CSE599d: Advanced Query Processing

Lecture 12: Modern Approaches to Yannakakis' Algorithm

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Announcements

- HW3 due: Friday Feb. 27

Review of YA

Acyclic Query

Q is acyclic if it admits a join tree, which is a tree T where:

- The nodes in T are in 1-1 correspondence with the atoms in Q.
- T satisfies the running intersection property: for any variable, the set of nodes that contain it forms a connected component.

YA for a Boolean Query

Choose a root of the join tree.

- Traverse the tree bottom-up and set $R_i := R_i \ltimes R_{\texttt{child}(i)}$.

$R_{\texttt{root}} = \emptyset$ then return FALSE. Otherwise return TRUE.

Runtime: $O(|\texttt{IN}|)$

Semijoin Reduction Algorithm

Yannakakis' algorithm for full semi-join reduction of an acyclic query Q.

- Traverse the tree bottom-up and set $R_i := R_i \ltimes R_{\texttt{child}(i)}$.
- Traverse the tree top-down and set $R_i := R_i \ltimes R_{\texttt{parent}(i)}$.

Runtime: $O(|\texttt{IN}|)$

YA for a Full Conjunctive Query

Phase 1: Semijoin Reduction.

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Phase 2: Join Computation. Initialize $\text{Out}_0 := \{()\}$ (empty tuple).

- Traverse the tree top-down and set $\text{Out}_i := \text{Out}_{i-1} \bowtie R_i$.

Return Out_n.

Runtime: $O(|\texttt{IN}| + |\texttt{OUT}|)$

YA for a Full Conjunctive Query

Phase 1: Semijoin Reduction.

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Runtime: $O(|\texttt{IN}| + |\texttt{OUT}|)$

GYO Acyclicity Test (Graham and Yu-Oszoyoglu)

Repeat:

- Remove an isolated variable (i.e. occurs in only one atom).
- Remove an ear (i.e. atom contain in another atom).

Q is a acyclic iff result is one empty edge.

Summary

- YA runs in time $O(|\texttt{IN}| + |\texttt{OUT}|)$.
- Semijoin reduction: first up, then down.
- Only for acyclic queries.
- Most SQL queries in practice are acyclic.

Main attraction today: Query Robustness

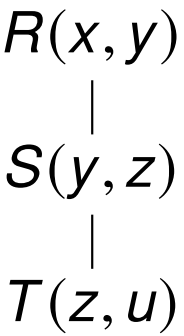
Limitations of Yannakakis' Algorithm

Limitations

- Requires additional (semi)-joins: joins are expensive!

- Requires a rigid join order.

Additional Joins



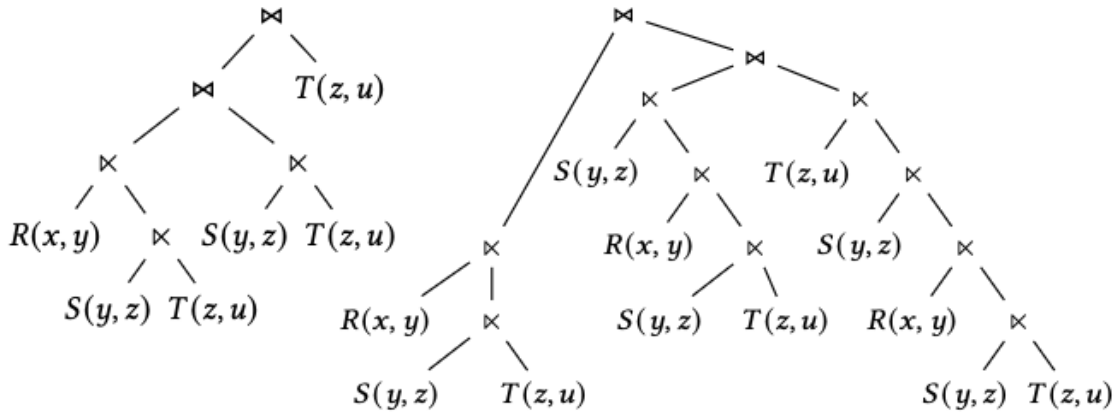
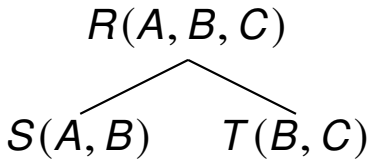


Figure 2: Semijoin plans induced by YA on join tree J_3 (Fig. 1a). Left: pass two and three combined. Right: all three passes.

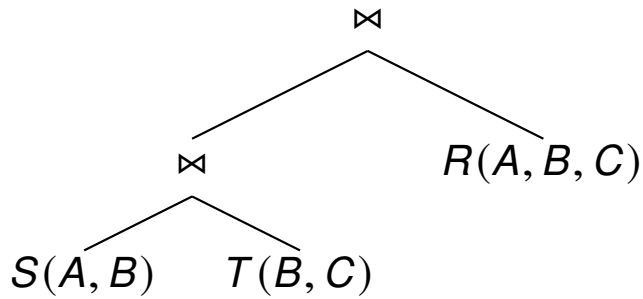
[Bekkers et al., 2025]

Rigid Join Order

Not every query plan without cross-products ensures optimality:



A join tree (acyclic query)



Not optimal [Zhao et al., 2025]:

$R = \{(1,1,1), (2,1,2), \ldots, (n,1,n)\}$
$S = \{(1,1), (2,1), \ldots, (n,1)\}$
$T = \{(1,1), (1,2), \ldots, (1,n)\}$

For optimality: every join must be an edge in the join tree

Approaches to Make YA Practical

- Use Bloom filters [Zhao et al., 2025]
- New physical operators: Lookup and Expand [Birler et al., 2024]
- Nested relations (factorized databases) [Bekkers et al., 2025]

Many others that we won't discuss.

Bloom Filters

Overview

We follow [Zhao et al., 2025]

- Replace semi-joins with a Bloom filter.
- Allow more flexibility for choosing a query plan.

Quick Review

A = array of m bits; $h_1, \ldots, h_k$ independent hash functions.

- Insert(v): set $A[h_i(v)] := 1$, for $i = 1, k$.
- Test(v): return $\bigwedge_{i=1,k} A[h_i(v)]$.
- One-sided guarantee: if Test(v) $= 0$ then v was not inserted.

For optimal FPR ε : $k = \frac{m}{n} \ln 2$ $\varepsilon = \exp\left(-\frac{m}{n} \ln^2 2\right)$

Main Heuristics

Instead of a semijoin: $\boxed{R := R \ltimes S}$

compute a Bloom filter on S, use it to probe R: $\boxed{R := R \ltimes_b S}$

If $|R| \geq |S|$ then $\boxed{R := R \ltimes_b S}$ is better than $\boxed{S := S \ltimes_b R}$

because $\varepsilon = \exp\left(-\frac{m}{n} \ln^2 2\right)$

Choosing a Join Trees

Ideal: all semi-joins are from small to large. Not always possible:

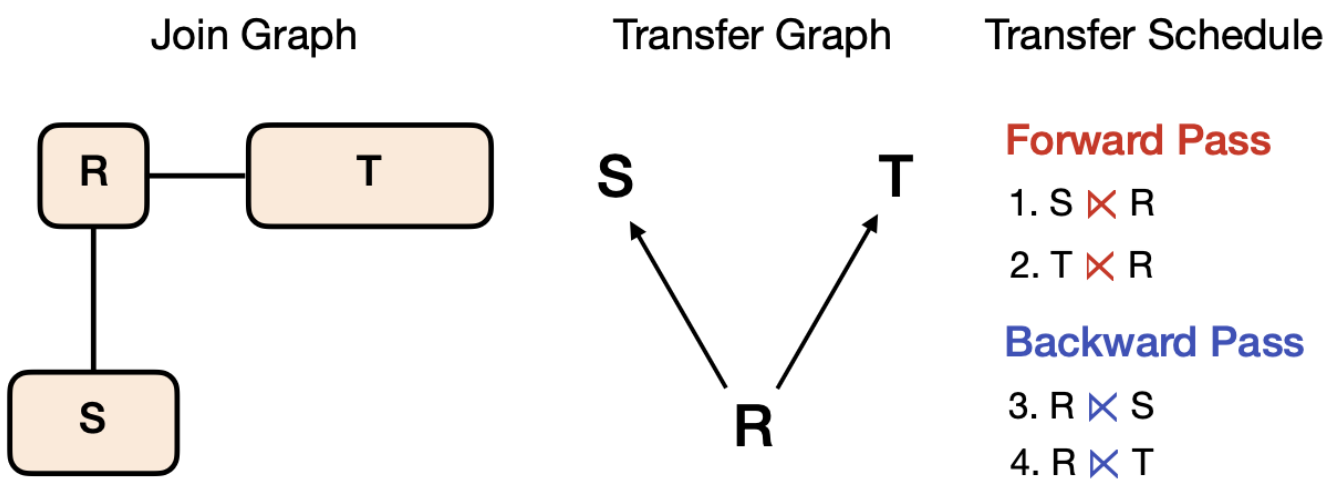


Fig. 2. An example of the `Small2Large` algorithm in the original Predicate Transfer

Alternative Characterization of Join Trees

Let G be the query graph of Q

what is that?

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$$\boxed{w(R,S) = |\text{attrs}(R) \cap \text{attrs}(S)|}$$

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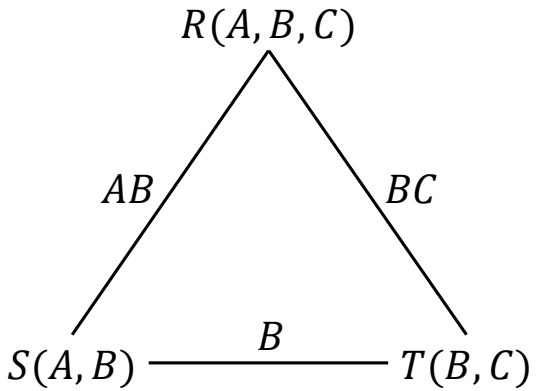

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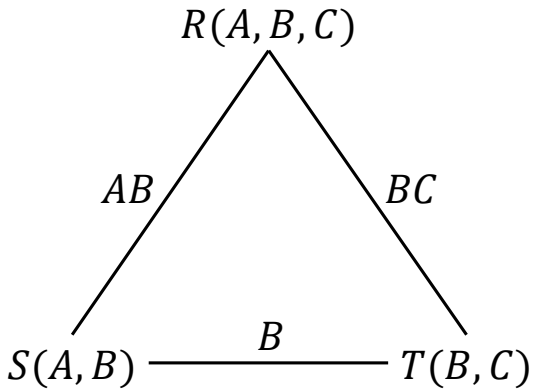
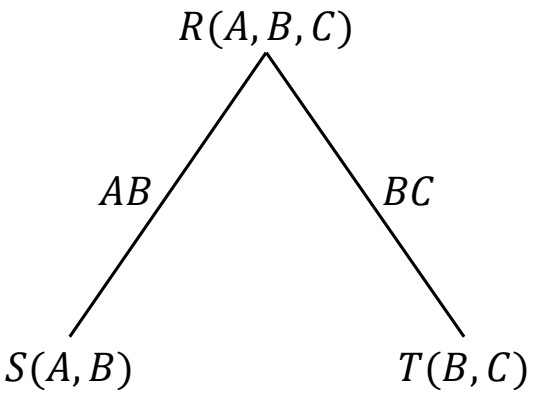


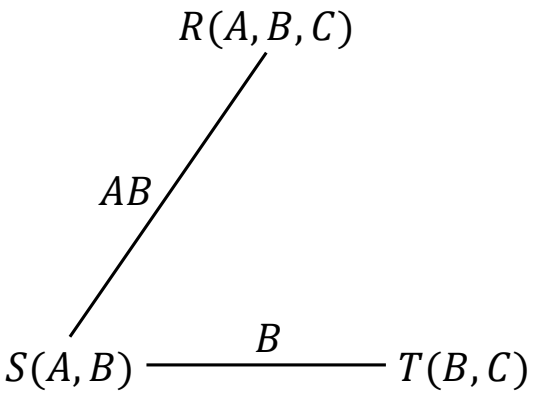
Theorem A tree $T \subseteq G$ is a join tree iff T is a maximal spanning tree of G.

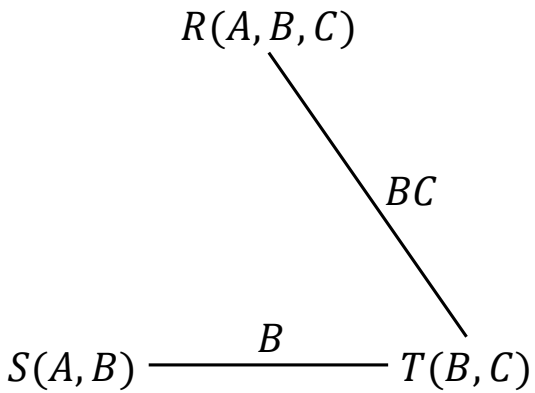
(Proof on next slides)

Proof (in class)

Which trees are join trees, and what are their weights?







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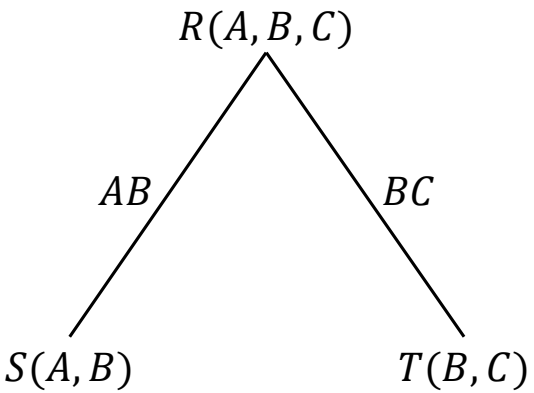

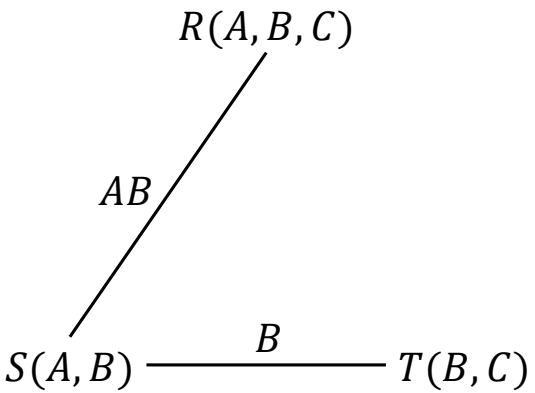

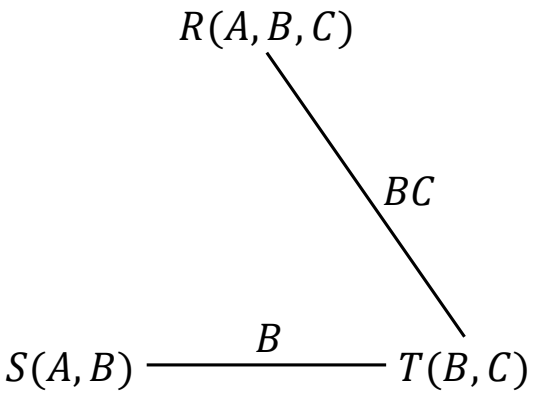

What is the weight of a join tree? of a non-join tree?

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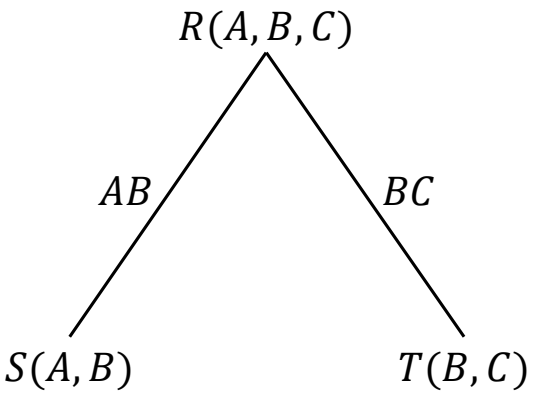

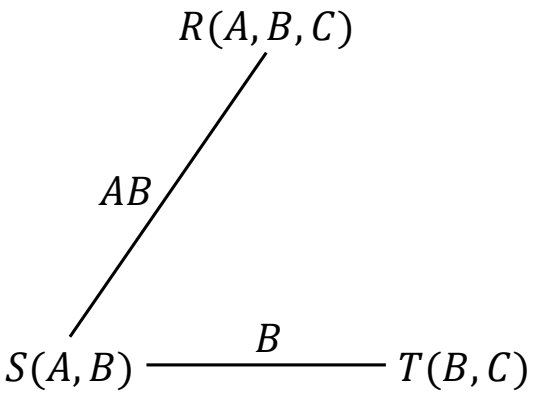

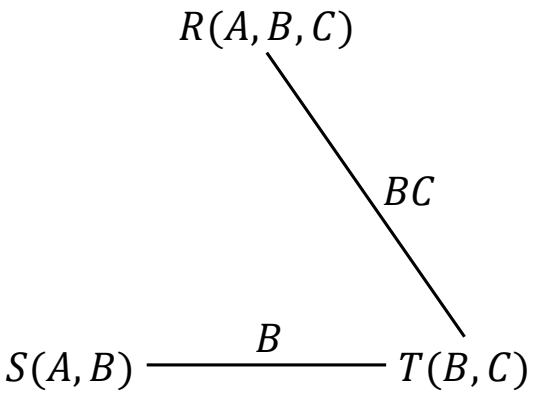

What is the weight of a join tree? of a non-join tree?

$\sum_i \texttt{arity}(R_i) - |\text{Vars}(Q)|$ for JT, strictly smaller otherwise

Choosing a Join Tree

Run Prim's algorithm for computing a maximal spanning tree.
Break ties in favor of larger relations.

Algorithm 1: `LargestRoot`

Input: join graph G_q
Output: tree T

$T \leftarrow \emptyset$; $\mathcal{R} \leftarrow$ all relations; $\mathcal{R}' \leftarrow \{R_{max}\}$;
while $\mathcal{R}' \neq \mathcal{R}$ **do**
  Find an edge $e = \{R, S\} \in E(G_q)$ with the largest weight such that $R \in \mathcal{R} \setminus \mathcal{R}', S \in \mathcal{R}'$. Choose the edge with the largest R to break ties;
  Add e to T with direction from R to S;
  $\mathcal{R}' \leftarrow \mathcal{R}' \cup \{R\}$;
end
return T;

At each tie we can choose between multiple join trees.

Choosing a Query Plan

The standard optimizer searches for an optimal bushy plan.

Problem: not every bushy plan guarantees optimality in the sense of YA.

Need to restrict all subplans to be safe.

Safe Join Order

Q' = a subquery (subset of atoms) of Q.

Q' is safe if for every fully reduced DB, $\boxed{Q'(DB) = \Pi_{\text{attrs}(Q')}(Q(DB))}$

This implies $|Q'(DB)| \leq |Q(DB)|$.

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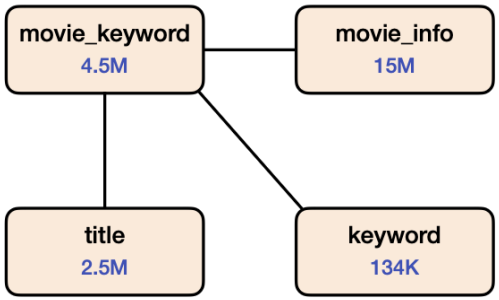
$Q = R(A,B,C) \bowtie S(A,B) \bowtie T(B,C)$, $Q' = S(A,B) \bowtie T(B,C)$ unsafe

We want every subplan to be safe

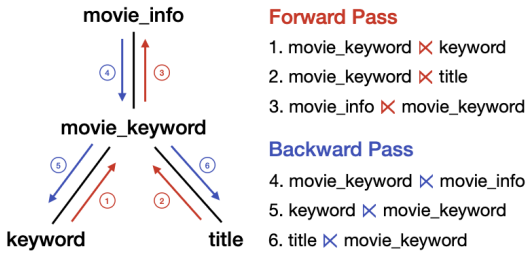
Testing for Safety

- Compute a maximal spanning tree T_0 for Q.
- Compute a maximal spanning tree T' for Q'.
- Extending T' to maximal spanning tree T for Q.
- If weight(T_0) = weight(T) then Q' is safe.

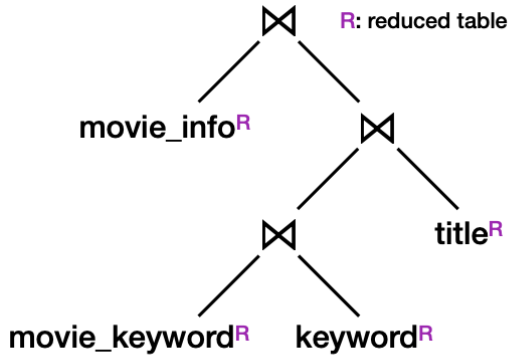
Putting it Together (by Example Only)



(a) Join Graph

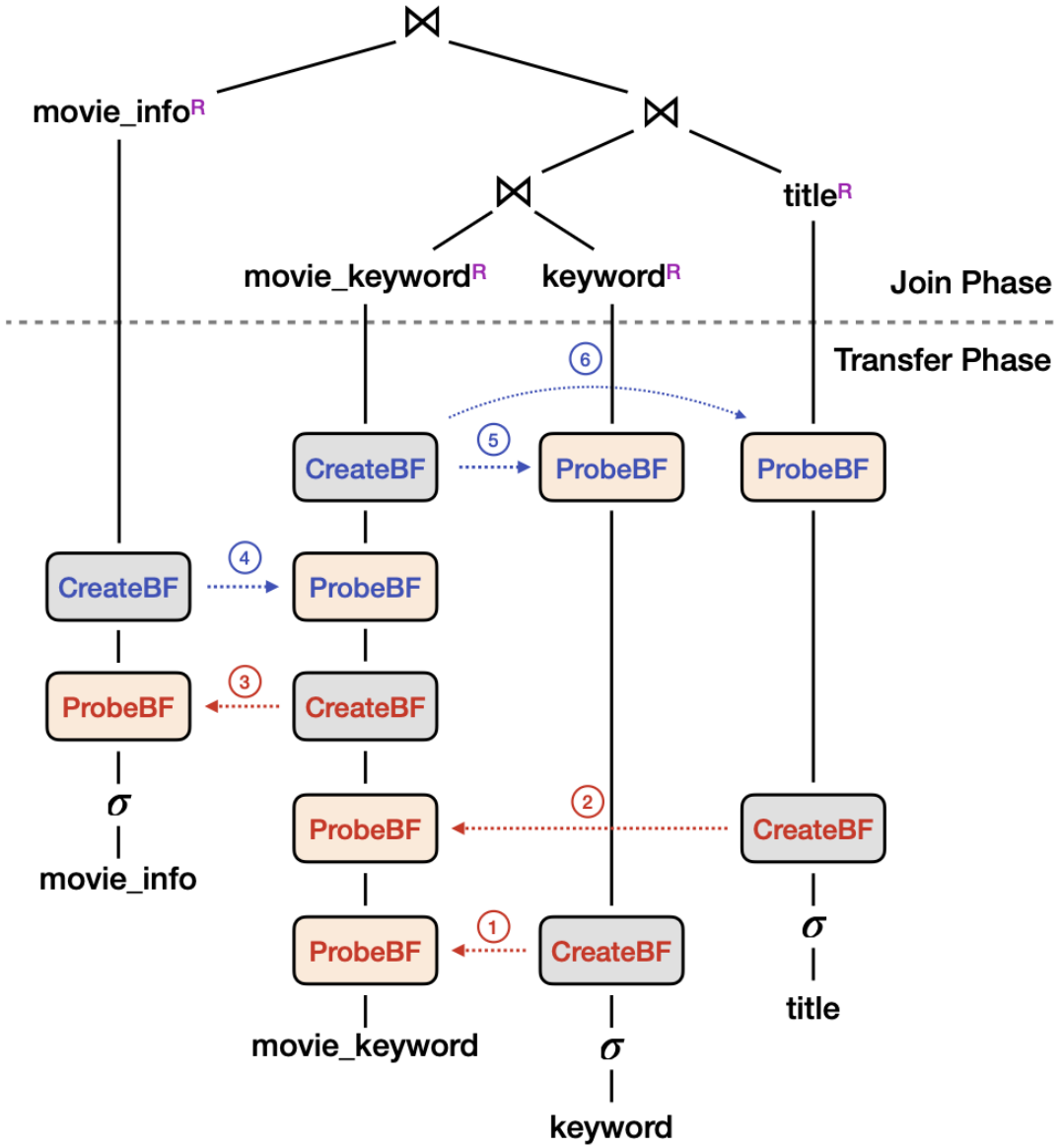


(b) Semi-Join Phase



(c) Join Phase

Putting it Together (by Example Only)



Discussion

- Bloom filter approach to YA: simple idea, more efficient than semijoins.
- But requires heavy engineering to incorporate in existing query engines.

Lookup and Expand

Overview

Goal: implement YA with minimum changes to an existing engine

[Birler et al., 2024]

Review: Hash-Join

```
1  # Hash table build
2  ht = {}
3  for k, v in buildInput:
4      ht[k] = v
5
6  # Hash table probe
7  for k, v in probeInput:
8      iterator = ht.find(k) # Lookup
9      if not iterator.done():
10         do: # Expand
11             produce(k, *iterator)
12             iterator.step()
13         while not iterator.done()
```

The probe phase has two steps: Lookup and Expand

Make them separate operators!

Lookup and Expand

Lookup returns pointer to the hash table entry, or NULL

Expand traverses the list at that entry.

```
1  def lookup_consume(produce, tuple, hashTable):
2    # Look for the key in the hash table
3    iterator = hashTable.find(tuple.key)
4    if iterator.done():
5      return
6    # Return tuple and iterator over matches
7    produce(tuple, iterator)
8
9  def expand_consume(produce, tuple):
10   # Extract the iterator from the tuple
11   currentMatch = tuple.iterator
12   do: # Loop over all matches
13     produce(tuple, *currentMatch)
14     currentMatch.step()
15   while not currentMatch.done()
```

(This is the push-based API from the Query Compiler paper in 544)

Examples

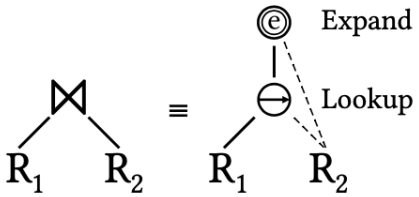


Figure 2: Binary hash join and equivalent Lookup & Expand.

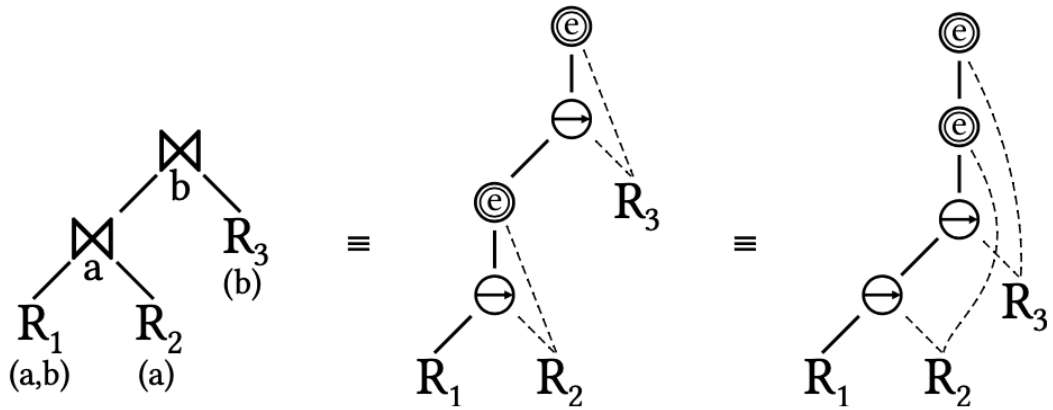


Figure 3: Threeway join, equivalent Lookup & Expand, and Lookup pushdown.

Example

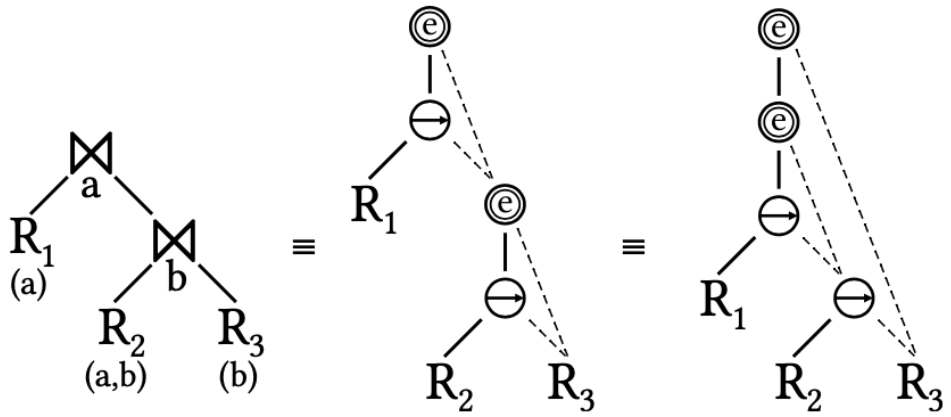


Figure 4: Threeway join, equivalent Lookup & Expand, and Expand pullup.

Discussion

- Lookup/Expand become independent operators, allows most freedom for the query optimizer.

- May still need to impose restrictions if we want the guarantees of YA.

Nested Relations

Main Idea

Represent the result of a join in a nested relations.

This idea is called factorized databases [Olteanu and Závodný, 2015]

This postpones the cross products inherent in a join, potentially leading to the benefit of YA.

Nested Relations

Nested schema: set of attributes and/or nested schemas.

Nested relation with schema $\{x, \{y\}, \{u, \{v\}\}\}$

x	$\{y\}$	$\{u, \{v\}\}$
1	10 20	a | m n b | k n p
2	...	

Nested Relational Algebra is Relational Algebra plus two operators:

$\texttt{nest}_x : \{x, y\} \rightarrow \{x, \{y\}\}$ a.k.a. `group-by` or γ.

$\texttt{unnest}_y : \{x, \{y\}\} \rightarrow \{x, y\}$ a.k.a. μ

Example: Using NRA for YA

$$R(x,y) \bowtie S(y,z) \bowtie T(z,u)$$

Several factorized representations are possible for the output:

$$\begin{aligned} P(y,z,\{u\}) &:= S(y,z) \ltimes_z \mathtt{nest}_z T(z,u) \\ F(x,\{y,\{z,\{u\}\}\}) &:= R(x,y) \ltimes_y \mathtt{nest}_y(P) \end{aligned}$$

For the query answer, unnest F.

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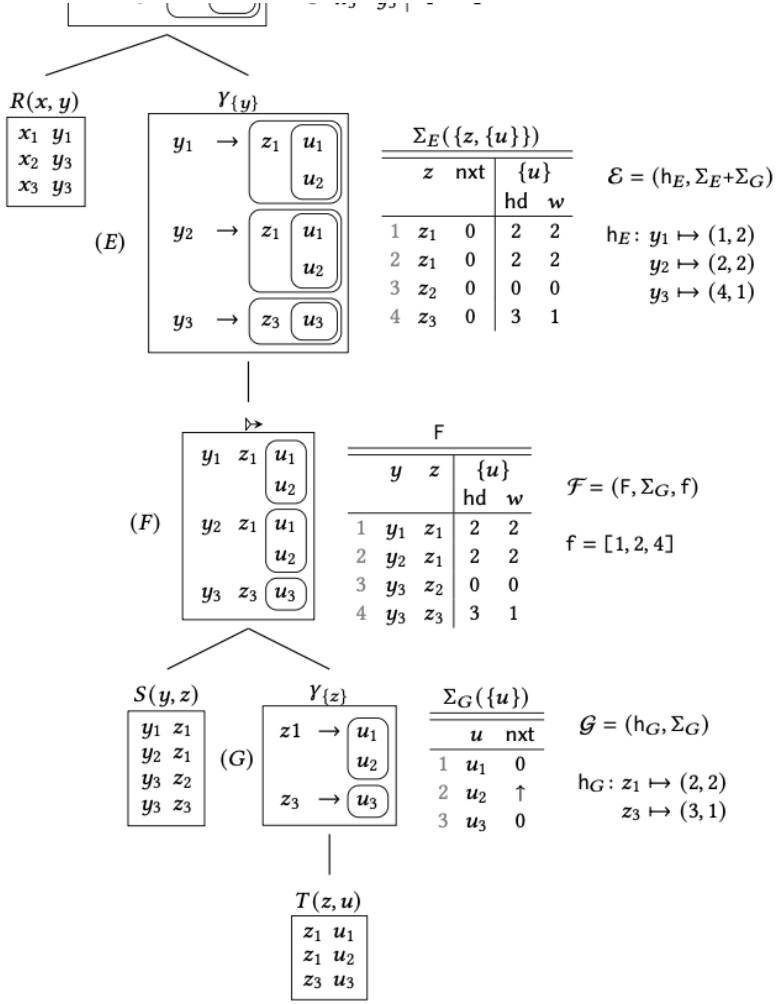
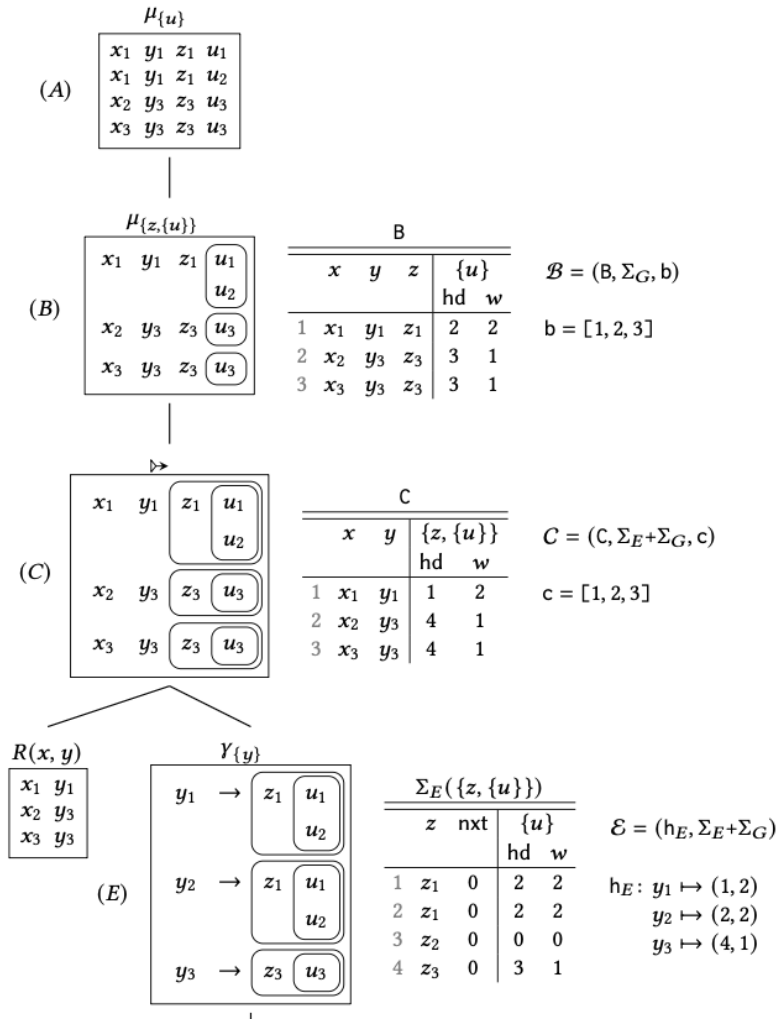
$$F(x,\{y,\{z,\{u\}\}\}) := R(x,y) \ltimes_y \texttt{nest}_y(P)$$

$$P(y,z,\{u\}) := [\text{same}]$$
$$F(\{x\},y,\{z,\{u\}\}) := \texttt{nest}_y R(x,y) \ltimes_y \texttt{nest}_y P$$

For the query answer, unnest F.

Example: Using NRA for YA





Main Takeaways

- Renewed interest in YA comes from the quest for robust query processing: less sensitive to cardinality estimation erros.

- Surprisingly, SQL Server already supports YA, without knowing!
  hfill[Zhao et al., 2026]


Bekkers, L., Neven, F., Vansummeren, S., and Wang, Y. R. (2025).
Instance-optimal acyclic join processing without regret: Engineering the yannakakis algorithm in column stores.
Proc. VLDB Endow., 18(8):2413–2426.


Birler, A., Kemper, A., and Neumann, T. (2024).
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Proc. VLDB Endow., 17(11):3215–3228.


Olteanu, D. and Závodný, J. (2015).
Size bounds for factorised representations of query results.
ACM Trans. Database Syst., 40(1):2:1–2:44.


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I can't believe it's not yannakakis: Pragmatic bitmap filters in microsoft SQL server.
In 16th Conference on Innovative Data Systems Research, CIDR 2026, Chaminade, CA, USA, January 18-21, 2026. www.cidrdb.org.


Zhao, J., Su, K., Yang, Y., Yu, X., Koutris, P., and Zhang, H. (2025).
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Proc. ACM Manag. Data, 3(3):146:1–146:28.