On Join Sampling and the Hardness of Combinatorial Output-Sensitive Join Algorithms

Based on the work of Shiyuan Deng, Shangqi Lu, and Yufei Tao (PODS 2023)

Presented by Jinchao Huang

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INTRODUCTION & MOTIVATION

WHAT IS A JOIN OPERATION?

- A fundamental operation in relational databases.
- Combines tuples from a set Q of multiple relations based on common attribute values.
- Example: Suppose $Q = \{R_{AB}, R_{BC}, R_{CA}\}$, then $Join(Q)$ is the set of all combinations of (a, b, c) where (a, b) is in R_{AB}, (b, c) is in R_{BC}, and (c, a) is in R_{CA}.

R_{AB}

A	B
0	1
0	2
1	1
2	1

R_{BC}

B	C
1	1
1	2
2	0
2	1

R_{CA}

C	A
0	1
1	0
2	1
2	2

Join(Q)

A	B	C
0	1	1
0	2	1
1	1	2
2	1	2

THE CHALLENGE: THE OUTPUT SIZE EXPLOSION

Joins are a primary performance bottleneck in database systems.

- The size of the join result, denoted OUT, can be massive.
- The theoretical upper bound on the output size is given by the AGM bound.
- In the worst case, for an input of size $\text{IN} = \sum |R|$:

$$\text{OUT} = \Omega(\text{IN}^{\rho^*})$$

  where ρ^* is the *fractional edge covering number* of the join query, a constant ≥ 1.
- For a simple 3-relation join, ρ^* can be 1.5. For more complex joins, it can be much larger.
- Even just writing the output can take $\Omega(\text{IN}^{\rho^*})$ time, which is prohibitive for large IN.

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MOTIVATION: WHY SAMPLE FROM A JOIN?

Many applications do not need the full join result. A small set of random samples is often sufficient.

- **Approximate Query Processing:** Estimate aggregates like `SUM(sales)` or `AVG(price)` over a large join result quickly.
- **Data Exploration & Visualization:** Get a quick "feel" for the data distribution without waiting for the full join.
- **Machine Learning:** Use samples as a training set for models.
- **Fair Representative Reporting:** Select a few diverse tuples to represent the overall distribution.

The Join Sampling Problem

Design a data structure to support *sampling query*, which extracts a uniform sample from the join result Join(Q). Additionally, the sample returned by each query must be independent.

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STATE OF THE ART VS. THE CONTRIBUTION

Let IN be the input size, OUT be the output size, and ρ^* be the fractional edge covering number.

- **State of the Art** [Chen and Yi, ICDT'20]:
  - After $\tilde{O}(\text{IN})$ preprocessing, a sample can be drawn in time:

$$\tilde{O}(\text{IN}^{\rho^*+1}/\max\{1, \text{OUT}\})$$

  - They posed it as an open problem to remove the extra factor of IN.
- **The Result** [Deng, Lu, and Tao, PODS'23]:
  - An $\tilde{O}(\text{IN})$-space fully dynamic data structure that supports tuple insertions/deletions in $\tilde{O}(1)$ time and draws a sample in time:

$$\tilde{O}(\text{IN}^{\rho^*}/\max\{1, \text{OUT}\}) \quad \text{w.h.p.}$$

  - A justification for the $O(IN^{\rho^*})$ running time of the worst-case optimal join evaluation algorithms even when $OUT << \text{IN}^{\rho^*}$.

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OUTLINE OF THE TALK

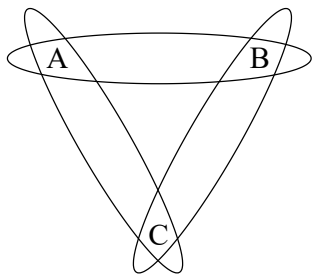
1. **Preliminaries:** The AGM Bound
   - A powerful tool for analyzing the maximum size of a join result.
2. **Core Technique:** The AGM Split Theorem
   - A geometric approach to recursively partition the data space.
3. **The Sampling Algorithm**
   - How to use the split theorem to build a fast sampling algorithm.
4. **Hardness Results & Conclusion**
   - Why the result is likely the best possible for combinatorial algorithms.

PRELIMINARIES: THE AGM BOUND

THE SCHEMA GRAPH AND FRACTIONAL EDGE COVERS

We can model a join query Q as a hypergraph $G = (\mathcal{X}, \mathcal{E})$.

- **Vertices** $\mathcal{X}$: The set of all attributes in the join (e.g., A, B, C).
- **Hyperedges** $\mathcal{E}$: The schema of each input relation (e.g., $\{A, B\}$, $\{B, C\}$, $\{C, A\}$).



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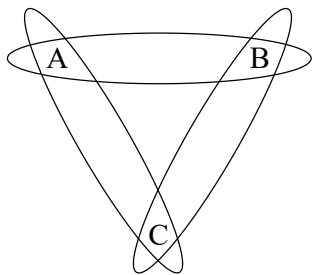

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THE AGM BOUND

Theorem (AGM Bound, Atserias et al. 2008)

For any fractional edge cover W, the size of the join result is bounded by:

$$|Join(Q)| \leq AGM_W(Q) := \prod_{e \in \mathcal{E}} |R_e|^{W(e)}$$

where R_e is the relation corresponding to edge e.

- This gives an instance-specific upper bound on the output size.
- To get a bound in terms of the total input size IN, we can minimize the total weight $\sum W(e)$.
- Let $\rho^* = \min_W \sum_{e \in \mathcal{E}} W(e)$ be the **fractional edge covering number**.

Corollary

$|Join(Q)| \leq IN^{\rho^*}$. (Remark: This bound is known to be tight in the worst case.)

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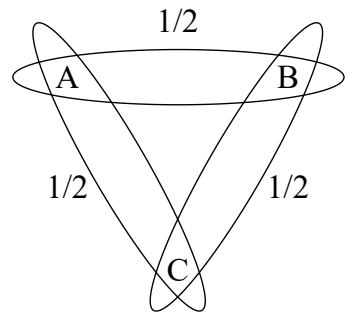
EXAMPLE: AGM BOUND FOR A TRIANGLE JOIN

Consider the triangle join $R_{AB} \bowtie R_{BC} \bowtie R_{AC}$.

- We need to find weights w_{AB}, w_{BC}, w_{AC} such that:
  - For attribute A: $w_{AB} + w_{AC} \geq 1$
  - For attribute B: $w_{AB} + w_{BC} \geq 1$
  - For attribute C: $w_{BC} + w_{AC} \geq 1$
- To minimize the sum $w_{AB} + w_{BC} + w_{AC}$, we can set: $w_{AB} = w_{BC} = w_{AC} = 1/2$
- The fractional edge covering number is $\rho^* = 1/2 + 1/2 + 1/2 = 1.5$.
- The AGM bound is $|\text{Join}(Q)| \leq |R_{AB}|^{0.5} |R_{BC}|^{0.5} |R_{AC}|^{0.5}$.
- The worst-case output size is $\text{OUT} = O(\text{IN}^{1.5})$.



CORE TECHNIQUE: THE AGM SPLIT THEOREM

A GEOMETRIC VIEWPOINT & BOX-INDUCED SUB-JOINS

- We view each result tuple as a point in d-dimensional space $\mathbb{N}^d$.
- A **box** B is a d-dimensional rectangle that acts as a filter.
- The box induces a **sub-join** $Q(B)$ by keeping only the input tuples that fall within the box.

Example: Box-Induced Sub-Join

Consider a 3D box for attributes (A, B, C): $B = [0,1] \times [1,1] \times [1,2]$.

$R_{AB}(B)$

A	B
0	1
~~0~~	~~2~~
1	1
~~2~~	~~1~~

$R_{BC}(B)$

B	C
1	1
1	2
~~2~~	~~0~~
~~2~~	~~1~~

$R_{CA}(B)$

C	A
~~0~~	~~1~~
1	0
2	1
~~2~~	~~2~~

Join(Q(B))

A	B	C
0	1	1
~~0~~	~~2~~	~~1~~
1	1	2
~~2~~	~~1~~	~~2~~

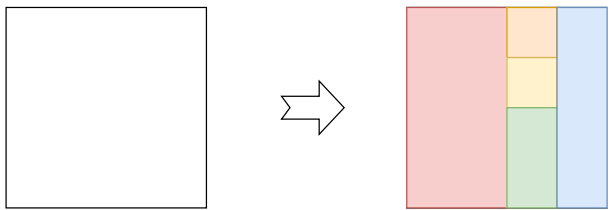
- We can still compute the AGM bound for sub-joins, which we denote as $\text{AGM}_W(B) := \text{AGM}_W(Q(B))$.

THE AGM SPLIT THEOREM

Theorem (AGM Split Theorem)

Fix an arbitrary fractional edge cover W, and assume the availability of count and median oracles. Given any box B with $AGM_W(B) \geq 2$, we can find in $\tilde{O}(1)$ time a set $\mathcal{C}$ of at most $2d + 1$ smaller boxes having these nice properties:

1. ***Partition:*** *The boxes in $\mathcal{C}$ are disjoint and their union is B. Formally, $B = \bigsqcup_{B' \in \mathcal{C}} B'$.*
2. ***Shrink:*** *For each $B' \in \mathcal{C}$, $AGM_W(B') \leq \frac{1}{2} AGM_W(B)$.*
3. ***Conserve:*** *$\sum_{B' \in \mathcal{C}} AGM_W(B') \leq AGM_W(B)$.*



THE SPLITTING STRATEGY

The split proceeds recursively, one dimension at a time, based on a lemma guaranteeing that any partition created by slicing a box along a single axis satisfies the ‘Conserve’ property (3).

- **Step 1: Find a split point.** Find the z_1 in the domain of X_1 that creates a "balanced" partition.
  - We choose the smallest z_1 such that the "left" part of the box has an AGM bound $\leq \frac{1}{2}\mathrm{AGM}_W(B)$. As a result, the "right" part also has an AGM bound $\leq \frac{1}{2}\mathrm{AGM}_W(B)$.
- **Step 2: Partition and Recurse.** This splits B into three pieces:
  - B_{left} and B_{right}: These are guaranteed to be "small" and are added to $\mathcal{C}$.
  - B_{mid}: A thin "slice" where the first attribute is fixed to z_1. We recursively apply the same process to this slice using the next attribute, X_2.
- This process is very fast, taking $\tilde{O}(d) = \tilde{O}(1)$ time per split.

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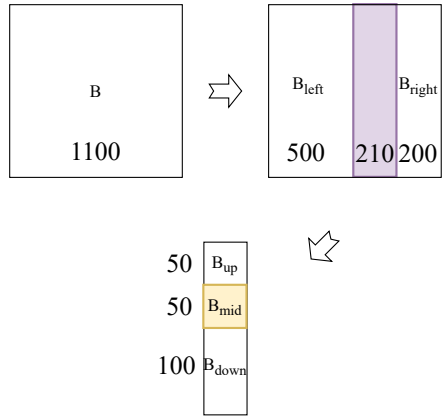
VISUALIZING THE SPLIT (2D EXAMPLE)

1. **Start with Box B.**
2. **Split on X_1 at z_1.**
   - B_{left} and B_{right} are final.
   - B_{mid} is the puple slice.
3. **Recurse on B_{mid}.**
4. **Split B_{mid} on X_2 at z_2.**
   - This creates B_{up}, B_{down}, and the final point B_{mid}.



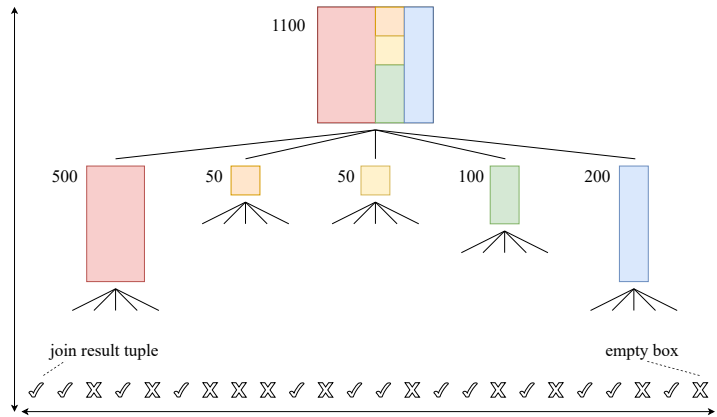
The final set of children for B would be $\{B_{left}, B_{right}, B_{up}, B_{down}, B_{mid}\}$.

THE SAMPLING ALGORITHM

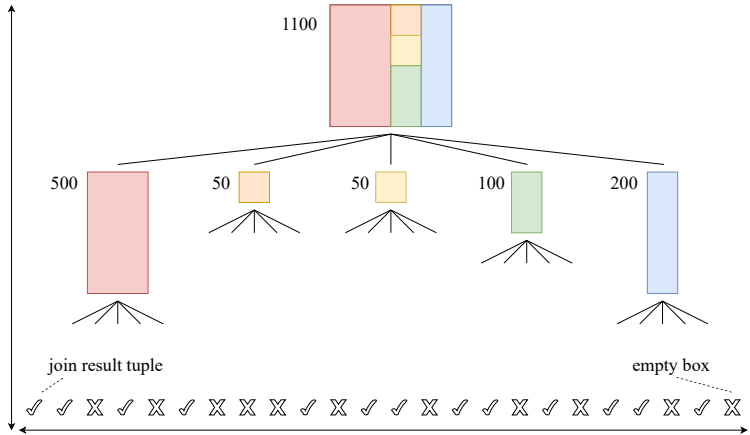
THE CONCEPTUAL AGM SPLIT TREE

We can use the AGM Split Theorem to get a conceptual decomposition tree.

- **Root:** The entire attribute space $\mathbb{N}^d$.
- **Children:** An internal box B is split into its children using the theorem.
- **Leaves:** Boxes with an AGM bound less than 2.



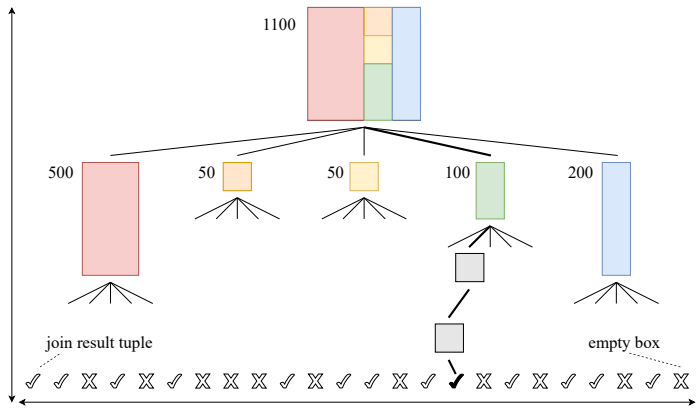
THE CONCEPTUAL AGM SPLIT TREE (CONT.)



- The height of this tree is $O(\log \mathrm{IN})$ because the AGM bound is halved at each level.
- We cannot afford to build this tree explicitly; it could have $\Omega(\mathrm{IN}^{\rho^*})$ leaves.

THE ALGORITHM IDEA: A RANDOM WALK ON A CONCEPTUAL TREE

- The AGM Split Theorem defines a conceptual AGM Split Tree.
- We cannot build this tree explicitly; it could have $\Omega(\text{IN}^{\rho^*})$ leaves.
- **Solution:** We don't build the tree. Instead, we generate a *single random path* on the fly.



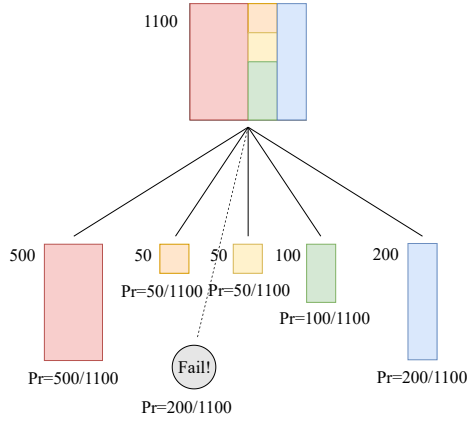
STEP 1: TRAVERSING THE TREE

At each internal node, we perform a weighted random choice to pick the next box in the path.

1. Split the current box B into children $\{B'_1, B'_2, \dots\}$.
2. Assign each child B'_j a probability:

$$\Pr[\text{choose } B'_j] = \frac{\mathrm{AGM}_W(B'_j)}{\mathrm{AGM}_W(B)}$$

3. Randomly select one child based on these weights to continue the walk.
4. There's a chance of "failure" if $\sum \mathrm{AGM}_W(B'_j) < \mathrm{AGM}_W(B)$.

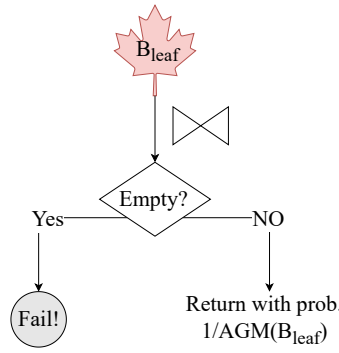


This process repeats until a leaf node is reached. Each step takes $\tilde{O}(1)$ time.

STEP 2: ARRIVING AT A LEAF

A leaf is a box B_{leaf} with $\text{AGM}_W(B_{leaf}) < 2$. It contains at most one join result tuple.

1. Compute the sub-join for B_{leaf}.
2. If it's empty, the attempt fails.
3. If it contains a single tuple u:
   - We perform one final probabilistic check.
   - Return u with probability $1/\text{AGM}_W(B_{leaf})$.
   - Otherwise, the attempt fails.



This final step ensures that every tuple in the entire join result has the exact same probability of being selected.

ANALYSIS OF THE ALGORITHM

- **Correctness:** The probability of the random walk reaching a specific leaf box B_{leaf} is $\text{AGM}_W(B_{leaf})/\text{AGM}_W(Q)$. The final step cancels out the $\text{AGM}_W(B_{leaf})$ term.
  - This means any given result tuple u is returned with probability exactly $1/\text{AGM}_W(Q)$. All result tuples are equally likely!
- **Success Probability:** The total probability of returning *any* tuple is:

$$\sum_{u \in \text{Join}(Q)} \Pr[\text{return } u] = \sum_{u \in \text{Join}(Q)} \frac{1}{\text{AGM}_W(Q)} = \frac{\text{OUT}}{\text{AGM}_W(Q)}$$

- **Running Time:**
  - A single run of the algorithm takes $\tilde{O}(1)$ time.
  - We expect to run it $\text{AGM}_W(Q)/\text{OUT}$ times to get one sample.
  - By choosing the optimal W, the total time to get a sample is $\tilde{O}(\text{IN}^{\rho^*}/\text{OUT})$ w.h.p.

HARDNESS RESULTS & CONCLUSION

HOW GOOD IS THE RESULT?

We achieved a sampling time of $\tilde{O}(\text{IN}^{\rho^*}/\text{OUT})$.

- When $\text{OUT} = \Omega(\text{IN}^{\rho^*})$, the time is $\tilde{O}(1)$, which is clearly optimal.
- But what if OUT is very small, e.g., OUT = 1? The time is $\tilde{O}(\text{IN}^{\rho^*})$. Can we do better?

The Hardness Question

Can a *combinatorial* algorithm achieve sampling time $\tilde{O}(\text{IN}^{\rho^*-\epsilon}/\text{OUT})$ for some constant $\epsilon > 0$, at least when $1 \leq \text{OUT} \leq \text{IN}^{\epsilon}$?

- A combinatorial algorithm is one that does not use techniques like fast matrix multiplication. All known practical join algorithms are combinatorial.

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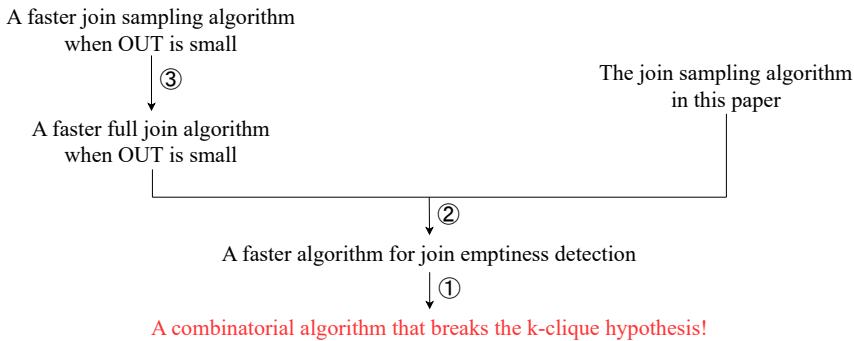
CONNECTION TO THE COMBINATORIAL K-CLIQUE HYPOTHESIS

Definition (Combinatorial k-Clique Hypothesis)

No combinatorial algorithm can detect if an n-vertex graph has a k-clique in $O(n^{k-\epsilon})$ time for any constant $\epsilon > 0$. This is a widely believed conjecture in fine-grained complexity.

We show a chain of reductions:



CONCLUSION

- We presented a dynamic data structure for the join sampling problem.
  - Achieves a sampling time of $\tilde{O}(\mathrm{IN}^{\rho^*}/\mathrm{OUT})$ w.h.p.
  - Supports dynamic updates in $\tilde{O}(1)$ time.
- The core technical contribution is the **AGM Split Theorem**, which enables a geometric, recursive decomposition of the problem space.
- We established a **hardness result**, showing that the sampling algorithm and the worst-case optimal join algorithm are likely the best possible for the class of combinatorial algorithms, by linking further improvements to the combinatorial k-clique hypothesis.
- This work not only solves a long-standing open problem but also deepens our understanding of the fundamental limits of join computation.

Thank you!