Distributed Slicing in Dynamic Systems

Antonio Fernández Anta, Vincent Gramoli, Ernesto Jiménez, Anne-Marie Kermarrec and Michel Raynal

***Abstract*—Peer to peer (P2P) systems have moved from application specific architectures to a generic service oriented design philosophy. This raised interesting problems in connection with providing useful P2P middleware services capable of dealing with resource assignment and management in a large-scale, heterogeneous and unreliable environment. The slicing problem consists of partitioning a P2P network into k groups (slices) of a given portion of the network nodes that share similar resource values. As the network is large and dynamic this partitioning is continuously updated without any node knowing the network size.**

In this paper, we propose the first algorithm to solve the slicing problem. We introduce the metric of slice disorder and show that the existing ordering algorithm cannot nullify this disorder. We propose a new algorithm that speeds up the existing ordering algorithm but that suffers from the same inaccuracy. Then, we propose another algorithm based on ranking that is provably convergent under reasonable assumptions. In particular, we notice experimentally that ordering algorithms suffer from resource-correlated churn while the ranking algorithm can cope with it. These algorithms are proved viable theoretically and experimentally.

Keywords: slice, gossip, churn, peer-to-peer, aggregation, large scale.

I. Introduction

The peer to peer (P2P) communication paradigm has now become the prevalent model to build large-scale distributed applications, like VoIP [2] and VOD [10], able to cope with both scalability and system dynamics. This is now a mature technology: P2P systems are moving from application-specific architectures to a generic-service oriented design philosophy. More specifically, P2P protocols integrate into platforms on top of which several applications, with various requirements, may cohabit. This leads to the interesting issue of resource assignment or how to allocate a set of nodes for a given application. Examples of targeted platforms for such a service are testbed platforms such as Planetlab [3] and video streaming platforms where some nodes are automatically selected to build an overlay depending on their observed stability [39].

Even in a single application, a P2P system should be able to balance the load taking into account that capabilities are heterogeneous at the peers. This ability would be of great interest since many works have unveiled the heavy-tailed distribution of storage space, bandwidth, and uptime of peers [34], [4], [37]. Currently, this heterogeneity has two drawbacks. First, the service guarantees offered by the P2P system are unpredictable and can consequently provide the clients with a poor quality of service. Second, when low capable peers are overloaded, the general performance of the system can be affected. For example, the completely decentralized P2P application, Gnutella, suffered from congestion when applied to large-scale systems [32] because nodes with a low bandwidth capability were queried. Consequently, modern P2P applications select specific nodes depending on their capabilities to improve the service. For example, outliers detection platforms [15] identify malicious nodes by propagating their associated suspicion values while Skype [2] elects super-nodes among nodes with high bandwidth that are not hidden behind a Firewall/NAT.

Large scale dynamic distributed systems consist of many participants that can join and leave at will. Identifying peers in such systems that have a similar level of power or capability (for instance, in terms of bandwidth, processing power, storage space, or uptime) in a completely decentralized manner is a difficult task. It is even harder to maintain this information in the presence of churn. Due to the intrinsic dynamics of contemporary P2P systems it is impossible to obtain accurate information about the capabilities (or even the identity) of the system participants. Consequently, no node is able to maintain accurate information about all other nodes. This disqualifies centralized approaches.

The slicing service enables peers in a large-scale unstructured network to self-organize into a partitioning, where partitions (*slices*) are equally-sized sets of nodes that share some similarities. Such slices can be either allocated to specific applications later on, or associated with specific roles (e.g., normal peers and superpeers). Given a set of nodes, each with a specific attribute value, the slicing problem is for each node to learn in which portion (or slice) of the system its attribute value belongs to. The existing result tried to approximate slices by ordering nodes depending on a random value drawn initially [23], leading to a result whose precision depends on the uniformity of the distribution of initial values. Among all random values drawn in a range r, if not exactly half of them belong to the lower half of r, then some nodes would never find their slice. As we show in this paper, this inaccuracy gets exacerbated in a dynamic environment where nodes may join and leave.

A preliminary version of this work appeared in the proceedings of ICDCS 2007 [12]. The additional material proves the convergence of the Ranking algorithm, proves the inaccuracy of the mod-JK algorithms and presents an extended related work.

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A. Contributions

This paper presents the first provably converging solution to the slicing problem provided that attribute values belong to some slice. More particularly, it presents two gossip-based solutions to slice the nodes according to their capability (reflected by an attribute value) in a distributed manner with high probability. The first algorithm of the paper improves the ordered slicing proposed algorithm [23] that we call the JK algorithm in the sequel of this paper. The second algorithm is a different approach based on rank approximation through statistical sampling.

In JK, each node i maintains a random number r_i, picked up uniformly at random (between 0 and 1), and an attribute value a_i, expressing its capability according to a given metric. Each peer periodically gossips with another peer j, randomly chosen among the peers it knows about. If the order between r_j and r_i is different from the order between a_j and a_i, random values are swapped between nodes. The algorithm ensures that eventually the order on the random values matches the order of the attribute ones. The quality of the ranking can then be measured by using a global disorder measure expressing the difference between the exact rank and the actual rank of each peer along the attribute value.

The first contribution of this paper is to locally compute a disorder measure so that a peer chooses the neighbor to communicate with in order to maximize the chance of decreasing the global disorder measure. The purpose of this approach is to speed up the convergence. We provide the analysis and experimental results of this improvement.

Then, we identify two issues that prevent accurate slicing and motivate us to find an alternative approach to this algorithm and JK.

On the one hand, once peers are ordered along the attribute values, the slicing in JK takes place as follows. Random values are used to calculate which slice a node belongs to. For example, a slice containing 20% of the best nodes according to a given attribute, will be composed of the nodes that end up holding random values greater than 0.8. The accuracy of the slicing (independent from the accuracy of the ranking) fully depends on the uniformity of the random value spread between 0 and 1 and the fact that the proportion of random values between 0.8 and 1 is approximately (but usually not exactly) 20% of the nodes. This observation means that the problem of ordering nodes based on uniform random values is not fully sufficient for determining slices.

On the other hand, another motivation for an alternative approach is related to churn and dynamism. It may well happen that the churn is actually correlated to the attribute value. For example, if the peers are sorted according to their connectivity potential, a portion of the attribute space (and therefore the random value space) might be suddenly affected. New nodes will then pick up new random values and eventually the distribution of random values will be skewed towards high values. If this happens we say that the churn is *attribute-correlated*.

The second contribution is an alternative algorithm solving these issues by approximating the rank of the nodes in the ordering locally, without the application of random values. The basic idea is that each node periodically estimates its rank along the attribute axis depending of the attributes it has seen so far. This algorithm is robust and lightweight due to its gossip-based communication pattern: each node communicates periodically with a restricted dynamic neighborhood that guarantees connectivity and provides a continuous stream of new samples. Based on continuously aggregated information, the node can determine the slice it belongs to with a decreasing error margin. We show that this algorithm provides accurate estimation and recovery ability in presence of attributes-correlated churn at the price of a slower convergence.

B. Roadmap

The rest of the paper is organized as follows: Section II surveys some related work. The system model is presented in Section III. The first contribution of an improved ordered slicing algorithm based on random values is presented in Section IV and the second algorithm based on dynamic ranking in Section V. Section VI concludes the paper.

II. Related Work

Original proposed solutions for ordering nodes came from the context of databases, where parallelizing query executions is used to improve efficiency. A large majority of the solutions in this area rely on centralized gathering or all-to-all exchange, which makes them unsuitable for large-scale networks.

A. Ordering Techniques

The *external sorting problem* [9] consists of providing a distributed sorting algorithm where the memory space of each processor does not necessarily depend on the input. This algorithm must output a sorted sequence of values distributed among processors. The solution proposed in [9] needs a global merge of the whole information, and thus it implies a centralization of information. Similarly, the *percentile finding* problem [21], which aims at dividing a set of values into equally sized sets, requires a logarithmic number of all-to-all message exchanges.

Other related problems are the selection problem and the ϕ-quantile search. The selection problem [13], [6] aims at determining the i^{th} smallest element with as few comparisons as possible. The *ϕ-quantile* search (with $\phi \in (0,1]$) is the problem of finding among n elements the $(\phi n)^{th}$ element. Even though these problems look similar to our problem, they aim at finding a specific node among all, while the distributed slicing problem aims at solving a global problem where each node maintains a piece of information. Additionally, solutions to the quantile search problem like the one presented in [26] use an approximation of the system size. The same holds for the algorithm in [33], which uses similar ideas to determine the distribution of a utility in order to isolate peers with high capability—i.e., super-peers.

A less related problem but with motivations similar to the slicing problem is the stratification problem [16] that differentiates peers based on their attributes in the context of incentive-based file sharing applications. Stratification defines one set of similar nodes for each single node while the slicing problem defines sets of similar nodes that are identical for all nodes. Finally, solving the more general problem of aggregating global information at each node can also solve the slicing problem without the need for gossip [5], however, typical solutions require multiple random walks per peer [14], a thousand of them was shown effective on some networks [11].

B. Slicing Variants

More recently, gossip-based protocols were used to discriminate nodes in a large network depending on their individual attributes. Some of them order nodes rather than slicing them [23], some assume a different model [30], [19], [28] and some aim at applying similar techniques to different contexts [8], [35], [36].

The *JK algorithm* is an algorithm that helps the node with the k^{th} smallest attribute value, among those in a system of size n, estimate its normalized index k/n. Initially, each node draws independently and uniformly a random value in the interval $(0, 1]$ which serves as its first estimate of its normalized index. Then, the nodes use a variant of Newscast [25] to gossip among each other to exchange random values when they find that the relative order of their random values and that of their attribute values do not match. As the algorithm exchanges random values among peers to reflect the order given by their attribute values, the estimate quality depends on the accuracy of the randomness of the values. T-Rank [29] proposed to solve a similar problem by ranking nodes and informing them about global information. More recently, a gossip-based protocol for ordering was also shown effective in renaming [17].

Sliver [18], [19] is a slicing protocol that adjusts the precision of slice membership by storing information about the global network at each individual node. Each node keeps track of the identity and attribute value it received so that it can distinguish between a duplicated information (the same attribute value from the same node received twice) from useful information (attribute values received from different nodes). The space needed at each is $O(n)$ as Sliver solves the slicing problem once a node obtains information about all the nodes of the network.

Slead [28] addresses the problem of Sliver by using Bloom filters to compress the global view of the system with a bounded memory footprint. It exploits a dynamic Bloom filter to adjust to the changes of the attribute value distribution, however, it prevents from adjusting the recency of information used to compute the slice membership. DSlead [27] improves Slead by adjusting the removal of stale information from the Bloom filter using a function of time. Other slicing solutions were investigated in the context of population protocols [7]. In this model, the nodes can neither store a large amount of information nor generate random numbers.

The absolute slicing problem [30] is a variant of the slicing problem in which the size of a slice represents a fixed number of nodes. The problem is different from the slicing problem in that the size is known when the algorithm starts. By contrast, in the slicing problem, nodes cannot be aware of the system size n. They ignore the exact number of nodes within one slice as this is a fraction of n. Our preliminary version of this work [12] was characterized as a typical gossip-based technique as it helps reaching a global result with local message exchanges in a large-scale system [8] but it did not include the proof of convergence that we present here.

Since then, the slicing problem has found applications to select nodes that can help bypass NAT [35], [36] in networks. First, Whisper [35] ensures the integrity of messages exchanged between the members of each slice, while ensuring confidentiality of the slice members to an external observer. It generalizes the slicing service to multiple dimensions, offering to segregate nodes into groups depending on the node attribute values. Second, RankSlicing [36] slices a peer-to-peer network to help bypassing NAT, but aims at connecting peers that are part of the same slice. It uses a similar notion of "age" as our ranking algorithm to assess the recency of information and discard stale information.

III. Model and Problem Statement

A. System Model

We consider a system Σ containing a set of n uniquely identified nodes.[1] The set of identifiers is denoted by $I \subset \mathbb{N}$. Each node can leave and new nodes can join the system at any time, thus the number of nodes is a function of time. Nodes may also crash. In this paper, we do not differentiate between a crash and a voluntary node departure.

Each node i maintains a fixed attribute value $a_i \in \mathbb{N}$, reflecting the node capability according to a specific metric. These attribute values over the network might have an arbitrary skewed distribution. Initially, a node has no global information neither about the structure or size of the system nor about the attribute values of the other nodes.

We can define a total ordering over the nodes based on their attribute value, with the node identifier used to break ties. Formally, we let i precede j if and only if $a_i < a_j$, or $a_i = a_j$ and $i < j$. We refer to this totally ordered sequence as the *attribute-based sequence*, denoted by $A.sequence$. The attribute-based rank of a node i, denoted by $\alpha_i \in \{1, ..., n\}$, is defined as the index of a_i in $A.sequence$. For instance, let us consider three nodes: 1, 2, and 3, with three different attribute values $a_1 = 50$, $a_2 = 120$, and $a_3 = 25$. In this case, the attribute-based rank of node 1 would be $\alpha_1 = 2$. In the rest of the paper, we assume that nodes are sorted according to a single attribute

[1] The value n is observed instantaneously but may vary over time.

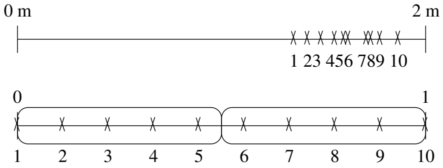

Fig. 1. Slicing of a population based on a height attribute.

and that each node belongs to a unique slice. The sorting along several attributes is out of the scope of this paper.

B. Distributed Slicing Problem

Let $\mathcal{S}_{l,u}$ denote the *slice* containing every node i whose normalized rank, namely $\frac{\alpha_i}{n}$, satisfies $l < \frac{\alpha_i}{n} \leq u$ where $l \in [0, 1)$ is the slice lower boundary and $u \in (0, 1]$ is the slice upper boundary so that all slices represent adjacent intervals $(l_1, u_1], (l_2, u_2]$... Let us assume that we partition the interval $(0, 1]$ using a set of slices, and this partitioning is known by all nodes. The distributed slicing problem requires each node to determine the slice it currently belongs to. Note that the problem stated this way is similar to the ordering problem, where each node has to determine its own index in $A.sequence$. However, the reference to slices introduces special requirements related to stability and fault tolerance, besides, it allows for future generalizations when one considers different types of categorizations.

Figure 1 illustrates an example of a population of 10 persons, to be sorted against their height. A partition of this population could be defined by two slices of the same size: the group of short persons, and the group of tall persons. This is clearly an example where the distribution of attribute values is skewed towards 2 meters. The rank of each person in the population and the two slices are represented on the bottom axis. Each person is represented as a small cross on these axes.[2] Each slice is represented as an oval. The slice $S_1 = \mathcal{S}_{0,\frac{1}{2}}$ contains the five shortest persons and the slice $S_2 = \mathcal{S}_{\frac{1}{2},1}$ contains the five tallest persons.

Observe that another way of partitioning the population could be to define the group of short persons as the group containing all the persons shorter than a predefined measure (e.g., $1.65m$) and the group of tall persons as that containing the persons taller than this measure. However, this way of partitioning would most certainly lead to have empty groups that contains no nodes (while a slice is almost surely non-empty). Since the distribution of attribute values is unknown and hard to predict, defining relevant groups is a difficult task. For example, if the distribution of the human heights were unknown, then the persons taller than $1m$ could be considered as tall and the persons shorter than $1m$ could be considered as short. In this case, the first of the two groups would be empty, while the second of the two groups would be as big as the whole system. Conversely, slices partition the population into subsets representing a predefined portion of this population. Therefore, in the rest of the paper, we consider slices as defined as a proportion of the network.

C. Facing Churn

Node churn, that is, the continuous arrival and departure of nodes is an intrinsic characteristic of P2P systems and may significantly impact the outcome, and more specifically the accuracy of the slicing algorithm. The easier case is when the distribution of the attribute values of the departing and arriving nodes are identical. In this case, in principle, the arriving nodes must find their slices, but the nodes that stay in the system are mostly able to keep their slice assignment. Even in this case however, nodes that are close to the border of a slice may expect frequent changes in their slice due to the variance of the attribute values, which is non-zero for any non-constant distribution. If the arriving and departing nodes have different attribute distributions, so that the distribution in the actual network of live nodes keeps changing, then this effect is amplified. However, we believe that this is a realistic assumption to consider that the churn may be correlated to some specific values (for example if the considered attribute is uptime mean or connectivity).

IV. Dynamic Ordering by Exchange of Random Values

This section proposes an algorithm for the distributed slicing problem improving upon the original JK algorithm [23], by considering a local measure of the global disorder function. In this section we present the algorithm along with the corresponding analysis and simulation results.

A. On Using Random Numbers to Sort Nodes

This Section presents the algorithm built upon JK. We refer to this algorithm as *mod-JK* (standing for modified JK). In JK, each node i generates a real number $r_i \in (0, 1]$ independently and uniformly at random. The key idea is to sort these random numbers with respect to the attribute values by swapping (i.e., exchanging) these random numbers between nodes, so that if $a_i < a_j$ then $r_i < r_j$. Eventually, the attribute values (that are fixed) and the random values (that are exchanged) should be sorted in the same order. That is, each node would like to obtain the x^{th} largest random number if it owns the x^{th} largest attribute value. Let $R.sequence$ denote the *random sequence* obtained by ordering all nodes according to their random number. Let $\rho_i(t)$ denote the index of node i in $R.sequence$ at time t. When not required, the time parameter is omitted.

To illustrate the above ideas, consider that nodes 1, 2, and 3 from the previous example have three distinct random values: $r_1 = 0.85$, $r_2 = 0.1$, and $r_3 = 0.35$. In this case, the index ρ_1 of node 1 would be 3. Since the attribute values are $a_1 = 50$, $a_2 = 120$, and $a_3 = 25$, the algorithm must achieve the following final assignment of random numbers: $r_1 = 0.35$, $r_2 = 0.85$, and $r_3 = 0.1$.

Once sorted, the random values are used to determine the portion of the network a peer belongs to.

[2] Note that the shortest (resp. largest) rank is represented by a cross at the extreme left (resp. right) of the bottom axis.

B. Definitions

1) View: Every node i keeps track of some neighbors and their age. The *age* of neighbor j is a timestamp, t_j, set to 0 when j becomes a neighbor of i. Thus, node i maintains an array containing the id, the age, the attribute value, and the random value of its neighbors. This array, denoted $\mathcal{N}_i$, is called the *view* of node i. The views of all nodes have the same size, denoted by c.

2) Misplacement: A node participates in the algorithm by exchanging its rank with a misplaced neighbor in its view. Neighbor j is misplaced if and only if

- $a_i > a_j$ and $r_i < r_j$, or
- $a_i < a_j$ and $r_i > r_j$.[3]

We can characterize these two cases by the predicate $(a_j - a_i)(r_j - r_i) < 0$.

3) Global Disorder Measure: In [23], a measure of the relative disorder of sequence $R.sequence$ with respect to sequence $A.sequence$ was introduced, called the *global disorder measure (GDM)* and defined, for any time t, as

$$GDM(t) = \frac{1}{n} \sum_i (\alpha_i - \rho(t)_i)^2.$$

The minimal value of GDM is 0, which is obtained when $\rho(t)_i = \alpha_i$ for all nodes i. In this case the attribute-based index of a node is equal to its random value index, indicating that random values are ordered.

C. Improved Ordering Algorithm

In this algorithm, each node i searches its own view $\mathcal{N}_i$ for misplaced neighbors. Then, one of them is chosen to swap random value with. This process is repeated until there is no global disorder. In this version of the algorithm, we provide each node with the capability of measuring disorder locally. This leads to a new heuristic for each node to determine the neighbor to exchange with which decreases most the disorder.

The proposed technique attempts to decrease the global disorder in each exchange as much as possible via selecting the neighbor from the view that minimizes the local disorder (or, equivalently, maximizes the order *gain*) as defined below. Referring to this disorder measure as a criterion, the decrease of the global criterion is related to the decrease of local criteria, similarly to [1].

```
Initial state of node $i$
$\mathcal{N}_i$, the view initially filled of some neighbor entries;
$c \geq k+1$, the view size.

Active thread at node $i$
for $j' \in \mathcal{N}_i$
    $t_{j'} \leftarrow t_{j'} + 1$
$j \leftarrow j'' : t_{j''} = \mathsf{max}_{j' \in \mathcal{N}_i}(t_{j'})$
$\mathsf{send}(\mathsf{REQ}', \mathcal{N}_i \setminus \{e_j\} \cup \{\langle i, 0 \rangle\})$ to $j$
$\mathsf{recv}(\mathsf{ACK}', \mathcal{N}_j)$ from $j$
$\mathit{duplicated\text{-}entries} = \{e : e.id \in \mathcal{N}_j \cap \mathcal{N}_i\}$
$\mathcal{N}_i^{init} \leftarrow \mathcal{N}_i$
$\mathcal{N}_i \leftarrow \mathcal{N}_j \setminus \mathit{duplicated\text{-}entries} \setminus \{e_i\}$
for $e_k \in \mathcal{N}_i^{init}$
    if $|\mathcal{N}_i| < c$
        $\mathcal{N}_i \leftarrow \mathcal{N}_i \cup \{e_k\}$

Passive thread at node $i$ activated upon reception
$\mathsf{recv}(\mathsf{REQ}', \mathcal{N}_j)$ from $j$
$\mathsf{send}(\mathsf{ACK}', \mathcal{N}_i)$ to $j$
$\mathit{duplicated\text{-}entries} = \{e \in \mathcal{N}_j : e.id \in \mathcal{N}_j \cap \mathcal{N}_i\}$
$\mathcal{N}_i \leftarrow \mathcal{N}_j \setminus \mathit{duplicated\text{-}entries}$
for $e_k \in \mathcal{N}_i^{init}$
    if $|\mathcal{N}_i| < c$
        $\mathcal{N}_i \leftarrow \mathcal{N}_i \cup \{e_k\}$
```

Fig. 2. Gossip-based neighborhood management using a variant of Cyclon.

For a node i to evaluate the gain of exchanging with a node j of its current view $\mathcal{N}_i$, we define its *local disorder measure* (abbreviated *LDM*$_i$). Let $LA.sequence_i$ and $LR.sequence_i$ be the local attribute sequence and the local random sequence of node i, respectively. These sequences are computed locally by i using the information $\mathcal{N}_i \cup \{i\}$. Similarly to $A.sequence$ and $R.sequence$, these are the sequences of neighbors where each node is ordered according to its attribute value and random number, respectively. Let, for any $j \in \mathcal{N}_i \cup \{i\}$, $\ell\rho_j(t)$ and $\ell\alpha_j(t)$ be the indices of r_j and a_j in sequences $LR.sequence_i$ and $LA.sequence_i$, respectively, at time (t). At any time t, the local disorder measure of node i is defined as:

$$LDM_i(t) = \frac{1}{c+1} \sum_{j \in \mathcal{N}_i(t) \cup \{i\}} (\ell\alpha_j(t) - \ell\rho_j(t))^2.$$

We denote by $G_{i,j}(t+1)$ the reduction on this measure that i obtains after exchanging its random value with node j between time t and $t+1$. We define it as:

$$\begin{aligned} G_{i,j}(t+1) &= LDM_i(t) - LDM_i(t+1), \\ G_{i,j}(t+1) &= [(\ell\alpha_i(t) - \ell\rho_i(t))^2 + (\ell\alpha_j(t) - \ell\rho_j(t))^2 - \\ &\quad (\ell\alpha_i(t) - \ell\rho_j(t))^2 - (\ell\alpha_j(t) - \\ &\quad \ell\rho_i(t))^2] \frac{1}{c+1}. \end{aligned} \tag{1}$$

The heuristic used chooses for node i the misplaced neighbor j that maximizes $G_{i,j}(t+1)$.

1) Sampling uniformly at random: The algorithm relies on the fact that potential misplaced nodes are found so that they can swap their random numbers thereby increasing order. If the global disorder is high, it is very likely that any given node has misplaced neighbors in its view to exchange with. Nevertheless, as the system gets ordered, it becomes more unlikely for a node i to have misplaced neighbors. In this stage the way the view is composed plays a crucial role: if fresh samples from the network are not available, convergence can be slower than optimal.

Several protocols may be used to provide a random and dynamic sampling in a P2P system such as Newscast [25], Cyclon [38] or Lpbcast [22]. They differ mainly by their *closeness* to the uniform random sampling of the neighbors and the way they handle churn. In this paper, we chose to use a variant of the Cyclon protocol, to construct and update the views, as it is reportedly the best approach to achieve a uniform random neighbor set for all nodes [20].

[3] Note that j is not misplaced in case $a_i = a_j$, regardless of values r_i and r_j.

```
Initial state of node $i$
(1)  $period_i$, initially set to a constant;
$r_i$, a random value chosen in $(0,1]$; $a_i$, the attribute value;
$slice_i \leftarrow \perp$, the slice $i$ belongs to; $\mathcal{N}_i$, the view;
$gain_{j'}$, a real value indicating the gain achieved by
    exchanging with $j'$;
$gain\text{-}max = 0$, a real.

Active thread at node $i$
(2)  wait($period_i$)
(3)  recompute-view$()_i$
(4)  for $j' \in \mathcal{N}_i$
(5)    if $gain_{j'} \geq gain\text{-}max$ then
(6)      $gain\text{-}max \leftarrow gain_{j'}$
(7)      $j \leftarrow j'$
(8)  end for
(9)  send(REQ, $r_i, a_i$) to $j$
(10) recv(ACK, $r'_j$) from $j$
(11) $r_j \leftarrow r'_j$
(12) if $(a_j - a_i)(r_j - r_i) < 0$ then
(13)   $r_i \leftarrow r_j$
(14)   $slice_i \leftarrow \mathcal{S}_{l,u}$ such that $l < r_i \leq u$

Passive thread at node $i$ activated upon reception
(15) recv(REQ, $r_j, a_j$) from $j$
(16) send(ACK, $r_i$) to $j$
(17) if $(a_j - a_i)(r_j - r_i) < 0$ then
(18)   $r_i \leftarrow r_j$
(19)   $slice_i \leftarrow \mathcal{S}_{l,u}$ such that $l < r_i \leq u$
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Fig. 3. Dynamic ordering by exchange of random values.

2) Description of the algorithm: The algorithm is presented in Figure 3. The active thread at node i runs the membership (gossiping) procedure (recompute-view$()_i$) and the exchange of random values periodically using the algorithm presented in Figure 2. Each node i maintains a view $\mathcal{N}_i$ containing one entry per neighbor. Node i copies its view, selects the oldest neighbor j of its view, removes the entry e_j of j from the copy of its view, and finally sends the resulting copy to j. When j receives the view, j sends its own view back to i discarding possible pointers to i, and i and j update their view with the one they receive by firstly keeping the entries they received. In the original Cyclon a subset $1 \leq \ell \leq c$ of the view is tossed uniformly at random to be exchanged. In our version, the whole view is simply exchanged so that no pseudo-random generator is used to select a subset of the view. This corresponds to fixing the original subset to the entire view, $\ell = c$.

The algorithm for exchanging random values from node i starts by measuring the ordering that can be gained by swapping with each neighbor (Lines 4–8). Then, i chooses the neighbor $j \in \mathcal{N}_i$ that maximizes gain $G_{i,k}$ for any of its neighbor k. Formally, i finds $j \in \mathcal{N}_i$ such that for any $k \in \mathcal{N}_i$, we have

$$G_{i,j}(t+1) \quad \geq \quad G_{i,k}(t+1). \tag{2}$$

Using the definition of $G_{i,j}$ in Equation (1), Equation (2) is equivalent to

$$\begin{aligned} \ell\alpha_i(t)\ell\rho_j(t) + \ell\alpha_j(t)\ell\rho_i(t) - \ell\alpha_j(t)\ell\rho_j(t) \quad &\geq \\ \ell\alpha_i(t)\ell\rho_k(t) + \ell\alpha_k(t)\ell\rho_i(t) - \ell\alpha_k(t)\ell\rho_k(t). \end{aligned} \tag{3}$$

In Figure 3 of node i, we refer to $gain_j$ as the value of $\ell\alpha_i(t)\ell\rho_j(t) + \ell\alpha_j(t)\ell\rho_i(t) - \ell\alpha_j(t)\ell\rho_j(t)$.

From this point on, i exchanges its random value r_i with the random value r_j of node j (Line 11). The passive threads are executed upon reception of a message. In Figure 3, when j receives the random value r_i of node i, it sends back its own random value r_j for the exchange to occur (Lines 15–16). Observe that the attribute value of i is also sent to j, so that j can check if it is correct to exchange before updating its own random number (Lines 17–18). Node i does not need to receive attribute value a_j of j, since i already has this information in its view and the attribute value of a node never changes over time.

D. Analysis of Slice Misplacement

In mod-JK, as in JK, the current random number r_i of a node i determines the slice s_i of the node. The objective of both algorithms is to reduce the global disorder as quickly as possible. Algorithm mod-JK consists of choosing one neighbor among the possible neighbors that would have been chosen in JK, plus the GDM of JK has been shown to fit an exponential decrease. Consequently mod-JK experiences also an exponential decrease of the global disorder. Eventually, JK and mod-JK ensure that the disorder has fully disappeared. For further information, please refer to [23].

However, the accuracy of the slices heavily depends on the uniformity of the random value spread between 0 and 1. It may happen, that the distribution of the random values is such that some peers decide upon a wrong slice. Even more problematic is the fact that this situation is unrecoverable unless a new random value is drawn for all nodes. This may be considered as an inherent limitation of the approach. For example, consider a system of size 2, where nodes 1 and 2 have the random values $r_1 = 0.1$, $r_2 = 0.4$. If we are interested in creating two slices S_1 and S_2 of equal size ($S_1 = \mathcal{S}_{0,\frac{1}{2}}$ and $S_2 = \mathcal{S}_{\frac{1}{2},1}$), both nodes will wrongly believe to belong to the same slice S_1, since r_1 and r_2 belong to $(0, \frac{1}{2}]$. This wrong estimate holds even after perfect ordering of the random values.

Therefore, an important step is to characterize the inaccuracy of slice assignment and how likely it may happen. To this end, we lower bound the deviation of random values distribution from the mean, and the probability that this happen with only two slices. First of all, consider a slice S_p of length p. In a network of n nodes, the number of nodes that will fall into this slice is a random variable X with a binomial distribution with parameters n and p. The standard deviation of X is therefore $\sqrt{np(1-p)}$. This means that the relative proportional expected difference from the mean (i.e., np) can be approximated as $\sqrt{(1-p)/(np)}$, which is very large if p is small, in fact, goes to infinity as p tends to zero, although a very large n compensates for this effect. For a reasonably large network, however, a constant number of slices results in a relatively large value p and a very low variance.

To stay with this random variable, the following result bounds, with high probability, its deviation from its mean.

Lemma 4.1: For any $\beta \in (0,1]$, a slice S_p of length

$p \in (0,1]$ has a number of peers $X \in [(1-\beta)np, (1+\beta)np]$ with probability at least $1-\epsilon$ as long as $p \geq \frac{3}{\beta^2 n}\ln(2/\epsilon)$.

Proof: The way nodes choose their random number is like drawing n times, with replacement and independently uniformly at random, a value in the interval $(0,1]$. Let $X_1, ..., X_n$ be the n corresponding independent identically distributed random variables such that:

$$\begin{cases} X_i &= 1 \text{ if the value drawn by node } i \text{ belongs to } S_p \text{ and} \\ X_i &= 0 \text{ otherwise.} \end{cases}$$

We denote $X = \sum_{i=1}^{n} X_i$ the number of elements of interval S_p drawn among the n drawings. The expectation of X is np. From now on we compute the probability that a bounded portion of the expected elements are misplaced. Two Chernoff bounds [31] give:

$$\left.\begin{array}{ll} \Pr[X \geq (1+\beta)np] & \leq e^{-\frac{\beta^2 np}{3}} \\ \Pr[X \leq (1-\beta)np] & \leq e^{-\frac{\beta^2 np}{2}} \end{array}\right\}$$

$\Rightarrow \Pr[|X - np| \geq \beta np] \leq 2e^{-\frac{\beta^2 np}{3}}$,
with $0 < \beta \leq 1$. That is, the probability that more than (β time the number expected) elements are misplaced regarding to interval S_p is bounded by $2e^{-\frac{\beta^2 np}{3}}$. We want this to be at most ϵ. This yields the result. ■

To measure the effect discussed above during the simulation experiments, we introduce the slice disorder measure (SDM) as the sum over all nodes i of the distance between the slice i actually belongs to and the slice i believes it belongs to. For example (in the case where all slices have the same size), if node i belongs to the 1^{st} slice (according to its attribute value) while it thinks it belongs to the 3^{rd} slice (according to its rank estimate) then the distance for node i is $|1-3| = 2$. Formally, for any node i, let S_{u_i,l_i} be the actual correct slice of node i and let $S_{\hat{u_i},\hat{l_i}}(t)$ be the slice i estimates as its slice at time t. The slice disorder measure is defined as:

$$SDM(t) = \sum_i \frac{1}{u_i - l_i} \left| \frac{u_i + l_i}{2} - \frac{\hat{u_i} + \hat{l_i}}{2} \right|.$$

$SDM(t)$ is minimal (equals 0) if for all nodes i, we have $S_{\hat{u_i},\hat{l_i}}(t) = S_{u_i,l_i}$.

In fact, it is simple to show that, in general, the probability of dividing n peers into two slices of the same size is less than $\sqrt{2/n\pi}$. This value is very small even for moderate values of n. Hence, it is highly possible that the random number distribution does not lead to a perfect division into slices.

E. Simulation Results

We present simulation results using PeerSim [24], using a simplified cycle-based simulation model, where all messages exchanges are atomic, so messages never overlap. First, we compare the performance of the two algorithms: JK and mod-JK. Second, we study the impact of concurrency that is ignored by the cycle-based simulations.

1) Performance comparison: We compare the time taken by these algorithms to sort the random values according to the attribute values (i.e., the node with the j^{th} largest attribute value of the system value obtains the j^{th} random value). In order to evaluate the convergence speed of each algorithm, we use the slice disorder measure as defined in Section IV-D.

We simulated 10^4 participants in 100 equally sized slices (when unspecified), each with a view size $c = 20$. Figure 4(a) illustrates the difference between the global disorder measure and the slice disorder measure while Figure 4(b) presents the evolution of the slice disorder measure over time for JK, and mod-JK.

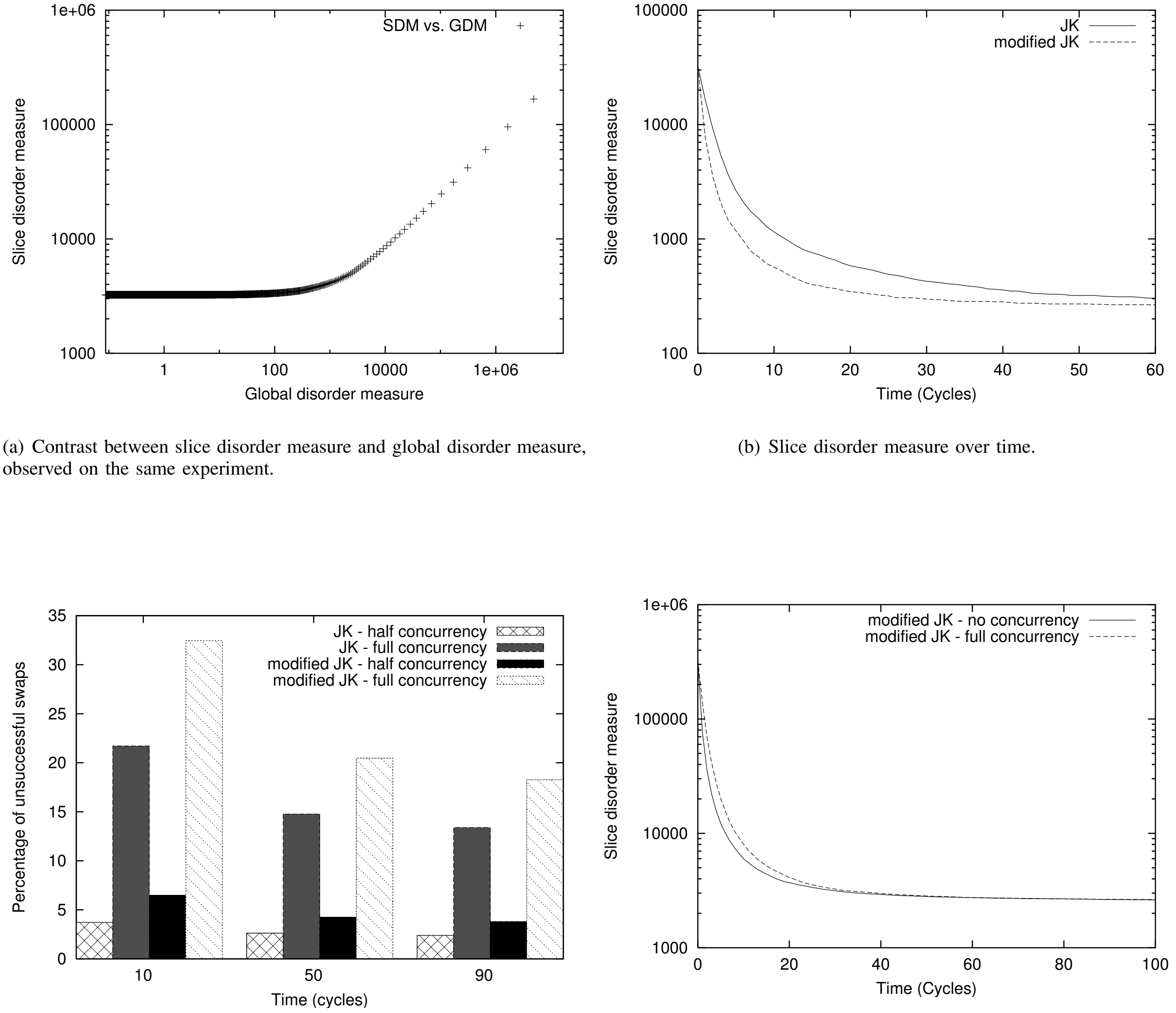
Figure 4(a) shows the different values to which the global disorder measure and the slice disorder measure converge. When values are sufficiently large, the GDM and SDM seem tightly related: if GDM increases then SDM increases too. Conversely, there is a significant difference between the GDM and SDM when the values are relatively low: the GDM reaches 0 while the SDM is lower bounded by a positive value. This is because the algorithm does lead to a totally ordered set of nodes, while it still does not associate each node with its correct slice. Consequently the GDM is not sufficient to rightly estimate the performance of our algorithms. Note that the different scales of the axes of Figure 4(a) do not change the result but helps visualizing the relatively high value of the SDM at which the GDM reaches 0.

Figure 4(b) shows the slice disorder measure to compare the convergence speed of our algorithm to that of JK with 10 equally sized slices. Our algorithm converges significantly faster than JK. Note that none of the algorithm reaches zero SDM, since they are both based on the same idea of sorting randomly generated values. Besides, since they both used an identical set of randomly generated values, both converge to the same SDM.

2) Remark: For the sake of fairness JK and mod-JK are compared using the same underlying view management protocol in our simulation: the variant of Cyclon. Nevertheless, we simulated JK on top of Newscast as it appeared in [23] (running a single cycle of Newscast in each cycle of JK, as for Cyclon and its variant in mod-JK). As expected, the convergence speed of JK was even slower due to the difference between the clustering coefficient of the communication graph obtained by Newscast and Cyclon, respectively [20]. The comparison of the underlying view management protocols both in terms of randomness and fault-tolerance is out of the scope of this paper.

F. Concurrency

The simulations are cycle-based and at each cycle an algorithm step is done atomically so that no other execution is concurrent. More precisely, the algorithms are simulated such that in each cycle, each node updates its view before sending its random value or its attribute value. Given this implementation, the cycle-based simulator does not allow us to realistically simulate concurrency, and a drawback is that view is up-to-date when a message is sent. In the following we artificially introduce concurrency (so that



(a) Contrast between slice disorder measure and global disorder measure, observed on the same experiment.

(b) Slice disorder measure over time.

(c) Percentage of unsuccessful swaps in the ordering algorithms.

(d) Convergence speed under high concurrency.

Fig. 4. Comparison of the original JK and our modified JK algorithms in terms of slice disorder measure and the amount of useless received messages due to concurrency.

view might be out-of-date) into the simulator and show that it has only a slight impact on the convergence speed.

Adding concurrency raises some realistic problems due to the use of non-atomic push-pull [22] in each message exchange. That is, concurrency might lead to other problems because of the potential staleness of views: unsuccessful swaps due to useless messages. Technically, the view of node i might indicate that j has a random value r while this value is no longer up-to-date. This happens if i has lastly updated its view before j swapped its random value with another j'. Moreover, due to asynchrony, it could happen that by the time a message is received this message has become useless. Assume that node i sends its random value r_i to j in order to obtain r_j at time t and j receives it by time $t + \delta$. With no loss of generality assume $r_i > r_j$. Then if j swaps its random value with j' such that $r'_j > r_i$ between time t and $t + \delta$, then the message of i becomes *useless* and the expected swap does not occur (we call this an *unsuccessful swap*).

Figure 4(d) indicates the impact of concurrent message exchange on the convergence speed while Figure 4(c) shows the amount of useless messages that are sent. Now, we explain how the concurrency is simulated. Let the *overlapping messages* be a set of messages that mutually overlap: it exists, for any couple of overlapping messages, at least one instant at which they are both in-transit. For each algorithm we simulated *(i)* full concurrency: in a given cycle, all messages are overlapping messages; and *(ii)* half concurrency: in a given cycle, each message is an overlapping message with probability $\frac{1}{2}$. Generally, we see that increasing the concurrency increases the number of useless messages. Moreover, in the modified version of JK, more messages are ignored than in the original JK algorithm. This is due to the fact that some nodes (the most misplaced ones) are more likely targeted which increases the number of concurrent messages arriving at the same nodes. Since a node i ignored more likely a message when it receives more messages during the same cycle, it comes out that concentrating message sending at some targets increases the number of useless messages.

Figure 4(d) compares the convergence speed under full concurrency and no concurrency. We omit the curve of half-concurrency since it would have been similar to the two other curves. Full-concurrency impacts on the convergence speed very slightly.

V. Dynamic Ranking by Sampling of Attribute Values

In this section we propose an alternative algorithm for the distributed slicing problem. This algorithm circumvents some of the problems identified in the previous approach by continuously ranking nodes based on observing attribute value information. Random values no longer play a role, so non-perfect uniformity in the random value distribution is no longer a problem. Besides, this algorithm is not sensitive to churn even if it is correlated with attribute values.

In the remaining part of the paper we refer to this new algorithm as the ranking algorithm while referring to JK and mod-JK as the ordering algorithms. Here, we elaborate on the drawbacks arising from the ordering algorithms relying on the use of random values that are solved by the ranking approach.

1) Impact of attribute correlated with dynamics: As already mentioned, the ordering algorithms rely on the fact that random values are uniformly distributed. However, if the attribute values are not constant but correlated with the dynamic behavior of the system, the distribution of random values may change from uniform to skewed quickly. For instance, assume that each node maintains an attribute value that represents its own lifetime. Although the algorithm is able to quickly sort random values, so nodes with small lifetime will obtain the small random values, it is more likely that these nodes leave the system sooner than other nodes. This results in a higher concentration of high random values and a large population of the nodes wrongly estimate themselves as being part of the higher slices.

2) Inaccurate slice assignments: As discussed in previous sections in detail, slice assignments will typically be imperfect even when the random values are perfectly ordered. Since the ranking approach does not rely on ordering random nodes, this problem is not raised: the algorithm guarantees eventually perfect assignment in a static environment.

3) Concurrency side-effect: In the previous ordering algorithms, a non negligible amount of messages are sent unnecessarily. The concurrency of messages has a drastic effect on the number of useless messages as shown previously, slowing down convergence. In the ranking algorithm concurrency has no impact on convergence speed because all received messages are taken in account. This is because the information encapsulated in a message (the attribute value of a node) is guaranteed to be up to date, as long as the attribute values are constant, or at least change slowly.

A. Ranking Algorithm Specification

The pseudocode of the ranking algorithm is presented in Figure 5. As opposed to the ordering algorithm of the previous section, the ranking algorithm does not assign random initial unalterable values as candidate ranks. Instead, the ranking algorithm improves its rank estimate each time a new message is received.

The ranking algorithm works as follows. Periodically each node i updates its view $\mathcal{N}_i$ following an underlying protocol that provides a uniform random sample (Line 3); later, we simulate the algorithm using the variant of Cyclon protocol presented in Section IV-C2. Node i computes its rank estimate (and hence its slice) by comparing the attribute value of its neighbors to its own attribute value. This estimate is set to the ratio of the number of nodes with a lower attribute value that i has seen over the total number of nodes i has seen (Line 15). Node i looks at the normalized rank estimate of all its neighbors. Then, i selects the node j_1 closest to a slice boundary (according to the rank estimates of its neighbors). Node i selects also a random neighbor j_2 among its view (Line 12). When those two nodes are selected, i sends an update message, denoted by a flag UPD, to j_1 and j_2 containing its attribute value (Line 13–14).

The reason why a node close to the slice boundary is selected as one of the contacts is that such nodes need more samples to accurately determine which slice they belong to (subsection V-B shows this point). This technique introduces a bias towards them, so they receive more messages.

Upon reception of a message from node i, the passive threads of j_1 and j_2 are activated so that j_1 and j_2 compute their new rank estimate r_{j_1} and r_{j_2}. The estimate of the slice a node belongs to, follows the computation of the rank estimate. Messages are not replied, communication is one-way, resulting in identical message complexity to JK and mod-JK.

B. Theoretical Analysis

The following Theorem shows a lower bound on the probability for a node i to accurately estimate the slice it belongs to. This probability depends not only on the number of attribute exchanges but also on the rank estimate of i.

Theorem 5.1: Let p be the normalized rank of i and let $\hat{p}$ be its estimate. For node i to exactly estimate its slice with confidence coefficient of $100(1-\alpha)\%$, the number of

```
**Initial state of node $i$**
  $period_i$, initially set to a constant; $r_i$, a value in $(0,1]$; $a_i$, the attribute value; $b$, the closest slice boundary to node $i$; $g_i$, the counter of encountered attribute values; $l_i$, the counter of lower attribute values; $slice_i \leftarrow \perp$; $\mathcal{N}_i$, the view.

**Active thread at node $i$**
  wait($period_i$)
  recompute-view()$_i$
  $dist\text{-}min \leftarrow \infty$
  for $j' \in \mathcal{N}_i$
      $g_i \leftarrow g_i + 1$
      if $a_{j'} \leq a_i$ then $\ell_i \leftarrow \ell_i + 1$
      if dist$(a_{j'}, b) < dist\text{-}min$ then
          $dist\text{-}min \leftarrow$ dist$(a_{j'}, b)$
          $j_1 \leftarrow j'$
  end for
  Let $j_2$ be a random node of $\mathcal{N}_i$
  send(UPD, $a_i$) to $j_1$
  send(UPD, $a_i$) to $j_2$
  $r_i \leftarrow \ell_i / g_i$
  $slice \leftarrow \mathcal{S}_{l,u}$ such that $l < r_i \leq u$

**Passive thread at node $i$ activated upon reception**
  recv(UPD, $a_j$) from $j$
  if $a_j \leq a_i$ then $\ell_i \leftarrow \ell_i + 1$
  $g_i \leftarrow g_i + 1$
  $r_i \leftarrow \ell_i / g_i$
  $slice \leftarrow \mathcal{S}_{l,u}$ such that $l < r_i \leq u$
```

Fig. 5. Dynamic ranking by exchange of attribute values.

messages i must receive is:

$$\left(Z_{\frac{\alpha}{2}} \frac{\sqrt{\hat{p}(1-\hat{p})}}{d}\right)^2,$$

where d is the distance between the rank estimate of i and the closest slice boundary, and $Z_{\frac{\alpha}{2}}$ represents the endpoints of the confidence interval.

Proof: Each time a node receives a message, it checks whether or not the attribute value is larger or lower than its own. Let $X_1, ..., X_k$ be k $(k > 0)$ independent identically distributed random variables described as follows. $X_j = 1$ with probability $\frac{i}{n} = p$ (indicating that the attribute value is lower) and $j \in \{1, ..., k\}$, otherwise $X_j = 0$ (indicating the attribute value is larger). By the central limit theorem, we assume $k > 30$ and we approximate the distribution of $X = \sum_{j=1}^{k} X_j$ as the normal distribution. We estimate X by $\hat{X} = \sum_{j=1}^{k} \hat{X}_j$ and p by $\hat{p} = \frac{\hat{X}}{k}$.

We want a confidence coefficient with value $1 - \alpha$. Let Φ be the standard normal distribution function, and let $Z_{\frac{\alpha}{2}}$ be $\Phi^{-1}(1 - \frac{\alpha}{2})$. Now, by the Wald large-sample normal test in the binomial case, where the standard deviation of $\hat{p}$ is $\sigma(\hat{p}) = \frac{\sqrt{\hat{p}(1-\hat{p})}}{\sqrt{k}}$, we have:

$$\begin{aligned} \left|\frac{\hat{p} - p}{\sigma(\hat{p})}\right| &\leq Z_{\frac{\alpha}{2}} \\ \hat{p} - Z_{\frac{\alpha}{2}}\sigma(\hat{p}) \quad \leq \quad p &\leq \quad \hat{p} + Z_{\frac{\alpha}{2}}\sigma(\hat{p}). \end{aligned}$$

Next, assume that $\hat{p}$ falls into the slice $S_{l,u}$, with l and u its lower and upper boundaries, respectively. Then, as long as $\hat{p} - Z_{\frac{\alpha}{2}}\sqrt{\frac{\hat{p}(1-\hat{p})}{k}} > l$ and $\hat{p} + Z_{\frac{\alpha}{2}}\sqrt{\frac{\hat{p}(1-\hat{p})}{k}} \leq u$, the slice estimate is exact with a confidence coefficient of $100(1-\alpha)\%$. Let $d = \min(\hat{p} - l, u - \hat{p})$, then we need

$$\begin{aligned} d &\geq Z_{\frac{\alpha}{2}}\sqrt{\frac{\hat{p}(1-\hat{p})}{k}}, \\ k &\geq \left(Z_{\frac{\alpha}{2}} \frac{\sqrt{\hat{p}(1-\hat{p})}}{d}\right)^2. \end{aligned}$$

■

To conclude, under reasonable assumptions every node estimates its slice with confidence coefficient $100(1-\alpha)\%$, after a finite number of message receipts. Moreover a node closer to the slice boundary needs more messages than a node far from the boundary.

C. Simulation Results

This section evaluates the ranking algorithm by focusing on three different aspects. First, the performance of the ranking algorithm is compared to the performance of the ordering algorithm[4] in a large-scale system where the distribution of attribute values does not vary over time. Second, we investigate if sufficient uniformity is achievable in reality using a dedicated protocol. Third, the ranking algorithm and ordering algorithm are compared in a dynamic system where the distribution of attribute values may change. Finally, a sliding window technique is given to prevent the SDM from increasing.

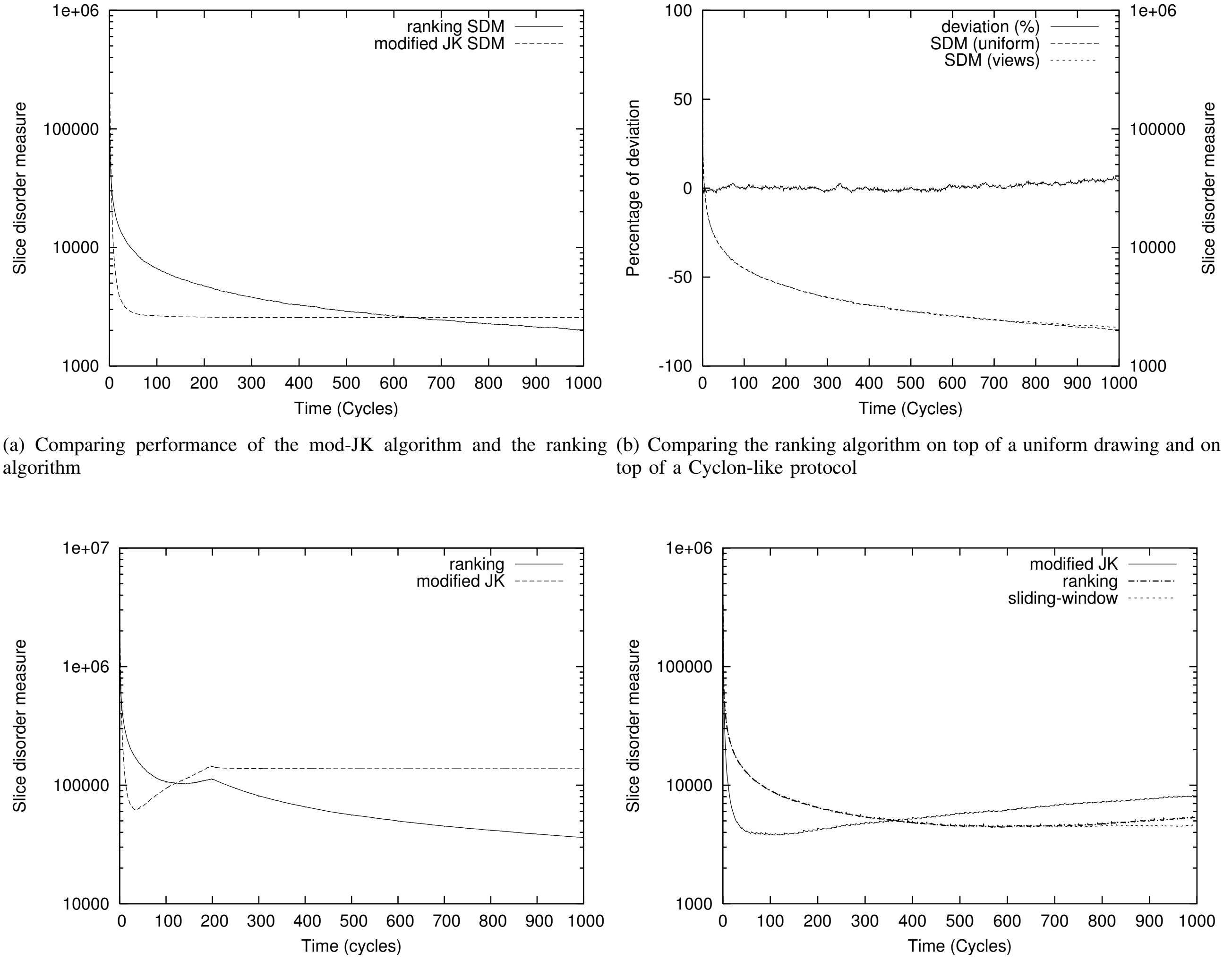
For this purpose, we ran two simulations, one for each algorithms. The system contains (initially) 10^4 nodes and each view contains 10 uniformly drawn random nodes and is updated in each cycle. The number of slices is 100, and we present the evolution of the slice disorder measure over time.

1) Performance comparison in the static case: Figure 6(a) compares the ranking algorithm to the mod-JK algorithm while the distribution of attribute values do not change over time (varying distribution is simulated below).

The difference between the mod-JK algorithm and the ranking algorithm indicates that the ranking algorithm gives a more precise result (in terms of node to slice assignments) than the mod-JK algorithm. More importantly, the slice disorder measure obtained by the mod-JK algorithm is lower bounded while the one of the ranking algorithm is not. Consequently, this simulation shows that the mod-JK algorithm might fail in slicing the system while the ranking algorithm keeps improving its accuracy over time as the convergence statement of Theorem 5.1 confirmed.

2) Feasibility of the ranking algorithm: Figure 6(b) shows that the ranking algorithm does not need artificial uniform drawing of neighbors. Indeed, an underlying view management protocol might lead to similar performance results. In the presented simulation we used an artificial protocol, drawing neighbors randomly at uniform in each cycle of the algorithm execution, and the variant of the Cyclon view management protocol presented above. Those underlying protocols are distinguished on the figure using

[4] We omit comparison with JK since the performance obtained with mod-JK are either similar or better.



(a) Comparing performance of the mod-JK algorithm and the ranking algorithm

(b) Comparing the ranking algorithm on top of a uniform drawing and on top of a Cyclon-like protocol

(c) Effect of burst of attribute-correlated churn on the convergence of the mod-JK algorithm and the ranking algorithm

(d) Effect of a low and regular attribute-correlated churn on the convergence of the modified JK algorithm and the ranking algorithm

Fig. 6. Evaluation of the mod-JK and the ranking protocols with uniform and Cyclon-like sampling, and under continuous and burst of attribute-correlated churn.

terms "uniform" (for the former one) and "views" (for the latter one). As said previously, the Cyclon protocol [38] consists of exchanging views between neighbors such that the communication graph produced shares similarities with a random graph. This figure shows that both cases give very similar results. The SDM legend is on the right-handed vertical axis while the left-handed vertical axis indicates what percentage the SDM difference represents over the total SDM value. At any time during the simulation (and for both type of algorithms) its value remains within plus or minus 7%. The two SDM curves of the ranking algorithm almost overlap. Consequently, the ranking algorithm and the variant of Cyclon presented in subection IV-C2 achieve very similar result.

To conclude, the variant of Cyclon algorithm presented in the previous section can be easily used with the ranking algorithm to provide the shuffling of views. More generally, an underlying distributed protocol that shuffles the view among nodes may provide nearly-optimal results.

3) Performance comparison in the dynamic case: In Figure 6(c) each of the two curves represents the slice disorder measure obtained over time using the mod-JK algorithm and the ranking algorithm respectively. We simulate the churn such that 0.1% of nodes leave and 0.1% of the nodes join in each cycle during the 200 first cycles. We observe how the SDM converges. The churn is reasonably and pessimistically tuned compared to recent experimental evaluations [37] of the session duration in three well-known P2P systems.[5]

The distribution of the churn is correlated to the attribute value of the nodes. The leaving nodes are the nodes with the lowest attribute values while the entering nodes have higher

[5] In [37], roughly all nodes have left the system after 1 day while there are still 50% of nodes after 25 minutes. In our case, assuming that in average a cycle lasts one second would lead to more than 54% of leave in 9 minutes.

attribute values than all nodes already in the system. The parameter choices are motivated by the need of simulating a system in which the attribute value corresponds to the (fixed) session duration of nodes, for example.

The churn introduces a significant disorder in the system which counters the fast decrease. When, the churn stops, the ranking algorithm readapts well the slice assignments: the SDM starts decreasing again. However, in the mod-JK algorithm, the convergence of SDM gets stuck. This leads to a poor slice assignment accuracy.

In Figure 6(d), each of the two curves represent the slice disorder measure obtained over time using the mod-JK algorithm, the ranking algorithm, and a modified version of the ranking algorithm using attribute values recorded in a sliding-window, respectively. (The simulation obtained using sliding windows is described in the next subsection.) The churn is diminished and made more regular than in the previous simulation such that 0.1% of nodes leave and 0.1% of nodes join every 10 cycles.

The curves fits a fast decrease (superlinear in the number of cycles) at the beginning of the simulation. At first cycles, the ordering gain is significant making the impact of churn negligible. This phenomenon is due to the fact that SDM decreases rapidly when the system is fully disordered. Later on, however, the decrease slope diminishes and the churn effect reduces the amount of nodes with a low attribute value while increasing the amount of nodes with a large attribute value. This unbalance leads to a messy slice assignment, that is, each node must quickly find its new slice to prevent the SDM from increasing. In the mod-JK algorithm the SDM starts increasing from cycle 120. Conversely, with the ranking algorithm the SDM starts increasing not earlier than at cycle 730. Moreover the increase slope is much larger in the former algorithm than in the latter one.

Even though the performance of the ranking algorithm is much better, its adaptiveness to churn is not surprising. Unlike the mod-JK algorithm, the ranking one keeps re-estimating the rank of each node depending on the attribute values present in the system. Since the churn increases the attribute values present in the system, nodes tend to receive more messages with higher attribute values and less messages with lower attribute values, which turns out to keep the SDM low, despite churn. Further on, we propose a solution based on sliding-window technique to limit the increase of the SDM in the ranking algorithm.

To conclude, the results show that when the churn is related to the attribute (e.g., attribute represents the session duration, uptime of a node), then the ranking algorithm is better suited than the mod-JK algorithm.

4) Sliding-window for limiting the SDM increase: In Figure 6(d), the "sliding-window" curve presents a slightly modified version of the ranking algorithm that encompasses SDM increase due to churn correlated to attribute values. Here, we present this enrichment.

In Section V, the ranking algorithm specifies that each node takes into account all received messages. More precisely, upon reception of a new message each node i recomputes immediately its rank estimate and the slice it thinks it belongs to without remembering the attribute values it has seen. Consequently the messages received long-time ago have as much importance as the fresh messages in the estimate of i. The drawback, as it appeared in Figure 6(d) of Section IV-E, is that if the attribute values are correlated to churn, then the precision of the algorithm might diminish.

To cope with this issue, the previous algorithm can be easily enriched in the following way. Upon reception of a message, each node i records an information about the attribute value received in a fixed-size ordered set of values. Say this set is a first-in first-out buffer such that only the most recent values remain. Right after having recorded this information, node i can re-compute its rank estimate and its slice estimate based on the most relevant piece of information (having discarded the irrelevant piece). Consequently, the estimate would rely only on fresh attribute values encountered so that the algorithm would be more tolerant to changes (e.g., dynamics or non-uniform evolution of attribute values). Of course, since the analysis (cf. Section V-B) shows that nodes close to the slice boundary require a large number of attribute values for estimating precisely their estimates, it would be unaffordable to record all these last attribute values encountered due to space limitation.

Actually, the only necessary relevant information of a message is simply whether it contains a lower attribute value than the attribute value of i, or not. Consequently, a single bit per message would be sufficient to record the necessary information (e.g., adding a 1 meaning that the attribute value is lower, and 0 otherwise). Thus, even though a node i would require 10^4 messages to rightly estimate its slice (with high probability), node i simply needs to allocate an array of size $10^4/(8*1000) = 1,25$ kB.

As expected, Figure 6(d) shows that the sliding-window method applied to the ranking algorithm prevents its SDM from increasing. Consequently, at some point in time, the resulting slice assignment may become even more accurate.

VI. Conclusion

Peer to peer systems may now be turned into general frameworks on top of which several applications might cohabit. To this end, allocating resources to applications, while resources are heterogeneously spread over the system, require specific algorithms to partition the network in a relevant way. The sorting algorithm proposed in [23] provided a first attempt to "slice" the network, taking into account the potential heterogeneity of nodes. This algorithm relies on each node drawing a random value uniformly and swapping continuously those random values, with candidate nodes, so that the order between attributes values (reflecting the capabilities of nodes) and random ones match.

In this paper, we first proposed an improvement over the initial algorithm resulting in the faster mod-JK algorithm. This improvement comes from a judicious choice of candidate nodes to swap values. Each node makes this choice depending on the potential decrease of the disorder measure it can compute locally.

Our second contribution is the definition of the slice disorder measure. The slice disorder measure evaluates how nodes wrongly estimate the slice they belong to. We showed that the proposed global disorder measure cannot indicate whether nodes found their slice. That is, the slice disorder measure is necessary to show that an algorithm solves the distributed slicing problem.

Using the slice disorder measure, we identified two issues related to the use of static random values. The first one refers to the fact that slice assignment heavily depends on the degree of uniformity of the initial random value. In particular, we showed that ordering algorithms do not converge to a sliced networks. The second is related to the fact that once sorted along one attribute axis, the churn (or failures) might be correlated to the attribute, therefore leading to a unrecoverable skewed distribution of the random values. This phenomenon results in a wrong slice assignment despite the system seems to be rightly ordered.

Last but not least, we provided a ranking algorithm that accurately maintains slices of the system even in the presence of churn. This algorithm minimizes the effect of correlated churn on slice disorder and recovers efficiently after a period of correlated churn. For this purpose, nodes continuously re-estimate their rank relatively to other nodes based on their sampling of the network. The convergence speedup of the first algorithm and the accuracy of the second algorithm are proved through theoretical analysis and simulations.

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