Computing Personalized PageRank Quickly by Exploiting Graph Structures

Takanori Maehara[‡§] Takuya Akiba[†§] Yoichi Iwata[†§] Ken-ichi Kawarabayashi[‡§]
‡National Institute of Informatics, †The University of Tokyo
§JST, ERATO, Kawarabayashi Large Graph Project
‡{maehara, k_keniti}@nii.ac.jp, †{t.akiba, y.iwata}@is.s.u-tokyo.ac.jp

ABSTRACT

We propose a new scalable algorithm that can compute Personalized PageRank (PPR) very quickly. The Power method is a state-of-the-art algorithm for computing exact PPR; however, it requires many iterations. Thus reducing the number of iterations is the main challenge.

We achieve this by exploiting graph structures of web graphs and social networks. The convergence of our algorithm is very fast. In fact, it requires up to 7.5 times fewer iterations than the Power method and is up to five times faster in actual computation time.

To the best of our knowledge, this is the first time to use graph structures explicitly to solve PPR quickly. Our contributions can be summarized as follows.

1. We provide an algorithm for computing a tree decomposition, which is more efficient and scalable than any previous algorithm.
2. Using the above algorithm, we can obtain a *core-tree decomposition* of any web graph and social network. This allows us to decompose a web graph and a social network into (1) the *core*, which behaves like an expander graph, and (2) a small tree-width graph, which behaves like a *tree* in an algorithmic sense.
3. We apply a direct method to the small tree-width graph to construct an LU decomposition.
4. Building on the LU decomposition and using it as *preconditoner*, we apply GMRES method (a state-of-the-art advanced iterative method) to compute PPR for whole web graphs and social networks.

1. INTRODUCTION

1.1 Large Graphs

Very large scale datasets and graphs are ubiquitous in today's world; the World Wide Web, online social networks, and huge search and query-click logs are regularly collected and processed by search engines. Therefore, designing scalable systems for analyzing, processing, and mining huge real-world graphs have become issues for all of computer science.

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The main problem is that modern graph datasets are huge. The best example is the World Wide Web, which currently consists of over one trillion links and is expected to exceed tens of trillions in the near future. Facebook [20] also consists of over 800 million active users, with hundreds of billions of friend links. In addition, Twitter [31] has over 41 million users with 1.47 billion social interactions. Examples of large graph datasets are not only limited to the web and social networks. Biological networks are also comprised of large graph dataset.

Despite the size of these graphs, it is still necessary to perform computations with the data. One of the most well-known graph computation problems is computing Personalized PageRank (PPR) [38] that is described as follows.

Problem 1 (Personalized PageRank problem).

- *Given: an input graph G with n vertices, and a personalized vector $b \in \mathbb{R}^n$*
- *Output: $x \in \mathbb{R}^n$ (PPR scores for all vertices of G with respect to the personalized vector b)*

As used by the Google search engine, PPR exploits the linkage structure of the web to compute global *importance* scores, which can be used to influence the ranking of search results. PPR and other personalized random walk based measures are very effective in various applications such as link prediction [34] and friend recommendation [8] in social networks.

1.2 Difficulty

Current graph systems can handle graphs with more than ten billion edges by distributing the computation. However, efficient large-scale computation of web graphs and social networks still remains a significant challenge.

Existing graph frameworks partition the graph into small pieces and handle the graph problem simultaneously for each piece to obtain a solution by looking at all solutions for small pieces. However, the main difficulty is that web graphs and social networks cannot be readily decomposed into small pieces, which can be processed in parallel. Finding efficient graph cuts, which minimize communication between pieces and are also balanced is a very difficult problem [33]. This problem makes MapReduce [17] inefficient for computing such graphs, as has been pointed by many researchers [13, 35, 36].

1.3 Our Purpose

In this paper, we shall look at a somewhat different direction. Parallel computations are useful; however, it would

definitely be best for them to adapt the fastest algorithm to compute PPR. To the best of our knowledge, either

- the Power method (a variant of an *iterative method*) is adapted to compute PPR, or
- some efficient *approximation* algorithms based on a Monte Carlo method are proposed to compute PPR (Section 8).

To date, approximation algorithms based on a Monte Carlo method have been extensively studied because the Power method suffers from slow convergence speed, especially for large-scale graphs. There are many accelerating methods that are designed to speed up the convergence procedure. Among them, iterative methods based on the Arnoldi process have been proposed [44]; however according to [44] and our analysis (Section 7), this can accelerate by at most 50%, and sometimes it requires more time.

Thus the main challenge to adapt an iterative method to solve PPR is

> reducing the number of iterations of an iterative method to speed up the convergence procedure.

It is not desirable to relax exactness, i.e., we require algorithms that can compute PPR $x \in \mathbb{R}^n$ such that $\|x - x^*\| \leq \epsilon\|x^*\|$ for very small $\epsilon > 0$, where $x^* \in \mathbb{R}^n$ is a vector of the optimal PPR. The *accuracy* of the algorithm is ϵ. According to [32], it should be less than 10^{-9}.

1.4 Main Contributions

It is well-known that web graphs and social networks are *sparse*. Moreover, common structural properties of these networks have been extensively studied [2, 33]. By building upon and generalizing these properties, our main contribution is to achieve the above purpose by exploiting not only sparsity of these networks, but also *graph properties*. We implemented and applied our algorithm to graphs with billions of edges, and indeed it ran within 10 minutes.

How do we achieve this? To answer this question, it is convenient to explain when iterative methods converge quickly in terms of theoretical justification. It is known that iterative methods converge very quickly when the gap between the first and the second eigenvalue is large, i.e., the spectral gap is large (Section 2.2). It is also known that (1) when a graph G is close to random this would happen, but on the other hand, (2) when G is close to a tree, then this is far from true[1] (experiments were performed to support these facts; Section 6.4). Thus, intuitively, if a given graph contains a large tree as an induced subgraph, then the convergence of iterative methods would be slow. This is the key idea in our algorithm and has motivated us to analyze the structures of web graphs and social networks more closely.

As mentioned above, web graphs and social networks cannot be readily decomposed into small pieces. However, they can be decomposed into two parts such that one part is a *core*, and the other is *almost a tree* [33]. Moreover, concerning the core, we have the following information:

> The *core* part of web graphs and social networks tends to be an *expander* graph [33] (See Section 2.2 for the exact definition of expander graphs, but they have some similarity with random graphs).

[1]This is true for undirected graphs, but it is not well-established for digraphs. That is why we perform some experiments.

This is the main reason why they cannot be decomposed into small pieces. On the other hand, this property is a good situation for iterative methods, because expander graphs exhibit rapid convergence for iterative methods (Section 6.4). Our proposed algorithm takes advantage of this *core* property, together with the *almost a tree* part. For the core part, an iterative method works very well; however, it does not work well for the *almost a tree* part (Section 6.4). What about the *almost a tree* part? There is another method; namely a *direct method*. This method can take advantage of trees because it can handle them very quickly; however it does not work well for the core (Section 6.3).

To obtain a faster algorithm for PPR, we could attempt to combine the two methods, i.e., an iterative method for the *core* and a direct method for the *almost a tree* part. However there are several issues to be resolved. In particular, what are the exact structural properties of the *core* part and the *almost a tree* part? What kind of decomposition is required to apply this idea? How do we combine an iterative method with a direct method?

We can answer the first two questions by employing our *core-tree-decomposition* method. At a high level, this method allows us to decompose any graph into the *core* part and the *almost a tree* part such that

1. the *core* part behaves like an expander graph, thus making the convergence of an iterative method very fast, and
2. the *almost a tree* part is of small tree-width (i.e., it behaves like a tree in an algorithmic sense; Section 2.3). This allows us to apply a direct method that runs in linear time (Section 6.1).

Moreover, such a decomposition can be computed efficiently (Section 5).

Another important key idea of our algorithm is the combination of an iterative method with a direct method. Specifically, a direct method quickly provides an LU decomposition of the almost a tree part. We plug this decomposition into the *preconditioner*[2] of an iterative method. It is well-known that an iterative method can be accelerated by preconditioning, which is also the case for our algorithm. In fact we can apply an advanced iterative method, GMRES [42], for whole networks. This results in an algorithm that can compute PPR very quickly. To support this claim, we implemented our algorithm for graphs with at least one billion (or even ten billion) edges and compared it with a state-of-the-art algorithm (i.e., the Power method) and an additional suggested accelerated method [44]. From these comparisons, the convergence is up to 7.5 times fewer than the Power method for the number of iterations, and up to five times faster than the Power method in actual computation time. In addition, our algorithm is much faster than algorithms [44] for large graphs.

In summary our main technical contributions are as follows:

1. We exploit more detailed structures of web graphs and social networks. Specifically, we propose a novel core-tree-decomposition for web graphs and social networks, such that not only *core-whisker* structure [33] but also *expander-like* core together with the small tree-width part is obtained. Moreover, we can compute this decomposition very quickly.

[2]For the precise definition, see Section 3.1

2. We use an LU decomposition (to the small tree-width part) as a preconditioner for an advanced iterative method (i.e., GMRES). To the best of our knowledge, this is the first time to use an LU decomposition, applied to a subgraph of an entire graph as a preconditioner, for an iterative method for quick convergence. This is due to the core property.

Note that the first point concerns the preprocessing of our algorithm, and the second point is to compute PPR. Let us point out that our preprocessing is also efficient. In fact, even if we take our preprocessing time into account to compute PPR, our proposed algorithm is still 2–4 times faster than the Power method. In applications, we may have to handle millions of query requests simultaneously; in this case once we perform one efficient preprocessing for a large network (say once a day, because the network may change in a single day), our query algorithm can handle millions of query requests up to five times more efficiently than the Power method

This paper is organized as follows: In Section 2, we present key concepts in our proposed algorithm; namely *expander* and *core-tree-decompositions*. In Section 3, we present two major approaches to compute PPR (i.e., directed methods and iterative methods) and then present *preconditioner* of iterative methods which play a key role in our algorithm. We then present an overview of our proposed algorithm in Section 4. We give more details concerning our preprocessing to construct core-tree-decompositions in Section 5. Section 6 gives theoretical analysis and experimental verification of our algorithm. To demonstrate the performance of the proposed algorithm, we conducted experiments on several web graphs and social networks, and compared the results with other existing methods. The results are discussed in Section 7. Related work is given in Section 8, and we conclude our paper in Section 9.

2. PRELIMINARIES

In this section, we formally define our key concepts: core-tree-decompositions and an expander graph. A core-tree-decomposition is a generalization of the well-known tree-decomposition. We first introduce basic notations from graph theory and matrices, which are needed in our paper, and then define tree-decomposition and tree-width.

2.1 Basic Notation

Let $G = (V, E)$ be a graph, where V is the vertex set and E is the edge set. We use n and m to denote the number of vertices and edges of a graph, respectively. For a vertex set $S \subseteq V$, let $e(S)$ be the set of edges between S and $V \setminus S$. We define $d(S) := |e(S)|$. For a vertex $v \in V$, $d_G(v)$ is the *degree* of v. If G is a digraph, then $d^-(v)$ is the number of edges whose tail is v.

We are also interested in the matrix A that arises from a graph. Formally, given a digraph G, we are interested in the *adjacency* matrix; We set the vertex set $V(G) = \{1, \ldots, n\}$. Then, $A(i, j) = 1$ if there is an edge from i to j. The *transition* matrix P of G is $P = AD^{-1}$, where D is a diagonal matrix and $D(i, i) = d(i)^{-1}$.

2.2 Expander Graph

Generally, an *expander graph* [27] is a sparse graph in which each subset of the vertices *that is not too large* has a *large* boundary (i.e., globally connected). One of the key properties presented in our paper is that our core is close to an expander graph (Section 6.2). Here, we formally define an expander graph. Whether or not a given graph G is close to an expander is a key in our paper. We will discuss how to determine this at the end of this subsection.

To define an expander graph formally, we need some more definitions. For a vertex set $S \subseteq V$,

$$\mu(S) := \sum_{v \in S} d(v),$$

and the *conductance* is defined as $\phi(S) := d(S)/\mu(S)$. The *conductance* of an undirected graph G is

$$\phi(G) := \min_{S \subseteq V : \mu(S) \leq \mu(V)/2} \phi(S).$$

We say that a graph G is an η-*expander* if $\phi(G) \geq \eta$. Intuitively, if the conductance η is large, we say that G is *globally connected*. In this case we say that G is an *expander*. It is known that expander graphs behave like *random graphs* [4].

The quantity $\phi(G)$ is NP-complete to compute. However, the following inequality of Jerrum and Sinclair [29] states that we can approximately determine η by looking at the second eigenvalue λ_2 of the transition matrix of a graph:

$$\eta^2/16 \leq 1 - \lambda_2 \leq \eta. \quad (1)$$

Indeed, from spectral graph theory [14], expander graphs and eigenvalue distribution are closely related, and moreover the second eigenvalue of an expander graph is relatively small compared to the first eigenvalue. On the other hand, if G is far from an expander (i.e., $\phi(G)$ is small), according to (1), the eigenvalues are scattered in the unit circle. For example, if G is a binary tree, by taking the left half of the tree as S, $\phi(G)$ is close to zero. THus that the second eigenvalue λ_2 is close to one by (1) and hence the second eigenvalue is scattered nearly in the unit circle. This means that the gap between the first eigenvalue (which is also scattered in the unit circle) and the second one is very small.

Note that (1) can be extended for a directed graph [15]. Therefore, to determine whether a given graph G is close to an expander the easiest way seems the following:

> look at the eigenvalues (and their distribution) of the transition matrix of G.

This is discussed in greater detail in Section 6.2.

2.3 Tree-decomposition

One of the main tools used in this paper is a core-tree-decomposition, which is based on a tree-decomposition. Let us define tree-decomposition and tree-width. Let G be an undirected graph, T a tree and let $\mathcal{V} = \{V_t \subseteq V(G) \mid t \in V(T)\}$ be a family of vertex sets indexed by the vertices t of T. A pair $(T, \mathcal{V})$ (or $(V_t)_{t \in T}$) is called a *tree-decomposition of* G if it satisfies the following three conditions [6, 39]:

1. $V(G) = \bigcup_{t \in T} V_t$,
2. for every edge $e \in E(G)$ there exists a $t \in T$ such that both ends of e lie in V_t,
3. if $t, t', t'' \in V(T)$ and t' lie on the path of T between t and t'', then $V_t \cap V_{t''} \subseteq V_{t'}$.

Each V_t is sometimes called a *bag*. The width of $(T, \mathcal{V})$ (or $(V_t)_{t \in T}$) is the number $\max\{|V_t| - 1 \mid t \in T\}$, and tree-width $\mathrm{tw}(G)$ of G is the minimum width of any tree-decomposition

of G. In a sense, tree-width is a measure how close a given graph is to a tree. Specifically, if tree-width is small, it behaves like a tree. This is a good situation from an algorithmic perspective. Indeed, if the width d of a given graph G is small, then we can apply a dynamic programming approach to G [6], much like it can be applied to a tree.

2.4 Core-tree-decomposition

Finally, we introduce the most important concept of this paper. We say that G has a *core-tree-decomposition of width* d if a tree-decomposition $(T, \mathcal{V})$ satisfies the following conditions.

1. r is a root of the tree T.
2. For all $t \in T \setminus \{r\}$, $|V_t| \leq d$.
3. For $W = V(G) \setminus V_r$, there is an ordering W of $v_1, \ldots,$ such that for each $l > 0$ with $W_l = \{v_{l+1}, \ldots, \}$, $N(v_l) \cap W_l$ is contained in V_t for some $t \in T \setminus \{r\}$, where $N(v_l)$ denotes the neighbor of v_l.

The bag V_r is called the *core part*, and it is the only bag that has more than d vertices. Sometimes we call W the *small tree-width part*. The third condition is necessary when applying a direct method. Indeed, our direct method starts with v_1, and proceeds in the order of W. As will be explained in Section 3 later, the order of W is important to analyze the time complexity of the direct method. In addition, the last statement "$N(v_l) \cap W_l$ is contained in V_t for some $t \in T \setminus \{r\}$" is important because this allows us to keep the small tree-width graph even after adding edges in the directed method (Section 6.1).

The purpose of our core-tree-decomposition is as follows.

1. We want to *steal* as many vertices in the core as possible so that the *stolen* vertices induce a graph W of small tree-width. If the remaining core is also small (i.e., less than or equal to d vertices), then the tree-width is at most d. Therefore we first want to take d such that the core size is as small as possible.
2. If we are stuck with *stealing* vertices from the core and the remaining core contains more than d vertices, the core no longer induces a graph of tree-width d. This means that this core contains a highly connected subgraph that behaves like an expander graph. In this case we want to take d such that this core is as close to an expander as possible.

In Section 5, given d, we propose an efficient algorithm to obtain our core-tree-decomposition of width d. In Section 7 (and Table 4), we discuss the selection of d.

3. BASIC ALGORITHMS

In this section, we briefly introduce definitions and basic facts about PageRank. Given a directed graph $G = (V, E)$. Let P be a transition matrix of G and let $b : V \to \mathbb{R}$ be a stochastic vector, called *personalized vector*. The *personalized PageRank* (PPR) is the solution x of the following equation:

$$x = \alpha P x + (1 - \alpha) b, \quad \text{or} \quad (I - \alpha P)x = (1 - \alpha)b. \qquad (2)$$

Here, $\alpha \in (0, 1)$ is called the *teleportation constant*, which is usually set to 0.85. By setting $A = I - \alpha P$ in (2), we only need to solve a linear system $Ax = b$.

When solving a linear system $Ax = b$, we are interested in *accurate linear solvers*, i.e., algorithms that can compute $x \in \mathbb{R}^n$ such that $\|x - x^*\| \leq \epsilon \|x^*\|$ for very small $\epsilon > 0$, where $x^* \in \mathbb{R}^n$ is a vector such that $Ax^* = b$. The *accuracy* of the algorithm is ϵ. In this paper we always set $\epsilon < 10^{-9}$.

There are two major approaches to solve a linear system $Ax = b$. The first is direct methods, which are essentially variants of Gaussian elimination that lead to exact solutions. The second is iterative methods. Let us look at these two methods more closely.

Direct method. The most naive direct method is to compute the inverse matrix explicitly and then apply the inverse. However, this method is quite impractical because the inverse matrix often becomes dense even if the original matrix is sparse. Hence, rather than computing the explicit inverse, computing an LU decomposition is more desirable. An *LU decomposition* is a matrix factorization of the form $A = LU$, where L is a lower triangular matrix with unit diagonals and U is an upper triangular matrix. This decomposition can be obtained from Gaussian elimination or from more sparse-matrix-friendly algorithms [16].

When applying an LU decomposition to A, we do not have to permute rows and columns to avoid pivots that are zero. However, the choice of which row and column to eliminate can have significant impact on the running time of the algorithm [5, 25]. Formally, the choice of elimination ordering corresponds to the choice of a permutation matrix Π, for which we factor $\Pi^\top A \Pi = LU$. By carefully choosing elimination ordering, we can often obtain a factorization of the form LU in which both L and U are sparse and can be computed quickly.

For a matrix A that arises from a graph, this procedure has a very clear graph theoretical interpretation. The rows and columns correspond to vertices. When we eliminate the row and column corresponding to a vertex, the resulting matrix is obtained from the original matrix of a graph in which that vertex has been removed but all of its neighbors become a clique (which we call *fill-in*). Thus,

> the number of entries in L and U depends linearly on the sum of degrees of vertices when they are eliminated, and the time complexity to compute L and U is proportional to the sum of the squares of degrees of the eliminated vertices (i.e., fill-in).

In our algorithm, we actually fix the order of vertices W that would be eliminated; let $W = \{v_1, v_2, \ldots, v_q\}$. Our algorithm proceeds as follows:

> We first delete v_1, and all of its neighbors become a clique. We then move on $v_2, \ldots, v_q$ in this order, and for v_i, we add edges between any nonadjacent vertices in $N_{v_i} \cap W_i$, which is bounded by $|V_{t'}|^2$, where the bag $V_{t'}$ contains all the vertices of $N(v_i) \cap W_i$ for some $t' \in T \setminus \{r\}$.
>
> Thus the order of the vertices to be eliminated is very important, and moreover the smaller degrees of the eliminated vertices are, the smaller the time complexity to compute L and U is.

We use this key fact explicitly in our analysis for our algorithm (Section 6.1).

A few studies have applied a direct method to compute PPR [22, 23]. However, as discussed in Section 7, the computational cost of a direct method largely depends on graph structures. For most graphs, the computational time is too

expensive. Thus a direct method can only be applied to a very restricted class of networks.

Iterative method. Iterative algorithms for solving linear systems $Ax = b$ produce successively better approximate solutions. The fundamental iterative method is the Power iteration (aka. Jacobi algorithm), which iterates $x^{(t+1)} = (I - A)x^{(t)} + b$. The convergence property of the Power iteration depends on the spectral radius of matrix $I - A$. The convergence rate is $O(\lambda^t)$, where λ is the spectral radius of $I - A$.

Here, we focus on computing PPR. Since $A = I - \alpha P$, where P is the transition matrix of a given graph G, the above iteration reduces to the following form:

$$x^{(t+1)} = \alpha P x^{(t)} + (1 - \alpha)b.$$

This is known as the *PageRank iteration* and the convergence rate is $O(\alpha^t)$. The PageRank iteration has been widely used for computing PPR in real applications.

The Krylov subspace method [41] is a modern framework of iterative algorithms that contains many methods such as CG (conjugate gradient) method, BiCG (biconjugate gradient) method, and GMRES (generalized minimal residual) method. The basic idea of the Krylov subspace method is to maintain all vectors $x^{(1)}, \ldots, x^{(t)}$ of the Power iteration to construct a better solution for the linear equation. More precisely, for the linear equation $Ax = b$, the Krylov subspace method generates a subspace $\mathcal{K}_t(A, b) := \mathrm{span}\{b, Ab, \ldots, A^{t-1}b\}$, and then finds the best approximate solution in $\mathcal{K}_t(A, b)$. In particular, the GMRES method [42] solves the following problem iteratively:

$$x^{(t+1)} = \underset{x \in \mathcal{K}_{t+1}(A,b)}{\arg\min} \|b - Ax\|.$$

Note that this problem can be solved efficiently by (modified) Gram-Schmidt orthogonalization.

The convergence rate of GMRES has been well studied [19, 42]. Essentially, it is fast if eigenvalues of A are clustered and far from the origin, and the condition number $\kappa(U) := \|U^{-1}\|\|U\|$ of the eigenvector matrix U is small.

Krylov subspace methods are regarded by numerical analysts as state-of-the-art for solving large sparse linear equations. However, with respect to computing PPR, it has been reported that Krylov methods do not outperform simple Power iteration [18, 26] especially for web graphs. In comparison of Krylov subspace methods and Power iterations to compute PPR, Gleich, Zhukov, and Berkhin [26] have stated the following:

> Although the Krylov methods have highest average convergence rate and fastest convergence by number of iterations, on some graphs, the actual run time can be longer than the run time for simple Power iterations.

3.1 Preconditioning

An important technique for iterative methods is *preconditioning*, which accelerates iterative methods significantly. This method is usually adapted if $Ax = b$ has a poor convergence property. A good preconditioner for a matrix A is another matrix M that approximates A such that it is easy to solve systems of linear equations in M (rather than in A). Specifically, let M be a non-singular matrix, called *preconditioner*. Preconditioning is the transformation of a linear equation that applies the preconditioner: $MAx = Mb$. Needless to say, preconditioning does not changes the solution of the linear equation. However, in some cases, if we choose a preconditioner M carefully, the convergence property of MA becomes better than A. Thus iterative methods converge quickly.

In most situations, ideally M should be be close to A^{-1}. Indeed, the best preconditioner is $M = A^{-1}$, because this converges the linear equation $MAx = Mb$ in exactly one step. However, this is obviously not an option because computing A^{-1} would be very expensive. Thus, we use an LU decomposition that is obtained from the small tree-width part (i.e., a subgraph that behaves like a tree), as a preconditioner. The experiments in Section 7 show that this preconditioner actually yields fast convergence. We also provide theoretical analysis for this fact in Section 6.

4. OVERVIEW OF OUR ALGORITHM

We now give an overview of our algorithm. At a high level, our algorithm consists of the following three parts. Given an input graph G,

1. we first find a core-tree-decomposition.
2. For the *small tree-width part*, we use a direct method to obtain an LU decomposition.
3. The LU decomposition is used as the preconditioner of an iterative method. Using this preconditioner, we apply the GMRES method to G.

Note that the first two parts are for preprocessing, and the last part computes PPR. Let us look at these two parts more closely.

4.1 Preprocessing for Small Tree-Width Part

For the preprocessing part, we first compute a core-tree-decomposition $(T, \mathcal{V})$ of width d for a given graph G and a constant d. This can be performed using the algorithm described in Section 5. The time complexity is $O(dn + m)$. As mentioned before, we need to choose d such that the core part is as close to an expander as possible (or as small as possible). In Section 7 (and Table 4), we discuss how to choose d; however we conclude that $d = 100$ is the average case, and hereafter we fix d.

As defined previously, the core-tree-decomposition gives rise to the following ordering.

> $W = \{v_1, \ldots, v_l\}$ such that for $i < j$, $d(v_i) \leq d(v_j)$. Note that $W = V(G) \setminus V_r$. Moreover, for each $i > 0$ with $W_i = \{v_{i+1}, \ldots, v_l\}$, $N(v_i) \cap W_i$ is contained in V_t for some $t \in T - r$.

Then the transition matrix P of G can be partitioned into 2×2 blocks:

$$P = \left[\begin{array}{c|c} P[W, W] & P[W, V_r] \\ \hline P[V_r, W] & P[V_r, V_r] \end{array}\right].$$

Finally, we compute an LU decomposition of the graph induced by W: $LU = I - \alpha P[W, W]$. This can be performed using a direct method starting with v_1, and proceeding in the order of W. The pseudo code is given in Algorithm 1.

Section 6.1 shows that the total number of fill-ins for W is bounded by $\sum_{t \in T-r} |V_t|^2$. This gives rise to a good upper bound for the time complexity of our algorithm for the small

Algorithm 1 Preprocessing.

1: Compute a core-tree-decomposition $(T, \mathcal{V})$ with fill-in of width d ($d \leq 1000$ is fixed at the beginning), with the ordering of G.
2: Let $W = V(G) \setminus V_r$. Compute an LU decomposition of $|W| \times |W|$ submatrix of $I - \alpha P[W, W]$ by using a direct method starting with v_1, and proceeds in the ordering of W.

Algorithm 2 Fast Personalized PageRank.

1: Solve $(I - \alpha P)x = (1 - \alpha)b$ by preconditioned GMRES with the preconditioner M in (3).
2: **return** x

tree-width part because the time complexity to obtain an LU decomposition for W is proportional to the number of fill-ins, which is at most $d \times n$ time.

4.2 Computing PPR: Core Part

Once a core-tree-decomposition of width d and an LU decomposition of W is obtained, we can compute PPR efficiently by applying the preconditioned GMRES algorithm. The preconditioner is the following block diagonal matrix.

$$M = \begin{bmatrix} (I - \alpha P[W, W])^{-1} & O \\ O & I \end{bmatrix}. \quad (3)$$

Thus, our linear equation is transformed as follows.

$$\begin{bmatrix} I & -\alpha(I - \alpha P[W, W])^{-1} P[W, V_r] \\ -\alpha P[V_r, W] & I - \alpha P[V_r, V_r] \end{bmatrix} x = (1 - \alpha) \begin{bmatrix} (I - \alpha P[W, W])^{-1} b[W] \\ b[V_r] \end{bmatrix},$$

where $b[W]$ and $B[V_r]$ denote the W and V_r components of b. We can evaluate the above efficiently using the LU decomposition of $(I - \alpha P[W, W])$. The pseudo code is given in Algorithm 2.

The number of iterations of the preconditioned GMRES depends on the graph structure; thus it is difficult to estimate in advance. However, if the core of a graph is close to expander, the number of iterations is much lesser than that in the Power method; see Section 6.4.

4.3 Total Time Complexity

Here we estimate the time complexity of our algorithm. For the preprocess part, as in Section 4.1, the time complexity is $O(dn + m)$ time. For computing PPR, the time complexity is $O(K'm)$, where K' is the number of iterations of our algorithm. However, as mentioned before, $K' \leq K/5$, where K is the number of iterations of the Power method. Note that both K and K' are determined when all PPR scores have errors less than 10^{-9}.

From our experiments (Tables 2 and 3), in most of the cases, our preprocessing (CT + LU in Table 2) is much faster than PPR computation (Table 3).

5. CORE-TREE-DECOMPOSITION ALGORITHM

In this section, we give a detailed description of our algorithm for constructing a core-tree-decomposition. A naive algorithm for the decomposition can be obtained by extending the well-known *min-degree heuristic* [10]; however, its scalability is highly limited because of its costly clique materialization. To construct the decompositions for large networks, we propose a new algorithm with several orders of magnitude better scalability using the new idea of a *star-based representation*. Our method is also based on the min-degree heuristic; thus we first explain this heuristic (Section 5.1), and then present our new algorithm (Section 5.2).

Algorithm 3 Min-degree heuristic.

1: Repeatedly reduce a vertex with minimum degree to generate a list of bags until all the vertices have degree larger than d.
2: Add a bag with all the remaining vertices to the list as the root bag.
3: Construct a tree of these bags.

Here, we are only interested in undirected graphs (but our input graph is directed). Thus we ignore the direction of each edge of the input graph, and then we apply the following algorithms to the resulting undirected graph.

5.1 Min-degree Heuristic Algorithm

Our algorithms is based on the *min-degree heuristic* [10], which is a standard tree-decomposition algorithm in practice [2, 43, 45]. Here, we present a modified version of the min-degree heuristic that takes a parameter d and computes a core-tree-decomposition with fill-ins of width d.

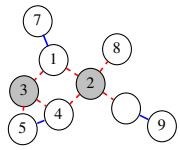
At a high level, the algorithm first generates a list of bags, and then constructs a tree of these bags (Algorithm 3). To generate a list of bags, the algorithm repeatedly *reduces* a vertex with degree at most d. The reduction of vertex v includes of three steps. First, we create a new bag V_v including v and all its neighbors. Second, we change the graph G by removing node v. Third, we create a clique among those vertices in $V_v \setminus \{v\}$. After reducing all vertices with degree at most d, we create a bag V_r that includes all the remaining vertices, and that corresponds to the *core* (note that this can be very large). Then, we construct the tree of the tree decomposition from the list of bags. We set the parent of bag V_v as bag V_p, where $(V_v \setminus \{v\}) \subseteq V_p$. We can always find the valid parent because all neighbors of a reduced vertex are contained in a clique.

Drawback of Scalability. Even if we assume that the adjacency lists are managed in hash tables and operations on edges can be performed in $O(1)$ time, reducing vertex v takes $\Theta(|V_v|^2)$ time. Thus, in total, the algorithm takes $\Theta(\sum_{t \in T \setminus \{r\}} |V_t|^2)$ time. Furthermore, we need to materialize edges of cliques; hence space consumption is also too large. Therefore, even if we use a relatively small parameter d (e.g., 100), it becomes impractical to apply the described algorithm to large-scale networks.

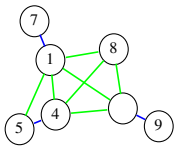
5.2 Proposed Core-Tree-Decomposition Algorithm

5.2.1 Overview

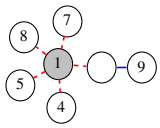
The idea behind our method is to *virtually* conduct the min-degree heuristic algorithm to avoid costly clique materialization. Rather than naively inserting all the edges of the cliques, we introduce *star-based representation* to maintain clique edges efficiently. In this representation, all operations on graphs used in the min-degree heuristic correspond to simple operations, such as modification of roles of vertices



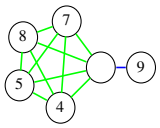
(a) A star-based representation of a graph.



(b) The represented graph.



(c) The star-based representation after reducing vertex 1.



(d) The represented graph after reducing vertex 1.

Figure 1: Star-based representation and reduction. The white vertices are normal vertices, and gray vertices are hub vertices.

and *contraction* of edges, which leads to improved scalability of several orders of magnitude.

Star-based Representation. Here we deal with two kinds of graphs: A *(star-based) representation graph* is what we store and maintain in the memory, and a *represented graph* corresponds to a virtual snapshot of a graph represented by a representation graph that would be maintained by the naive min-degree heuristic algorithm.

In the star-based representation, each vertex belongs to one of the following two types: *normal vertices* or *hub vertices*. Two hub vertices are never connected, i.e., edges connect either two normal vertices or a normal vertex and a hub vertex. The represented graph can be obtained by a representation graph by *(1)* adding edges to make its neighbors a clique for all hub vertices and *(2)* removing hub vertices. For example, the representation graphs shown in Figures 1a and 1c represents the graphs shown in Figures 1b and 1d, respectively.

Overall Algorithm. At a high level, our algorithm conducts the min-degree heuristic (Algorithm 3) on virtually represented graphs, i.e., it repeatedly reduces vertices with degree at most d in the represented graph to generate a list of bags. Then our algorithm constructs the tree of the bags. To construct the tree, we use the same tree construction algorithm. Therefore, as noted before, the main difference here is that, during the reduction phase, we do not maintain the represented graph itself. We manage the star-based representation graph instead. Thus, we explain how to reduce vertices using star-based representation for enumerating bags.

Reducing a Vertex. First, for a easier case, we consider a situation in which we reduce vertex v, whose neighbors are all normal vertices. To remove v and make its neighbors a clique in the represented graph, we must alter the vertex type of v from normal to hub.

Let us now consider a general situation, where some of v's neighbors in the representation graph are hub vertices. One of the challenges here is the fact that no direct edges can exist in the representation graph between some of v's neighbors due to these neighbor hub vertices. To make v's neighbors a clique in the represented graph, we must create a new hub vertex that is connected to all these neighbors.

Rather than creating such a new hub from scratch, the new hub can be efficiently composed by contracting v and all the neighboring hub vertices. Contraction of two vertices means removing the edge between them and merging two endpoints. For example, reducing the vertex 1 in the represented graph shown in Figure 1b corresponds to contracting vertices 1, 2, and 3 in the representation graph depicted in Figure 1a, thus yielding the representation graph in Figure 1c. By doing so, as we will discuss in Section 5.2.2, the time complexity becomes almost linear to the output size using proper data structures. Moreover, we never add any new edge to the representation graph. Therefore, the number of edges in the representation graph never increases; thus, space consumption is also kept in linear.

5.2.2 Details

Finding a Vertex to Reduce: Precisely finding a vertex with minimum degree is too costly because we must track the degree of all vertices. Therefore, we approximately find a vertex with minimum degree by using a priority queue as follows. First, we insert all vertices into the priority queue, and use their current degree as keys. To find a vertex to reduce, we pop a vertex with the smallest key from the priority queue. If its current degree is the same as the key, then we reduce the vertex. Otherwise, we reinsert the vertex to the priority queue with its new degree.

Data Structures: We manage adjacency lists in hash tables to operate edges in constant time. To efficiently contract edges, we manage groups of vertices and merge adjacency lists, similar to the weighted quick-find algorithm [46].

Core-tree-decomposition Ordering: For our total PPR algorithm, in addition to the decomposition, we also require ordering of vertices $V(G) \setminus V_r$ that satisfies the conditions specified in Section 2.4. Actually, this can be obtained easily by the order of vertices to be reduced. It is easy to see that this ordering satisfies the conditions.

Time Complexity: As we contract vertices similar to the weighted quick-find algorithm, the expected total time consumed for edge contractions is $O(m)$ time [30]. Reducing a vertex v takes approximately $O(d')$, where d' is the degree of v. Therefore, we expect that the proposed algorithm computes a core-tree-decomposition in $\sum_{i<d} id_i + O(m)$ time, where d_i is the number of vertices of degree i. In Section 6.1, we point out $\sum_{i<d} id_i \leq d/10 \times n$. In particular, it runs in linear time if d is a constant.

6. THEORETICAL ANALYSIS AND EXPERIMENTAL VERIFICATION

Let $G = (T_r, \mathcal{V})$ be a rooted tree-decomposition of width d and V_r corresponding to the core. Here, we give a theoretical analysis of our proposed algorithm. Then we justify it by performing several experiments.

We first show that our algorithm to construct an LU decomposition for a small tree-width part is very efficient. This can be qualified by giving an upper bound for fill-in (Section 6.1), which is also an upper bound for the time complexity to construct an LU decomposition. Our next empirical results imply that the core V_r is very close to an expander graph (Section 6.2). So far, we have examined undirected graphs.

In Sections 6.3 and 6.4, we show that a direct method works very well for small tree-width graphs; however a direct method does not work well for expander graphs. Moreover, an iterative method works very well for expander graphs, but does not for small tree-width graphs. These two facts would clarify theoretical hypothesis for our proposed algorithm. Thus, we need to look at directed graphs for this purpose. We also perform some experiments to support these facts.

6.1 How Many "Fill-in"?

Here, we estimate an upper bound for the number of fill-in. As in Algorithm 1, our algorithm starts with v_1 and proceeds in the order of W. Let us consider v_i. The number of fill-in for v_i is exactly same as that of non-edges between any nonadjacent vertices in $N_{v_i} \cap W_i$, which is bounded by $|V_{t'}|^2$, where the bag $V_{t'}$ contains all the vertices of $N(v_i) \cap W_i$ for some $t' \in T \setminus \{r\}$. It follows that the number of fill-in is at most $\sum_{t \in T \setminus \{r\}} |V_t|^2$. By our construction of the core-tree-decomposition, naively $\sum_{t \in T \setminus \{r\}} |V_t|^2$ is proportional to $\sum_{i<d} i^2 d_i$, where d_i is the number of vertices of degree i in $V(G) \setminus V_r$. Note that we keep the small tree-width graph even after adding edges.

To estimate $\sum_{i<d} i^2 d_i$ more accurately, we must look at the distribution of the bag size of the core-tree-decompositions of the graphs shown in Figure 2[3]. As is shown, many bags are small, and only a few bags are large. This can be explained from a theoretical perspective. A *scale-free network* is a network whose degree distribution follows a power law, at least asymptotically. That is, the fraction $P(k)$ of vertices in the network having degree exactly k for large values of k can be described as follows:

$$P(k) \sim k^{-\gamma},$$

where γ is a parameter whose value is typically in the range $2 < \gamma < 3$. Many networks are observed to be scale-free, including social networks and web graphs. Our core-tree-decomposition is based on minimum degree heuristic, which depends on degree distribution. Therefore, in practice, $\sum_{i<d} id_i \leq \sum_{i<d} i \times n/i^2 \leq d/10 \times n$ and $\sum_{i<d} i^2 d_i \leq \sum_{i<d} i^2 \times n/i^2 \leq d \times n$.

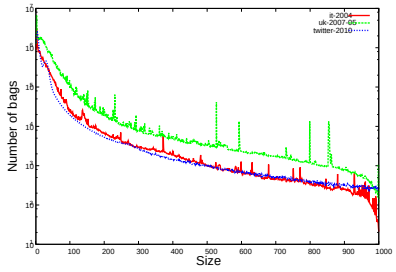
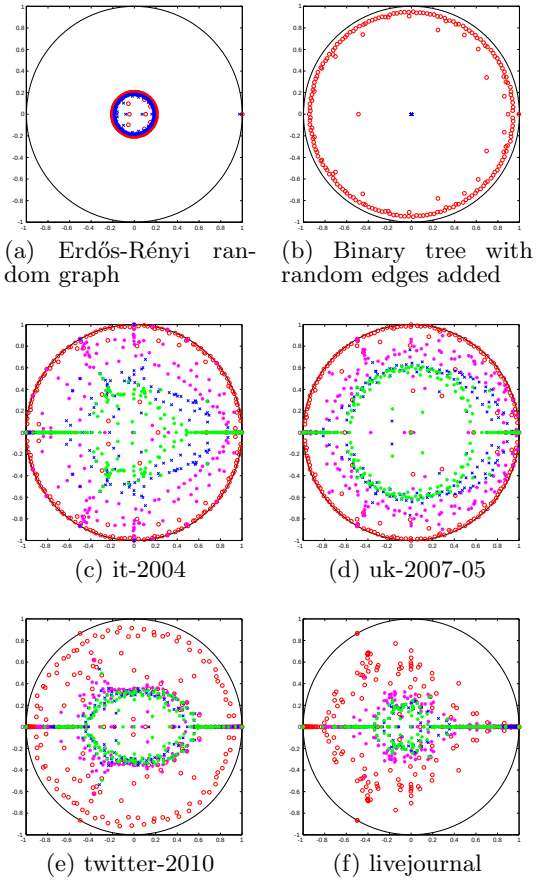


Figure 2: Distribution of bag sizes.

6.2 How Close the Core is to Expander?

As explained previously, we determine how close the core of real networks is to expander by evaluating the distribution of the eigenvalues of the transition matrix. For two synthetic networks (a typical expander graph and a typical non-expander graph), two real web graphs (it-2004 and uk-2007-05), and two real social networks (twitter-2010 and livejournal)[4], we compute 200 *extreme* eigenvalues of the transition matrix of their cores and their whole networks, respectively, using the Arnoldi method [40]. The results are shown in Figure 3. The transition matrices are not necessarily symmetric; thus, eigenvalues may not be real. In fact, they contain both the real part and the imaginary part, as shown in Figure 3.



(a) Erdős-Rényi random graph (b) Binary tree with random edges added

(c) it-2004 (d) uk-2007-05

(e) twitter-2010 (f) livejournal

Figure 3: Extreme eigenvalues of typical networks on complex plane; x axis is for the real part and y axis is for the imaginary part. Red points are the distribution of eigenvalues of the whole network, purple points are that of the core with $d = 10$, blue points are that of the core with $d = 100$, and green points are that of the core with $d = 1000$. For (a) and (b), there are only red and blue points.

Figure 3a indicates a directed version of an Erdös-Rényi random graph, which is supposed to be a typical expander graph, and Figure 3b indicates a directed complete binary tree with a few random edges added, which is a typical non-expander graph (i.e., a small tree-width graph). As explained previously, a given network is close to expander if the eigenvalues are clustered near the origin. This can be also qualified by Figures 3a and 3b.

For real networks (Figures 3c–3f), the eigenvalues of the whole networks (red points) are scattered, similar to the distribution of a non-expander graph (Figure 3b). On the other hand, the eigenvalues of the core (blue points) are relatively

[3]Datasets are explained in Section 7.

[4]Again, datasets are explained in Section 7.

clustered near the origin, similar to the distribution of an expander graph (Figure 3a). These results suggest that

> real networks are non-expanders but the core of each network is closer to an expander.

6.3 Direct Method Is Fast on Small Tree-Width Graphs

From the analysis in Section 6.1, if a graph is of tree-width d then the number of fill-in is $O(nd)$. Thus, the number of nonzero elements in L and U is $O(m + nd)$. Therefore, if the tree-width of a given graph is larger, then it is expected to take much more time to find an LU decomposition.

We now verify this discussion for real networks by finding an LU decomposition for typical synthetic undirected networks (i.e., Erdős-Rényi and binary tree with random edges added). The tree-width of an Erdős-Rényi random graph is $O(n)$ [24], and the tree-width of a binary-tree is $O(1)$. Both graphs have $m = O(n)$ edges; however the computational time required to find an LU decomposition (and hence for a direct method) is quite different (Figure 4). This coincides with the above theoretical observation.

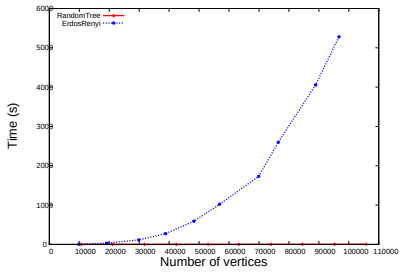


Figure 4: Computational time of LU decomposition.

Note that in the literature for a sparse direct method, many re-ordering methods are proposed to reduce the number of fill-ins [5, 25]; however if a graph has a large tree-width, any ordering cannot reduce the computational cost, as shown in Figure 4. Therefore, we conclude that decomposing a graph into the small tree-width part and the *core* part is more important than finding a better ordering.

6.4 Iterative Method Is Fast on Expander Graphs

Here, we show that iterative methods, in particular GMRES, converge quickly if a network is close to expander.

Let us start with the analysis of the Power iteration. The Power iteration for PPR is given by

$$x^{(t+1)} = \alpha P x^{(t)} + (1-\alpha)b.$$

To simplify the following discussion, we assume $x^{(0)} = (1-\alpha)b$. By substituting the left side to the right side iteratively, we obtain

$$x^{(t)} = (1-\alpha)\left[I + \alpha P + \cdots + \alpha^{t-1}P^{t-1}\right] b$$

and hence the residual $r^{(t)} = (1-\alpha)b - (I - \alpha P)x^{(t)}$ satisfies

$$\|r^{(t)}\| \leq \alpha^t \|P^t r^{(0)}\|. \tag{4}$$

The standard analysis of PPR uses this formula and applies the Perron-Frobenius theorem to show that the convergence rate is $O(\alpha^t)$ [38]. However, we should take advantage of an expander graph; thus more detailed analysis is required.

Suppose that the transition matrix P is diagonalizable, i.e., $U^{-1}PU = \mathrm{diag}(\lambda_1, \ldots, \lambda_n)$ for an eigenvector matrix $U = [v_1 \ldots v_n]$. Without loss of generality, we may assume that $1 = \lambda_1 \geq |\lambda_2| \geq \cdots \geq |\lambda_n|$. Then, by expanding $r^{(0)} = (1-\alpha)b$ by the eigenvectors of P as

$$r^{(0)} = \beta_1 u_1 + \cdots + \beta_n u_n, \tag{5}$$

and substituting to (4), we obtain

$$\|r^{(t)}\| \leq \alpha^t \sum_{i=1}^{n} |\lambda_i|^t |\beta_i|. \tag{6}$$

As explained before in the case of an expander graph, the second eigenvalue of an expander graph is relatively small compared to the first eigenvalue [14]. Therefore, all terms except for the first converge rapidly; thus the Power iteration converges quickly. However, this does not give us improvement. The asymptotic convergence rate of the Power iteration is still $O(\alpha^t)$ because the first eigenvector component is a bottleneck.

To take the advantage of expander, we have a closer look at the GMRES algorithm. We consider Embree [19]'s result, which is a generalization of (6). Here, let κ_i be the condition number of i'th eigenvalue λ_i, which is defined as $\kappa_i = \|u_{Li}\|\|u_{Ri}\|/|u_{Li}^* u_{Ri}|$, where u_{Li} and u_{Ri} are the left and right eigenvectors of λ_i, respectively. Then, for *any polynomial* $p(z)$ of degree t and $p(0) = 1$, we have the following bound [19]:

$$\|r^{(t)}\| \leq \sum_{i=1}^{n} |p(1-\alpha\lambda_i)|\kappa_i. \tag{7}$$

Generally, we do not know the optimal polynomial p to minimize the right side of (7) which gives tight convergence estimation. However, by using some explicit polynomial p, we can obtain an upper bound of convergence estimation.

Let us first use a simple polynomial $p(z) = (1-z)^t$. Thus (7) gives

$$\|r^{(t)}\| \leq \alpha^t \sum_{i=1}^{n} |\lambda_i|^t \kappa_i,$$

which is a similar form of (6). This implies that GMRES requires at most the same number of iterations of Power iteration. To take further advantage of the expander property, let us use $p(z) \propto (1-\alpha-z)(1-z)^{t-1}$. Then, (7) gives

$$\|r^{(t)}\| \leq K\alpha^t \sum_{i=2}^{n} |\lambda_i|^t \kappa_i$$

for some constant K. We emphasize that the summation starts from $i = 2$, i.e., the term for $i = 1$ is removed. This shows that GMRES can remove the effect of the first eigenvector component, which is the bottleneck of the Power iteration. Thus the convergence rate of GMRES is at least $O(|\alpha\lambda_2|^t)$. This significantly improves the Power iteration when a given graph is an expander, i.e., $|\lambda_2| \ll 1$.

We verify the above discussion empirically by applying Power iteration and GMRES to typical synthetic networks. Consider an Erdős-Rényi random graph and a binary tree with random edges, whish are typical expander and non-expander graphs, respectively. We plot the error curves of

Table 1: Dataset information.[5]

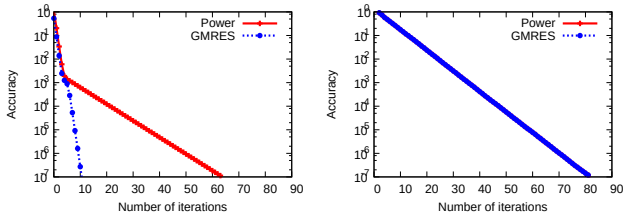
name	n	m
in-2004	1,382,908	16,917,053
it-2004	41,291,549	1,150,725,436
uk-2007-05	105,896,555	3,738,733,648
twitter-2010	41,652,230	1,468,365,182
web-BerkStan	685,230	7,600,505
web-Google	875,713	5,105,049
web-NotreDame	325,728	1,497,134
web-Stanford	281,903	2,312,497
livejournal	5,284,457	77,402,652
flickr	1,846,198	22,613,981
orkut	3,072,441	223,534,301

the Power iteration and GMRES for these networks in Figure 5. Observe that the error curve for an expander graph is shown in Figure 5a. Both the Power iteration and GMRES have a steeper slope in the first few iterations. However, in the latter iterations, the slope of GMRES stays steep, but the slope of the Power iteration becomes gentle. This result implies that

> iterative methods are fast for expander graphs. In particular, GMRES can exploit much more information on expander graphs than the Power iteration.

Next, we examine the error curves for non-expander graphs. The results are shown in Figure 5b. We can see that the error curves of the Power iteration and GMRES are completely overlapped, because, as there are too many larger eigenvalues, there is no good polynomial p that shows the rapid convergence of GMRES. Since the computational cost of a single iteration of GMRES is more expensive than that of the Power iteration [18, 26], we can conclude that

> GMRES cannot outperform the Power iteration for non-expander graphs.



(a) Erdős-Rényi random graph (b) Binary tree with random edges

Figure 5: Comparison between the Power iteration and GMRES.

7. EXPERIMENTAL EVALUATION

We conducted experiments on several web graphs as well as a few social networks. The purpose of the experiments is to demonstrate performance of our proposed algorithm for both the preprocessing and the computation for PPR.

All experiments are conducted on an Intel Xeon E5-2690 2.90GHz CPU with 256GB memory and running Ubuntu 12.04. Our algorithm is implemented in C++ and compiled with g++v4.6 with -O3 option. We use 10 directed and 1 undirected (orkut) networks shown in Table 1.

[5]in-2004, it-2004, uk-2007-05, and twitter-2010 data sets are available at `http://law.di.unimi.it/datasets.php` [11, 12]. web-BerkStan web-Google, web-NotreDame, and web-Stanford data sets are available at `http://snap.stanford.edu/data/index.html` [3, 33]. livejournal, flickr, and orkut data sets are available at `http://socialnetworks.mpi-sws.org/datasets.html` [37].

Table 2: Preprocessing; width $d = 100$.

name	CT dec[s]	core size	LU dec[s]
in-2004	0.39	41,475	1.41
it-2004	162.90	4,309,140	43.45
uk-2007-05	528.26	13,009,914	101.47
twitter-2010	197.32	7,513,858	16.81
web-BerkStan	2.02	36,823	0.83
web-Google	2.22	41,693	0.83
web-NotreDame	0.42	5,252	0.31
web-Stanford	0.70	10,393	0.35
livejournal	33.81	1,174,081	3.74
flickr	12.91	148,385	0.88
orkut	28.53	1,950,126	1.13

Preprocessing. The experimental results for the preprocessing phase are shown in Table 2. For these networks we set the width d of the core-tree-decomposition as $d = 100$. We also perform the preprocessing phase with varying d. The results will be given later; however, $d = 100$ is the average case (i.e., CT+LU in Table 2) for many datasets. Thus let us fix $d = 100$ for the moment. We perform our algorithm 100 times and take the average.

For these networks, the computational time to construct a core-tree-decomposition (CT in Table 2) and an LU decomposition (LU in Table 2) is essentially proportional to the number of vertices and edges. However it varies significantly among the networks. The size of the core also varies among the networks

These experiments show that we can perform our preprocessing very quickly to obtain both a core-tree-decomposition and an LU decomposition of the small tree-width part.

Personalized PageRank computation and comparison to other algorithms. The experimental results for the PPR computation phase are shown in Table 3. We take the personalized vector b such that the number of nonzero elements is four, and these nonzero elements are randomly chosen[6] All algorithms in Table 3 must compute $x \in \mathbb{R}^n$ such that $\|x - x^*\| \leq 10^{-9}\|x^*\|$, where $x^* \in \mathbb{R}^n$ is a vector of the optimal PPR (accuracy 10^{-9} in Table 3). We set $\alpha = 0.85$, as it is widely used. We perform our algorithm 100 times and take the average.

We compare our algorithm with the Power method and the naive GMRES method [44](Note that no preconditioning is performed).

First, let us look at our algorithm, the preconditioned GMRES, and the Power method, and the naive GMRES method. The proposed algorithm is 2–5 times faster than the Power method and 1.5–6 times faster than the naive GMRES method. Even if we consider the preprocessing time into account for the query time, our proposed algorithm is 2-4 times faster than the Power method and the naive GMRES method. Note that the number of iterations of our algorithm is very small, say 5 times less than the Power method. These results suggest that if we handle millions of query requests simultaneously, then once we have performed one efficient preprocessing for a large network (e.g., once a

[6]In word sense disambiguation, the number of query nodes is 2.2 on average, see [9].

Table 3: Solving PPR; accuracy 10^{-9}.

name	precond. GMRES		Power		naive GMRES	
	time[s]	iteration	time[s]	iteration	time[s]	iteration
in-2004	2.55	23	4.65	108	8.44	64
it-2004	136.08	21	321.65	104	572.33	74
uk-2007-05	576.98	26	1078.10	103	1626.06	73
twitter-2010	540.49	22	1824.23	106	1434.89	50
web-BerkStan	0.91	15	2.48	107	6.09	74
web-Google	1.88	27	2.40	107	4.91	64
web-NotreDame	0.18	17	0.61	102	0.98	71
web-Stanford	0.48	20	0.82	106	1.70	60
livejournal	21.20	21	69.11	106	35.79	37
flickr	3.50	18	11.35	108	7.18	37
orkut	41.69	21	120.33	74	46.99	24

Table 4: Computational time for various bag sizes d. PPR column shows the number of iterations in parenthesis.

	it-2004			twitter-2010		
d	CT[s]	LU[s]	PPR[s]	CT[s]	LU[s]	PPR[s]
10	8.87	10.48	148.44(26)	17.77	14.06	540.78(23)
20	24.58	14.71	142.79(25)	39.05	15.61	547.89(23)
50	78.94	26.60	134.35(23)	107.73	15.35	589.16(23)
100	162.90	43.45	136.08(21)	197.32	16.81	540.49(22)
200	276.96	70.86	148.40(21)	353.61	19.74	547.51(22)
500	476.99	219.24	160.97(20)	958.65	21.67	577.86(22)
1000	690.73	563.77	168.15(19)	2265.78	21.53	557.14(22)

day because the network may change in a single day), our algorithm can handle millions of query requests up to five times more efficiently than the Power method and the naive GMRES method.

Bag size and computational time. As mentioned above, $d = 100$ is the average case for many datasets; however, sometimes our algorithm runs faster if d is smaller. This is the case for a web graph (it-2004) and a social network (twitter-2010). The results are shown in Table 4. For these two datasets, the time for PPR (i.e., our proposed query phase) does not vary significantly. Therefore, we can obtain a slightly faster algorithm (for CT + LU + PPR).

Here we present theoretical justification. First, Let us look at Figures 3c and 3d for web graphs and Figures 3e and 3f for social networks. We compute 200 "extreme" eigenvalues of the whole networks and of only their cores for the cases $d = 10$, 100, and 1000, respectively, by using the Arnoldi method [40]. We can conclude that as d increases, the eigenvalues of the cores of web graphs are clustered closer to the origin. This means that as d increases, the core of web graphs gets closer to an expander (similar to the distribution of an expander graph (Figure 3a)). On the other hand, as d increases, the eigenvalues of the cores of social networks are first clustered closer to the origin, but then stay for a while. This means that, for social networks, we can stop at some value of d. Indeed, $d = 100$ seems sufficient for social networks.; however for web graphs, we can increase d.

8. RELATED WORK

We discuss previous work related to PPR computation.

Several approximate approaches have been proposed focusing on efficient computation for PPR. However, none of them seems to guarantee an accurate solution. Their outputs differ from those of iterative methods. Therefore, it is difficult for these approximate approaches to compare the quality of real applications with ours.

Having said that, Jeh and Widom have suggested a framework that provides a scalable solution for PPR for vertices that belong to a highly linked subset of hub vertices [28]. Their approach is based on the observation that relevance scores for a given distribution can be approximated as a linear combination of those from a single vertex in hubs. They compute approximate relevance scores for a given distribution using relevance scores that can be precomputed from hubs. Fogaras et al. [21] proposed a Monte Carlo based algorithm for PPR. To compute approximate relevance scores, they used fingerprints of several vertices; a fingerprint of a vertex is a random walk starting from the vertex. They first preprocess fingerprints by simulating random walks, and then approximate relevance distributions from the ending vertices of these random walks. They approximated relevance scores by exploiting the linearity property of PPR. Avrachenkov et al. [7] and Bahmani, Chowdhury, and Goel [8], independently, improved the Monte Carlo method.

9. CONCLUSION

In this paper, by exploiting graph structures of web graphs and social networks, we have proposed a GMRES (a state-of-the-arts advanced iterative method) based algorithm to compute the personalized PageRank for web graphs and social networks. The convergence of the algorithm is very fast. In fact, it is as much as 7.5 times less than the Power method for the number of iterations and as much as five times faster than the Power method in actual computation time. Even if we consider the preprocessing time into account for the query time, the proposed algorithm is 2-4 times faster than the Power method. In addition, we can implement our algorithm for graphs with billions of edges. If we must handle millions of query requests simultaneously, then once we have performed a single efficient preprocessing for a large network (once a day because the network may change in a single day), our algorithm can handle millions of query requests up to five times more efficiently.

Finally, we would mention that our experimental results imply that web graphs and social networks are different in the structure of core-tree-decomposition. In [1], we extend this idea and analyze several real networks via core-tree-decomposition.

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