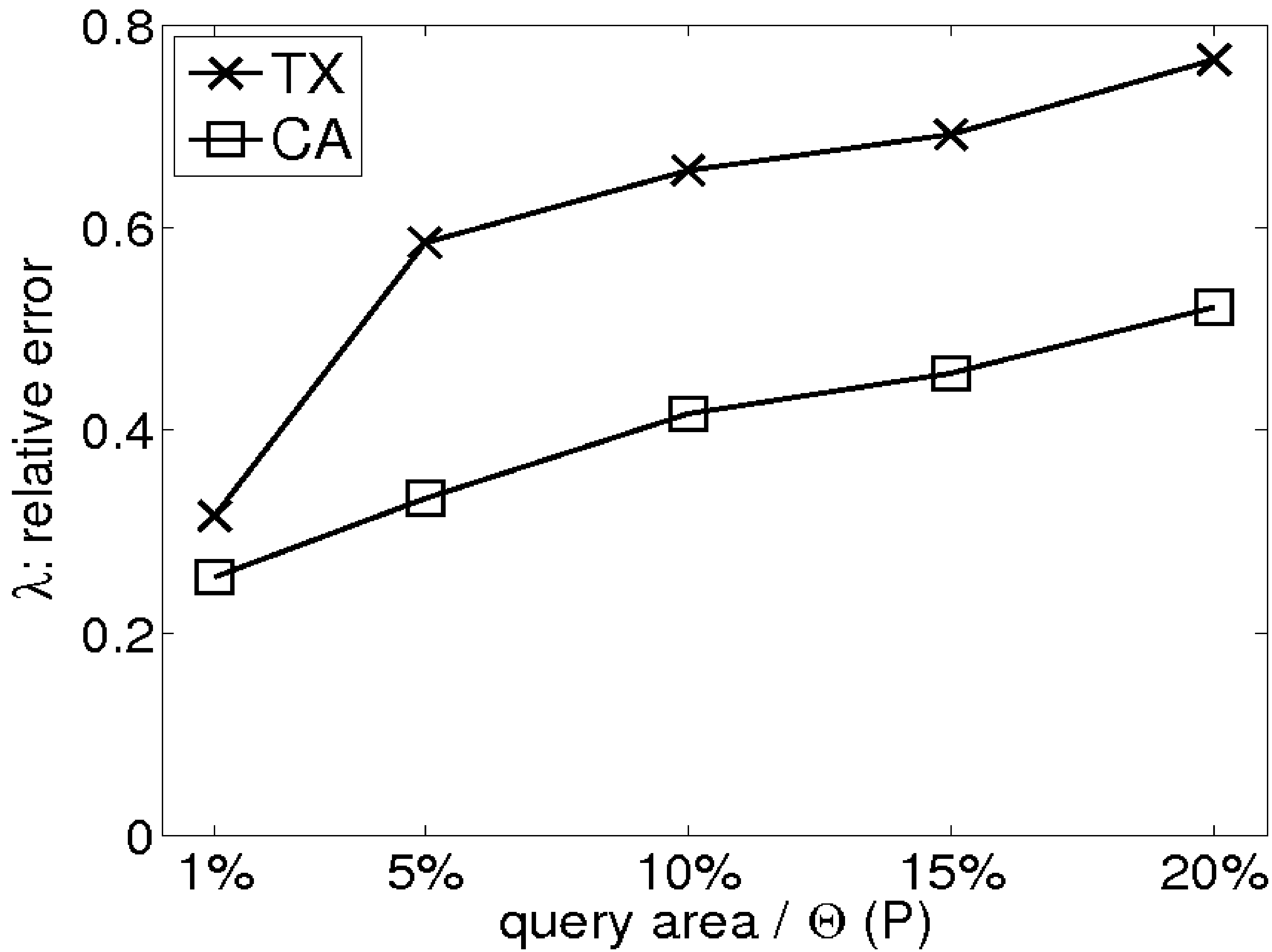


CA data set

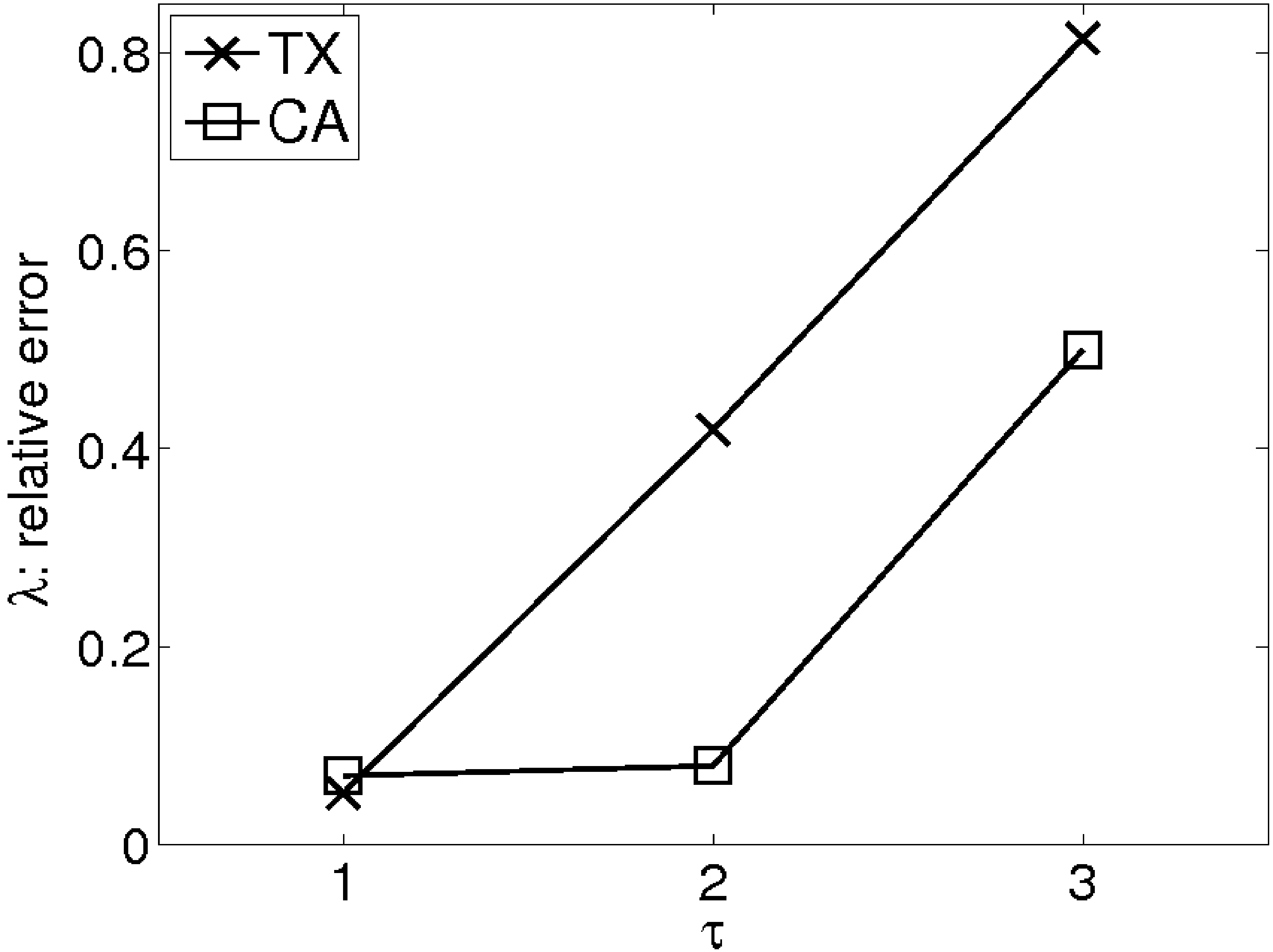
Selectivity estimation: relative errors



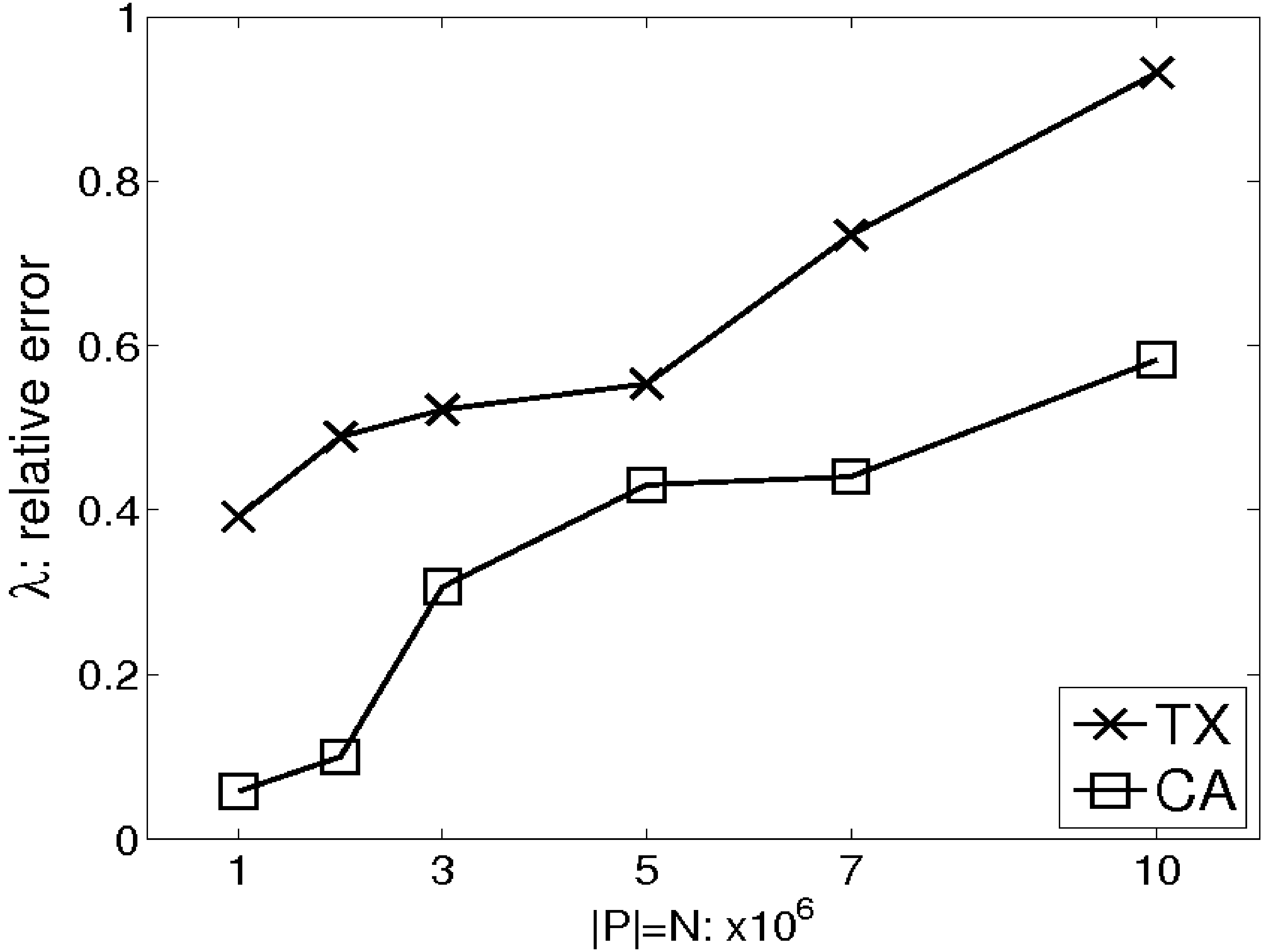
Selectivity estimation: relative errors



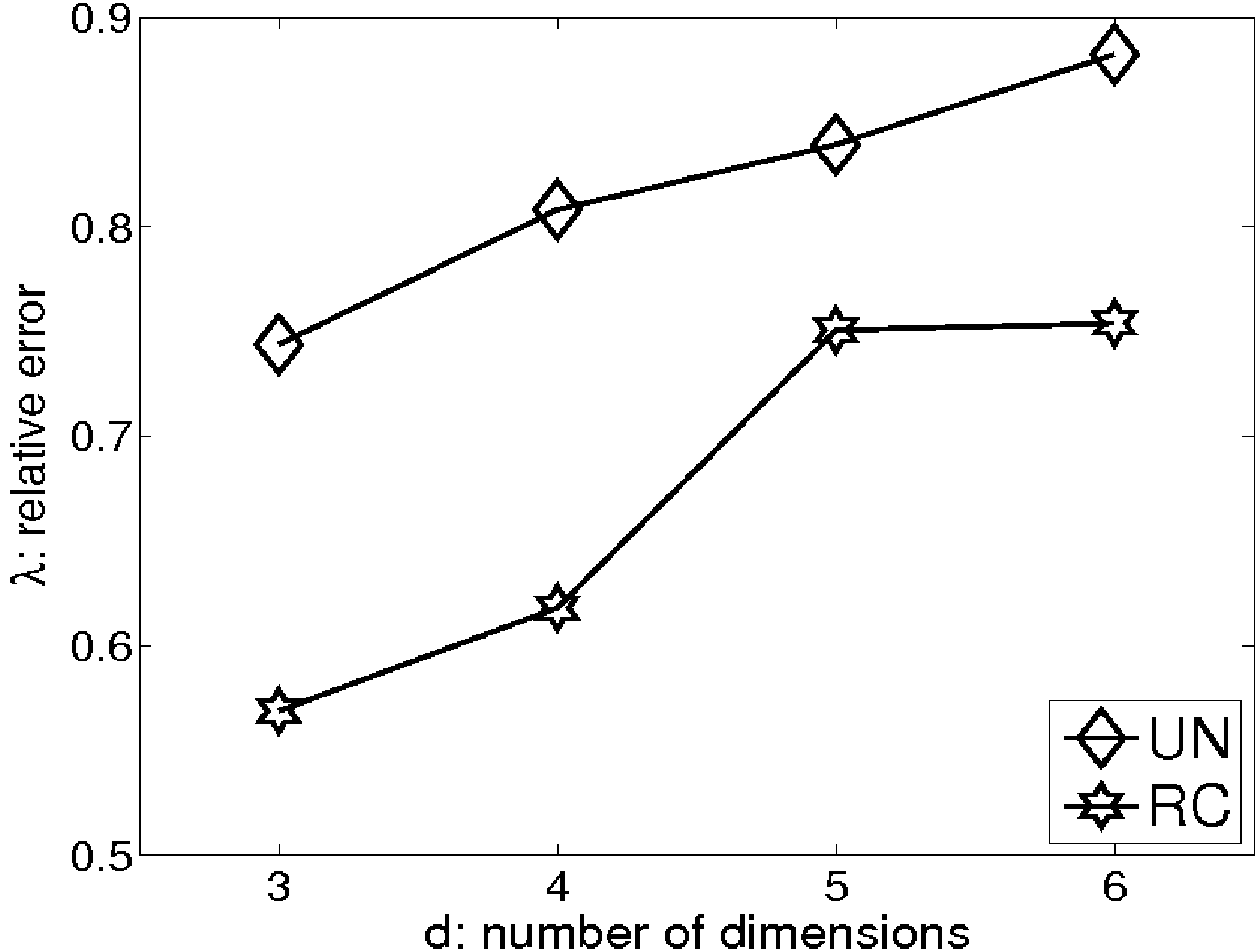
Selectivity estimation: relative errors



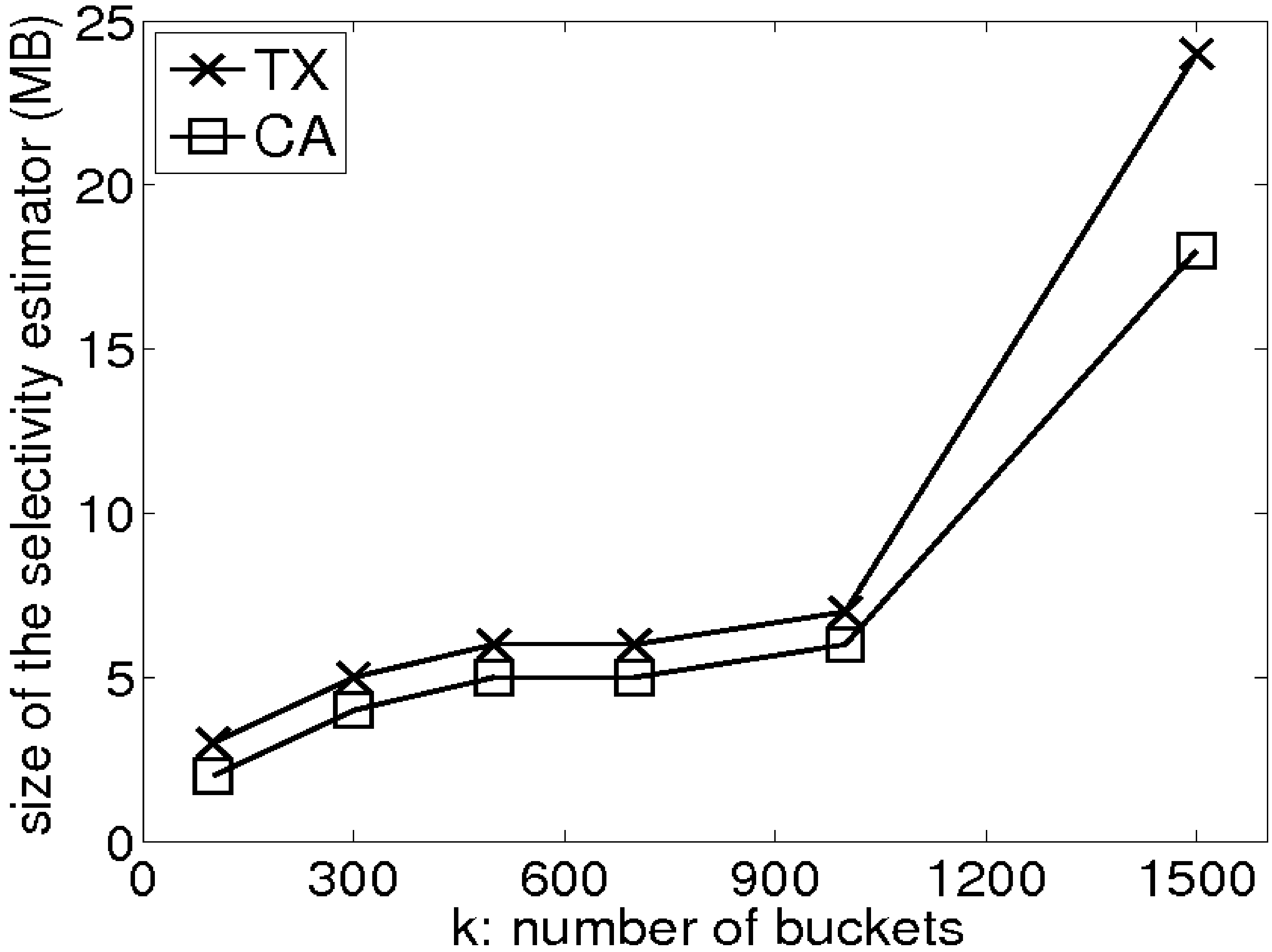
Selectivity estimation: relative errors



Selectivity estimation: relative errors



Selectivity estimation: cost of the adaptive estimator



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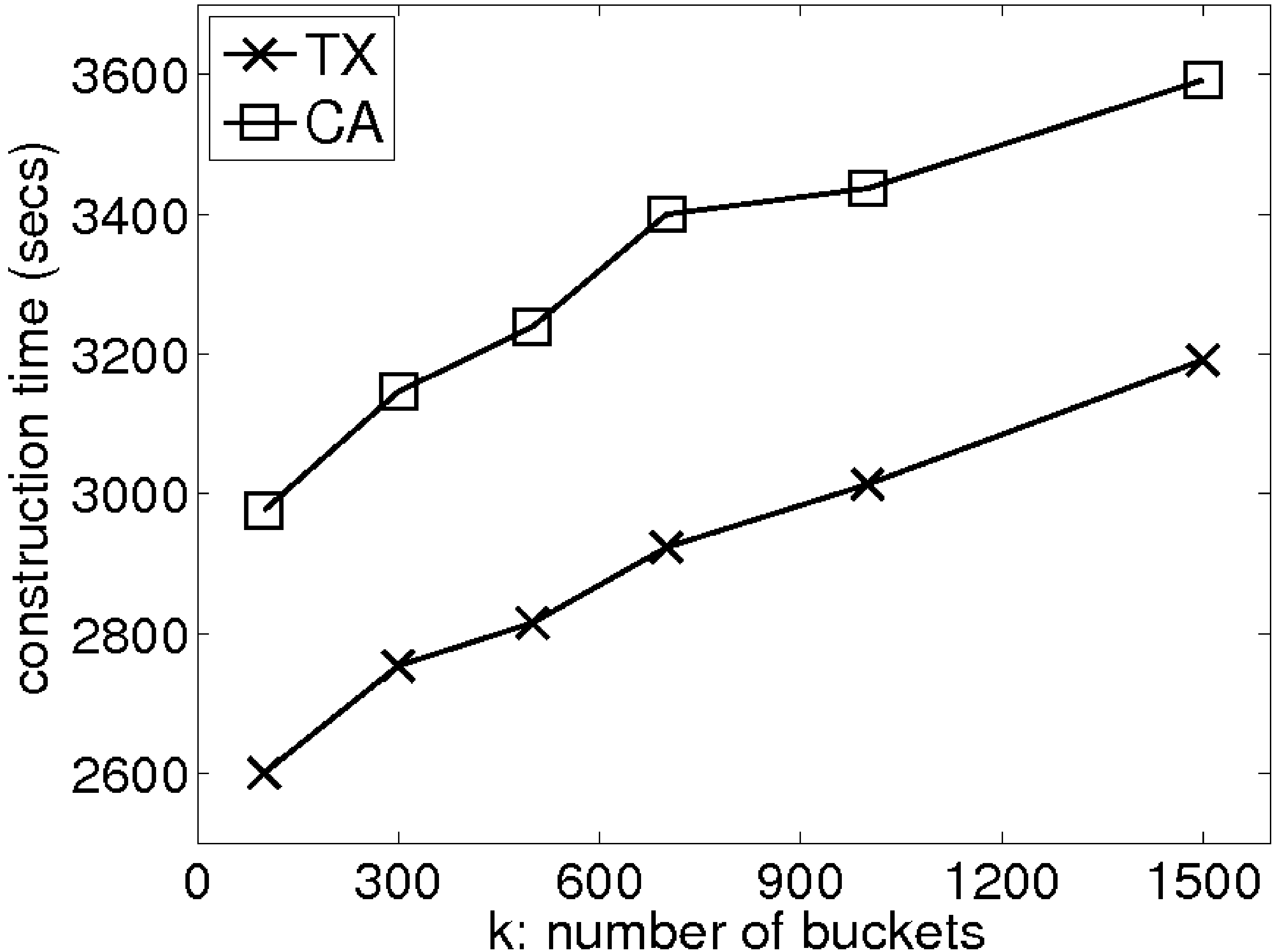

Conclusions

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- We designed MHR-tree for spatial approximate string queries.
- We designed novel selectivity estimator for SAS range queries, which take into account both the spatial and string distributions.
- Future work includes examining spatial approximate sub-string queries, and using the KMV synopsis to improve the performance.

The End

THANK YOU

Q and A