

Bala-Join: Balancing the Workload in Distributed Hash Join

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ABSTRACT

Distributed Hash Join (Dist-HJ) is fundamental to distributed databases. Under Dist-HJ, the build and probe table shall be first redistributed to multiple compute nodes, each of which then performs a local HASH JOIN afterwards. However, the prevalent use of hash partitioning in the former phase often leads to uneven load distribution if data is skewed, resulting in inferior join performance. In this paper, we introduce *Bala-Join*, a comprehensive and adaptive solution to balance the load in Dist-HJ execution.

Our approach consists of a novel redistribution strategy, namely Balanced Partition and Partial Replication (BPPR) algorithm and a distributed online skewed value detector. BPPR achieves balanced redistribution of skewed data through a multi-cast mechanism to improve computational performance and reduce network overhead. The online detector is tailored to the BPPR algorithm and provides real-time skewed value information to BPPR in an imperceptible manner while minimizing additional overhead. The detector only accounts for 2%-6% extra cost compared to BPPR, which is superior to existing solutions. Our experimental study shows that Bala-Join, compared to the latest Dist-HJ solutions, exhibits much better throughput *i.e.*, by 25%-61%.

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1 INTRODUCTION

2 INTRODUCTION

Traditional relational database management systems (RDBMSs) compile a given SQL query and generate the corresponding query

execution plan (QEP) through a query optimizer. QEP is a tree structure consisting of a set of physical operators showing how a given SQL query will be processed step by step. Among dozens of predefined operators, HASH JOIN is one of the fundamental operators extensively studied and used [17, 22, 31]. Given two relations, R and S , HASH JOIN will run as follows: (1) Use the smaller relation, say R , to build a hash table in memory. (2) Scan each element in S , check the elements in the hash table that match S with respect to the join condition. At this point, R and S are called the **build table** and the **probe table**, respectively.

In most of Shared-Nothing [30] distributed RDBMS (*e.g.*, CockroachDB [32], TiDB [15], Spanner [6]), HASH JOIN must be executed in a distributed manner, *i.e.*, Distributed Hash Join (Dist-HJ). In these environments, both storage and computation differ significantly from the single-node environment: 1) From the data *storage* perspective, each table tends to be distributed across multiple *data* nodes. 2) From a *computational* aspect, the distributed environment comprises multiple compute nodes, and thus the execution of Dist-HJ needs to be re-designed. For convenience of description, we functionally abstract the nodes in the distributed environment into *data*, *compute*, and *response* nodes. *Data* nodes temporarily store parts of R and S , which could be either raw tables or intermediate ones. The concatenation of all the *data* nodes constitutes the complete R and S . *Compute* nodes are responsible for performing HASH JOIN computation over the records acquired from the *data* nodes. *Response* nodes are not complementary and are applicable only when there is no subsequent operator along the QEP. The general process of the three types of nodes collaborating to perform Dist-HJ can be summarized in the following three steps:

- **Redistribution:** When the Dist-HJ process is initiated, the nodes where R and S (as well as the intermediate tables) reside have already been determined, so the data need to be redistributed to multiple *compute* nodes for HASH JOIN task.
- **Computation:** Each *compute* node performs local HASH JOIN computations on the shares of records shares it receives.
- **Aggregation:** This step only applies when HASH JOIN is the final step in the QEP, results produced by each *compute* node need to be aggregated to the response node. Otherwise, *i.e.*, the QEP contains subsequent operations after HASH JOIN, the results produced by the *compute* nodes become intermediate tables, and these *compute* nodes subsequently transform into *data* nodes, serving as a data source

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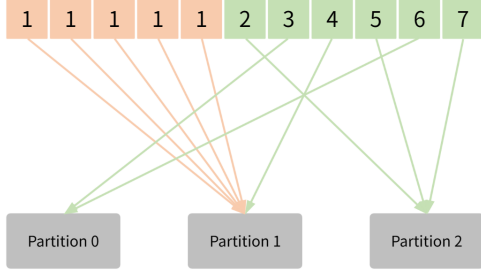


Figure 1: Hash partitioning over skewed data

to provide input for subsequent operations, *e.g.*, another HASH JOIN.

In particular, the redistribution phase is fundamental in a Dist-HJ solution. It is essential to consider task load balance and network overhead simultaneously, as both factors can affect the performance of Dist-HJ. Shared-Nothing distributed database management systems (DDBMSs) often employ hash partitioning to redistribute data from different *data* nodes to *compute* nodes over the network based on the hash values derived from the joined columns. When there is skewed data in the joined columns, which is a universal phenomenon in practice [10, 27, 37], hash partitioning will lead to an excessive imbalance among nodes, significantly degrading the performance of Dist-HJ [2].

Figure 1 shows the process of hash partitioning following a hash function $hash(x) = x \bmod 3$, values 1-7 are distributed among Partition 0, 1, and 2 according to the hash results. For simplicity, suppose that a node is in charge of a partition. Clearly, value 1 is skewed, which is hash-distributed to Partition 1. As a result, the node where Partition 1 resides will undertake much more computational tasks than the other nodes. A study by Barthels et al. [2] shows that in an 8-server cluster, the time cost for a Dist-HJ algorithm using hash partitioning is 3.3 times higher than in a skewed dataset (Zipf distribution, factor of 1.2), compared with non-skewed data with the same volume. Previous studies [2, 24, 27] have extensively examined the challenges of traditional redistribution with skewed data, identifying three main limitations.

- Hash partitioning of skewed data will result in uneven data distribution, leading to certain hotspot nodes. Those nodes bear too much computational load, and this imbalance will make some other nodes idle and wait, resulting in the “long-tail effect”;
- When a large amount of skewed data is sent to some of the hotspot nodes, it may lead to a network congestion towards these nodes;
- From the perspective of the whole cluster, when there is skewed data, the new nodes cannot disperse the burden on the hotspot nodes, thus limiting the horizontal scalability of the cluster and the space for performance improvement.

Therefore, addressing the skewed issue within Dist-HJ solutions is crucial to improve the performance of DDBMS clusters. This entails two main challenges: handling skewed data and detecting skewed values, the latter acting as a prerequisite for the former.

The handling of skewed data aims to distribute the data as evenly as possible across *compute* nodes during the redistribution phase. The common idea [26, 27, 37] is to treat skewed data separately.

Although finer granularity can improve balance, it adds extra computational and network overhead. Current algorithms (*i.e.*, PnR [38] and PRPD [37]) typically focus on either balance or network overhead, thus limiting their overall performance.

In a distributed environment, the detection of skewed values can be viewed as a global streaming frequent item mining task, presenting real-time performance and accuracy challenges. The common practice [3, 16] is to deploy detectors on each node, aggregating the results to form a consensus on skewed values. Both the deployment and aggregation phases introduce additional storage and network costs.

Generally, strategies for detecting skewness and redistribution algorithms handling skewed data are studied separately rather than deeply integrated, limiting the overall join performance. Furthermore, due to the diverse architectures of DDBMSs, the adaptability of solutions is another issue that needs to be addressed.

In this paper, we propose a adaptive technical solution, namely Bala-Join (Dist-HJ with near-balanced load and network overhead), to improve the performance of Dist-HJ in data-skewed environments. Bala-Join consists of a run-time skewed values detector and a novel redistribution strategy, namely Balanced Partition and Partial Replication (BPPR). The former, can identify skewed values within intermediate join tables at run-time, while the latter is adaptable to different fine-grained skew scenarios and consistently performs well. Specifically, the technical contribution of this work can be summarized as follows.

- We propose a novel algorithm for handling skewed data: the Balanced Partition and Partial Replication (BPPR) algorithm. The Balanced Partition mechanism of the algorithm balances overall throughput with network overhead, demonstrating high adaptability and stability. We also theoretically prove the correctness of the BPPR and the balance of load it preserves.
- We present a distributed runtime-skewed value detector tailored for BPPR. The strategy with the Active-Signaling and Asynchronous-Pulling (ASAP) mechanism provides imperceptibly skewed value information in real time to BPPR while minimizing additional overhead costs.
- We conducted a series of experimental studies to evaluate the performance of BPPR, the distributed detector, and the overall Bala-Join solution.

The rest of this paper is organized as follows. Section 3 reviews related works. In Section 4, we discuss the limitations of PRPD and PnR, and then propose the BPPR algorithm. We introduce the distributed skewness detector and the ASAP mechanism in Section 5. Section 6 covers the details of the experimental setups and shows the evaluation results. Section 7 concludes the paper.

3 RELATED WORKS

3.1 Skewed data detection

Skewed data detection strategies can be classified into two categories: static strategies and dynamic ones. Static detection typically takes place during the preparatory phase before a join operation. Since static data inherently contains statistical information, they can be pre-processed by analyzing table or column statistics and

sampling [10, 20, 26, 33]. The static solution can not work when the HASH JOIN is not the first operator in QEP.

Dynamic detection typically occurs at runtime, with uncertain data sources and scales. Skewed value information can only be obtained based on historical data that has already been received. This issue can be categorized as the problem of frequent item-set mining in data streams. Dynamic detection algorithms can be broadly classified into three categories: sampling-based algorithms, counter-based algorithms, and sketch-based algorithms.

Sampling-based algorithms [8, 12, 23] obtain data samples by randomly sampling or taking regular interval samples from the data stream.

Counter-based algorithms [23, 24] use counters or counting structures to track the occurrences of different items. Specifically, the Space Saving algorithm [24] use a list of k counters to track the top- k most frequent elements. If an element is in the list, its counter is incremented. If the list is not full, the element is added with a counter initialized to 1. When the list is full, the algorithm finds the element with the smallest counter, increases its counter, and replaces it with the new element.

Sketch-based algorithms [4, 7] use data sketches to estimate frequent items. Specifically, Count Sketch [4] uses a hash table and two matrices to estimate the frequency of occurrence of elements in a data stream. Count-Min Sketch [7] uses a hash table composed of multiple hash functions to perform estimation.

Several efforts have also been made in distributed dynamic detection. Parallel Spacing Saving [3] introduces a distributed parallel version of Space-Saving and proves its accuracy. LD-Sketch [16] is a sketch-based algorithm that maintains multiple frequent items and their counters within each bucket of the sketch. The distributed version of LD-Sketch reports elements that are frequent on a selected set of nodes as frequent items.

3.2 Joins over skewed data

Previous research [10] defined four types of data skew, namely the Tuple Placement Skew (TPS), the Selectivity Skew (SS), the Redistribution Skew (RS) and the Join Product Skew (JPS). In most DDBMS, effective data distribution techniques are commonly employed, and database administrators typically select appropriate partitioning columns for data distribution. Consequently, TPS is exceptionally rare in practical scenarios. A well-performing hash function can be chosen to mitigate it, even if it does occur. SS is induced by query predicates and is closely related to query relevance; research in this area is limited. RS and JPS are two prominent skew types, with research in this domain typically classified into three categories.

The first category of algorithms models the data skew as a traditional task scheduling problem. In the case of Dist-HJ, the join tables are divided into smaller partitions (e.g., range partitions [10] or hash buckets [1, 9, 14, 20, 34–36]) and then distributed to all processing units for individual local computation. Since task scheduling problems are NP-complete, various well-known heuristic algorithms (e.g., LPT [13] and MULTIFIT [5]) have been employed in such algorithms [1, 10, 14, 20, 34–36]. These algorithms propose different approaches based on distinct cost models. They estimate the Join cost using the number of tuples on each processing unit,

with the aim of balancing the number of tuples from join tables on each processing unit to avoid Redistribution Skew (RS).

The second category of algorithms employs advanced models [1, 9, 10, 19, 29, 39, 40]. Instead of pre-estimating execution time like the first type, it adapts in real time, adjusting workloads among processing units. If one unit is overloaded, its tasks shift to less-crowded units. [10] introduces the Virtual Processor Scheduling (VPS) for this, using $|R| + |S| + |R \bowtie S|$ to gauge the join costs. [1] employs output and work functions for cost estimation. [9] considers systems with uneven processing unit configurations. [29] relies on shared virtual memory to shift tasks away from busy units. [19] observes the processing speeds of join tables. [40] offers single-stage and two-stage scheduling, the latter involving a central processor managing tasks. Fastjoin [39] periodically reallocates workloads to address stream processing imbalances.

The third category of algorithms takes a different approach by focusing on micro-level adjustments to balance computational loads rather than handle data skew on a macro-scale. PRPD [37] assumes data to be randomly distributed across units. On each unit, skewed tuples in one join table remain local, while corresponding tuples from another table are broadcasted to all units, thereby achieving workload balance. Flow-Join [27] refines PRPD by applying Symmetric Fragment Replicate (SFR) for skewed values in both join tables, which performs well in large high-speed networks. [26] offers Track Join, an algorithm that reduces network traffic by optimizing data transmission plans for each unique join value. [11] introduces FGSD, a fine-grained method to improve load balancing in MapReduce flows, thus reducing task times. Inspired by prior work in [27, 37], the PnR algorithm is presented in [38]. Departing from the traditional focus on minimizing network data transfer, PnR targets near-perfect workload balancing across processing units and excels in high-speed network conditions.

4 BALANCED PARTITION AND PARTIAL REPLICATION

4.1 Limitation of PRPD and PnR

In this section, we study the major limitations of existing solutions, including Grace Hash Join, PRPD, and PnR.

Grace Hash Join: Grace Hash Join (GraHJ) [21] is a widely used implementation for Dist-HJ in Shared-Nothing architectures. For join tables R (build table) and S (probe table), GraHJ employs a hash function to partition both R and S into an equal number of partitions, ensuring that each partition of R can fit in memory for the construction of the hash table. Using the same hash function for R and S , the elements that match in R and S end up in the same partition, ensuring the correctness of the result. After partitioning, each partition contains a subset of R and S . The partitions are independent, and each must only perform its own HASH JOIN calculation. The union of the results from all partitions constitutes the final output. Figure 2 illustrates the partitioning mechanism of GraHJ.

PRPD: While GraHJ performs well in most distributed scenarios, its efficiency can decrease when the data is skewed, increasing network data transmission. PRPD [37], optimized for skewed data, improves performance without affecting regular data. During the redistribution phase, PRPD categorizes elements in table S as either

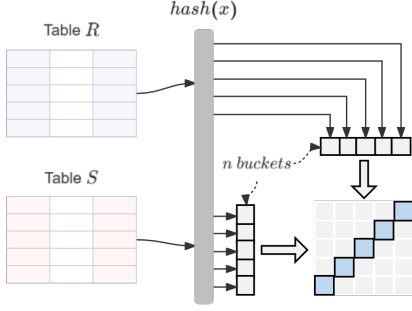


Figure 2: Partitioning of join tables in GraHJ.

non-skewed or skewed: (a) Non-skewed elements follow GraHJ’s redistribution logic. (b) Skewed elements are kept locally. The corresponding elements in table R are then duplicated in all nodes. This strategy balances workload and minimizes network transmission, especially when skewed elements are uniformly distributed between nodes. However, PRPD introduces an element of uncertainty due to the unpredictable distribution of skewed data, making it less stable than other load-balancing approaches.

Figure 3(a) illustrates the core idea of the PRPD algorithm. In the given example, *node 0* and *node 1* act as both *data* nodes and *compute* nodes. S contains 10 elements, among which the elements of value 1 are skewed. The skewed elements in S in both *node 0* and *node 1* are retained locally, while the skewed elements of value 1 of table R are replicated in both *node 0* and *node 1*. The rest elements in R and S are redistributed according to GraHJ.

PnR: PnR selects to evenly redistribute skewed elements to achieve a balance of workload all *compute* nodes. As shown in Figure 3(b), all the skewed elements of value 1 in S are initially located at *node 0*. PnR divides these elements evenly, keeping one partition in *node 0* while redistributing the other to *node 1*. In implementation, PnR achieves an even distribution by randomly sending skewed elements to *compute* nodes. The corresponding skewed elements of the value 1 in R are also distributed across both nodes. The figure only shows how skewed elements in S are handled. The treatment of skewed elements in table R is similar to that of S .

PRPD focuses on optimizing network overhead, while PnR emphasizes on load balancing. Both algorithms have their merits in specific scenarios, but may face limitations in more generalized situations.

Figure 3(c) shows how PRPD performs under different data distributions. Here, the vertical bars indicates the count of specific values in the probe and build tables, which showcase three types of data distribution scenarios. Clearly, when the difference of the volume between the build table and the probe is not too large (e.g., with identical magnitude), it results in substantial network overhead.

- Optimal Conditions:** In this scenario, elements in the probe table are evenly distributed across three *data* nodes. For illustration, we assume that elements in the build table are also balanced. After redistribution, the elements in both tables are balanced across all *compute* nodes.
- Uneven Probe Table Distribution:** In this case, the data volume on *node 2* significantly exceeds that on nodes 0

and 1. Following PRPD’s redistribution strategy, *node 2* will suffer from a much heavier load, while *node 0* has a lighter one, causing a decline in the overall performance.

- Large Build Table:** Here, elements in both the probe and build tables are evenly distributed across the three *data* nodes, but their volumes are nearly identical. Broadcasting the build table in this scenario results in substantial network overhead, leading to performance degradation.

These scenarios indicate that PRPD’s strategy may not be sufficiently nuanced to provide optimal performance in every case.

Compared to PRPD, PnR has significant advantages in the computation phase. The average redistribution strategy ensures an absolute balance of the workload of each *compute* node and has no requirements for the distribution of the data itself, resulting in better stability. However, in the redistribution phase, PnR’s strategy is theoretically more time-consuming than PRPD for the following reasons:

- Massive Network Transmission:** The average redistribution strategy of PnR leads to the transmission of a large number of skewed elements into the network, which can cause large network overhead.
- Uneven Redistribution Task Among Nodes:** Redistribution tasks involve data splitting and distribution, leading to uneven redistribution workloads among nodes. As shown in Figure 3(d), it is evident that *node 2* faces a higher redistribution workload compared to *node 0* and *node 1*. This disparity depends not only on the computational time for processing data but also on the network conditions: *node 2* sends more data, which is more likely to cause network congestion than *node 1*.
- Large Build Table:** In PnR, the handling of the build table involves broadcasting the elements corresponding to the skewed values of the probe table. When the sizes of the two tables are similar, the network data traffic caused by broadcasting the build table’s data may even exceed that of the probe table.

The limitations stem from their different motivations. PRPD excels in poor network conditions by reducing network overhead, while PnR aims for optimal use of computational resources and performs best in good network environments.

Each of PRPD and PnR suffers from limitations in either the computational or the redistribution phase. In light of this, we present a novel solution, Balanced Partition and Partial Replication (BPPR), to achieve satisfactory performance in both the computation and redistribution phases.

4.2 Algorithm details of BPPR

Before presenting the details of BPPR, we shall first introduce some notions. Assuming Dist-HJ is employed in a n -nodes cluster to accomplish: $R \bowtie_{R.a=S.b} S$, where R and S are two tables, either intermediate or raw. Each of R and S may be distributed in multiple *data* nodes. The data residing in node i is represented as R^i and S^i , subsets of R and S , respectively. The relationships between these subsets and their parent tables are governed by: $R = \bigcup_{i=0}^{n-1} R^i$, $S = \bigcup_{i=0}^{n-1} S^i$.

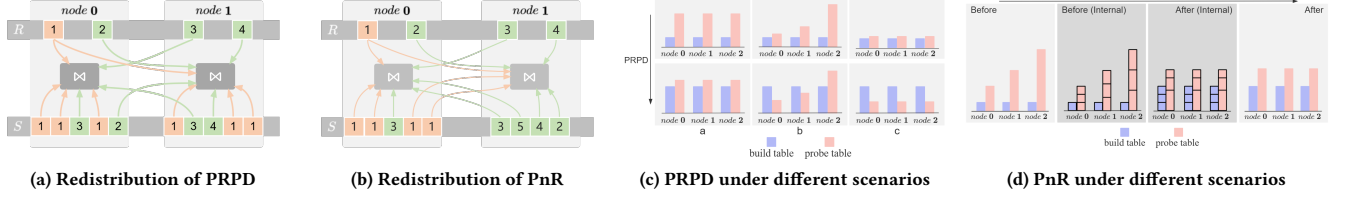


Figure 3: Strategy and limitation of PRPD and PnR

Table 1: Notations

Symbol	Description
R, S	build table and probe table in Dist-HJ
R^i, S^i	partition of R, S at node i
\widehat{R}, \widehat{S}	skewed data in R, S
$\widetilde{R}, \widetilde{S}$	non-skewed data in R, S
R_b^i	data in R^i that intersects with \widehat{S}
R_h^i	data in R^i that does not intersect with \widehat{S}
\widetilde{S}^i	partition of \widetilde{S} at node i
\widehat{S}^i	partition of \widehat{S} at node i
$U(x)$ (resp., $U^i(x)$)	set of nodes to which element x (resp., on node i) can be distributed during the execution of BPPR
$U_{loc}(x)$	set of nodes where element x is kept local
$C(x, U(x))$	node selection function to choose a node from $U(x)$
S_{hash}^i	data from \widetilde{S} that node i receives through hash distribution
S_{bal}^i	data from \widehat{S} that node i receives through a balanced distribution
\mathcal{R}_{hash}^i	data from $R_b^0, R_b^1, \dots, R_b^{n-1}$ that node i receives through hash distribution
\mathcal{R}_{bal}^i	data from $R_h^0, R_h^1, \dots, R_h^{n-1}$ that node i receives through partial replication
$R(x)$	number of element x in R
\widehat{S}^{ij}	data distributed to node j from \widehat{S}^i

R and S may contain skewed tuples, represented as \widehat{R} and \widehat{S} . For instance, \widehat{R} is a set of skewed values that frequently recur in table R . Skewed values are identified by a frequency threshold λ . If a value x in the $R.a$ column appears with a frequency at least as high as λ , it is considered skewed and belongs to $\widehat{R}.a$. The function $f(x)$ denotes the frequency of x , either relative or absolute.

$$f(x | x \in \widehat{R}.a) \geq \lambda, \quad f(x | x \in \widehat{S}.b) \geq \lambda \quad (1)$$

In contrast, tables R and S also contain non-skewed data, denoted as \widetilde{R} and \widetilde{S} , respectively. Obviously, $R = \widetilde{R} \cup \widehat{R}, S = \widetilde{S} \cup \widehat{S}$.

BPPR follows the general workflow of Dist-HJ, but with a different redistribution phase, containing an extra partitioning sub-step. The purpose of this step is to partition the subsets of tables S and R on each node into skewed and non-skewed parts, such that the skewed data can be processed correctly in the subsequent phases.

Step 1, Partition. In a distributed computing environment, it is typical for each *data* node to hold a subset of tables R and S , denoted as R^i and S^i for node i .

Partitioning S^i : S^i on each node is divided into two partitions, \widetilde{S}^i and \widehat{S}^i .

Partitioning R^i : The partition of R^i at each node is passively determined by \widehat{S}^i . The details can be described as follows:

$$R_b^i = \{t \mid t.a \in R^i.a, t.a \in \widehat{S}.b\} \quad (2)$$

$$R_h^i = \{t \mid t.a \in R^i.a, t.a \notin \widehat{S}.b\} \quad (3)$$

Step 2, Redistribution. During the redistribution phase, R^i and S^i are redistributed on each node. After partitioning, R^i and S^i are divided into four partitions: $\widetilde{S}^i, \widehat{S}^i, R_b^i$, and R_h^i . These partitions are redistributed as follows:

\widetilde{S}^i : This partition contains the non-skewed data from S on node i . The elements are hash-distributed, achieving nearly even distribution across n nodes.

\widehat{S}^i : This partition contains the skewed data from S on node i . The elements are distributed in a balanced manner, and each element of the skewed value is targeted to a specific subset of nodes. The selection of these target nodes can be flexible and could encompass some (or even all) nodes. The set can automatically expand when the balance condition is not satisfied, and the sequence generated determines which node will be included in the set next. For each skewed value, the sequence generator on each node can generate the same sequence. It will be introduced in detail in Section 4.4. For any given skewed value x , the candidate set of target nodes is denoted as $U(x)$, with a choice function $C(x, U(x))$ determining the final destination. $U(x)$ and $C(x, U(x))$ satisfy the following relationship:

$$U(x) \subseteq \{0, 1, 2, \dots, n-1\}, x \in \widehat{S} \quad (4)$$

$$C(x, U(x)) = i, i \in U(x) \quad (5)$$

R_b^i : According to Equation (2), all the elements in R_b^i correspond to those in \widehat{S} . Since \widehat{S}^i redistributed to each *data* node is balanced, each element $x \in R_b^i$ must be sent to the nodes specified by $U(x)$, which we refer to as *Partial Replication*.

R_h^i : Based on Equations (2) and 3, R_b^i and R_h^i are complementary sets. Specifically, R_b^i is the set related to \widehat{S}^i , while R_h^i is essentially the set not related to \widehat{S}^i . Elements in R_h^i undergo a hash distribution.

Step 3, Computation. During the computation phase, each *compute* node receives the redistributed data from the *data* nodes according to **Step 2**. Consequently, each *compute* node will receive four sets of data (shown in Figure 4):

S_{hash}^i : This set is composed of partial data from \widetilde{S}^i across n *data* nodes. During the redistribution phase, \widetilde{S}^i on each node is hash-distributed to multiple *compute* nodes. S_{hash}^i thus consists of the data from $\widetilde{S}^0, \widetilde{S}^1, \dots, \widetilde{S}^{n-1}$ that has been hash-distributed to node i . Hence S_{hash}^i can be represented by the following formula:

$$S_{hash}^i = \{t \mid (\text{hash}(t.b) \bmod n) = i, t \in \bigcup_{i=0}^{n-1} \widetilde{S}^i\} \quad (6)$$

S_{bal}^i : This set is derived from the \widehat{S}^i sent by n data nodes, where \widehat{S}^i represents the skewed elements of S at node i . During the redistribution phase, the element $t \in \widehat{S}^i$ is sent to the node $C(t.b, U(t.b))$. Specifically, for *compute* node i , S_{bal}^i contains element t when $C(t.b, U(t.b)) = i$. Therefore, S_{bal}^i is the data set of elements of $\widehat{S}^0, \widehat{S}^1, \dots, \widehat{S}^{n-1}$ where $C(t.b, U(t.b)) = i$. S_{bal}^i can be represented by the following formula:

$$S_{bal}^i = \{t \mid C(t.b, U(t.b)) = i, t \in \bigcup_{i=0}^{n-1} \widehat{S}^i\} \quad (7)$$

\mathcal{R}_{hash}^i : This set consists of partial data from R_b^i across n data nodes. R_b^i is the set that does not intersect with the skewed values of S and is hash-distributed during the redistribution phase. Therefore, \mathcal{R}_{hash}^i is similar to S_{hash}^i and represents the data hashed to node i from $R_b^0, R_b^1, \dots, R_b^{n-1}$. \mathcal{R}_{hash}^i can be represented as:

$$\mathcal{R}_{hash}^i = \{t \mid (\text{hash}(t.a) \bmod n) = i, t \in \bigcup_{i=0}^{n-1} R_b^i\} \quad (8)$$

\mathcal{R}_{bal}^i : This set includes elements from R_b^i . During redistribution, each element in R_b^i is replicated to nodes in $U(t.a)$. \mathcal{R}_{bal}^i may contain duplicate elements to ensure correctness of HASH JOIN result. It consists of elements from $R_b^0, R_b^1, \dots, R_b^{n-1}$ where $U(t.a)$ contains node i . It can be formally defined as follows:

$$\mathcal{R}_{bal}^i = \{t \mid i \in U(t.a), t \in \bigcup_{i=0}^{n-1} R_b^i\} \quad (9)$$

Upon receiving the above four data sets, each *compute* node must first perform local HASH JOIN as follows:

$$\mathcal{R}_{bal}^i \bowtie_{a=b} S_{bal}^i \quad (10)$$

$$\mathcal{R}_{hash}^i \bowtie_{a=b} S_{hash}^i \quad (11)$$

The local result for *compute* node i can be represented by the following equation:

$$R_{a=b}^i \bowtie S^i = (\mathcal{R}_{bal}^i \bowtie_{a=b} S_{bal}^i) \cup (\mathcal{R}_{hash}^i \bowtie_{a=b} S_{hash}^i) \quad (12)$$

Step 4, Union. After the computation phase, each *compute* node obtains local results. To aggregate these into a final result, a coordinating node is required to integrate the outputs from all *compute* nodes. The mathematical representation of this aggregation and integration process is as follows:

$$R \bowtie_{R.a=S.b} S = \bigcup_{i=0}^{n-1} (R_{a=S.b}^i \bowtie S^i) \quad (13)$$

Overall, instead of considering every single skewed values at the micro-level (as PRPD and PnR), BPPR handles data skew from a macro perspective and improves the overall performance significantly. In the case of PnR, for example, it ensures that elements of the probe table S are evenly distributed across all nodes. Differently, in BPPR, these elements are distributed only to the node set $U(x)$ and might not be evenly distributed. Although the distribution of elements with a single value in BPPR is uneven, the overall distribution is balanced, which shall be justified in our empirical study in Section 6.

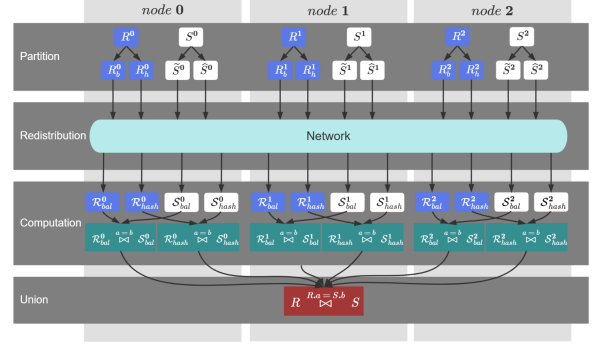


Figure 4: 3-steps illustration of BPPR (3 Nodes)

4.3 Correctness study of BPPR

In this part, we shall study the correctness of BPPR. As discussed in Section 4.1, for elements with the same values in the build and probe table, there exist several different combinations of distribution strategies, referred to as *pairing strategy*. Figure 3(a) shows two examples: 1) Elements of non-skewed values 2, 3, and 4 in the probe table are hash-distributed, and the join-able elements in the build table are also hash-distributed (denoted as *hash-hash* pairing strategy). 2) Elements of skewed value 1 in the probe table are kept local, while the join-able elements in the build table are broadcast to all nodes (denoted as *local-broadcast* pairing strategy).

In general, there are four distribution strategies (i.e., *hash*, *broadcast*, *keep local*, *random*) and three types of pairing strategies (i.e., *hash-hash*, *local-broadcast*, and *random-broadcast*) in PRPD and PnR. From the perspective of each of these strategies, we can infer:

THEOREM 4.1. *In the computation of HASH JOIN, suppose the actual result is denoted by Z . When skewed values x in the probe table are distributed across multiple nodes while values x in the build table are replicated to all nodes, the result Z' from the operation $R \bowtie_{R.a=S.b} S$ matches Z .*

This theory summarizes the *local-broadcast* and *random-broadcast* pairing strategies. The difference lies in the final distribution of elements from the probe table. Next, we will study the correctness of the three pairing strategies in sequence. Let $R(x)$ (resp., $S(x)$) denote the count of tuples corresponding to x in R (resp., S), after performing a HASH JOIN, the number of tuples with respect to x in the correct result should be $S(x) \times R(x)$.

- (1) *hash-hash*: HASH JOIN is essentially an intersection operation. Only when a value x appears in both the probe and build table will there be a calculation result related to x . In the *hash-hash* strategy, no matter where the value x is distributed among the *data* nodes, using the same hash function will always send it to the same *compute* node. Therefore, this node will have $S(x)$ elements from the probe table and $R(x)$ elements from the build table. After a local HASH JOIN, the result count is $S(x) \times R(x)$, ensuring the correctness of this strategy for handling single value results.
- (2) *local-broadcast*: In the *hash-hash* strategy, computation result generation for any value is always on a single node. However, with the *local-broadcast* strategy, these calculations spread across multiple nodes. Suppose value x from the probe table distributes in set $U_{loc}(x)$, where $U_{loc}(x) \in$

$\{0, 1, \dots, n-1\}$, then the nodes involved are those in $U_{loc}(x)$. While the elements corresponding to x in S are kept local, the count of such elements at node i is $S^i(x)$, $i \in U_{loc}(x)$, satisfying the following:

$$S(x) = \sum_{i=0}^{n-1} S^i(x), \quad i \in U_{loc}(x) \quad (14)$$

Elements corresponding to x in R are broadcasted to all nodes, therefore, the count of such elements at node i is $R^i(x)$, which can be represented as:

$$R^i(x) = R(x), \quad i \in \{0, 1, \dots, n-1\} \quad (15)$$

Then the count of results generated on node i is $S^i(x) \cdot R^i(x)$ and the final result count is:

$$\sum_{i=0}^{n-1} S^i(x) \cdot R^i(x), \quad i \in U_{loc}(x) \quad (16)$$

By merging Equations (14), 15, and 16, we derive:

$$\sum_{i=0}^{n-1} S^i(x) \cdot R^i(x) = \sum_{i=0}^{n-1} S^i(x) \cdot R(x) = S(x) \cdot R(x) \quad (17)$$

At this point, the correctness of single-value pairing under the *local-broadcast* strategy has been proven.

- (3) *random-broadcast*: The *random-broadcast* strategy is similar to the *local-broadcast* strategy. The difference is that calculations and result generation for a single value under the *random-broadcast* strategy are performed on all *compute* nodes. Regardless of how x in the probe table S distributes across *data* nodes originally, each *compute* node ends up with the same count of x elements. The number of x elements that node i obtains from S is denoted as $S^i(x)$.

$$S^i(x) = \frac{S(x)}{n} \quad (18)$$

Elements of value x in R are broadcasted to all nodes. The count of such elements on node i is $R^i(x)$, with the same representation as Equation (15). The final count of results is:

$$\sum_{i=0}^{n-1} S^i(x) \cdot R^i(x) \quad (19)$$

The above equation, combined with Equations (14) and 18, can be simplified to:

$$\sum_{i=0}^{n-1} S^i(x) \cdot R^i(x) = \sum_{i=0}^{n-1} \frac{S(x)}{n} \cdot R(x) = S(x) \cdot R(x) \quad (20)$$

This equation proves the correctness of single-value pairing under the *random-broadcast* strategy.

Although Theorem 4.1 guarantees the accuracy of the BPPR, it can contain redundant calculations, especially in the *local-broadcast* pairing strategy. Specifically, when a value x in the probe table is distributed across the set of nodes $U_{loc}(x)$, broadcasting its corresponding elements from the build table to all nodes is excessive. In fact, broadcasting elements of the build table beyond $U_{loc}(x)$ does not affect the validity equation. Therefore, we can refine Theorem 4.1 into the following:

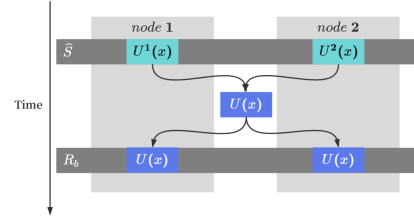


Figure 5: Consensus process for forming the node set $U(x)$ (2 nodes)

THEOREM 4.2. In a HASH JOIN operation, suppose that the actual result is denoted by Z . If the skewed values x from the probe table are distributed to the node set $U(x)$, and the values x from the build table are replicated to the same node set $U(x)$, then the result Z' of the operation $R \bowtie_{R.a=S.b} S$ is equivalent to Z .

During the redistribution phase of BPPR, there are two pairing strategies, i.e., the *hash-hash* pairing strategy of \widehat{S}^i and R_b^i , and the BPPR pairing strategy of \widehat{S}^i and R_b^i . Their computation phases correspond to Equations (10) and (11), respectively. The correctness of the results for the *hash-hash* pairing strategy has been proven by Theorem 4.1, and for the BPPR pairing strategy it follows Theorem 4.2. In all, the accuracy of the BPPR algorithm is guaranteed.

4.4 Sequence generator

Recall that in step 2 of Section 4.2, \widehat{S}^i on each *data* node is distributed in a balanced manner, the set of nodes to which \widehat{S}^i is sent depends on the usage of a sequence generator. In the following, we shall present a sequence generator in order to form an imperceptible consensus among *data* nodes.

Without a sequence generator, the BPPR pairing strategy requires two synchronization steps. As shown in Figure 5, each *data* node generates an individual node set $U^i(x)$ when processing partition data \widehat{S}^i . Since $U^i(x)$ of each *data* node is different and does not satisfy Theorem 4.2, this leads to the first synchronization process to obtain a global $U(x)$.

$$U(x) = \bigcup_{i=0}^{n-1} U^i(x) \quad (21)$$

Afterwards, $U(x)$ must be synchronized with the partition R_b^i of the data nodes, informing them which nodes the data should be distributed. This means that R_b^i on the *data* node i must wait to generate $U^i(x)$. In BPPR, $U^i(x)$ continuously grows until \widehat{S}^i is fully processed.

The sequence generator is designed to achieve the first synchronization. It generates a fixed sequence for each value, with the sequence elements and length related to the number of nodes n , and $U^i(x)$ expands accordingly.

Algorithm 1 illustrates the generation of the sequence. Lines 5-12 detail the sequence generation process, with Line 6 generating a temporary string to calculate the hash value. Line 7 generates a sequence element *number* by performing a hash-modulus operation on the temporary string. Lines 8-9 conditionally add the element to the sequence. After iterations, the final sequence is returned.

Algorithm 1 Sequence Generation Algorithm**Input:** value to generate the sequence x , number of nodes n **Output:** *sequence*

```

1: procedure GENERATESEQUENCE( $x, n$ )
2:    $sequence \leftarrow []$ 
3:    $sequence.add(hash(x) \bmod n)$ 
4:    $epoch \leftarrow 0$ 
5:   while  $sequence.size < n$  do
6:      $hashString \leftarrow String(x) + String(epoch)$ 
7:      $number \leftarrow Hash(hashString) \bmod n$ 
8:     if  $number \notin sequence$  then
9:        $sequence.add(number)$ 
10:    end if
11:     $epoch++$ 
12:  end while
13:  return  $sequence$ 
14: end procedure

```

Algorithm 2 Node Set Update Algorithm**Input:** value to update the node set x , node set to be updated $U(x)$, generated sequence *sequence*

```

1: procedure UPDATEU( $x, U(x), sequence$ )
2:    $size \leftarrow U(x).size$ 
3:   if  $size == sequence.size$  then
4:     return  $U(x)$ 
5:   end if
6:    $U(x).add(sequence[size])$ 
7:   return
8: end procedure

```

Algorithm 2 details the process for updating the node set $U(x)$. It adds an element to the node set $U(x)$. Lines 3-5 determine whether the size of the node set $U(x)$ is equal to *sequence*, and otherwise new elements must be added to $U(x)$ (Line 6).

With the sequence generator, every *data* node can employ Algorithm 1 to generate a sequence for value x . Even without any communication between nodes, the generated sequences are identical among these nodes. In particular, though the time complexity of Algorithm 1 is linear to n , the sequences can be created once and reused later. Once every node imperceptibly obtains the same sequence for x , we can use it as the node set $U(x)$ to achieve the first synchronization. However, this method is not flexible enough, we shall present a balanced partition algorithm in subsequent sections. By putting both the generator and partitioning together, better performance can be achieved.

4.5 Balanced partition algorithm

Recall that at the *data* node level, under the BPPR pairing strategy, we need to balanced partition the probe table S , or more specifically, the \widehat{S}^i partition of S^i . At the *data* node, \widehat{S}^i will undergo further partitioning (balanced repartitioning), and each subpartition after this will be sent to a *compute* node. Here, the sub-partitions are denoted as \widehat{S}^{ij} , $j \in \{0, 1, \dots, n-1\}$, indicating that these sub-partition data originate from \widehat{S}^i and will be sent to the j^{th} *compute* node.

To ensure that the data in \widehat{S}^i is balanced at the macro level after repartitioning, we define a balance factor B^i as follows:

$$B^i = (\max_j |\widehat{S}^{ij}| - \min_j |\widehat{S}^{ij}|) / \max_j |\widehat{S}^{ij}| \quad (22)$$

Obviously, the balance factor reflects the degree of data balance among the subpartitions. The smaller B^i , the more balanced the subpartitions are. When repartitioning \widehat{S}^i for balance, a threshold B_c can be set to control the balance factor during repartitioning, that is, $B^i \leq B_c$.

After all *data* nodes complete the balanced repartitioning of \widehat{S}^i and send the sub-partitions, the data volume received by *compute* node j is \widehat{S}^j :

$$|\widehat{S}^j| = \sum_{i=0}^{n-1} |\widehat{S}^{ij}| \quad (23)$$

Ultimately, the balance factor B of \widehat{S} among the *compute* nodes can be calculated as:

$$B = (\max_j |\widehat{S}^j| - \min_j |\widehat{S}^j|) / \max_j |\widehat{S}^j| \quad (24)$$

THEOREM 4.3. *In the case of balanced partitioning, if the balance factor B^i between subpartitions for each data node is below the threshold B_c , it follows that the general balance factor B among compute nodes after redistribution will also be below B_c .*

PROOF. This statement can be proven through the transformation of inequalities. Transform Equation (22) into the following inequality:

$$\max_j \widehat{S}^{ij} - \min_j \widehat{S}^{ij} \leq B_c \cdot \max_j \widehat{S}^{ij} \quad (25)$$

Apply summation transformation to the inequality:

$$\sum_{i=0}^{n-1} (\max_j \widehat{S}^{ij} - \min_j \widehat{S}^{ij}) \leq \sum_{i=0}^{n-1} (B_c \cdot \max_j \widehat{S}^{ij}) \quad (26)$$

Shifting the summation gives:

$$\max_j (\sum_{i=0}^{n-1} \widehat{S}^{ij}) - \min_j (\sum_{i=0}^{n-1} \widehat{S}^{ij}) \leq B_c \cdot \max_j (\sum_{i=0}^{n-1} \widehat{S}^{ij}) \quad (27)$$

Divide both sides by $\max_j (\sum_{i=0}^{n-1} \widehat{S}^{ij})$:

$$\frac{\max_j (\sum_{i=0}^{n-1} \widehat{S}^{ij}) - \min_j (\sum_{i=0}^{n-1} \widehat{S}^{ij})}{\max_j (\sum_{i=0}^{n-1} \widehat{S}^{ij})} \leq B_c \quad (28)$$

Substitute into the inequality using Equation (23) to obtain:

$$\frac{\max_j \widehat{S}^j - \min_j \widehat{S}^j}{\max_j \widehat{S}^j} \leq B_c \quad (29)$$

By combining this with Equation (24), we obtain:

$$B \leq B_c \quad (30)$$

□

Algorithm 3 shows the detailed process of the balanced partitioning algorithm. According to Theorem 4.3, we only need to ensure that the balance factor B^i of each *data* node after partitioning is below the threshold B_c . Upon inputting the partition data \widehat{S}^i , the algorithm will ultimately return a set of sub-partitions, denoted *partition*, that satisfy the condition $B^i \leq B_c$.

Lines 1-15 calculate the balance factor based on Equation (22). The calculation of the balance factor has linear time complexity. Nevertheless, in the actual implementation, this computation can be optimized to a constant time complexity. As shown in Line 23, each subpartition only adds one element at a time. Thus, by maintaining *maxVal*, *minVal*, and the element count for each subpartition, we can simply update *maxVal* and *minVal* when a new element is added to a subpartition. Lines 16-19 initialize the partition set as *n* empty subpartitions. Lines 20-35 iterate over each element in \widehat{S}^i and balance the partition. Lines 23-25 perform a test partition by inserting element *t* into the previously selected sub-partition, calculating a testing balance factor, which later serves as the basis for adaptive sub-partition choices. Lines 27-33 aim to reselect a sub-partition ID when *balanceFactor* > B_c . Line 28 picks a subpartition from the set $U(t)$, choosing the one with the fewest elements. If the subpartition chosen in line 28 is the same as the last, it would still exceed the balance factor threshold. In this case, Lines 30-31 update $U(t)$ and then reselect a sub-partition. Line 34 identifies the ultimately chosen subpartition ID, which satisfies the balance factor threshold, and adds element *t* to it. Finally, Line 36 returns the subpartition set *i.e.*, *partition*.

5 DETECTION OF SKEWED ELEMENTS

Recall that our ultimate goal is to propose a universal Dist-HJ solution for skewed data scenarios, while the effectiveness of the BPPR algorithm depends on the skewness information. That is, there still exists a gap between BPPR and a universal Dist-HJ solution, namely the detection of skewed values at runtime.

In this section, we will further introduce a distributed strategy for detecting skewed values at run-time.

5.1 Detector in single-node environment

In distributed databases, as queries and computations involve the coordination of multiple nodes, the input data for each operation is typically data streams. Therefore, we start with a skewness detector from data streams in a single-node environment, and then expand it to distributed settings. As discussed in Section 3, existing skewness detection strategies can be classified into counter-based techniques and sketch-based techniques.

We employ Space-Saving Algorithm [24], a counter-based technique, as the building block in the distributed detection strategy of this paper. The core idea of Space-Saving is to maintain frequency information about a subset of the elements in the data stream. Specifically, it preserves the frequencies of the *k* elements using *k* counters. Each counter is updated to estimate the frequency of the corresponding element. Lightweight data structures are used to sort these elements according to their estimated frequencies.

Algorithm 4 outlines the process of the Space-Saving Algorithm. In particular, on Line 14, when *monitorList* reaches its capacity and a new element *e* is to replace e_{min} , the *counter* retains the

Algorithm 3 Balanced Partition Algorithm

Input: partition of the current node \widehat{S}^i , thresholds for the balance factor B_c , number of nodes *n*

Output: set of the sub partitions after the balanced partitioning *partition*

```

1: procedure CALCULATEBALANCEFACTOR(partition)
2:   maxVal  $\leftarrow$  partition[0].size
3:   minVal  $\leftarrow$  partition[0].size
4:   for array in partition do
5:     size  $\leftarrow$  array.size
6:     if size > maxVal then
7:       maxVal  $\leftarrow$  size
8:     end if
9:     if size < minVal then
10:      minVal  $\leftarrow$  size
11:    end if
12:  end for
13:  balanceFactor  $\leftarrow$  (maxVal - minVal) / maxVal
14:  return balanceFactor
15: end procedure
16: partition  $\leftarrow$  []
17: for i = 0 to n - 1 do
18:   partition.add([])
19: end for
20: for t in  $\widehat{S}^i$  do
21:   U  $\leftarrow$  set of partition IDs corresponding to t i.e.,  $U(t)$ 
22:   lastID  $\leftarrow$  partition ID last selected by t
23:   partition[lastID].add(t)
24:   balanceFactor  $\leftarrow$  CALCULATEBALANCEFACTOR(partition)
25:   partition[lastID].delete(t)
26:   selectID  $\leftarrow$  lastID
27:   if balanceFactor >  $B_c$  then
28:     selectID  $\leftarrow$  ID of the sub-partition in set U with the
        fewest elements
29:     if selectID == lastID then
30:       Expanding the ID set U using Algorithm 2.
31:       selectID  $\leftarrow$  ID of the sub-partition in set U with the
        fewest elements
32:     end if
33:   end if
34:   partition[selectID].add(t)
35: end for
36: return partition

```

frequency information of the former element e_{min} . This counter is assigned directly to the element *e* and added to the *monitorList*.

The primary challenge of the Space-Saving Algorithm lies in efficiently updating elements and removing elements corresponding to the minimum count, as indicated in Lines 4-5 and 11-14. Following the suggestion of [27], we adopt the Space-Saving Algorithm based on a hash table and an ordered array as the detector for the single-node environment.

Algorithm 4 Space Saving Algorithm

Input: number of monitored elements k , data stream *Stream*
Output: monitor list *monitorList*

```

1: monitorList  $\leftarrow$  []
2: for element  $e$  in Stream do
3:   if  $e$  in monitorList then
4:     counter  $\leftarrow$  counter corresponding to  $e$ 
5:     counter ++
6:   else
7:     if monitorList.size <  $k$  then
8:       counter  $\leftarrow$  1
9:       monitorList add  $e$  and counter
10:    else
11:       $e_{min}$   $\leftarrow$  element with the lowest frequency among
        the monitored elements
12:      counter  $\leftarrow$  counter corresponding to  $e_{min}$ 
13:      monitorList remove  $e_{min}$  and its corresponding
        counter
14:      monitorList add  $e$  and counter
15:    end if
16:  end if
17: end for
18: return monitorList

```

5.2 Integration of BPPR and distributed detectors

We are now moving forward to integrate the detector into a distributed environment. A straightforward approach is to conduct local detection on each standalone node, aggregate the results, and then redistribute elements based on the skewed values obtained. However, this approach poses several challenges:

- (1) **Double Traversals of S :** Each *data* node must traverse the table S^i twice (once for local detection and again for redistribution). In distributed databases, *data* nodes often receive data in the form of data streams. Repeatedly traversing S^i can result in significant memory and I/O overhead.
- (2) **Independent Standalone Detection:** In a distributed environment, independently executing detection on each standalone node can lead to varying execution times. Faster nodes may become idle after completing their tasks, while slower ones can significantly hinder overall detection progress.
- (3) **Communication Overhead Due to Consensus:** Achieving consensus on local skewness information from all *data* nodes is essential. However, this requires unavoidable communication overhead between *data* nodes.

Therefore, carrying out a distributed detector is not a trivial task. In response to these challenges, distributed skewness detection must be tightly integrated with the BPPR algorithm. We propose Bala-Join (Balanced Hash Join) by embedding distributed skewness detection into the redistribution and computation phases of BPPR without altering its time complexity. In the following, we will describe the Bala-Join redistribution and computation phases with distributed skewness detector embedded.

Algorithm 5 Redistribution on Data Nodes

Input: data stream S^i, R^i , number of nodes n

```

1: for element  $e$  in  $S^i$  do
2:   Space Saving Algorithm Sampling Element  $e$ 
3:   if  $e$  in monitor list then
4:     selectNode  $\leftarrow$  select a node from  $U(e)$ 
5:     send  $e$  to selectNode
6:     signal selectNode that  $e$  is a skewed element
7:   else
8:     selectNode  $\leftarrow$   $\text{hash}(e) \bmod n$ 
9:     send element  $e$  to selectNode
10:  end if
11: end for
12: for element  $e$  in  $R^i$  do
13:   selectNode  $\leftarrow$   $\text{hash}(e) \bmod n$ 
14:   send element  $e$  to selectNode
15: end for
16: return

```

Redistribution According to the BPPR algorithm, both S^i and R^i on *data* node i are divided into four parts for redistribution. However, the partitioning process relies on the knowledge of skewed values, making it impossible to complete at this stage. Therefore, the way in which S^i and R^i are processed on a single *data* node differs from the original BPPR approach.

S^i : S^i takes the form of a data stream, its length unknown. Space-Saving deployed on S^i can process each element one after another in the data stream.

Skewed Elements: elements detected (by Space-Saving) to be skewed will be sent to a sub-partition, which is selected based on Lines 21-34 of Algorithm 3. A signal will be sent to the node that the element is skewed.

Non-skewed Elements: elements found to be non-skewed will be hash-distributed.

In fact, after the redistribution phase, S^i has been effectively partitioned into \widehat{S}^i and \widetilde{S}^i . Therefore, this process achieves three critical objectives for the data stream S^i : detection of local skewness, partitioning of S^i and redistribution of S^i .

R^i : R^i is also a data stream and no special treatment is applied to it. Instead, all its elements are directly hash-distributed. Following the redistribution phase described in Section 4.2, R^i must be partitioned into R_b^i and R_h^i . At this stage, all elements of the data stream are temporarily treated as part of the R_h^i partition. Consequently, the partitioning of R^i is not completed at this point.

Algorithm 5 outlines the pipeline of the Bala-Join redistribution phase integrated with local skewness detection.

Computation In the original computation phase of BPPR, each *compute* node receives four data partitions. With the introduction of distributed skewness detection, each *compute* node continues to receive these four partitions, but the sources of these data partitions are slightly different.

S_{hash}^i : S_{hash}^i is composed of elements hash-distributed from the \widehat{S}^i partitions of various *data* nodes to the current node.

Algorithm 6 Generation of \mathcal{R}_{bal}^i **Input:** set M^i , current node i , number of the nodes n **Output:** set \mathcal{R}_{bal}^i

```

1:  $\mathcal{R}_{bal}^i \leftarrow []$ 
2: for element  $t$  in  $M^i$  do
3:    $fetchNode \leftarrow hash(t) \bmod n$ 
4:   if  $fetchNode == i$  then
5:     continue
6:   end if
7:    $tSet \leftarrow$  all element  $t$  pulled from  $fetchNode$ 
8:    $\mathcal{R}_{bal}^i.add(tSet)$ 
9: end for
10: return  $\mathcal{R}_{bal}^i$ 

```

S_{bal}^i : S_{bal}^i has the same source of data as the original BPPR. It comprises skewed elements detected in various *data* nodes, which are sent to the current node based on balanced partitioning.

\mathcal{R}_{hash}^i : \mathcal{R}_{hash}^i consists of hash-distributed elements from R to the current node. The union of \mathcal{R}_{hash}^i from all *compute* nodes forms R , which is expressed as $R = \bigcup_{i=0}^{n-1} \mathcal{R}_{hash}^i$.

\mathcal{R}_{bal}^i : After redistribution, each *compute* node receives a set of skewed elements, denoted M^i . M^i consists of skewed elements informed by *data* nodes to node i . Let $q = hash(t) \bmod n$, $q \neq i$. For each element t in M^i , all the elements corresponding to t in R are pulled from *compute* node q . \mathcal{R}_{bal}^i is composed of all these elements and can be represented as:

$$\mathcal{R}_{bal}^i = \{t \mid t \in M^i, t \in R\} \quad (31)$$

Algorithm 6 shows how \mathcal{R}_{bal}^i is derived.

The *compute* node can calculate the local join result based on Equations (10) and 11 after obtaining data from the four partitions.

5.3 ASAP mechanism

To ensure the correctness of HASH JOINS, computing nodes need to be aware of the skewness information to obtain the required elements, which corresponds to the second synchronization process mentioned in Section 4.4. However, in a pipeline executor, waiting for all the elements to be detected and aggregated in order to obtain the global skewness values is impractical. The Bala-Join algorithm, enhanced with distributed skewness detection, imperceptibly establishes a consensus on global skewness information through the **Active-Signaling and Asynchronous-Pulling (ASAP)** mechanism. Specifically, regarding a skewed element x in S , the node receiving x is informed during the redistribution phase that element x is skewed. Then, in the computation phase, the node receiving element x asynchronously pulls all elements x from R .

Figure 6 illustrates the specific flow of the skewed element x under the ASAP mechanism. The Active-Signaling and Asynchronous-Pulling ensures that it does not disrupt the original redistribution process. Both active signaling and asynchronous pulling can be completed in a constant amount of time.

Based on Theorem 4.2, the ASAP mechanism ensures correctness when an element x is detected as skewed by the Space-Saving

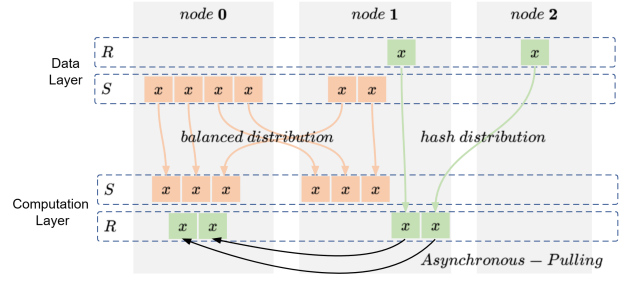


Figure 6: Flow of skewed element x under ASAP

algorithm. Next, we discuss the correctness of the results when the element x is falsely recognized as non-skewed on some *data* nodes. According to the BPPR algorithm, when a *data* node determines that the element x is not skewed, let $q = hash(x) \bmod n$, it will hash-distribute this element to node q and will not inform node q that the element x is skewed. On other *data* nodes, when element x is determined as skewed, it will be balanced distributed to the node set $U(x)$, and these nodes will be notified that element x is a skewed element. Here, the node set $U(x)$ must include the node q , which is determined by Algorithm 1. Therefore, the relevant nodes can still form a consensus. The Bala-Join algorithm, equipped with ASAP, has a robust tolerance for skewed value detection. Regardless of whether the skewed value detection is correct or not, it will only affect the *efficiency* of the algorithm rather than its *correctness*.

6 EVALUATION

6.1 Experimental setup

In this experiment, a total of approximately 12000 lines of experimental code were implemented in C++, supported with the Google open source framework GRPC. In the experimental environment, 1 ~ 8 Huawei cloud servers were adopted in Beijing, Shanghai and Guiyang, respectively, forming a cluster of 3 ~ 24 nodes. Each node follows the same configuration: a 4-core CPU, 8GB of memory, a general-purpose SSD, and the Ubuntu 18.04 operating system. The network between these servers supports an adjustable bandwidth of 1-300Mbit/s, which can simulate the environment of three remote servers with limited bandwidth.

We evaluated the performance of different redistribution strategies (including PRPD [37], PnR [38], and BPPR) specifically designed for skewed data. Afterward, we compare the performance of Bala-Join with other Dist-HJ baselines (with skewness detector) listed below.

- GraHJ: The popular Dist-HJ implementation [21] adopted by many off-the-shelf DDBMSs.
- Flow-Join: A latest Dist-HJ solution [27] with runtime skew detector.

In terms of experimental data, a synthetic dataset with Zipf [41] distribution was used, which was widely adopted in many existing works [16, 20, 27–29] for skewed data. The degree of data skewness is positively correlated with the Zipf factor z . In addition, we also adopted SSB-skew dataset [18] (scale factor is set to 10), which is a variation of the Star Schema Benchmark [25]. Notably, the degree of skewness is not configurable compared to the synthetic dataset,

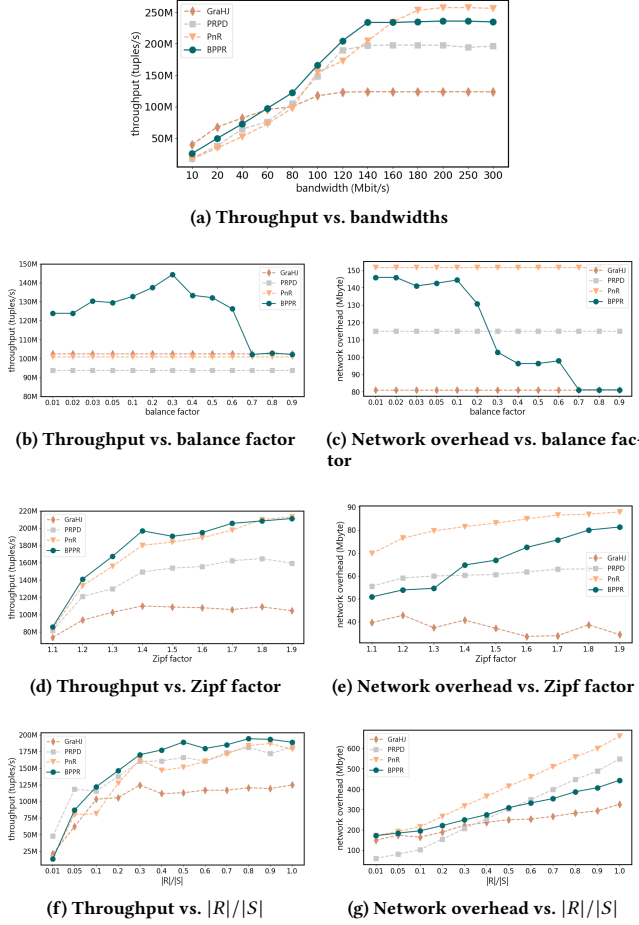


Figure 7: Comparison of distribution strategies in various scenarios

we can only test the performance of Dist-HJ for the join tasks over all the queries in the benchmark (see Sec 6.4).

Performance is evaluated from two main perspectives: efficiency and network overhead. Efficiency is measured by throughput, representing the number of result records produced every second. This offers a concise view of performance without delving into details like table sizes or execution time. On the other hand, network overhead reflects how an algorithm performs with respect to the network environment; higher transmission suggests more network strain.

6.2 Performance of BPPR

Firstly, we conducted a group of experiments to test distributed execution strategies in face of different skewness settings. Hereby, the skewness information is directly provided for each algorithm as an input knowledge.

Figure 7(a) shows the performance of four algorithms at different bandwidths of 10-300 Mbit/s. GraHJ has the lowest network transmission, while BPPR's transmission is 21% less than PnR but 14% more than PRPD. BPPR performs best at medium bandwidths

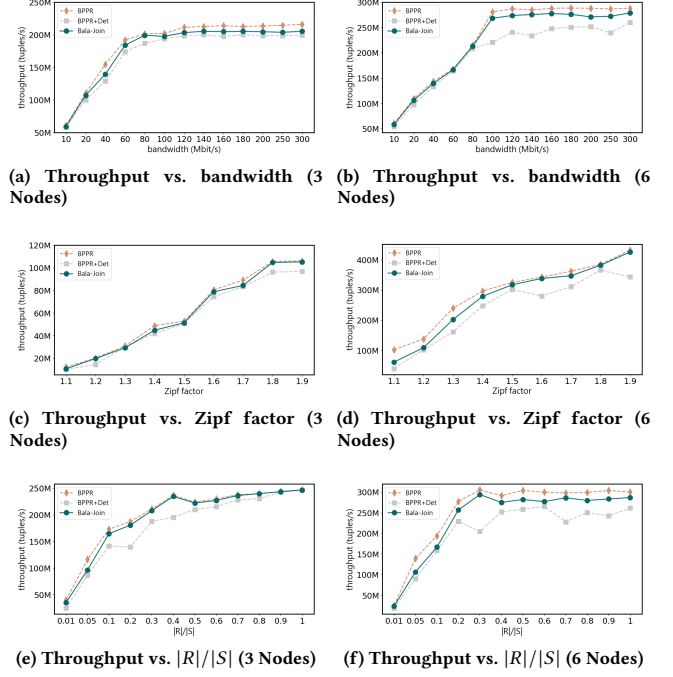


Figure 8: Cost of the runtime skewness detector

and is competitive at high bandwidths, especially when compared to GraHJ.

Figure 7(b) and Figure 7(c) explore the optimal value of the BPPR balance factor. As the balance factor increases, the throughput of BPPR increases in the beginning and achieves the highest value at a balance factor of 0.3. After that, the throughput drops and eventually becomes similar to GraHJ at 0.7.

Figure 7(d) and Figure 7(e) compare algorithms under different Zipf factors, which control the degree of skewness of the data. BPPR outperforms all the other algorithms in the aspect of throughput and ranks 2nd in the aspect of network overhead.

Figure 7(f) and Figure 7(g) test the performance for different $|R|/|S|$ ratios. BPPR remains stable, slightly inferior to PRPD when $|R|/|S|$ is less than 0.1.

Table 2 summarizes the average throughput and rankings of the four sets of experiments. It can be seen that BPPR has a stronger adaptability compared to PRPD and PnR, and it ranks the best in all the experimental settings.

Table 2: Average throughput and ranking of different algorithms over all experiments in Section 6.2

	Bandwidth	Balance Factor	Zipf Factor	$ R / S $	Comprehensive Ranking
BPPR	2144M (1)	1622M (1)	1602M (1)	1848M (1)	7216M (1)
PnR	2064M (2)	1312M (3)	1546M (2)	1646M (3)	6568M (2)
PRPD	1820M (3)	1218M (4)	1273M (3)	1776M (2)	6087M (3)
GraHJ	1367M (4)	1326M (2)	909M (4)	1239M (4)	4841M (4)

6.3 Performance of distributed detector

In this part, we test the performance of the distributed skewed element detector proposed in Section 5.2. Since the strategy is

deeply integrated with BPPR and results in Bala-Join, for fairness, we compare it with two other schemes: BPPR (without skewness detector), which directly provide skewed values to the BPPR algorithm, allowing us to observe any overheads introduced by our distributed runtime detector. BPPR with an independent skewness detector, referred to as BPPR+Det: which employs an independent Space-Saving detection algorithm [3] on BPPR.

By comparing the three schemes, we can evaluate the additional overhead introduced by the distributed detector. Since all of the systems use BPPR for skewed data processing, they do not exhibit any difference in terms of network overhead. The focus here is solely on comparing the throughput of these methods. In subsequent experiments, they are respectively abbreviated as BPPR, BPPR+Det, and Bala-Join, the latter being the strategy introduced in this paper.

Figures 8(a) and 8(b) show the throughput of different strategies in 3-node and 6-node clusters across various bandwidths. In both settings, the performance of Bala-Join lies between BPPR and BPPR+Det. We also test the performance of these strategies in different Zipf factors (Figure 8(c) and 8(d)) and $|R|/|S|$ ratios (Figure 8(e) and 8(f)).

Throughout all experiments, the Bala-Join curve is consistently between BPPR and BPPR+Det. This indicates that the distributed detector in Bala-Join introduces some overhead but is significantly better than simply putting a Space-Saving detector before BPPR, *i.e.*, BPPR+Det, justifying the challenges mentioned in Section 5.2. In general, the overhead of the proposed detector is about 5%, compared to BPPR. The 6-node setup often incurs more overhead than the 3-node setup.

Table 3 summarizes the average throughput per second for the three strategies in each scenario.

Table 3: Average throughput and ranking of different algorithms over all experiments in Section 6.3

	Bala-Join	BPPR+Det	BPPR
Bandwidth (3 nodes)	2319M	2232M(+4%)	2415M(-4%)
Zipf factor (3 nodes)	524M	500M(+5%)	548M(-4%)
$ R / S $ (3 nodes)	2327M	2141M(+9%)	2377M(-2%)
Bandwidth (6 nodes)	2868M	2602M(+10%)	2985M(-4%)
Zipf factor (6 nodes)	2468M	2151M(+15%)	2628M(-6%)
$ R / S $ (6 nodes)	2811M	2451M(+15%)	3030M(-6%)

6.4 Performance of comprehensive Dist-HJ solutions

Finally, we evaluate the comprehensive Dist-HJ solutions (the entire pipeline, including skewness detection, redistribution and computation). Figure 9 and Figure 10 show the comparison of solutions under different scenarios for 3-node and 6-node clusters, respectively. Table 4 summarizes the average throughput per second of each solution in various scenarios, as well as the improvement of our solution relative to Flow-Join and GraHJ.

Figure 11 shows the results for the top-2 joins that appear in the most number of queries in SSB-skew benchmark, within 24-node cluster (similar phenomenon has been observed in other cluster scales). The join predicates for both also lead to different degrees of

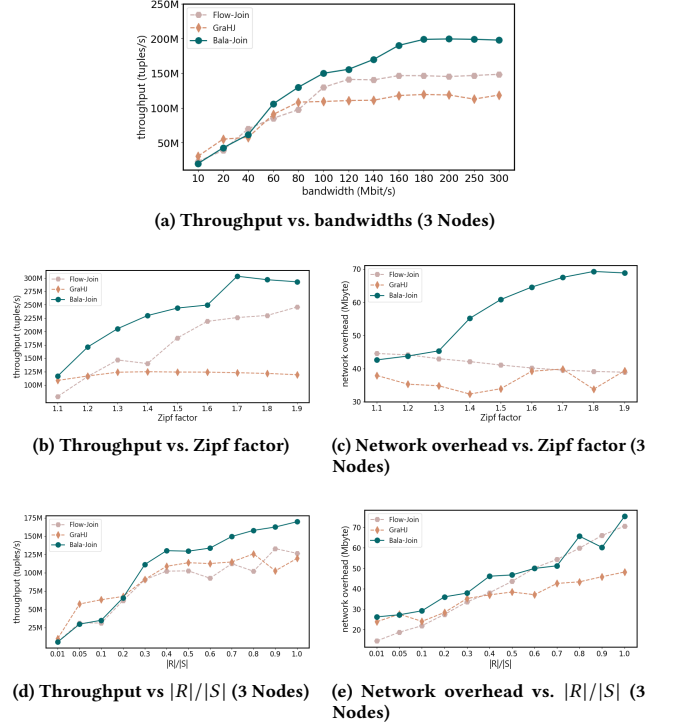


Figure 9: Comparison of Dist-HJ solutions in various scenarios (3 Nodes)

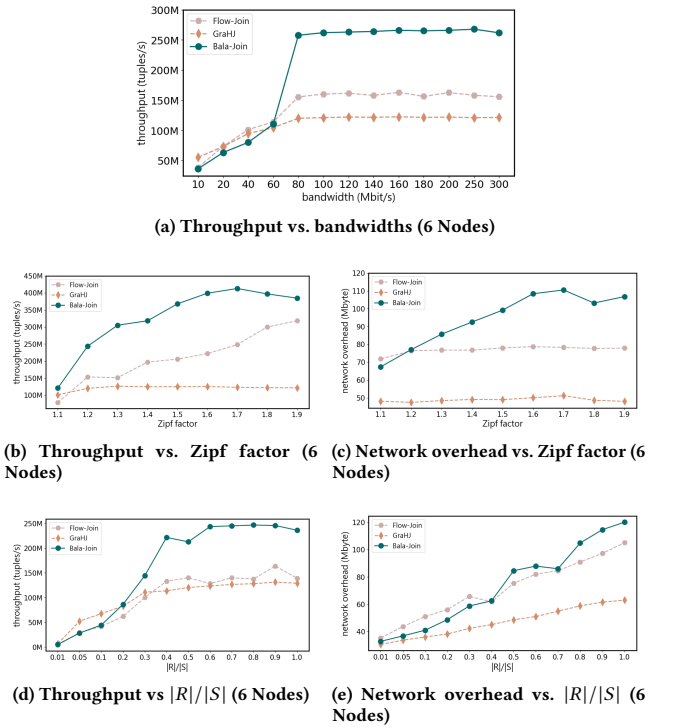


Figure 10: Comparison of Dist-HJ solutions in various scenarios (6 Nodes)

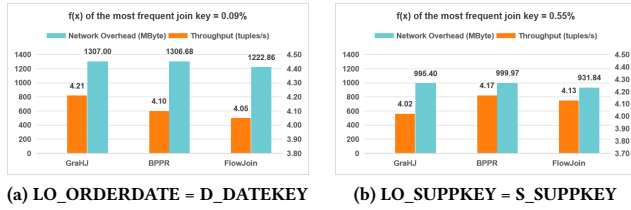


Figure 11: Performance of Dist-HJ solutions on SSB-skew

skew within the joined tuples. Similar to the results in the synthetic dataset, as the degree of skew increases, our solution outperforms GraHJ. Even at lower skew levels, the performance of Bala-Join is also superior to that of Flow Join. This occurs because tuples with identical values are placed next to each other during data splitting, allowing the detector to potentially classify the initially received tuples as skewed.

Among the above experimental scenarios, our comprehensive solution consistently outperforms Flow-Join in terms of throughput. However, it did not have an advantage over Flow-Join in the aspect of network overhead. Furthermore, Flow-Join, relying on its SFR strategy in the skewness processing, exhibited a trend of decreasing network overhead while the number of nodes in the cluster increases from 3 to 6. However, the results of our test scenarios still show how our solution strikes a better balance between network performance and computational performance. Despite the higher network overhead, our algorithm displays superior execution efficiency.

Table 4: Average throughput and ranking of different Dist-HJ implementations over all experiments in Section 6.4

	Bala-Join	Flow-Join	GraHJ
Bandwidth (3 nodes)	1818M	1460M(+25%)	1261M(+44%)
Zipf factor (3 nodes)	2106M	1594M(+32%)	1082M(+95%)
R / S (3 nodes)	1281M	994M(+29%)	1087M(+18%)
Bandwidth (6 nodes)	2659M	1761M(+51%)	1423M(+89%)
Zipf factor (6 nodes)	2953M	1870M(+58%)	1091M(+171%)
R / S (6 nodes)	1957M	1217M(+61%)	1192M(+65%)

7 CONCLUSIONS

Distributed Hash Join is a fundamental operator in distributed databases, the implementation of which in most DDBMSs is based on the principle of hash partitioning. Although this approach is straightforward to develop and maintain, the system experiences significant throughput degradation when confronted with data skewness. In this paper, we propose a BPPR algorithm to handle skewed data with high adaptability and outstanding performance. We also theoretically proved the accuracy of the algorithm. Subsequently, we propose a distributed skewness detection strategy tailored to the BPPR algorithm. It deeply couples with the BPPR algorithm and adopts the Active-Signaling and Asynchronous-Pulling (ASAP) mechanism. The mechanism imperceptibly enables the provision in real-time of skewness information to BPPR, limiting the additional overhead of skewed value detection. Experimental results justify that our comprehensive Dist-HJ solution, *i.e.*, Bala-Join,

effectively balances the network and computational performance, achieving superior overall efficiency.

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