Data-Intensive Text Processing with MapReduce

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CHAPTER 1

Introduction

MapReduce [31] is a programming model for expressing distributed computations on massive amounts of data and an execution framework for large-scale data processing on clusters of commodity servers. It was originally developed by Google and built on well-known principles in parallel and distributed processing dating back several decades. MapReduce has since enjoyed widespread adoption via an open-source implementation called Hadoop, whose development was led by Yahoo (now an Apache project). Today, a vibrant software ecosystem has sprung up around Hadoop, with significant activity in both industry and academia.

This book is about scalable approaches to processing large amounts of text with MapReduce. Given this focus, it makes sense to start with the most basic question: Why? There are many answers to this question, but we focus on two. First, "big data" is a fact of the world, and therefore an issue that real-world systems must grapple with. Second, across a wide range of text processing applications, more data translates into more effective algorithms, and thus it makes sense to take advantage of the plentiful amounts of data that surround us.

Modern information societies are defined by vast repositories of data, both public and private. Therefore, any practical application must be able to scale up to datasets of interest. For many, this means scaling up to the web, or at least a non-trivial fraction thereof. Any organization built around gathering, analyzing, monitoring, filtering, searching, or organizing web content must tackle large-data problems: "web-scale" processing is practically synonymous with data-intensive processing. This observation applies not only to well-established internet companies, but also countless startups and niche players as well. Just think, how many companies do you know that start their pitch with "we're going to harvest information on the web and. . . "?

Another strong area of growth is the analysis of user behavior data. Any operator of a moderately successful website can record user activity and in a matter of weeks (or sooner) be drowning in a torrent of log data. In fact, logging user behavior generates so much data that many organizations simply can't cope with the volume, and either turn the functionality off or throw away data after some time. This represents lost opportunities, as there is a broadly-held belief that great value lies in insights derived from mining such data. Knowing what users look at, what they click on, how much time they spend, etc. leads to better business decisions and competitive advantages. Broadly, this is known as business intelligence, which encompasses a wide range of technologies including data warehousing, data mining, and analytics.

How much data are we talking about? A few examples: Google grew from processing 100 TB of data a day in 2004 [31] to processing 20 PB a day in 2008 [32]. In April 2009, a blog post[1] was written about eBay's two enormous data warehouses: one with 2 petabytes of user data, and the other with 6.5 petabytes of user data spanning 170 trillion records and growing by 150 billion new records per day. Shortly thereafter, Facebook revealed[2] similarly impressive numbers, boasting of 2.5 petabytes of user data, growing at about 15 terabytes per day. Petabyte datasets are rapidly becoming the norm, and the trends are clear: our ability to store data is fast overwhelming our ability to process what we store. More distressing, increases in capacity are outpacing improvements in bandwidth such that our ability to even *read* back what we store is deteriorating [63]. Disk capacities have grown from tens of megabytes in the mid-1980s to about a couple of terabytes today (several orders of magnitude); on the other hand, latency and bandwidth have improved relatively little in comparison (in the case of latency, perhaps 2× improvement during the last quarter century, and in the case of bandwidth, perhaps 50×). Given the tendency for individuals and organizations to continuously fill up whatever capacity is available, large-data problems are growing increasingly severe.

Moving beyond the commercial sphere, many have recognized the importance of data management in many scientific disciplines, where petabyte-scale datasets are also becoming increasingly common [13]. For example:

- The high-energy physics community was already describing experiences with petabyte-scale databases back in 2005 [12]. Today, the Large Hadron Collider (LHC) near Geneva is the world's largest particle accelerator, designed to probe the mysteries of the universe, including the fundamental nature of matter, by recreating conditions shortly following the Big Bang. When it becomes fully operational, the LHC will produce roughly 15 petabytes of data a year.[3]

- Astronomers have long recognized the importance of a "digital observatory" that would support the data needs of researchers across the globe—the Sloan Digital Sky Survey [102] is perhaps the most well known of these projects. Looking into the future, the Large Synoptic Survey Telescope (LSST) is a wide-field instrument that is capable of observing the entire sky every few days. When the telescope comes online around 2015 in Chile, its 3.2 gigapixel primary camera will produce approximately half a petabyte of archive images every month [11].

- The advent of next-generation DNA sequencing technology has created a deluge of sequence data that needs to be stored, organized, and delivered to scientists for

[1] http://www.dbms2.com/2009/04/30/ebays-two-enormous-data-warehouses/
[2] http://www.dbms2.com/2009/05/11/facebook-hadoop-and-hive/
[3] http://public.web.cern.ch/public/en/LHC/Computing-en.html

> further study. Given the fundamental tenant in modern genetics that genotypes explain phenotypes, the impact of this technology is nothing less than transformative [74]. The European Bioinformatics Institute (EBI), which hosts a central repository of sequence data called EMBL-bank, has increased storage capacity from 2.5 petabytes in 2008 to 5 petabytes in 2009 [99]. Scientists are predicting that, in the not-so-distant future, sequencing an individual's genome will be no more complex than getting a blood test today—ushering a new era of personalized medicine, where interventions can be specifically targeted for an individual.

Increasingly, scientific breakthroughs will be powered by advanced computing capabilities that help researchers manipulate, explore, and mine massive datasets [50]—this has been hailed as the emerging "fourth paradigm" of science [51] (complementing theory, experiments, and simulations). In other areas of academia, particularly computer science, systems and algorithms incapable of scaling to massive real-world datasets run the danger of being dismissed as "toy systems" with limited utility. Large data is a fact of today's world and data-intensive processing is fast becoming a necessity, not merely a luxury or curiosity.

Although large data comes in a variety of forms, this book is primarily concerned with processing large amounts of text, but touches on other types of data as well (e.g., relational and graph data). The problems and solutions we discuss mostly fall into the disciplinary boundaries of natural language processing (NLP) and information retrieval (IR). Recent work in these fields is dominated by a data-driven, empirical approach, typically involving algorithms that attempt to capture statistical regularities in data for the purposes of some task or application. There are three components to this approach: data, representations of the data, and some method for capturing regularities in the data. The first is called *corpora* (singular, corpus) by NLP researchers and *collections* by those from the IR community. Aspects of the representations of the data are called *features*, which may be "superficial" and easy to extract, such as the words and sequences of words themselves, or "deep" and more difficult to extract, such as the grammatical relationship between words. Finally, algorithms or models are applied to capture regularities in the data in terms of the extracted features for some application. One common application, classification, is to sort text into categories. Examples include: Is this email spam or not spam? Is this word a part of an address? The first task is easy to understand, while the second task is an instance of what NLP researchers call named-entity detection, which is useful for local search and pinpointing locations on maps. Another common application is to rank texts according to some criteria—search is a good example, which involves ranking documents by relevance to the user's query. Another example is to automatically situate texts along a scale of "happiness", a task known as sentiment analysis, which has been applied to everything from understanding political discourse in the blogosphere to predicting the movement of stock prices.

There is a growing body of evidence, at least in text processing, that of the three components discussed above (data, features, algorithms), data probably matters the most. Superficial word-level features coupled with simple models in most cases trump sophisticated models over deeper features and less data. But why can't we have our cake and eat it too? Why not both sophisticated models *and* deep features applied to lots of data? Because inference over sophisticated models and extraction of deep features are often computationally intensive, they often don't scale.

Consider a simple task such as determining the correct usage of easily confusable words such as "than" and "then" in English. One can view this as a supervised machine learning problem: we can train a classifier to disambiguate between the options, and then apply the classifier to new instances of the problem (say, as part of a grammar checker). Training data is fairly easy to come by—we can just gather a large corpus of texts and assume that writers make correct choices (the training data may be noisy, since people make mistakes, but no matter). In 2001, Banko and Brill [8] published what has become a classic paper in natural language processing exploring the effects of training data size on classification accuracy, using this task as the specific example. They explored several classification algorithms (the exact ones aren't important), and not surprisingly, found that more data led to better accuracy. Across many different algorithms, the increase in accuracy was approximately linear in the log of the size of the training data. Furthermore, with increasing amounts of training data, the accuracy of different algorithms converged, such that pronounced differences in effectiveness observed on smaller datasets basically disappeared at scale. This led to a somewhat controversial conclusion (at least at the time): machine learning algorithms really don't matter, all that matters is the amount of data you have. This led to an even more controversial conclusion, delivered somewhat tongue-in-cheek: we should just give up working on algorithms and simply spend our time gathering data.

As another example, consider the problem of answering short, fact-based questions such as "Who shot Abraham Lincoln?" Instead of returning a list of documents that the user would then have to sort through, a question answering (QA) system would directly return the answer: John Wilkes Booth. This problem gained interest in the late 1990s, when natural language processing researchers approached the challenge with sophisticated linguistic processing techniques such as syntactic and semantic analysis. Around 2001, researchers discovered a far simpler approach to answering such questions based on pattern matching [18, 37, 64]. Suppose you wanted the answer to the above question. As it turns out, you can simply search for the phrase "shot Abraham Lincoln" on the web and look for what appears to its left. Or better yet, look through multiple instances of this phrase and tally up the words that appear to the left. This simple approach works surprisingly well, and has become known as the redundancy-based approach to question answering. It capitalizes on the insight that in a very large text

collection (i.e., the web), answers to commonly-asked questions will be stated in obvious ways, such that pattern-matching techniques suffice to extract answers accurately.

Yet another example concerns smoothing in web-scale language models [16]. A language model is a probability distribution that characterizes the likelihood of observing a particular sequence of words, estimated from a large corpus of texts. They are useful in a variety of applications, such as speech recognition (to determine what the speaker is more likely to have said) and machine translation (to determine which of possible translations is the most fluent, as we will discuss in Chapter 6.4). Since there are infinitely many possible strings, and probabilities must be assigned to all of them, language modeling is a more challenging task than simply keeping track of which strings were seen how many times: some number of likely strings will never have been seen at all, even with lots and lots of training data! Most modern language models make the Markov assumption: in a n-gram language model, the conditional probability of a word is given by the $n-1$ previous words. Thus, by the chain rule, the probability of a sequence of words can be decomposed into the product of n-gram probabilities. Nevertheless, an enormous number of parameters must still be estimated from a training corpus: potentially V^n parameters, where V is the number of words in the vocabulary. Even if we treat every word on the web as the training corpus to estimate the n-gram probabilities from, most n-grams—in any language, even English—will never have been seen. To cope with this sparseness, researchers have developed a number of smoothing techniques [24, 73], which all share the basic idea of moving probability mass from observed to unseen events in a principled manner. Smoothing approaches vary in effectiveness, both in terms of intrinsic and application-specific metrics. In 2007, Brants et al. [16] described language models trained on up to two trillion words.[4] Their experiments compared a state-of-the-art approach known as Kneser-Ney smoothing [24] with another technique the authors affectionately referred to as "stupid backoff".[5] Not surprisingly, stupid backoff didn't work as well as Kneser-Ney smoothing on smaller corpora. However, it was simpler and could be trained on *more* data, which ultimately yielded better language models. That is, a simpler technique on more data beat a more sophisticated technique on less data.

Recently, three Google researchers summarized this data-driven philosophy in an essay titled *The Unreasonable Effectiveness of Data* [45].[6] Why is this so? It boils down to the fact that language *in the wild*, just like human behavior in general, is messy. Unlike, say, the interaction of subatomic particles, human *use* of language is not constrained by succinct, universal "laws of grammar". There are of course rules

[4] As an side, it is interesting to observe the evolving definition of *large* over the years. Banko and Brill's paper in 2001 was titled *Scaling to Very Very Large Corpora for Natural Language Disambiguation*, and dealt with a corpus containing a billion words.

[5] As in, so stupid it couldn't possibly work.

[6] This title was inspired by a classic article titled *The Unreasonable Effectiveness of Mathematics in the Natural Sciences* [108].

that govern the formation of words and sentences—for example, that verbs appear before objects in English, and that subjects and verbs must agree in number—but real-world language is affected by a multitude of other factors as well: people invent new words and phrases all the time, authors occasionally make mistakes, groups of individuals write within a shared context, etc. The Argentine writer Jorge Luis Borges wrote a famous allegorical one-paragraph story about fictional society in which the art of cartography had gotten so advanced that their maps were as big as the lands they were describing.[7] The world, he would say, is the best description of itself. In the same way, the more observations we gather about language use, the more accurate a description we have about language itself. This, in turn, translates into more effective algorithms and systems.

So, in summary, why large data? In some ways, the first answer is similar to the reason people climb mountains: because they're there. But the second answer is even more compelling. Data is the rising tide that lifts all boats—more data leads to better algorithms and systems for solving real-world problems. Now that we've addressed the *why*, let's tackle the *how*. Let's start with the obvious observation: data-intensive processing is beyond the capabilities of any individual machine and requires clusters—which means that large-data problems are fundamentally about organizing computations on dozens, hundreds, or even thousands of machines. This is exactly what MapReduce does, and the rest of this book is about the *how*.

1.1 COMPUTING IN THE CLOUDS

For better or for worse, MapReduce cannot be untangled from the broader discourse on cloud computing. True, there is substantial promise in this new paradigm of computing, but unwarranted hype by the media and popular sources threatens its credibility in the long run. In some ways, cloud computing is simply brilliant marketing. Before clouds, there were grids,[8] and before grids, there were vector supercomputers, each having claimed to be the best thing since sliced bread.

So what exactly is cloud computing? This is one of those questions where ten experts will give eleven different answers; in fact, countless papers have been written simply to attempt to define the term (e.g., [4, 21, 105], just to name a few examples).

[7] *On Exactitude in Science* [14].

[8] What *is* the difference between cloud computing and grid computing? Although both tackle the fundamental problem of how best to bring computational resources to bear on large and difficult problems, they start with different assumptions. Whereas clouds are assumed to be relatively homogeneous servers that reside in a datacenter or are distributed across a relatively small number of datacenters controlled by a single organization, grids are assumed to be a less tightly-coupled federation of heterogeneous resources under the control of distinct but cooperative organizations. As a result, grid computing tends to deal with tasks that are coarser-grained, and must deal with the practicalities of a federated environment, e.g., verifying credentials across multiple administrative domains. Grid computing has adopted a middleware-based approach for tackling many of these issues.

Here we offer up our own thoughts and attempt to explain how cloud computing relates to MapReduce and data-intensive processing.

At the most superficial level, everything that used to be called web applications has been rebranded to become "cloud applications", which includes what we have previously called web 2.0 sites. In fact, anything running inside a browser that gathers and stores user-generated content now qualifies as an example of cloud computing. This includes social-networking services such as Facebook, video-sharing sites such as YouTube, web-based email services such as Gmail, and applications such as Google Docs. In this context, the cloud simply refers to the servers that power these sites, and user data is said to reside "in the cloud". The accumulation of vast quantities of user data creates large-data problems, many of which are suitable for MapReduce. To give two concrete examples: a social-networking site analyzes connections in the enormous globe-spanning graph of friendships to recommend new connections. An online email service analyzes messages and user behavior to optimize ad selection and placement. These are all large-data problems that have been tackled with MapReduce.[9]

Another important facet of cloud computing is what's more precisely known as utility computing [91, 21]. As the name implies, the idea behind utility computing is to treat computing resource as a metered service, like electricity or natural gas. The idea harkens back to the days of time-sharing machines, and in truth isn't very different from this antiquated form of computing. Under this model, a "cloud user" can dynamically provision any amount of computing resources from a "cloud provider" on demand and only pay for what is consumed. In practical terms, the user is paying for access to virtual machine instances that run a standard operating system such as Linux. Virtualization technology (e.g., [9]) is used by the cloud provider to allocate available physical resources and enforce isolation between multiple users that may be sharing the same hardware. Once one or more virtual machine instances have been provisioned, the user has full control over the resources and can use them for arbitrary computation. Virtual machines that are no longer needed are destroyed, thereby freeing up physical resources that can be redirected to other users. Resource consumption is measured in some equivalent of machine-hours and users are charged in increments thereof.

Both users and providers benefit in the utility computing model. Users are freed from upfront capital investments necessary to build datacenters and substantial reoccurring costs in maintaining them. They also gain the important property of elasticity—as demand for computing resources grow, for example, from an unpredicted spike in customers, more resources can be seamlessly allocated from the cloud without an interruption in service. As demand falls, provisioned resources can be released. Prior to the advent of utility computing, coping with unexpected spikes in demand was fraught with

[9]The first example is Facebook, a well-known user of Hadoop, in exactly the manner as described [46]. The second is, of course, Google, which uses MapReduce to continuously improve existing algorithms and to devise new algorithms for ad selection and placement.

challenges: under-provision and run the risk of service interruptions, or over-provision and tie up precious capital in idle machines that are depreciating.

From the utility provider point of view, this business also makes sense because large datacenters benefit from economies of scale and can be run more efficiently than smaller datacenters. In the same way that insurance works by aggregating risk and redistributing it, utility providers aggregate the computing demands for a large number of users. Although demand may fluctuate significantly for each user, overall trends in aggregate demand should be smooth and predictable, which allows the cloud provider to adjust capacity over time with less risk of either offering too much (resulting in inefficient use of capital) or too little (resulting in unsatisfied customers). In the world of utility computing, Amazon Web Services currently leads the way and remains the dominant player, but a number of other cloud providers populate a market that is becoming increasingly crowded. Most systems are based on proprietary infrastructure, but there is at least one, Eucalyptus [78], that is available open source. Increased competition will benefit cloud users, but what direct relevance does this have for MapReduce? The connection is quite simple: processing large amounts of data with MapReduce requires access to clusters with sufficient capacity. However, not everyone with large-data problems can afford to purchase and maintain clusters. This is where utility computing comes in: clusters of sufficient size can be provisioned only when the need arises, and users pay only as much as is required to solve their problems. This lowers the barrier to entry for data-intensive processing and makes MapReduce much more accessible.

A generalization of the utility computing concept is "everything as a service", which is itself a new take on the age-old idea of outsourcing. A cloud provider offering customers access to virtual machine instances is said to be offering infrastructure as a service, or IaaS for short. However, this may be too low level for many users. Enter platform as a service (PaaS), which is a rebranding of what used to be called hosted services in the "pre-cloud" era. Platform is used generically to refer to any set of well-defined services on top of which users can build applications, deploy content, etc. This class of services is best exemplified by Google App Engine, which provides the backend datastore and API for anyone to build highly-scalable web applications. Google maintains the infrastructure, freeing the user from having to backup, upgrade, patch, or otherwise maintain basic services such as the storage layer or the programming environment. At an even higher level, cloud providers can offer software as a service (SaaS), as exemplified by Salesforce, a leader in customer relationship management (CRM) software. Other examples include outsourcing an entire organization's email to a third party, which is commonplace today. What does this proliferation of service have to do with MapReduce? No doubt that "everything as a service" is driven by desires for greater business efficiencies, but scale and elasticity play important roles as well. The cloud allows seamless expansion of operations without the need for careful planning and

supports scales that may otherwise be difficult or cost-prohibitive for an organization to achieve.

Finally, cloud services, just like MapReduce, represents the search for an appropriate level of abstraction and beneficial divisions of labor. IaaS is an abstraction over raw physical hardware—an organization might lack the capital, expertise, or interest in running datacenters, and therefore pays a cloud provider to do so on its behalf. The argument applies similarly to PaaS and SaaS. In the same vein, the MapReduce programming model is a powerful abstraction that separates the *what* from the *how* of data-intensive processing.

1.2 BIG IDEAS

Tackling large-data problems requires a distinct approach that sometimes runs counter to traditional models of computing. In this section, we discuss a number of "big ideas" behind MapReduce. To be fair, all of these ideas have been discussed in the computer science literature for some time (some for decades), and MapReduce is certainly not the first to adopt these approaches. Nevertheless, the engineers at Google deserve tremendous credit for pulling these various threads together and demonstrating the power of these ideas on a scale previously unheard of.

Scale "out", not "up". For data-intensive workloads, a large number of commodity low-end servers (i.e., the scaling "out" approach) is preferred over a small number of high-end servers (i.e., the scaling "up" approach). The latter approach of purchasing symmetric multi-processing (SMP) machines with a large number of processor sockets (dozens, even hundreds) and a large amount of shared memory (hundreds or even thousands of gigabytes) is not cost effective, since the costs of such machines do not scale linearly (i.e., a machine with twice as many processors is often significantly more than twice as expensive). On the other hand, the low-end server market overlaps with the high-volume desktop computing market, which has the effect of keeping prices low due to competition, interchangeable components, and economies of scale.

Barroso and Hölzle's recent treatise of what they dubbed "warehouse-scale computers" [10] contains a thoughtful analysis of the two approaches. The Transaction Processing Council (TPC) is a neutral, non-profit organization whose mission is to establish objective database benchmarks. Benchmark data submitted to that organization are probably the closest one can get to a fair "apples-to-apples" comparison of cost and performance for specific, well-defined relational processing applications. Based on TPC-C benchmarks results from late 2007, a low-end server platform is about four times more cost efficient than a high-end shared memory platform from the same vendor. Excluding storage costs, the price/performance advantage of the low-end server increases to about a factor of twelve.

What if we take into account the fact that communication between nodes in a high-end SMP machine is orders of magnitude faster than communication between nodes in a commodity network-based cluster? Since workloads today are beyond the capability of any *single* machine (no matter how powerful), the comparison is more accurately between a smaller cluster of high-end machines and a larger cluster of low-end machines (network communication is unavoidable in both cases). Barroso and Hölzle model these two approaches under workloads that demand more or less communication, and conclude that a cluster of low-end servers approaches the performance of the equivalent cluster of high-end servers—the small performance gap is insufficient to justify the price premium of the high-end servers. For data-intensive applications, the conclusion is clear: scaling "out" is superior to scaling "up", and MapReduce is explicitly designed around clusters of commodity low-end servers.

Move processing to the data. In traditional high-performance computing (HPC) applications (e.g., for climate or nuclear simulations), it is commonplace for a supercomputer to have "processing nodes" and "storage nodes" linked together by a high-capacity interconnect. Many data-intensive workloads are not very processor-demanding, which means that the separation of compute and storage creates a bottleneck in the network. As an alternative to moving data around, it is more efficient to move the processing around. That is, MapReduce assumes an architecture where processors and storage (disk) are co-located. In such a setup, we can take advantage of data locality by running code on the processor directly attached to the block of data we need. The distributed file system is responsible for managing the data over which MapReduce operates.

Process data sequentially and avoid random access. Data-intensive processing by definition means that the relevant datasets are too large to fit in memory and must be held on disk. Seek times for random disk access are fundamentally limited by the mechanical nature of the devices: read heads can only move so fast, and platters can only spin so rapidly. As a result, it is desirable to avoid random data access, and instead organize computations so that data is processed sequentially. A simple scenario[10] poignantly illustrates the large performance gap between sequential operations and random seeks: assume a 1 terabyte database containing 10^{10} 100-byte records. Given reasonable assumptions about disk latency and throughput, a back-of-the-envelop calculation will show that updating 1% of the the records (by accessing and then mutating each record) will take about a month on a single machine. On the other hand, if one simply reads the entire database and rewrites all the records (mutating those that need updating), the

[10] Adapted from a post by Ted Dunning on the Hadoop mailing list.

process would finish in under a work day on a single machine. Sequential data access is, literally, orders of magnitude faster than random data access.[11]

The development of solid-state drives is unlikely the change this balance for at least two reasons. First, the cost differential between traditional magnetic disks and solid-state disks remains substantial: large-data will for the most part remain on mechanical drives, at least in the near future. Second, although solid-state disks have substantially faster seek times, order-of-magnitude differences in performance between sequential and random access still remain.

MapReduce is primarily designed for batch processing over large datasets. To the extent possible, all computations are organized into long streaming operations that take advantage of the aggregate bandwidth of many disks in a cluster. Many aspects of MapReduce's design explicitly trade latency for throughput.

Hide system-level details from the application developer. According to many guides on the practice of software engineering written by experienced industry professionals, one of the key reasons why writing code is difficult is because the programmer must simultaneously keep track of many details in short term memory all at once—ranging from the mundane (e.g., variable names) to the sophisticated (e.g., a corner case of an algorithm that requires special treatment). This imposes a high cognitive load and requires intense concentration, which leads to a number of recommendations about a programmer's environment (e.g., quiet office, comfortable furniture, large monitors, etc.). The challenges in writing distributed software are greatly compounded—the programmer must manage details across several threads, processes, or machines. Of course, the biggest headache in distributed programming is that code runs concurrently in unpredictable orders, accessing data in unpredictable patterns. This gives rise to race conditions, deadlocks, and other well-known problems. Programmers are taught to use low-level devices such as mutexes and to apply high-level "design patterns" such as producer–consumer queues to tackle these challenges, but the truth remains: concurrent programs are notoriously difficult to reason about and even harder to debug.

MapReduce addresses the challenges of distributed programming by providing an abstraction that isolates the developer from system-level details (e.g., locking of data structures, data starvation issues in the processing pipeline, etc.). The programming model specifies simple and well-defined interfaces between a small number of components, and therefore is easy for the programmer to reason about. MapReduce maintains a separation of *what* computations are to be performed and *how* those computations are actually carried out on a cluster of machines. The first is under the control of the programmer, while the second is exclusively the responsibility of the execution framework or "runtime". The advantage is that the execution framework only needs to be designed once and verified for correctness—thereafter, as long as the

[11] For more detail, Jacobs [53] provides real-world benchmarks in his discussion of large-data problems.

developer expresses computations in the programming model, code is guaranteed to behave as expected. The upshot is that the developer is freed from having to worry about system-level details (e.g., no more debugging race conditions and addressing lock contention) and can instead focus on algorithm or application design.

Seamless scalability. For data-intensive processing, it goes without saying that scalable algorithms are highly desirable. As an aspiration, let us sketch the behavior of an ideal algorithm. We can define scalability along at least two dimensions. First, in terms of data: given twice the amount of data, the same algorithm should take at most twice as long to run, all else being equal. Second, in terms of resources: given a cluster twice the size, the same algorithm should take no more than half as long to run. Furthermore, an ideal algorithm would maintain these desirable scaling characteristics across a wide range of settings: on data ranging from gigabytes to petabytes, on clusters consisting of a few to a few thousand machines. Finally, the ideal algorithm would exhibit these desired behaviors without requiring any modifications whatsoever, not even tuning of parameters.

Other than for embarrassingly parallel problems, algorithms with the characteristics sketched above are, of course, unobtainable. One of the fundamental assertions in Fred Brook's classic *The Mythical Man-Month* [19] is that adding programmers to a project behind schedule will only make it fall further behind. This is because complex tasks cannot be chopped into smaller pieces and allocated in a linear fashion, and is often illustrated with a cute quote: "nine women cannot have a baby in one month". Although Brook's observations are primarily about software engineers and the software development process, the same is also true of algorithms: increasing the degree of parallelization also increases communication costs. The algorithm designer is faced with diminishing returns, and beyond a certain point, greater efficiencies gained by parallelization are entirely offset by increased communication requirements.

Nevertheless, these fundamental limitations shouldn't prevent us from at least striving for the unobtainable. The truth is that most current algorithms are far from the ideal. In the domain of text processing, for example, most algorithms today assume that data fits in memory on a single machine. For the most part, this is a fair assumption. But what happens when the amount of data doubles in the near future, and then doubles again shortly thereafter? Simply buying more memory is not a viable solution, as the amount of data is growing faster than the price of memory is falling. Furthermore, the price of a machine does not scale linearly with the amount of available memory beyond a certain point (once again, the scaling "up" vs. scaling "out" argument). Quite simply, algorithms that require holding intermediate data in memory on a single machine will simply break on sufficiently-large datasets—moving from a single machine to a cluster architecture requires fundamentally different algorithms (and reimplementations).

Perhaps the most exciting aspect of MapReduce is that it represents a small step toward algorithms that behave in the ideal manner discussed above. Recall that the programming model maintains a clear separation between *what* computations need to occur with *how* those computations are actually orchestrated on a cluster. As a result, a MapReduce algorithm remains fixed, and it is the responsibility of the execution framework to execute the algorithm. Amazingly, the MapReduce programming model is simple enough that it is actually possible, in many circumstances, to *approach* the ideal scaling characteristics discussed above. We introduce the idea of the "tradeable machine hour", as a play on Brook's classic title. If running an algorithm on a particular dataset takes 100 machine hours, then we should be able to finish in an hour on a cluster of 100 machines, or use a cluster of 10 machines to complete the same task in ten hours.[12] With MapReduce, this isn't so far from the truth, at least for some applications.

1.3 WHY IS THIS DIFFERENT?

> "Due to the rapidly decreasing cost of processing, memory, and communication, it has appeared inevitable for at least two decades that parallel machines will eventually displace sequential ones in computationally intensive domains. This, however, has not happened." — Leslie Valiant [104][13]

For several decades, computer scientists have predicted that the dawn of the age of parallel computing was "right around the corner" and that sequential processing would soon fade into obsolescence (consider, for example, the above quote). Yet, until very recently, they have been wrong. The relentless progress of Moore's Law for several decades has ensured that most of the world's problems could be solved by single-processor machines, save the needs of a few (scientists simulating molecular interactions or nuclear explosions, for example). Couple that with the inherent challenges of concurrency, and the result has been that parallel processing and distributed systems have largely been confined to a small segment of the market and esoteric upper-level electives in the computer science curriculum.

However, all of that changed around the middle of the first decade of this century. The manner in which the semiconductor industry had been exploiting Moore's Law simply ran out of opportunities for improvement: faster clocks, deeper pipelines, superscalar architectures, and other tricks of the trade reached a point of diminishing returns that did not justify continued investment. This marked the beginning of an entirely new strategy and the dawn of the multi-core era [81]. Unfortunately, this radical shift in hardware architecture was not matched at that time by corresponding advances in how software could be easily designed for these new processors (but not for

[12] Note that this idea meshes well with utility computing, where a 100-machine cluster running for one hour would cost the same as a 10-machine cluster running for ten hours.

[13] Guess when this was written? You may be surprised.

lack of trying [75]). Nevertheless, parallel processing became an important issue at the forefront of everyone's mind—it represented the only way forward.

At around the same time, we witnessed the growth of large-data problems. In the late 1990s and even during the beginning of the first decade of this century, relatively few organizations had data-intensive processing needs that required large clusters: a handful of internet companies and perhaps a few dozen large corporations. But then, everything changed. Through a combination of many different factors (falling prices of disks, rise of user-generated web content, etc.), large-data problems began popping up everywhere. Data-intensive processing needs became widespread, which drove innovations in distributed computing such as MapReduce—first by Google, and then by Yahoo and the open source community. This in turn created more demand: when organizations learned about the availability of effective data analysis tools for large datasets, they began instrumenting various business processes to gather even more data—driven by the belief that more data leads to deeper insights and greater competitive advantages. Today, not only are large-data problems ubiquitous, but technological solutions for addressing them are widely accessible. Anyone can download the open source Hadoop implementation of MapReduce, pay a modest fee to rent a cluster from a utility cloud provider, and be happily processing terabytes upon terabytes of data within the week. Finally, the computer scientists are right—the age of parallel computing has begun, both in terms of multiple cores in a chip or multiple machines in a cluster.

Why is MapReduce important? In practical terms, it provides a very effective tool for tackling large-data problems. But beyond that, MapReduce is important in how it has changed the way we organize computations at a massive scale. MapReduce represents the first step away from the von Neumann model that has served as the foundation of computer science over the last half plus century. Valiant called this a *bridging model* [104], a conceptual bridge between the physical implementation of a machine and the software that is to be executed on that machine. Until recently, the von Neumann model has served us well: Hardware designers focused on efficient implementations of the von Neumann model and didn't have to think much about actual software that would run on the machines. Similarly, the software industry developed software targeted at the model without worrying about the hardware details. The result was extraordinary growth: chip designers churned out successive generations of increasingly powerful processors, and software engineers were able to develop applications in high-level languages that exploited those processors.

Today, however, the von Neumann model isn't sufficient anymore: we can't treat a multi-core processor or a large cluster as an agglomeration of many von Neumann machine instances communicating over some interconnect. Such a view places too much burden on the software developer to effectively take advantage of available computational resources—it simply is the wrong level of abstraction. MapReduce can be viewed

as the first breakthrough in the quest for new abstractions that allow us to organize computations, not over individual machines, but over entire clusters. As Barroso puts it, the datacenter *is* the computer [83].

As anyone who has taken an introductory computer science course knows, abstractions manage complexity by hiding details and presenting well-defined behaviors to users of those abstractions. They, inevitably, are imperfect—making certain tasks easier but others more difficult, and sometimes, impossible (in the case where the detail suppressed by the abstraction is exactly what the user cares about). This critique applies to MapReduce: it makes certain large-data problems easier, but suffers from limitations as well. This means that MapReduce is not the final word, but rather the first in a new class of models that will allow us to more effectively organize computations at a massive scale.

So if MapReduce is only the beginning, what's next beyond MapReduce? We're getting ahead of ourselves, as we can't meaningfully answer this question before thoroughly understanding what MapReduce can and cannot do well. This is exactly the purpose of this book: let us now begin our exploration.

1.4 WHAT THIS BOOK IS NOT

Actually, not quite yet... A final word before we get started. This book is about MapReduce algorithm design, particularly for text processing applications. Although our presentation most closely follows implementations in the Hadoop open-source implementation of MapReduce, this book is explicitly *not* about Hadoop programming. We don't for example, discuss APIs, driver programs for composing jobs, command-line invocations for running jobs, etc. For those aspects, we refer the reader to Tom White's excellent book, "Hadoop: The Definitive Guide", published by O'Reilly [107].

CHAPTER 2

MapReduce Basics

The only feasible approach to tackling large-data problems today is to divide and conquer, a fundamental concept in computer science that is introduced very early in typical undergraduate curricula. The basic idea is to partition a large problem into smaller pieces, each of which is tackled in parallel by different workers—which may be threads in a processor core, cores in a multi-core processor, multiple processors in a machine, or many machines in a cluster. Intermediate results from each individual worker are then combined to yield the final output.[1]

The general principles behind divide-and-conquer algorithms are broadly applicable to a wide range of problems. However, the details of their implementations are varied and complex. For example, the following are just some of the issues that need to be addressed:

- How do we split up a large problem into smaller tasks?
- How do we assign tasks to workers distributed across a potentially large number of machines?
- How do we ensure that workers get the data they need?
- How do we coordinate synchronization among the different workers?
- How do we share partial results from one worker that is needed by another?
- How do we accomplish all of the above in the face of software errors and hardware faults?

In a traditional parallel or distributed programming environments, the developer needs to explicitly address all of the above issues. In the shared memory programming, the programmer needs to explicitly coordinate access to shared data structures through synchronization primitives such as mutexes, to explicitly handle process synchronization through devices such as barriers, and to remain ever vigilant for common problems such as deadlocks and race conditions. Language extensions, like OpenMP for shared memory parallelism,[2] or libraries implementing the Message Passing Interface (MPI) for cluster-level parallelism,[3] provide logical abstractions that hide details of operating system synchronization and communications primitives. However, even with these

[1] We note that promising technologies such as quantum or biological computing could potentially induce a paradigm shift, but unfortunately they are far from being sufficiently mature to solve real world problems.
[2] http://www.openmp.org/
[3] http://www.mcs.anl.gov/mpi/

extensions, developers are still burdened to keep track of how resources are made available to workers. Additionally, these frameworks are designed to scale out computational resources and have only rudimentary support for dealing with very large amounts of input data. When using existing parallel computing approaches for large-data computation, the programmer must devote a significant amount of attention to low-level system details, which detracts from higher-level problem solving.

One of the most significant advantages of MapReduce is that it provides an abstraction that hides many system-level details from the programmer. Therefore, a developer can focus on what computations need to be performed, as opposed to how those computations are actually carried out or how to get the data to the processes that depend on them. Like OpenMP and MPI, MapReduce provides a means to distribute computation without burdening the programmer with the details of distributed computing (but at a different level of granularity). However, organizing and coordinating large amounts of computation is only part of the challenge. Large-data processing by definition requires bringing data and code together for computation to occur—no small feat for datasets that are terabytes and perhaps petabytes in size! MapReduce addresses this challenge by providing a simple abstraction for the developer, transparently handling most of the details behind the scenes in a scalable, robust, and efficient manner. As we mentioned in Chapter 1, instead of moving large amounts of data around, it is far more efficient, if possible, to move the code to the data. This is operationally realized by spreading data across the local disks of machines in a cluster and running processes on machines that hold the data. The complex task of managing storage in such a processing environment is handled by the distributed file system that underlies MapReduce.

This chapter introduces the MapReduce programming model and the underlying distributed file system. We start in Chapter 2.1 with an overview of functional programming, from which MapReduce draws its inspiration. Chapter 2.2 introduces the basic programming model, focusing on mappers and reducers. Chapter 2.3 discusses the role of the execution framework in actually running MapReduce programs (called jobs). Chapter 2.4 fills in additional details by introducing partitioners and combiners, which provide greater control over data flow. MapReduce would not be practical without a tightly-integrated distributed file system that manages the data being processed; Chapter 2.5 covers this in detail. Tying everything together, a complete cluster architecture is described in Chapter 2.6 before the chapter ends with a summary.

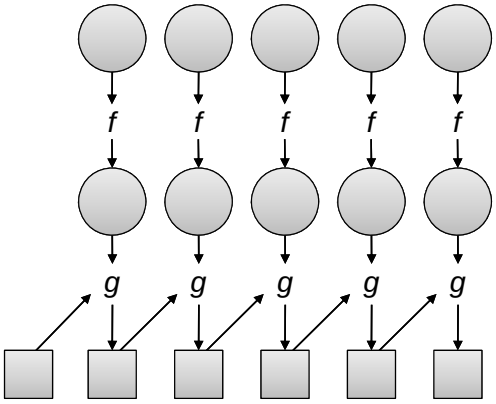


Figure 2.1: Illustration of *map* and *fold*, two higher-order functions commonly used together in functional programming: *map* takes a function f and applies it to every element in a list, while *fold* iteratively applies a function g to aggregate results.

2.1 FUNCTIONAL PROGRAMMING ROOTS

MapReduce has its roots in functional programming, which is exemplified in languages such as Lisp and ML.[4] A key feature of functional languages is the concept of higher-order functions, or functions that can accept other functions as arguments. Two commonly built-in higher order functions are *map* and *fold*, illustrated in Figure 2.1. Given a list, *map* takes as an argument a function f (that takes a single argument) and applies it to all elements in a list (the top part of the diagram). Given a list, *fold* takes as arguments a function g (that takes two arguments) and an initial value: g is first applied to the initial value and the first item in a list, the result of which is stored in an intermediate variable. This intermediate variable and the next item in the list serve as the arguments to a second application of g, the results of which are stored in the intermediate variable. This process repeats until all items in the list have been consumed; *fold* then returns the final value of the intermediate variable. Typically, *map* and *fold* are used in combination. For example, to compute the sum of squares of a list of integers, one could map a function that squares its argument (i.e., $\lambda x.x^2$) over the input list, and then fold the resulting list with the addition function (more precisely, $\lambda x \lambda y.x + y$) using an initial value of zero.

We can view *map* as a concise way to represent the transformation of a dataset (as defined by the function f). In the same vein, we can view *fold* as an aggregation operation, as defined by the function g. One immediate observation is that the appli-

[4]However, there are important characteristics of MapReduce that make it non-functional in nature—this will become apparent later.

cation of f to each item in a list (or more generally, to elements in a large dataset) can be parallelized in a straightforward manner, since each functional application happens in isolation. In a cluster, these operations can be distributed across many different machines. The *fold* operation, on the other hand, has more restrictions on data locality—elements in the list must be "brought together" before the function g can be applied. However, many real-world applications do not require g to be applied to *all* elements of the list. To the extent that elements in the list can be divided into groups, the fold aggregations can proceed in parallel. Furthermore, for operations that are commutative and associative, significant efficiencies can be gained in the *fold* operation through local aggregation and appropriate reordering.

In a nutshell, we have described MapReduce. The map phase in MapReduce roughly corresponds to the *map* operation in functional programming, whereas the reduce phase in MapReduce roughly corresponds to the *fold* operation in functional programming. As we will discuss in detail shortly, the MapReduce execution framework coordinates the map and reduce phases of processing over large amounts of data on large clusters of commodity machines.

Viewed from a slightly different angle, MapReduce codifies a generic "recipe" for processing large datasets that consists of two stages. In the first stage, a user-specified computation is applied over all input records in a dataset. These operations occur in parallel and yield intermediate output that is then aggregated by another user-specified computation. The programmer defines these two types of computations, and the execution framework coordinates the actual processing (very loosely, MapReduce provides a functional abstraction). Although such a two-phase processing structure may appear to be very restrictive, many interesting algorithms can actually be expressed quite concisely—especially if one decomposes complex algorithms into a sequence of MapReduce jobs. Subsequent chapters in this book will focus on how a number of algorithms can be implemented in MapReduce.

2.2 MAPPERS AND REDUCERS

Key-value pairs form the basic data structure in MapReduce. For a collection of web pages, keys may be URLs and values may be the actual HTML content. For a graph, keys may represent nodes and values represent adjacency lists of those nodes (see Chapter 5 for more details). Part of the design of MapReduce algorithms involves imposing this structure on arbitrary datasets. It is not necessary for the keys to be meaningful, but keys are often used to uniquely identify input data.

In MapReduce, the programmer defines a mapper and a reducer with the following signatures:

map: $(k_1, v_1) \rightarrow [(k_2, v_2)]$
reduce: $(k_2, [v_2]) \rightarrow [(k_3, v_3)]$

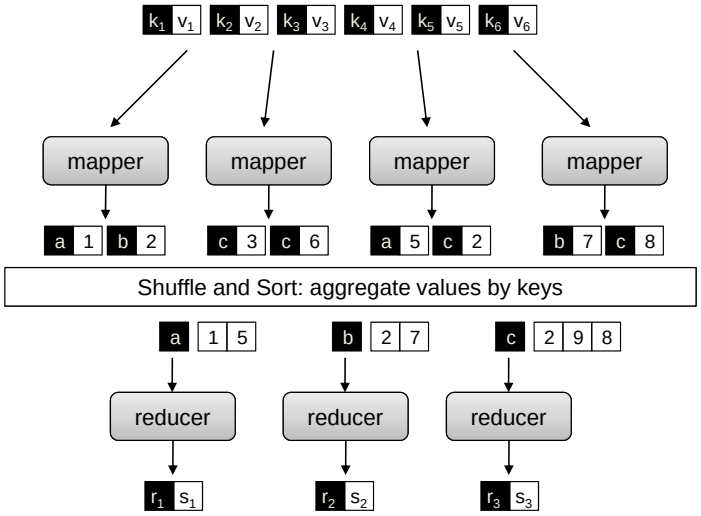


Figure 2.2: Simplified view of MapReduce. Mappers are applied to all input key-value pairs, which generate an arbitrary number of intermediate key-value pairs. Reducers are applied to all values associated with the same key. Between the map and reduce phases lies a barrier that involves a large distributed sort and group by.

The input to a MapReduce job starts as data stored on the underlying distributed file system (see Chapter 2.5). The mapper is applied to every input key-value pair (split across an arbitrary number of files) to generate an arbitrary number of intermediate key-value pairs (the convention [...] is used throughout this book to denote a list). The reducer is applied to all values associated with the same intermediate key to generate output key-value pairs.[5] Implicit between the map and reduce phases is a distributed "group by" operation on intermediate keys. Intermediate data arrive at each reducer in order, sorted by the key. However, no ordering relationship is guaranteed for keys across different reducers. Output key-value pairs from each reducer are written persistently back onto the distributed file system (whereas intermediate key-value pairs are transient and not preserved). The output ends up in r files on the distributed file system, where r is the number of reducers. For the most part, there is no need to consolidate reducer output, since the r files often serve as input to yet another MapReduce job. Figure 2.2 illustrates this two-stage processing structure.

A simple word count algorithm in MapReduce is shown in Figure 2.3. This algorithm counts the number of occurrences of every word in a text collection, which may be the first step in, for example, building a unigram language model (i.e., probability

[5]This characterization, while conceptually accurate, is a slight simplification. See Chapter 2.6 for more details.

```
1: class Mapper
2:     method Map(docid a, doc d)
3:         for all term t ∈ doc d do
4:             Emit(term t, count 1)

1: class Reducer
2:     method Reduce(term t, counts [c1, c2, ...])
3:         sum ← 0
4:         for all count c ∈ counts [c1, c2, ...] do
5:             sum ← sum + c
6:         Emit(term t, count sum)
```

Figure 2.3: Pseudo-code for the word count algorithm in MapReduce. The mapper emits an intermediate key-value pair for each word in a document. The reducer sums up all counts for each word.

distribution over words in a collection). Input key-values pairs take the form of (docid, doc) pairs stored on the distributed file system, where the former is a unique identifier for the document, and the latter is the text of the document itself. The mapper takes an input key-value pair, tokenizes the document, and emits an intermediate key-value pair for every word: the word itself serves as the key, and the integer one serves as the value (denoting that we've seen the word once). The MapReduce execution framework guarantees that all values associated with the same key will be brought together in the reducer. Therefore, in our word count algorithm, we simply need to sum up all counts (ones) associated with each word. The reducer does exactly this, and emits final key-value pairs with the word as the key, and the count as the value. Final output is written to the distributed file system, one file per reducer. Words within each file will be sorted by alphabetical order, and each file will contain roughly the same number of words. The partitioner, which we discuss later in Chapter 2.4, controls the assignment of words to reducers. The output can be examined by the programmer or used as input to another MapReduce program.

To provide a bit more implementation detail: pseudo-code provided in this book roughly mirrors how MapReduce programs are written in Hadoop, the open-source Java implementation. Mappers and reducers are objects that implement the Map and Reduce methods, respectively. In Hadoop, a mapper object is initialized for each map task (associated with a particular sequence of key-value pairs called an input split) and the Map method is called on each key-value pair by the execution framework. In configuring a MapReduce job, the programmer provides a hint on the number of map tasks to run, but the execution framework (see next section) makes the final determination based on the physical layout of the data (more details in Chapter 2.5

and Chapter 2.6). The situation is similar for the reduce phase: a reducer object is initialized for each reduce task, and the Reduce method is called once per intermediate key. In contrast with number of map tasks, the programmer can precisely specify the number of reduce tasks. We will return to discuss the details of Hadoop job execution in Chapter 2.6, which is dependent on an understanding of the distributed file system (covered in Chapter 2.5). To reiterate: although the presentation of algorithms in this book closely mirrors the way they would be implemented in Hadoop, our focus is on algorithm design and conceptual understanding—not actual Hadoop programming. For that, we would recommend Tom White's book [107].

What are the restrictions on mappers and reducers? Mappers and reducers can express arbitrary computations over their inputs. However, one must generally be careful about use of external resources since multiple mappers or reducers would be contending for those resources. For example, it may be unwise for a mapper to query an external SQL database, since that would introduce a scalability bottleneck on the number of map tasks that could be run in parallel (since they might all be simultaneously querying the database). In general, mappers can emit an arbitrary number of intermediate key-value pairs, and they need not be of the same type as the input key-value pairs. Similarly, reducers can emit an arbitrary number of final key-value pairs, and they can differ in type from the intermediate key-value pairs. Although not permitted in functional programming, mappers and reducers can have side effects. This is a powerful and useful feature: for example, preserving state across multiple inputs is central to the design of many MapReduce algorithms (see Chapter 3). Such algorithms can be understood as having side effects that only change state that is *internal* to the mapper or reducer. While the correctness of such algorithms may be more difficult to guarantee (since the function's behavior depends not only on the current input but on previous inputs), most potential synchronization problems are avoided since internal state is private only to individual mappers and reducers. In other cases (see Chapter 4.3 and Chapter 6.5), it may be useful for mappers or reducers to have *external* side effects, such as writing files to the distributed file system. Since many mappers and reducers are run in parallel, and the distributed file system is a shared global resource, special care must be taken to ensure that such operations avoid synchronization conflicts. One strategy is to write a temporary file that is renamed upon successful completion of the mapper or reducer [31].

In addition to the "canonical" MapReduce processing flow, other variations are also possible. MapReduce programs can contain no reducers, in which case mapper output is directly written to disk (one file per mapper). For embarrassingly parallel problems, e.g., parse a large text collection or independently analyze a large number of images, this would be a common pattern. The converse—a MapReduce program with no mappers—is not possible, although in some cases it is useful for the mapper to implement the identity function and simply pass input key-value pairs to the reducers. This

has the effect of sorting and regrouping the input for reduce-side processing. Similarly, in some cases it is useful for the reducer to implement the identity function, in which case the program simply sorts and groups mapper output. Finally, running identity mappers and reducers has the effect of regrouping and resorting the input data (which is sometimes useful).

2.3 THE EXECUTION FRAMEWORK

To be precise, MapReduce can refer to three distinct but related concepts. First, MapReduce is a programming model, which is the sense discussed above. Second, MapReduce can refer to the execution framework (i.e., the "runtime") that coordinates the execution of programs written in this particular style. Finally, MapReduce can refer to the software implementation of the programming model and the execution framework: for example, Google's proprietary implementation vs. the open-source Hadoop implementation.[6] For the most part, usage should be clear from context, but for additional clarity we refer specifically to Hadoop when discussing features of the open-source implementation that may or may not be shared by other implementations.

So what exactly does the MapReduce execution framework do? In short, it takes over where the programmer leaves off. A MapReduce program consists of code packaged with configuration parameters (such as input and output paths), and is referred to as a job. The programmer submits the MapReduce job to the submission node of a cluster (in Hadoop, this is called the jobtracker) and waits for the job to run. The runtime transparently handles all other aspects of execution, on clusters ranging from a few to a few thousand nodes. Specific responsibilities include:

Scheduling. Each MapReduce job is divided into smaller units called tasks (see Chapter 2.6 for more details). For example, a map task may be responsible for processing a certain block of input key-value pairs (called an input split in Hadoop); similarly, a reduce task may handle a portion of the intermediate key space. It is not uncommon for MapReduce jobs to have thousands of individual tasks that need to be assigned to nodes in the cluster. In many cases, the number of tasks exceeds the capacity of the cluster, making some amount of sequential processing inevitable. Another aspect of scheduling involves coordination among tasks belonging to different jobs (e.g., from different users): how can a large, shared resource support several users simultaneously in a predictable, transparent, policy-driven fashion?

Data/code co-location. The phrase *data distribution* is misleading, since one of the key ideas behind MapReduce is to move the code, not the data. However, the more general point remains—in order for computation to occur, we need to somehow feed

[6] And in fact, there are many implementations of MapReduce, e.g., targeted specifically for multi-core processors [90], for GPGPUs [49], for the CELL architecture [89], etc.

data to the code. In MapReduce, this issue is inexplicably intertwined with scheduling and relies heavily on the design of the underlying distributed file system. To achieve data locality, the scheduler starts tasks on the machine that holds a particular block of data (i.e., on its local drive) needed by the task. This has the effect of moving code to the data. If this is not possible (e.g., a machine is already running too many tasks), new tasks will be started elsewhere, and the necessary data will be streamed over the network. An important optimization here is to prefer machines that are on the same rack (in the data center) as the machine with the relevant data block, since inter-rack bandwidth is significantly less than intra-rack bandwidth.

Synchronization. In general, synchronization refers to the mechanisms by which multiple concurrently running processes "join up", for example, to share intermediate results or otherwise exchange state information. In MapReduce, synchronization is accomplished by a barrier between the map and reduce phases of processing. Intermediate key-value pairs must be grouped by key, which is accomplished by a large distributed sort involving all the nodes that executed map tasks and all the nodes that will execute reduce tasks. This necessarily involves copying intermediate data over the network, and therefore the process is commonly known as "shuffle and sort". A MapReduce job with m mappers and r reducers involves $m \times r$ distinct copy operations, since each mapper may have intermediate output going to every reducer.

Note that reducers cannot start until all the mappers have finished, since the execution framework cannot otherwise guarantee that all values associated with the same key have been gathered. This is an important departure from functional programming: in a *fold* operation, the aggregation function g is a function of the intermediate value and the next item in the list—which means that values can be lazily generated and aggregation can begin as soon as values are available. In contrast, the reducer in MapReduce receives *all* values associated with the same key at once. Although reducers must wait for all mappers to finish before they start processing, it is possible to start copying intermediate key-value pairs over the network to the nodes running the reducers before the mappers have finished—this is a common optimization and implemented in Hadoop.

Error and fault handling. The MapReduce execution framework must accomplish all the tasks above in an environment where errors and faults are the norm, not the exception. Since MapReduce was explicitly designed around low-end commodity servers, the runtime must be especially resilient. In large clusters, disk failures are common [87] and RAM experiences more errors than one might expect [93]. Large datacenters suffer from both planned outages (e.g., system maintenance and hardware upgrades) and unexpected outages (e.g., power failure, connectivity loss, etc.).

And that's just hardware. No software is bug free—exceptions must be appropriately trapped, logged, and recovered from. Large-data problems have a penchant for

uncovering obscure corner cases in code that is otherwise thought to be "bulletproof".[7] Furthermore, any sufficiently large dataset will contain corrupted data or records that are mangled beyond a programmer's imagination—resulting in errors that one would never think to check for or trap. The MapReduce execution framework must thrive in this hostile environment.

2.4 PARTITIONERS AND COMBINERS

We have thus far presented a simplified view of MapReduce. There are two additional elements that complete the programming model: partitioners and combiners.

Partitioners are responsible for dividing up the intermediate key space and assigning intermediate key-value pairs to reducers. In other words, the partitioner specifies the node to which an intermediate key-value pair must be copied. Within each reducer, keys are processed in sorted order (which is how the "group by" is implemented). The simplest partitioner involves computing the hash value of the key and then taking the mod of that value with the number of reducers. This assigns approximately the same number of keys to each reducer (dependent on the quality of the hash function). Note, however, that the partitioner only considers the key and ignores the value—therefore, a roughly-even partitioning of the key space may nevertheless yield large differences in the number of key-values pairs sent to each reducer (since different keys may have different numbers of associated values).

Combiners are an optimization in MapReduce that allow for local aggregation before the shuffle and sort phase. We can motivate the need for combiners by considering the word count algorithm in Figure 2.3, which emits a key-value pair for each word in the collection. Furthermore, all these key-value pairs need to be copied across the network, and so the amount of intermediate data will be larger than the input collection itself. This is clearly inefficient. One solution is to perform local aggregation on the output of each mapper, i.e., to compute a local count for a word over all the documents processed by the mapper. With this modification, the number of intermediate key-value pairs will be at most the number of unique words in the collection times the number of mappers (and typically far smaller because each mapper may not encounter every word).

The combiner in MapReduce supports such an optimization. One can think of combiners as "mini-reducers" that take place on the output of the mappers, prior to the shuffle and sort phase. Each combiner operates in isolation and therefore does not have access to intermediate output from other mappers. Like the reducer, the combiner is provided keys and all values associated with each key. It can emit any number of key-value pairs, but the keys and values must be of the same type as the reducer (i.e., the combiner and reducer must have the exact same method signature). In cases where an operation is both associative and commutative (e.g., addition or multiplication),

[7] For example, Hadoop has unearthed several bugs in Sun's JVM.

reducers can directly serve as combiners. In general, however, reducers and combiners are not interchangeable.

In many cases, proper use of combiners can spell the difference between an impractical algorithm and an efficient algorithm. This topic will be discussed in Chapter 3.1, which focuses various techniques for local aggregation. It suffices to say for now that a combiner can significantly reduce the amount of data that needs to be copied over the network, resulting in much faster algorithms.[8]

The complete MapReduce model is shown in Figure 2.4. Output of the mappers are processed by the combiners, which perform local aggregation to cut down on the number of intermediate key-value pairs. The partitioner determines which reducer will be responsible for processing a particular key, and the execution framework uses this information to copy the data to the right location during the shuffle and sort phase. Therefore, a complete MapReduce job consists of code for the mapper, reducer, combiner, and partitioner, along with job configuration parameters. The execution framework handles everything else.

2.5 THE DISTRIBUTED FILE SYSTEM

So far, we have mostly focused on the *processing* aspect of data-intensive processing, but it is important to recognize that without data, there is nothing to compute on. In high-performance computing (HPC) and many traditional cluster architectures, storage is viewed as a distinct and separate component from computation. Implementations vary widely, but network-attached storage (NAS) and storage area networks (SAN) are common; supercomputers often have dedicated subsystems for handling storage (separate nodes, and often even separate networks). Regardless of the details, the processing cycle remains the same at a high level: the compute nodes fetch input from storage, load into memory, process the data, and then write back the results (with perhaps intermediate checkpointing for long-running processes).

As dataset sizes increase, more compute capacity is required for processing. But as compute capacity grows, the link between the compute nodes and the storage becomes a bottleneck. At that point, one could invest in higher performance and necessarily more expensive networks (10 gigabit Ethernet), or special-purpose interconnects such as InfiniBand (also expensive). In most cases, this is not a cost-effective solution, as the price of networking equipment increases non-linearly with performance (e.g., a switch with ten times the capacity is more than ten times more expensive). Alternatively, one

[8] A note on the implementation of combiners in Hadoop: by default, the execution framework reserves the right to use combiners at its discretion. In reality, this means that a combiner may be invoked one, two, or multiple times. In addition, combiners in Hadoop may actually be invoked in the reduce phase, i.e., after key-value pairs have been copied over the reducer, but before the user reducer code runs. As a result, reducers must be carefully written so that it can be executed in these different environments. Chapter 3 discusses this in more detail.

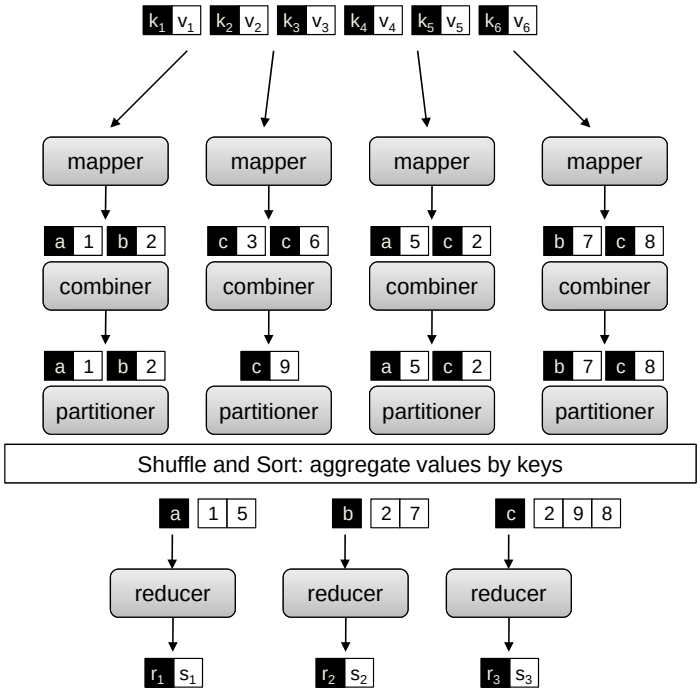


Figure 2.4: Complete view of MapReduce, illustrating combiners and partitioners in addition to mappers and reducers. Combiners can be viewed as "mini-reducers" in the map phase. Partitioners determine which reducer is responsible for a particular key.

could abandon the separation of computation and storage as distinct components in a cluster. The distributed file system (DFS) that underlies MapReduce adopts exactly this approach. The Google File System (GFS) [41] supports Google's proprietary implementation of MapReduce; in the open-source world, HDFS (Hadoop Distributed File System) is an open-source implementation of GFS that supports Hadoop. Although MapReduce doesn't necessarily require the distributed file system, it is difficult to realize many of the advantages of the programming model without a storage substrate that behaves much like the DFS.[9]

The main idea behind the distributed file system is to divide user data into blocks and spread those blocks across the local disks of nodes in the cluster. Blocking data, of course, is not a new idea, but DFS blocks are significantly larger than block sizes in typical single-machine file systems (64 MB by default). The distributed file system

[9]However, there is evidence that existing POSIX-based distributed cluster file systems (e.g., GPFS or PVFS) can serve as a replacement for HDFS, when properly tuned or modified for MapReduce workloads [103, 3]. This, however, remains an experimental use case.

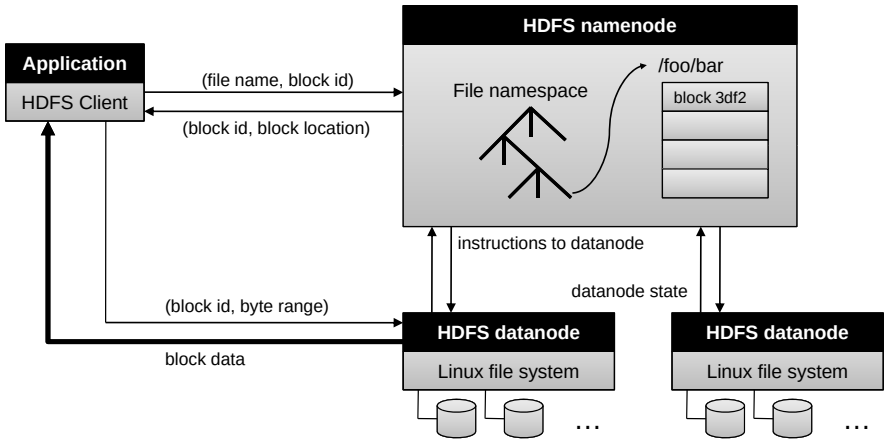


Figure 2.5: Architecture of HDFS illustrating the master–slave architecture. The namenode is responsible for maintaining the file namespace and directs clients to datanodes that actually hold the data.

adopts a master–slave architecture in which the master maintains the file namespace (metadata, directory structure, file to block mapping, location of blocks, and access permissions) and the slaves manage the actual data blocks. In GFS, the master is called the GFS master, and the slaves are called GFS chunkservers. In Hadoop, the same roles are filled by the namenode and datanodes, respectively. This book adopts the Hadoop terminology, although for most basic file operations GFS and HDFS work much the same way. The architecture of HDFS is shown in Figure 2.5, redrawn from a similar diagram describing GFS by Ghemawat et al. [41].

In HDFS, an application client wishing to read a file (or a portion thereof) must first contact the namenode to determine where the actual data is stored. In response to the client request, the namenode returns the relevant block id and the location where the block is held (i.e., which datanode). The client then contacts the datanode to retrieve the data. Blocks are themselves stored on standard single-machine file systems, so HDFS lies on top of the standard OS stack (e.g., Linux). An important feature of the design is that data is never moved through the namenode. Instead, all data transfer occurs directly between clients and datanodes; communications with the namenode only involves transfer of metadata.

By default, HDFS stores three separate copies of each data block to ensure both reliability, availability, and performance (multiple copies result in more opportunities to exploit data locality). In large clusters, the three replicas are spread across two physical racks, so HDFS is resilient towards two common failure scenarios: individual datanode crashes and failures in networking equipment that brings an entire rack offline.

Replicating blocks across physical machines also increase opportunities to co-located data and processing in the scheduling of MapReduce jobs (more details later). The namenode is in periodic communication with the datanodes to ensure proper replication of all the blocks: if there are too many replicas, extra copies are discarded; if there aren't enough replicas, the namenode directs the creation of additional copies.[10]

To create a new file and write data to HDFS, the application client first contacts the namenode, which updates the file namespace after checking permissions and making sure the file doesn't already exist. The namenode allocates a new block on a suitable datanode, and the application is directed to stream data directly to it. From the initial datanode, data is further propagated to additional replicas. In the most recent release of Hadoop as of this writing (release 0.20.1), files are immutable—they cannot be modified after creation. There are current plans to officially support file appends in the near future, which is a feature already present in GFS.

In summary, the HDFS namenode has the following responsibilities:

- Namespace management. The namenode is responsible for maintaining the file namespace, which includes metadata, directory structure, file to block mapping, location of blocks, and access permissions. These data are held in memory for fast access and all mutations are persistently logged.

- Coordinating file operations. The namenode directs application clients to datanodes for read operations, and allocates blocks on suitable datanodes for write operations. All data transfers occur directly between clients and datanodes. When a file is deleted, HDFS does not immediately reclaim the available physical storage; rather, blocks are lazily garbage collected.

- Maintaining overall health of the file system. The namenode is in periodic contact with the datanodes via heartbeat messages to ensure the integrity of the system. If the namenode observes that a data block is under-replicated (fewer copies are stored on datanodes than specified replication factor), it will direct the creation of new replicas. Finally, the namenode is also responsible for rebalancing the file system. During the course of normal operations, certain datanodes may end up holding more blocks than others; rebalancing involves moving blocks from datanodes with more blocks to datanodes with fewer blocks. This leads to better load balancing and more even disk utilization.

Since GFS and HDFS were specifically designed to support Google's proprietary and the open-source implementation of MapReduce, respectively, they were designed with a number of assumptions about the operational environment, which in term influenced

[10]Note that the namenode coordinates the replication process, but data transfer occurs directly from datanode to datanode.

the design of the system. Understanding these choices is critical to designing effective MapReduce algorithms:

- The file system stores a relatively modest number of large files. The definition of "modest" varies by the size of the deployment, but in HDFS multi-gigabyte files are common (if not encouraged). There are several reasons why lots of small files are strongly dispreferred. Since the namenode must hold all file metadata in memory, this presents an upper bound on both the number of files and blocks that can be supported. Large multi-block files represent a more efficient use of namenode memory than many single-block files (each of which consumes less space than a single block size). In addition, mappers in a MapReduce job use individual files as a basic unit for splitting input data. At present, there is no default mechanism that allows a mapper to process multiple files. As a result, mapping over many small files will yield as many mappers as there are files. This results in two potential problems: first, the startup costs of mappers may become significant compared to the time spent actually processing input key-value pairs; second, this may result in an excessive amount of across-the-network copy operations during the "shuffle and sort" phase (recall that a MapReduce job with m mappers and r reducers involves $m \times r$ distinct copy operations).

- Workloads are batch oriented, dominated by long streaming streams and large sequential writes. As a result, high sustained bandwidth is more important than low latency. This exactly describes the nature of MapReduce jobs, which are batch operations on large amounts of data. Due to the common-case workload, both HDFS and GFS do not implement any form of data caching.[11]

- Applications are aware of the characteristics of the distributed file system. Neither HDFS nor GFS present a general POSIX-compliant API, but rather support only a subset of possible file operations. This simplifies the design of the distributed file system, and in essence pushes part of the data management onto the end application. On rationale for this decision is that each application knows best how to handle data specific to that application, for example, in terms of resolving inconsistent sates and optimizing the layout of data structures.

- The file system is deployed in an environment of cooperative users. There is no discussion of security in the original GFS paper, but HDFS explicitly assumes a datacenter environment where only authorized users have access. File permissions in HDFS are only meant to prevent unintended operations and can be easily circumvented.

[11] Although since the distributed file system is built on top of a standard operating system such as Linux, there is still OS-level caching.

- The system is built from unreliable but inexpensive commodity components. As a result, failures are the norm rather than the exception. HDFS is designed around a number of self-monitoring and self-healing mechanisms to robustly cope with common failure modes.

Finally, some discussion is necessary to understand the single-master design of HDFS and GFS. It has been demonstrated that in large-scale distributed systems, simultaneously providing consistency, availability, and partition tolerance is impossible—this is Brewer's so-called CAP Theorem [42]. Since partitioning is unavoidable in large-data systems, the real tradeoff is between consistency and availability. A single-master design trades availability for consistency and significantly simplifies implementation. If the master (HDFS namenode or GFS master) goes down, the entire file system become unavailable, which trivially guarantees that the file system will never be in an inconsistent state. An alternative design might involve multiple masters that jointly manage the file namespace—such an architecture would increase availability (if one goes does, others can step in) at the cost of consistency, not to mention requiring a far more complex implementation.

The single-master design of the distributed file system is a well-known design weakness, since if the master goes offline, the entire file system and all MapReduce jobs running on top of it will grind to a halt. This weakness is mitigated in part by the lightweight nature of file system operations. Recall that no data is ever moved through the namenode and that all communication between clients and datanodes involve only metadata. Because of this, the namenode rarely is the bottleneck, and for the most part avoids load-induced crashes. In practice, this single point of failure is not as severe a limitation as it may appear—with diligent monitoring of the namenode, mean time between failure measured in months are not uncommon for production deployments. Furthermore, the Hadoop community is well-aware of this problem and has developed several reasonable workarounds—for example, a warm standby namenode that can be quickly switched over when the primary namenode fails. The open source environment and the fact that many organizations already depend on Hadoop for production systems virtually guarantees that more effective solutions will be developed over time.

2.6 HADOOP CLUSTER ARCHITECTURE

Putting everything together, the architecture of a complete Hadoop cluster is shown in Figure 2.6. The HDFS namenode runs the namenode daemon. The job submission node runs the jobtracker, which is the single point of contact for a client wishing to execute a MapReduce job. The jobtracker monitors the progress of running MapReduce jobs and is responsible for coordinating the execution of the mappers and reducers. Typically, these services run on two separate machines, although in smaller clusters they are often co-located. The bulk of a Hadoop cluster consists of slave nodes (only three of which

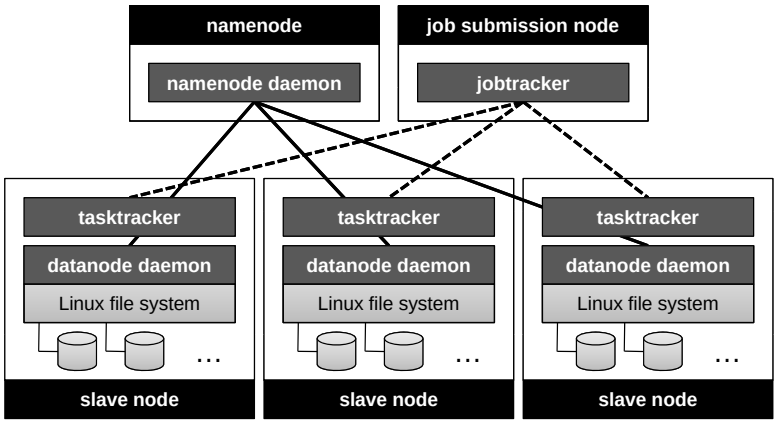


Figure 2.6: Architecture of a complete Hadoop cluster, which consists for three separate components: a namenode, a job submission node, and a number of slave nodes. Each of the slave nodes runs a tasktracker for executing map and reduce tasks and a datanode daemon for serving HDFS data.

are shown in the figure) that run both a tasktracker, which is responsible for actually running code, and a datanode daemon, for serving HDFS data.

A Hadoop MapReduce job is divided up into a number of map tasks and reduce tasks. Tasktrackers periodically send heartbeat messages to the jobtracker that also doubles as a vehicle for task allocation. If a tasktracker is available to run tasks (in Hadoop parlance, has empty task slots), the return acknowledgment of the tasktracker heartbeat contains task allocation information. The number of reduce tasks is equal to the number of reducers specified by the programmer. The number of map tasks, on the other hand, depends on many factors: the number of mappers specified by the programmer serves as a hint to the execution framework, but the actual number of tasks depends on both the number of input files and the number of HDFS data blocks occupied by those files. Each map task is assigned a sequence of input key-value pairs, called an input split in Hadoop. Input splits are computed automatically and the execution framework strives to align them to HDFS block boundaries so that each map task is associated with a single data block. In scheduling map tasks, the jobtracker tries to take advantage of data locality—if possible, map tasks are scheduled on the slave machine that holds the input split, so that the mapper will be processing local data. The alignment of input splits with HDFS block boundaries simplifies task scheduling. If it is not possible to run a map task on local data, it becomes necessary to stream input key-value pairs across the network. Since large clusters are organized into racks, with

far greater intra-rack bandwidth than inter-rack bandwidth, the execution framework strives to at least place map tasks on a rack which has a copy of the data block.

Although conceptually in MapReduce one can think of the mapper being applied to all input key-value pairs and the reducer being applied to all values associated with the same key, actual job execution is a bit more complex. In Hadoop, mappers are Java objects with a Map method (among others). A mapper object is instantiated for every map task by the tasktracker. The life-cycle of this object begins with instantiation, where a hook is provide in the API to run programmer-specified code. This means that mappers can read in "side data", providing an opportunity to load state, static data sources, dictionaries, etc. After initialization, the Map method is called (by the execution framework) on all key-value pairs in the input split. Since these method calls occur in the context of the same Java object, it is possible to preserve state across multiple input key-value pairs within the same map task—this is an important property to exploit in the design of MapReduce algorithms, as we will see in the next chapter. After all key-value pairs in the input split have been processed, the mapper object provides an opportunity to run programmer-specified termination code. This, too, will be important in the design of MapReduce algorithms.

The actual execution of reducers is similar to that of the mappers. Each reducer object is instantiated for every reduce task. The Hadoop API provides hooks for programmer-specified initialization and termination code. After initialization, for each intermediate key in the partition (defined by the partitioner), the execution framework repeatedly calls the Reduce method with an intermediate key and an iterator over all values associated with that key. The programming model also guarantees that intermediate keys will be presented to the Reduce method in sorted order. Since this occurs in the context of a single object, it is possible to preserve state across multiple intermediate keys (and associated values) within a single reduce task. Once again, this property will be critical in the design of MapReduce algorithms and will be discussed in the next chapter.

2.7 SUMMARY

This chapter provides a basic overview of the MapReduce programming model, starting with its roots in functional programming and continuing with a description of mappers, reducers, partitioners, and combiners. Significant attention is also given to the underlying distributed file system, which is a tightly-integrated component of the MapReduce environment. Given this basic understanding, we now turn out attention to the design of MapReduce algorithms.

CHAPTER 3

MapReduce algorithm design

A large part of the power of MapReduce comes from its simplicity: in addition to preparing the input data, the programmer needs only to implement the mapper, the reducer, and optionally, the combiner and the partitioner. All other aspects of execution are handled transparently by the execution framework—on clusters ranging from a few to a few thousand nodes, over datasets ranging from gigabytes to petabytes. However, this also means that any conceivable algorithm that a programmer wishes to develop must be expressed in terms of a small number of rigidly-defined components that must fit together in very specific ways. It may not appear obvious how a multitude of algorithms can be recast into this programming model. The purpose of this chapter is to provide, primarily through examples, a guide to MapReduce algorithm design. These examples illustrate what can be thought of as "design patterns" for MapReduce, which instantiate arrangements of components and specific techniques designed to handle frequently-encountered situations. Two of these design patterns are used in the scalable inverted indexing algorithm we'll present later in Chapter 4; concepts presented here will show up again in Chapter 5 (graph processing) and Chapter 6 (expectation-maximization algorithms).

Synchronization is perhaps the most tricky aspect of designing MapReduce algorithms (or for that matter, parallel and distributed algorithms in general). Other than embarrassingly-parallel problems, processes running on separate nodes in a cluster must, at some point in time, come together—for example, to distribute partial results from nodes that produced them to the nodes that will consume them. Within a single MapReduce job, there is only one opportunity for cluster-wide synchronization—during the shuffle and sort stage where intermediate key-value pairs are copied from the mappers to the reducers. Beyond that, mappers and reducers run in isolation without any mechanisms for direct communication. Furthermore, the programmer has little control over many aspects of execution, for example:

- *Where* a mapper or reducer runs (i.e., on which node in the cluster).
- *When* a mapper or reducer begins or finishes.
- *Which* input key-value pairs are processed by a specific mapper.
- *Which* intermediate key-value pairs are processed by a specific reducer.

Nevertheless, the programmer does have a number of tools for synchronization, controlling execution, and managing the flow of data in MapReduce. In summary, they are:

1. The ability to construct complex data structures as keys and values to store and communicate partial results.
2. The ability to hold state in both mappers and reducers across multiple input or intermediate keys.
3. The ability to control the sort order of intermediate keys, and therefore the order in which a reducer will encounter particular keys.
4. The ability to control the partitioning of the key space, and therefore the set of keys that will be encountered by a particular reducer.

Finally, it is important to realize that many algorithms cannot be expressed as a single MapReduce job. One must often decompose complex algorithms into a sequence of jobs, which requires orchestrating data so that the output of one job becomes the input to the next. Many algorithms are iterative in nature, requiring repeated execution until some convergence criteria—graph algorithms in Chapter 5 and expectation-maximization algorithms in Chapter 6 behave in exactly this way. Often, the convergence check itself cannot be easily expressed in MapReduce; the standard solution is an external (non-MapReduce) program that serves as a "driver" to coordinate MapReduce iterations.

This chapter explains how various techniques to control code execution and data flow can be applied to design algorithms in MapReduce. The focus is both on scalability—ensuring that there are no inherent bottlenecks as algorithms are applied to increasingly larger datasets—and efficiency—ensuring that algorithms do not needlessly consume resources and thereby reducing the cost of parallelization. The gold standard, of course, is linear scalability: an algorithm running on twice the amount of data should take only twice as long. Similarly, an algorithm running on twice the number of nodes should only take half as long.

This chapter is organized as follows:

- Chapter 3.1 introduces the important concept of local aggregation in MapReduce and strategies for designing efficient algorithms that minimize the amount of partial results that need to be copied across the network. The proper use of combiners is discussed in depth, as well as the "in-mapper combining" design pattern.
- Chapter 3.2 uses the example of building word co-occurrence matrices on large text corpora to illustrate two common design patterns, which we have dubbed "pairs" and "stripes". These two approaches are useful in a large class of problems that require keeping track of joint events across a large number of observations.

- Chapter 3.3 shows how co-occurrence counts can be converted into relative frequencies using a pattern known as "order inversion". The sequencing of computations in the reducer can be recast as a sorting problem, where pieces of intermediate data are sorted into exactly the order that is required to carry out a series of computations. Often, a reducer needs to compute an aggregate statistic on a set of elements before individual elements can be processed. Normally, this would require two passes over the data, but with the "order inversion" design pattern, the aggregate statistic can be computed in the reducer before the individual elements are encountered. This may seem counter-intuitive: in the reducer, how can we compute a statistic from a set of elements before encountering elements of that set? As it turns out, clever sorting of special key-value pairs enables exactly this.
- Chapter 3.4 provides a general solution to the problem of sorting values associated with a key in the reduce phase. We call this technique "value-to-key conversion".
- Chapter 3.5 approaches the topic of how to perform joins on relational datasets, covering techniques for "reduce-side" and "map-side" joins.

3.1 LOCAL AGGREGATION

In the context of data-intensive distributed processing, the single most important aspect of synchronization is the exchange of intermediate results, from the processes that produced them to the processes that will ultimately consume them. In a cluster environment, with the exception of embarrassingly-parallel problems, this necessarily involves transferring data over the network. Furthermore, in Hadoop, intermediate results are written to local disk before being sent over the network. Since network and disk latencies are relatively expensive compared to other operations, reductions in the amount of intermediate data translate into increases algorithmic efficiency. In MapReduce, local aggregation of intermediate results is one of the keys to efficient algorithms. Through use of the combiner and by taking advantage of the ability to preserve state across multiple inputs, it is often possible to substantially reduce both the number and size of key-value pairs that need to be shuffled from the mappers to the reducers.

To begin, we illustrate various techniques for local aggregation using the simple word count example presented in Chapter 2.2. For convenience, Figure 3.1 repeats the pseudo-code of the basic algorithm, which is quite simple: the mapper emits an intermediate key-value pair for each term observed, with the term itself as the key and a value of one; reducers sum up the partial counts to arrive at the final count.

The first technique for local aggregation is the combiner, already discussed in Chapter 2.4. Combiners provide a general mechanism within the MapReduce framework to reduce the amount of intermediate data generated by the mappers—recall that they can be understood as "mini-reducers" that process the output of mappers. In this

```
1: class Mapper
2:     method Map(docid a, doc d)
3:         for all term t ∈ doc d do
4:             Emit(term t, count 1)

1: class Reducer
2:     method Reduce(term t, counts [c1, c2, ...])
3:         sum ← 0
4:         for all count c ∈ counts [c1, c2, ...] do
5:             sum ← sum + c
6:         Emit(term t, count sum)
```

Figure 3.1: Pseudo-code for the basic word count algorithm in MapReduce (repeated from Figure 2.3).

example, the combiners aggregate term counts across the documents processed by each mapper. This results in a reduction in the number of intermediate key-value pairs that need to be shuffled across the network—from the order of *total* number of terms in the collection to the order of the number of *unique* terms in the collection.[1]

An improvement on the basic algorithm is shown in Figure 3.2 (the mapper is modified but the reducer remains the same as in Figure 3.1 and therefore is not repeated). An associative array (i.e., Map in Java) is introduced inside the mapper to tally up term counts within a single document: instead of emitting a key-value pair for every term in the document, this version emits a key-value pair for every unique term in each document. Given that some words appear frequently within a document, this can yield substantial savings in the number of intermediate key-value pairs emitted, especially for long documents.

This basic idea can be taken one step further, as illustrated in the variant of the word count algorithm in Figure 3.3 (once again, only the mapper is modified). The workings of this algorithm critically depends on the details of how mappers and reducers in Hadoop are actually executed, discussed in Chapter 2.6. The mapper begins by initializing an associative array, in the method Initialize, prior to processing any input key-value pairs. Since it is possible to preserve state across multiple calls of the

[1] More precisely, if the combiners take advantage of all opportunities for local aggregation, the algorithm would generate at most $m \times V$ intermediate key-value pairs, where m is the number of mappers and V is the vocabulary size (number of unique terms in the collection), since every term could have been observed in every mapper. However, there are two additional factors to consider. Due to the Zipfian nature of term distributions, most terms will not be observed by most mappers (for example, terms that occur only once will by definition only be observed by one mapper). On the other hand, combiners in Hadoop are treated as *optional* optimizations, so there is no guarantee that the execution framework will take advantage of all opportunities for partial aggregation.

```
1: class Mapper
2:     method Map(docid a, doc d)
3:         H ← new AssociativeArray
4:         for all term t ∈ doc d do
5:             H{t} ← H{t} + 1                    ▷ Tally counts for entire document
6:         for all term t ∈ H do
7:             Emit(term t, count H{t})
```

Figure 3.2: Pseudo-code for the improved MapReduce word count algorithm that uses an associative array to aggregate term counts on a per-document basis.

```
1: class Mapper
2:     method Initialize
3:         H ← new AssociativeArray
4:     method Map(docid a, doc d)
5:         for all term t ∈ doc d do
6:             H{t} ← H{t} + 1                    ▷ Tally counts across documents
7:     method Close
8:         for all term t ∈ H do
9:             Emit(term t, count H{t})
```

Figure 3.3: Pseudo-code for the improved MapReduce word count algorithm that demonstrates the "in-mapper combining" design pattern.

Map method (for each input key-value pair), we can continue to accumulate partial term counts in an associative array *across* multiple documents, and emit key-value pairs only when the mapper has processed all documents. That is, the emission of intermediate data is deferred until the Close method in the pseudo-code, after the Map method has been applied to all input key-value pairs of the input data split to which the mapper was assigned.

With this technique, we are in essence incorporating combiner functionality directly into the mapper—this is a sufficiently common design pattern in MapReduce that it's worth giving it a name, "in-mapper combining", so that we can refer to the pattern more conveniently from now on. There are several advantages to this approach. First, it provides control over when local aggregation occurs and how it exactly takes place. In contrast, the semantics of the combiner is underspecified in MapReduce. For example, Hadoop makes no guarantees on how many times the combiner is applied, or that it is even applied at all. The combiner is provided as a semantics-preserving optimization to the execution framework, which has the *option* of using it, perhaps multiple times,

or not at all.[2] In some cases, this indeterminism is unacceptable, which is exactly why programmers often choose to perform their own local aggregation in the mappers.

Second, in-mapper combining will typically be more efficient than using actual combiners. One reason for this is the additional overhead associated with actually materializing the key-value pairs. Combiners reduce the amount of intermediate data that is shuffled across the network, but don't actually reduce the number of key-value pairs that are emitted by the mappers in the first place. With the algorithm in Figure 3.2, intermediate key-value pairs are still generated on a per-document basis,[3] only to be "compacted" by the combiners. This process involves unnecessary object creation and destruction (garbage collection takes time), and furthermore, object serialization and deserialization (when intermediate key-value pairs fill the in-memory buffer holding map outputs and need to be temporarily spilled to disk). In contrast, with in-mapper combining, the mappers will generate only those key-value pairs that need to be shuffled across the network to the reducers.

There are, however, drawbacks to the in-mapper combining technique. First, it breaks the functional programming underpinnings of MapReduce, since state is being preserved across multiple input key-value pairs. Ultimately, this isn't a big deal, since pragmatic concerns for efficiency often trump theoretical "purity", but there are practical consequences as well. Preserving state across multiple input instances means that algorithmic behavior may depend on the order in which input key-value pairs are encountered. This creates the potential for ordering-dependent bugs, which are difficult to debug on large datasets. Second, there is a fundamental scalability bottleneck associated with the in-mapper combining technique. It critically depends on having sufficient memory to store intermediate results until the mapper has completely processed all key-value pairs in an input split. For the word count example, the memory footprint is bound by the vocabulary size, since it is possible that a mapper encounters every term in the collection. Heap's Law, a well-known result in information retrieval, accurately models the growth of vocabulary size as a function of the collection size—the somewhat surprising fact is that the vocabulary size never stops growing.[4] Therefore, the algorithm in Figure 3.3 will scale only up to a point, beyond which the associative array holding the partial term counts will no longer fit in memory.

One common solution to limiting memory usage when using the in-mapper combining technique is to "block" input key-value pairs and "flush" in-memory data structures periodically. The idea is simple: instead of emitting intermediate data only after

[2] In fact, Hadoop may choose to run the combiner in the reduce phase of processing during the merging of partial results from different mappers.

[3] In Hadoop, these key-value pairs are held in memory and "spilled" into temporary files on disk when the buffer fills up to a certain point.

[4] In more detail, Heap's Law relates the vocabulary size V to the collection size as follows: $V = kT^b$, where T is the number of tokens in the collection. Typical values of the parameters k and b are: $30 \leq k \leq 100$ and $b \sim 0.5$ ([72], p. 81).

every key-value pair has been processed, emit partial results after processing every n key-value pairs. This is straightforwardly implemented with a counter variable that keeps track of number input key-value pairs that have been processed. As an alternative, the mapper could keep track of its own memory footprint and flush intermediate key-value pairs once memory usage has crossed a certain threshold. In both approaches, either the block size or the memory usage threshold needs to be determined empirically, which can be quite tricky: with too large a value, the mapper may run out of memory, but with too small a value, opportunities for local aggregation may be lost. Furthermore, in Hadoop physical memory is split between multiple tasks that may be running on a node concurrently; these tasks are all competing for finite resources, but since the tasks are not aware of each other, it is difficult to coordinate resource consumption effectively.

In MapReduce algorithms, the extent to which efficiency can be increased through local aggregation depends on the size of the intermediate key space, the distribution of keys themselves, and the number of key-value pairs that are emitted by each individual map task. Opportunities for aggregation, after all, come from having multiple values associated with the same key (whether one uses combiners or employs the in-mapper combining technique). In the word count example, local aggregation is possible only because many words are encountered multiple times within a map task. In other cases, however, this may not be the case, as we'll see in the next section.

Although use of combiners can yield dramatic reductions in algorithm running time, care must be taken in applying them. Since combiners in Hadoop are viewed as optional optimizations, the correctness of the algorithm cannot depend on computations performed by the combiner or depend on them even being run at all. As a result, the types of the input key-value pairs and output key-value pairs of the combiner must be identical to those of the reducer. In other words, combiners and reducers must have the same method signatures. In cases where the reduce computation is both commutative and associative, the reducer can also be used (unmodified) as the combiner (as is the case with the word count example). In the general case, however, combiners and reducers are not interchangeable.

Consider a simple example: we have a large dataset where input keys are strings and input values are integers, and we wish to compute the mean of all integers associated with the same key (rounded to the nearest integer). A real-world example might be a large user log from a popular website, where keys represent user ids and values represent some measure of activity such as elapsed time for a particular session—the task would correspond to computing the mean session length on a per-user basis, which would be useful for understanding user demographics. Figure 3.4 shows the pseudo-code of a simple algorithm for accomplishing this task that does not involve combiners. We use an identity mapper, which simply passes all input key-value pairs to the reducers

```
1: class Mapper
2:     method Map(string t, integer r)
3:         Emit(string t, integer r)

1: class Reducer
2:     method Reduce(string t, integers [r_1, r_2, ...])
3:         sum ← 0
4:         cnt ← 0
5:         for all integer r ∈ integers [r_1, r_2, ...] do
6:             sum ← sum + r
7:             cnt ← cnt + 1
8:         r_avg ← sum/cnt
9:         Emit(string t, integer r_avg)
```

Figure 3.4: Pseudo-code for the basic MapReduce algorithm that computes the mean of values associated with the same key.

(appropriately grouped and sorted). The reducer keeps track of the running sum and the number of integers encountered. This information is used to compute the mean once all values are processed. The mean is then emitted as the output value in the reducer.

This algorithm will indeed work, but suffers from the same drawbacks as the basic word count algorithm in Figure 3.1: it requires shuffling all key-value pairs from mappers to reducers across the network, which is highly inefficient. Unlike in the word count example, the reducer cannot be used as a combiner in this case. Consider what would happen if one did: the combiner would compute the mean of an arbitrary subset of values associated with the same key, and the reducer would compute the mean of those values. The result is clearly different from the mean of the original values, and therefore the algorithm would not produce the correct result.[5]

So how might we properly take advantage of combiners? An attempt is shown in Figure 3.5. The mapper remains the same, but we have added a combiner that partially aggregates results by computing the numeric components necessary to arrive at the mean. The combiner receives each string and the associated list of integer values, from which it computes the sum of those values and the number of integers encountered (i.e., the count). The sum and count are packaged into a complex value object (a pair), and emitted as the output of the combiner, with the same string as the key. In the reducer, pairs of partial sums and counts can be aggregated to arrive at the mean. Up until now, all keys and values in our algorithms have been primitives (string, integers,

[5] There is one condition under which this algorithm *would* produce the correct result: if each combiner computed the mean of equal-size subsets of the values. However, since such fine-grained control over the combiners is impossible in MapReduce, such a scenario is highly unlikely.

```
1: class Mapper
2:     method Map(string t, integer r)
3:         Emit(string t, integer r)

1: class Combiner
2:     method Combine(string t, integers [r_1, r_2, ...])
3:         sum ← 0
4:         cnt ← 0
5:         for all integer r ∈ integers [r_1, r_2, ...] do
6:             sum ← sum + r
7:             cnt ← cnt + 1
8:         Emit(string t, pair (sum, cnt))                ▷ Separate sum and count

1: class Reducer
2:     method Reduce(string t, pairs [(s_1, c_1), (s_2, c_2) ...])
3:         sum ← 0
4:         cnt ← 0
5:         for all pair (s, c) ∈ pairs [(s_1, c_1), (s_2, c_2) ...] do
6:             sum ← sum + s
7:             cnt ← cnt + c
8:         r_avg ← sum/cnt
9:         Emit(string t, integer r_avg)
```

Figure 3.5: Pseudo-code for an incorrect first attempt at introducing combiners to compute the mean of values associated with each key. The mismatch between value types between violates the MapReduce programming model.

etc.)—however, there are no prohibitions in MapReduce for more complex types. In fact, this is a key strategy for designing MapReduce algorithms that we outlined at the beginning of the chapter, to which we will frequently return throughput this book.

Unfortunately, this algorithm will not work. Recall that combiners and reducers must have exactly the same method signature, i.e., their input and output key-value types must be exactly the same. This is clearly not the case since there is a mismatch in both the input value type and output value type between the combiner and reducer. To understand why this restriction is necessary in the programming model, remember that combiners are optimizations that cannot change the correctness of the algorithm. So let us remove the combiner and see what happens: the output value type of the mapper is integer, so the reducer expects to receive a list of integers as values. But the reducer actually expects a list of pairs! The correctness of the algorithm is contingent

```
1: class Mapper
2:     method Map(string t, integer r)
3:         Emit(string t, pair (r, 1))

1: class Combiner
2:     method Combine(string t, pairs [(s_1, c_1), (s_2, c_2) ...])
3:         sum ← 0
4:         cnt ← 0
5:         for all pair (s, c) ∈ pairs [(s_1, c_1), (s_2, c_2) ...] do
6:             sum ← sum + s
7:             cnt ← cnt + c
8:         Emit(string t, pair (sum, cnt))

1: class Reducer
2:     method Reduce(string t, pairs [(s_1, c_1), (s_2, c_2) ...])
3:         sum ← 0
4:         cnt ← 0
5:         for all pair (s, c) ∈ pairs [(s_1, c_1), (s_2, c_2) ...] do
6:             sum ← sum + s
7:             cnt ← cnt + c
8:         r_avg ← sum/cnt
9:         Emit(string t, pair (r_avg, cnt))
```

Figure 3.6: Pseudo-code for a MapReduce algorithm that computes the mean of values associated with each key that correctly takes advantage of combiners.

on the combiner running on the output of the mappers, and more specifically, that the combiner is run exactly once.[6] This violates the MapReduce programming model.

Another stab at the algorithm is shown in Figure 3.6, and this time, the algorithm is correct. In the mapper we emit a pair consisting of the integer and one as the value—this corresponds to a partial count over one instance. The combiner separately aggregates the partial sums and the partial counts, and emits pairs with updated sums and counts. The reducer is similar to the combiner, except that the mean is computed at the end. In essence, this algorithm transforms a non-associative operation (mean of numbers) into an associative operation (element-wise sum of a pair of numbers, with an additional division at the very end).

Let us verify the correctness of this algorithm by repeating the previous exercise: What would happen if no combiners were run? With no combiners, the mappers would

[6] Recall from our previous discussion that Hadoop makes no guarantees on how many times combiners are called; it could be zero, one, or multiple times.

```
1: class Mapper
2:     method Initialize
3:         S ← new AssociativeArray
4:         C ← new AssociativeArray
5:     method Map(string t, integer r)
6:         S{t} ← S{t} + r
7:         C{t} ← C{t} + 1
8:     method Close
9:         for all term t ∈ S do
10:            Emit(term t, pair (S{t}, C{t}))
```

Figure 3.7: Pseudo-code for a MapReduce algorithm that computes the mean of values associated with each key that exploits in-mapper combining. Only the mapper is shown here; the reducer is the same as in Figure 3.6

send pairs (as values) directly to the reducers. There would be as many intermediate pairs as there were input key-value pairs, and each of those would consist of an integer and one. The reducer would still arrive at the correct sum and count, and hence the mean would be correct. Now add in the combiners: the algorithm would remain correct, no matter how many times they run, since the combiners merely aggregate partial sums and counts to pass along to the reducers. Note that although the input and output key-value types of the combiner and reducer must be identical, the semantics of those types need not be the same. In this case, the input and output values of the combiners hold the partial sum and partial count in a pair. This is the same for the input to the reducer, but the output value of the reducer holds the mean (no longer the sum) in a pair. The lesson here is that the programmer must carefully keep track of not only key-value types, but the semantics of those types.

Finally, in Figure 3.7, we present an even more efficient algorithm that exploits the in-mapper combining technique. Inside the mapper, the partial sums and counts associated with each string are held in memory across input key-value pairs. Intermediate key-value pairs are emitted only after the entire input split has been processed; similar to before, the value type is a pair consisting of the sum and count. The reducer is exactly the same as in Figure 3.6. In this algorithm, combiners are not necessary because there are no opportunities for partial aggregation outside the mapper. Moving partial aggregation from the combiner directly into the mapper is subjected to all the tradeoffs and caveats discussed earlier this section, but in this case the memory footprint of the data structures for holding intermediate data is likely to be modest, making this variant algorithm an attractive option.

3.2 PAIRS AND STRIPES

One common approach for synchronization in MapReduce is to construct complex keys and values in such a way that data necessary for a computation are naturally brought together by the execution framework. We first touched on this technique in the previous section, in the context of "packaging" partial sums and counts in a complex value that is passed from mapper to combiner to reducer. Building on previously published work [38, 66], this section introduces two common design patterns we have dubbed "pairs" and "stripes" that exemplify this strategy.

As a running example, we focus on the problem of building word co-occurrence matrices from large corpora, a common task in corpus linguistics and statistical natural language processing. Formally, the co-occurrence matrix of a corpus is a square $N \times N$ matrix where N corresponds to the number of unique words in the corpus (i.e., the vocabulary size). A cell m_{ij} contains the number of times word w_i co-occurs with word w_j within a specific context—a natural unit such as a sentence or a certain window of m words (where m is an application-dependent parameter). Note that the upper and lower triangles of the matrix are identical since co-occurrence is a symmetric relation, though in the general case relations between words need not be symmetric.

This task is quite common in text processing and provides the starting point to many other algorithms, e.g., for computing statistics such as pointwise mutual information [26], for unsupervised sense clustering [94], and more generally, a large body of work in lexical semantics based on distributional profiles of words, dating back to Firth [39] and Harris [47] in the 1950s and 1960s. The task also has applications in information retrieval (e.g., automatic thesaurus construction [95] and stemming [110]), and other related fields such as text mining. More importantly, this problem represents a specific instance of the task of estimating distributions of discrete joint events from a large number of observations, a very common task in statistical natural language processing for which there are nice MapReduce solutions. Indeed many of the concepts here are used when we discuss expectation-maximization algorithms in Chapter 6.

Beyond text processing, a number of problems in many application domains share similar characteristics. For example, a large retailer might mine point-of-sale transaction records to identify correlated product purchases (e.g., customers who buy *this* tend to also buy *that*), which would assist in inventory management and product placement on shelves. Similarly, an intelligence analyst might wish to identify associations between re-occurring financial transactions that are otherwise unrelated, which might provide a clue in thwarting terrorist activity. The algorithms discussed in this section can be adapted to tackle these related problems.

It is obvious that the space requirement for the word co-occurrence problem is $O(N^2)$, where N is the size of the vocabulary, which for real-world English corpora can be hundreds of thousands of words, or even millions of words in web-scale collections.

```
1: class Mapper
2:     method Map(docid a, doc d)
3:         for all term w ∈ doc d do
4:             for all term u ∈ Neighbors(w) do
5:                 Emit(pair (w, u), count 1)        ▷ Emit count for each co-occurrence

1: class Reducer
2:     method Reduce(pair p, counts [c_1, c_2, ...])
3:         s ← 0
4:         for all count c ∈ counts [c_1, c_2, ...] do
5:             s ← s + c                              ▷ Sum co-occurrence counts
6:         Emit(pair p, count s)
```

Figure 3.8: Pseudo-code for the "pairs" approach for computing word co-occurrence matrices from large corpora.

The computation of the word co-occurrence matrix is quite simple if the entire matrix fits into memory—however, in the case where the matrix is too big to fit in memory, a naïve implementation on a single machine can be very slow as memory is paged to disk. Although compression techniques can increase the size of corpora for which word co-occurrence matrices can be constructed on a single machine, it is clear that there are inherent scalability limitations. We describe two MapReduce algorithms for this task that can scale to large corpora.

Pseudo-code for the first algorithm, dubbed the "pairs" approach, is shown in Figure 3.8. As usual, document ids and the corresponding contents make up the input key-value pairs. The mapper processes each input document and emits intermediate key-value pairs with each co-occurring word pair as the key and the integer one (i.e., the count) as the value. This is straightforwardly accomplished by two nested loops: the outer loop iterates over all words (the left element in the pair), and the inner loop iterates over all neighbors of the first word (the right element in the pair). The neighbors of a word can either be defined in terms of a sliding window or some other contextual unit such as a sentence. The MapReduce execution framework guarantees that all values associated with the same key are brought together in the reducer. Thus, in this case the reducer simply sums up all the values associated with the same co-occurring word pair to arrive at the absolute count of the joint event in the corpus, which is then emitted as the final key-value pair. Each pair corresponds to a cell in the word co-occurrence matrix. This algorithm illustrates the use of complex keys in order to coordinate distributed computations.

An alternative approach, dubbed the "stripes" approach, is presented in Figure 3.9. Like the pairs approach, co-occurring word pairs are generated by two nested

```
1: class Mapper
2:     method Map(docid a, doc d)
3:         for all term w ∈ doc d do
4:             H ← new AssociativeArray
5:             for all term u ∈ Neighbors(w) do
6:                 H{u} ← H{u} + 1                ▷ Tally words co-occurring with w
7:             Emit(Term w, Stripe H)

1: class Reducer
2:     method Reduce(term w, stripes [H_1, H_2, H_3, ...])
3:         H_f ← new AssociativeArray
4:         for all stripe H ∈ stripes [H_1, H_2, H_3, ...] do
5:             Sum(H_f, H)                        ▷ Element-wise sum
6:         Emit(term w, stripe H_f)
```

Figure 3.9: Pseudo-code for the "stripes" approach for computing word co-occurrence matrices from large corpora.

loops. However, the major difference is that instead of emitting intermediate key-value pairs for each co-occurring word pair, co-occurrence information is first stored in an associative array, denoted H. The mapper emits key-value pairs with words as keys and corresponding associative arrays as values, where each associative array encodes the co-occurrence counts of the neighbors of a particular word (i.e., its context). The MapReduce execution framework guarantees that all associative arrays with the same key will be brought together in the reduce phase of processing. The reducer performs an element-wise sum of all associative arrays with the same key, accumulating counts that correspond to the same cell in the co-occurrence matrix. The final associative array is emitted with the same word as the key. In contrast to the pairs approach, each final key-value pair encodes a row in the co-occurrence matrix.

It is immediately obvious that the pairs algorithm generates an immense number of key-value pairs compared to the stripes approach. However, the values in the stripes approach are far more complex (and comes with serialization and deserialization overhead). Both algorithms can benefit from the use of combiners, since the respective operations in their reducers (addition and element-wise sum of associative arrays) are both commutative and associative. However, combiners with the stripes approach have more opportunities to perform local aggregation because the key space is the vocabulary—associative arrays can be merged whenever a word is encountered multiple times by a mapper. In contrast, the key space in the pairs approach is the cross of the vocabulary with itself, which is far larger—counts can be aggregated only when the same

co-occurring word pair is observed multiple times by an individual mapper (which is less likely than observing multiple occurrences of a word, as in the stripes case).

For both algorithms, the in-mapper combining optimization discussed in the previous section can also be applied; the modification is sufficiently straightforward that we leave the implementation as an exercise for the reader. However, the above caveats remain: there will be far fewer opportunities for partial aggregation in the pairs approach due to the sparsity of the intermediate key space. The sparsity of the key space also limits the effectiveness of in-memory combining, since the mapper may run out of memory to store partial counts before all documents are processed, necessitating some mechanism to periodically emit key-value pairs (which further limits the opportunities to perform partial aggregation). Similarly, for the stripes approach, memory management will also be more complex than in the simple word count example. For common terms, the associative array may grow to be quite large, necessitating some mechanism to periodically flush in-memory structures.

It is also important to consider potential bottlenecks of either algorithm. The stripe approach makes the assumption that, at any point in time, each associative array is small enough to fit into memory—otherwise, memory paging will significantly impact performance. The size of the associative array is bounded by the vocabulary size, which is itself unbounded with respect to corpus size (recall the previous discussion of Heap's Law). Therefore, as the sizes of corpora increase, this will become an increasingly pressing issue—perhaps not for gigabyte-sized corpora, but certainly for terabyte-sized corpora that will be commonplace tomorrow. The pairs approach, on the other hand, does not suffer from this limitation, since it does not need to hold intermediate data in memory.

Given this discussion, which approach is faster? Here, we present previously-published results [66] that empirically answered this question. We have implemented both algorithms in Hadoop and applied them to a corpus of 2.27 million documents from the Associated Press Worldstream (APW) totaling 5.7 GB.[7] Figure 3.10 compares the running time of the pairs and stripes approach on different fractions of the corpus, with a co-occurrence window size of two. These experiments were performed on a cluster with 19 slave machines, each with two single-core processors.

Results demonstrate that the stripes approach is far more efficient than the pairs approach: 666 seconds (∼11 minutes) compared to 3758 seconds (∼62 minutes) for the entire corpus (improvement by a factor of 5.7). The mappers in the pairs approach generated 2.6 billion intermediate key-value pairs, totaling 31.2 GB. After the combiners, this was reduced to 1.1 billion key-value pairs, which quantifies the amount of

[7]This was a subset of the English Gigaword corpus (version 3) distributed by the Linguistic Data Consortium (LDC catalog number LDC2007T07). Prior to working with Hadoop, the corpus was first preprocessed. All XML markup was removed, followed by tokenization and stopword removal using standard tools from the Lucene search engine. All tokens were replaced with unique integers for a more efficient encoding.

intermediate data transferred across the network. In the end, the reducers emitted a combined total of 142 million final key-value pairs (the number of non-zero cells in the co-occurrence matrix). On the other hand, the mappers in the stripes approach generated 653 million intermediate key-value pairs totaling 48.1 GB; after the combiners, only 28.8 million key-value pairs were left. The reducers emitted a total of 1.69 million final key-value pairs (the number of rows in the co-occurrence matrix). As expected, the stripes approach provided more opportunities for combiners to aggregate intermediate results, thus greatly reducing network traffic in the shuffle and sort phase. Figure 3.10 also shows that both algorithms exhibit highly desirable scaling characteristics—linear in the amount of input data. This is confirmed by a linear regression applied to the running time data, which yields an R^2 value close to one.

An additional series of experiments explored the scalability of the stripes approach along another dimension: the size of the cluster. These experiments were made possible by Amazon's EC2 service, which allows anyone to rapidly provision clusters of varying sizes for limited durations (for more information, refer back to our discussion of utility computing in Chapter 1.1). Virtualized computation units in EC2 are called instances, and the user is charged only for the instance-hours consumed. Figure 3.11 shows the running time of the stripes algorithm (on the same corpus, same setup as before), on varying cluster sizes, from 20 slave "small" instances all the way up to 80 slave "small" instances (along the x-axis). Running times are shown with solid squares. The alternate set of axes shows the scaling characteristics of various cluster sizes. The circles plot the relative size and speedup of the EC2 experiments, with respect to the 20-instance cluster. These results show highly desirable linear scaling characteristics (once again, confirmed by a linear regression with an R^2 value close to one).

Viewed abstractly, the pairs and stripes algorithms represent two different approaches to counting co-occurring events from a large number of observations. This general description captures the gist of many algorithms in fields as diverse as text processing, data mining, and bioinformatics. For this reason, these two design patterns are broadly useful and frequently observed in a variety of applications.

3.3 COMPUTING RELATIVE FREQUENCIES

Let us build on the pairs and stripes algorithms presented in the previous section and continue with our running example of constructing the word co-occurrence matrix M for a large corpus. Recall that in this large square $N \times N$ matrix, where N corresponds to the vocabulary size, cell m_{ij} contains the number of times word w_i co-occurs with word w_j within a specific context. The drawback of absolute counts is that it doesn't take into account the fact that some words appear more frequently than others. Word w_i may co-occur frequently with w_j simply because one of the words is very common. A simple remedy is to convert absolute counts into relative frequencies, $f(w_j|w_i)$. That

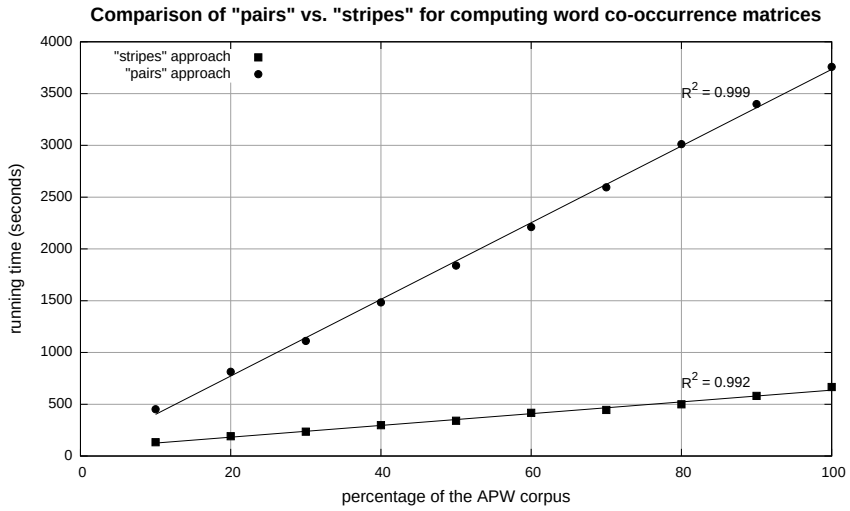


Figure 3.10: Running time of the "pairs" and "stripes" algorithms for computing word co-occurrence matrices on different fractions of the APW corpus. The cluster used for this experiment contained 19 slaves, each with two single-core processors.

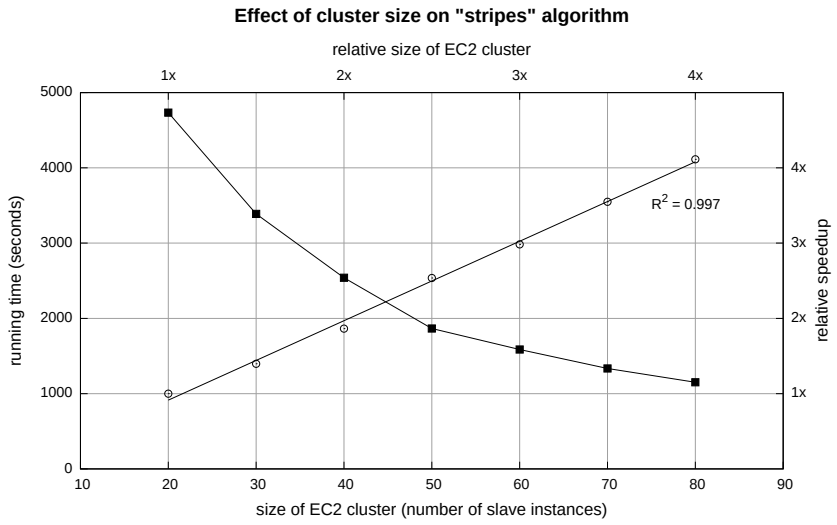


Figure 3.11: Running time of the stripes algorithm on the APW corpus with clusters of different sizes from EC2. Alternate axes (circles) plot scaling characteristics in terms increasing cluster size.

is, what proportion of the time when w_j appears does it a appear in the context of w_i? This can be computed using the following equation:

$$f(B|A) = \frac{c(A, B)}{\sum_{B'} c(A, B')} \tag{3.1}$$

Here, $c(\cdot, \cdot)$ indicates the number of times a particular co-occurring word pair is observed in the corpus. We need the count of the joint event (word co-occurrence), divided by what is known as the marginal (the sum of the counts of the conditioning variable co-occurring with anything else).

Computing relative frequencies with the stripes approach is straightforward. In the reducer, counts of all words that co-occur with the conditioning variable (A in the above example) are available in the associative array. Therefore, it suffices to sum all those counts to arrive at the marginal (i.e., $\sum_{B'} c(A, B')$), and then divide all the joint counts by the marginal to arrive at the relative frequency for all words. This implementation requires minimal modification to the original stripes algorithm in Figure 3.9, and illustrates the use of complex data structures to coordinate distributed computations in MapReduce. Through appropriate structuring of keys and values, one can use the MapReduce execution framework to bring together all the pieces of data required to perform a computation. Note that, as with before, this algorithm also assumes that each associative array fits into memory.

How might one compute relative frequencies with the pairs approach? In the pairs approach, the reducer would receive (A, B) as the key and the count as the value. From this alone it is not possible to compute $f(B|A)$ since we do not have the marginal. Fortunately, as in the mapper, the reducer can preserve state across multiple keys. Inside the reducer, we can store in memory all the words that co-occur with A and their counts, in essence building the associative array in the stripes approach. To make this work, we must define the sort order of the pair so that keys are first sorted by the left word, and then by the right word. Given this ordering, we can easily detect if all pairs associated with the word we are conditioning on (A) have been encountered. At that point we can go back through the in-memory buffer, compute the relative frequencies, and then emit them in the final key-value pairs.

There is one more modification necessary to make this algorithm work. We must ensure that all pairs with the same left word are sent to the same reducer. This, unfortunately, does not happen automatically: recall that the default partitioner is based on the hash value of the intermediate key, modulo the number of reducers. For a complex key, the raw byte representation is used to compute the hash value. As a result, there is no guarantee that, for example, (dog, aardvark) and (dog, zebra) are assigned to the same reducer. To produce the desired behavior, we must define a custom partitioner

that only pays attention to the left word (i.e., the hash of the pair should be the hash of the left word only).

This algorithm will indeed work, but it suffers from the same drawback as the stripes approach: as the size of the corpus grows, so does that vocabulary size, and at some point there will not be sufficient memory to store all co-occurring words and their counts for the word we are conditioning on. For computing the co-occurrence matrix, the advantage of the pairs approach is that it doesn't suffer from any memory bottlenecks. Is there a way to modify the basic pairs approach so that this advantage is retained?

As it turns out, such an algorithm is indeed possible, although it requires the coordination of several mechanisms in MapReduce. The insight lies in properly sequencing data presented to the reducer. If it were possible to somehow compute (or otherwise obtain access to) the marginal in the reducer before processing the joint counts, the reducer can simply divide the joint counts by the marginal to compute the relative frequency. The notion of "before" and "after" can be captured in the ordering of key-value pairs, which can be explicitly controlled by the programmer. That is, the programmer can define the sort order of keys so that data needed earlier is presented to the reducer before data that is needed later. However, we still need to compute the marginal counts. Recall that in the basic pairs algorithm, each mapper emits a key-value pair with the co-occurring word pair as the key. To compute relative frequencies, we modify the mapper so that it additionally emits a "special" key of the form $(A, *)$, with a value of one, that represents the contribution of the word pair to the marginal. Through use of combiners, these partial marginal counts will be aggregated before being sent to the reducers. Alternatively, the in-mapper combining technique can be used to keep track of the marginals.

In the reducer, we must make sure that the special key-value pairs representing the partial marginal contributions are processed before the normal key-value pairs representing the joint counts. This is accomplished by defining the sort order of the keys so that pairs with the special symbol of the form $(A, *)$ are ordered before any other key-value pairs where the left word is A. In addition, as with before we must also properly define the partitioner to pay attention to only the left word in each pair. With the data properly sequenced, the reducer can directly compute the relative frequencies.

A concrete example is shown in Figure 3.12, which lists the sequence of key-value pairs that a reducer might encounter. First, the reducer will be presented with the special key $(\text{dog}, *)$ and a number of values, each of which represents partial marginal contributions from the map phase (shown here with combiners performing partial aggregation). The reducer accumulates these counts to arrive at the marginal, $\sum_{B'} c(\text{dog}, B')$. The reducer holds on to this value as it processes subsequent keys. After $(\text{dog}, *)$, the reducer will encounter a series of keys representing joint counts; let's say the first of these is the key $(\text{dog}, \text{aardvark})$. Associated with this key will be a list values represent-

key	**values**	
$(\text{dog}, *)$	{6327, 8514, ...}	compute marginal: $\sum_{B'} c(\text{dog}, B') = 42908$
$(\text{dog}, \text{aardvark})$	{2,1}	$f(\text{aardvark}\|\text{dog}) = 3/42908$
$(\text{dog}, \text{aardwolf})$	{1}	$f(\text{aardwolf}\|\text{dog}) = 1/42908$
...		
$(\text{dog}, \text{zebra})$	{2,1,1,1}	$f(\text{zebra}\|\text{dog}) = 5/42908$
$(\text{doge}, *)$	{682, ...}	compute marginal: $\sum_{B'} c(\text{doge}, B') = 1267$
...		

Figure 3.12: Example of the sequence of key-value pairs presented to the reducer in the pairs algorithm for computing relative frequencies.

ing partial joint counts from the map phase (two separate values in this case). Summing these counts will yield the final joint count, i.e., the number of times dog and aardvark co-occur in the entire collection. At this point, since the reducer already knows the marginal, simple arithmetic suffices to compute the relative frequency. All subsequent joint counts are processed in exactly the same manner. When the reducer encounters the next special key-value pair $(\text{doge}, *)$, the reducer resets its internal state and starts to accumulate the marginal all over again. Observe that the memory requirements for this algorithm are minimal, since only the marginal (an integer) needs to be stored. No buffering of individual co-occurring word counts are necessary, and therefore we have eliminated the scalability bottleneck of the previous algorithm.

This design pattern, which we call "order inversion", occurs surprisingly often and across applications in many domains. It is so named because through proper coordination, we can access the result of a computation in the reducer before processing the data needed for that computation. The key insight is to convert the sequencing of computations into a sorting problem. In most cases, an algorithm requires data in some fixed order: by controlling how keys are sorted and how the key space is partitioned, we can present data to the reducer in the order necessary to perform the proper computations. This greatly cuts down on the amount of partial results that a reducer needs to hold in memory.

To summarize, the specific application of the order inversion design pattern for computing relative frequencies requires the following:

- Emitting a special key-value pair for each co-occurring word pair in the mapper to capture its contribution to the marginal.

- Controlling the sort order of pairs so that the key-value pairs holding the marginal contributions are presented to the reducer before any of the pairs representing the joint word co-occurrence counts.

- Defining a custom partitioner to ensure that all pairs with the same left word are shuffled to the same reducer.
- Preserving state across multiple keys in the reducer to first compute the marginal based on the special key-value pairs and then dividing the joint counts by the marginals to arrive at the relative frequencies.

As we will see in Chapter 4, this design pattern is also used in inverted index construction to properly set compression parameters for postings lists.

3.4 SECONDARY SORTING

MapReduce sorts intermediate key-value pairs by the keys during the shuffle and sort phase, which is very convenient if computations inside the reducer rely on sort order (e.g., the order inversion design pattern described in the previous section). However, what if in addition to sorting by key, we also need to sort by value? Consider the example of sensor data from a scientific experiment: there are m sensors each taking readings on continuous basis, where m is potentially a large number. A dump of the sensor data might look something like the following, where ... after each timestamp represents the actual sensor readings.

$(t_1, m_1, \ldots)$
$(t_1, m_2, \ldots)$
$(t_1, m_3, \ldots)$
...
$(t_2, m_1, \ldots)$
$(t_2, m_2, \ldots)$
$(t_2, m_3, \ldots)$

Suppose we wish to reconstruct the activity at each individual sensor over time. A MapReduce program to accomplish this might map over all the raw data and emit the sensor id as the intermediate key, with the rest of the data as the value:

$$m_1 \rightarrow (t_1, \ldots)$$

This would bring all readings from the same sensor together in the reducer. However, since MapReduce makes no guarantees about the ordering of values associated with the same key, the sensor readings will not likely be in temporal order. The simple solution is to buffer all the readings in memory and then sort by timestamp before additional processing.

By now, it should be apparent that any in-memory buffering of data will introduce a scalability bottleneck. What if we are working with a high frequency sensor or sensor readings over a long period of time? What if the sensor readings themselves are large

complex objects? This approach may not scale in these cases—the reducer runs out of memory to buffer all values associated with the same key.

This is a common problem, since in many applications we wish to first group together data one way (e.g., by sensor id), and then sort the groupings another way (e.g., by time). Fortunately, there is a general purpose solution, which we call the "value-to-key conversion" design pattern. The basic idea is to move part of the value into the intermediate key to form a more complex composite key, and let the MapReduce execution framework handle the sorting.

In the above example, instead of emitting the sensor id as the key, we would now emit the sensor id and the timestamp as a composite key:

$$(m_1, t_1) \rightarrow (\ldots)$$

The sensor reading itself now occupies the value. Of course, we must define the sort order of the keys to first sort by the sensor id (on the left) and then by the timestamp (on the right). We must also implement a custom partitioner so that all pairs associated with the same sensor are shuffled to the same reducer.

Properly orchestrated, the key-value pairs will be presented to the reducer in the correct sorted order:

$$(m_1, t_1) \rightarrow (\ldots)$$
$$(m_1, t_2) \rightarrow (\ldots)$$
$$(m_1, t_3) \rightarrow (\ldots)$$
$$\ldots$$

However, note that sensor readings are now split across multiple keys, so the reducer will need to preserve state and keep track of when readings associated with the next sensor begins. Note that this approach can be arbitrarily extended to tertiary, quaternary, etc. sorting.

The basic tradeoff between the two approaches discussed above is where sorting is performed. One can explicitly implement secondary sorting in the reducer, which is generally faster but suffers from a scalability bottleneck. Through value-to-key conversion, sorting is offloaded to the MapReduce execution framework. This typically results in many more keys to sort, but distributed sorting is a task that the MapReduce runtime should excel at, since it lies at the heart of the programming model.

3.5 RELATIONAL JOINS

One popular application of Hadoop is data-warehousing. In an enterprise setting, a data warehouse serves as a vast repository of data, holding everything from sales transactions to product inventories. Typically, the data is relational in nature, but increasingly data warehouses are used to store semi-structured data (e.g., query logs) as well as

unstructured data. Data warehouses form a foundation for business intelligence applications designed to provide decision support. It is widely believed that insights gained by mining historical, current, and prospective data can yield competitive advantages.

Traditionally, data warehouses have been implemented through relational databases, particularly those optimized for a specific workload known as online analytical processing (OLAP). A number of vendors offer parallel databases, but often customers find that they simply cannot scale to the crushing amounts of data an organization needs to deal with today. Cost is another factor, as parallel databases are often quite expensive—on the order of tens of thousands of dollars per terabyte of user data. Over the past few years, Hadoop has gained popularity as a platform for data-warehousing. Hammerbacher [46], for example, discusses Facebook's experiences with scaling up business intelligence applications with Oracle databases, which they ultimately abandoned in favor of a Hadoop-based solution developed in-house called Hive (which is now an open-source project).

Given successful applications of Hadoop to data-warehousing, it makes sense to examine MapReduce algorithms for manipulating relational data. This chapter focuses specially on performing relational joins in MapReduce. We should stress here that even though Hadoop has been applied to process relational data, Hadoop *is not a database*. There is an ongoing debate between advocates of parallel databases and proponents of MapReduce regarding the merits of both approaches for data warehousing applications. Dewitt and Stonebraker, two well-known figures in the database community, famously decried MapReduce as "a major step backwards". They ran a series of benchmarks that demonstrated the supposed superiority of column-oriented parallel databases [84, 101]. However, see Dean and Ghemawat's counterarguments [33] and recent attempts at hybrid architectures [1].

We shall refrain here from participating in this lively debate, and instead focus on presenting algorithms. The following illustrates how one might use MapReduce to perform a relational join on two datasets, generically named R and S. Let us suppose R that looks something like the following:

$(k_1, R_1, \ldots)$
$(k_2, R_2, \ldots)$
$(k_3, R_3, \ldots)$
$\ldots$

where k_n is the key we would like to join on, R_n is a unique id for the record, and the $\ldots$ after R_n denote other parts of the record (not important for our purposes). Similarly, suppose S looks something like this:

$(k_1, S_1, \ldots)$
$(k_3, S_2, \ldots)$

$(k_8, S_3, \ldots)$
$\ldots$

where k_n is the join key, S_n is a unique id for the record, and the $\ldots$ after S_n denotes other parts of the record that are unimportant for our purposes.

The first approach to relational joins is what's known as a "reduce-side join". The idea is quite simple: we map over both datasets and emit the join key as the intermediate key, and the complete record itself as the intermediate value. Since MapReduce guarantees that all values with the same key are brought together, all records will be grouped by the join key—which is exactly what we need to perform the join operation. In more detail, there are three different cases to consider.

The first and simplest is a *one-to-one* join, where at most one record from R and one record from S share the same join key. In this case, the algorithm sketched above will work fine. The reducer will be presented keys and lists of values along the lines of the following:

$k_{23} \rightarrow [(R_{64}, \ldots), (S_{84}, \ldots)]$
$k_{37} \rightarrow [(R_{68}, \ldots)]$
$k_{59} \rightarrow [(S_{97}, \ldots), (R_{81}, \ldots)]$
$k_{61} \rightarrow [(S_{99}, \ldots)]$
$\ldots$

Since we've emitted the join key as the intermediate key, we can remove it from the value to save a bit of space. If there are two values associated with a key, then we know that one must be from R and the other must be from S—remember that MapReduce makes no guarantees about value ordering, so the first value might be from R or from S. We can proceed now to join the two records and perform additional computations (e.g., filter by some other attribute). If there is only one value associated with a key, this means that no record in the other dataset shares the join key, so the reducer does nothing.

Let us now consider the *one-to-many* join. Assume that records in R have unique join keys, so that R is the "one" and S is the "many". The above algorithm will still work, but when processing each key in the reducer, we have no idea when the value corresponding to the record from R will be seen, since values are arbitrarily ordered. The easiest solution is to buffer all values in memory, pick out the record from R, and then cross it with every record from S to perform the join. As we have seen several times already, this creates a scalability bottleneck since we may not have sufficient memory to hold all the records with the same join key.

This is a problem that requires a secondary sort, and the solution lies in the value-to-key conversion design pattern we just presented. In the mapper, instead of simply emitting the join key as the intermediate key, we instead create a composite

key consisting of the join key and the record id (from either R or S). Two additional changes are required: First, we must define the sort order of the keys to first sort by the join key, and then sort all record ids from R before all record ids from S. Second, we must define the partitioner to pay attention to only the join key, so that all composite keys with the same join key arrive at the same reducer.

After applying the value-to-key conversion design pattern, the reducer will be presented keys and values along the lines of the following:

$(k_{82}, R_{105}) \rightarrow (\ldots)$
$(k_{82}, S_{98}) \rightarrow (\ldots)$
$(k_{82}, S_{101}) \rightarrow (\ldots)$
$(k_{82}, S_{137}) \rightarrow (\ldots)$
$\ldots$

Since both the join key and the record id are present in the intermediate key, we can remove them from the value to save space. Whenever the reducer encounters a new join key, it is guaranteed that the associated value will be the relevant record from R. The reducer can hold this record in memory and then proceed to join it with records from S in subsequent steps (until a new join key is encountered). Since the MapReduce execution framework performs the sorting, there is no need to buffer records, and therefore we have eliminated the scalability bottleneck.

Finally, let us consider the *many-to-many* join case. Assuming that R is the smaller dataset, the above algorithm will also work. Consider what will happen at the reducer:

$(k_{82}, R_{105}) \rightarrow (\ldots)$
$(k_{82}, R_{124}) \rightarrow (\ldots)$
$\ldots$
$(k_{82}, S_{98}) \rightarrow (\ldots)$
$(k_{82}, S_{101}) \rightarrow (\ldots)$
$(k_{82}, S_{137}) \rightarrow (\ldots)$
$\ldots$

All the records from R with the same join key will be encountered first, which the reducer can hold in memory. As the reducer processes each S record, it is joined with all the R records. Of course, we are assuming that the R records will fit into memory, which is a limitation of this algorithm (and why we want to control the sort order so that the smaller dataset comes first).

The basic idea behind the reduce-side join is to repartition the two datasets by the join key. This isn't particularly efficient since it requires shuffling both datasets across the network. However, what if the two datasets are already partitioned and sorted in the same way? For example, suppose R and S are both divided into ten files, each sorted by the join key. Further suppose that the join keys are partitioned in exactly the same

manner. In this case, we simply need to join the first file of R with the first file of S, the second file with R with the second file of S, etc. This can be accomplished in what's known as a *map-side join*. We map over one of the datasets and inside the mapper read the corresponding part of the other dataset to perform the join.[8] No reducer is required, unless the user wishes to repartition or perform further process on the results.

A map-side join is far more efficient than a reduce-side join since there is no need to shuffle the datasets over the network. But is it realistic to expect that the stringent conditions required for map-side joins are satisfied? In many cases, *yes*. The reason is that relational joins happen within the broader context of a workflow, which may include multiple steps. Therefore, the datasets that are to be joined may be the output of previous processes (either MapReduce jobs or other code). If the workflow is known in advance and relatively static, we can engineer the previous processes to generate output sorted and partitioned in a way that will make efficient map-side joins possible (in MapReduce, by using a custom partitioner and controlling the sort order of key-value pairs). For *ad hoc* data analysis, reduce-side joins are a more general, albeit less efficient, solution. Consider the case where datasets have multiple keys that one might wish to join on—then no matter how the data is organized, map-side joins will require repartitioning of the data. Alternatively, it is always possible to repartition a dataset using an identity mapper and reducer. But of course, this incurs the cost of shuffling data over the network.

There is a final restriction to bear in mind when using map-side joins with the Hadoop implementation of MapReduce. We assume here that the datasets to be joined were produced by a previous MapReduce job, and the restriction applies to the kinds of keys the reducers in this job may emit. The Hadoop framework permits reducers to emit keys that are different from the the input key whose values they are processing (that is, input and output keys need not be the same type).[9] However, if the output key of a reducer is different from the input key, then the output dataset from the reducer will not necessarily be partitioned in a manner consistent with the specified partitioner (since it applies to the *input* keys rather than the *output* keys). Since map-side joins depend on consistent partitioning (and sorting) of keys, the reducers used to generate data that will participate in a later map-side join *must not* emit any key but the one they are currently processing.

In addition to these two approaches to joining relational data that leverage the MapReduce framework to bring together records that share a common join key, there is also a *memory-backed join*. This is applicable when one of the two datasets completely fits into memory. In this situation, we can load the dataset into memory inside every mapper, in an associative array to facilitate access to records based on the join key.

[8] Note that this almost always implies a non-local read.

[9] The example code given in Google's MapReduce publication suggests that this may not be supported by their implementation [31].

The mappers are applied over the larger dataset, and for each input key-value pair, the mapper checks to see if there is a record with the same join key from the in-memory dataset. There is also an extension to this approach for cases where neither datasets fit into memory: a distributed key-value store can be used to hold one dataset in memory across multiple machines while mapping over another; the mappers could then query this distributed key-value store in parallel and perform joins if the join keys match. The open source caching system `memcached` can be used for exactly this purpose, and therefore we've dubbed this approach memcached join. For further reading, this approach is detailed in a technical report [67].

3.6 SUMMARY

This chapter provides a guide on the design of MapReduce algorithms. In particular, we present a number of "design patterns" that capture effective solutions to common problems. In summary, they are:

- "In-mapper combining", where the functionality of the combiner is moved into the mapper. Instead of emitting intermediate output for every input key-value pair, the mapper aggregates partial results across multiple input records and only emits intermediate key-value pairs after some amount of local aggregation is performed.
- The related patterns "pairs" and "stripes" for keeping track of joint events from a large number of observations. In the pairs approach, we keep track of each joint event separately, whereas in the stripes approach we keep track of all events that co-occur with the same event. Although the stripes approach is significantly more efficient, it requires memory on the order of the size of the event space, which presents a scalability bottleneck.
- "Order inversion", where the main idea is to convert the sequencing of computations into a sorting problem. Through careful orchestration, we can send the reducer the result of a computation before it encounters the data necessary to produce that computation.
- "Value-to-key conversion", which provides a scalable solution for secondary sort. By moving the value (or part thereof) into the key, we can exploit the MapReduce execution framework itself for sorting.

Ultimately, controlling synchronization in the MapReduce programming model boils down to effective use of the following techniques:

1. Constructing complex keys and value types that bring together data necessary for a computation (used in all of the above design patterns).

2. Preserving state across multiple inputs in the mapper and reducer (used in in-mapper combining, order inversion, and value-to-key conversion).

3. Controlling the sort order of intermediate keys (used in order inversion and value-to-key conversion).

4. Controlling the partitioning of the intermediate key space (used in order inversion and value-to-key conversion).

This concludes an overview of MapReduce algorithm design in general. It should be clear by now that although the programming model forces one to express algorithms in terms of a small set of rigidly-defined components, there are many tools at one's disposal to shape the flow of computation. In the next few chapters, we will focus on specific classes of MapReduce algorithms: inverted indexing in Chapter 4, graph processing in Chapter 5, and expectation-maximization in Chapter 6.

CHAPTER 4

Inverted Indexing for Text Retrieval

Web search is the quintessential large-data problem. Given an information need expressed as a short query consisting of a few terms, the system's task is to retrieve relevant web objects (web pages, PDF documents, PowerPoint slides, etc.) and present them to the user. How large is the web? It is difficult to compute exactly, but even a conservative estimate would place the size at several tens of billions of pages, totaling hundreds of terabytes (considering text alone). In real-world applications, users demand results quickly from a retrieval engine—query latencies longer than a few hundred millisecond will try a user's patience. Fulfilling these requirements is quite an engineering feat, considering the amounts of data involved!

Nearly all retrieval engines for full-text search today rely on a data structure called an inverted index, which given a term provides access to the list of documents that contain the term. In information retrieval parlance, objects to be retrieved are generically called "documents" even though in actuality they may be web pages, PDFs, or even fragments of code. Given a user query, the retrieval engine uses the inverted index to score documents that contain the query terms with respect to some ranking model, taking into account features such as term matches, term proximity, attributes of the terms in the document (e.g., bold, appears in title, etc.), as well as the hyperlink structure of the documents (e.g., PageRank [82], which we'll discuss in Chapter 5, or related metrics such as HITS [56] and SALSA [60]). The web search problem thus decomposes into two components: construction of the inverted index (the indexing problem) and ranking documents given a query (the retrieval problem).

The two components of the web search problem have very different requirements. Inverted indexing is for the most part an offline problem. The indexer must be scalable and efficient, but does not need to operate in real time. Indexing is usually a batch process that runs periodically, although the periodicity is often dynamically adjusted for different types of documents (for example, contrast government regulations with news sites). Even for rapidly changing sites, a delay of a few minutes is usually tolerable. Furthermore, since the amount of data the changes rapidly is relatively small, running small indexing jobs at greater frequencies is an adequate solution. Retrieval, on the other hand, is an online problem that demands sub-second response time. Individual users expect low query latencies, but query throughput is equally important since a retrieval engine must serve many users concurrently. Furthermore, query loads are highly variable, depending on the time of day, and can exhibit "spikey" behavior due to special

circumstances (e.g., occurrence of a natural disaster). On the other hand, resource consumption for the indexing problem is more predictable.

However, before inverted indexing can begin, we must first acquire the documents. Research collections for information retrieval are widely available for a variety of genres ranging from blogs to newswire text.[1] In the web context, however, document acquisition often requires crawling, which is the process of traversing the web by repeatedly following hyperlinks and storing downloaded pages for subsequent processing. Effective and efficient web crawling is as much as an art as it is a science, with established best practices but many common pitfalls as well. We explicitly do not cover this problem, and simply assume that, one way or another, one already has access to a large collection of documents. For researchers who wish to explore web-scale retrieval, there is fortunately an available test collection called ClueWeb09 that contains one billion web pages in ten languages (totally 25 terabytes) crawled by Carnegie Mellon University in early 2009.[2]

This chapter focuses on the indexing problem and presents various solutions in MapReduce. Chapter 4.1 begins with an overview of the inverted index structure. Chapter 4.2 discusses the baseline inverted indexing algorithm that is presented in Dean and Ghemawat's original MapReduce paper [31]. We point out a scalability bottleneck in that algorithm, which leads to a revised version presented in Chapter 4.3. Index compression is discussed in Chapter 4.4, which fills in missing details on building compact index structures. Since MapReduce is primarily designed for batch-oriented processing, it does not provide an adequate solution for the retrieval problem, an issue discussed in Section 4.5.

4.1 INVERTED INDEXES

The structure of an inverted index is illustrated in Figure 4.1. In its basic form, an inverted index consists of postings lists, one associated with each term that appears in the collection.[3] A postings list is comprised of individual postings, each of which consists of a document id and a *payload*—information about occurrences of the term in the document. The simplest payload is. . . nothing! For simple boolean retrieval, no additional information is needed in the posting other than the document id; the existence of the posting itself indicates that presence of the term in the document. The most common payload, however, is term frequency (*tf*), or the number of times the term occurs in the document. More complex payloads include positions of every occurrence of the term in

[1] As an interesting side note, in the 1990s, such collections were distributed via postal mail on CD-ROMs, and later, on DVDs. Nowadays, collections are so large that it has become common practice to ship hard drives around the world.

[2] `http://boston.lti.cs.cmu.edu/Data/clueweb09/`

[3] In information retrieval parlance, *term* is preferred over *word* since documents are processed (e.g., tokenization and stemming) into basic units that are often not words in the linguistic sense.

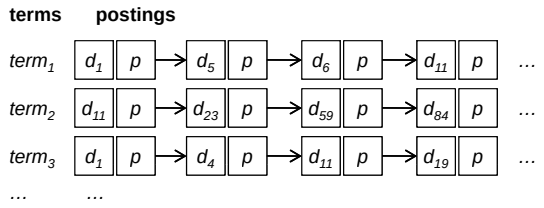


Figure 4.1: Simple illustration of an inverted index. Each term is associated with a list of postings. Each posting is comprised of a document id and a payload, denoted as p in this case. An inverted index provides quick access to documents that contain a term.

the document (to support phrase queries and document scoring based on term proximity), properties of the term (such as if it occurred in the page title or not, to support document ranking based on notions of importance), or even the results of additional linguistic processing (for example, indicating that the term is part of a place name, to support address searches). In the example shown in Figure 4.1, we see that $term_1$ occurs in $\{d_1, d_5, d_6, d_{11}, \ldots\}$, $term_2$ occurs in $\{d_{11}, d_{23}, d_{59}, d_{84}, \ldots\}$, and $term_3$ occurs in $\{d_1, d_4, d_{11}, d_{19}, \ldots\}$. In terms of actual implementation, we assume that documents can be identified by a unique integer ranging from 1 to n, where n is the total number of documents.[4] Generally, postings are sorted by document id, although other sort orders are possible as well.

Given a query, retrieval involves fetching postings lists associated with query terms and traversing the postings to compute the result set. In the simplest case, boolean retrieval involves set operations (union for boolean OR and intersection for boolean AND) on postings lists, which can be accomplished very efficiently since the postings are sorted by document id. In the general case, however, query–document scores must be computed. Partial document scores are stored in structures called *accumulators*. At the end (i.e., once all postings have been processed), the top k documents are then extracted to yield a ranked list of results for the user.

Generally, it is possible hold the entire vocabulary (i.e., dictionary of all the terms) in memory. However, in most cases, postings are too large to store in memory and must be held on disk, usually in compressed form (more details in Chapter 4.4). Query evaluation, therefore, necessarily involves random disk access and "decoding" of the postings. One important aspect of the retrieval problem is to organize disk operations such that random seeks are minimized. The size of an inverted index varies, depending on the payload stored in each posting. If only term frequency is stored, a well-optimized inverted index can be an order magnitude smaller than the original document collection.

[4]It is preferable to start numbering the documents at one since it is not possible to encode zero with many common compression schemes used in information retrieval; see Chapter 4.4.

```
1: class Mapper
2:     procedure Map(docid n, doc d)
3:         H ← new AssociativeArray
4:         for all term t ∈ doc d do
5:             H{t} ← H{t} + 1
6:         for all term t ∈ H do
7:             Emit(term t, posting ⟨n, H{t}⟩)

1: class Reducer
2:     procedure Reduce(term t, postings [⟨a_1, f_1⟩, ⟨a_2, f_2⟩ ...])
3:         P ← new List
4:         for all posting ⟨a, f⟩ ∈ postings [⟨a_1, f_1⟩, ⟨a_2, f_2⟩ ...] do
5:             Append(P, ⟨a, f⟩)
6:         Sort(P)
7:         Emit(term t, postings P)
```

Figure 4.2: Pseudo-code of the inverted indexing algorithm in MapReduce. Mappers emit postings keyed by terms, the execution framework groups postings by term, and the reducers write postings lists to disk.

The inverted index would easily be several times larger if positional information for term occurrences were also stored.

Since the focus of this chapter is MapReduce algorithms for inverted indexing, and not information retrieval in general, we provide a few pointers for additional reading: a survey article by Zobel and Moffat [112] is an excellent starting point on indexing and retrieval algorithms; a number of general information retrieval textbooks have been recently published [72, 29]; while outdated in many other respects, the textbook *Managing Gigabytes* [109] remains an excellent source for index compression techniques.

4.2 INVERTED INDEXING: BASELINE IMPLEMENTATION

Dean and Ghemawat's original paper [31] showed that MapReduce was designed from the very beginning with inverted indexing as an application. Although very little space was devoted to describing the algorithm, it is relatively straightforward to fill in the missing details: this basic algorithm is shown in Figure 4.2.

Input to the mapper consists of document ids (keys) paired with the actual content (values). Individual documents are processed in parallel by the mappers. First, each document is analyzed and broken down into its component terms. The processing pipeline differs depending on the application and type of document, but for web pages typically involves stripping out HTML tags, tokenizing, case folding, removing

stopwords, and stemming. Once the document has been analyzed, term frequencies are computed by iterating over all the terms and keeping track of counts. Lines (4) and (5) in pseudo-code reflect the process of computing term frequencies, but hides the details of document processing. After this histogram has been built, the mapper then iterates over all terms. For each term, a pair consisting of the document id and the term frequency is created. Each pair, denoted by $\langle a, H\{t\}\rangle$ in the pseudo-code, represents an individual posting. The mapper then emits an intermediate key-value pair with the term as the key and the posting as the value, in line (7) in the mapper pseudo-code. Although as presented here only the term frequency is stored in the posting, the algorithm can be easily augmented to store additional information (e.g., term positions) in the payload.

In the shuffle and sort phase, the MapReduce runtime essentially performs a large, distributed "group by" of the postings by term. Without any additional effort by the programmer, the execution framework brings together all the postings that belong in the same postings list. The tremendously simplifies the task of the reducer, which simply needs to gather together all the postings and write them to disk. The reducer begins by initializing an empty list and then appends all postings associated with the same key (term) to the list. The postings are then sorted by document id, and the entire postings list is emitted as a value, with the term as the key. Typically, the postings list is first compressed, but we leave this aside for now (see Chapter 4.3). The final key-value pairs are written to disk and comprise the inverted index. Since each reducer writes its output in a separate file in the distributed file system, our final index will be split across r files, where r is the number of reducers. There is no need to further consolidate these files. Separately, we must also build an index to the postings lists themselves for the retrieval engine: this is typically in the form of mappings from term to (file, byte offset) pairs, so that given a term, the retrieval engine can fetch its corresponding postings list by opening the correct file and seeking to the appropriate byte offset position.

Execution of the complete algorithm is illustrated in Figure 4.3 with a toy example consisting of three documents, three mappers, and two reducers. Intermediate key-value pairs (from the mappers) and the final key-value pairs comprising the inverted index (from the reducers) are shown in the boxes with dotted lines. Postings are shown as pairs of boxes, with the document id on the left, and the term frequency on the right.

The MapReduce programming model provides a very concise expression of the inverted indexing algorithm. Its implementation is similarly concise: the basic algorithm can be implemented in as few as a couple of dozen lines of code in Hadoop. Such an implementation can be completed as a week-long programming assignment in a computer science course [55, 65] by advanced undergraduates and first-year graduate students. In a non-MapReduce indexer, a significant fraction of the code is devoted to grouping postings by term, given constraints imposed by memory and disk (e.g., memory capacity is limited, disk seeks are slow, etc.). In MapReduce, the programmer

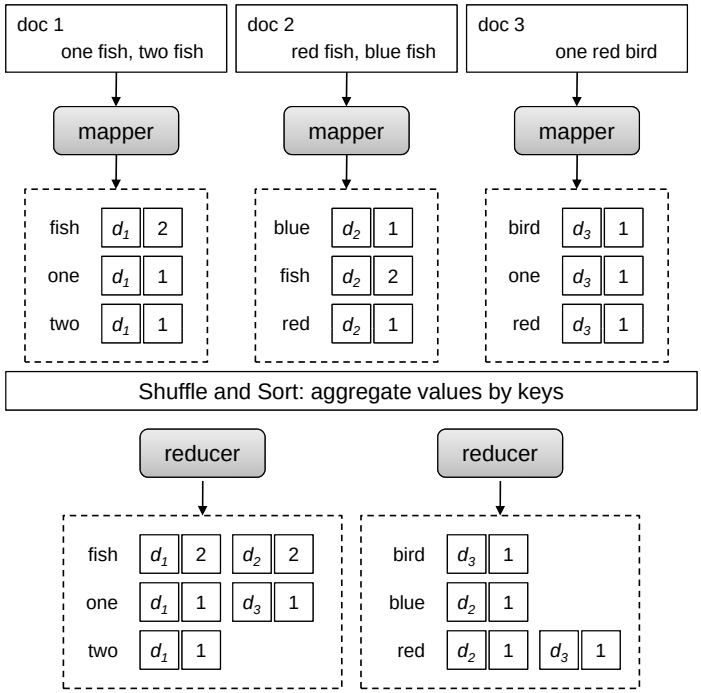


Figure 4.3: Simple illustration of the MapReduce inverted indexing algorithm with three mappers and two reducers. Postings are shown as pairs of boxes (document id, *tf*).

does not need to worry about any of these issues—most of the heavy lifting is performed by the execution framework.

4.3 INVERTED INDEXING: REVISED IMPLEMENTATION

The inverted indexing algorithm presented in the previous section serves as a reasonable baseline. However, there is a significant scalability bottleneck: it assumes that there is sufficient memory to hold all postings associated with the same term, since all postings are buffer in memory prior to being sorted. Since the MapReduce execution framework makes no guarantees about the ordering of values associated with the same key, the reducer must first buffer all postings and then perform an in-memory sort before the postings can be written out to disk. As collections become larger, postings lists will grow longer, and at some point in time, the reducer will run out of memory.

There is a simple solution to this problem. Since the execution framework guarantees that keys arrive at each reducer in sorted order, one way to overcome the scalability

```
1: class Mapper
2:     method Map(docid n, doc d)
3:         H ← new AssociativeArray
4:         for all term t ∈ doc d do
5:             H{t} ← H{t} + 1
6:         for all term t ∈ H do
7:             Emit(tuple ⟨t, n⟩, tf H{t})

1: class Reducer
2:     method Initialize
3:         t_prev ← ∅
4:         P ← new PostingsList
5:     method Reduce(tuple ⟨t, n⟩, tf [f])
6:         if t ≠ t_prev ∧ t_prev ≠ ∅ then
7:             Emit(term t, postings P)
8:             P.Reset()
9:         P.Add(⟨n, f⟩)
10:        t_prev ← t
11:    method Close
12:        Emit(term t, postings P)
```

Figure 4.4: Pseudo-code of a scalable inverted indexing algorithm in MapReduce. This forms the core of the algorithm used in Ivory.

bottleneck is to let the MapReduce runtime do the sorting for us. Instead of emitting key-value pairs of the following type:

$$(\text{term } t, \text{posting } \langle n, f \rangle)$$

We emit intermediate key-value pairs of the type:

$$(\text{tuple } \langle t, n \rangle, \text{tf } f)$$

In other words, the key is a tuple containing the term and the document number, while the value is the term frequency. This is exactly an example of the "value-to-key conversion" design pattern introduced in Chapter 3.4. The programming model ensures that the postings arrive in the correct order. This, combined with the fact that reducers can hold state across multiple keys, allows postings lists to be created with minimal memory usage. As a detail, remember that we must define a custom partitioner to ensure that all tuples with the same term are shuffled to the same reducer.

The revised MapReduce inverted indexing algorithm is shown in Figure 4.4. The mapper remains unchanged for the most part, other than differences in the intermediate

key-value pairs. The Reduce method is called for each key (i.e., $\langle t, n \rangle$), and by design, there will only be one value associated with each key. For each key-value pair, a posting can be directly added to the postings list. Since the postings are guaranteed to arrive in the correct order, they can be incrementally encoded in compressed form—thus ensuring a small memory footprint. Finally, when all postings associated with the same term have been processed (i.e., $t \neq t_{prev}$), the entire postings list is emitted. The final postings list must be written out in the Close method. As with the baseline algorithm, payloads can be easily changed: by simply replacing the intermediate value f (term frequency) with whatever else is desired (e.g., term positional information).

There is one more detail that is omitted in Dean and Ghemawat's original algorithm [31]. Since almost all retrieval models take into account document length, this information also needs to be computed. Although it is straightforward to express this computation as another MapReduce job, this task can actually be folded into the inverted indexing process. When processing the terms in each document, the document length is known, and can be written out as "side data" directly to HDFS. We can take advantage of the ability for a mapper to hold state across the processing of multiple documents in the following manner: an in-memory associative array is created to store document lengths, which is populated as each document is processed.[5] When the mapper finishes processing input records, document lengths are written out to HDFS (i.e., in the Close method). Thus, document length data ends up in m different files, where m is the number of mappers; these files are then consolidated into a more compact representation.

4.4 INDEX COMPRESSION

We return to the question of how postings are actually compressed and stored on disk. Let us consider the canonical case where each posting consists of a document id and the term frequency. A naïve implementation might represent the first as a four-byte integer[6] and the second is represented as a two-byte short. Thus, a postings list might be encoded as follows:

$$[(5, 2), (7, 3), (12, 1), (49, 1), (51, 2), \ldots]$$

where each posting is represented by a pair in parentheses. Note that all brackets, parentheses, and commas are only included to enhance readability; in reality the postings would be represented as a long stream of numbers. This naïve implementation would require six bytes per posting; using this scheme, the entire inverted index wouldn't be that much smaller than the collection itself. Fortunately, we can do significantly better.

[5] In general, there is no worry about insufficient memory to hold these data.
[6] However, note that $2^{32} - 1$ is "only" 4,294,967,295, which isn't sufficient for the entire web.

The first trick is to encode *differences* between document ids as opposed to the document ids themselves. Since the postings are sorted by document ids, the differences (called *d*-gaps) must be positive integers greater than zero. The above postings list, represented in this manner:

$$[(5, 2), (2, 3), (5, 1), (37, 1), (2, 2), \ldots]$$

Of course, we must actually encode the first document id. We haven't lost any information, since the original document ids can be easily reconstructed from the *d*-gaps. However, it's not obvious that we've reduced the space requirements either, since the largest *d*-gap is one less than the number of documents in the collection.

This is where the second trick comes in, which is to represent the *d*-gaps in a way such that it takes less space for smaller numbers. Similarly, we want to apply the same techniques to compress the term frequencies, since for the most part they are also small values. But to understand how this is done, we need to take a detour into compression techniques, particularly for coding integers. Compression, in general, can be characterized as either *loseless* or *lossy*: it's fairly obvious that loseless compression is required in this context.

As a preface, it is important to understand that all compression techniques represent a time–space tradeoff. That is, we reduce the amount of space on disk necessary to store data, but at the cost of extra processor cycles must be spent coding and decoding data. Therefore, it is possible that compression reduces size but also speed, but if the two factors are properly balanced, we can achieve the best of both worlds: smaller *and* faster. This is the case for the integer coding techniques we discuss below.

4.4.1 BYTE-ALIGNED CODES

In most programming languages, an integer is encoded in 4 bytes and holds a value between 0 and $2^{32} - 1$, inclusive.[7] This means that 1 and 4,294,967,295 both occupy four bytes—obviously, encoding *d*-gaps this way doesn't yield any reduce size.

A simple approach to compression is to only use as many bytes as is necessary to represent the integer. This is known as variable-length integer coding and accomplished by using the high order bit of every byte as the *continuation bit*, which is set to 1 in the last byte or zero elsewhere. As a result, we have 7 bits per byte for coding the value, which means that $0 \leq n < 2^7$ can be expressed with 1 byte, $2^7 \leq n < 2^{14}$ with 2 bytes, $2^{14} \leq n < 2^{21}$ with 3, and $2^{21} \leq n < 2^{28}$ with 4 bytes. This scheme can be extended to code arbitrarily-large integers. As a concrete example, the two numbers:

127, 128

would be coded as such:

[7] We limit our discussion to *unsigned* integers, since *d*-gaps are always positive (and greater than zero).

1 1111111 0 0000001 1 0000000

The above code contains two code words, the first consisting of 1 byte, and the second consisting of 2 bytes. Of course, the spaces are there only for readability.

Variable-length integers are byte-aligned because the code words fall along byte boundaries. Since most architectures are optimized to read and write bytes, such schemes are very efficient. Note that with variable-length integer coding there is never any ambiguity about where one code word ends and the next begins.

4.4.2 BIT-ALIGNED CODES

The advantage of byte-aligned codes is that they can be coded and decoded quickly. The downside, however, is that they *must* consume multiples of eight bits, even when fewer bits might suffice. In bit-aligned codes, on the other hand, code words can occupy any number of bits, meaning that boundaries can fall anywhere. Since modern architectures and programming languages are designed around bytes, in practice coding and decoding bit-aligned codes require processing bytes and appropriately shifting or masking bits. Generally, this isn't a big deal, since bit-level operations are fast on modern processors.

One additional challenge with bit-aligned codes is that we need a mechanism to delimit code words, i.e., tell where the last ends and the next begins, since there are no byte boundaries to guide us. To address this issue, most bit-align codes are so-called prefix codes (confusingly, they are also called prefix-free codes), in which no valid code word is a prefix of any other valid code word. For example, coding $0 \leq x < 3$ with $\{0, 1, 01\}$ is not a valid prefix code, since 0 is a prefix of 01, and so we can't tell if 01 is two code words or one. On the other hand, $\{00, 01, 1\}$ is a valid prefix code, such that a sequence of bits:

0001101001010100

can be unambiguously segmented into:

00 01 1 01 00 1 01 01 00

and decoded without any additional delimiters.

One of the simplest prefix codes is unary code. An integer $x > 0$ is coded as $x - 1$ one bits followed by a zero bit. Note that unary codes do not allow the representation of zero, which is fine since d-gaps and term frequencies should never be zero.[8] As an example, 4 in unary code is 1110. With unary code we can code x in x bits, which although economical for small values, becomes inefficient for even moderately large values. Unary codes are rarely used in practice, but form a component of other coding schemes. Unary codes of the first ten positive integers are shown in Figure 4.5.

[8] As a note, different sources describe slightly formulations of the same coding scheme. Here, we adopt the conventions in the classic IR text *Managing Gigabytes* [109].

			Golomb	
x	unary	γ	$b = 5$	$b = 10$
1	0	0	0:00	0:000
2	10	10:0	0:01	0:001
3	110	10:1	0:10	0:010
4	1110	110:00	0:110	0:011
5	11110	110:01	0:111	0:100
6	111110	110:10	10:00	0:101
7	1111110	110:11	10:01	0:1100
8	11111110	1110:000	10:10	0:1101
9	111111110	1110:001	10:110	0:1110
10	1111111110	1110:010	10:111	0:1111

Figure 4.5: The first ten positive integers in unary, γ, and Golomb ($b = 5, 10$) codes.

Elias γ code is an efficient coding scheme that is widely used in practice. A integer $x > 0$ is broken into two components, $1 + \lfloor \log_2 x \rfloor$ ($= n$, the length), which is coded in unary code, and $x - 2^{\lfloor \log_2 x \rfloor}$ ($= r$, the remainder), which is in binary.[9] The unary component n specifies the number of bits required to code x, and the binary component codes the remainder r in $n - 1$ bits. As an example, consider $x = 10$: $1 + \lfloor \log_2 10 \rfloor = 4$, which is 1110. The binary component codes $x - 2^3 = 2$ in $4 - 1 = 3$ bits, which is 010. Putting both together, we arrive at 1110:010.[10] Working in reverse, it is easy to unambiguously decode a bit stream of γ codes: First, we read a unary code c_u, which is a prefix code. This tells us that the binary portion is written in $c_u - 1$ bits, which we then read as c_b. We can then reconstruct x as $2^{c_u - 1} + c_b$. For $x < 16$, γ codes occupy less than a full byte, which makes them more compact than variable-length integer codes. Since term frequencies for the most part are relatively small, γ codes make sense for them and can yield substantial space savings. For reference, the γ codes of the first ten positive integers are shown in Figure 4.5. A variation on γ code is δ code, where the n portion of the γ code is coded in γ code itself (as opposed to unary code). For smaller values γ codes are more compact, but for larger values, δ codes take less space.

Unary and γ codes are parameterless, but even better compression can be achieved with parameterized codes. A good example of this is Golomb codes. For some parameter b, an integer $x > 0$ is coded in two parts: first, we compute $q = \lfloor (x - 1)/b \rfloor$ and encode $q + 1$ in unary; then, we code the remainder $r = x - qb - 1$ in truncated binary. This is accomplished as follows: if b is a power of two, then truncated binary is exactly the

[9] Note that $\lfloor x \rfloor$ is the floor function, which maps x to the largest integer not greater than x, so, e.g., $\lfloor 3.8 \rfloor = 3$. This is the default behavior in many programming languages when casting from a floating-point type to an integer type.

[10] The extra colon is inserted only for readability; it's not part of the final code, of course.

same as normal binary, requiring $\log_2 b$ bits.[11] Otherwise, we code the first $2^{\lfloor \log_2 b \rfloor + 1} - b$ values of r in $\lfloor \log_2 b \rfloor$ bits and code the rest of the values of r by coding $r + 2^{\lfloor \log_2 b \rfloor + 1} - b$ in ordinary binary representation using $\lfloor \log_2 b \rfloor + 1$ bits. In this case, the r is coded in either $\lfloor \log_2 b \rfloor$ or $\lfloor \log_2 b \rfloor + 1$ bits, and unlike ordinary binary coding, truncated binary codes are prefix codes. As an example, if $b = 5$, then r can take the values $\{0, 1, 2, 3, 4\}$, which would be coded with the following code words: $\{00, 01, 10, 110, 111\}$. For reference, Golomb codes of the first ten positive integers are shown in Figure 4.5 for $b = 5$ and $b = 10$. Researchers have shown that Golomb compression works very well for *d*-gaps, and is optimal with the following parameter setting:

$$b \approx 0.69 \times \frac{df}{N} \tag{4.1}$$

where *df* is the document frequency of the term, and N is the number of documents in the collection.[12]

Putting everything together, standard best practices for postings compression is to represent *d*-gaps with Golomb codes and term frequencies with γ codes [109, 112]. If positional information is desired, we can use the same trick to encode differences between positions using γ codes.

4.4.3 POSTINGS COMPRESSION

Having completed our detour into integer compression techniques, we can now return to the scalable inverted indexing algorithm shown in Figure 4.4 and discuss how postings lists can be properly compressed. Coding term frequencies with γ codes is easy since they are parameterless. Compressing *d*-gaps with Golomb codes, however, is a bit tricky, since two parameters are required: the size of the document collection and the number of postings for a particular postings list (i.e., document frequency, or *df*). The first is easy to obtain and can be passed into the reducer as a constant. The *df* of a term, however, is not known until all the postings have been processed—and unfortunately, the parameter must be known before any posting is coded. A two-pass solution that involves first buffering the postings (in memory) would suffer from the memory bottleneck we've been trying to avoid in the first place.

To get around this problem, we need to somehow inform the reducer of a term's *df* before any of its postings arrive. This can be solved with the order inversion design pattern introduced in Chapter 3.3 to compute relative frequencies. The solution is to have the mapper emit special keys of the form $\langle t, * \rangle$ to communicate partial document

[11] This special case is known as Rice codes.

[12] For details as to why this is the case, we refer to reader elsewhere [109], but here's the intuition: under reasonable assumptions, the appearance of postings can be modeled as a sequence of independent Bernoulli trials, which implies a certain distribution of *d*-gaps. From this we can derive an optimal setting of b.

frequencies. That is, inside the mapper, in addition to emitting intermediate key-value pairs of the following form:

$$(\text{tuple } \langle t, n \rangle, \text{tf } f)$$

also emit special intermediate key-value pairs like this:

$$(\text{tuple } \langle t, * \rangle, \text{df } n)$$

In practice, we accomplish this by applying the in-mapper combining design pattern (see Chapter 3.1). The mapper holds an in-memory associative array that keeps track of how many documents a term has been observed in (i.e., the local document frequency of the term for the subset of documents processed by the mapper). Once the mapper has processed all input records, special keys of the form $\langle t, * \rangle$ are emitted with the partial *df* as the value.

To ensure that these special keys arrive first, we define the sort order of the tuple so that the special symbol $*$ precedes all documents (part of the order inversion design pattern). Thus, for each term, the reducer will first encounter the $\langle t, * \rangle$ key, associated with a list of values representing partial *df*s originating from each mapper. Summing all these partial contributions will yield the term's *df*, which can then be used to set the Golomb compression parameter b. This allows the postings to be incrementally compressed as they are encountered in the reducer—memory bottlenecks are eliminated since we do not need to buffer postings in memory.

4.5 WHAT ABOUT RETRIEVAL?

Thus far, we have only focused on MapReduce algorithms for inverted indexing. What about for retrieval? It should be fairly obvious that MapReduce, which was designed for large batch operations, is a poor solution for retrieval. Since users demand sub-second response times, every aspect of retrieval must be optimized for low latency, which is exactly the opposite tradeoff made in MapReduce. Recall the basic retrieval problem: we must look up postings lists corresponding to query terms and systematically traverse those postings lists to compute query–document scores, and then return the top k results to the user. Looking up postings implies random disk seeks, since for the most part postings are too large to fit into memory (leaving aside caching for now). Unfortunately, random access is not a forte of the distributed file system underlying MapReduce—such operations require multiple round-trip network exchanges (and associated latencies). In Hadoop, the client must first obtain the location of the desired data block from the namenode before the correct datanode can be contacted for the actual data (of course, access will typically require a random disk seek on the datanode).

Real-world distributed web search architectures are exceedingly complex and their exact architectures are closely guarded secrets. However, the general strategies employed

to achieve scalability, reliability, and speed are well known. Partitioning and replication are the keys to achieving all three properties. An index of the web is by no means a monolithic entity. It couldn't possibly be: since query evaluation requires looking up and traversing postings lists, running time would grow roughly linearly with size of the document collection. To get around this, search engines must divide up the web in independent, smaller collections—called partitions or shards. Most adopt a two-dimensional partitioning strategy: first, the web is divided into "layers" by document quality; then, each layer is partitioned "vertically" into smaller, more manageable pieces. Retrieval is accomplished by a number of query brokers, which receive requests from the clients, forwards them to servers responsible for each partition, and then assembles the results. Typically, most systems employ a multi-phase strategy that involves searching the top layer of high quality documents first, and then backing off to subsequent layers if no suitable results could be found. Finally, query evaluation can benefit immensely from caching: individual postings or even results of entire queries [7]. This is made possible by the Zipfian distribution of queries, with very frequent queries at the head of the distribution dominating the total number of queries.

On a large-scale, reliability of service is provided by replication, both in terms of multiple machines serving the same partition within a single datacenter, but also replication across geographically-distributed datacenters. This creates at least two query routing problems: since it makes sense to serve clients from the closest datacenter, a service must route queries to the appropriate location. Within a single datacenter, a service needs to properly balance load across replicas. Note that intrinsically, partitioning provides added reliability in the sense that if documents are spread across many partitions, individual failures might not even be noticeable from the user's point of view.

4.6 CHAPTER SUMMARY

The phrase "search the web" is technically inaccurate, in that one actually searches the inverted index constructed from crawling the web. This chapter focused on the problem of how those structures are built.

MapReduce was designed from the very beginning with inverted indexing in mind. Although Dean and Ghemawat's original MapReduce paper [31] sketches an algorithm for this problem, it is lacking in details and suffers from a scalability bottleneck. We present an improvement of the original indexing algorithm that address this scalability bottleneck. An important component of the inverted indexing process is compression of postings lists, which otherwise could grow quite large. Researchers have spent quite some effort exploring different coding schemes, and we present a summary of best practices: use Golomb codes for compressing d-gaps and γ codes for term frequencies and other small values. Finally, we showed how compression can be integrated into a scalable MapReduce algorithm for inverted indexing.

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, social networks (manifest in the flow of email, phone call patterns, connections on social networking sites, etc.), and transportation networks (roads, flight routes, 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 the hyperlink graph, 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 is 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 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.

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

- Graph clustering. Can a large graph be divided into components that are relatively disjoint (for example, as measured by inter-component links)? 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).

- 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 [44].

- 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 everything from jobseekers looking for employment to singles looking for dates.

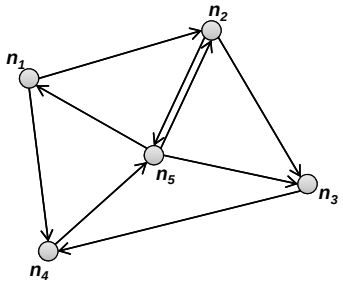
- Maximum flow. In a weighted directed graph with two special nodes called the source and the sink, the max flow problem involves computing the amount of "traffic" that can be sent from source to sink given various flow capacities defined by edge weights. Transportation companies (airlines, shipping, 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 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 (see also another recent article that discusses graph algorithms with MapReduce [27]).[2]

This chapter is organized as follows: we begin in Chapter 5.1 with an introduction to graph representations, and then explore two classic graph algorithms in MapReduce:

[2] As a side note, Google recently published a short description of a system called Pregel [70], based on Valiant's Bulk Synchronous Parallel model [104], for large-scale graph algorithms.



	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 as adjacency lists (right).

parallel breadth-first search (Chapter 5.2) and PageRank (Chapter 5.3). Before concluding with a summary, Chapter 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 i to node 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 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

[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.

web. In this chapter, we assume processing of sparse graphs, although we will return to this issue in Chapter 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. 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.

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 lowest-cost or lowest-weight paths). Such problems are a staple in undergraduate algorithms 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 Figure 5.2, adapted from a classic algorithms textbook often known as *CLR* [28]. 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 priority queue of vertices with priorities equal to their distance d values.

```
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)
```

Figure 5.2: Pseudo-code for Dijkstra's algorithm, which is based on maintaining a priority queue of nodes with priorities equal to their distance from the source node. At each iteration, the algorithm expands the node with the shortest distance and updates distances to all reachable nodes.

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 Figure 5.2 only computes the shortest distances. The actual paths can be recovered by storing "backpointers" for every node indicating a fragment of the shortest path.

An sample trace of the algorithm running on a simple graph is shown in Figure 5.3 (example also adapted from *CLR* [28]). 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 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,

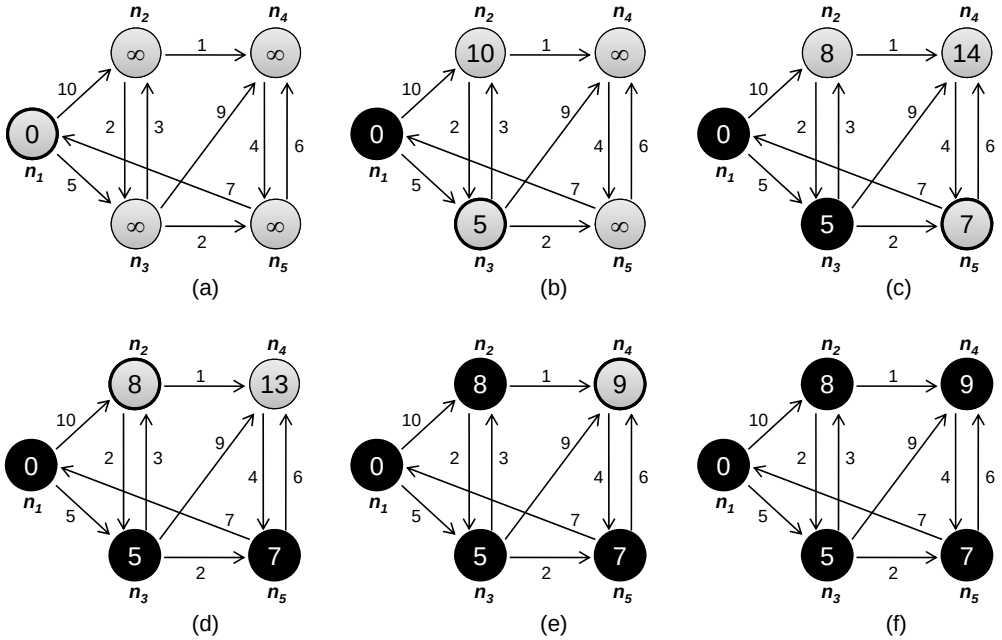


Figure 5.3: Example of Dijkstra's algorithm applied to a simple graph with five nodes, with the n_1 as the source and edge distances as indicated. Parts (a)–(e) show the running of the algorithm at each iteration, with the current distance inside the node. Nodes with thicker borders are those being expanded; nodes that have already been expanded are shown in black.

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 a 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 go through one of the nodes in M that contain an outgoing edge to n: we need to examine all $m \in M$ and find the m_s 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 Figure 5.4. 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

```
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)
```

Figure 5.4: Pseudo-code for parallel breath-first search in MapReduce: 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.

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 I can reach node n with a distance d, then I must be able to reach all the nodes that are connected to n with distance $d + 1$. After shuffle and short, reducers will receive keys corresponding to the destination node ids and distances corresponding to all paths that lead 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 (Figure 5.4, line 4 in the mapper). In the reducer, we must distinguish the node data structure from distance values (Figure 5.4, 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.[4]

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 is 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. 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 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.

[4]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.

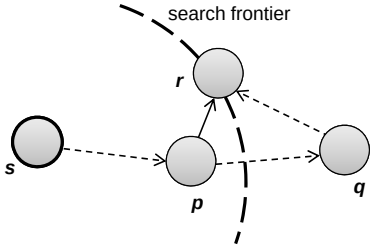


Figure 5.5: In the single source shortest path problem with arbitrary edge distances, the shortest path from source s to node r may go outside the current search frontier, in which case we will not find the shortest distance to r until the search frontier expands to cover q.

Up till 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 Figure 5.4, 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 5.5, 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 discovered yet, since it lies outside the search frontier.[5] 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. In fact, it is not difficult to construct graphs that will elicit this worse case behavior: Figure 5.6 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

[5] 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.

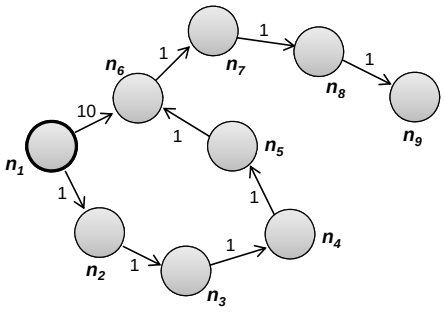


Figure 5.6: A sample graph that elicits worst-case behavior for parallel breadth-first search. Eight iterations are required to discover shortest distances to all nodes.

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 sequential 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.[6] 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 that contains the nodes sorted by distances—this is not possible in MapReduce because the programming model provides no 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:

[6] Unless the algorithm discovers an instance of the situation described in Figure 5.5, in which case, updated distances will propagate inside the search frontier.

- The graph structure is represented as 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 are limited to the 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, while the reducer computation is the Min function. As we will see in the next section, the MapReduce algorithm for PageRank works in much the same way.

5.3 PAGERANK

PageRank [82] 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 room full of web surfing monkeys. Each monkey 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 surfing monkeys. 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 [60] and HITS [56] (also known as "hubs and authorities").

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

But enough about random web surfing monkeys. 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 later on. 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 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 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, [6, 43]). 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

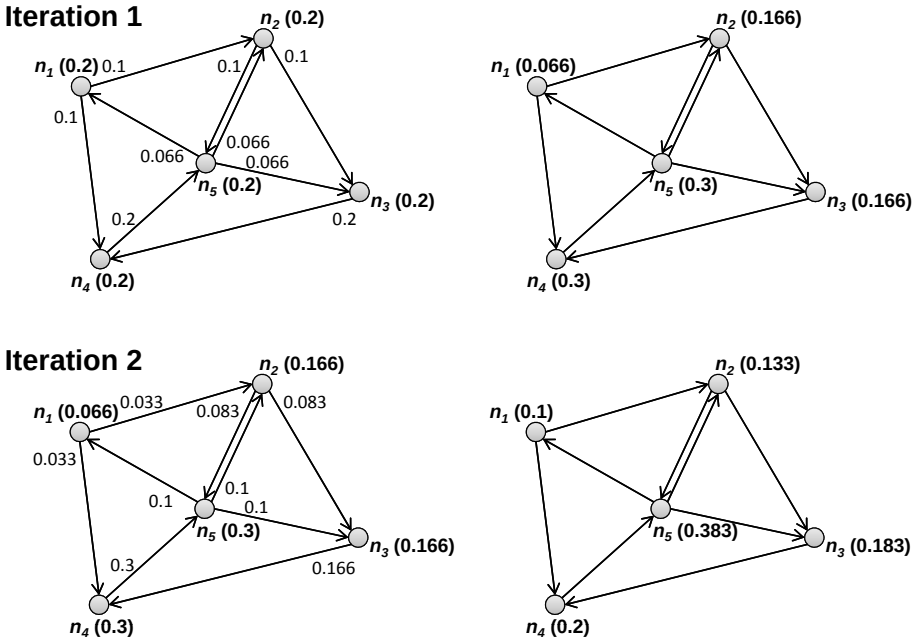


Figure 5.7: PageRank toy example showing two iterations, top and bottom. Left graphs show PageRank values at the beginning of each iteration and how much PageRank mass is passed to each neighbor. Right graphs show updated PageRank values at the end of each iteration.

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 in terms of itself 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 the incoming links. This algorithm iterates until PageRank values don't change anymore.

Figure 5.7 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.

```
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                       ▷ Sums incoming PageRank contributions
9:         M.PageRank ← s
10:        Emit(nid m, node M)
```

Figure 5.8: Pseudo-code for PageRank in MapReduce. 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 in each destination node. Each MapReduce job corresponds to one iteration of the algorithm.

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 monkey is at n_1 with a probability of 0.2, then he 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 Figure 5.8; it is simplified in that we continue to ignore the random jump factor and assume no dangling

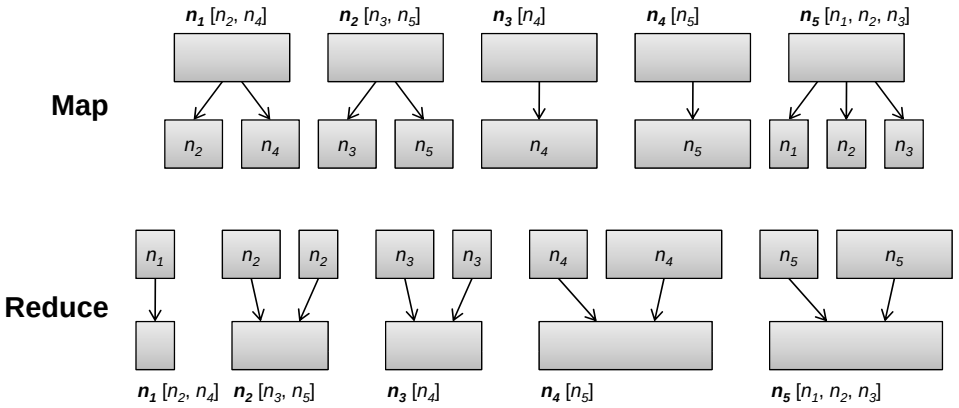


Figure 5.9: Illustration of the MapReduce PageRank algorithm corresponding to the first iteration in Figure 5.7. Size of boxes are proportion to the PageRank values. During the map phase, PageRank mass is distributed evenly to nodes on each node's adjacency list (shown at the very top). Intermediate values are keyed by node (shown in the boxes). In the reduce phase, all partial PageRank contributions are summed together to arrive at updated values.

nodes (complications that we will return to later). An illustration of the running algorithm is shown in Figure 5.9 for the first iteration of the toy graph in Figure 5.7. The algorithm maps over the nodes, and for each node compute 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 been downloaded yet. If we simply run

the algorithm in Figure 5.8 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. We can determine how much missing PageRank mass there is by instrumenting the algorithm in Figure 5.8 with counters: whenever the mapper processes a node with an empty adjacency list, it emits no intermediate key-value pairs, but keeps track of the node's PageRank value in the counter. At the end of the algorithm, we can access the counter to find out how much PageRank mass was lost at all the dangling nodes—this is the amount of mass we must now distribute 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 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. Note that 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 including running a fixed number of iterations (useful if one wishes to bound algorithm running time) or stopping when the *rank* of PageRank values no longer changes. The latter is useful for some applications that only care about comparing the PageRank of two pages and does 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 [82], convergence on a graph with 322 million edges was reached in 52 iterations. 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 work.[7]

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 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 as 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.

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 even the in-mapper combining pattern described in Chapter 3.1, can be used to decrease the running time of graph iterations. It is straightforward to

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

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 a mapper, combiners are useless. This implies that it would be desirable to partition large graphs into smaller components where there are many intra-component links, but fewer inter-component links. This way, we can arrange the data such that nodes in the same components are handled by the same mapper—thus maximizing opportunities for combiners to work.

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 is 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 [76]. For example, in a social network, we might sort nodes representing users by zip code, as opposed to by last name—based on 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. Resorting records using MapReduce is a relatively cheap operation—however, whether the efficiencies gained by this crude form of partitioning is worth the extra time taken in performing the sort is an empirical question that will depend on the actual graph structure and algorithm.

5.5 SUMMARY

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 as 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.

In MapReduce, it is not possible to maintain global data structures accessible and mutable by all the mappers and reducers. One implication of this is that an algorithm

cannot communicate partial results from one arbitrary node to another. Instead, information can only propagate along graph edges—which gives rise to the structure of algorithms discussed above.

CHAPTER 6

EM Algorithms for Text Processing

Until the end of the 1980s, text processing systems tended to rely on large numbers of manually written rules to analyze, annotate, and transform text input, usually in a deterministic way. This rule-based approach can be appealing: a system's behavior can generally be understood and predicted precisely, and, when errors surface, they can be corrected by writing new rules or refining old ones. However, rule-based systems suffer from a number of serious problems. They are brittle with respect to the natural variation found in language, and developing systems that can deal with inputs from diverse domains is very labor intensive. Furthermore, when these systems fail, they often do so catastrophically, unable to offer even a "best guess" as to what the desired analysis of the input might be.

In the last 20 years, the rule-based approach has largely been abandoned in favor of more data-driven methods, where the "rules" for processing the input are inferred automatically from large corpora of examples, called *training data*. The basic strategy of the data-driven approach is to start with a processing algorithm capable of capturing how any instance of the *kinds* of inputs (e.g., sentences or emails) can relate to any instance of the kinds of outputs that the final system should produce (e.g., the syntactic structure of the sentence or a classification of the email as spam). At this stage, the system can be thought of as having the potential to produce any output for any input, but they are not distinguished in any way. Next, a *learning algorithm* is applied which refines this process based on the training data—generally attempting to make the model perform as well as possible at predicting the examples in the training data. The learning process, which often involves iterative algorithms, typically consists of activities like ranking rules, instantiating the content of rule templates, or determining parameter settings for a given model. This is known as *machine learning*, an active area of research.

Data-driven approaches have turned out to have several benefits over rule-based approaches to system development. Since data-driven systems can be trained using examples actual data of the kind that they will eventually be used to process, they tend to deal with the complexities found in real data more robustly than rule-based systems do. Second, developing training data tends to be far less expensive than developing rules. For some applications, significant quantities of training data may even exist for independent reasons (e.g., translations of text into multiple languages are created by authors wishing to reach an audience speaking different languages, not because they are generating training data for a data-driven machine translation system). These advantages come at the cost of systems that often behave internally quite differently than a

human-engineered system. As a result, correcting errors that the trained system makes can be quite challenging.

Data-driven information processing systems can be constructed using variety of mathematical techniques, but in this chapter we focus on *statistical models*, which probabilistically relate inputs from an input set $\mathcal{X}$ (e.g., sentences, documents, etc.), which are always *observable*, to annotations from a set $\mathcal{Y}$, which is the space of possible annotations or analyses that the system should predict. This model may take the form of either a *joint model* $\Pr(x, y)$ which assigns a probability to every pair $\langle x, y \rangle \in \mathcal{X} \times \mathcal{Y}$ or a *conditional model* $\Pr(y|x)$, which assigns a probability to every $y \in \mathcal{Y}$, given an $x \in \mathcal{X}$. For example, to create a statistical spam detection system, we might have $\mathcal{Y} = \{\text{SPAM}, \text{NOTSPAM}\}$ and $\mathcal{X}$ be the set of all possible email messages. For machine translation, $\mathcal{X}$ might be the set of Arabic sentences and $\mathcal{Y}$ the set of English sentences.[1]

There are three closely related, but distinct challenges in statistical text-processing. The first is model selection. This entails selecting a representation of a joint or conditional distribution over the desired $\mathcal{X}$ and $\mathcal{Y}$. For a problem where $\mathcal{X}$ and $\mathcal{Y}$ are very small, one could imagine representing these probabilities in look-up tables. However, for something like email classification or machine translation, where the model space is infinite, the probabilities cannot be represented directly, and must be computed algorithmically. As an example of such models, we introduce *hidden Markov models* (HMMs), which define a joint distribution over sequences of inputs and sequences of annotations. The second challenge is *parameter estimation* or *learning*, which involves the application of a optimization algorithm and training criterion to select the parameters of the model to optimize the model's performance (with respect to the given training criterion) on the training data.[2] The parameters of a statistical model are the values used to compute the probability of some event described by the model. In this chapter we will focus on one particularly simple training criterion for parameter estimation, *maximum likelihood estimation*, which says to select the parameters that make the training data most probable under the model, and one learning algorithm that attempts to meet this criterion, called expectation maximization (EM). The final challenge for statistical modeling is the problem of *decoding*, or, given some x, using the model to select an annotation y. One very common strategy is to select y according to the following criterion:

$$y^* = \arg\max_{y \in \mathcal{Y}} \Pr(y|x)$$

[1] In this chapter, we will consider discrete models only. They tend to be sufficient for text processing, and their presentation is simpler than models with continuous densities. It should be kept in mind that the sets $\mathcal{X}$ and $\mathcal{Y}$ may still be countably infinite.

[2] We restrict our discussion in this chapter to models with finite numbers of parameters and where the learning process refers to setting those parameters. Inference in and learning of so-called *nonparameteric models*, which have an infinite number of parameters and have become important statistical models for text processing in recent years, is beyond the scope of this chapter.

In a conditional (or *direct*) model, this is a straightforward search for the best y under the model. In a joint model, the search is also straightforward, on account of the definition of conditional probability:

$$y^* = \arg\max_{y \in \mathcal{Y}} \Pr(y|x) = \arg\max_{y \in \mathcal{Y}} \frac{\Pr(x, y)}{\sum_{y'} \Pr(x, y')} = \arg\max_{y \in \mathcal{Y}} \Pr(x, y)$$

The specific form that the search takes will depend on how the model is represented. Our focus in this chapter will primarily be on the second problem: learning parameters for models, but we will touch on the third problem as well.

Machine learning is often categorized as either *supervised* or *unsupervised*. Supervised learning of statistical models simply means that the model parameters are estimated from training data consisting of pairs of inputs and annotations, that is $\mathcal{Z} = \langle \langle x_1, y_1 \rangle, \langle x_2, y_2 \rangle, \ldots \rangle$ where $\langle x_i, y_i \rangle \in \mathcal{X} \times \mathcal{Y}$ and y_i is the *gold standard* (i.e., correct) annotation of x_i. While supervised models often attain quite good performance, they are often uneconomical to use, since the training data requires each object that is to be classified (to pick a specific task), x_i to be paired with its correct label, y_i. In many cases, these gold standard training labels must be generated by a process of *expert annotation*, meaning that each x_i must be manually labeled by a trained individual. Even when the annotation task is quite simple for people to carry out (e.g., in the case of spam detection), the number of potential examples that could be classified (representing a subset of $\mathcal{X}$, which may of course be infinite in size) will far exceed the amount of data that can be annotated. As the annotation task becomes more complicated (e.g., when predicting more complicated structures like sequences of labels or when the annotation task requires specialized expertise), annotation becomes far more challenging.

Unsupervised learning, on the other hand, requires only that its training data consist of a representative collection of objects that should be annotated, that is $\mathcal{Z} = \langle x_1, x_2, \ldots \rangle$ where $x_i \in \mathcal{X}$, but *without* any example annotations. While it may at first seem counterintuitive that meaningful annotations can be learned without any examples of the desired annotations being given, the learning criteria and model structure (which crucially define the space of possible annotations, $\mathcal{Y}$ and the process by which annotations relate to observable inputs) make it possible to induce annotations by relying on regularities in the unclassified training instances. While a thorough discussion of unsupervised learning is beyond the scope of this book, we focus on a particular class of algorithms—expectation maximization (EM) algorithms—that can be used to learn the parameters of a joint model $\Pr(x, y)$ from incomplete data (i.e., data where some of the variables in the model cannot be observed; in the case of unsupervised learning, the y_i's are unobserved). Expectation maximization algorithms fit naturally into the MapReduce paradigm, and are used to solve a number of problems of interest in text processing. Furthermore, these algorithms can be quite computationally expen-

sive, since they generally require repeated evaluations of the training data. MapReduce therefore provides an opportunity not only to scale to larger amounts of data, but also to improve efficiency bottlenecks at scales they where non-parallel solutions could be utilized.

This chapter is organized as follows. In Chapter 6.1 we describe maximum likelihood estimation for statistical models, show how this is generalized to models where not all variables are observable, and then describe expectation maximization (EM). We then describe hidden Markov models (HMMs), a very versatile class of models that uses EM for parameter estimation. In Chapter 6.3 we describe how EM algorithms can be expressed in MapReduce, and then in Chapter 6.4 we look at a case study of word alignment for statistical machine translation. We conclude by looking at similar algorithms that are appropriate for supervised learning tasks in Chapter 6.5 and summarizing in Chapter 6.6.

6.1 EXPECTATION MAXIMIZATION

Expectation maximization (EM) algorithms [35] are a family of iterative optimization algorithms for learning probability distributions from incomplete data. They are extensively utilized in statistical natural language processing where one seeks to infer latent linguistic structure from unannotated text. To name just a few applications, EM algorithms have been used to find part-of-speech sequences, constituency and dependency trees, alignments between texts in different languages, alignments between acoustic signals and their transcriptions, as well as for numerous other clustering and structure discovery problems.

Expectation maximization generalizes the principle of maximum likelihood estimation to the case where the values of some variables are unobserved (specifically, those characterizing the latent structure that is sought).

6.1.1 MAXIMUM LIKELIHOOD ESTIMATION

Maximum likelihood estimation (MLE) is a criterion for fitting the parameters θ of a statistical model to some given data $\mathbf{x}$. Specifically, it says to select the parameter settings θ^* such that the likelihood of given of the training data using the model is maximized:

$$\theta^* = \arg\max_{\theta} \Pr(X = \mathbf{x}; \theta) \tag{6.1}$$

To illustrate, consider the simple marble game shown in Figure 6.1. In this game, a marble is released at the position indicated by the black dot, and it bounces down into one of the cups at the bottom of the board, being diverted to the left or right by the peg (indicated by a triangle) in the center. Our task is to construct a model that

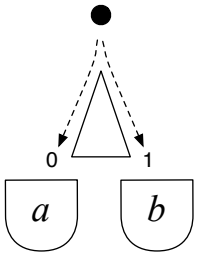


Figure 6.1: A simple marble game where a released marble takes one of two paths. This game that can be modeled using a Bernoulli random variable with parameter p, which indicates the probability that the marble will go to the right when it hits the peg.

predicts into which cup the ball will drop. A "rule-based" approach might be to take exact measurements of the board and construct a physical model that we can use to predict the behavior of the ball. Given sophisticated enough measurements, this could certainly lead to a very accurate model. However, the construction of this model would be quite time consuming and difficult.

A statistical approach, on the other hand, might be to assume that the behavior of a marble in this game be modeled using a Bernoulli random variable Y with parameter p. That is, the value of the random variable indicates whether path 0 or 1 is taken. We also define a random variable X whose value is the label of the cup that a marble ends up in; note that X is deterministically related to Y, so an observation of X is equivalent to an observation of Y.

To estimate the parameter p of the statistical model of our game, we need some *training data*, so we drop 10 marbles into the game which end up in cups $\mathbf{x} = \langle b, b, b, a, b, b, b, b, b, a \rangle$.

What is the maximum likelihood estimate of p given this data? By assuming that our samples are independent and identically distributed (i.i.d.), we can write the likelihood of our data as follows:[3]

$$\begin{aligned} \Pr(\mathbf{x}; p) &= \prod_{i=1}^{10} p^{\delta(x_i, a)} (1-p)^{\delta(x_i, b)} \\ &= p^2 \cdot (1-p)^8 \end{aligned}$$

Since log is a monotonically increasing function, maximizing $\log \Pr(\mathbf{x}; p)$ will give us the desired result. We can do this differentiating with respect to p and finding where

[3]In this equation, δ is the Kroneker delta function which evaluates to 1 where its arguments are equal and 0 otherwise.

the resulting expression equals 0:

$$\begin{aligned} \frac{d \log \Pr(\mathbf{x}; p)}{dp} &= 0 \\ \frac{d[2 \cdot \log p + 8 \cdot \log(1-p)]}{dp} &= 0 \\ \frac{2}{p} - \frac{8}{1-p} &= 0 \end{aligned}$$

Solving for p yields 0.2, which is the intuitive result. Furthermore, it is straightforward to show that in N trials where N_0 marbles followed path 0 to cup a, and N_1 marbles followed path 1 to cup b, the maximum likelihood estimate of p is $N_1/(N_0 + N_1)$.

While this model only makes use of an approximation of the true physical process at work when the marble interacts with the game board, it is an empirical question whether the model works well enough in practice to be useful. Additionally, while a Bernoulli trial is an extreme approximation of the physical process, if insufficient resources were invested in building a physical model, the approximation may perform better than the more complicated "rule-based" model. This sort of dynamic is found often in text processing problems: given enough data, astonishingly simple models can outperform complex knowledge-intensive models that attempt to simulate complicated processes.

6.1.2 A LATENT VARIABLE MARBLE GAME

To see where latent variables might come into play in modeling, consider a more more complicated variant of our marble game shown in Figure 6.2. This version consists of three pegs that influence the marble's path, and the marble may end up in one of three cups. Note that both paths 1 and 2 lead to cup b.

To construct a statistical model of this game, we again assume that the behavior of a marble interacting by a peg can be modeled with a Bernoulli random variable. Since there are three pegs, we have three random variables with parameters $\theta = \langle p_0, p_1, p_2 \rangle$, corresponding to the probabilities that the marble will go to the right at the top, left, and right pegs. We further define a random variable X taking on values from $\{a, b, c\}$ indicating what cup the marble ends in, and Y, taking on values from $\{0, 1, 2, 3\}$ indicating which path was taken. Note that the full joint distribution $\Pr(X = x, Y = y)$ is determined by θ.

How should the parameters θ be estimated? If it were possible to observe the paths taken by marbles as they were dropped into the game, it would be trivial to estimate the parameters for our model using the maximum likelihood estimator—we would simply need to count the number of times the marble bounced left or right at each peg. If N_x counts the number of times a marble took path x in N trials, this is:

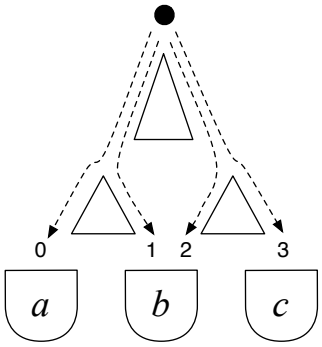


Figure 6.2: A more complicated marble game where the released marble takes one of four paths. We assume that we can only determine which bucket the marble ends up in, not the specific path taken.

$$p_0 = \frac{N_2 + N_3}{N} \qquad p_1 = \frac{N_1}{N_0 + N_1} \qquad p_2 = \frac{N_3}{N_2 + N_3}$$

However, we wish to consider the case where the paths taken are *unobservable* (imagine an opaque sheet covering the center of game board), but where we can see what cup a marble ends in. In other words, we want to consider the case where we have *partial* data. This is exactly the problem encountered in unsupervised learning: there is a statistical model describing the relationship between two sets of variables (X's and Y's), and there is data available from just one of them. Furthermore, such algorithms are quite useful in text processing, where latent variables may describe latent linguistic structures of the observed variables, such as parse trees or part of speech tags, or alignment structures relating sets of observed variables.

6.1.3 MLE WITH LATENT VARIABLES

Formally, we are considering the problem of estimating the parameters for statistical models of the from $\Pr(\mathbf{x}, \mathbf{y}; \theta)$ which describe not only observable variables $\mathbf{x}$ but latent, or hidden, variables $\mathbf{y}$.

In these models, since only $\mathbf{x}$ is observable, we must define our optimization criterion to be the maximization of the *marginal* likelihood, that is, summing over all settings of the latent variables $\mathcal{Y}$:[4]

[4]For this description, we assume that the variables in our model take on discrete values. Not only does this simplify exposition, but discrete models are widely used in text processing.

$$\theta^* = \arg\max_\theta \sum_{\mathbf{y}\in\mathcal{Y}} \Pr(\mathbf{x}, \mathbf{y}; \theta)$$

Unfortunately, in many cases, this maximum cannot be computed analytically, but the iterative hill-climbing approach of expectation maximization can be used instead.

6.1.4 EXPECTATION MAXIMIZATION

Expectation maximization (EM) is an iterative algorithm that finds a successive series of parameter estimates $\theta^{(0)}$, $\theta^{(1)}$, ... that improve the marginal likelihood of the the training data. That is, EM guarantees:

$$\sum_{\mathbf{y}\in\mathcal{Y}} \Pr(\mathbf{x}, \mathbf{y}; \theta^{(i+1)}) \geq \sum_{\mathbf{y}\in\mathcal{Y}} \Pr(\mathbf{x}, \mathbf{y}; \theta^{(i)})$$

The algorithm starts with some initial set of parameters $\theta^{(0)}$ and then updates them using two steps: expectation (E-step), which computes the posterior distribution over the latent variables given the observable data $\mathbf{x}$ and a set of parameters $\theta^{(i)}$,[5] and maximization (M-step), which computes new parameters $\theta^{(i+1)}$ maximizing the expected log likelihood of the joint distribution with respect to the distribution computed in the E-step. The process then repeats with these new parameters. The algorithm terminates when the likelihood remains unchanged.[6] In more detail, the steps are as follows:

E-step. Compute the posterior probability of the hidden variable assignments $\mathbf{y}$ given the observed data $\mathbf{x}$ and the current parameter settings, that is:

$$\Pr(\mathbf{y}|\mathbf{x}; \theta^{(i)}) = \frac{\Pr(\mathbf{x}, \mathbf{y}; \theta^{(i)})}{\sum_{\mathbf{y}'} \Pr(\mathbf{x}, \mathbf{y}'; \theta^{(i)})} \tag{6.2}$$

M-step. New parameter settings that maximize the expected log-probability of the joint distribution according to the conditional distribution given the observed data and current parameters (which was computed in the E-step).

$$\theta^{(i+1)} = \arg\max_\theta \mathbb{E}_{\Pr(\mathbf{y}|\mathbf{x};\theta^{(i)})} \log \Pr(\mathbf{x}, \mathbf{y}; \theta) \tag{6.3}$$

The effective application of EM requires that both the E-step and the M-step consist of tractable computations. Specifically, summing over the space of hidden variable assignments must not be intractable. Depending on the independence assumptions made in

[5] The term 'expectation' is used since the values computed in terms of the posterior distribution $\Pr(\mathbf{y}|\mathbf{x}; \theta^{(i)})$ that are required to solve the M-step have the form of an expectation (with respect to this distribution).

[6] The final solution is only guaranteed to be a *local maximum*, but if the model is fully convex, it will also be the global maximum.

the model, this may be achieved in through techniques such as dynamic programming, but some models may require intractable computations.

6.1.5 AN EM EXAMPLE

Let's look at how to estimate the parameters from our latent variable marble game from Chapter 6.1.2 using EM. We assume training data $\mathbf{x}$ consisting of N observations of X with N_a, N_b, and N_c indicating the number of marbles ending in cups a, b, and c. We start with some parameters $\theta^{(0)} = \langle p_0^{(0)}, p_1^{(0)}, p_2^{(0)} \rangle$ that have been randomly initialized to values between 0 and 1.

E-step. We need to compute the distribution $\Pr(Y|X = \mathbf{x}; \theta^{(i)})$. We first assume that our training samples $\mathbf{x}$ are i.i.d:

$$\Pr(Y|X = \mathbf{x}) = \Pr(Y|X = x) \cdot \frac{N_x}{N}$$

Next, we observe that $\Pr(Y = 0|X = a) = 1$ and $\Pr(Y = 3|X = c) = 1$ since cups a and c fully determine the value of the path variable Y. The posterior probability of paths 1 and 2 are only non-zero when X is b:

$$\Pr(1|b; \theta^{(i)}) = \frac{(1 - p_0^{(i)})p_1^{(i)}}{(1 - p_0^{(i)})p_1^{(i)} + p_0^{(i)}(1 - p_2^{(i)})} \qquad \Pr(2|b; \theta^{(i)}) = \frac{p_0^{(i)}(1 - p_2^{(i)})}{(1 - p_0^{(i)})p_1^{(i)} + p_0^{(i)}(1 - p_2^{(i)})}$$

M-step. We now need to maximize the expectation $\log \Pr(X, Y)$ (which will be a function in terms of the three parameter variables) over the distribution we computed in the E step. The non-zero terms in the expectation are as follows:

X	Y	$\Pr(Y\|X; \theta^{(i)})$	$\log \Pr(X, Y; \theta)$
a	0	N_a/N	$\log(1 - p_0) + \log(1 - p_1)$
b	1	$\Pr(1\|b; \theta^{(i)}) \cdot N_b/N$	$\log(1 - p_0) + \log p_1$
b	2	$\Pr(2\|b; \theta^{(i)}) \cdot N_b/N$	$\log p_0 + \log(1 - p_2)$
c	3	N_c/N	$\log p_0 + \log p_2$

Multiplying across each row and adding from top to bottom yields the expectation we wish to maximize. These can each be optimized independently using differentiation. The resulting optimal values are expressed in terms of the counts in $\mathbf{x}$ and $\theta^{(i)}$:

$$p_0 = \frac{\Pr(2|b; \theta^{(i)}) \cdot N_b + N_c}{N} \qquad p_1 = \frac{\Pr(1|b; \theta^{(i)}) \cdot N_b}{N_a + \Pr(1|b; \theta^{(i)}) \cdot N_b} \qquad p_2 = \frac{N_c}{\Pr(2|b; \theta^{(i)}) \cdot N_b + N_c}$$

It is worth noting that the form of these expressions is quite similar to the fully observed maximum likelihood estimate. However, rather than depending on *exact* path counts, the statistics used are the *expected* path counts, given $\mathbf{x}$ and parameters $\theta^{(i)}$.

Typically, the values computed at the end of the M-step would serve as new parameters for another iteration of EM. However, the example we have presented here is quite simple and the model converges to a global optimum after a single iteration. For most models, EM requires several iterations to converge, and it may not find a global optimum. However, as is often the case, EM only finds a locally optimal solution, so the value of the final parameters depends on the values chose for $\theta^{(0)}$.

6.2 HIDDEN MARKOV MODELS

To give a more substantial and useful example of models whose parameters may be estimated using EM, we turn to hidden Markov models (HMMs). HMMs are models of data that is ordered *sequentially* (temporally, from left to right, etc.), such as words in a sentence, base pairs in a gene, or letters in a word. These simple but powerful models have been used in applications as diverse as speech recognition [54], information extraction [96], gene finding [100], part of speech tagging [30], stock market forecasting [48], and word alignment of parallel (translated) texts [106].

In an HMM, the data being modeled is posited to have been generated from an underlying *Markov process*, which is a stochastic process consisting of a finite set of states where the probability of entering a state at time $t+1$ depends only on the the state of the process at time t [92]. Alternatively, one can view a Markov process as a probabilistic variant of a finite state machine, where transitions are taken probabilistically. The states of this Markov process are, however, not directly observable (i.e., *hidden*). Instead, at each time step, an observable token (e.g., a word, base pair, or letter) is emitted according to a probability distribution conditioned on the identity of the state that the underlying process is in.

A hidden Markov model $\mathcal{M}$ is defined as a tuple $\langle \mathcal{S}, \mathcal{O}, \theta \rangle$. $\mathcal{S}$ is a finite set of states, which generate symbols from a finite observation vocabulary $\mathcal{O}$. Following convention, we assume that variables q, r, and s refer to states in $\mathcal{S}$, and o refers to symbols in the observation vocabulary $\mathcal{O}$. This model is parameterized by the tuple $\theta = \langle A, B, \pi \rangle$ consisting of an $|\mathcal{S}| \times |\mathcal{S}|$ matrix A of *transition probabilities*, where $A_q(r)$ gives the probability of transitioning from state q to state r; an $|\mathcal{S}| \times |\mathcal{O}|$ matrix B of *emission probabilities*, where $B_q(o)$ gives the probability that symbol o will be emitted from state q; and an $|\mathcal{S}|$-dimensional vector π, where π_q is the probability that the process starts in state q.[7] These matrices may be dense, but for many applications sparse

[7] This is only one possible definition of an HMM, but it is one that is useful for many text processing problems. In alternative definitions, initial and final states may be handled differently, observations may be emitted during

parameterizations are useful. We further stipulate that $A_q(r) \geq 0$, $B_q(o) \geq 0$, and $\pi_q \geq 0$ for all q, r, and o, as well as that:

$$\sum_{r \in \mathcal{S}} A_q(r) = 1 \ \forall q \qquad \sum_{o \in \mathcal{O}} B_q(o) = 1 \ \forall q \qquad \sum_{q \in \mathcal{S}} \pi_q = 1$$

A sequence of observations of length τ is generated as follows:

Step 0, let $t = 1$ and select an initial state q according to the distribution π.

Step 1, an observation symbol from $\mathcal{O}$ is emitted according to the distribution B_q.

Step 2, a new q is drawn according to the distribution A_q.

Step 3, t is incremented, if $t \leq \tau$, the process repeats from Step 1.

Since all events generated by this process are conditionally independent, the joint probability of this sequence of observations and the state sequence used to generate it is the product of the individual event probabilities.

Figure 6.3 shows a simple example of a hidden Markov model for part-of-speech tagging, which is the task of assigning to each word in an input sentence its grammatical category (one of the first steps in analyzing textual content). States $\mathcal{S} = \{\text{DET}, \text{ADJ}, \text{NN}, \text{V}\}$ correspond to the parts of speech (determiner, adjective, noun, and verb), and observations $\mathcal{O} = \{\texttt{the}, \texttt{a}, \texttt{green}, \ldots\}$ are a subset of the English words. This example illustrates a key intuition behind many applications of HMMs: states correspond to equivalence classes or clustering of observations, and a single observation type may associated with several clusters (in this example, the word `wash` can be generated by an NN or V, since wash can either be a noun or a verb).

6.2.1 THREE QUESTIONS FOR HIDDEN MARKOV MODELS

There are three fundamental questions associated with hidden Markov models:[8]

1. Given a model $\mathcal{M} = \langle \mathcal{S}, \mathcal{O}, \theta \rangle$, and an observation sequence of symbols from $\mathcal{O}$, $\mathbf{x} = \langle x_1, x_2, \ldots, x_\tau \rangle$, what is the probability that $\mathcal{M}$ generated the data (summing over all possible state sequences, $\mathcal{Y}$)?

$$\Pr(\mathbf{x}) = \sum_{\mathbf{y} \in \mathcal{Y}} \Pr(\mathbf{x}, \mathbf{y}; \theta)$$

2. Given a model $\mathcal{M} = \langle \mathcal{S}, \mathcal{O}, \theta \rangle$ and an observation sequence $\mathbf{x}$, what is the most likely sequence of states that generated the data?

$$\mathbf{y}^* = \arg\max_{\mathbf{y} \in \mathcal{Y}} \Pr(\mathbf{x}, \mathbf{y}; \theta)$$

the transition between states, or continuous-valued observations may be emitted, for example, from a Gaussian distribution.

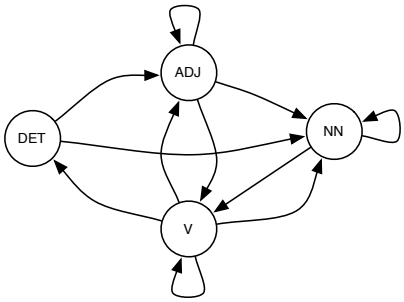
[8]The organization of this section is based in part on ideas from Lawrence Rabiner's HMM tutorial [88].

Initial probabilities:

DET	ADJ	NN	V
0.5	**0.1**	**0.3**	**0.1**

Transition probabilities:

	DET	ADJ	NN	V
DET	**0**	**0**	**0**	**0.5**
ADJ	**0.3**	**0.2**	**0.1**	**0.2**
NN	**0.7**	**0.7**	**0.4**	**0.2**
V	**0**	**0.1**	**0.5**	**0.1**



Emission probabilities:

DET		ADJ		NN		V	
the	**0.7**	**green**	**0.1**	**book**	**0.3**	**might**	**0.2**
a	**0.3**	**big**	**0.4**	**plants**	**0.2**	**wash**	**0.3**
		old	**0.4**	**people**	**0.2**	**washes**	**0.2**
		might	**0.1**	**person**	**0.1**	**loves**	**0.1**
				John	**0.1**	**reads**	**0.19**
				wash	**0.1**	**books**	**0.01**

Example outputs:

John might wash
NN V V

the big green person loves old plants
DET ADJ ADJ NN V ADJ NN

plants washes books books books
NN V V NN V

Figure 6.3: An example HMM that relates part-of-speech tags to vocabulary items in an English-like language. Possible (probability > 0) transitions for the Markov process are shown graphically. In the example outputs, the state sequence corresponding to the emissions is written below the emitted symbols.

3. Given a set of states $\mathcal{S}$, an observation vocabulary $\mathcal{O}$, and a series of ℓ i.i.d. observation sequences $\langle \mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_\ell \rangle$, what are the parameters $\theta = \langle A, B, \pi \rangle$ that maximize the likelihood of the training data?

$$\theta^* = \arg\max_\theta \prod_{i=1}^{\ell} \sum_{\mathbf{y} \in \mathcal{Y}} \Pr(\mathbf{x}_i, \mathbf{y}; \theta)$$

Using our definition of an HMM, the answers to the first two questions are in principle quite trivial to compute: by iterating over all state sequences $\mathcal{Y}$, the probability that each generated $\mathbf{x}$ can be computed by looking up and multiplying the relevant probabilities in A, B, and π, and then summing the result or taking the maximum. And, as we hinted at in the previous section, the third question can be answered using EM. Unfortunately, even with all the distributed computing power MapReduce makes available, we will quickly run into trouble if we try to use this naïve strategy since there are $|\mathcal{S}|^\tau$ distinct state sequences of length τ, making exhaustive enumeration computationally intractable. Fortunately, because the underlying model behaves exactly the same whenever it is in some state, regardless of how it got to that state, we can use *dynamic programming* algorithms to answer all of the above questions without summing over exponentially many sequences.

6.2.2 THE FORWARD ALGORITHM

Given some observation sequence, for example $\mathbf{x} = \langle \texttt{John}, \texttt{might}, \texttt{wash} \rangle$, Question 1 asks what is the probability that this sequence was generated by an HMM $\mathcal{M} = \langle \mathcal{S}, \mathcal{O}, \theta \rangle$. For the purposes of illustration, we assume that $\mathcal{M}$ is defined as shown in Figure 6.3.

There are two possibilities to compute the probability of $\mathbf{x}$ having been generated by $\mathcal{M}$. The first is to compute the sum over the joint probability of $\mathbf{x}$ and every possible labeling $\mathbf{y}' \in \{\langle \textsc{det}, \textsc{det}, \textsc{det} \rangle, \langle \textsc{det}, \textsc{det}, \textsc{nn} \rangle, \langle \textsc{det}, \textsc{det}, \textsc{v} \rangle, \ldots\}$. As indicated above this is not feasible for most sequences, since the set of possible labels is exponential in the length of $\mathbf{x}$.

Fortunately, we can make use of what is known as the *forward algorithm* to compute the desired probability in polynomial time. We assume a model $\mathcal{M} = \langle \mathcal{S}, \mathcal{O}, \theta \rangle$ as defined above. This algorithm works by recursively computing the answer to a related question: what is the probability that the process is in state q at time t and has generated $\langle x_1, x_2, \ldots, x_t \rangle$? Call this probability $\alpha_t(q)$. The $\alpha_t(q)$ is a two dimensional matrix (of size $|\mathbf{x}| \times |\mathcal{S}|$), called a *trellis*. It is easy to see that the values of $\alpha_1(q)$ can be computed as the product of two independent probabilities: the probability of starting in state q and the probability of state q generating x_1:

$$\alpha_1(q) = \pi_q \cdot B_q(x_1)$$

From this, it's not hard to see that the values of $\alpha_2(r)$ for every r can be computed in terms of the $|\mathcal{S}|$ values in $\alpha_1(\cdot)$ and the observation x_2:

$$\alpha_2(r) = B_r(x_2) \cdot \sum_{q \in \mathcal{S}} \alpha_1(q) \cdot A_q(r)$$

This works because there are $|\mathcal{S}|$ different ways to get to state r at time $t = 2$: starting from state $1, 2, \ldots, |\mathcal{S}|$ and transitioning to state r. Furthermore, because a Markov process's behavior is determined only by the state it is in at some time (not by how it got to that state), $\alpha_t(r)$ can always be computed in terms of the $|\mathcal{S}|$ values in $\alpha_{t-1}(\cdot)$ and the observation x_t:

$$\alpha_t(r) \quad = \quad B_r(x_t) \cdot \sum_{q \in \mathcal{S}} \alpha_{t-1}(q) \cdot A_q(r)$$

We have now shown how to compute the probability of being in any state q at any time t using the forward algorithm. The probability of the full sequence is the probability of being in time t and in *any* state, so the answer to Question 1 can be computed simply by summing over α values at time $|\mathbf{x}|$ for all states:

$$\Pr(\mathbf{x}; \theta) = \sum_{q \in \mathcal{S}} \alpha_{|\mathbf{x}|}(q)$$

In summary, there are two ways of computing the probability that a sequence of observations $\mathbf{x}$ was generated by $\mathcal{M}$: exhaustive enumeration and summing and the forward algorithm. Figure 6.4 illustrates the two possibilities. The upper panel shows the naive exhaustive approach, enumerating all 4^3 possible labels $\mathbf{y}'$ of $\mathbf{x}$ and computing their joint probability $\Pr(\mathbf{x}, \mathbf{y}')$. Summing over all $\mathbf{y}'$, the marginal probability of $\mathbf{x}$ is found to be 0.00018. The lower panel shows the forward trellis, consisting of 4×3 cells. Summing over the final column also yields 0.00018.

6.2.3 THE VITERBI ALGORITHM

Given an observation sequence $\mathbf{x}$, the second question we might want to ask of $\mathcal{M}$ is what is the most likely sequence of states that generated the observations. As with the previous question, the naive approach to solving this problem is to enumerate all possible labels and find the one with the highest joint probability. Continuing with the example observation sequence $\mathbf{x} = \langle \texttt{John}, \texttt{might}, \texttt{wash} \rangle$, examining the chart of probabilities in the upper panel of Figure 6.4 shows that $\mathbf{y}^* = \langle \text{NN}, \text{V}, \text{V} \rangle$ is the most likely sequence of states under our example HMM.

However, a more efficient answer to Question 2 can be computed using the same intuition as we used in the forward algorithm: determine the best state sequence for

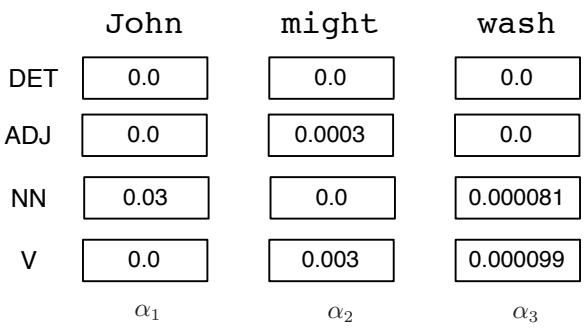
John	might	wash	$p(x,y)$
DET	DET	DET	0.0
DET	DET	ADJ	0.0
DET	DET	NN	0.0
DET	DET	V	0.0
DET	ADJ	DET	0.0
DET	ADJ	ADJ	0.0
DET	ADJ	NN	0.0
DET	ADJ	V	0.0
DET	NN	DET	0.0
DET	NN	ADJ	0.0
DET	NN	NN	0.0
DET	NN	V	0.0
DET	V	DET	0.0
DET	V	ADJ	0.0
DET	V	NN	0.0
DET	V	V	0.0

John	might	wash	$p(x,y)$
ADJ	DET	DET	0.0
ADJ	DET	ADJ	0.0
ADJ	DET	NN	0.0
ADJ	DET	V	0.0
ADJ	ADJ	DET	0.0
ADJ	ADJ	ADJ	0.0
ADJ	ADJ	NN	0.0
ADJ	ADJ	V	0.0
ADJ	NN	DET	0.0
ADJ	NN	ADJ	0.0
ADJ	NN	NN	0.0
ADJ	NN	V	0.0
ADJ	V	DET	0.0
ADJ	V	ADJ	0.0
ADJ	V	NN	0.0
ADJ	V	V	0.0

John	might	wash	$p(x,y)$
NN	DET	DET	0.0
NN	DET	ADJ	0.0
NN	DET	NN	0.0
NN	DET	V	0.0
NN	ADJ	DET	0.0
NN	ADJ	ADJ	0.0
NN	ADJ	NN	0.000021
NN	ADJ	V	0.000009
NN	NN	DET	0.0
NN	NN	ADJ	0.0
NN	NN	NN	0.0
NN	NN	V	0.0
NN	V	DET	0.0
NN	V	ADJ	0.0
NN	V	NN	0.00006
NN	V	V	0.00009

John	might	wash	$p(x,y)$
V	DET	DET	0.0
V	DET	ADJ	0.0
V	DET	NN	0.0
V	DET	V	0.0
V	ADJ	DET	0.0
V	ADJ	ADJ	0.0
V	ADJ	NN	0.0
V	ADJ	V	0.0
V	NN	DET	0.0
V	NN	ADJ	0.0
V	NN	NN	0.0
V	NN	V	0.0
V	V	DET	0.0
V	V	ADJ	0.0
V	V	NN	0.0
V	V	V	0.0

$$\Pr(\mathbf{x}) = \sum_{\mathbf{y} \in \mathcal{Y}} \Pr(\mathbf{x}, \mathbf{y}; \theta) = 0.00018$$



$$\Pr(\mathbf{x}) = \sum_{q \in \mathcal{S}} \alpha_3(q) = 0.00018$$

Figure 6.4: Computing the probability of the sequence $\langle \texttt{John}, \texttt{might}, \texttt{wash} \rangle$ under the HMM given in Figure 6.3 by explicitly summing over all sequence labels (upper panel) and using the forward algorithm (lower panel).

a short sequence and extend this to easily compute the best sequence for longer ones. This is known as the Viterbi algorithm. We define $\gamma_t(q)$, the Viterbi probability, to be the most probable sequence of states of ending in state q at time t and generating observations $\langle x_1, x_2, \ldots, x_t \rangle$. Since we wish to be able to reconstruct the sequence of states, we define $bp_t(q)$, the "backpointer", to be the state used in this sequence at time $t-1$. The base case for the recursion is as follows (the state index of -1 is used as a place-holder since there is no previous best state at time 1):

$$\begin{aligned} \gamma_1(q) &= \pi_q \cdot B_q(x_1) \\ bp_1(q) &= -1 \end{aligned}$$

The recursion is similar to that of the forward algorithm, except rather than summing over previous states, the *maximum* value of all possible trajectories into state r at time t is computed. Note that the backpointer just records the index of the originating state—a separate computation is not necessary.

$$\begin{aligned} \gamma_t(r) &= \max_{q \in \mathcal{S}} \gamma_{t-1}(q) \cdot A_q(r) \cdot B_r(x_t) \\ bp_t(r) &= \arg\max_{q \in \mathcal{S}} \gamma_{t-1}(q) \cdot A_q(r) \cdot B_r(x_t) \end{aligned}$$

To compute the best sequence of states, $\mathbf{y}^*$, the state with the highest probability best path at time $|\mathbf{x}|$ is selected, and then the backpointers are followed, recursively, to construct the rest of the sequence:

$$\begin{aligned} y^*_{|\mathbf{x}|} &= \arg\max_{q \in \mathcal{S}} \gamma_{|\mathbf{x}|}(q) \\ y^*_{t-1} &= bp_t(y_t) \end{aligned}$$

Figure 6.5 illustrates a Viterbi trellis, including backpointers that has been used to compute the most likely state sequence.

6.2.4 PARAMETER ESTIMATION FOR HMMS

We now turn to the Question 3: given a set of states $\mathcal{S}$ and observation vocabulary $\mathcal{O}$, what are the parameters $\theta^* = \langle A, B, \pi \rangle$ that maximize the likelihood of a set of training examples, $\langle \mathbf{x}_1, \mathbf{x}_2, \ldots, \mathbf{x}_\ell \rangle$?[9] Since our model is constructed in terms of variables whose values we cannot observe (the state sequence) in the training data, we may train it to optimize the marginal likelihood (summing over *all* state sequences) of $\mathbf{x}$ using EM. Deriving the EM update equations requires only the application of the techniques

[9]Since an HMM models sequences, its training data consists of a collection of example sequences.

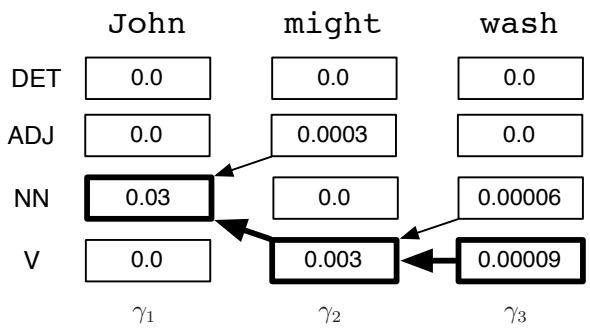


Figure 6.5: Computing the most likely state sequence that generated ⟨`John`, `might`, `wash`⟩ under the HMM given in Figure 6.3 using the Viterbi algorithm. The most likely state sequence is highlighted in bold and could be recovered programmatically by following backpointers from the maximal probability cell in the last column to the first column.

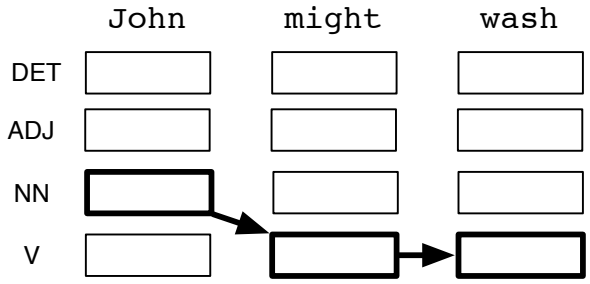


Figure 6.6: A "fully observable" HMM training instance. The output sequence is at the top of the figure, and the states used are shown in the trellis below.

presented earlier in this chapter and some differential calculus. However, since the formalism is cumbersome, we will skip a detailed derivation, but readers interested in more information can find it in the relevant citations [54, 88].

In order to make the update equations as intuitive as possible, consider a fully observable HMM, that is, one where both the emissions and the state sequence are observable in all ℓ training instances. In this case, a training instance can be depicted as shown in Figure 6.6. When this is the case, such as when we have a corpus of sentences in which all words have already been tagged with their parts of speech, the maximum likelihood estimate for the parameters can be computed in terms of the counts of the number of times the process transitions from state q to state r in all training instances, $T(q \rightarrow r)$, and the number of times that state q emits symbol o, $O(q \uparrow o)$, and the

number of times the process starts in state q, $I(q)$. In this example, the process starts in state NN, there is one NN $\rightarrow$ V transition, one V $\rightarrow$ V transition, NN emits `John`, and V emits `might` and `wash`. We also define $N(q)$ to be the number of times the process enters state q. The maximum likelihood estimates of the parameters in the fully observable case are:

$$\pi_q = \frac{I(q)}{\ell = \sum_r I(r)} \qquad A_q(r) = \frac{T(q \rightarrow r)}{N(q) = \sum_{r'} T(q \rightarrow r')} \qquad B_q(o) = \frac{O(q \uparrow o)}{N(q) = \sum_{o'} O(q \uparrow o')} \tag{6.4}$$

For example, to compute the emission parameters from state NN, we simply need to keep track of the number of times process is in state NN and what symbol it generates at each of these times. Transition probabilities are computed similarly: to compute, for example, the distribution $A_{\text{DET}}(\cdot)$, that is, the probabilities of transitioning away from state DET, we count the number of times the process is in state DET, and keep track of what state it transitioned into at the next time step. This counting and normalizing be accomplished using the exact same counting and relative frequency algorithms that we described in Chapter 3.3. Thus, in the fully observable case, parameter estimation is not a new algorithm at all, but one we have seen before.

How should the model parameters be estimated when the state sequence is not provided? It turns out that the update equations have the satisfying form where the optimal parameter values for iteration $i + 1$ are expressed in terms of the *expectations* of the counts referenced in the fully observed case, according to the posterior distribution over the latent variables given the observations $\mathbf{x}$ and the parameters $\theta^{(i)}$:

$$\pi_q = \frac{\mathbb{E}[I(q)]}{\ell} \qquad A_q(r) = \frac{\mathbb{E}[T(q \rightarrow r)]}{\mathbb{E}[N(q)]} \qquad B_q(o) = \frac{\mathbb{E}[O(q \uparrow o)]}{\mathbb{E}[N(q)]} \tag{6.5}$$

Because of the independence assumptions made in the HMM, the update equations consist of $2 \cdot |\mathcal{S}| + 1$ independent optimization problems, just as was the case with the 'observable' HMM. Solving for the initial state distribution, π, is one problem; there are $|\mathcal{S}|$ solving for the transition distributions $A_q(\cdot)$ from each state q; and $|\mathcal{S}|$ solving for the the emissions distributions $B_q(\cdot)$ from each state q. Furthermore, we note that the following must hold:

$$\mathbb{E}[N(q)] = \sum_{r \in \mathcal{S}} \mathbb{E}[T(q \rightarrow r)] = \sum_{o \in \mathcal{O}} \mathbb{E}[O(q \uparrow o)]$$

As a result, the optimization problems (i.e., Equations 6.4) require completely independent sets of statistics, which we will utilize later to facilitate efficient parallelization in MapReduce.

How can the expectations in Equation 6.5 be understood? In the fully observed training case, between every time step, there is exactly one transition taken and the

source and destination state are observable. By progressing through the Markov chain, we can let each transition count as '1', and we can accumulate the total number of times each kind of transition was taken (by each kind, we simply mean the number of times that one state follows another, for example, the number of times NN follows DET). These statistics can then in turn be used to compute the MLE for an 'observable' HMM, as described above. However, when the transition sequence is not observable (as is most often the case), we can instead imagine that at each time step, *every* possible transition (there are $|\mathcal{S}|^2$ of them, and typically $|\mathcal{S}|$ is quite small) is taken, with a particular probability. The probability used is the *posterior probability* of the transition, given the model and an observation sequence (we describe how to compute this value below). By summing over all the time steps in the training data, and using this probability as the 'count' (rather than '1' as in the observable case), we compute the *expected count* of the number of times a particular transition was taken, given the training sequence. Furthermore, since the training instances are statistically independent, the value of the expectations can be computed by processing each training instance independently and summing the results.

Similarly for the necessary emission counts (the number of times each symbol in $\mathcal{O}$ was generated by each state in $\mathcal{S}$), we assume that any state could have generated the observation. We therefore must compute the probability of being in every state at each time point, which is then the size of the emission 'count'. By summing over all time steps we compute the expected count of the number of times that a particular state generated a particular symbol. These two sets of expectations, which are written formally here, are sufficient to execute the M-step.

$$\mathbb{E}[O(q \uparrow o)] = \sum_{i=1}^{|\mathbf{x}|} \Pr(y_i = q|\mathbf{x};\theta) \cdot \delta(x_i, o) \tag{6.6}$$

$$\mathbb{E}[T(q \rightarrow r)] = \sum_{i=1}^{|\mathbf{x}|-1} \Pr(y_i = q, y_{i+1} = r|\mathbf{x};\theta) \tag{6.7}$$

Posterior probabilities. The expectations necessary for computing the M-step in HMM training are sums of probabilities that a particular transition is taken, given an observation sequence, and that some state emits some observation symbol, given an observation sequence. These are referred to as posterior probabilities, indicating that they are the probability of some event whose distribution we have a prior belief about, after addition evidence (here, the model parameters characterize our prior beliefs, and the observation sequence is the evidence) has been taken into consideration. Both posterior probabilities can be computed by combining the forward probabilities, $\alpha_t(\cdot)$, which give the probability of reaching some state at time t, by any path, and gen-

erating the observations $\langle x_1, x_2, \ldots, x_t \rangle$, with *backward probabilities*, $\beta_t(\cdot)$, which give the probability of starting in some state at time t and generating the rest of the sequence $\langle x_{t+1}, x_{t+2}, \ldots, x_{|\mathbf{x}|} \rangle$, using any sequence of states to do so. The algorithm for computing the backward probabilities is given below. Once the forward and backward probabilities have been computed, the state transition posterior probabilities and the emission posterior probabilities can be written as follows:

$$\Pr(y_i = q|\mathbf{x};\theta) = \alpha_i(q) \cdot \beta_i(q) \quad (6.8)$$

$$\Pr(y_i = q, y_{i+1} = r|\mathbf{x};\theta) = \alpha_i(q) \cdot A_q(r) \cdot B_r(x_{i+1}) \cdot \beta_{i+1}(r) \quad (6.9)$$

Equation 6.8 is the probability being state q at time i, given $\mathbf{x}$, and the correctness of the expression should be relatively clear from the definitions of forward and backward probabilities. The intuition for Equation 6.9, the probability of taking a particular transition at a particular time, is also not complicated: it is the product of four conditionally independent probabilities, the probability of getting to state q at time i, having generated the first part of the sequence, the probability of taking transition $q \rightarrow r$ (which is specified in in the parameters, θ), the probability of generating x_{i+1} from state r (also specified in θ), and the probability of generating the rest of the sequence, along any path. A visualization of the quantities used in computing this probability is shown in Figure 6.7. In this illustration, we assume an HMM with $\mathcal{S} = \{\mathrm{s}_1, \mathrm{s}_2, \mathrm{s}_3\}$ and $\mathcal{O} = \{\mathtt{a}, \mathtt{b}, \mathtt{c}\}$.

The backward algorithm. Like the forward and Viterbi algorithms introduced above to answer Questions 1 and 2, the backward algorithm uses dynamic programming to incrementally compute $\beta_t(\cdot)$. Its base case starts at time $|\mathbf{x}|$, and is defined as follows:

$$\beta_{|\mathbf{x}|}(q) = 1$$

To understand intuition for this base case, keep in mind that since the backward probabilities $\beta_t(\cdot)$ are the probability of generating the remainder of the sequence *after* time t (as well as being in some state), and since there is nothing left to generate after time $|\mathbf{x}|$, the probability must be 1. The recursion is defined as follows:

$$\beta_t(q) = \sum_{r \in \mathcal{S}} \beta_{t+1}(r) \cdot A_q(r) \cdot B_r(x_{t+1})$$

Unlike the forward and Viterbi algorithms, the backward algorithm is computed from right to left and makes no reference to the start probabilities, π.

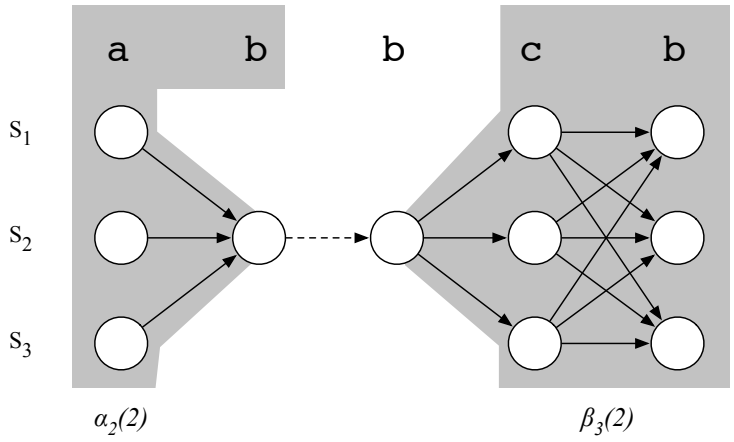


Figure 6.7: Using forward and backward probabilities to compute the posterior probability of the dashed transition, given the observation sequence `a b b c b`. The shaded area on the left corresponds to the forward probability $\alpha_2(\mathrm{S}_2)$, and the shaded area on the right corresponds to the backward probability $\beta_3(\mathrm{S}_2)$.

6.2.5 FORWARD-BACKWARD TRAINING: SUMMARY

In the preceding section, we have shown how to compute all quantities needed to find the parameter settings $\theta^{(i+1)}$ using EM training with a hidden Markov model $\mathcal{M} = \langle \mathcal{S}, \mathcal{O}, \theta^{(i)} \rangle$. To recap: each training instance $\mathbf{x}$ is processed independently, using the parameter settings of the current iteration, $\theta^{(i)}$. For each $\mathbf{x}$ in the training data, the forward and backward probabilities are computed using the algorithms given above (for this reason, this training algorithm is often referred to as the forward-backward algorithm). The forward and backward probabilities are in turn used to compute expected number of times the underlying Markov process enters into each state, the number of times each state generates each output type, and the number of times each state transitions into each other state. These expectations are summed over all training instances, completing the E-step. The M-step involves normalizing the expected counts computed in the E-step using the calculations in Equation 6.5, which yields $\theta^{(i+1)}$. The process then repeats from the E-step using the new parameters. The number of iterations required for convergence but depends on the quality of the initial parameters, and the complexity of the model. For some applications, only a handful of iterations are used, whereas for others, hundreds may be required.

Practical considerations. HMMs have a non-convex likelihood surface (meaning that if has the equivalent of many hills and valleys in the number of dimensions corre-

sponding to the number of parameters in the model). As a result, EM training is only guaranteed to find a local maximum, and the quality of the learned model may vary considerably, depending on the initial parameters that are used. Strategies for optimal selection of initial parameters depend on the phenomena being modeled. Additionally, if some parameter is assigned a probability of 0 (either as an initial value or during one of the M-step parameter updates), EM will never change this in future iterations. This can be useful, since it provides a way of constraining the structures of the Markov model; however, one must be aware of this behavior.

Another pitfall to be avoided when implementing HMMs is arithmetic underflow. HMMs typically define a massive number of sequences, and so the probability of any one of them is often vanishingly small—so small that they often underflow standard floating point representations. A very common solution to this problem is to represent probabilities using their logarithms (since probabilities are always non-negative, this is well defined). Note that expected counts do not typically have this problem and can be represented using normal floating point numbers. When probabilities are stored as logs, the product of two values is computed simply by adding them together. However, addition of probabilities is also necessary—we are, after all, summing over all settings of the latent variables! It 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 also include a `log1p` function which computes $\log(1 + x)$ with higher precision than the naive implementation would have when x is very small (such as it often is when working with probabilities). Its use may further improve the accuracy of implementations that use log probabilities.

6.3 EM IN MAPREDUCE

Expectation maximization algorithms fit quite naturally into the MapReduce paradigm. Although the model being optimized determines the details of the the required computations, MapReduce instantiations of EM algorithms have a number of characteristics:

- Each iteration of EM is one MapReduce job.
- A controlling process (i.e., driver program) spawns the MapReduce jobs, keeps track of the number of iterations and convergence criteria.
- Model parameters $\theta^{(i)}$, which are static for the duration of the MapReduce job, are loaded by each mapper from HDFS or other data provider.
- Mappers map over independent training instances, computing partial latent variable posteriors (or summary statistics, such as expected counts).

- Reducers sum together the required training statistics *and* solve one or more of the M-step optimization problems.
- Combiners, which sum together the training statistics, are often quite effective at reducing the amount of data that must be written to disk.

The degree of parallelization that can be attained depends on the statistical independence assumed in the model and in the derived quantities required to solve the optimization problems in the M-step. Since parameters are estimated from a collection of samples that are assumed to be i.i.d., the E-step can generally be parallelized effectively since every training instance can be processed independently of the others. In the limit, in fact, each independent training instance could be processed by a separate mapper!

Reducers, however, must aggregate the statistics necessary to solve the optimization problems as required by the model. The degree to which these may be solved independently depends on the structure of the model, and this constrains the number of reducers that may be used. Fortunately, many common models require solving several independent optimization problems in the M-step. In this situation, a number of reducers may be run in parallel. Still, it is possible that in the worst case, the M-step optimization problem will not decompose into independent subproblems, making it necessary to use only a single reducer.

6.3.1 HMM TRAINING IN MAPREDUCE

As we would expect, the training of hidden Markov models parallelizes well in MapReduce. The process can be summarized as follows: in each iteration, mappers process training instances, emitting expected event counts computed using the forward-backward algorithm introduced in Chapter 6.2.4. Reducers aggregate the expected counts, completing the E-step, and then generate parameter estimates for the upcoming iteration using the updates given in Equation 6.5.

This parallelization strategy is effective for several reasons. First, the majority of the computational effort in HMM training is the running of the forward and backward algorithms. Since there is no limit on the number of mappers that may be run, the full computational resources of a cluster may be brought to bear to solve this problem. Second, since the M-step of an HMM training iteration with $|\mathcal{S}|$ states in the model consists of $2 \cdot |\mathcal{S}| + 1$ independent optimization problems that require non-overlapping sets of statistics, this may be exploited to let as many as $2 \cdot |\mathcal{S}| + 1$ reducers run in parallel. While the optimization problem is computationally trivial, being able to reduce in parallel helps avoid the data bottleneck that would harm performance if only a single reducer is used.

The quantities that are required to solve the M-step optimization problem are quite similar to the relative frequency estimation example discussed in Chapter 3.3; however, rather than counts of observed events, we aggregate *expected* counts of events.

As a result of the similarity, we can employ the *stripes* representation for aggregating sets of related values, as described in Chapter 3.2. A *pairs* approach that requires less memory at the cost of slower performance is also feasible.

HMM training mapper. The pseudo-code for the HMM training mapper is given in Figure 6.8. The input consists of key-value pairs that are pairs of an opaque id and a value that is a training instance (e.g., a sentence). For each training instance, $2n + 1$ stripes are emitted with unique keys, and every training instance emits the same set of keys. Each unique key corresponds to one of the independent optimization problems that will be solved in the M-step. The outputs are:

1. the probabilities that unobserved Markov process begins in each state q, with a unique key designating that the values are initial state counts;

2. the expected number of times that state q generated each emission symbol o (the set of emission symbols included will be just those found in each training instance $\mathbf{x}$), with a key indicating that the associated value is a set of *emission* counts from state q; and

3. the expected number of times state q transitions to each state r, with a key indicating that the associated value is a set of *transition* counts from state q.

HMM training reducer. The reducer for one iteration of HMM training, shown together with an optional combiner in Figure 6.9, aggregates the count collections associated for each key by summing them. When the values for each key have been completely aggregated, the associative array contains all of the statistics necessary to compute a subset of the parameters for the next EM iteration. The optimal parameter settings for the following iteration are computed simply by computing the relative frequency of each event with respect to its expected count at the current iteration. The new computed parameters are emitted from the reducer and will be written to HDFS. Note that they will be spread across $2 \cdot |\mathcal{S}| + 1$ keys, representing initial state probabilities, π, transition probabilities, A_q for each state q, and emission probabilities, B_q for each state q.

6.4 CASE STUDY: WORD ALIGNMENT FOR STATISTICAL MACHINE TRANSLATION

To illustrate the real-world benefits of using MapReduce to solve EM problems, we turn to the problem of word alignment, which is an important task in statistical machine

```
1: class Mapper
2:     method Initialize(integer iteration)
3:         ⟨S, O⟩ ← ReadModel
4:         θ ← ⟨A, B, π⟩ ← ReadModelParams(iteration)
5:     method Map(sample id, sequence x)
6:         α ← Forward(x, θ)                                  ▷ cf. Section 6.2.2
7:         β ← Backward(x, θ)                                 ▷ cf. Section 6.2.4
8:         I ← new AssociativeArray                           ▷ Initial state expectations
9:         for all q ∈ S do                                   ▷ Loop over states
10:            I{q} ← α_1(q) · β_1(q)
11:        O ← new Vector of AssociativeArray                 ▷ Emission expectations
12:        for t = 1 to |x| do                                ▷ Loop over observations
13:            for all q ∈ S do                               ▷ Loop over states
14:                O[q]{x_t} ← O[q]{x_t} + α_t(q) · β_t(q)
15:            t ← t + 1
16:        T ← new Vector of AssociativeArray                 ▷ Transition expectations
17:        for t = 1 to |x| − 1 do                            ▷ Loop over observations
18:            for all q ∈ S do                               ▷ Loop over states
19:                for all r ∈ S do                           ▷ Loop over states
20:                    T[q]{r} ← T[q]{r} + α_t(q) · A_q(r) · B_r(x_{t+1}) · β_{t+1}(r)
21:            t ← t + 1
22:        Emit(string 'initial', stripe I)
23:        for all q ∈ S do                                   ▷ Loop over states
24:            Emit(string 'emit from ' + q, stripe O[q])
25:            Emit(string 'transit from ' + q, stripe T[q])
```

Figure 6.8: Pseudo-code for a mapper for EM training for hidden Markov models. Mappers map over training instances, that is, sequences of observations $\mathbf{x}_i$, and generate the expected counts of initial states, emissions, and transitions taken to generate the sequence.

translation that is typically solved using models whose parameters are learned with EM.

We begin by giving a brief introduction to statistical machine translation and the phrase-based translation approach; for more a comprehensive introduction, refer to [57, 69]. Fully automated translation has been studied since the earliest days of electronic computers. After the successes with code-breaking during Word War II, there was considerable optimism that translation would be another soluble problem. In the early years, work on translation was dominated by manual attempts to encode linguistic

```
1: class Combiner
2:     method Combine(string t, stripes [C_1, C_2, ...])
3:         C_f ← new AssociativeArray
4:         for all stripe C ∈ stripes [C_1, C_2, ...] do
5:             Sum(C_f, C)
6:         Emit(string t, stripe C_f)
```

```
1: class Reducer
2:     method Reduce(string t, stripes [C_1, C_2, ...])
3:         C_f ← new AssociativeArray
4:         for all stripe C ∈ stripes [C_1, C_2, ...] do
5:             Sum(C_f, C)
6:         z ← 0
7:         for all ⟨k, v⟩ ∈ C_f do
8:             z ← z + v
9:         P_f ← new AssociativeArray                ▷ Final parameters vector
10:        for all ⟨k, v⟩ ∈ C_f do
11:            P_f{k} ← v/z
12:        Emit(string t, stripe P_f)
```

Figure 6.9: Pseudo-code for the reducer for EM training for HMMs. The HMMs considered in this book are fully parameterized by multinomial distributions, so reducers do not require special logic to handle different kinds of model parameters since they are all of the same type.

knowledge into computers—another instance of the 'rule-based' approach we described in the introduction to this chapter. These early attempts failed to live up to the admittedly optimistic expectations. For a number of years, the idea of fully automated translation was viewed with skepticism. Not only was constructing a translation system labor intensive, but translation pairs had to be worked on independently, meaning that improvements in a Russian-English translation system could not often be leveraged to improve a French-English system.

After languishing for a number of years, the field was reinvigorated in the late 1980s when researchers at IBM pioneered the development of *statistical machine translation* (SMT), which took a data-driven approach to solving the problem of machine translation, attempting to improve both the quality of translation while reducing the cost of developing systems [20]. The core idea of SMT is to equip the computer to *learn* how to translate, using example translations which are produced for other purposes, and modeling the process as a statistical process with some parameters θ relating strings

in a source language (typically denoted as $\mathbf{f}$) to strings in a target language (typically denoted as $\mathbf{e}$):

$$\mathbf{e}^* = \arg\max_{\mathbf{e}} \Pr(\mathbf{e}|\mathbf{f};\theta)$$

With the statistical approach, translation systems can be developed cheaply and quickly for any language pair, as long as there is sufficient training data available. Furthermore, improvements in learning algorithms and statistical modeling can yield benefits in many translation pairs at once, rather than being specific to individual language pairs. Thus, SMT, like many other topics we are considering in this book, is an attempt to leverage the vast quantities of textual data that is available to solve problems that would otherwise require considerable manual effort to encode specialized knowledge. Since the advent of statistical approaches to translation, the field has grown tremendously and numerous statistical models of translation have been developed, with many incorporating quite specialized knowledge about the behavior of natural language as biases in their learning algorithms.

6.4.1 STATISTICAL PHRASE-BASED TRANSLATION

One approach to statistical translation that is simple yet powerful is called *phrase-based translation* [58]. We provide a rough outline of the process since it is representative of most state-of-the-art statistical translation systems (such as the one used inside Google translate). Phrase-based translation works by learning how strings of words, called *phrases*, translate between languages.[10] Example phrase pairs for Spanish-English translation might include $\langle$*los estudiantes*, *the students*$\rangle$, $\langle$*los estudiantes*, *some students*$\rangle$, and $\langle$*soy*, *i am*$\rangle$. From a few hundred thousand sentences of example translations, many millions of such phrase pairs may be automatically learned. The starting point is typically a parallel corpus (also called *bitext*), which contains *pairs* of sentences in two languages that are translations of each other.[11] The parallel corpus is then annotated with *word alignments*, which indicate which words in one language correspond to words in the other. By using these word alignments as a skeleton, phrases can be extracted from the sentence that is likely to preserve the meaning relationships represented by the word alignment. While an explanation of the process is not necessary here, we mention it as a motivation for learning a word alignment, which we show below how to compute with EM. After phrase extraction, each phrase pair is associated with a number of scores which, taken together, are used to compute the phrase translation probability, a conditional probability that reflecting how likely the source phrase is to

[10] Phrases are simply sequences of words; they are not required to correspond to the definition of a phrase in any linguistic theory.

[11] Parallel corpora are frequently generated as the byproduct of an organization's effort to disseminate information in multiple languages, for example, proceedings of the Canadian Parliament in French and English, and text generated by the United Nations in many different languages.

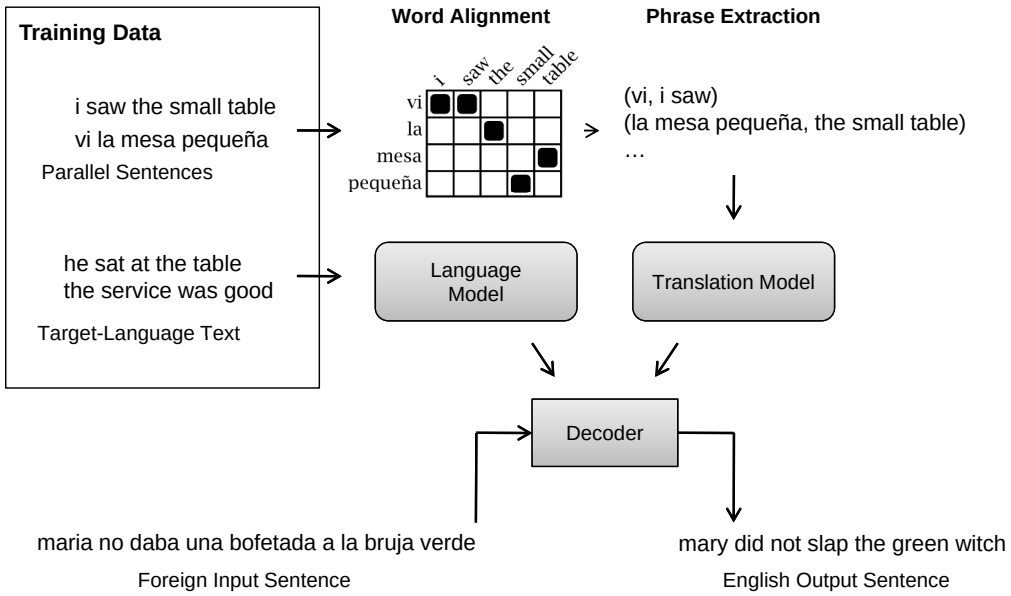


Figure 6.10: The standard phrase-based machine translation architecture. The translation model is constructed from phrases extracted from a word-aligned parallel corpus. The language model is estimated from a monolingual corpus. Both serve as input to the decoder, which performs the actual translation.

translate into the target phrase. We briefly note that although EM could be utilized to learn the phrase translation probabilities, this is not typically done in practice since the maximum likelihood solution turns out to be quite bad for this problem. The collection of phrase pairs and their scores are referred to as the *translation model*. In addition to the translation model, phrase-based translation depends on a *language model*, which gives the probability of a string in the target language. The translation model attempts to preserve meaning during the translation processing, and the target language model is supposed to ensure that the out put is fluent and grammatical. The phrase-based translation process is summarized in Figure 6.10.

A language model gives the probability that a string of words $\mathbf{w} = \langle w_1, w_2, \ldots, w_n \rangle$, written as w_1^n for short, is a string in the target language. By the chain rule of probability, we get:

$$\Pr(w_1^n) = \Pr(w_1)\Pr(w_2|w_1)\Pr(w_3|w_1^2)\ldots\Pr(w_n|w_1^{n-1}) = \prod_{k=1}^{n}\Pr(w_k|w_1^{k-1}) \qquad (6.10)$$

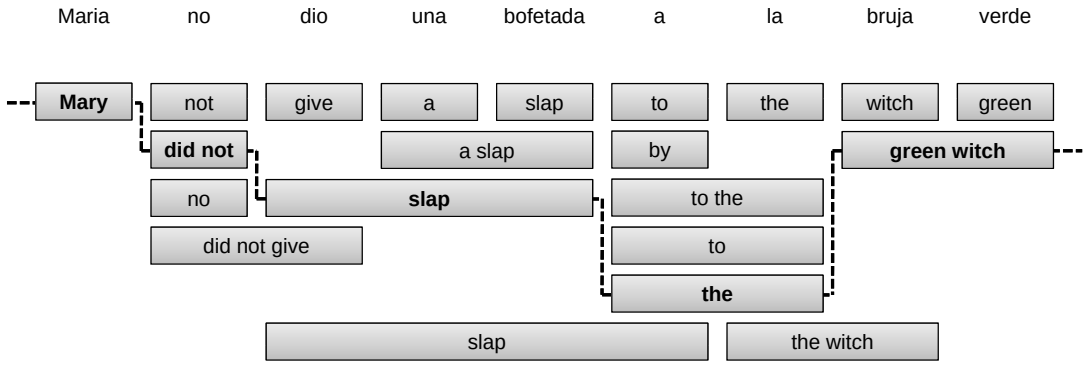


Figure 6.11: Translation coverage of the sentence *Maria no dio una bofetada a la bruja verde* by a phrase-based model. One possible translation path is indicated with a dashed line.

Due to extremely large number of parameters involved in estimating such a model directly, it is customary to make the *Markov assumption*, that the sequence histories only depends on prior local context. That is, an n-gram language model is equivalent to a *(n-1)th*-order Markov model. Thus, we can approximate $P(w_k|w_1^{k-1})$ as follows:

$$\text{bigrams:} \quad P(w_k|w_1^{k-1}) \approx P(w_k|w_{k-1}) \tag{6.11}$$
$$\text{trigrams:} \quad P(w_k|w_1^{k-1}) \approx P(w_k|w_{k-1}w_{k-2}) \tag{6.12}$$
$$n\text{-grams:} \quad P(w_k|w_1^{k-1}) \approx P(w_k|w_{k-n+1}^{k-1}) \tag{6.13}$$

The probabilities used in computing $\Pr(w_1^n)$ based on an n-gram language model are generally estimated from a monolingual corpus of target language text. Since only target language text is necessary (without any additional annotation), language modeling has been well served by large-data approaches that take advantage of the vast quantities of text available on the web.

To translate an input sentence $\mathbf{f}$, the phrase-based *decoder* creates a matrix of all translation possibilities of all substrings in the input string, as an example illustrates in Figure 6.11. A sequence of phrase pairs is selected such that each word in $\mathbf{f}$ is translated exactly once.[12] The decoder seeks to find the translation that maximizes the product of the translation probabilities of the phrases used and the language model probability of the resulting string in the target language. Because the phrase translation probabilities are independent of each other, and the Markov assumption made in the language model, this may be done efficiently using dynamic programming. For a detailed introduction to phrase-based decoding, we refer the reader to a recent textbook by Koehn [57].

[12]The phrases must not necessarily be selected in a strict left-to-right order (being able to vary the order of the phrases used is necessary since languages may express the same ideas using different word orders).

6.4.2 BRIEF DIGRESSION: LANGUAGE MODELING WITH MAPREDUCE

Statistical machine translation provides the context for a brief digression on distributed parameter estimation for language models using MapReduce, and provides another example illustrating the effectiveness data-driven approaches in general. We briefly touched upon this work in Chapter 1. Even after making the Markov assumption, training n-gram language models still requires estimating an enormous number of parameters: potentially V^n, where V is the number of words in the vocabulary. For higher-order models (e.g., 5-grams) used in real-world applications, the number of parameters can easily exceed the number of words from which to estimate those parameters. In fact, most n-grams will never be observed in a corpus, no matter how large. To cope with this sparseness, researchers have developed a number of smoothing techniques [73], which all share the basic idea of moving probability mass from observed to unseen events in a principled manner. For many applications, a state-of-the-art approach is known as Kneser-Ney smoothing [24].

In 2007, Brants et al. [16] reported experimental results that answered an interesting question: given the availability of large corpora (i.e., the web), could a simpler smoothing strategy, applied to more text, beat Kneser-Ney in a machine translation task? It should come as no surprise that the answer is *yes*. Brants et al. introduced a technique known as "stupid backoff" that was exceedingly simple and so naïve that the resulting model didn't even define a valid probability distribution (it assigned "scores" as opposed to probabilities). The simplicity, however, afforded an extremely scalable implementations in MapReduce. With smaller corpora, stupid backoff didn't work as well as Kneser-Ney in generating accurate and fluent translations. However, as the amount of data increased, the gap between stupid backoff and Kneser-Ney narrowed, and eventually disappeared with sufficient data. Furthermore, with stupid backoff it was possible to train a language model on more data than was feasible with Kneser-Ney smoothing. Applying this language model to a machine translation task yielded better results than a (smaller) language model trained with Kneser-Ney smoothing.

The role of the language model in statistical machine translation is to select fluent, grammatical translations from a large hypothesis space: the more training data a language model has access to, the better its description of relevant language phenomena and hence its ability to select good translations. Once again, large data triumphs! For more information about estimating language models using MapReduce, we refer the reader to a forthcoming book from Morgan & Claypool [17].

6.4.3 WORD ALIGNMENT

Word alignments, which are necessary for learning phrase-based translation models (as well as many other more sophisticated translation models), can be learned automatically using EM. In this section, we introduce a popular alignment model based on HMMs.

In the statistical model of word alignment considered here, the observable variables are the words in the source and target sentences (conventionally written using the variables $\mathbf{f}$ and $\mathbf{e}$, respectively), and their alignment is a latent variable. To make this model tractable, we assume that words are translated independently of one another, which means that the model's parameters include the probability of any word in the source language translating to any word in the target language. While this independence assumption is problematic in many ways, it results in a simple model structure that admits efficient inference yet produces reasonable alignments. Alignment models that make this assumption generate a string $\mathbf{e}$ in the target language by selecting words in the source language according to a lexical translation distribution. The indices of the words in $\mathbf{f}$ used to generate each word in $\mathbf{e}$ are stored in an alignment variable, $\mathbf{a}$.[13] This means that the variable a_i indicates the source word position of the i^{th} target word generated, and $|\mathbf{a}| = |\mathbf{e}|$. Using these assumptions, the probability of an alignment and translation can be written as follows:

$$\Pr(\mathbf{e}, \mathbf{a}|\mathbf{f}) = \underbrace{\Pr(\mathbf{a}|\mathbf{f}, \mathbf{e})}_{\text{Alignment probability}} \times \underbrace{\prod_{i=1}^{|\mathbf{e}|} \Pr(e_i|f_{a_i})}_{\text{Lexical probability}}$$

Since we have parallel corpora consisting of only $\langle \mathbf{f}, \mathbf{e} \rangle$ pairs, we can learn the parameters for this model using EM and treating $\mathbf{a}$ as a latent variable. However, to combat data sparsity in the alignment probability, we must make some further simplifying assumptions. By letting the probability of an alignment depend only on the position of the previous aligned word we capture a valuable insight (namely, that words that are nearby in the source language will tend to be nearby in the target language), and our model acquires the structure of an HMM [106]:

$$\Pr(\mathbf{e}, \mathbf{a}|\mathbf{f}) = \underbrace{\prod_{i=1}^{|\mathbf{e}|} \Pr(a_i|a_{i-1})}_{\text{Transition probability}} \times \underbrace{\prod_{i=1}^{|\mathbf{e}|} \Pr(e_i|f_{a_i})}_{\text{Emission probability}}$$

This model can be trained using the forward-backward algorithm described in the previous section, summing over all settings of $\mathbf{a}$, and the best alignment for a sentence pair can be found using the Viterbi algorithm.

To properly initialize this HMM, it is conventional to further simplify the alignment probability model, and use this simpler model to learn initial lexical translation

[13] In the original presentation of statistical lexical translation models, a special null word is added to the source sentences, which permits words to be inserted 'out of nowhere'. Since this does not change any of the important details of the training, we omit it from our presentation for simplicity of presentation.

(emission) parameters for the HMM. The favored simplification is to assert that all alignments are uniformly probable:

$$\Pr(\mathbf{e}, \mathbf{a}|\mathbf{f}) = \frac{1}{|\mathbf{f}|^{|\mathbf{e}|}} \times \prod_{i=1}^{|\mathbf{e}|} \Pr(e_i|f_{a_i})$$

This model is known as IBM Model 1. It is attractive for initialization because it is convex everywhere, and therefore EM will learn the same solution regardless of initialization. Finally, while the forward-backward algorithm could be used to compute the expected counts necessary for training this model ($A_q(r)$ would just be set to a fixed value for all q and r), the uniformity assumption means that the expected emission counts can be estimated in time $O(|\mathbf{e}| \cdot |\mathbf{f}|)$, rather than time $O(|\mathbf{e}| \cdot |\mathbf{f}|^2)$ required by the forward-backward algorithm.

6.4.4 EXPERIMENTS

We now compare the training time of a highly optimized C++ implementation of an HMM word aligner called Giza++ that runs on a single core [79] with our own Java-based Hadoop implementation (these results were previously reported elsewhere [38]). Training time is shown for both Model 1 and the HMM alignment model on the optimized, single-core implementation in Figure 6.12. There are three things to observe. First, the running time scales linearly with the size of the training data. Second, the HMM is a constant factor slower than Model 1. Third, the alignment process is quite slow as the size of the training data grows. At one million sentences, a single iteration takes over three hours to complete!

In Figure 6.13 we plot the average running time of our MapReduce implementation running on a cluster consisting of 19 slave nodes, each with 2 cores. For reference, we plot points indicating what 1/38 of the running time of the Giza++ iterations would be at each data size, which gives a rough indication of what an 'ideal' parallelization could achieve, assuming that there was no overhead associated with distributing computation across these machines. Three things may be observed in the results. First, as the amount of data increases, the relative cost of the overhead of the overhead associated with distributing data, marshaling and aggregating counts, decreases. At one million sentence pairs of training data, the HMM alignment iterations begin to approach optimal runtime efficiency. Second, Model 1, which we observe is light on computation, does not approach the theoretical performance of an ideal parallelization, and in fact, has almost the same running time as the HMM alignment algorithm. We conclude that the overhead associated with distributing and aggregating data is significant compared to the Model 1 computations, although a comparison with Figure 6.12 indicates that the MapReduce implementation is still substantially faster than the single core implementation, at least

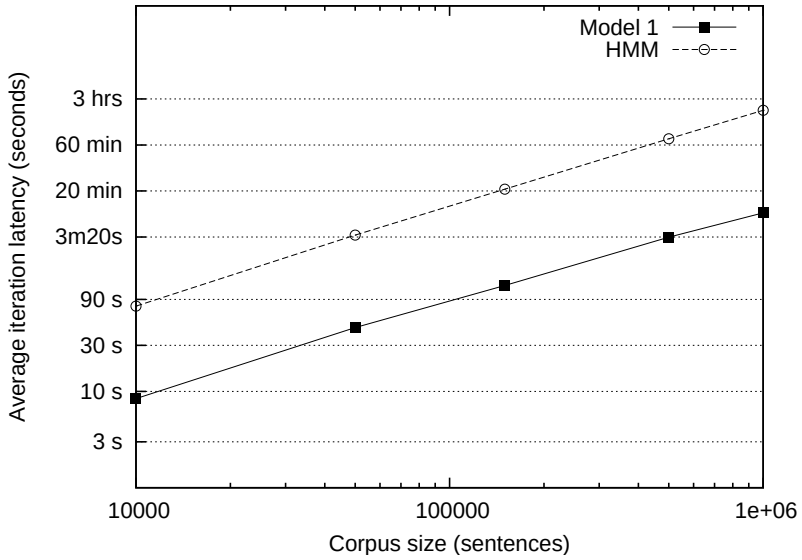


Figure 6.12: Running times of Giza++ for Model 1 and HMM training iterations at various corpus sizes.

once a certain training data size is reached. Finally, we note that, in comparison to the running times of the single-core implementation, at large data sizes, there is a significant advantage to using the distributed implementation, even of Model 1.

Why are these results important? Perhaps the most significant reason is that the quantity of parallel data that is available to train statistical machine translation models is ever increasing, and as is the case with so many problems we have encountered, more data leads to improvements in translation quality [38]. Recently a corpus of 1 billion words of French-English data was mined automatically from the web and released publicly [22].[14] Single core solutions to model construction simply cannot keep pace with the amount of translated data that is constantly being produced. Fortunately, we have shown that existing modeling algorithms can be expressed naturally and effectively using MapReduce, which means that we can take advantage of this data. Furthermore, our results show that even at data sizes that may be tractable on single machines, significant performance improvements are attainable using MapReduce implementations. This improvement reduces experimental turnaround times, which allows researchers to more quickly explore the solution space—which will, we hope, lead to rapid new developments in statistical machine translation.

[14] http://www.statmt.org/wmt10/translation-task.html

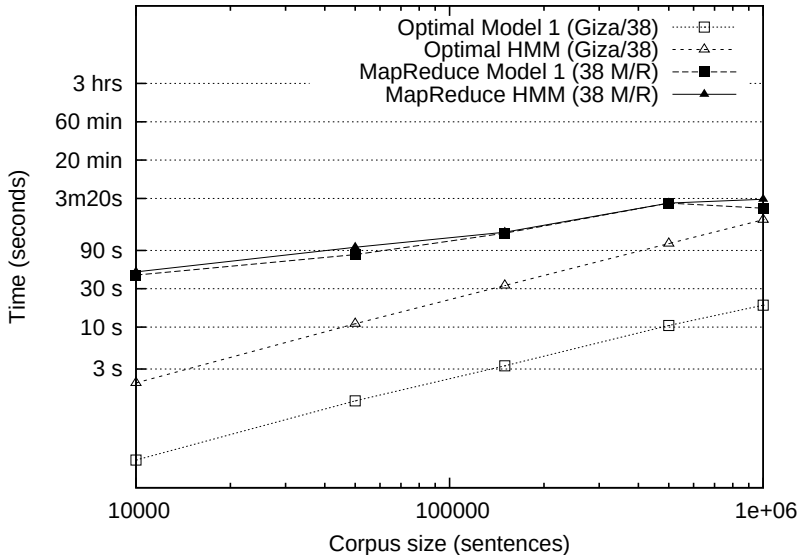


Figure 6.13: Running time for our MapReduce implementation of Model 1 and HMM training iterations at various corpus sizes. For an reference, the 1/38 running time of the Giza++ runtime is shown.

For the reader interested in statistical machine translation, there is an open source Hadoop-based MapReduce implementation of a training pipeline for phrase-based translation that includes word alignment, phrase extraction, and phrase scoring [40].

6.5 EM-LIKE ALGORITHMS

This chapter has focused on expectation maximization algorithms and their realization in the MapReduce programming paradigm. These important algorithms are indispensable for learning models with latent structure from unannotated data, and they can be implemented quite naturally in MapReduce. We now explore some related learning algorithms that are similar to EM but can be used to solve more general problems, and discuss their implementation.

In this section we focus on *gradient-based optimization*, which refers to a class of techniques used to optimize any objective function, provided it is differentiable with respect to the parameters being optimized. Gradient-based optimization is particularly useful in the learning of maximum entropy (maxent) [77] and conditional random field (CRF) [59] models that have a exponential form and are trained to maximize conditional likelihood. In addition to being widely used supervised classification models in text processing (meaning that during training, both the data and its annotation must be

observable), their gradients take the form of expectations. As a result, the techniques, such as the forward-backward algorithm we developed for computing expected values for EM in models with certain independence assumptions, can be reused in the optimization of these models.

6.5.1 GRADIENT-BASED OPTIMIZATION AND LOG-LINEAR MODELS

Gradient-based optimization refers to a class of iterative optimization algorithms that use the derivatives of a function to find the parameters that yield a minimal or maximal value of that function. Obviously, these algorithms are only applicable in cases where a useful objective exists, is differentiable, and its derivatives can be efficiently evaluated. Fortunately, this is the case for many important problems of interest in text processing. For the purposes of this discussion, we will give examples in terms of minimizing functions.

Assume that we have some real-valued function $F(\theta)$ where θ is a k-dimensional vector and that F is differentiable with respect to θ. Its gradient is defined as:

$$\nabla F(\theta) = \left\langle \frac{\partial F}{\partial \theta_1}(\theta), \frac{\partial F}{\partial \theta_2}(\theta), \ldots, \frac{\partial F}{\partial \theta_k}(\theta) \right\rangle$$

The gradient has two crucial properties that are exploited in gradient-based optimization. First, the gradient ∇F is a vector field that points in the direction of the greatest increase of F and whose magnitude indicates the rate of increase. Second, if θ^* is a (local) minimum of F, then the following is true:

$$\nabla F(\theta^*) = 0$$

An extremely simple gradient-based minimization algorithm produces a series of parameter estimates $\theta^{(1)}, \theta^{(2)}, \ldots$ by starting with some initial parameter settings $\theta^{(1)}$ and updating parameters through successive iterations according to the following rule:

$$\theta^{(i+1)} = \theta^{(i)} - \eta^{(i)} \nabla F(\theta^{(i)}) \tag{6.14}$$

The parameter $\eta^{(i)} > 0$ is a learning rate which indicates how quickly the algorithm moves along the gradient during iteration i. Provided this value is small enough so that F decreases, this strategy will find a local minimum of F; however, while simple, this update strategy may converge slowly, and proper selection of η is non-trivial. More sophisticated algorithms perform updates that are informed by approximations of the second derivative, which are estimated by successive evaluations of $\nabla F(\theta)$, and can converge much more rapidly [68].

Gradient-based optimization in MapReduce. Gradient-based optimization algorithms can often be implemented effectively in MapReduce. Like EM, where the

structure of the model determines the specifics of the realization, the details of the function being optimized determines how it should best be implemented, and not every function optimization problem will be a good fit for MapReduce. Nevertheless, MapReduce implementations of gradient-based optimization tend to have the following characteristics:

- Each optimization iteration is one MapReduce job.
- The objective should decompose linearly across training instances. This implies that the gradient also decomposes linearly, and therefore mappers can process materials in parallel. The values they emit are pairs $\langle F(\theta), \nabla F(\theta) \rangle$ that are linear components of the objective and gradient.
- Evaluation of the function and its gradient should be computationally expensive because they require processing lots of data. This make parallelization with MapReduce worthwhile.
- Whether more than one reducer can run in parallel depends on the specific optimization algorithm being used. Some, like the trivial algorithm of Equation 6.14 treat the dimensions of θ independently, whereas many are sensitive to global properties of $\nabla F(\theta)$. In the latter case, only a single reducer may be run.
- Reducer(s) sum the component objective/gradient pairs, computing the total objective and gradient and run the optimization algorithm and emitting $\theta^{(i+1)}$.
- Many optimization algorithms are stateful and must persist their state between optimization iterations. This may either be emitted together with $\theta^{(i+1)}$ or written to the distributed file system as a side effect of the reducer. Such external side effects must be handled carefully; refer to Chapter 2.2 for a discussion.

Parameter learning for log-linear models. Gradient-based optimization techniques can be quite effectively used to learn the parameters of probabilistic models with a log-linear parameterization [71]. While a comprehensive introduction to these models is beyond the scope of this book, such models are used extensively in text processing applications, and their training using gradient-based optimization, which can otherwise be computationally quite expensive, can be implemented effectively using MapReduce. We therefore include a brief summary.

Log-linear models are particularly useful for *supervised* learning (unlike the unsupervised models learned with EM), where an annotation $\mathbf{y} \in \mathcal{Y}$ is available for every $\mathbf{x} \in \mathcal{X}$ in the training data. In this case, it is possible to directly model the conditional distribution of label given input:

$$\Pr(\mathbf{y}|\mathbf{x};\theta) = \frac{\exp \sum_i \theta_i \cdot H_i(\mathbf{x},\mathbf{y})}{\sum_{\mathbf{y}'} \exp \sum_i \theta_i \cdot H_i(\mathbf{x},\mathbf{y}')}$$

In this expression, H_i are real-valued functions sensitive to features of the input and labeling. The parameters of the model may be selected so as to minimize the negative conditional log likelihood of a set of training instances $\langle \langle \mathbf{x},\mathbf{y} \rangle_1, \langle \mathbf{x},\mathbf{y} \rangle_2, \ldots \rangle$, which we assume to be i.i.d.:

$$F(\theta) = \sum_{\langle \mathbf{x},\mathbf{y} \rangle} -\log \Pr(\mathbf{y}|\mathbf{x};\theta) \tag{6.15}$$

$$\theta^* = \arg\min_{\theta} F(\theta) \tag{6.16}$$

As Equation 6.15 makes clear, the objective decomposes linearly across training instances, meaning it can be optimized quite well in MapReduce. The gradient derivative of F with respect to θ_i can be shown to have the following form [98]:[15]

$$\frac{\partial F}{\partial \theta_i}(\theta) = \sum_{\langle \mathbf{x},\mathbf{y} \rangle} \left[H_i(\mathbf{x},\mathbf{y}) - \mathbb{E}_{\Pr(\mathbf{y}'|\mathbf{x};\theta)}[H_i(\mathbf{x},\mathbf{y}')] \right]$$

The expectation in the second part of the gradient's expression can be computed using a variety of techniques. However, as we saw with EM, when very large event spaces are being modeled, as is the case when with sequence labeling, enumerating all possible values $\mathbf{y}$ can become computationally intractable. And, as was the case with HMMs, Independence assumptions can be used to enable efficient computation using dynamic programming. In fact, the forward-backward algorithm introduced in Chapter 6.2.4 can, with only minimal modification, be used to compute the expectation $\mathbb{E}_{\Pr(\mathbf{y}'|\mathbf{x};\theta)}[H_i(\mathbf{x},\mathbf{y}')]$ needed in CRF sequence models, as long as the feature functions respect the same Markov assumption that is made in HMMs. For more information about inference in CRFs using the forward-backward algorithm, we refer the reader to Sha et al. [97].

As we saw in the previous section, MapReduce offers significant speed ups when training iterations require running the forward-backward algorithm, and the same pattern of results holds when training linear CRFs.

6.6 SUMMARY

This chapter has focused on learning the parameters of statistical models from data, using expectation maximization algorithms or gradient-based optimization techniques. We focused especially on EM algorithms for three reasons. First, these algorithms can be expressed naturally in the MapReduce programming model, making them a good

[15] This assumes that when $\langle \mathbf{x},\mathbf{y} \rangle$ is present the model is fully observed; i.e., there are no additional latent variables.

example of how to express a commonly-used algorithm in this new paradigm. Second, many models, such as the widely-used hidden Markov model (HMM), that are trained using EM make independence assumptions that permit an high degree of parallelism to be used during both the E- and M-steps, making them particularly well-positioned to take advantage of large clusters. Finally, EM algorithms are *unsupervised* learning algorithms, which means that they have access to far more training data than comparable supervised approaches. This is quite important. In Chapter 1, when we hailed large data as the "rising tide that lifts all boats" to yield more effective algorithms, we were mostly referring to unsupervised approaches, given that manual effort required to generate annotated data remains a bottleneck in many supervised approaches. Data acquisition for unsupervised algorithms is often as simple as crawling specific web sources, given the enormous quantities of data available "for free". This, combined with the ability of MapReduce to process large datasets in parallel, provides researchers with an effective strategy for developing increasingly-effective applications.

Since EM algorithms are relatively expensive computationally, even for small amounts of data, this led us to consider how related supervised learning models (which typically have much less training data available), can also be implemented in MapReduce. The discussion demonstrates that not only does MapReduce provide a means for coping with ever-increasing amounts of data, but it is also useful for parallelizing expensive computations. Although MapReduce has been designed with mostly data-intensive applications in mind, the ability to leverage clusters of commodity hardware to parallelize computationally-expensive algorithms is an important use case.

CHAPTER 7

Closing Remarks

The need to process enormous quantities of data has never been greater. Not only are terabyte- and petabyte-scale datasets rapidly becoming commonplace, but there is consensus that great value lies buried in them, waiting to be unlocked by the right computational tools. In the commercial sphere, business intelligence—driven by the ability to gather data from a dizzying array of sources—promises to help organizations better understand their customers and the marketplace, leading to better business decisions and competitive advantages. For engineers building information processing tools and applications, larger datasets lead to more effective algorithms for a wide range of tasks. In the natural sciences, the ability to analyze massive amounts of raw data may provide the key to unlocking the secrets of the cosmos or the mysteries of life.

In the preceding chapters, we have shown how MapReduce can be exploited to solve a variety of problems related to text processing at scales that would have been unthinkable a few years ago. However, no tool—no matter how powerful or flexible—can be perfectly adapted to every job, so it is only fair to discuss the limitations of the MapReduce programming model and survey alternatives. Chapter 7.1 covers *online learning algorithms* and *Monte Carlo simulations*, which are examples of a class of algorithm that require preserving global state. As we have seen, this is difficult in MapReduce. Chapter 7.2 discusses alternative models, and the book concludes in Chapter 7.3.

7.1 LIMITATIONS OF MAPREDUCE

As we have seen throughout this book, solutions to many interesting problems in text processing do not require global synchronization. As a result, they can be expressed naturally in MapReduce. However, there are many examples of algorithms that depend crucially on the existence of shared global state during processing, making them difficult to implement in MapReduce.

The first example is online learning. Recall from Chapter 6 the concept of learning as the setting of parameters in a statistical model. Both EM and the gradient-based learning algorithms we described are instances of what are known as *batch learning algorithms*. This means simply that the full "batch" of training data is processed before any updates to the model parameters are made. On one hand, this is quite reasonable: updates are not made until the full evidence of the training data has been weighed against the model. An earlier update would seem, in some sense, to be hasty. However, it is generally the case that more frequent updates can lead to *more* rapid convergence of the model (in terms of number of training instances processed), even though those

updates are made by considering less data [15]. Thinking in terms of gradient optimization (see Chapter 6.5), online learning algorithms can be understood as computing an approximation of the true gradient, using only a few training instances. Although only an approximation, the gradient computed from a small subset of training instances is often quite reasonable, and the aggregate behavior of multiple updates tends to even out errors that are made. In the limit, updates can be made after *every* training instance.

Unfortunately, implementing online learning algorithms in MapReduce is problematic. The model parameters in a learning algorithm can be viewed as shared global state, which must be updated as the model is evaluated against training data. All processes performing the evaluation (presumably the mappers) must have access to this state. In a batch learner, where updates occur in a reducer (or, alternatively, in driver code), synchronization of this resource is enforced by the MapReduce framework. However, with online learning, these updates must occur after processing smaller numbers of instances. This means that the framework must be altered to support faster processing of smaller datasets, which goes against its original design. Since MapReduce was specifically optimized for batch operations over large amounts of data, such a style of computation would likely result in inefficient use of resources. Another approach is to abandon shared global state and run independent instances of the training algorithm in parallel (on different portions of the data). A final solution is then arrived at by merging individual results. Experiments, however, show that the merged solution is inferior to the output of running the training algorithm on the entire dataset [36].

A related difficulty occurs when running what are called *Monte Carlo simulations*, which are used to perform inference in probabilistic models where evaluating or representing the model exactly is impossible. The basic idea is quite simple: samples are drawn from the random variables in the model to simulate its behavior, and then simple frequency statistics are computed over the samples. This sort of inference is particularly useful when dealing with so-called *nonparametric models*, which are models whose structure is not specified in advance, but is rather inferred from training data. For an illustration, imagine learning a hidden Markov model, but inferring the number of states, rather than having them specified. Being able to parallelize Monte Carlo simulations would be tremendously valuable, particularly for unsupervised learning applications where they have been found to be far more effective than EM-based learning (which requires specifying the model). Although recent work [5] has shown that the delays in synchronizing sample statistics due to parallel implementations do not necessarily damage the inference, MapReduce offers no natural mechanism for managing the global shared state that would be required for such an implementation.

The problem of global state is sufficiently pervasive that there has been substantial work on solutions. One approach is to build a distributed datastore capable of maintaining the global state. But such a system would need to be highly scalable to be used

in conjunction with MapReduce. Google's BigTable [23], which is a sparse, distributed, persistent multidimensional sorted map built on top of GFS, fits the bill, and has been used in exactly this manner. Amazon's Dynamo [34], which is a distributed key-value store (with a very different architecture), might also be useful in this respect, although it wasn't originally designed with such an application in mind. Unfortunately, it is unclear if the open-source implementations of these two systems (HBase and Cassandra, respectively) are sufficiently mature to handle the low-latency and high-throughput demands of maintaining global state in the context of massively distributed processing.

7.2 ALTERNATIVE COMPUTING PARADIGMS

Streaming algorithms [2] represent an alternative programming model for dealing with large volumes of data with limited computational and storage resources. This programming model assumes that data is presented to the algorithm as one or more *streams* of inputs that are processed in order, and only once. The model is agnostic with respect to the source of these streams, which could be files in a distributed file system, but more interestingly, data from an "external" source such as feeds, sensors, or some other data gathering device. Stream processing is very attractive for working with time-series data (news feeds, tweets, sensor readings, etc.), which is something that is very difficult in MapReduce. Furthermore, since streaming algorithms are comparatively simple (because there is only so much that can be done with a particular training instance), they can often take advantage of modern GPUs, which have a large number of (relatively simple) functional units [75]. In the context of text processing, streaming algorithms have been applied to language modeling [62], translation modeling [61], and detecting the first mention of news event in a stream [85].

The idea of stream processing has been generalized in the Dryad framework as arbitrary dataflow graphs [52, 111]. A Dryad job is a directed acyclic graph where each vertex represents developer-specified computations and edges represent data channels that capture dependencies. The dataflow graph is a logical computation graph that is automatically mapped onto physical resources by the framework. At runtime, channels are used to transport partial results between vertices, and can be realized using files, TCP pipes, or shared memory.

Another system worth mentioning is Google's Pregel [70], which implements a programming model inspired by Valiant's Bulk Synchronous Parallel (BSP) model [104]. Pregel was specifically designed for large-scale graph algorithms, but unfortunately there are few published details.

What is the significance of these developments? The power of MapReduce derives from providing an abstraction that allows developers to harness the power of large clusters. As anyone who has taken an introductory computer science course would know, abstractions manage complexity by hiding details and presenting well-defined behaviors

to users of those abstractions. This process makes certain tasks easier, but others more difficult if not impossible. MapReduce is certainly no exception to this generalization, and one of the goals of this book has been to give the reader a better understanding of what's easy to do in MapReduce and what its limitations are. But of course, this begs the obvious question: What other abstractions are available in the massively-distributed datacenter environment? Are there more appropriate computational models that would allow us to tackle classes of problems that are difficult for MapReduce?

Dryad and Pregel are alternative answers to these questions. They share in providing an abstraction for large-scale distributed computations, separating the *what* from the *how* of computation and isolating the developer from the details of concurrent programming. They differ, however, in how distributed computations are conceptualized: functional-style programming, arbitrary dataflows, or BSP. These conceptions represent different tradeoffs between simplicity and expressivity: for example, Dryad is more flexible than MapReduce, and in fact, MapReduce can trivially implemented in Dryad. However, it remains unclear, at least at present, which approach is more appropriate for different classes of applications. Looking forward, we can certainly expect the development of new models and a better understanding of existing ones. MapReduce is not the end, and perhaps not even the best. It is merely the first of many approaches to harness large-scaled distributed computing resources.

Even within the Hadoop/MapReduce ecosystem, we have already observed the development of alternative approaches for expressing distributed computations. For example, there is a proposal to add a third *merge* phase after map and reduce to better support relational operations [25]. Pig [80], which is inspired by Google's Sawzall [86], can be described as a lightweight "scripting language" for manipulating large datasets. Although Pig scripts are ultimately compile down to Hadoop jobs by the execution engine, constructs in the language (called *Pig Latin*) allow developers to specify data transformations (filtering, joining, grouping, etc.) at a much higher level. Similarly, Facebook's Hive [46], another open-source project, provides an abstraction on top of Hadoop that allows users to issue SQL queries against large relational datasets stored in HDFS. Although Hive queries (in HiveQL) compile down to Hadoop jobs by the query engine, they provide a data analysis tool for users who are already comfortable with relational databases.

7.3 MAPREDUCE AND BEYOND

The capabilities necessary to tackle large-data problems are already within reach by many and will continue to become more accessible over time. By scaling "out" with commodity servers, we have been able to economically bring large clusters of machines to bear on problems of interest. But this has only been possible with corresponding innovations in software and how computations are organized on a massive scale. Im-

portant ideas include moving processing to data, as opposed to the other way around, and emphasizing throughput over latency for batch tasks by sequential scans through data and avoiding random seeks. Most important of all, however, is the development of new abstractions that hide system-level details from the application developer. These abstractions are at the level of entire datacenters, and provide a model through which programmers can reason about computations at a massive scale in a fault-tolerant fashion. This, in turn, paves the way for innovations in scalable algorithms that can run on petabyte-scale datasets.

None of these points are new or particularly earth-shattering—computer scientists working in the area of parallel and distributed systems have known about these principles for decades. However, MapReduce is unique in that, for the first time, all these ideas came together, and was demonstrated on practical problems at scales unseen before, both in terms of computational resources and the impact of the daily lives of millions. The engineers at Google deserve a tremendous amount of credit for that. However, if that were the end of the story, the power of these ideas would have had only limited impact within a single organization. The engineers (and executives) at Yahoo deserve an equal amount of credit for sharing MapReduce with the rest of the world through the Hadoop implementation, making a powerful tool even more potent by coupling it with the vibrancy of the open-source ecosystem. Add to that the advent of utility computing, which eliminates capital investments associated with cluster infrastructure, large-data processing capabilities are available today "to the masses" with a relatively low barrier to entry.

The golden age of massively distributed computing is finally upon us. The computer is dead. The datacenter *is* the computer.

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