Chapter 5

Graph Algorithms

Graphs are ubiquitous in modern society: examples encountered by almost everyone on a daily basis include the hyperlink structure of the web (simply known as the web graph), social networks (manifest in the flow of email, phone call patterns, connections on social networking sites, etc.), and transportation networks (roads, bus routes, flights, etc.). Our very own existence is dependent on an intricate metabolic and regulatory network, which can be characterized as a large, complex graph involving interactions between genes, proteins, and other cellular products. This chapter focuses on graph algorithms in MapReduce. Although most of the content has nothing to do with text processing *per se*, documents frequently exist in the context of some underlying network, making graph analysis an important component of many text processing applications. Perhaps the best known example is PageRank, a measure of web page quality based on the structure of hyperlinks, which is used in ranking results for web search. As one of the first applications of MapReduce, PageRank exemplifies a large class of graph algorithms that can be concisely captured in the programming model. We will discuss PageRank in detail later this chapter.

In general, graphs can be characterized by nodes (or vertices) and links (or edges) that connect pairs of nodes.[1] These connections can be directed or undirected. In some graphs, there may be an edge from a node to itself, resulting in a self loop; in others, such edges are disallowed. We assume that both nodes and links may be annotated with additional metadata: as a simple example, in a social network where nodes represent individuals, there might be demographic information (e.g., age, gender, location) attached to the nodes and type information attached to the links (e.g., indicating type of relationship such as "friend" or "spouse").

Mathematicians have always been fascinated with graphs, dating back to Euler's paper on the *Seven Bridges of Königsberg* in 1736. Over the past few centuries, graphs have been extensively studied, and today much is known about their properties. Far more than theoretical curiosities, theorems and

[1] Throughout this chapter, we use *node* interchangeably with *vertex* and similarly with *link* and *edge*.

algorithms on graphs can be applied to solve many real-world problems:

- Graph search and path planning. Search algorithms on graphs are invoked millions of times a day, whenever anyone searches for directions on the web. Similar algorithms are also involved in friend recommendations and expert-finding in social networks. Path planning problems involving everything from network packets to delivery trucks represent another large class of graph search problems.

- Graph clustering. Can a large graph be divided into components that are relatively disjoint (for example, as measured by inter-component links [59])? Among other applications, this task is useful for identifying communities in social networks (of interest to sociologists who wish to understand how human relationships form and evolve) and for partitioning large graphs (of interest to computer scientists who seek to better parallelize graph processing). See [158] for a survey.

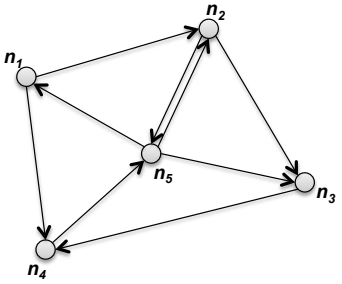
- Minimum spanning trees. A minimum spanning tree for a graph G with weighted edges is a tree that contains all vertices of the graph and a subset of edges that minimizes the sum of edge weights. A real-world example of this problem is a telecommunications company that wishes to lay optical fiber to span a number of destinations at the lowest possible cost (where weights denote costs). This approach has also been applied to wide variety of problems, including social networks and the migration of Polynesian islanders [64].

- Bipartite graph matching. A bipartite graph is one whose vertices can be divided into two disjoint sets. Matching problems on such graphs can be used to model job seekers looking for employment or singles looking for dates.

- Maximum flow. In a weighted directed graph with two special nodes called the source and the sink, the max flow problem involves computing the amount of "traffic" that can be sent from source to sink given various flow capacities defined by edge weights. Transportation companies (airlines, shipping, etc.) and network operators grapple with complex versions of these problems on a daily basis.

- Identifying "special" nodes. There are many ways to define what special means, including metrics based on node in-degree, average distance to other nodes, and relationship to cluster structure. These special nodes are important to investigators attempting to break up terrorist cells, epidemiologists modeling the spread of diseases, advertisers trying to promote products, and many others.

A common feature of these problems is the scale of the datasets on which the algorithms must operate: for example, the hyperlink structure of the web, which contains billions of pages, or social networks that contain hundreds of



	n_1	n_2	n_3	n_4	n_5
n_1	0	1	0	1	0
n_2	0	0	1	0	1
n_3	0	0	0	1	0
n_4	0	0	0	0	1
n_5	1	1	1	0	0

adjacency matrix

n_1	$[n_2, n_4]$
n_2	$[n_3, n_5]$
n_3	$[n_4]$
n_4	$[n_5]$
n_5	$[n_1, n_2, n_3]$

adjacency lists

Figure 5.1: A simple directed graph (left) represented as an adjacency matrix (middle) and with adjacency lists (right).

millions of individuals. Clearly, algorithms that run on a single machine and depend on the entire graph residing in memory are not scalable. We'd like to put MapReduce to work on these challenges.[2]

This chapter is organized as follows: we begin in Section 5.1 with an introduction to graph representations, and then explore two classic graph algorithms in MapReduce: parallel breadth-first search (Section 5.2) and PageRank (Section 5.3). Before concluding with a summary and pointing out additional readings, Section 5.4 discusses a number of general issue that affect graph processing with MapReduce.

5.1 Graph Representations

One common way to represent graphs is with an adjacency matrix. A graph with n nodes can be represented as an $n \times n$ square matrix M, where a value in cell m_{ij} indicates an edge from node n_i to node n_j. In the case of graphs with weighted edges, the matrix cells contain edge weights; otherwise, each cell contains either a one (indicating an edge), or a zero (indicating none). With undirected graphs, only half the matrix is used (e.g., cells above the diagonal). For graphs that allow self loops (a directed edge from a node to itself), the diagonal might be populated; otherwise, the diagonal remains empty. Figure 5.1 provides an example of a simple directed graph (left) and its adjacency matrix representation (middle).

Although mathematicians prefer the adjacency matrix representation of graphs for easy manipulation with linear algebra, such a representation is far from ideal for computer scientists concerned with efficient algorithmic implementations. Most of the applications discussed in the chapter introduction involve *sparse* graphs, where the number of *actual* edges is far smaller than the

[2]As a side note, Google recently published a short description of a system called Pregel [98], based on Valiant's Bulk Synchronous Parallel model [148], for large-scale graph algorithms; a longer description is anticipated in a forthcoming paper [99]

number of *possible* edges.[3] For example, in a social network of n individuals, there are $n(n-1)$ possible "friendships" (where n may be on the order of hundreds of millions). However, even the most gregarious will have relatively few friends compared to the size of the network (thousands, perhaps, but still far smaller than hundreds of millions). The same is true for the hyperlink structure of the web: each individual web page links to a minuscule portion of all the pages on the web. In this chapter, we assume processing of sparse graphs, although we will return to this issue in Section 5.4.

The major problem with an adjacency matrix representation for sparse graphs is its $O(n^2)$ space requirement. Furthermore, most of the cells are zero, by definition. As a result, most computational implementations of graph algorithms operate over adjacency lists, in which a node is associated with neighbors that can be reached via outgoing edges. Figure 5.1 also shows the adjacency list representation of the graph under consideration (on the right). For example, since n_1 is connected by directed edges to n_2 and n_4, those two nodes will be on the adjacency list of n_1. There are two options for encoding undirected graphs: one could simply encode each edge twice (if n_i and n_j are connected, each appears on each other's adjacency list). Alternatively, one could order the nodes (arbitrarily or otherwise) and encode edges only on the adjacency list of the node that comes first in the ordering (i.e., if $i < j$, then n_j is on the adjacency list of n_i, but not the other way around).

Note that certain graph operations are easier on adjacency matrices than on adjacency lists. In the first, operations on incoming links for each node translate into a column scan on the matrix, whereas operations on outgoing links for each node translate into a row scan. With adjacency lists, it is natural to operate on outgoing links, but computing anything that requires knowledge of the incoming links of a node is difficult. However, as we shall see, the shuffle and sort mechanism in MapReduce provides an easy way to group edges by their destination nodes, thus allowing us to compute over incoming edges with in the reducer. This property of the execution framework can also be used to invert the edges of a directed graph, by mapping over the nodes' adjacency lists and emitting key–value pairs with the destination node id as the key and the source node id as the value.[4]

5.2 Parallel Breadth-First Search

One of the most common and well-studied problems in graph theory is the *single-source shortest path* problem, where the task is to find shortest paths from a source node to all other nodes in the graph (or alternatively, edges can be associated with costs or weights, in which case the task is to compute

[3] Unfortunately, there is no precise definition of sparseness agreed upon by all, but one common definition is that a sparse graph has $O(n)$ edges, where n is the number of vertices.

[4] This technique is used in *anchor text inversion*, where one gathers the anchor text of hyperlinks pointing to a particular page. It is common practice to enrich a web page's standard textual representation with all of the anchor text associated with its incoming hyperlinks (e.g., [107]).

Algorithm 5.1 Dijkstra's algorithm

Dijkstra's algorithm is based on maintaining a global priority queue of nodes with priorities equal to their distances from the source node. At each iteration, the algorithm expands the node with the shortest distance and updates distances to all reachable nodes.

```
1:  DIJKSTRA(G, w, s)
2:      d[s] ← 0
3:      for all vertex v ∈ V do
4:          d[v] ← ∞
5:      Q ← {V}
6:      while Q ≠ ∅ do
7:          u ← EXTRACTMIN(Q)
8:          for all vertex v ∈ u.ADJACENCYLIST do
9:              if d[v] > d[u] + w(u, v) then
10:                 d[v] ← d[u] + w(u, v)
```

lowest-cost or lowest-weight paths). Such problems are a staple in undergraduate algorithm courses, where students are taught the solution using Dijkstra's algorithm. However, this famous algorithm assumes sequential processing—how would we solve this problem in parallel, and more specifically, with MapReduce?

As a refresher and also to serve as a point of comparison, Dijkstra's algorithm is shown in Algorithm 5.1, adapted from Cormen, Leiserson, and Rivest's classic algorithms textbook [41] (often simply known as *CLR*). The input to the algorithm is a directed, connected graph $G = (V, E)$ represented with adjacency lists, w containing edge distances such that $w(u, v) \geq 0$, and the source node s. The algorithm begins by first setting distances to all vertices $d[v], v \in V$ to ∞, except for the source node, whose distance to itself is zero. The algorithm maintains Q, a global priority queue of vertices with priorities equal to their distance values d.

Dijkstra's algorithm operates by iteratively selecting the node with the lowest current distance from the priority queue (initially, this is the source node). At each iteration, the algorithm "expands" that node by traversing the adjacency list of the selected node to see if any of those nodes can be reached with a path of a shorter distance. The algorithm terminates when the priority queue Q is empty, or equivalently, when all nodes have been considered. Note that the algorithm as presented in Algorithm 5.1 only computes the shortest distances. The actual paths can be recovered by storing "backpointers" for every node indicating a fragment of the shortest path.

A sample trace of the algorithm running on a simple graph is shown in Figure 5.2 (example also adapted from *CLR*). We start out in (a) with n_1 having a distance of zero (since it's the source) and all other nodes having a distance of ∞. In the first iteration (a), n_1 is selected as the node to expand (indicated by the thicker border). After the expansion, we see in (b) that n_2

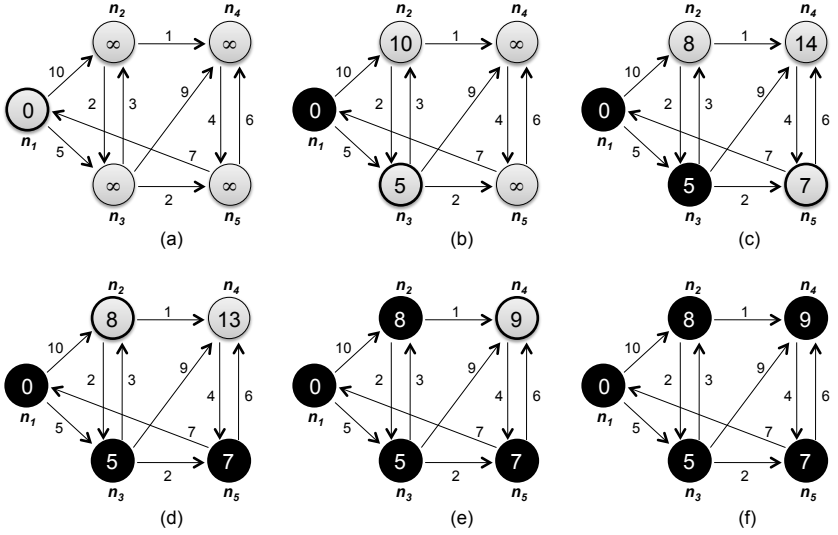


Figure 5.2: Example of Dijkstra's algorithm applied to a simple graph with five nodes, with n_1 as the source and edge distances as indicated. Parts (a)–(e) show the running of the algorithm at each iteration, with the current distance inside the node. Nodes with thicker borders are those being expanded; nodes that have already been expanded are shown in black.

and n_3 can be reached at a distance of 10 and 5, respectively. Also, we see in (b) that n_3 is the next node selected for expansion. Nodes we have already considered for expansion are shown in black. Expanding n_3, we see in (c) that the distance to n_2 has decreased because we've found a shorter path. The nodes that will be expanded next, in order, are n_5, n_2, and n_4. The algorithm terminates with the end state shown in (f), where we've discovered the shortest distance to all nodes.

The key to Dijkstra's algorithm is the priority queue that maintains a globally-sorted list of nodes by current distance. This is not possible in MapReduce, as the programming model does not provide a mechanism for exchanging global data. Instead, we adopt a brute force approach known as parallel breadth-first search. First, as a simplification let us assume that all edges have unit distance (modeling, for example, hyperlinks on the web). This makes the algorithm easier to understand, but we'll relax this restriction later.

The intuition behind the algorithm is this: the distance of all nodes connected directly to the source node is one; the distance of all nodes directly connected to those is two; and so on. Imagine water rippling away from a rock dropped into a pond—that's a good image of how parallel breadth-first search works. However, what if there are multiple paths to the same node? Suppose we wish to compute the shortest distance to node n. The shortest path must

Algorithm 5.2 Parallel breath-first search

The mappers emit distances to reachable nodes, while the reducers select the minimum of those distances for each destination node. Each iteration (one MapReduce job) of the algorithm expands the "search frontier" by one hop.

```
1: class Mapper
2:     method Map(nid n, node N)
3:         d ← N.Distance
4:         Emit(nid n, N)                          ▷ Pass along graph structure
5:         for all nodeid m ∈ N.AdjacencyList do
6:             Emit(nid m, d + 1)                  ▷ Emit distances to reachable nodes

1: class Reducer
2:     method Reduce(nid m, [d1, d2, ...])
3:         d_min ← ∞
4:         M ← ∅
5:         for all d ∈ counts [d1, d2, ...] do
6:             if IsNode(d) then
7:                 M ← d                           ▷ Recover graph structure
8:             else if d < d_min then              ▷ Look for shorter distance
9:                 d_min ← d
10:        M.Distance ← d_min                      ▷ Update shortest distance
11:        Emit(nid m, node M)
```

go through one of the nodes in M that contains an outgoing edge to n: we need to examine all $m \in M$ to find m_s, the node with the shortest distance. The shortest distance to n is the distance to m_s plus one.

Pseudo-code for the implementation of the parallel breadth-first search algorithm is provided in Algorithm 5.2. As with Dijkstra's algorithm, we assume a connected, directed graph represented as adjacency lists. Distance to each node is directly stored alongside the adjacency list of that node, and initialized to ∞ for all nodes except for the source node. In the pseudo-code, we use n to denote the node id (an integer) and N to denote the node's corresponding data structure (adjacency list and current distance). The algorithm works by mapping over all nodes and emitting a key-value pair for each neighbor on the node's adjacency list. The key contains the node id of the neighbor, and the value is the current distance to the node plus one. This says: if we can reach node n with a distance d, then we must be able to reach all the nodes that are connected to n with distance $d+1$. After shuffle and sort, reducers will receive keys corresponding to the destination node ids and distances corresponding to all paths leading to that node. The reducer will select the shortest of these distances and then update the distance in the node data structure.

It is apparent that parallel breadth-first search is an iterative algorithm, where each iteration corresponds to a MapReduce job. The first time we run the algorithm, we "discover" all nodes that are connected to the source. The second iteration, we discover all nodes connected to those, and so on. Each iteration

of the algorithm expands the "search frontier" by one hop, and, eventually, all nodes will be discovered with their shortest distances (assuming a fully-connected graph). Before we discuss termination of the algorithm, there is one more detail required to make the parallel breadth-first search algorithm work. We need to "pass along" the graph structure from one iteration to the next. This is accomplished by emitting the node data structure itself, with the node id as a key (Algorithm 5.2, line 4 in the mapper). In the reducer, we must distinguish the node data structure from distance values (Algorithm 5.2, lines 5–6 in the reducer), and update the minimum distance in the node data structure before emitting it as the final value. The final output is now ready to serve as input to the next iteration.[5]

So how many iterations are necessary to compute the shortest distance to all nodes? The answer is the diameter of the graph, or the greatest distance between any pair of nodes. This number is surprisingly small for many real-world problems: the saying "six degrees of separation" suggests that everyone on the planet is connected to everyone else by at most six steps (the people a person knows are one step away, people that they know are two steps away, etc.). If this is indeed true, then parallel breadth-first search on the global social network would take at most six MapReduce iterations. For more serious academic studies of "small world" phenomena in networks, we refer the reader to a number of publications [61, 62, 152, 2]. In practical terms, we iterate the algorithm until there are no more node distances that are ∞. Since the graph is connected, all nodes are reachable, and since all edge distances are one, all discovered nodes are guaranteed to have the shortest distances (i.e., there is not a shorter path that goes through a node that hasn't been discovered).

The actual checking of the termination condition must occur outside of MapReduce. Typically, execution of an iterative MapReduce algorithm requires a non-MapReduce "driver" program, which submits a MapReduce job to iterate the algorithm, checks to see if a termination condition has been met, and if not, repeats. Hadoop provides a lightweight API for constructs called "counters", which, as the name suggests, can be used for counting events that occur during execution, e.g., number of corrupt records, number of times a certain condition is met, or anything that the programmer desires. Counters can be defined to count the number of nodes that have distances of ∞: at the end of the job, the driver program can access the final counter value and check to see if another iteration is necessary.

Finally, as with Dijkstra's algorithm in the form presented earlier, the parallel breadth-first search algorithm only finds the shortest distances, not the actual shortest paths. However, the path can be straightforwardly recovered. Storing "backpointers" at each node, as with Dijkstra's algorithm, will work, but may not be efficient since the graph needs to be traversed again to reconstruct the path segments. A simpler approach is to emit paths along with

[5]Note that in this algorithm we are overloading the value type, which can either be a distance (integer) or a complex data structure representing a node. The best way to achieve this in Hadoop is to create a wrapper object with an indicator variable specifying what the content is.

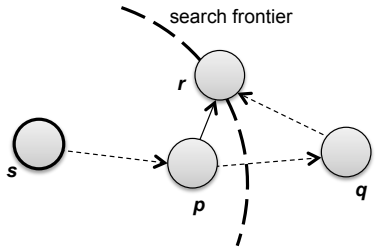


Figure 5.3: In the single source shortest path problem with arbitrary edge distances, the shortest path from source s to node r may go outside the current search frontier, in which case we will not find the shortest distance to r until the search frontier expands to cover q.

distances in the mapper, so that each node will have its shortest path easily accessible at all times. The additional space requirements for shuffling these data from mappers to reducers are relatively modest, since for the most part paths (i.e., sequence of node ids) are relatively short.

Up until now, we have been assuming that all edges are unit distance. Let us relax that restriction and see what changes are required in the parallel breadth-first search algorithm. The adjacency lists, which were previously lists of node ids, must now encode the edge distances as well. In line 6 of the mapper code in Algorithm 5.2, instead of emitting $d+1$ as the value, we must now emit $d+w$ where w is the edge distance. No other changes to the algorithm are required, but the termination behavior is very different. To illustrate, consider the graph fragment in Figure 5.3, where s is the source node, and in this iteration, we just "discovered" node r for the very first time. Assume for the sake of argument that we've already discovered the shortest distance to node p, and that the shortest distance to r so far goes through p. This, however, does not guarantee that we've discovered the shortest distance to r, since there may exist a path going through q that we haven't encountered yet (because it lies outside the search frontier).[6] However, as the search frontier expands, we'll eventually cover q and all other nodes along the path from p to q to r—which means that with sufficient iterations, we will discover the shortest distance to r. But how do we know that we've found the shortest distance to p? Well, if the shortest path to p lies within the search frontier, we would have already discovered it. And if it doesn't, the above argument applies. Similarly, we can repeat the same argument for all nodes on the path from s to p. The conclusion is that, with sufficient iterations, we'll eventually discover all the shortest distances.

So exactly how many iterations does "eventually" mean? In the worst case, we might need as many iterations as there are nodes in the graph minus one.

[6]Note that the same argument does not apply to the unit edge distance case: the shortest path cannot lie outside the search frontier since any such path would necessarily be longer.

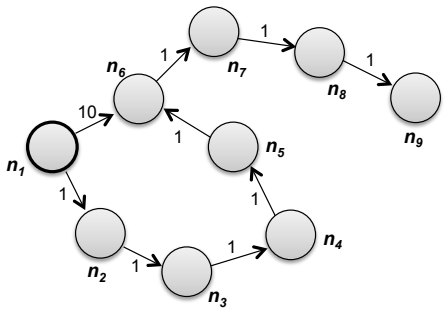


Figure 5.4: A sample graph that elicits worst-case behavior for parallel breadth-first search. Eight iterations are required to discover shortest distances to all nodes from n_1.

In fact, it is not difficult to construct graphs that will elicit this worse-case behavior: Figure 5.4 provides an example, with n_1 as the source. The parallel breadth-first search algorithm would not discover that the shortest path from n_1 to n_6 goes through n_3, n_4, and n_5 until the fifth iteration. Three more iterations are necessary to cover the rest of the graph. Fortunately, for most real-world graphs, such extreme cases are rare, and the number of iterations necessary to discover all shortest distances is quite close to the diameter of the graph, as in the unit edge distance case.

In practical terms, how do we know when to stop iterating in the case of arbitrary edge distances? The algorithm can terminate when shortest distances at every node no longer change. Once again, we can use counters to keep track of such events. Every time we encounter a shorter distance in the reducer, we increment a counter. At the end of each MapReduce iteration, the driver program reads the counter value and determines if another iteration is necessary.

Compared to Dijkstra's algorithm on a single processor, parallel breadth-first search in MapReduce can be characterized as a brute force approach that "wastes" a lot of time performing computations whose results are discarded. At each iteration, the algorithm attempts to recompute distances to all nodes, but in reality only useful work is done along the search frontier: inside the search frontier, the algorithm is simply repeating previous computations.[7] Outside the search frontier, the algorithm hasn't discovered any paths to nodes there yet, so no meaningful work is done. Dijkstra's algorithm, on the other hand, is far more efficient. Every time a node is explored, we're guaranteed to have already found the shortest path to it. However, this is made possible by maintaining a global data structure (a priority queue) that holds nodes sorted by distance—this is not possible in MapReduce because the programming model does not

[7]Unless the algorithm discovers an instance of the situation described in Figure 5.3, in which case, updated distances will propagate inside the search frontier.

provide support for global data that is mutable and accessible by the mappers and reducers. These inefficiencies represent the cost of parallelization.

The parallel breadth-first search algorithm is instructive in that it represents the prototypical structure of a large class of graph algorithms in MapReduce. They share in the following characteristics:

- The graph structure is represented with adjacency lists, which is part of some larger node data structure that may contain additional information (variables to store intermediate output, features of the nodes). In many cases, features are attached to edges as well (e.g., edge weights).
- The MapReduce algorithm maps over the node data structures and performs a computation that is a function of features of the node, intermediate output attached to each node, and features of the adjacency list (outgoing edges and their features). In other words, computations can only involve a node's internal state and its local graph structure. The results of these computations are emitted as values, keyed with the node ids of the neighbors (i.e., those nodes on the adjacency lists). Conceptually, we can think of this as "passing" the results of the computation along outgoing edges. In the reducer, the algorithm receives all partial results that have the same destination node, and performs another computation (usually, some form of aggregation).
- In addition to computations, the graph itself is also passed from the mapper to the reducer. In the reducer, the data structure corresponding to each node is updated and written back to disk.
- Graph algorithms in MapReduce are generally iterative, where the output of the previous iteration serves as input to the next iteration. The process is controlled by a non-MapReduce driver program that checks for termination.

For parallel breadth-first search, the mapper computation is the current distance plus edge distance (emitting distances to neighbors), while the reducer computation is the Min function (selecting the shortest path). As we will see in the next section, the MapReduce algorithm for PageRank works in much the same way.

5.3 PageRank

PageRank [117] is a measure of web page quality based on the structure of the hyperlink graph. Although it is only one of thousands of features that is taken into account in Google's search algorithm, it is perhaps one of the best known and most studied.

A vivid way to illustrate PageRank is to imagine a random web surfer: the surfer visits a page, randomly clicks a link on that page, and repeats ad infinitum. PageRank is a measure of how frequently a page would be encountered

by our tireless web surfer. More precisely, PageRank is a probability distribution over nodes in the graph representing the likelihood that a random walk over the link structure will arrive at a particular node. Nodes that have high in-degrees tend to have high PageRank values, as well as nodes that are linked to by other nodes with high PageRank values. This behavior makes intuitive sense: if PageRank is a measure of page quality, we would expect high-quality pages to contain "endorsements" from many other pages in the form of hyperlinks. Similarly, if a high-quality page links to another page, then the second page is likely to be high quality also. PageRank represents one particular approach to inferring the quality of a web page based on hyperlink structure; two other popular algorithms, not covered here, are SALSA [88] and HITS [84] (also known as "hubs and authorities").

The complete formulation of PageRank includes an additional component. As it turns out, our web surfer doesn't just randomly click links. Before the surfer decides where to go next, a biased coin is flipped—heads, the surfer clicks on a random link on the page as usual. Tails, however, the surfer ignores the links on the page and randomly "jumps" or "teleports" to a completely different page.

But enough about random web surfing. Formally, the PageRank P of a page n is defined as follows:

$$P(n) = \alpha \left(\frac{1}{|G|} \right) + (1 - \alpha) \sum_{m \in L(n)} \frac{P(m)}{C(m)} \tag{5.1}$$

where $|G|$ is the total number of nodes (pages) in the graph, α is the random jump factor, $L(n)$ is the set of pages that link to n, and $C(m)$ is the out-degree of node m (the number of links on page m). The random jump factor α is sometimes called the "teleportation" factor; alternatively, $(1 - \alpha)$ is referred to as the "damping" factor.

Let us break down each component of the formula in detail. First, note that PageRank is defined recursively—this gives rise to an iterative algorithm we will detail in a bit. A web page n receives PageRank "contributions" from all pages that link to it, $L(n)$. Let us consider a page m from the set of pages $L(n)$: a random surfer at m will arrive at n with probability $1/C(m)$ since a link is selected at random from all outgoing links. Since the PageRank value of m is the probability that the random surfer will be at m, the probability of arriving at n from m is $P(m)/C(m)$. To compute the PageRank of n, we need to sum contributions from all pages that link to n. This is the summation in the second half of the equation. However, we also need to take into account the random jump: there is a $1/|G|$ chance of landing at any particular page, where $|G|$ is the number of nodes in the graph. Of course, the two contributions need to be combined: with probability α the random surfer executes a random jump, and with probability $1 - \alpha$ the random surfer follows a hyperlink.

Note that PageRank assumes a community of honest users who are not trying to "game" the measure. This is, of course, not true in the real world, where an adversarial relationship exists between search engine companies and

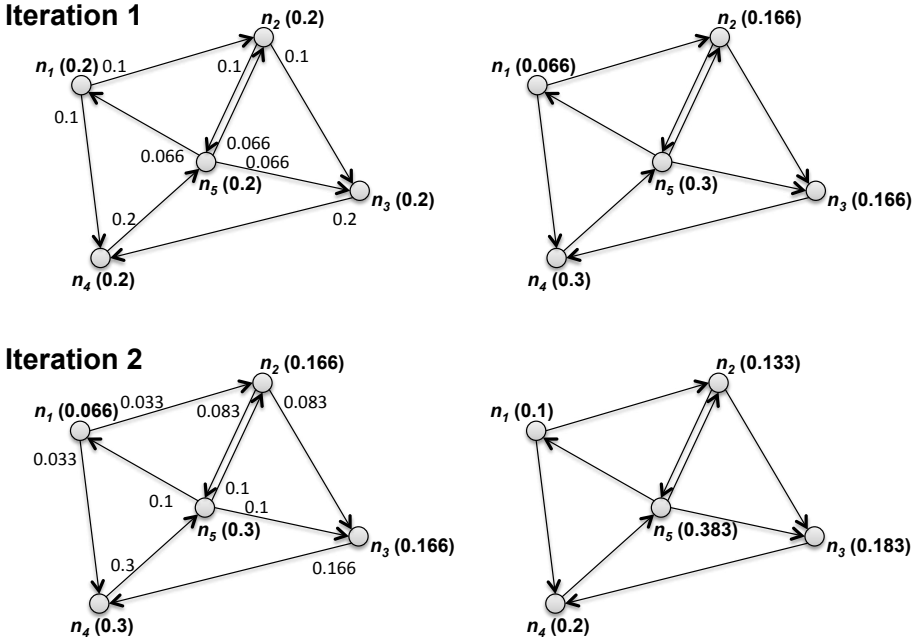


Figure 5.5: PageRank toy example showing two iterations, top and bottom. Left graphs show PageRank values at the beginning of each iteration and how much PageRank mass is passed to each neighbor. Right graphs show updated PageRank values at the end of each iteration.

a host of other organizations and individuals (marketers, spammers, activists, etc.) who are trying to manipulate search results—to promote a cause, product, or service, or in some cases, to trap and intentionally deceive users (see, for example, [12, 63]). A simple example is a so-called "spider trap", a infinite chain of pages (e.g., generated by CGI) that all link to a single page (thereby artificially inflating its PageRank). For this reason, PageRank is only one of thousands of features used in ranking web pages.

The fact that PageRank is recursively defined translates into an iterative algorithm which is quite similar in basic structure to parallel breadth-first search. We start by presenting an informal sketch. At the beginning of each iteration, a node passes its PageRank contributions to other nodes that it is connected to. Since PageRank is a probability distribution, we can think of this as spreading probability mass to neighbors via outgoing links. To conclude the iteration, each node sums up all PageRank contributions that have been passed to it and computes an updated PageRank score. We can think of this as gathering probability mass passed to a node via its incoming links. This algorithm iterates until PageRank values don't change anymore.

Figure 5.5 shows a toy example that illustrates two iterations of the algorithm. As a simplification, we ignore the random jump factor for now (i.e., $\alpha = 0$) and further assume that there are no dangling nodes (i.e., nodes with no outgoing edges). The algorithm begins by initializing a uniform distribution of PageRank values across nodes. In the beginning of the first iteration (top, left), partial PageRank contributions are sent from each node to its neighbors connected via outgoing links. For example, n_1 sends 0.1 PageRank mass to n_2 and 0.1 PageRank mass to n_4. This makes sense in terms of the random surfer model: if the surfer is at n_1 with a probability of 0.2, then the surfer could end up either in n_2 or n_4 with a probability of 0.1 each. The same occurs for all the other nodes in the graph: note that n_5 must split its PageRank mass three ways, since it has three neighbors, and n_4 receives all the mass belonging to n_3 because n_3 isn't connected to any other node. The end of the first iteration is shown in the top right: each node sums up PageRank contributions from its neighbors. Note that since n_1 has only one incoming link, from n_3, its updated PageRank value is smaller than before, i.e., it "passed along" more PageRank mass than it received. The exact same process repeats, and the second iteration in our toy example is illustrated by the bottom two graphs. At the beginning of each iteration, the PageRank values of all nodes sum to one. PageRank mass is preserved by the algorithm, guaranteeing that we continue to have a valid probability distribution at the end of each iteration.

Pseudo-code of the MapReduce PageRank algorithm is shown in Algorithm 5.3; it is simplified in that we continue to ignore the random jump factor and assume no dangling nodes (complications that we will return to later). An illustration of the running algorithm is shown in Figure 5.6 for the first iteration of the toy graph in Figure 5.5. The algorithm maps over the nodes, and for each node computes how much PageRank mass needs to be distributed to its neighbors (i.e., nodes on the adjacency list). Each piece of the PageRank mass is emitted as the value, keyed by the node ids of the neighbors. Conceptually, we can think of this as passing PageRank mass along outgoing edges.

In the shuffle and sort phase, the MapReduce execution framework groups values (piece of PageRank mass) passed along the graph edges by destination node (i.e., all edges that point to the same node). In the reducer, PageRank mass contributions from all incoming edges are summed to arrive at the updated PageRank value for each node. As with the parallel breadth-first search algorithm, the graph structure itself must be passed from iteration to iteration. Each node data structure is emitted in the mapper and written back out to disk in the reducer. All PageRank mass emitted by the mappers are accounted for in the reducer: since we begin with the sum of PageRank values across all nodes equal to one, the sum of all the updated PageRank values should remain a valid probability distribution.

Having discussed the simplified PageRank algorithm in MapReduce, let us now take into account the random jump factor and dangling nodes: as it turns out both are treated similarly. Dangling nodes are nodes in the graph that have no outgoing edges, i.e., their adjacency lists are empty. In the hyperlink graph of the web, these might correspond to pages in a crawl that have not

Algorithm 5.3 PageRank (simplified)

In the map phase we evenly divide up each node's PageRank mass and pass each piece along outgoing edges to neighbors. In the reduce phase PageRank contributions are summed up at each destination node. Each MapReduce job corresponds to one iteration of the algorithm. This algorithm does not handle dangling nodes and the random jump factor.

```
1: class Mapper
2:     method Map(nid n, node N)
3:         p ← N.PageRank/|N.AdjacencyList|
4:         Emit(nid n, N)                          ▷ Pass along graph structure
5:         for all nodeid m ∈ N.AdjacencyList do
6:             Emit(nid m, p)                      ▷ Pass PageRank mass to neighbors

1: class Reducer
2:     method Reduce(nid m, [p1, p2, ...])
3:         M ← ∅
4:         for all p ∈ counts [p1, p2, ...] do
5:             if IsNode(p) then
6:                 M ← p                           ▷ Recover graph structure
7:             else
8:                 s ← s + p                       ▷ Sum incoming PageRank contributions
9:         M.PageRank ← s
10:        Emit(nid m, node M)
```

been downloaded yet. If we simply run the algorithm in Algorithm 5.3 on graphs with dangling nodes, the total PageRank mass will not be conserved, since no key-value pairs will be emitted when a dangling node is encountered in the mappers.

The proper treatment of PageRank mass "lost" at the dangling nodes is to redistribute it across all nodes in the graph evenly (cf. [22]). There are many ways to determine the missing PageRank mass. One simple approach is by instrumenting the algorithm in Algorithm 5.3 with counters: whenever the mapper processes a node with an empty adjacency list, it keeps track of the node's PageRank value in the counter. At the end of the iteration, we can access the counter to find out how much PageRank mass was lost at the dangling nodes.[8] Another approach is to reserve a special key for storing PageRank mass from dangling nodes. When the mapper encounters a dangling node, its PageRank mass is emitted with the special key; the reducer must be modified to contain special logic for handling the missing PageRank mass. Yet another approach is to write out the missing PageRank mass as "side data" for each map task (using the in-mapper combining technique for aggregation); a final pass in the driver program is needed to sum the mass across all map tasks.

[8] In Hadoop, counters are 8-byte integers: a simple workaround is to multiply PageRank values by a large constant, and then cast as an integer.

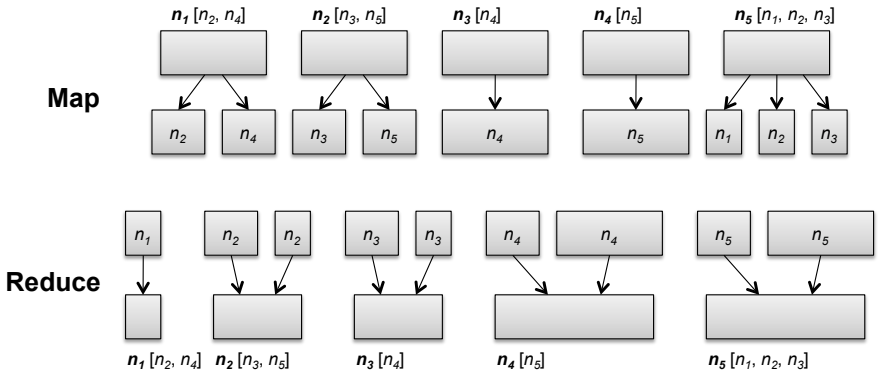


Figure 5.6: Illustration of the MapReduce PageRank algorithm corresponding to the first iteration in Figure 5.5. The size of each box is proportion to its PageRank value. During the map phase, PageRank mass is distributed evenly to nodes on each node's adjacency list (shown at the very top). Intermediate values are keyed by node (shown inside the boxes). In the reduce phase, all partial PageRank contributions are summed together to arrive at updated values.

Either way, we arrive at the amount of PageRank mass lost at the dangling nodes—this then must be redistribute evenly across all nodes.

This redistribution process can be accomplished by mapping over all nodes again. At the same time, we can take into account the random jump factor. For each node, its current PageRank value p is updated to the final PageRank value p' according to the following formula:

$$p' = \alpha \left(\frac{1}{|G|} \right) + (1 - \alpha) \left(\frac{m}{|G|} + p \right) \tag{5.2}$$

where m is the missing PageRank mass, and $|G|$ is the number of nodes in the entire graph. We add the PageRank mass from link traversal (p, computed from before) to the share of the lost PageRank mass that is distributed to each node ($m/|G|$). Finally, we take into account the random jump factor: with probability α the random surfer arrives via jumping, and with probability $1 - \alpha$ the random surfer arrives via incoming links. Note that this MapReduce job requires no reducers.

Putting everything together, one iteration of PageRank requires two MapReduce jobs: the first to distribute PageRank mass along graph edges, and the second to take care of dangling nodes and the random jump factor. At end of each iteration, we end up with exactly the same data structure as the beginning, which is a requirement for the iterative algorithm to work. Also, the PageRank values of all nodes sum up to one, which ensures a valid probability distribution.

Typically, PageRank is iterated until convergence, i.e., when the PageRank values of nodes no longer change (within some tolerance, to take into account, for example, floating point precision errors). Therefore, at the end of each iteration, the PageRank driver program must check to see if convergence has been reached. Alternative stopping criteria include running a fixed number of iterations (useful if one wishes to bound algorithm running time) or stopping when the *ranks* of PageRank values no longer change. The latter is useful for some applications that only care about comparing the PageRank of two arbitrary pages and do not need the actual PageRank values. Rank stability is obtained faster than the actual convergence of values.

In absolute terms, how many iterations are necessary for PageRank to converge? This is a difficult question to *precisely* answer since it depends on many factors, but generally, fewer than one might expect. In the original PageRank paper [117], convergence on a graph with 322 million edges was reached in 52 iterations (see also Bianchini et al. [22] for additional discussion). On today's web, the answer is not very meaningful due to the adversarial nature of web search as previously discussed—the web is full of spam and populated with sites that are actively trying to "game" PageRank and related hyperlink-based metrics. As a result, running PageRank in its unmodified form presented here would yield unexpected and undesirable results. Of course, strategies developed by web search companies to combat link spam are proprietary (and closely-guarded secrets, for obvious reasons)—but undoubtedly these algorithmic modifications impact convergence behavior. A full discussion of the escalating "arms race" between search engine companies and those that seek to promote their sites is beyond the scope of this book.[9]

5.4 Issues with Graph Processing

The biggest difference between MapReduce graph algorithms and single-machine graph algorithms is that with the latter, it is usually possible to maintain global data structures in memory for fast, random access. For example, Dijkstra's algorithm uses a global priority queue that guides the expansion of nodes. This, of course, is not possible with MapReduce—the programming model does not provide any built-in mechanism for communicating global state. Since the most natural representation of large sparse graphs is with adjacency lists, communication can only occur from a node to the nodes it links to, or to a node from nodes linked to it—in other words, passing information is only possible within the local graph structure.[10]

[9] For the interested reader, the proceedings of a workshop series on Adversarial Information Retrieval (AIRWeb) provide great starting points into the literature.

[10] Of course, it is perfectly reasonable to compute derived graph structures in a preprocessing step. For example, if one wishes to propagate information from a node to all nodes that are within two links, one could process graph G to derive graph G', where there would exist a link from node n_i to n_j if n_j was reachable within two link traversals of n_i in the original graph G.

This restriction gives rise to the structure of many graph algorithms in MapReduce: local computation is performed on each node, the results of which are "passed" to its neighbors. With multiple iterations, convergence on the global graph is possible. The passing of partial results along a graph edge is accomplished by the shuffling and sorting provided by the MapReduce execution framework. The amount of intermediate data generated is on the order of the number of edges, which explains why all the algorithms we have discussed assume sparse graphs. For dense graphs, MapReduce running time would be dominated by copying intermediate data across the network, which in the worst case is $O(n^2)$ in the number of nodes in the graph. Since MapReduce clusters are designed around commodity networks (e.g., gigabit Ethernet), MapReduce algorithms are often impractical on large, dense graphs.

Combiners and the in-mapper combining pattern described in Section 3.1 can be used to decrease the running time of graph iterations. It is straightforward to use combiners for both parallel breadth-first search and PageRank since Min and sum, used in the two algorithms, respectively, are both associative and commutative. However, combiners are only effective to the extent that there are opportunities for partial aggregation—unless there are nodes pointed to by multiple nodes being processed by an individual map task, combiners are not very useful. This implies that it would be desirable to partition large graphs into smaller components where there are many intra-component links and fewer inter-component links. This way, we can arrange the data such that nodes in the same component are handled by the same map task—thus maximizing opportunities for combiners to perform local aggregation.

Unfortunately, this sometimes creates a chick-and-egg problem. It would be desirable to partition a large graph to facilitate efficient processing by MapReduce. But the graph may be so large that we can't partition it except with MapReduce algorithms! Fortunately, in many cases there are simple solutions around this problem in the form of "cheap" partitioning heuristics based on reordering the data [106]. For example, in a social network, we might sort nodes representing users by zip code, as opposed to by last name—based on the observation that friends tend to live close to each other. Sorting by an even more cohesive property such as school would be even better (if available): the probability of any two random students from the same school knowing each other is much higher than two random students from different schools. Another good example is to partition the web graph by the language of the page (since pages in one language tend to link mostly to other pages in that language) or by domain name (since inter-domain links are typically much denser than intra-domain links). Resorting records using MapReduce is both easy to do and a relatively cheap operation—however, whether the efficiencies gained by this crude form of partitioning are worth the extra time taken in performing the resort is an empirical question that will depend on the actual graph structure and algorithm.

Finally, there is a practical consideration to keep in mind when implementing graph algorithms that estimate probability distributions over nodes (such as PageRank). For large graphs, the probability of any particular node is

often so small that it underflows standard floating point representations. A very common solution to this problem is to represent probabilities using their logarithms. When probabilities are stored as logs, the product of two values is simply their sum. However, addition of probabilities is also necessary, for example, when summing PageRank contribution for a node. This can be implemented with reasonable precision as follows:

$$a \oplus b = \begin{cases} b + \log(1 + e^{a-b}) & a < b \\ a + \log(1 + e^{b-a}) & a \geq b \end{cases}$$

Furthermore, many math libraries include a `log1p` function which computes $\log(1+x)$ with higher precision than the naïve implementation would have when x is very small (as is often the case when working with probabilities). Its use may further improve the accuracy of implementations that use log probabilities.

5.5 Summary and Additional Readings

This chapter covers graph algorithms in MapReduce, discussing in detail parallel breadth-first search and PageRank. Both are instances of a large class of iterative algorithms that share the following characteristics:

- The graph structure is represented with adjacency lists.
- Algorithms map over nodes and pass partial results to nodes on their adjacency lists. Partial results are aggregated for each node in the reducer.
- The graph structure itself is passed from the mapper to the reducer, such that the output is in the same form as the input.
- Algorithms are iterative and under the control of a non-MapReduce driver program, which checks for termination at the end of each iteration.

The MapReduce programming model does not provide a mechanism to maintain global data structures accessible and mutable by all the mappers and reducers.[11] One implication of this is that communication between pairs of arbitrary nodes is difficult to accomplish. Instead, information typically propagates along graph edges—which gives rise to the structure of algorithms discussed above.

Additional Readings. The ubiquity of large graphs translates into substantial interest in scalable graph algorithms using MapReduce in industry, academia, and beyond. There is, of course, much beyond what has been covered in this chapter. For additional material, we refer readers to the following: Kang et al. [80] presented an approach to estimating the diameter of large graphs using MapReduce and a library for graph mining [81]; Cohen [39] discussed

[11] However, maintaining globally-synchronized state may be possible with the assistance of other tools (e.g., a distributed database).

a number of algorithms for processing undirected graphs, with social network analysis in mind; Rao and Yarowsky [128] described an implementation of label propagation, a standard algorithm for semi-supervised machine learning, on graphs derived from textual data; Schatz [132] tackled the problem of DNA sequence alignment and assembly with graph algorithms in MapReduce. Finally, it is easy to forget that parallel graph algorithms have been studied by computer scientists for several decades, particular in the PRAM model [77, 60]. It is not clear, however, to what extent well-known PRAM algorithms translate naturally into the MapReduce framework.