Parallel and Distributed Algorithms

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January 15, 2007

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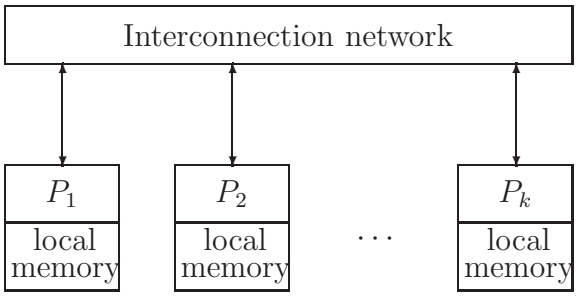
Chapter 1

Introduction

We consider two models of parallel computing, multicomputers and multiprocessors. A **multicomputer** consists of processors (such as workstations or personal computers) and an interconnection network. Processors communicate by exchanging point-to-point messages. These messages are routed by an interconnection network composed of switches which cooperate according to various network technologies such as Fast Ethernet, Gigabit Ethernet, Myrinet or InfiniBand.

Each processor has direct access only to its local memory and has to communicate any request for missing information. Thus multicomputers are *distributed memory* computers with the advantage of a large aggregate memory capacity and the disadvantage of (possibly) slow access time.



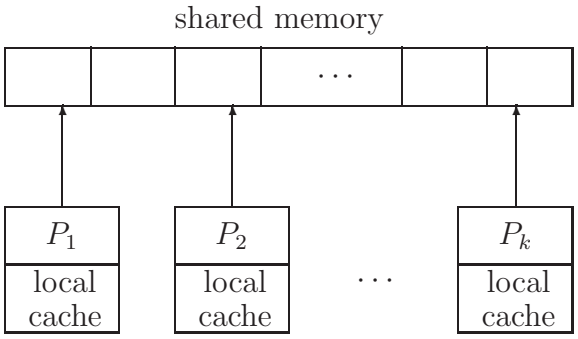
k processors in a distributed memory model.

The performance of a multicomputer program is determined by its *compute time* (the time spent by processors when computing on their local data) and its *communication time* (the time spent when sending, receiving or waiting for messages). Typically, the communication performance is the weak spot of a multicomputer. Fast Ethernet or Gigabit Ethernet have *latencies*[1] of 100 μs, the latest generations of Myrinet and InfiniBand have latencies of

[1]The latency of a link is defined as the time from the start of a transmission to the end of the reception for a short message.

as low as 2μs and 1.32 μs respectively, but still a simple compute step is by a factor of a few thousands faster than a simple communication step. Moreover, although the bandwidth of Fast Ethernet (100 Mbit/sec), Gigabit Ethernet (1 Gbit/sec), Myrinet (1,92 Gbit/sec) and InfiniBand (up to 10 Gbit/sec) seems considerable, current technologies do not allow to transport long message streams without interruption and thus slow down communication time even further. On the other hand, due to the inexpensive switching technology, multicomputers reach a superior performance/price ratio.

Multiprocessors form the second important parallel computer model. A multiprocessor consists of several CPUs which access their local cache directly and access a *shared memory* with special hardware to cut down on communication costs. However, in affordable multiprocessors, only few processors are supported.[2] The production cost of multiprocessors has been reduced considerably and multiprocessors such as multicore Pentiums or multicore Opterons have reached the mass market.



k processors in a shared memory model.

It is not inevitable that multicomputers and multiprocessors are competing parallel computer models. Just to the contrary, hybrid systems, i.e., clusters of multiprocessors such as the CSC cluster in Frankfurt, are becoming standard and receive special software support (MPI version 2).

We assume throughout that all processors work according to the same program. This is a reasonable restriction, since parallel programs should be portable to parallel systems of arbitrary sizes; moreover this approach is still flexible, since processors have different a priori information such as their ID and hence we can emulate multiple programs within the single-program restriction.

We allow asynchronous computing for multicomputers, but require multiprocessors to be fully synchronous. As a consequence, our algorithms for multicomputers are easily applicable for real life clusters, whereas our algorithms for multiprocessors, at least at this

[2]This multiprocessor model is also called a *centralized multiprocessor*. A *distributed multiprocessor* uses an interconnection network to exchange messages between different processors and is capable to support more processors. Whereas a multiprocessor has a single global address space, a multicomputer has disjoint local address spaces.

moment in time, live in a "theoretical world" of synchronous computation with shared memory access and insignificant communication delays. This ideal setting is currently unrealistic, but it allows us to investigate fundamental questions such as a classification of computing problems into parallelizable respectively inherently sequential problems.

The mathematical prerequisites are described in the following sections. After introducing "communication patterns" we design and analyze parallel algorithms for the message passing paradigm in Part I. Algorithmic problems and their solutions for shared memory models are described in Part II. When is it possible to design superfast parallel algorithms? In Chapter 9 we encounter a large class of problems which in all likelihood do not possess superfast parallel algorithms: if one problem in this class is solvable superfast, then all problems in this class are. We conclude in Part III with a short survey of some important distributed algorithms.

We recommend the following references: [Q04, GGKK03] for message passing, [Ja92] and [KR90] for PRAMs, [GHR95] for Chapter 9 and [AW04, L96, T00] for distributed algorithms.

Exercise 1
We call a problem *parallelizable*, if it can be solved by a parallel algorithm with poly(n) processors in time poly($\log_2 n$). A problem is *efficiently parallelizable*, if additionally the product of running time and the number of processors is by at most a factor of poly($\log_2 n$) larger than the running time of the best sequential algorithm. Which of the following problems "seem" parallelizable, respectively efficiently parallelizable?

(1) Input: n numbers $z_1, \ldots, z_n$ with n bits each.
Output: The binary representation of the sum $z_1 + \cdots + z_n$.

(2) Input: Two numbers x and y with n bits each.
Output: The binary representation of $\lfloor x/y \rfloor$.

(3) Input: Two $n \times n$ matrices A and B with entries from $\{0, 1\}$.
Output: The product matrix $(c_{i,j})_{i,j}$ with $c_{i,j} = \bigvee_{k=1}^{n} a_{i,k} \wedge b_{k,j}$.

(4) Input: The $n \times n$ matrix A whose entries are n-bit integers.
Output: The determinant of A.

(5) Input: A directed graph G and two distinguished nodes s and t.
Output: Accept, if there is a path in G from s to t.

(6) Input: A directed graph G with weighted edges and two distinguished nodes s and t.
Output: The length of a shortest path from s to t.

(7) Input: A directed graph G.
Output: The ordering of nodes in which depth-first search visits the nodes.

(8) Input: An undirected graph G.
Output : A maximal independent set, i.e., an independent set which cannot be enlarged.

1.1 Asymptotic Notation

Some of the results are asymptotic, and we use the standard asymptotic notation: for two functions $f, g : \mathbb{N} \to \mathbb{R}$, we write $f = O(g)$ if $f(n) \leq cg(n)$ for all $n \geq N$, where N is a suitably large threshold and $c > 0$ is a suitably large constant. We write $f = \Omega(g)$ if $g = O(f)$, and $f = \Theta(g)$ if $f = O(g)$ and $g = O(f)$. If the limit of the ratio f/g tends to 0 as the variables of the functions tend to infinity, we write $f = o(g)$. Finally, $f \sim g$ denotes that $f = (1 + o(1))g$, i.e., that f/g tends to 1 when the variables tend to infinity. If x is a real number, then $\lceil x \rceil$ denotes the smallest integer not less than x, and $\lfloor x \rfloor$ denotes the greatest integer not exceeding x.

1.2 Important Inequalities

Recall that the *inner product* of two vectors $x = (x_1, \ldots, x_n)$ and $y = (y_1, \ldots, y_n)$ in $\mathbb{R}^n$ is defined by:

$$\langle x, y \rangle = x_1 y_1 + \cdots + x_n y_n.$$

The *norm* (or *length*) of a vector $x = (x_1, \ldots, x_n)$ is the number

$$\|x\| = \langle x, x \rangle^{1/2} = \left(\sum_{i=1}^{n} x_i^2 \right)^{1/2}.$$

A real-valued function $f(x)$ is convex (resp. concave) iff

$$f(\lambda x + (1 - \lambda)y) \leq \lambda f(x) + (1 - \lambda) f(y) \text{ (resp. } f(\lambda x + (1 - \lambda)y) \geq \lambda f(x) + (1 - \lambda) f(y))$$

for any $0 \leq \lambda \leq 1$. From a geometrical point of view, the convexity of f implies that if we draw a line l through points $(x, f(x))$ and $(y, f(y))$, then the graph of the curve $f(z)$ must lie below that of $l(z)$ for $z \in [x, y]$. Thus, for a function f to be convex it is sufficient that its second derivative is nonnegative.

The following basic inequality, known as the *Cauchy–Schwarz inequality*, bounds the inner product of two vectors in terms of their norms.

Lemma 1.1 (Cauchy–Schwarz Inequality) *If x and y are vectors in $\mathbb{R}^n$, then*

$$| \langle x, y \rangle | \leq \|x\| \cdot \|y\|.$$

That is, if $x_1, \ldots, x_n$ and $y_1, \ldots, y_n$ are real numbers then

$$\left(\sum_{i=1}^{n} x_i y_i \right)^2 \leq \left(\sum_{i=1}^{n} x_i^2 \right) \left(\sum_{i=1}^{n} y_i^2 \right).$$

Proof: We consider the inner product $\langle u, v\rangle$ of two vectors u and v of norm 1. The value of the inner product coincides with the cosine of the angle between u and v and is therefore at most one. Thus the claim follows, if we replace u by $\frac{x}{\|x\|}$ and v by $\frac{y}{\|y\|}$. □

We also need an estimate of $1 - x$ in terms of the e-function.

Lemma 1.2 *For any $x > -1$:*

$$e^{x/(1+x)} \leq 1 + x \leq e^x.$$

Moreover, $1 + x \leq e^x$ holds for all $x \in \mathbb{R}$.

Proof: We first consider the case $x \geq 0$. The natural logarithm is a concave function and therefore the slope of the secant through $(1, 0)$ and $(1+x, \ln(1+x))$ is bounded from below by the slope of the tangent in $(1 + x, \ln(1 + x))$ and bounded from above by the slope of the tangent in $(1, 0)$. Thus we get the inequality

$$\frac{1}{1+x} \leq \frac{\ln(1+x) - \ln(1)}{(1+x) - 1} = \frac{\ln(1+x)}{x} \leq 1 \tag{1.1}$$

or equivalently

$$\frac{x}{1+x} \leq \ln(1+x) \leq x. \tag{1.2}$$

Thus the first claim follows for $x \geq 0$ by exponentiation. For $x \in]-1, 0]$ we only have to observe that this time the inequality

$$1 \leq \frac{\ln(1+x) - \ln(1)}{(1+x) - 1} \leq \frac{1}{1+x}$$

holds: the argument is analogous to proof of inequality (1.1). We once again obtain inequality (1.2), and thus have shown the claim, if we multiply (1.1) by the negative number x.

But then we also obtain $1 + x \leq e^x$ for all real numbers, since $1 + x$ is nonpositive for $x \leq -1$ and e^x is always positive. □

Lemma 1.3 (Jensen's Inequality) *If $0 \leq \lambda_i \leq 1$, $\sum_{i=1}^r \lambda_i = 1$ and f is convex, then*

$$f\left(\sum_{i=1}^r \lambda_i x_i\right) \leq \sum_{i=1}^r \lambda_i f(x_i).$$

Proof: Easy induction on the number r of summands. For $r = 2$ this is true, so assume the inequality holds for the number of summands up to r, and prove it for $r + 1$. For this

it is enough to replace the sum of the first two terms in $\lambda_1 x_1 + \lambda_2 x_2 + \ldots + \lambda_{r+1} x_{r+1}$ by the term

$$(\lambda_1 + \lambda_2)\left(\frac{\lambda_1}{\lambda_1 + \lambda_2} x_1 + \frac{\lambda_2}{\lambda_1 + \lambda_2} x_2\right)$$

and apply the induction hypothesis. □

Jensen's inequality immediately yields the following useful inequality between the arithmetic and geometric means.

Lemma 1.4 *Let $a_1, \ldots, a_n$ be non-negative numbers. Then*

$$\frac{1}{n}\sum_{i=1}^{n} a_i \geq \left(\prod_{i=1}^{n} a_i\right)^{1/n}. \tag{1.3}$$

Proof: Let $f(x) = 2^x$, $\lambda_1 = \ldots = \lambda_n = 1/n$ and $x_i = \log_2 a_i$, for all $i = 1, \ldots, n$. By Jensen's inequality

$$\frac{1}{n}\sum_{i=1}^{n} a_i \;=\; \sum_{i=1}^{n} \lambda_i f(x_i) \geq f\left(\sum_{i=1}^{n} \lambda_i x_i\right) = 2^{\left(\sum_{i=1}^{n} x_i\right)/n} = \left(\prod_{i=1}^{n} a_i\right)^{1/n}.$$

□

1.3 Graphs

An *undirected graph* is a pair $G = (V, E)$ consisting of a set V, whose members are called *nodes* (or *vertices*), and a family E of 2-element subsets of V, whose members are called *edges*. A node v is *incident* with an edge e if $v \in e$. The two nodes incident with an edge are its *endpoints*, and the edge *joins* its endpoints. Two nodes u, v of G are *adjacent*, or *neighbors*, if $\{u, v\}$ is an edge of G. In a *directed* graph edges are not 2-element subsets $\{u, v\}$, but ordered pairs (u, v) of nodes instead.

The number $d(u)$ of neighbors of a node u is its *degree*. The degree of a graph is the maximal degree of its nodes.

A *walk* of length k in G is a sequence $v_0, e_1, v_1 \ldots, e_k, v_k$ of nodes and edges such that $e_i = \{v_{i-1}, v_i\}$. A walk without repeated nodes is a *path*. A *cycle* of length k is a walk $v_0, \ldots, v_k$ such that $v_0 = v_k$ and $v_0, \ldots, v_{k-1}$ is a path. The *distance* between two nodes is the minimum length of a path between them.

A *Hamiltonian cycle* is a cycle containing all nodes of the graph. Note that a Hamiltonian cycle traverses every node exactly once. An *Euler cycle* is a walk which starts and ends at the same node and includes every edge exactly once.

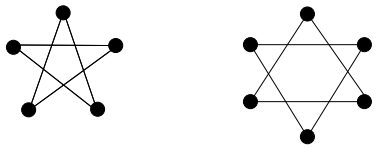


Figure 1.1: The first graph is a cycle of length 5. The second graph consists of two cycles of length 3.

A (connected) *component* in a graph is a set of its nodes such that there is a path between any two of them. A graph is *connected* if it consists of one component. A *subgraph* is obtained by deleting edges and nodes. A *spanning subgraph* is obtained by deleting edges only. An *induced subgraph* is obtained by deleting nodes (together with all the edges incident to them).

A *forest* is a graph without cycles. A *tree* is a connected graph without cycles.

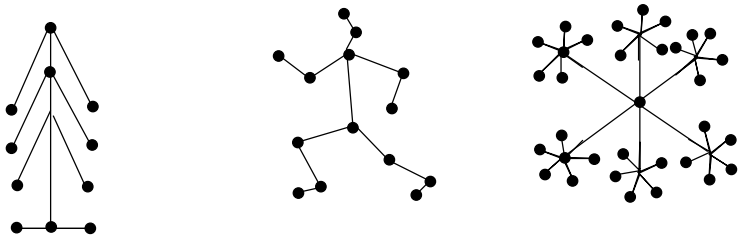


Figure 1.2: A forest consisting of three trees.

In a *rooted* tree one node r is declared as root. Nodes of degree 1 are called *leaves*. The *depth* of a node u in such a tree is the distance between u and the root. Nodes of the same depth form a *level* of a tree. The depth of a tree is the maximum depth of its leaf. A tree is *binary* if the root has degree 2 and all other non-leaves have degree 3. A *complete binary* tree T_d of depth d is a binary tree such that all leaves have depth d.

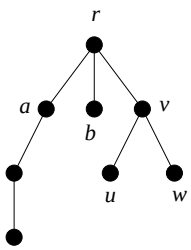


Figure 1.3: A rooted tree of depth 3; u and w are children of v, and v is their parent; a, b and v are on the same level.

A *complete graph* or *clique* is a graph in which every pair of nodes is adjacent. An *independent set* in a graph is a set of nodes with no edges between them. The greatest integer r such that G contains an independent set of size r is the *independence number* of G, and is denoted by $\alpha(G)$. A graph is *bipartite* if its node set can be partitioned into two independent sets.

A *legal coloring* of $G = (V, E)$ is an assignment of colors to each node so that adjacent nodes receive different colors and hence it can be interpreted as a partition of the node set V into independent sets. The minimum number of colors required for a legal coloring is the *chromatic number* $\chi(G)$ of G.

Exercise 2
(a) Show that every rooted binary tree with N leaves has depth at least $\log_2 N$.
(b) Let T be a rooted binary tree with N leaves, and let d_i be the depth of the ith leaf. Show that then the so called *Kraft inequality* holds: $\sum_{i=1}^{N} 2^{-d_i} \leq 1$. Hint: associate with each leaf a binary string.
(c) Show that always $\chi(G) \geq |V|/\alpha(G)$.

1.4 Some Basics from Probability Theory

A *finite probability space* consists of a finite set Ω (a *sample space*) and a function

$$\text{prob} : \Omega \to [0, 1]$$

(a *probability distribution*), such that $\sum_{x\in\Omega} \text{prob}\,[x] = 1$. A probability space is a representation of a random experiment, where we choose a member of Ω at random and $\text{prob}\,[x]$ is the probability that x is chosen.

Elements $x \in \Omega$ are called *sample points* and subsets $A \subseteq \Omega$ are called *events*. The probability of an event is defined by

$$\text{prob}\,[A] = \sum_{x\in A} \text{prob}\,[x]\,,$$

i.e., the probability that a member of A is chosen.

Some elementary properties follow directly from the definitions. For any two events A and B (here and throughout $\bar{A} = \Omega \setminus A$ stands for the complement of A):

(1) $\text{prob}\,[A \cup B] = \text{prob}\,[A] + \text{prob}\,[B] - \text{prob}\,[A \cap B]$;
(2) $\text{prob}\left[\bar{A}\right] = 1 - \text{prob}\,[A]$;
(3) $\text{prob}\,[A \cap B] \geq \text{prob}\,[A] - \text{prob}\left[\bar{B}\right]$;
(4) If $B_1, \ldots, B_m$ is a partition of Ω, then $\text{prob}\,[A] = \sum_{i=1}^{m} \text{prob}\,[A \cap B_i]$.

For two events A and B, the *conditional probability of A given B*, denoted $\text{prob}\,[A|B]$, is the probability that A occurs if one knows that B has occurred. Formally, we define

$$\text{prob}\,[A|B] = \frac{\text{prob}\,[A \cap B]}{\text{prob}\,[B]},$$

when $\text{prob}\,[B] \neq 0$. For example, if we are choosing an integer uniformly from $\{1, \ldots, 6\}$, if A is the event that the number is 2 and if B is the event that the number is even, then $\text{prob}\,[A|B] = 1/3$, whereas $\text{prob}\,[B|A] = 1$.

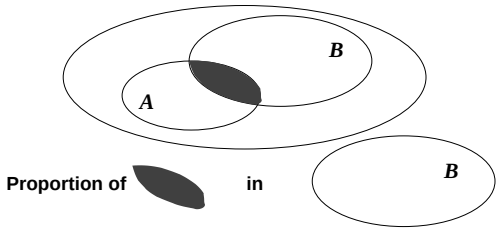


Figure 1.4: Interpretation of $\text{prob}\,[A|B]$ in the case of the uniform distribution.

Two events A and B are *independent* $\text{prob}\,[A \cap B] = \text{prob}\,[A] \cdot \text{prob}\,[B]$. Note that this is equivalent to $\text{prob}\,[A|B] = \text{prob}\,[A]$ as well as to $\text{prob}\,[B|A] = \text{prob}\,[B]$. Hence, in the case of uniform distribution we have that the events A and B are independent iff the proportion $|A|/|\Omega|$ of the event A in the whole sample space is equal to the proportion $|A \cap B|/|B|$ of the sub-event $A \cap B$ of A in the event B.

It is worth to note that "independence" has nothing to do with "disjointness" of events: if, say, $\text{prob}\,[A] > 0$, $\text{prob}\,[B] > 0$ and $A \cap B = \emptyset$, then the events A and B *are* dependent!

Example 1.1 We describe the "Monty Hall problem". In a game show a price is hidden behind one of three doors. A contestant guesses one of the three doors and the show master Monty Hall opens another door which does not hide the price. The contestant has the option to change her choice. What should she do? We consider the events

- P_i: the price is behind door i,
- C_i: the contestant's first choice is door i,
- M_i: Monty Hall opens door i.

We assume without loss of generality that the contestant opens first door 1 and that Monte Hall opens door 2; moreover we assume that both choices are according to the uniform distribution. We determine the conditional probabilities prob[$P_1 \mid C_1, M_2$] and

prob[$P_3 \mid C_1, M_2$] and observe that prob[$P_1 \mid C_1, M_2$] + prob[$P_3 \mid C_1, M_2$] = 1 holds, since the price is not behind door 2. By definition of conditional probabilities we get

$$\begin{aligned} \text{prob}[\, P_1 \mid C_1, M_2 \,] \cdot \text{prob}[\, C_1, M_2] &= \text{prob}[\, C_1, M_2 \mid P_1 \,] \cdot \text{prob}[\, P_1 \,] \text{ and} \\ \text{prob}[\, P_3 \mid C_1, M_2 \,] \cdot \text{prob}[\, C_1, M_2] &= \text{prob}[\, C_1, M_2 \mid P_3 \,] \cdot \text{prob}[\, P_3 \,]. \end{aligned}$$

We determine the right hand sides and obtain

$$\text{prob}[\, P_1 \mid C_1, M_2 \,] \cdot \text{prob}[\, C_1, M_2] = (\frac{1}{3} \cdot \frac{1}{2}) \cdot \frac{1}{3},$$

since Monty Hall can open doors 2 and 3. On the other hand we have

$$\text{prob}[\, P_3 \mid C_1, M_2 \,] \cdot \text{prob}[\, C_1, M_2] = (\frac{1}{3} \cdot 1) \cdot \frac{1}{3},$$

since Monty Hall can only open door 2. Thus we get

$$\text{prob}[\, P_3 \mid C_1, M_2 \,] \cdot \text{prob}[\, C_1, M_2] = 2 \cdot \text{prob}[\, P_1 \mid C_1, M_2 \,] \cdot \text{prob}[\, C_1, M_2]$$

and obtain prob[$P_3 \mid C_1, M_2$] = $\frac{2}{3}$ and prob[$P_1 \mid C_1, M_2$] = $\frac{1}{3}$: The contestant should always change her choice!

A *random variable* is a function $X : \Omega \to \mathbb{R}$ of the sample space. For example, if X is an integer uniformly chosen from $\{1, \ldots, n\}$, then $Y = 2X$ and $Z =$ "the number of prime divisors of X" are both random variables, and so is X itself. The *distribution* of a random variable X is the function $f : \Omega \to [0, 1]$ defined as $f(i) = \text{prob}\,[X = i]$, where here and in what follows prob $[X = i]$ denotes the probability of the event $A = \{x \in \Omega : X(x) = i\}$. An *indicator random variable* for the event A is a random 0-1 variable X with

$$X(\omega) = \begin{cases} 1 & \text{if } \omega \in A; \\ 0 & \text{otherwise.} \end{cases}$$

Example 1.2 The solution to the "Monty Hall problem" can be formulated concisely when using random variables. Let W be the random variable describing the first choice of the contestant and let T be the random variable describing the correct door. The Change-strategy finds the correct door, if W and T disagree and this event happens with probability $\frac{2}{3}$.

Random variables $X_1, \ldots, X_n$ are called *independent*, iff for all $x_1, \ldots, x_n \in \mathbb{R}$

$$\text{prob}[\, X_1 = x_1 \wedge \cdots \wedge X_n = x_n \,] = \prod_{i=1}^{n} \text{prob}[\, X_i = x_i \,].$$

The random variables are called k-wise independent, if $X_{i_1}, \ldots, X_{i_k}$ is independent for any subset $\{i_1, \ldots, i_k\} \subseteq \{1, \ldots, n\}$ of k elements.

Observe that repeated experiments correspond to independent random variables. Moreover independent random variables $X_1, \ldots, X_n$ are k-wise independent for any $k < n$. The reverse implication is false.

Exercise 3
Construct random variables X_1, X_2, X_3, which are pairwise independent, but not independent.

A fundamental probabilistic measure is the expected value of a random variable. The expectation is defined for any real-valued random variable X, and intuitively, it is the value that we would expect to obtain if we repeat a random experiment several times and determine the average of the outcomes of X. More formally, the *expected value* (or *expectation* or *mean*) of X is defined as the sum

$$\mathrm{E}[X] = \sum_i i \cdot \mathrm{prob}[X = i]$$

over all numbers i in the range of X. For example, if X is the number of spots on the top face when we roll a fair die, then the expected number of spots is $\mathrm{E}[X] = \sum_{i=1}^{6} \frac{i}{6} = 3.5$.

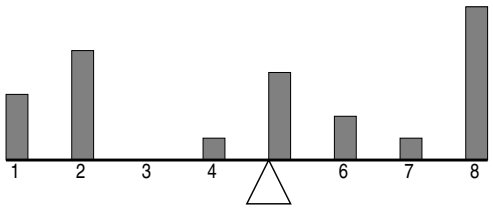


Figure 1.5: Interpretation of the expected value as the "mass-center": the objects have weights $p_i = \mathrm{prob}[X = a_i]$ on the x-axis in positions a_i $(i = 1, \ldots, n)$.

It is important to note that the expected value $\mathrm{E}[X]$ does not have to lie in the range of X. For example, if the random variable X assumes each value in the set $\{0, 1, 9, 10\}$ with probability $1/4$ then $\mathrm{E}[X] = 0 \cdot \frac{1}{4} + 1 \cdot \frac{1}{4} + 9 \cdot \frac{1}{4} + 10 \cdot \frac{1}{4} = 5$, the number which lies far away from the possible values $0, 1, 9, 10$ of X. Do not always expect the "expected"! And indeed, in many cases the expected value $\mathrm{E}[X]$ says not much about the behaviour of the random variable X. The expectation is only "reliable", if one can show that the probability of X being far away from $\mathrm{E}[X]$ is small. The estimates of these probabilities are given by Markov, Chernoff and Chebyshev inequalities which we will prove soon.

The "distance" between a random variable X and its expectation $\mathrm{E}[X]$ is measured by its *variance* which is defined as

$$\mathrm{Var}[X] = \mathrm{E}\left[(X - \mathrm{E}[X])^2\right].$$

A very useful property of the expectation is its *linearity*. The property is so useful because it applies to *any* random variables.

Theorem 1.5 (Linearity of Expectation) *For any random variables X, Y and real numbers a, b*

$$\mathrm{E}[a \cdot X + b \cdot Y] = a \cdot \mathrm{E}[X] + b \cdot \mathrm{E}[Y].$$

Proof: Let $x_1, \ldots, x_n$ and $y_1, \ldots, y_m$ be the elements in the range of X and Y, respectively. Since for any real number a we have

$$\mathrm{E}[a \cdot X] = \sum_{i=1}^{n} a \cdot x_i \cdot \mathrm{prob}[X = x_i] = a \cdot \sum_{i=1}^{n} x_i \cdot \mathrm{prob}[X = x_i] = a \cdot \mathrm{E}[X],$$

it is enough to prove that $\mathrm{E}[X + Y] = \mathrm{E}[X] + \mathrm{E}[Y]$.

Since the events $Y = y_j$ for different y_j's are disjoint, we have that $\mathrm{prob}[X = x_i] = \sum_{j=1}^{m} \mathrm{prob}[X = x_i, Y = y_j]$, and similarly for $\mathrm{prob}[Y = y_j]$. Hence

$$\begin{aligned}
\mathrm{E}[X + Y] &= \sum_{i=1}^{n}\sum_{j=1}^{m}(x_i + y_j)\mathrm{prob}[X = x_i, Y = y_j] \\
&= \sum_{i=1}^{n}\sum_{j=1}^{m} x_i \mathrm{prob}[X = x_i, Y = y_j] + \sum_{j=1}^{m}\sum_{i=1}^{n} y_j \mathrm{prob}[X = x_i, Y = y_j] \\
&= \sum_{i=1}^{n} x_i \mathrm{prob}[X = x_i] + \sum_{j=1}^{m} y_j \mathrm{prob}[Y = y_j] \\
&= \mathrm{E}[X] + \mathrm{E}[Y].
\end{aligned}$$

□

Exercise 4

(a) Show that the variance can be computed by the formula $\mathrm{Var}[X] = \mathrm{E}\left[X^2\right] - (\mathrm{E}[X])^2$.

(b) Show that we always have $\mathrm{Var}[a \cdot X + b] = a^2 \cdot \mathrm{Var}[X]$.

(c) Let X and Y be independent random variables. Show that then $\mathrm{E}[X \cdot Y] = \mathrm{E}[X] \cdot \mathrm{E}[Y]$ and $\mathrm{Var}[X + Y] = \mathrm{Var}[X] + \mathrm{Var}[Y]$.

(d) Let X be a non-negative integer-valued random variable. Show that $\mathrm{E}\left[X^2\right] \geq \mathrm{E}[X]$, $\mathrm{prob}[X = 0] \geq 1 - \mathrm{E}[X]$ and $\mathrm{E}[X] = \sum_{x=1}^{\infty} \mathrm{prob}[X \geq x]$.

(e) Use the Cauchy–Schwarz inequality to show that, for any random variable X, $\mathrm{E}[X]^2 \leq \mathrm{E}\left[X^2\right]$.

(f) We have n letters going to n different persons and n envelopes with their addresses. We insert each letter into an envelope independently from each other at random (several letters may go in the same envelope). What is the expected number of correct matches?

(g) Recall that the *length* (or the *norm*) $\|v\|$ of a vector $v \in \mathbb{R}^n$ is the square root of the scalar product $\langle v, v \rangle$. Prove that for any vectors $v_1, \ldots, v_n$ in $\{+1, -1\}^n$ there are scalars $\epsilon_1, \ldots, \epsilon_n \in \{+1, -1\}$ such that

$$\|\epsilon_1 v_1 + \cdots + \epsilon_n v_n\| \leq n.$$

Hint: Choose the ϵ_i's independently at random to be $+1$ or -1 with probability $1/2$, and use the linearity of expectation to evaluate the expected length of the vector $\sum \epsilon_i v_i$ by computing the square of that quantity.

The method of generating functions There is a general method to compute the expectation $\mathrm{E}[X]$ and the variance $\mathrm{Var}[X]$ for an arbitrary discrete random variable $X : \Omega \to \mathbb{N}$. Set $p_k = \mathrm{prob}[X = k]$ and define the *generating function* of X by

$$F_X(x) := \sum p_k x^k,$$

where the sum is over all k's in the range of X.

Theorem 1.6 *For every discrete random variable X we have:*

$$F_X(1) = 1 \tag{1.4}$$

$$\mathrm{E}[X] = F_X'(1) \tag{1.5}$$

$$\mathrm{Var}[X] = F_X''(1) + \mathrm{E}[X] - \mathrm{E}[X]^2 \tag{1.6}$$

Proof: The first equality is just the definition of the probability distribution: $F_X(1) = \sum p_k = 1$. Taking the first derivative $F_X'(x) = \sum k p_k x^{k-1}$ we obtain that $F_X'(1) = \sum k p_k = \mathrm{E}[X]$. Finally, taking the second derivative $F_X''(x) = \sum k(k-1) p_k x^{k-2}$ we obtain that

$$F_X''(1) = \sum k(k-1)p_k = \sum k^2 p_k - \sum k p_k = \mathrm{E}\left[X^2\right] - \mathrm{E}[X].$$

Thus, if we add $\mathrm{E}[X]$ and subtract $\mathrm{E}[X]^2$ on the right hand, then we obtain precisely the variance $\mathrm{Var}[X]$. □

We mention some often used distributions of random variables.

Uniform distribution This is the simplest distribution for a random variable $X : \Omega \to \mathbb{R}$ and it is given by

$$p_k = \mathrm{prob}[X = k] = \frac{1}{|\Omega|}.$$

In this case we also say that X is *uniformly distributed*.

Exercise 5
What is are expectation and the variance of a uniformly distributed random variable?

Binomial distribution We say that a random variable X is *binomially distributed* with parameters n and k, provided

$$\mathrm{prob}[X = k] = \binom{n}{k} p^k (1-p)^{n-k}$$

for any $0 \le k \le n$. If $X_1, \ldots, X_n$ are n independent random variables with $\mathrm{prob}[X_i = 1] = p$ and $\mathrm{prob}[X_i = 0] = 1 - p$, then $\mathrm{prob}[X_1 + \cdots + X_n = k] = \binom{n}{k} p^k (1-p)^{n-k}$. Hence we may set $X = X_1 + \cdots + X_n$ and $\mathrm{prob}[X = k]$ is the probability that k out of n repeated

experiments succeed. The expectation of X is $\mathrm{E}[X] = \sum_{i=1}^{n} \mathrm{E}[X_i] = np$. The variance is also easy to compute. By the linearity of expectation

$$\mathrm{E}\left[X^2\right] = \mathrm{E}\left[(\sum X_i)^2\right] = \sum_i \mathrm{E}\left[X_i^2\right] + \sum_{i \neq j} \mathrm{E}\left[X_i \cdot X_j\right].$$

Since X_i, X_j are pairwise independent, $\mathrm{E}[X_i \cdot X_j] = \mathrm{E}[X_i] \cdot \mathrm{E}[X_j]$. Hence

$$\mathrm{E}\left[X^2\right] = np + 2 \cdot \binom{n}{2} \cdot p^2 = np + n(n-1)p^2 = (np)^2 + np(1-p),$$

and the variance of X is $\mathrm{Var}[X] = \mathrm{E}[X^2] - (\mathrm{E}[X])^2 = np(1-p)$.

Geometric distribution We toss a coin until we receive heads for the first time. Let X be the number of attempts. Hence, X is defined on the set $\Omega = \{\mathrm{Tail}^n \cdot \mathrm{Head} \mid n \in \mathbb{N}\}$. (This time we have countably infinite sample points.) If p is the probability for Heads, then we get

$$p_k = \mathrm{prob}[X = k] = q^{k-1} \cdot p, \qquad \text{where } q = 1 - p.$$

To compute the expectation and the variance for such a random variable we use the method of generating functions (see Theorem 1.6). The generating function of X is

$$F_X(x) = \sum_{t=1}^{\infty} q^{t-1} p x^t = px \cdot \sum_{t=0}^{\infty} q^t x^t = \frac{px}{1 - qx}$$

The first and the second derivatives of F_X are

$$F'_X(x) = \frac{(1-qx)p + pxq}{(1-qx)^2} = \frac{p}{(1-qx)^2}$$

and

$$F''_X(x) = \frac{2pq}{(1-qx)^3}.$$

Hence, by Theorem 1.6,

$$\mathrm{E}[X] = F'_X(1) = \frac{p}{(1-q)^2} = \frac{1}{p}$$

and

$$\mathrm{Var}[X] = F''_X(1) + \mathrm{E}[T] - \mathrm{E}[Y]^2 = \frac{2pq}{p^3} + \frac{1}{p} - \frac{1}{p^2} = \frac{1-p}{p^2}.$$

Exercise 6

A *random source* Q produces zeroes and ones, such that the probability for a one is p at any time. We have access to Q, but do not know p. Our task is is to construct a perfect random source which emits a one with probability $\frac{1}{2}$. Hence we can watch the stream of random bits of Q and have to construct perfect random bits.

Design a perfect random source from Q, such that the expected number of Q-bits, required to produce one truly random bit, is at most $\frac{1}{p \cdot (1-p)}$.

Hint: consider two successive bits of Q.

Exercise 7
We have access to a random source S which emits the bit 0 (resp. 1) with probability $\frac{1}{2}$.

- We want to produce the distribution $(p_1, \ldots, p_n)$. Design an algorithm which outputs i with probability p_i. You should only use the expected number of $O(\log_2 n)$ bits from S. Observe that $p_1, \ldots, p_n \geq 0$ are arbitrary real numbers summing to one.
- Determine the worst-case number of bits from S, if we have to solve the above problem for $p_1 = p_2 = p_3 = \frac{1}{3}$.

Exercise 8
We are playing against an adversary. The adversary thinks of two numbers and writes each number, invisible to us, on a separate piece of paper. We randomly pick one piece of paper, read the number and then have the option, to either keep the number or exchange it against the other number. Let x be the number we finally have and let y be the other number. Then our possibly negative gain is the difference $x - y$.

- we consider strategies of the form *"'Return numbers $< t$ and keep numbers $\geq t$"'*. Analyze the expected gain $E_{x,y}(\mathrm{gain}(S_t))$ of this strategy in dependence on t, x and y.
- Design a randomized strategy, whose expected gain is positive for arbitrary $x \neq y$.

Exercise 9
We play a game with success probability $p = 1/2$. If we win the game, we double our stake. If we lose, we lose our stake completely. We consider the following strategy.

```
i:=0
REPEAT
    put down the stake 2^i$
    i:=i+1
UNTIL(I win for the first time)
```

Determine the expected gain of this strategy and the expected amount of money required to carry out the strategy.

Example 1.3 *Determining the average salary without making the own salary public.*
n persons $1, \ldots, n$ want to determine their average salary, but no one wants to make their salary public. If all persons are honest, then the average salary should be computed correctly. If however some k persons are liars, then they should not be able to gather any information, except for the total sum of salaries.

Algorithm 1.7 **A protocol**

(1) Let M be sufficiently large number which is known to be larger than the sum of salaries.

Each person i chooses numbers $X_{i,1}, \ldots, X_{i,i-1}, X_{i,i+1}, \ldots X_{i,n} \in \{0, \ldots, M-1\}$ at random and communicates $X_{i,j}$ to person j.

(2) If G_i is the salary of person i, then she determines the residue

$$S_i = G_i + \sum_{j,j\neq i}^{n} X_{j,i} - \sum_{j,j\neq i}^{n} X_{i,j} \bmod M.$$

(3) Each person i announces S_i and then $\sum_i S_i \bmod M$ is determined.

Commentary: If all persons are honest, then we have

$$\sum_i S_i \bmod M \equiv \sum_i G_i + \sum_{i,j,j\neq i}^{n} X_{j,i} - \sum_{i,j,j\neq i}^{n} X_{i,j} \bmod M \equiv \sum_i G_i \bmod M = \sum_i G_i.$$

Thus $\frac{1}{n} \cdot \sum_j S_j$ is the wanted average salary.

Why is this protocol safe? Suppose the last k persons are liars. We set $S_i^* = G_i + \sum_{j=1,j\neq i}^{n-k} X_{j,i} - \sum_{j=1,j\neq i}^{n-k} X_{i,j} \bmod M$. An honest person makes

$$S_i = S_i^* + \sum_{j=n-k+1}^{n} X_{j,i} - \sum_{j=n-k+1}^{n} X_{i,j} \bmod M$$

public. Observe that $\sum_{i=1}^{n-k} S_i^* = \sum_{i=1}^{n-k} G_i$ holds.

Exercise 10
Show: Any combination $(s_2^*, \ldots, s_{n-k}^*)$ of values of the random variables $S_2^*, \ldots, S_{n-k}^*$ is produced with probability $M^{-(n-k-1)}$. Thus the random variables $S_2^*, \ldots, S_{n-k}^*$ are independent.

According to the problem, the random variables $S_2^*, \ldots, S_{n-k}^*$ are independent and uniformly distributed over $\{0, \ldots, M-1\}$. With the same argument this statement also holds for $S_2, \ldots, S_{n-k}$ and the liars learn nothing, since each sequence of $n-k-1$ values occurs with probability $\frac{1}{M^{n-k-1}}$.

We investigate the probability of large deviations from the expected value. The following estimates are particularly helpful.

Markov's Inequality Let X be a non-negative random variable and $a > 0$ a real number. Then

$$\text{prob}\,[X > a] \leq \frac{\text{E}\,[X]}{a}.$$

Proof: By the definition of the expected value we have

$$\text{E}\,[X] = \sum_x x \cdot \text{prob}\,[X = x] \geq \sum_{x>a} a \cdot \text{prob}\,[X = x] = a \cdot \text{prob}\,[X > a]\,.$$

□

Chebycheff's Inequality Let X be a random variable. Then for any real $t > 0$,

$$\text{prob}\left[|X - \text{E}[X]| > t\right] \leq \frac{\text{Var}[X]}{t^2}.$$

Proof: We define the random variable $Y = (X - \text{E}[X])^2$, and apply Markov's inequality. This yields

$$\text{prob}\left[|X - \text{E}[X]| > t\right] = \text{prob}\left[Y > t^2\right] \leq \text{E}[Y]/t^2 = \text{Var}[X]/t^2.$$

□

Chernoff's Inequalities These inequalities are special (and hence, more informative) cases of Markov's inequality applied to sums of independent random 0-1 variables.

Theorem 1.8 *Let $X_1, \ldots, X_n$ be arbitrary independent binary random variables, where $p_i = \text{prob}[X_i = 1]$ is the success probability of X_i. Then $N = \sum_{i=1}^n p_i$ is the expected number of successes and we get*

$$\begin{aligned}
\text{prob}\left[\sum_{i=1}^n X_i > (1+\beta)\cdot N\right] &\leq \left(\frac{e^\beta}{(1+\beta)^{1+\beta}}\right)^N \leq e^{-N\cdot\beta^2/3} \\
\text{prob}\left[\sum_{i=1}^n X_i < (1-\beta)\cdot N\right] &\leq \left(\frac{e^{-\beta}}{(1-\beta)^{1-\beta}}\right)^N \leq e^{-N\cdot\beta^2/2}
\end{aligned}$$

for any $\beta > 0$ (resp. $0 < \beta \leq 1$ in the second case).

Proof: We only show the first inequality. We obtain with the Markov inequality for an arbitrary $\alpha > 0$

$$\begin{aligned}
\text{prob}\left[\sum_{i=1}^n X_i > t\right] &= \text{prob}\left[e^{\alpha\cdot\sum_{i=1}^n X_i} > e^{\alpha\cdot t}\right] \\
&\leq e^{-\alpha\cdot t}\cdot\text{E}\left[e^{\alpha\cdot\sum_{i=1}^n X_i}\right] \\
&= e^{-\alpha\cdot t}\cdot\prod_{i=1}^n \text{E}\left[e^{\alpha\cdot X_i}\right].
\end{aligned}$$

In the last equality we have utilized that $\text{E}[Y_1\cdot Y_2] = \text{E}[Y_1]\cdot\text{E}[Y_2]$ holds, if Y_1 and Y_2 are independent random variables. We replace t by $(1+\beta)\cdot N$, α by $\ln(1+\beta)$ and obtain

$$\begin{aligned}
\text{prob}\left[\sum_{i=1}^n X_i > (1+\beta)\cdot N\right] &\leq e^{-\alpha\cdot(1+\beta)\cdot E}\cdot\prod_{i=1}^n \text{E}\left[e^{\alpha\cdot X_i}\right] \\
&= (1+\beta)^{-(1+\beta)\cdot N}\cdot\prod_{i=1}^n \text{E}\left[(1+\beta)^{X_i}\right].
\end{aligned}$$

The claim follows, since $\mathrm{E}\left[(1+\beta)^{X_i}\right] = p_i(1+\beta) + (1-p_i) = 1 + \beta \cdot p_i \leq e^{\beta \cdot p_i}$. □

Exercise 11
Let $x \leq 1$ be arbitrary. Show

$$\frac{e^x}{(1+x)^{1+x}} = e^{x-(1+x)\ln(1+x)} \leq e^{-x^2/3}.$$

Exercise 12
Let $X_1, \ldots, X_n$ be binary, independent random variables with $p_i = \mathrm{prob}\,[X_i = 1]$. Assume that $N^* \geq \sum_{i=1}^n p_i$. Show that

$$\mathrm{prob}\left[\sum_{i=1}^n X_i > (1+\beta) \cdot N^*\right] \leq \left(\frac{e^\beta}{(1+\beta)^{1+\beta}}\right)^{N^*} \leq e^{-\beta^2 \cdot N^*/3}$$

holds for any $\beta > 0$.

Exercise 13
Show the second Chernoff inequality.

Example 1.4 We would like to obtain the expected value of an experiment X. The experiment however is quite unstable, i.e., its variance is quite large. We boost X, that is we repeat the experiment k times. If X_i is the result of the ith repetition, then we set $Y = \frac{1}{k} \cdot \sum_{i=1}^k X_i$ and observe that the random variables $X_1, \ldots, X_k$ are independent and in particular

$$\mathrm{Var}\,[Y] = \frac{1}{k^2} \cdot \sum_{i=1}^k \mathrm{Var}\,[X_i] = \frac{1}{k^2} \cdot \sum_{i=1}^k \mathrm{Var}\,[X] = \frac{1}{k} \cdot \mathrm{Var}\,[X]$$

holds. We have reduced variance by the factor k and the expected value remains stable, since $\mathrm{E}\,[Y] = \mathrm{E}\left[\frac{1}{k} \cdot \sum_{i=1}^k X_i\right] = \frac{1}{k} \cdot \sum_{i=1}^k \mathrm{E}\,[X] = \mathrm{E}\,[X]$. The Chebycheff inequality implies the inequality

$$\mathrm{prob}\,[|Y - \mathrm{E}\,[X]\,| > t] = \mathrm{prob}\,[|Y - \mathrm{E}\,[Y]\,| > t] \leq \frac{\mathrm{Var}\,[Y]}{t^2} = \frac{\mathrm{Var}\,[X]}{k \cdot t^2}$$

and large deviations from the expected value have become more improbable.

Assume we know that Y lies, with probability at least $p = 1-\varepsilon$, within the "confidence interval" $T = [\mathrm{E}\,[X] - \delta, \mathrm{E}\,[X] + \delta\ ]$. Is it possible to drive p fast towards one? This time we repeat the experiment Y m times and obtain again independent random variables $Y_1, \ldots, Y_m$. We use the median M of $Y_1, \ldots, Y_m$ to obtain an estimate of the expected value. How large is the probability, that M does not belong to the confidence interval T?

Y belongs to T with probability at least p. If the median lies outside of T, then at least $\frac{m}{2}$ estimates Y_j lie outside of T, whereas at most $(1-p) \cdot m = \varepsilon \cdot m$ Y_is are expected to

lie outside of T. We apply the Chernoff inequality and observe that $(1 + \frac{1-2\cdot\varepsilon}{2\cdot\varepsilon}) \cdot \varepsilon \cdot m = \frac{m}{2}$ holds. We set $\lambda = \frac{1-2\cdot\varepsilon}{2\cdot\varepsilon}$ and get

$$\text{prob}\,[M \notin T] \leq e^{-\varepsilon\cdot m\cdot\lambda^2/3} = e^{-(1-2\cdot\varepsilon)^2\cdot m/(12\cdot\varepsilon)}.$$

Thus the probability of error decreases negative exponentially, provided $\varepsilon < \frac{1}{2}$.

Part I

Distributed Memory

Chapter 2

Communication Patterns

How should we distribute information efficiently? Of course the answer depends on the algorithmic context, but a few basic "communication patterns" such as trees, meshes and hypercube architectures are distinguished.

We model a communication pattern by an undirected graph of processes where we introduce an edge between processes p and q, whenever p and q communicate. How do we determine whether a given undirected graph $G = (V, E)$ is a "good" communication pattern? Important parameters are its degree, diameter and bisection width.

- The degree of G is the maximal degree of a node.
- The diameter of G is the maximal distance between any two nodes. Whenever possible we should keep the diameter as small as possible, since the time to route information between distant nodes is governed by the diameter.

  However the diameter is not the whole story behind a fast computation. Important is also the "bisection width" of the network.
- The bisection width of G is the minimal number of edges, whose removal disconnects the graph into two halves with sizes differing by at most one.

  Observe that bisection width b implies that b edges have to carry all information from one half to the other and hence a large bisection width is of uttermost importance to avoid bottlenecks. Moreover a large bisection width also provides robustness against link- and process-failures.

  However a large bisection width comes with the price of complex communications.

We discuss trees, meshes and hypercube architectures in the following sections and evaluate these most successful communication patterns with respect to degree, diameter and bisection width. Certainly a further fundamental component when evaluating architectures is to determine how well an architecture is suited to implement important algorithmic design principles such as for instance the Divide & Conquer method. Hypercube architectures

turn out to be particularly well suited for this task. Finally we should also mention that hypercube architectures are good choices to implement interconnection networks. We return to this subject in Section 2.3.3, where we describe randomized routing on the hypercube.

Exercise 14
A permutation network is a directed acyclic graph with n sources $s_1, \ldots, s_n$ and n sinks $t_1, \ldots, t_n$. We call its edges *links* and its nodes *switches*. Each switch has two inputs x_0 and x_1, two outputs y_0 and y_1 and two states *neutral* and *exchange*. In the exchange state the switch exchanges x_0 and x_1 (i.e., $y_i = x_{1-i}$), whereas inputs are left unchanged in the neutral state (i.e., $y_i = x_i$). We demand that the network can implement any permutation π of $\{1, \ldots, n\}$ by properly setting switches such that s_i reaches $t_{\pi(i)}$.

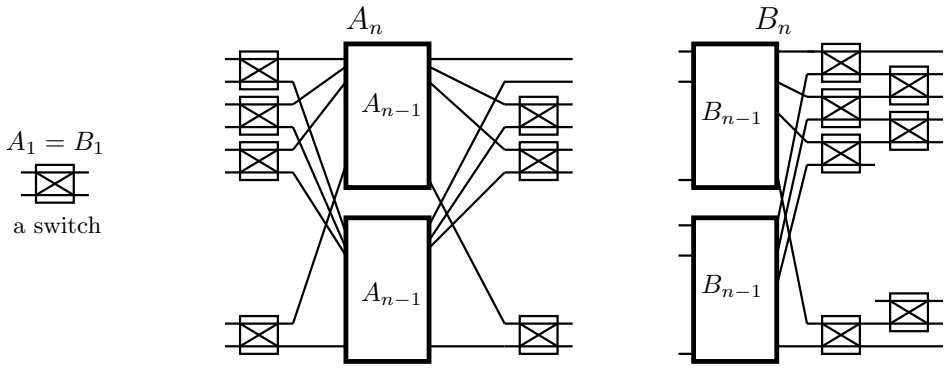


Figure 2.1: The networks A_n and B_n

(a) Prove or disprove: A_n is a family of permutation networks.

(b) Prove or disprove: B_n is a family of permutation networks.

(c) Show that A_n and B_n are composed of $O(n \cdot \log_2 n)$ switches.

(d) Show that any permutation network with n sources and sinks requires $\Omega(n \cdot \log_2 n)$ switches.

2.1 Trees

The broadcast problem is possibly the most fundamental problem with trees as communication pattern.

Example 2.1 In broadcasting a process P sends a message to the remaining $p-1$ processes. Let T be a balanced binary tree with root P and depth at most $\lfloor \log_2 p \rfloor$. The broadcast is started by root P who sends its message to its two children. Then the message is passed from one generation to the next and reaches all processes in $\lfloor \log_2 p \rfloor$ steps.

Exercise 15
Let p be a power of two. Assume that a node has to broadcast a message to its $p-1$ colleagues. Is it a good idea to organize the broadcast by a binary tree or are more general tree shapes better?

Let T_k be an ordered, complete binary tree of depth k. Complete binary trees have the big advantage of the small diameter $2k$ allowing algorithms to use at most $O(k)$ communication steps. The big disadvantage is the bottleneck structure of trees: if nodes outside of the subtree $T_k(v)$ with root v require information held by nodes of $T_k(v)$, then this information has to travel across bottleneck v.

Example 2.2 A further prominent example of a tree algorithm is the tournament approach of determining the minimum among n keys. We assign the keys to the leaves of T_k such that each leaf obtains $\frac{n}{2^k}$ keys. First we let all leaves determine their minimum in parallel. Then the respective minimal keys are passed upwards from the children to their parents, who determine the minimum and pass it upwards themselves. We set $p = 2^{k+1} - 1$ and we have computed the minimum of n keys with p processors in $O(\log_2 p + \frac{n}{p})$ compute steps and $\log_2 p$ communication steps. Is it possible to obtain the same performance with just $p = 2^k$ processors?

We considerably generalize the class of problems solvable on binary trees by considering the important class of prefix problems.

Definition 2.1 A set U and an operation $* : U \times U \to U$ is given. We demand that operation $*$ is associative, i.e., we require that

$$x * (y * z) = (x * y) * z$$

holds for all $x, y, z \in U$. The prefix problem for the input sequence $x_1, x_2, \ldots, x_n \in U$ is to determine all prefixes

$$\begin{array}{l} x_1 \\ x_1 * x_2 \\ x_1 * x_2 * x_3 \\ \quad\vdots \\ x_1 * x_2 * \cdots * x_n \end{array}$$

The prefix problem has many applications. For instance

- An array A of m cells is given and we assume that a cell is either empty or stores a value. We would like to remove all empty cells. We set $U = \mathbb{N}$ and

$$x_i := \begin{cases} 1 & A[i] \text{ is non-empty,} \\ 0 & \text{otherwise.} \end{cases}$$

  Finally we choose addition as our operation $*$. If cell i is not empty, then $A[i]$ has to be moved to cell $x_1 + x_2 + \cdots + x_i$.

- The problem of determining the minimum is a prefix problem, if we define operation $*$ by

$$x * y = \min\{x, y\}.$$

Observe that $x_1 * \cdots * x_n$ is the minimum of $x_1, \ldots, x_n$.

- The reals with addition or multiplication define a prefix problem.

- Let U be a class of functions which is closed under composition, i.e., if $f, g \in U$, then $f \circ g \in U$. We choose the operation $*$ as the the composition of functions and observe that $*$ is associative.

- A Mealey machine is a deterministic finite automaton, which produces an output whenever reading a letter. Let $\mathcal{M}$ be a Mealey machine with state set Q, program δ and input alphabet Σ. Observe that $\mathcal{M}$ defines a function

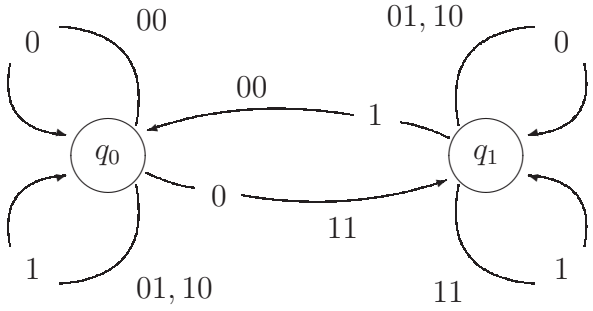
$$f_a : Q \to Q \quad \text{with} \quad f_a(q) := \delta(q, a)$$

for each letter $a \in \Sigma$. Therefore, with initial state q_0 and input word $w = w_1 w_2 \ldots w_n$, we obtain the sequence of states

$$\begin{array}{ccccccccc} & & & & & & & & q_0, \\ & & & & & & & f_{w_1} & (q_0), \\ & & & & f_{w_2} & \circ & f_{w_1} & (q_0), \\ & & & & \vdots & & & & \\ f_{w_n} & \circ & \cdots & \circ & f_{w_2} & \circ & f_{w_1} & (q_0) \end{array}$$

Thus we have reduced the problem of determining the sequence of states to the prefix problem with $U = \{ f \mid f : Q \to Q \}$ and $*$ as the composition of functions, provided we work on the sequence $f_{w_1}, \ldots, f_{w_n}$ instead of on input w. Observe however that in this case the evaluation of $*$ takes time proportional to $|Q|$.

- In particular, we have reduced the problem of adding two n-bit numbers $x_1 x_2 \ldots x_n$ and $y_1 y_2 \ldots y_n$ to a prefix problem, since the Mealey machine



A Mealey machine for addition.

performs addition, if we choose $\Sigma = \{0,1\}^2$ as input alphabet. q_0 is the starting state and we move to q_1, whenever a carry has to be remembered. The last letter has to be 00. Retrieving the output bits is now easy, since the ith output bit is determined by $x_{n-i+1}y_{n-i+1}$ and the ith state q_{i-1}.

Exercise 16
We would like to solve a bidiagonal system $A \cdot x = b$ of linear equations, that is all entries of the $n \times n$ matrix A are zero with the exception of entries of the form $(i, i-1)$ or (i, i). We also require that all entries of the main diagonal are non-zero since otherwise the system is not be solvable. Define a prefix problem whose solution determines x.

Exercise 17
We recursively define the language of a well-formed brackets:

- () is well formed,
- if K_1 and K_2 are well-formed, then so is (K_1) and K_1K_2.

Determine how to decide in parallel whether a given expression of brackets is well-formed.

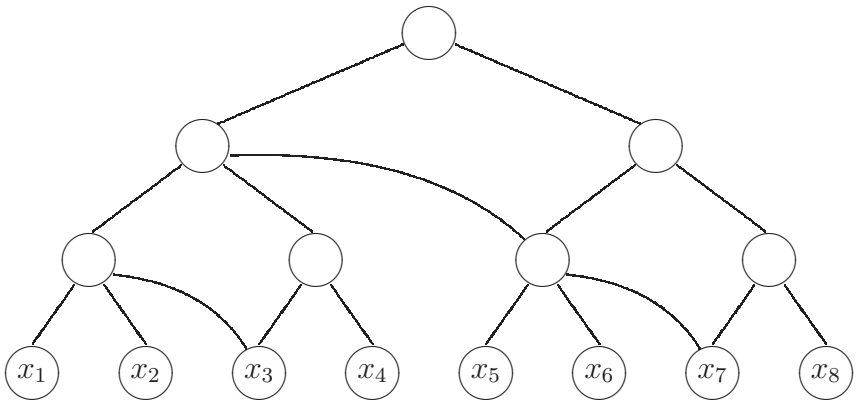
Exercise 18
In the segmented prefix problem, besides an array A and an associative operation $*$, an additional 0-1 array B is given. The array B partitions A into segments, where a segment starts in position i whenever $B[i] = 1$. The task is to determine all prefix sums, but restricted to the segments defined by B.

For instance, if we choose the operation addition:

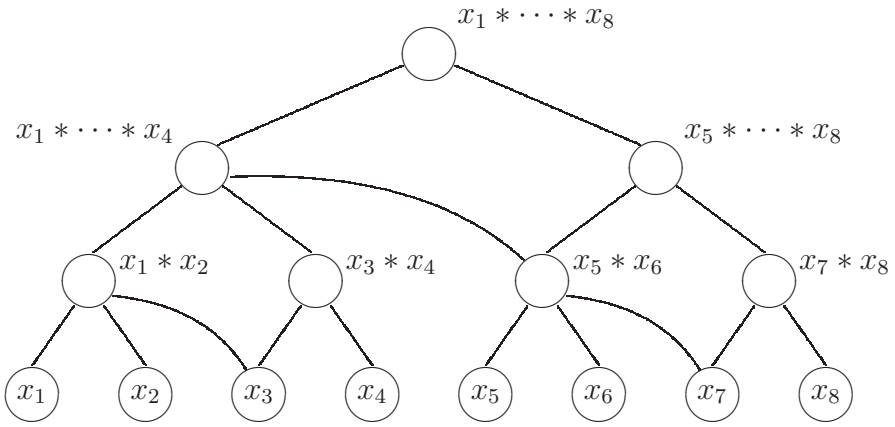
	1	2	3	4	5	6	7	8
A	4	2	6	-2	6	7	0	-3
B	1	0	0	1	0	1	0	0
	4	6	12	-2	4	7	7	4

Define a new operation $*_{B,*}$, which depends on B and $*$ only, such that $*_{B,*}$ determines the "segment sums" as prescribed by B.

We describe a fast evaluation of the prefix problem, assuming that the operation $*$ can be quickly evaluated. Our communication pattern T_k^* is an extension of the complete binary T_k: we introduce diagonal edges linking a left child to its leftmost nephew.



We first make the unrealistic assumption that we have $p = 2n-1$ processors (with $n = 2^k$) and assign input x_i to the ith leaf. The computation proceeds in phases. In Phase 1 the input is moved up the tree and each interior node, upon receiving x and y from its children, computes $z = x * y$, stores the result z and hands z over to its parent.



T_3^* after phase 1.

In the second phase the computation is moving down again.

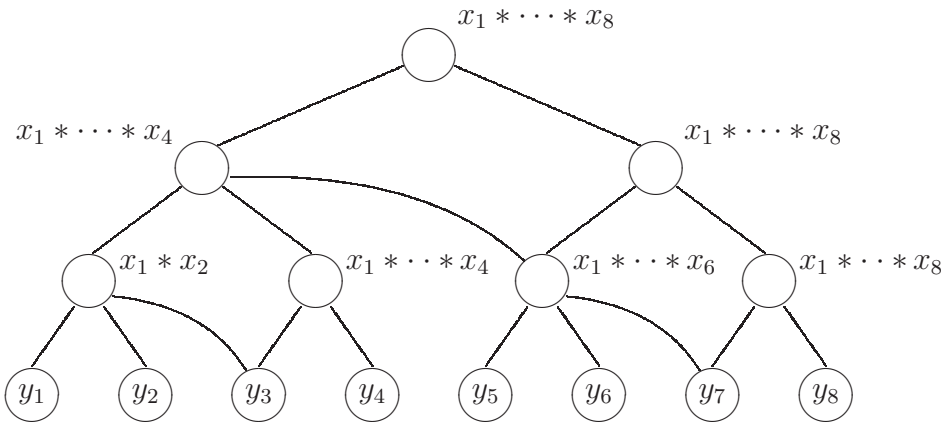
- The root broadcasts a "pay attention" signal down the tree. Moreover the result of the root is passed down to its right child.

- Assume that v receives the pay attention signal from the root and that it currently stores the result z_v. v computes the new value z'_v.

  Case 1: If v is a left child, which does "sit" on the leftmost path, then it sets $z'_v = z_v$ and sends z'_v to its nephew and its right child.

  Case 2: If v is a left child, which does not "sit" on the leftmost path, then it reads the data x it receives from its uncle and computes $z'_v = x * z_v$. It sends z'_v to its nephew and its right child as well as x to its left child.

  Case 3: If v is a right child, then it reads the data x it receives from its parent, sets $z'_v = x$ and sends z'_v to its right child.



After phase 2.

Observe that we have to provide a priori information to nodes. In particular, the root should know its prominent position, leaves should know that they have inputs and each inner node should be able to differentiate between its children, nephews and parent.

Exercise 19
(a) Show how to solve the prefix problem on the complete binary tree T_k.

(b) Show how to solve the prefix problem with $n = 2^k$ processors with no loss in running time.

(c) Assume that we only have $p = 2^k$ processors available with $p < n$. Each evaluation of $*$ may cost time $O(1)$. Show how to solve the prefix problem with p processors in $O(\frac{n}{p} + \log_2 p)$ compute steps and in $O(\log_2 p)$ communication steps in which elements of U are communicated.

Theorem 2.2 *Assume that we can evaluate a $*$-product in time ℓ. Then the prefix problem for n elements can be solved with p processors in $O(\ell \cdot (\frac{n}{p} + \log_2 p))$ compute steps and in $O(\log_2 p)$ communication steps involving elements from U. In particular, two n-bit numbers can be added with p processors in $O(\frac{n}{p} + \log_2 p)$ compute steps.*

Exercise 20
Assume that p is a power of two. Show how to sort n keys (with $p < n$) on $T_{\log_2 p}$ in time $O(n + \frac{n}{p} \cdot \log_2 \frac{n}{p})$. We demand that each leaf stores at the beginning and at the end $\frac{n}{p}$ keys. Moreover we require that at most one key can be exchanged between neighbors. Is it possible to sort faster, if we can work on T_s for arbitrarily large s and sort by comparing keys?

2.2 Meshes

Definition 2.3 The *d-dimensional mesh* $M_d(m)$ is an undirected graph whose nodes are all m^d possible vectors $x = (x_1, \ldots, x_d)$ with $x_i \in \mathbb{Z}_m := \{0, 1, \ldots, m-1\}$. Two nodes x and y are connected by an edge iff $\sum_{i=1}^{d} |x_i - y_i| = 1$. Hence, x and y are connected iff there is a coordinate i such that $y = (x_1, \ldots, x_{i-1}, x_i \pm 1, x_{i+1}, \ldots, x_d)$.

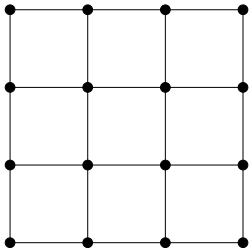


Figure 2.2: The 2-dimensional mesh $M_2(4)$.

We also call $M_1(m)$ a one-dimensional array. Further important meshes are the two- and three-dimensional meshes $M_2(m)$ and $M_3(m)$ as well as the d-dimensional hypercube $M_d(2)$ which we investigate in the next section. Observe that $M_d(m)$ has degree at most $2d$ and diameter $d \cdot (m-1)$.

To obtain an upper bound on the bisection width, we fix the first component per vector and remove all m^{d-1} edges connecting the nodes with vectors $(m/2-1, x_2, \ldots, x_d)$ and $(m/2, x_2, \ldots, x_d)$. We have disconnected the node set into the two components $V_1 = \{i, x_2, \ldots, x_d) \mid 0 \leq i < \frac{m}{2}, 0 \leq x_2, \ldots, x_d < m\}$ and $V_2 = \{i, x_2, \ldots, x_d) \mid \frac{m}{2} \leq i < m, 0 \leq x_2, \ldots, x_d < m\}$. We show in the next section, that our upper bound is tight for the d-dimensional hypercube. The moderate bisection width however has its price: if a problem requires us to exchange information between V_1 and V_2, then this information has to be carried across the bottleneck of m^{d-1} edges.

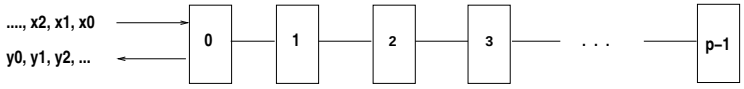
Exercise 21
A *finite impulse response* (FIR) *filter* of order p receives a data stream $x_0, x_1, \ldots$ and outputs the data stream $y_0, y_1, \ldots$ with

$$y_t = \sum_{k=0}^{p-1} a_k \cdot x_{t-k}$$

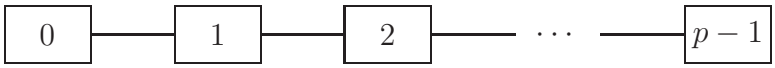
for $t \geq p-1$. Hence FIR produces the output stream

$$\begin{array}{lcl} y_p & = & a_0 \cdot x_{p-1} + a_1 \cdot x_{p-2} + \cdots + a_{p-1} \cdot x_0 \\ y_{p+1} & = & a_0 \cdot x_p + a_1 \cdot x_{p-1} + \cdots + a_{p-1} \cdot x_1 \\ y_{p+2} & = & a_0 \cdot x_{p+1} + a_1 \cdot x_p + \cdots + a_{p-1} \cdot x_2 \\ & \vdots & \end{array}$$

Show how to construct a FIR filter with the help of a linear array with p processors so that x_t is input at step t and y_t is output at step at most $t + 2p$.



Example 2.3 We consider the linear array with p processors.



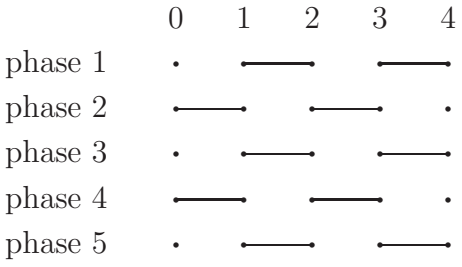
We have two distinguished nodes 0 and $p-1$ which do not have a left, respectively no right neighbor. All other nodes i have a left neighbor $i-1$ and a right neighbor $i+1$. We assume that p is odd and show how to parallelize Bubblesort.

Algorithm 2.4 **Odd-even transposition sort.**
// Each node receives $\frac{n}{p}$ elements.

(1) Each node sorts its subsequence with Quicksort;

(2) for $k = 1$ to p do
    if (k is odd) then
        for $i = 1$ to $\lfloor \frac{p}{2} \rfloor$ pardo
            node $2 \cdot i$ sends its sorted sequence to left neighbor $j = 2 \cdot i - 1$.
            j merges the two sorted sequences,
            keeps the smaller half and returns the larger half to neighbor $2 \cdot i$;
    else
        for $i = 1$ to $\lfloor \frac{p}{2} \rfloor$ pardo
            node $2 \cdot i$ sends its sorted sequence to right neighbor $j = 2 \cdot i + 1$.
            j merges the two sorted sequences,
            keeps the larger half and returns the smaller half to neighbor $2 \cdot i$;

We have used pseudo-code, which uses standard "sequential statements" such as the for-do loop, but also has "parallel statements" such as the for-pardo loop which dictates a parallel execution. In particular, Algorithm 2.4 runs sequentially for exactly p steps, where in an odd (resp. even) step all even nodes transmit their sequences to their left (resp. right) neighbor in parallel. The odd nodes compare and return the larger (resp. smaller) half in parallel.



Pattern of comparisons

Theorem 2.5 *Odd-even transposition sort (OETS) sorts n keys on a linear array with p processors. OETS executes $O(\frac{n}{p} \cdot \log_2 \frac{n}{p} + n)$ compute steps and p communication steps involving messages of length n/p.*

We first investigate the resources required by odd-even transposition sort. In the first step each node runs Quicksort for a sequence of length n/p and hence time $O(\frac{n}{p} \cdot \log_2 \frac{n}{p})$ is sufficient. In every of the subsequent p steps a merging step is executed which runs in linear time $O(n/p)$. Obviously we have p communication steps in which sequences of length n/p are exchanged.

To show that OETS sorts correctly we first verify the important 0-1 principle which applies to *oblivious comparison-exchange* algorithms. The only operation of a comparison-exchange algorithm is to compare two keys in positions i and j and to swap dependent on the outcome of the comparison. For the algorithm to be oblivious the choice of i and j is pre-specified and does *not* depend on the outcome of previous comparisons.

Lemma 2.6 The 0-1 principle.
An oblivious comparison-exchange algorithm sorts correctly iff it sorts 0-1 sequences correctly.

Proof: It suffices to show that an oblivious comparison-exchange algorithm $\mathcal{A}$ sorts correctly, if it sorts 0-1 sequences correctly. Assume otherwise and there will be a sequence $x = (x_1, \ldots, x_n)$ which is incorrectly sorted. Let π be an order type of x, i.e., we have

$$x_{\pi(1)} \leq x_{\pi(2)} \leq \cdots \leq x_{\pi(n)},$$

and assume that $\mathcal{A}$ determines the wrong order type σ. We determine the smallest k such that $x_{\sigma(k)}$ is "out of order", that is k is minimal with $x_{\pi(k)} < x_{\sigma(k)}$. Hence there is $l > k$ with $\sigma(l) = \pi(k)$. We concentrate on $x_{\pi(k)}$ and define the 0-1 sequence

$$y_i = \begin{cases} 0 & x_i \leq x_{\pi(k)}, \\ 1 & x_i > x_{\pi(k)}. \end{cases}$$

Observe that $y_{\sigma(k)} = 1$ and $y_{\sigma(l)} = 0$. Since $x_i \leq x_j \Rightarrow y_i \leq y_j$, the sequence y produces the same outcome of comparisons as sequence x. Thus algorithms $\mathcal{A}$ "claims" the sequence

$$y_{\sigma(1)} \leq \cdots \leq y_{\sigma(k)} \leq \cdots \leq y_{\sigma(l)} \cdots$$

of inequalities. Bad luck, since $y_{\sigma(k)} = 1$ and $y_{\sigma(l)} = 0$, and $\mathcal{A}$ does not sort 0-1 sequences after all. □

Proof of Theorem 2.5. We apply the 0-1 principle and have to show that Algorithm 2.4 sorts an arbitrary sequence x of zeroes and ones. We first observe that, with the possible exception of the first step, the n/p rightmost ones move right in every step until node $p-1$

is reached. (One of the n/p rightmost ones is not moved in the first step, if it initially occupies an even node.)

What happens to a one among the second block of n/p rightmost ones? Any one belonging to the rightmost block is moving right from step two onwards and hence will not delay a one from the "runner-up block" after step 1. Thus, if a one from the runner-up block is unlucky, then it is blocked in the first step by ones from the rightmost block and hence, sitting on an odd node, wins the next comparison against bits from the left neighbor and stays put as well. Thus the worst that can happen is that ones from the runner-up block move right after step 2 until they reach node $p-2$.

An inductive argument shows that ones from the ith rightmost block move right after step i until they reach node $p-i$. But then their distance is at most $(p-i)-0 = p-i$ and they will reach their destination in the $p-i$ steps $i+1,\ldots,p$. □

Let us analyze the running time of Algorithm 2.4 in dependence on the number p of nodes. If $p \leq \log_2 n$, then Quicksort dominates and Algorithm 2.4 runs in time proportional to $\frac{n}{p} \cdot \log_2 \frac{n}{p} = O(\frac{n}{p} \cdot \log_2 n)$. We have reached a perfect parallelization in this case, since the best sequential sorting algorithm runs in time $O(n \cdot \log_2 n)$. For $p > \log_2 n$ we have $n = \Omega(\frac{n}{p} \cdot \log_2 \frac{n}{p} + n)$ and the p merging steps dominate and force Algorithm 2.4 to run in linear time $O(n)$. Thus there is no gain in running time when working with $\omega(\log_2 n)$ nodes. Is Algorithm 2.4 a good sorting algorithm? The answer is certainly "yes", if we have to compute on a linear array.

Exercise 22
(a) Let G be an undirected graph with bisection width w and $p \leq n$ nodes. Show that any sorting algorithm requires $\Omega(n/w)$ compute steps to sort n keys on G, provided only keys can be communicated.

(b) Show that $\Omega(n)$ compute steps are required, when n keys are sorted on the linear array and only keys can be communicated. This claim holds for any number p of nodes.

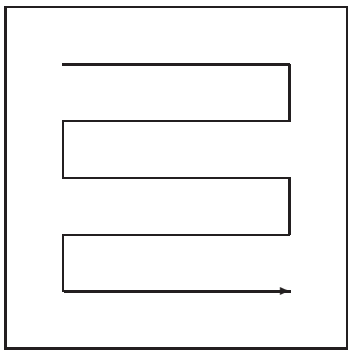
(c) Show that any sorting algorithm on the two-dimensional $\sqrt{p} \times \sqrt{p}$ mesh requires $\Omega(\frac{n}{\sqrt{p}})$ compute steps to sort n keys, when only keys can be communicated.

We define the *work* of a parallel algorithm as the product of the worst-case running time and the number of processors and observe that the work of Algorithm 2.4 is bounded by $O(p \cdot \frac{n}{p} \cdot \log_2 \frac{n}{p} + p \cdot n) = O(n \cdot \log_2 \frac{n}{p} + p \cdot n)$: for $p = O(\log_2 n)$ the work of Algorithm 2.4 is therefore bounded by $O(n \cdot \log_2 n)$. However each communication step involves sending/receiving n/p keys and it dominates the compute step of merging two sorted sequences of length n/p.

If we have the option of designing a communication pattern tailor-made for sorting, then we can achieve work $O(n \log_2 n)$ and running time $O(\frac{n}{p} \cdot \log_2 n)$ for larger choices of p. For instance let us have a look at the two-dimensional mesh.

We use the odd-even transposition sort to describe *shearsort*, a sorting algorithm to sort n^2 keys on the two-dimensional $n \times n$ mesh $M_2(n)$. Shearsort works in $2 \cdot \log_2 n$ phases, if n is a power of two. In odd phases it sorts all rows in parallel and in even phases all columns

are sorted in parallel. To sort odd rows all smaller keys move left, to sort even rows all smaller keys move right and to sort columns all smaller keys move up. All sorting steps utilize the odd-even transposition sort for linear arrays. We show with the 0-1 principle that the final sequence determined by shearsort is sorted in snakelike order.



Lemma 2.7 *Shearsort is correct.*

Proof: We say that a row is *clean*, if it consists only of zeroes or only of ones, and *dirty* otherwise. Assume that n is a power of two. We claim that at any time we have clean 0-rows, followed by at most $n/2^k$ dirty rows and finally only clean 1-rows appear. The claim is correct for $k = 0$, since we have initially at most n dirty rows. To show the inductive step for $k + 1$, we consider two rows in positions $2i - 1$ and $2i$. First both rows are sorted individually in snakelike order.

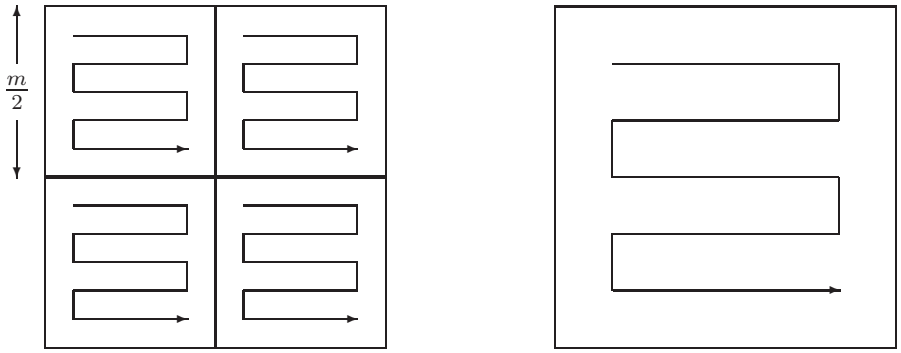
Case 1: the number of zeroes of row $2i$ is at least as large as the number of ones of row $2i-1$. After the first step of column sorting, row $2i-1$ turns into a clean 0-row. Subsequent steps of the column sort move the new 0-row upwards until it hits another 0-row.

Case 2: the number of zeroes of row $2i$ is less than the number of ones of row $2i - 1$. After the first step of column sorting, row $2i$ turns into a clean 1-row. Subsequent steps of of the column sort move the new 1-row downwards until it hits another 1-row. □

Now assume that we work with p instead of n^2 processors which we imagine to be arranged in a $\sqrt{p} \times \sqrt{p}$ mesh of processors. We use the checkerboard decomposition and assign all keys $x_{k,l}$ with $k \in \{(i-1) \cdot \sqrt{\frac{n}{p}} + 1, \ldots, i \cdot \sqrt{\frac{n}{p}}\}$ and $l \in \{(j-1) \cdot \sqrt{\frac{n}{p}} + 1, \ldots, j \cdot \sqrt{\frac{n}{p}}\}$ to processor (i, j). Each processor uses quicksort to sort its n/p keys in time $O(\frac{n}{p} \cdot \log_2 \frac{n}{p})$. Any application of odd-even transposition sort involves $\sqrt{p}$ processors and hence runs in time $O(\sqrt{p} \cdot \frac{n}{p}) = O(\frac{n}{\sqrt{p}})$. Since shearsort applies odd-even transposition sort $2 \log_2 p$ times we obtain the following result.

Theorem 2.8 *If $p \leq n$, then shearsort sorts n keys in time $O(\frac{n}{p} \cdot \log_2 \frac{n}{p} + \frac{n}{\sqrt{p}} \cdot \log_2 p)$ on $M_2(\sqrt{p})$. It uses $O(\sqrt{p} \cdot \log_2 p)$ point-to-point communication steps involving $\frac{n}{p}$ keys.*

Observe that the work of shearsort is bounded by $O(n \cdot \log_2 \frac{n}{p} + \sqrt{p} \cdot n \cdot \log_2 p)$. Hence its work is bounded by $O(n \cdot \log_2 n \cdot \log_2 \log_2 n)$, whenever $p \leq \log_2^2 n$. However we can do better. Our next approach sorts n keys recursively on the two-dimensional mesh $M_{\sqrt{n}}$: we recursively sort the four quadrants of $M_{\sqrt{n}}$ in snakelike order. Then we sort the rows in snakelike order followed by sorting the columns. Finally we sort the "snake" with $2 \cdot \sqrt{n}$ steps of odd-even transposition sort.

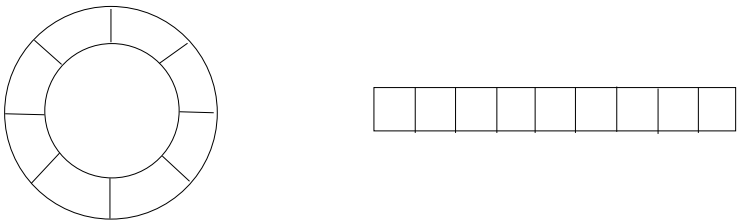


Exercise 23
Let n be a power of two. Show that the recursive algorithm sorts n keys in $O(\sqrt{n})$ compute steps on the two-dimensional $\sqrt{n} \times \sqrt{n}$ mesh.

Exercise 24
Show how to implement the recursive sorting procedure on $M_2(\log_2 n)$ such that n keys are sorted in $O(\frac{n}{\log_2 n})$ compute steps with $p = \log_2^2 n$ processors.

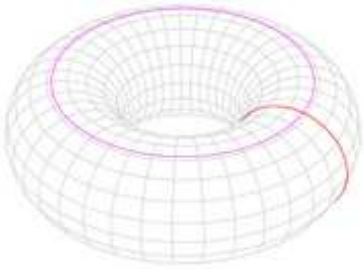
Moreover show that n keys can be sorted optimally (i.e., within work $O(n \cdot \log_2 n)$), whenever at most $p \leq \log_2^2 n$ processors are available. Observe that the odd-even transposition sort can sort n keys optimally whenever $p \leq \log_2 n$.

Exercise 25
(a) The n-cell ring results from the $(n+1)$-cell linear array by identifying the first and the last cell.



Show that an n-cell linear array can simulate an n-cell ring with a slowdown of at most 2. (You may assume that n is even.)

(b) The $n \times n$ torus results from the $n \times n$ two-dimensional mesh after identifying the first and last column as well as the first and last row.



Show that an $n \times n$ torus and an $n \times n$ mesh have equivalent computational power up to constant factors. In particular, show that an $n \times n$ mesh can simulate an $n \times n$ torus with a slowdown of at most two.

Exercise 26

(a) Assume that m divides n. Show how to simulate a mesh $M_2(n)$ on a mesh $M_2(m)$ with slowdown at most $O((n/m)^2)$. Can you do better?

(b) Show how to multiply two $n \times n$ matrices on a p-processor two-dimensional mesh in $O(n^3/p)$ steps for $p \leq n^2$. How efficient is this algorithm? (We assume that each processor receives $O(n^2/p)$ entries.)

2.3 Hypercube Architectures

We begin with another perspective on hypercubes.

Definition 2.9 The *d-dimensional hypercube* $Q_d = (V_d, E_d)$ has node set $V_d = \{0,1\}^d$. The edges of Q_d are partitioned into the sets

$$\{ \{w, w \oplus e_i\} \mid w \in \{0,1\}^d \}$$

of edges of dimension i (for $i = 1, \ldots, d$) where $e_i = (0, \ldots, 0, 1, 0, \ldots, 0)$ is a binary vector with a one in position i.

Observe that $M_d(2) = Q_d$. Nodes of Q_d are binary strings $u \in \{0,1\}^d$ of length d, and two nodes u, v are connected by an edge iff v can be obtained from u by flipping *exactly one* bit. Edges of dimension i correspond to flipping the ith bit.

Note that Q_d has 2^d nodes, $d \cdot 2^{d-1}$ edges and the (high) degree d. There is another equivalent recursive definition of the hypercube. The d-dimensional hypercube consists of two copies of the $(d-1)$-dimensional hypercube (the 0-hypercube and the 1-hypercube) with edges between corresponding nodes in the two subcubes: there is an edge between node $0x$ in the 0-hypercube and node $1x$ in the 1-hypercube for any $x \in \{0,1\}^{d-1}$.

We show that the d-dimensional hypercube $Q_d = (V_d, E_d)$ is a very robust graph in the following sense: consider how many edges must be removed to separate a subset $S \subseteq V_d$

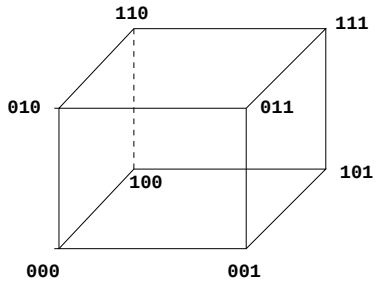


Figure 2.3: The 3-dimensional hypercube.

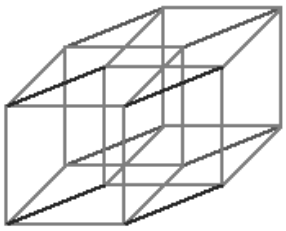


Figure 2.4: A 4-dimensional hypercube.

of nodes from the remaining nodes $\bar{S} = V_d - S$. Assume that S is the smaller set, i.e. $|S| \leq |\bar{S}|$. A *cut* $C(S, \bar{S})$ between S and $\bar{S}$ is a set of edges whose removal disconnects S and $\bar{S}$.

Theorem 2.10 *For every subset of nodes S with $|S| \leq |\bar{S}|$ we have $|C(S, \bar{S})| \geq |S|$.*

Proof: By induction on d. The base case $d = 1$ is trivial. For the induction step, take an arbitrary subset $S \subseteq V_d$ such that $|S| \leq |\bar{S}|$; hence, $|S| \leq 2^{d-1}$. Let $S_0 \subseteq S$ be the set of nodes of S in the 0-hypercube, and $S_1 \subseteq S$ be the set of nodes of S in the 1-hypercube.

Case 1: If $|S_0| \leq 2^{d-1}/2$ and $|S_1| \leq 2^{d-1}/2$, then applying the induction hypothesis to each of the subcubes shows that the number of edges between S and $\bar{S}$, even without considering edges between the 0-subcube and the 1-subcube, already exceeds $|S_0| + |S_1| = |S|$.

Case 2: Suppose $|S_0| > 2^{d-1}/2$. Then $|S_1| \leq 2^{d-1}/2$. By the induction hypothesis, the number of edges in $C(S, \bar{S})$ within the 0-subcube is at least $|\bar{S_0}| = 2^{d-1} - |S_0|$, and those within the 1-subcube is at least $|S_1|$. But now there must be at least $|S_0| - |S_1|$ edges in $C(S, \bar{S})$ between the two subcubes, since every node $0x \in S_0$ is connected with the *unique* node $1x$ in the 1-subcube and only $|S_1|$ edges connect nodes in S. Thus, the entire cut consists of at least $(2^{d-1} - |S_0|) + |S_1| + (|S_0| - |S_1|) = 2^{d-1}$ edges and we are done since $|S| \leq 2^{d-1}$. □

Corollary 2.11 *The bisection width of Q_d is 2^{d-1}.*

Proof: We already know that the bisection width of Q_d is at most 2^{d-1}. But Theorem 2.10 implies that at least 2^{d-1} edges must be removed to disconnect a subset of size 2^{d-1} and hence 2^{d-1} is a lower bound for the bisection width. □

Exercise 27
Let $G = (V, E)$ be an undirected graph. We say that a mapping $f : V \to V$ is an automorphism of G iff f is bijective and

$$\{u, v\} \in E \Leftrightarrow \{f(u), f(v)\} \in E$$

holds for all $u, v \in V$. Show that

$$(x_1, \ldots, x_d) \mapsto (x_{\pi(1)}, \ldots, x_{\pi(d)})$$

is an automorphism of Q_d for any permutation π of $\{1, \ldots, d\}$.

Why does the hypercube play a prominent role among communication patterns? There are several reasons.

- The diameter of Q_d is d and hence logarithmic in the number of nodes. Thus any two nodes can communicate after logarithmically many steps.
- The previous property also applies to the complete binary tree T_d. However T_d has severe bottlenecks, or, in other words, its bisection width is one: we partition T_d into two halves (of almost same size) when removing an edge that is incident to the root. But the bisection width of Q_d is 2^{d-1}.
- Q_d has good routing algorithms. A first algorithm is the bit-fixing strategy: when moving a packet from u to v, "fix" bits successively by moving the packet along those dimensions in which u and v differ. Bit-fixing is good for many routing problems, but may degenerate severely. It turns out that a randomized routing scheme (see Section 2.3.3) always does the job with high probability.
- A good network should be able able to simulate other important networks without significant congestion and delay. We show in this section that Q_d can simulate trees and meshes with ease.
- Q_d is tailor-made to simulate divide & conquer algorithms through its recursive structure.

Exercise 28
Show how to transpose a $2^d \times 2^d$ matrix on the hypercube Q_{2d} in time $O(d)$.

Hint: bit fixing does not work. Use a divide & conquer algorithm instead.

Exercise 29
Let $n = 2^d$. Show how to solve a solve a parallel prefix problem on the elements $x_0, x_1, \ldots, x_{n-1}$ in time $O(d)$ on Q_d. We assume that processor u receives the element $x_{|u|}$ as input, where $|u|$ is the number with binary representation u, and outputs $x_0 * \cdots * x_{|u|}$.

2.3.1 Simulating Trees and Meshes

We first worry about simulating trees. We have apparently bad news, since the complete binary tree T_d is not a subgraph of Q_{d+1}. Why? We observe that hypercube edges flip the parity of nodes and hence all nodes of Q_{d+1} corresponding to tree nodes of fixed depth have the same parity. But then the $2^{d-2} + 2^d > 2^d$ hypercube nodes corresponding to tree nodes of depth $d-2$ and d have the same parity and this is impossible since there are exactly 2^d hypercube nodes of parity zero respectively one in Q_{d+1}.

However we can simulate *normal* tree algorithms easily by *normal* algorithms on the hypercube.

Definition 2.12 **(a)** An algorithm with communication pattern T_d is a normal tree algorithm, if at any time only nodes of identical depth are used. Moreover, if only nodes of depth i are used at time t, then only nodes of depth $i-1$ or only nodes of depth $i+1$ are used at time $t+1$.

(b) We say that an edge $e = \{u, v\}$ of the hypercube Q_d is active at time t iff u and v exchange information at time t.

An algorithm with communication pattern Q_d is a normal hypercube algorithm iff at any time, edges of only one dimension are active and if edges of dimension i are active at time t, then at time $t+1$ edges of dimension $\begin{cases} 1 & i = d, \\ i+1 & \text{otherwise} \end{cases}$ or $\begin{cases} d & i = 1, \\ i-1 & \text{otherwise} \end{cases}$ are active.

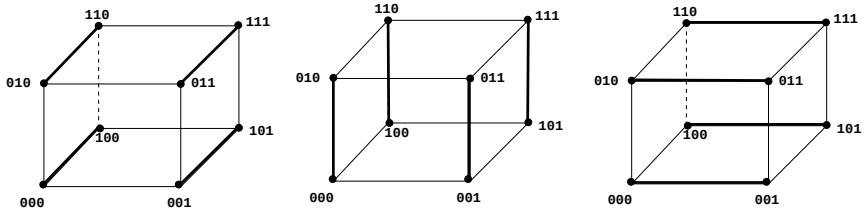


Figure 2.5: Three steps of a normal algorithm on Q_3.

Theorem 2.13 *Any normal tree algorithm on T_d can be simulated by a normal hypercube algorithms on Q_d without any slowdown. In particular, the hypercube algorithm sends no more messages than the normal tree algorithm.*

Proof: We label an edge of T_d leading to a left child by zero and an edge leading to a right child by one. Thus in particular, if label(v) is the 0-1 sequence of labels on the path from the root to v, then we can identify v by label(v). We simulate the tree node v by the hypercube node $v^* = \text{label}(\text{lm}(v))$, where lm($v$) is the leftmost leaf in the subtree with root v.

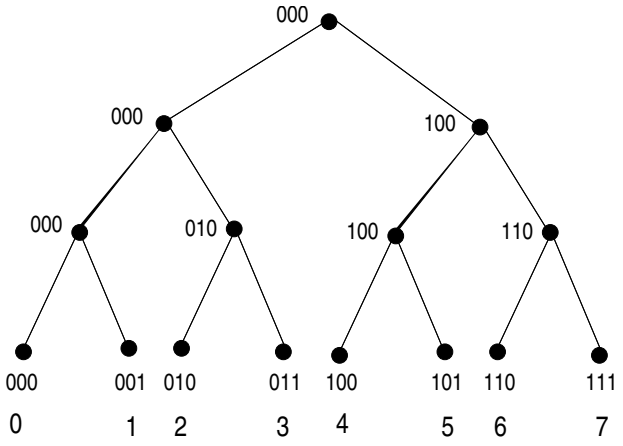


Figure 2.6: The leftmost leaf representation of tree nodes.

The mapping $v \mapsto v^*$ is not injective, since the $d+1$ tree nodes $\varepsilon, 0, 0^2, \ldots, 0^d$ for instance are all mapped to the hypercube node 0^d, but we also have the following positive properties:

- Tree nodes of same depth t are simulated by distinct hypercube nodes from the set $\{0,1\}^t \cdot 0^{d-t}$. Thus a communication with children is easy on hypercubes using the edges $\{w0^{d-t}, w10^{d-t-1}\}$ and a tree node and its left child are simulated by the same hypercube node.
- Edges to right children, originating in tree nodes from the same layer, are therefore mapped into hypercube edges of identical dimension.

Thus we may simulate any normal tree algorithm without slowdown. □

We show next how to embed a generalized class of meshes.

Definition 2.14 We define the generalized mesh $M_d(n_1, \ldots, n_d)$, for numbers $n_1, \ldots, n_d \in \mathbb{N}$, as the undirected graph with node set

$$V = \times_{i=1}^{d} \{1, \ldots, n_i\}.$$

As for conventional meshes we connect two nodes u and v iff their distance $\sum_{i=1}^{d} |u_i - v_i|$ is exactly one.

Theorem 2.15 *Assume that $n_1, \ldots, n_d$ are powers of 2. If*

$$D = \sum_{i=1}^{d} \log_2 n_i,$$

then $M_d(n_1, \ldots, n_d)$ is a subgraph of Q_D. In particular, any mesh algorithm $\mathcal{M}$ can be simulated by a hypercube algorithm which sends no more messages than $\mathcal{M}$.

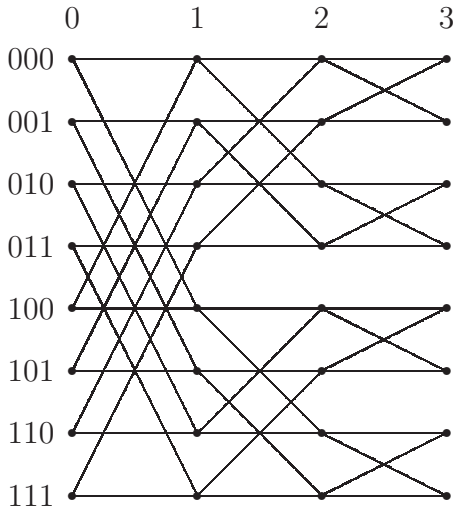
Proof: We first observe that the hypercube has a Hamiltonian path. (Why? Proceed inductively, run the Hamiltonian path first in the subcube $0\{0,1\}^d$, then "move up" into the subcube $1\{0,1\}^d$ and run the path backwards.)

Let P_j be a Hamiltonian path for the hypercube $Q_{\log_2 n_j}$. We map node $(i_1, \ldots, i_d)$ of $M_d(n_1, \ldots, n_d)$ to the hypercube node $v^1(i_1) \circ \cdots \circ v^d(i_d) \in Q_D$, where $v^j(i)$ is the ith node of P_j, and $\circ$ denotes the concatenation of strings.

The mapping is obviously injective. Moreover any edge of $M_d(n_1, \ldots, n_d)$ connects two nodes which differ in exactly one coordinate j and their difference (in absolute value) is one. Thus, if the first endpoint is mapped to $v^1(i_1) \circ \cdots \circ v^j(i_j) \circ \cdots \circ v^d(i_d)$, then the second endpoint is mapped to (say) $v^1(i_1) \circ \cdots \circ v^j(i_j + 1) \circ \cdots \circ v^d(i_d)$ and the two hypercube nodes are connected, since $v^j(i_j)$ and $v^j(i_j + 1)$ are connected in $Q_{\log_2 n_j}$. □

2.3.2 Butterflies

Q_d has however the severe disadvantage of a large degree. We therefore propose butterfly networks, a degree four network which is capable of simulating the hypercube quickly.



The butterfly network B_3.

Definition 2.16 The nodes of the *d-dimensional butterfly network* B_d are pairs (u, i) with $u \in \{0,1\}^d$ and $0 \leq i \leq d$. Nodes (u, i) and $(v, i + 1)$ are joined by a "horizontal edge" iff $u = v$ or by a "crossing edge" iff u and v differ only in their $(i + 1)$st bit. We say that $C_i := \{(w, i) \mid w \in \{0,1\}^d\}$ is the $i$the column and $R_w := \{(w, i) \mid 0 \leq i \leq d\}$ is the row of $w \in \{0,1\}^d$.

Butterfly networks are sometimes introduced differently by identifying the first and last column. This variant is called the *wrapped butterfly* B_d^*. Here are some important properties of B_d.

- *The recursive structure of* B_d: B_d is composed of two disjoint copies of B_{d-1} on columns $C_0, \ldots, C_{d-1}$. The first copy occupies the even rows R_{u0} and the second copy occupies the odd rows R_{u1} (for $u \in \{0,1\}^{d-1}$). (Observe that edges ending in a column C_i $(i < d)$ connect even with even and odd with odd rows.) Two more copies can be found on columns $C_1, \ldots, C_d$ with the first copy occupying rows R_{0u} and the second copy occupying rows R_{1u} (for $u \in \{0,1\}^{d-1}$).
- *The butterfly network* B_d *and the hypercube* Q_d: B_d is tailor-made to simulate parallel computations of the hypercube Q_d. The nodes of a row R_u play the role of node u of the hypercube. Observe moreover that hypercube edges of dimension i correspond to edges connecting nodes of C_{i-1} to nodes of C_i.

Lemma 2.17 *(a) The butterfly network* B_d *and the wrapped butterfly have the same number* $d \cdot 2^{d+1}$ *of edges and both have degree* 4. B_d *has* $(d+1) \cdot 2^d$ *nodes, the wrapped butterfly has* $d \cdot 2^d$ *nodes.*

(b) The diameter of B_d *is* $2 \cdot d$ *and decreases to* $\lfloor \frac{3d}{2} \rfloor$ *for the wrapped butterfly.*

(c) B_d *has bisection width* $\Theta(2^d)$ *and its wrapped version has bisection width* 2^d.

Exercise 30
Show Lemma 2.17 (a) and (b).

The advantage of the butterfly network is its low degree of 4, its disadvantage is the $O(d)$ delay in simulating arbitrary computations of Q_d. But wrapped butterflies are very fast when simulating normal algorithms on the hypercube.

Theorem 2.18 *If a normal algorithm on* Q_d *starts by communicating along dimension one, then it can be simulated on* B_d^* *with a slowdown of two. In particular, any hypercube algorithm* $\mathcal{H}$ *on* Q_d *can be simulated by a butterfly algorithm on* B_d^* *which sends twice as many messages as* $\mathcal{H}$.

In later applications we assume a slightly different perspective and interpret a row as a single process. Horizontal edges indicate successive time steps and crossing edges stand for hypercube communications. Thus we use butterfly communications to represent normal hypercube algorithms and achieve under this perspective no slowdown whatsoever.

A further important property of B_d or B_d^* is its fast simulation by smaller butterflies.

Exercise 31
Assume that $d < e$. Then any algorithm $\mathcal{B}_e$ on B_e can be simulated by an algorithm $\mathcal{B}_d$ on B_d which sends no more messages than $\mathcal{B}_e$ and actually may send fewer messages. The compute time of $\mathcal{B}_d$ grows by at most the factor 2^{e-d} in comparison to $\mathcal{B}_e$.

2.3.3 Routing on Hypercubes

Our goal is to implement the communication primitive "permutation routing": we are given a network $G = (V, E)$, a permutation $\pi : V \to V$ and assume that each node $v \in V$ wants to send a message packet P_v along some path from v to node $\pi(v)$. We require that only one packet may traverse an edge at any time and try to route all packets to their destination as quickly as possible. Hence we have to construct congestion-free routing.

We call a routing algorithm *conservative*, if the path of any packet only depends on the address $\pi(v)$ of the destination. This class of algorithms seems reasonable, but deterministic algorithms within this class are forced to fail!

Fact 2.1 *[KKT91] Let G be an undirected graph of N nodes. Assume that each node in G has at most D neighbors. Furthermore let A be a conservative, deterministic routing algorithm. Then there is a permutation π for which A requires at least $\Omega(\frac{\sqrt{N}}{D})$ steps.*

Exercise 32
Let $G = (V, E)$ be an arbitrary connected undirected graph with N nodes and degree D. A conservative routing algorithm is uniquely determined by the $\binom{N}{2}$ paths $\mathcal{P}(u, v)$ from u to v (with $u \neq v$). We define $\mathcal{P}(v)$ as the set of all such paths ending in v and $S_k(v)$ as the set of all nodes $x \in V$ which are traversed by at least k paths from $\mathcal{P}(v)$.

(a) Show that $|\mathcal{P}(v)| \leq |S_k(v)| + |S_k(v)| \cdot D \cdot (k-1)$ holds and hence $|S_k(v)| \geq N/(D(k-1)+1)$ follows. Hint: How many paths from $\mathcal{P}(v)$ run along an edge $\{u, w\}$ with $u \in S_k(v)$ and $w \in \overline{S_k(v)}$?

(b) Show that there is a node $x \in V$ and a permutation π of V such that at least $k = \sqrt{N/D}$ paths $\mathcal{P}(u, \pi(u))$ traverse x.

(c) Show that for any conservative routing algorithm $\mathcal{A}$ there is a permutation π of V for which $\mathcal{A}$ runs for at least $\Omega(\sqrt{N/D^3})$ steps.

Example 2.4 We consider the d-dimensional hypercube Q_d. The *bit-fixing strategy* checks the address bits beginning with position 1 and ending with position d. If position i is considered and the packet P_v with address $\pi(v)$ has reached node w, then the packet does not move, if w and $\pi(v)$ agree in their ith bit. Should they however disagree, then P_v is sent along the edge corresponding to bit i. (For instance, $(111, 011, 001, 000)$ is the bit-fixing path from $v = 111$ to $\pi(v) = 000$.)

Bit-fixing fails for the routing problem $(x, y) \to (y, x)$, where x (resp. y) is the first (resp. second) half of all bits of the sender v. What happens? The $\sqrt{2^d}$ packets of the sending nodes $(x, 0)$ clog the bottleneck $(0, 0)$.

Exercise 33
(a) We have to implement a partial routing problem on the d Butterfly network B_d, where some nodes in column C_d wish to communicate with nodes in column C_0. The goal is that the ith node (among nodes wishing to communicate) sends its packet to the ith node in column C_0. In other words, the order among packets to be sent is preserved and gaps are closed.

Show how to implement this routing problem in time $O(d)$. Hint: bit fixing.

(b) Our goal is to implement radix sort on B_d assuming that node (u, d) receives the key x_u. Show how to implement one phase of radix sort in time $O(d)$.

If we consider the d-dimensional hypercube Q_d, then d is the diameter, that is the maximal distance between any two nodes. Thus we should expect a good routing algorithm to run in time $O(d)$. However fact 2.1 forces the clearly unacceptable running time of $\Omega(\sqrt{\frac{2^d}{d}})$ in the worst-case. Randomized conservative algorithms however face no problems on the hypercube.

Algorithm 2.19 **Randomized routing on the hypercube**

(1) The permutation π describes the routing problem on the d-dimensional hypercube.

(2) **Phase 1:** Sending packets to a random destination.

each packet P_v chooses a destination $z_v \in \{0,1\}^d$ at random. Packet P_v then follows the bit-fixing path from v to z_v.

(3) **Phase 2:** Sending packets to the original destination.

Packet P_v follows the bit-fixing path from z_v to $\pi(v)$.

Observe that we do not require any queuing strategies whatsoever. The only requirement is that we send some packet along an edge e, if at least some packet is waiting in the queue of edge e. We begin with the analysis of phase one. The following observations are crucial.

- If two packets P_v and P_w meet at some time during the first phase, then they will not meet again later in phase one. (That is, if two packets P_v and P_w meet at some time and diverge at some later time then the two paths will be node-disjoint from that point on.)

- Assume that packet P_v runs along the path $(e_1, \ldots, e_k)$. Let $\mathcal{P}$ be the set of packets different from P_v which run along some edge in $\{e_1, \ldots, e_k\}$ during phase one. Observe that the waiting time of P_v is bounded by $|\mathcal{P}|$ from above.

The second observation is not obvious, since a packet P_w may repeatedly block a packet P_v. (Two packets block each other, if both belong to the same queue at some time.) Hence we establish this observation by induction on the size of $\mathcal{P}$. The basis $|\mathcal{P}| = 0$ is trivial and we assume $|\mathcal{P}| = n + 1$.

Exercise 34
Show that there is packet $P_w \in \mathcal{P}$, that blocks P_v at most once.

The packet P_w from the above exercise is only responsible for P_v waiting for one time step. We remove P_w from $\mathcal{P}$ and obtain the claim from the induction hypothesis. For the rest of the analysis we introduce the random variables

$$H_{v,w} = \begin{cases} 1 & P_v \text{ and } P_w \text{ run over at least one joint edge,} \\ 0 & \text{otherwise.} \end{cases}$$

Due to the last observation, the total waiting time of P_v during phase one is upper-bounded by $\sum_w H_{v,w}$. How large is the expected value of $\sum_w H_{v,w}$ and how likely are large deviations? Assume that W_i is the number of bit-fixing paths which traverse the ith edge of P_v. Then

$$\mathrm{E}\left[\sum_w H_{v,w}\right] \leq \frac{d}{2} \cdot \mathrm{E}\left[W_1\right]. \tag{2.1}$$

Why? The randomized routing of phase 1 guarantees that all edges carry the same expected load. In particular, all edges carry the expected load $E[W_1]$ of the first edge of P_v and the claim follows, since the path travelled by P_v has expected path length $\frac{d}{2}$. (Observe that the right hand side of (2.1) counts a colliding packet multiple times, namely once for each contested edge.)

We can determine the expected load $\mathrm{E}\left[W_1\right]$ as follows: the expected path length of a packet is $\frac{d}{2}$ and hence the $d \cdot 2^{d-1}$ edges of the hypercube all carry the same expected load

$$\mathrm{E}\left[W_1\right] = \frac{\frac{d}{2} \cdot 2^d}{d \cdot 2^{d-1}} = 1.$$

Thus we get $\mathrm{E}\left[\sum_w H_{v,w}\right] \leq \frac{d}{2}$ as a consequence of (2.1). We apply the Chernoff bound (Theorem 1.8) and get

$$\mathrm{prob}\left[\sum_w H_{v,w} \geq (1+\beta) \cdot \frac{d}{2}\right] \leq e^{-\beta^2 \cdot \frac{d}{2}/3}.$$

We set $\beta = 3$ and the probability of a total waiting time of at least $2 \cdot d$ is upper-bounded by $e^{-3 \cdot d/2}$. Since we are dealing with 2^d packets, the probability that some packet requires more than $2 \cdot d$ waiting steps is upper-bounded by $2^d \cdot e^{-3 \cdot d/2} \leq e^{-d/2}$. The analysis of the second phase is completely analogous and we can summarize.

Theorem 2.20 *The following statements hold with probability at least* $1 - 2 \cdot e^{-d/2}$*:*

(a) each packet reaches its destination in each phase after at most $3 \cdot d$ *steps,*

(b) each packet has reached its final destination after at most $6 \cdot d$ *steps.*

Exercise 35
In the routing problem for a general networks we assume that packets are to be routed according to a partially defined permutation.

Assume that we can sort n keys in time $t(n)$ on a given network $\mathcal{N}$. Show that any partial permutation can be routed in time $O(t(n))$ on $\mathcal{N}$.

Now assume that we are given an arbitrary undirected graph G with 2^d nodes and degree c. Then it can be shown that the set of edges of G is the union of at most c matchings, where a matching is a set of node-disjoint edges.

Exercise 36
Show that each edge of an undirected graph of degree c belongs to one of at most c matchings.

We can interpret each matching as a partially defined permutation which we know how to route in time $O(d)$ with high probability and hence we can simulate any graph with 2^d nodes and degree c in time $O(c \cdot d)$ on the d-dimensional hypercube.

Chapter 3

The Message Passing Interface

The message passing interface, MPI for short, is a message passing library standard which can be used in conjunction with conventional programming languages such as C, C++ or Fortran. Free versions of MPI libraries are available and MPI algorithms can be ported on a variety of different platforms, although the algorithmic performance may vary from platform to platform. Nowadays MPI is the de-facto standard when writing parallel scientific applications for high performance clusters.

MPI supports the point-to-point Send and Receive operations between a specified sending process and a specified receiving process through its *communication primitives*, the **MPI_Send** and **MPI_Recv** commands. MPI_Send basically takes as arguments the location of the data to be sent as well as the description of the receiving process. The arguments of its counterpart MPI_Recv describe the sending process and the memory location destined for the message.

There are several versions of send, dependent on whether *message buffering* is allowed, a matching "ready" message from the receiver is required or the entire communication has to terminate. The sending process starts communication after receiving a request from the recipient or after receiving a ready message from the recipient as reply to its own request to send. As long as the recipient has not replied, the sender either has to leave its send buffer unchanged or it may copy the send buffer into a system buffer. In both cases the particular version of send either allows communication to continue as a background process or it may force the sender to wait in order to synchronize communication. If the recipient has replied, the message is copied from its respective buffer into the communication buffer (such as the TCP/IP buffer) and the "bits flow into the cable".

A communication routine is *blocking*, if the completion of the call is dependent on certain events such as successful message delivery or message buffering. Network interfaces transport messages from the communication buffer to their target location without processor intervention and hence non-blocking communication helps to mask the communication overhead. Non-blocking operations are more efficient than blocking operations, but now unsafe memory access has to be avoided and additional code has to check the status of the

communication process running in the background. We mention the following variants of the send operation with MPI_Isend as the only non-blocking and MPI_Bsend, MPI_Ssend as at least "partially non-blocking" operations:

- **MPI_Send**: MPI copies short messages into a system buffer, where the message length depends on the system in use. For a long message the sender has to wait until the message is successfully delivered. (Blocking, send buffer can be reused.)
- **MPI_Ssend** (synchronous send): terminates only if all bits have left the send buffer and the receiver has begun reception. At this time sender and receiver have synchronized. (Blocking, send buffer can be reused.)
- **MPI_Bsend** (buffered send): If no matching receive operation is posted, then MPI copies the message into a user controlled buffer. The sender can resume work without waiting for the successful delivery of the message. (Blocking, send buffer can be reused.)
- **MPI_Isend** (immediate send): the request to send is posted immediately and the sender can resume work. (Non-blocking, send buffer should *not* be reused.)

Based on its communication primitives MPI supports a variety of *collective communication* functions, in which a group of processes cooperates to distribute or gather a set of values. This set of operations is based on the concept of a *communicator*, which defines a set of processes and attributes of this set. One such attribute is the topology of the communicator such as mesh topologies and general graph topologies. Processes receive coordinates and can be addressed by these coordinates.

We list the following fundamental collective communication functions assuming that p processes are participating.

- **MPI_Bcast** is a *one-to-all broadcast*, namely a specified value is to be sent to all processes of the communicator.
- **MPI_Scatter**, a *one-to-all personalized broadcast* sends messages $M_1, \ldots, M_p$ from a root process to all other processes of the communicator. In particular, the ith process of the communicator is to receive message M_i.
- **MPI_Gather** is the counterpart of MPI_Scatter. This time the ith process sends a message M_i to a specified root process.
- **MPI_Allgather** is an *all-to-all broadcast* operation: each process i specifies a message M_i that it wants to broadcast. At the completion of the all-to-all broadcast each process of the communicator has to know all messages $M_1, \ldots, M_p$.
- **MPI_Alltoall** is an *All-to-all personalized broadcast*: each process i specifies messages M_j^i that it wants to send to process j. At the completion of the broadcast process j has to know all messages $M_j^1, \ldots, M_j^p$.

Example 3.1 Assume that we want to determine the transpose of a $p \times p$ matrix A, where process i initially stores the ith row and is supposed to finally store the ith column. All we have to do is to implement an all-to-all personalized broadcast in which process i sends $M_j^i = A[i, j]$ to process j.

MPI also supplies collective communication functions in which data is manipulated.

- In **MPI_Reduce** an associative operation $*$ and a root process is distinguished. The result $M_1 * \cdots * M_p$ has to be assigned to the root process. One can choose for instance from the following list of operations: maximum, minimum, sum, product, and, or, xor, bitwise and, bitwise or, bitwise xor.
- **MPI_Allreduce** works as MPI_Reduce, but the result is distributed to all processes of the communicator.
- **MPI_Scan** is the prefix version of MPI_Reduce: process i has to receive the "sum" $M_1 * \cdots * M_i$.

The above MPI operations belong to MPI version 1. In Section 3.1 we analyze the communication resources required for each of the above MPI functions.

3.1 Analyzing MPI Programs: The LogGP Model

Already the analysis of a sequential algorithm is a challenge, since the speed of the processor, access times to caches, DRAM-memory and external memory differ considerably and, as a consequence, the new area of algorithm engineering is emerging. But counting the number of "dominant operations" (such as the number of additions and multiplications when computing a matrix-vector product or the number of comparisons when sorting) and taking the memory hierarchy (cache, main memory, external memory) into account one obtains in many cases reliable estimates of the actual running time. The situation for parallel algorithms on multicomputers is even more complex, since the cost of communicating overwhelms the cost of local computing or memory operations, slowing down the algorithm in some and being harmless in other cases.

Which characteristics of a parallel machine are of interest when evaluating a parallel algorithm? In the LogGP model [CKP93, AISS95] the following parameters are distinguished as crucial parameters when determining the algorithmic performance on a wide variety of parallel platforms and it is argued that these parameters suffice for an approximate estimate of the actual running time.

- **L** is an upper bound on the latency, which is the length of the time interval beginning when the first bit "'hits the cable"' and ending with receiving the last bit for a (short) point-to-point message of the *canonical message length* w.

- During the time interval of length **o** the processor involved in the communication process cannot perform any other operation. The overhead does depend on the variant of the send operation, for instance if message buffering is required. Therefore we single out the synchronous MPI_Ssend. Header information has to be supplied, the message has to be copied into the communication buffer and the sender-receiver handshake has to complete (verifying that the recipient is ready to receive).

- **g** is the gap parameter. g is defined as the minimum time interval between consecutive message transmissions or consecutive message receptions at a processor. $\frac{1}{g}$ is the available per-processor communication bandwidth.

- **G** is defined as the time per byte for long messages. $\frac{1}{G}$ is the available per-processor communication bandwidth for long messages.

- **P** is the number of processors.

The LogGP model has several advantages compared to other analysis models. For instance, it makes sense to differentiate overhead o and latency L (instead of considering $o + L + o$ as new latency), since the processor is free for L steps to compute locally, but occupied for o steps. Moreover short and long messages are treated differently to capture performance gains if the platform provides additional support for long messages. The model seems however rather coarse, since one does not distinguish between sending and receiving overheads o_S, o_R and also tacitly assumes that messages are routed without congestion. However the difference between o_R and o_S is not considerable and it makes sense to postulate congestion-free routing, since only "good" algorithms deserve an analysis.

The relative sizes of the various parameters vary from architecture to architecture. For instance the current Myrinet implementation of the CSC cluster has a bandwidth of 1,92 Gbit/sec and a latency of about 7μs, whereas Gigabit Ethernet has a bandwith of 1 Gbit/sec and a latency of about 100 μs. The canonical message length w is 16 KB and since $\frac{128Kbit}{1.92Gbit} \approx 66 \cdot 10^{-6}$ (resp. $\frac{128Kbit}{1Gbit} = 128 \cdot 10^{-6}$) we obtain $g \approx 66\mu s$ for Myrinet (resp. $g \approx 128\mu s$ for Gigabit Ethernet). Determining exact bounds for the overhead is difficult, but experiments give $o \approx 70\mu s$ as an approximation for MPI_Ssend on the Myrinet and gap and overhead almost coincide.

Below we assume that all parameters are measured as multiples of the processor cycle. We now describe implementations of the MPI functions discussed in the previous section and analyze our implementations in the LogGP model.

MPI_Send

When sending a small message (of length w), we incur the overhead o at the sending processor, the network latency L and the overhead o at the receiving processor. Moreover, if we send a long message of n bytes, then this message is broken up into $\lceil n/w \rceil$ messages of length w. The sending and receiving processors incur the overhead o for every partial

message, but only the larger of overhead and gap has to be counted. Moreover observe that only the latency of the last message is of relevance, since we may inject new messages after g steps. Thus the total delay for the n-byte message is

$$T_{\text{Send}} = o + (\lceil \frac{n}{w} - 1 \rceil) \cdot \max\{o, g\} + L + o = O(n) \tag{3.1}$$

processor cycles, if we assume a machine *without* additional support for long messages. The sending processor however loses "only" time $o + (\lceil \frac{n}{w} - 1 \rceil) \cdot o$. If however additional support for long messages is provided, then the k-byte message incurs the delay

$$T^*_{\text{Send}} = o + (n-1) \cdot G + L + o = O(n). \tag{3.2}$$

(The first byte goes after o steps "into the wire" and subsequent bytes follow in intervals of length G. The last byte exits the wire at time $o + (n-1) \cdot G + L$. Observe that the sending and receiving processor are kept busy only at the very beginning and at the very end. At all other times the processors may go back to their local computation and thus overlap computation with communication.)

Observe that (3.1) and (3.2) coincide for $k = 1$. Neither in (3.1) nor in (3.2) does latency play a decisive role for long messages. Dependent on the platform the difference between the breakup of long messages into short ones (see (3.1)) and supporting long messages directly (see (3.2)) can be considerable [AISS95].

MPI_Bcast

To analyze the **one-to-all broadcast** we have to first define the binomial trees B_k with 2^k nodes. B_0 is a singleton tree. If B_k is defined, then we obtain B_{k+1} from B_k by attaching the root r_2 of a second copy T_2 of B_k as child of the root r_1 of a first copy T_1. Observe that B_k has depth k.

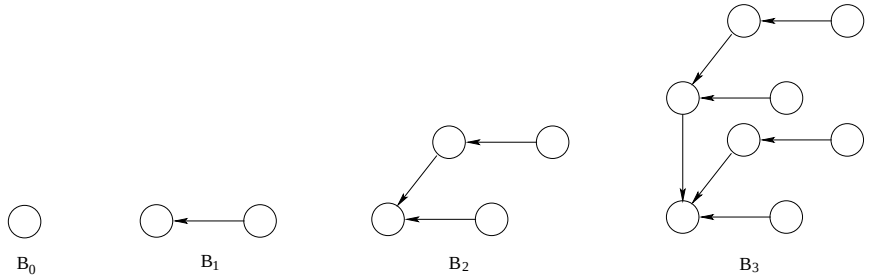


Figure 3.1: The first four binomial trees.

We assume that r broadcasts a message M of length w. r initiates the broadcast by sending M to process s. Now r continues with recursively broadcasting M in its tree T_1, whereas s broadcasts M in its tree T_2. The broadcast then proceeds recursively and is hence called

recursive doubling. To analyze the communication time we first observe that r feeds M after o cycles into the network. s receives M after $o + L + o$ steps and it can feed M after a total of $(o + L + o) + o$ cycles into the network. Thus a child of s receives M after $2 \cdot (o + L + o)$ cycles and, with an inductive argument, we obtain

$$T_{\text{Bcast}} \leq \lceil \log_2 p \rceil \cdot (o + L + o)$$

as the total number of required cycles. The gap parameter does not play a role, if $g \leq o + L + o$: in this case r sends its second message before s sends its first message.

The broadcasting problem in T_1 however is solved faster, since r_1 does not have to wait until r_2 receives M. Thus we can do better, if instead of using the binomial tree we use a tree with a higher fanout for the root r_1. The higher fanout helps us to keep r_1 busy sending messages while r_2 is waiting for M. The choice of the new fanout depends on the relative sizes of L, o and g; thus g does play a role in an optimal algorithm.

Exercise 37
Assume that the latency L, the overhead o, the gap g and the number p of processors is known. Design an efficient sequential algorithm which determines an optimal broadcast tree, that is a broadcast tree which supports a broadcast within minimal time.

Hint: use dynamic programming.

Exercise 38
Assume that we have to broadcast a message of general length n.

(a) Determine the number of cycles, if the binomial tree algorithm is used. What is the asymptotic performance?

(b) MPI uses binomial trees for short messages, but applies a combination of Scatter and Allgather for long messages. Sketch the details and analyze the performance.

MPI_Scatter and MPI_Gather

The communication pattern for **one-to-all personalized broadcast** is identical to the one-to-all broadcast and uses the binomial tree approach. However the source processor r_1 starts by sending the concatenated message $M_{p/2+1} \circ \cdots \circ M_p$ to r_2. This approach is recursively repeated by subsequent processors who break up the concatenation and propagate the corresponding substring of messages. To analyze the total communication time we assume that long messages are supported and obtain $o + (\frac{p}{2} \cdot n - 1) \cdot G + L + o$ cycles in the first round, if all messages have length n. Hence an inductive argument shows that

$$\begin{aligned} T_{\text{Scatter}} &\leq \lceil \log_2 p \rceil \cdot (o + L + o) + \sum_{k=1}^{\lceil \log_2 p \rceil} (\frac{p}{2^k} \cdot n - 1) \cdot G \\ &\leq \lceil \log_2 p \rceil \cdot (o + L + o) + p \cdot n \cdot G = O(p \cdot n) \end{aligned}$$

cycles suffice. Not surprisingly we can improve our approach by increasing the fanout of r_1 again to keep it busy while r_2 is waiting. Observe that the one-to-all personalized broadcast

is quite a bit more expensive than the simple broadcast, since G is weighted by p. The MPI_Gather operation is implemented analogously and requires the same resources.

MPI_Allgather

We describe two implementations of the **all-to-all broadcast**. We first use the linear array as communication pattern. In particular we pump all messages through the network once via pipelining: process i sends message M_i to process $i+1$. Then it waits for message M_{i-1} and forwards it immediately to process $i+1\ldots$ Hence the communication time is at most

$$T_{\text{Allgather},1} \leq (o + L + o) \cdot (p - 1),$$

if all messages have length w. Here we assume $g \leq o + L + o$.

In our second implementation we use the hypercube of dimension $\log_2 p$ as communication pattern and perform recursive doubling: processor $u = u_1u_2u'$ sends its message M_u to neighbor $\overline{u_1}u_2u'$, receives message $M_{\overline{u_1}u_2u'}$ in return and computes the concatenation $M_{0u_2u'} \circ M_{1u_2u'}$. This procedure is repeated for neighbor $u_1\overline{u_2}u'$ and afterwards u stores the concatenation $M_{00u'} \circ M_{10u'} \circ M_{01u'} \circ M_{11u'}$. Thus, if all messages have the same length n, we get

$$\begin{aligned} T_{\text{Allgather},2} &\leq \sum_{k=1}^{\lceil \log_2 p \rceil} [o + (\frac{p}{2^k} \cdot n - 1) \cdot G + L + o] \\ &\leq \lceil \log_2 p \rceil \cdot (o + L + o) + p \cdot n \cdot G = O(p \cdot n), \end{aligned}$$

provided all messages have the same length n. Thus MPI_Scatter and MPI_Allgather have identical upper bounds. Observe however that in both of our implementations for MPI_Allgather all processes are busy most of the time.

> **Exercise 39**
> What is the performance of the linear array approach, if all messages have same length n? Which approach, linear array or hypercube, is better assuming extra support for long messages?

In both implementations of Allgather all processors have to carry the same load whereas the tree implementation of Gather and Scatter are unbalanced and allow processors to continue with their local computations until their are called upon by their parent. Moreover, a higher root fanout improves Scatter, but since all processors in Allgather start simultaneously, comparable improvements cannot be obtained for Allgather. Thus from the perspective of the average load, it may be preferable to first run Gather followed by a broadcast.

All-To-All Personalized Broadcast

We show next an implementation of the **all-to-all personalized broadcast** which uses the $\log_2 p$-dimensional hypercube as its communication pattern. We have $p - 1$ phases. In

phase b, for $b \in \{0,1\}^{\log_2 p}$ with $b \neq 0$, processor v sends its message $M^v_{v \oplus b}$ to processor $v \oplus b$.

Exercise 40
Show how to construct edge-disjoint paths $v \to v \oplus b$ in the d-dimensional hypercube for each $b \in \{0,1\}^d$. Thus all communications of the above implementation are congestion-free when routed on the hypercube.

Hence the total communication time for MPI_Alltoall is

$$T_{\text{Alltoall}} = o + L + (\max\{o, g\} + L) \cdot (p-2) + o = T_{\text{Allgather},1},$$

if all messages have length w.

Exercise 41
Show that $T_{\text{Alltoall}} = O(p \cdot n)$, if all messages have length n.

Exercise 42
We consider a second implementation for the all-to-all personalized broadcast which also uses the $\log_2 p$-dimensional hypercube as its communication pattern. Initially processor v concatenates all messages M^v_u with $u_1 \neq v_1$ and sends the concatenation to processor $\overline{v_1} v_2 \cdots v_{\log_2 p}$. Processes continue to use bitfixing (along dimensions $2, \ldots, \log_2 p$) to eventually move all messages to their destination. In particular, in the jth iteration ($1 \leq j \leq \log_2 p$) processor v concatenates all currently stored messages whenever their jth destination bit differs from v_j and sends the concatenation to processor $v_1 \cdots v_{j-1} \overline{v_j} v_{j+1} \cdots v_{\log_2 p}$.

(a) Show that each processor sends exactly one half of its messages at any time. It receives the same number of messages that is sent.

(b) Determine the total communication time of the new implementation.

MPI_Reduce, MPI_Allreduce and MPI_Scan

We implement **MPI_Reduce** with binomial trees of depth $\log_2 p$ as communication pattern. Its communication cost is comparable with MPI_Broadcast for short messages. To implement **MPI_Allreduce** we execute MPI_Reduce, followed by MPI_Bcast. Finally, the communication resources required for **MPI_Scan** are comparable to the resources of MPI_Allreduce, if we utilize our algorithm of Section 2.1.

Let us summarize. The basic operations MPI_Send and MPI_Receive are of course the cheapest functions. Then come MPI_Bcast and MPI_Reduce followed by MPI_Allreduce and MPI_Scan which require twice the resources. The operations MPI_Scatter, MPI_Gather and MPI_Allgather are significantly more expensive. The leader of the pack in resource consumption is not surprisingly MPI_Alltoall.

In the following we use asymptotic estimates of the communication time. The corresponding bounds are only rough estimates, since the asymptotic notation hides large constants. Hence, if the parallel machine is known, then the machine-specific performance of the respective MPI-functions should be used instead.

3.2 Work, Speedup and Efficiency

Assume that a parallel algorithm $\mathcal{P}$ solves an algorithmic problem $\mathcal{A}$. When should we be satisfied with its performance? Assume that our algorithm uses p processors and runs in time $t_{\mathcal{P}}(n)$ for inputs of length n. Furthermore let us assume that any sequential algorithm for $\mathcal{A}$ runs in time at least $\Omega(t(n))$. Certainly we can simulate $\mathcal{P}$ by a sequential algorithm, which requires time $O(p)$ to simulate one parallel step of $\mathcal{P}$ and hence runs in time $O(p \cdot t_{\mathcal{P}}(n))$.[1] But any sequential algorithm for $\mathcal{A}$ requires time $\Omega(t(n))$ and hence

$$p \cdot t_{\mathcal{P}}(n) = \Omega(t(n))$$

follows. Thus

$$\mathbf{work}_{\mathcal{P}}(\mathbf{n}) = \mathbf{p} \cdot \mathbf{t}_{\mathcal{P}}(\mathbf{n}),$$

the work of $\mathcal{P}$ on inputs of size n, is an important performance parameter of $\mathcal{P}$. Observe that the performance of $\mathcal{P}$ is the better, the smaller $\text{work}_{\mathcal{P}}(n)$ is.

Theorem 3.1 *Assume that any sequential algorithm for $\mathcal{A}$ runs in time at least $\Omega(t(n))$ and let $\mathcal{P}$ be a parallel algorithm for $\mathcal{A}$. Then $work_{\mathcal{P}}(n) = \Omega(t(n))$ holds.*

Thus we can evaluate $\mathcal{P}$, if we compare its work with the running time of an (asymptotic) optimal sequential algorithm for $\mathcal{A}$, respectively with the asymptotic running time of the best, currently known algorithm —provided such an algorithm exists.

From now on we assume that $\mathcal{S}$ is a sequential algorithm for $\mathcal{A}$ and that $\mathcal{P}$ is a parallelization of $\mathcal{S}$: any operation performed by $\mathcal{S}$ is also performed by some processor of $\mathcal{P}$. Let $t_{\mathcal{S}}(n)$ be the running time of $\mathcal{S}$. We define the **speedup** $S_{\mathcal{P}}(n)$ of $\mathcal{P}$ by

$$S_{\mathcal{P}}(n) = \frac{t_{\mathcal{S}}(n)}{t_{\mathcal{P}}(n)}$$

and the **efficiency** $E_{\mathcal{P}}(n)$ of $\mathcal{P}$ by

$$E_{\mathcal{P}}(n) = \frac{S_{\mathcal{P}}(n)}{p} = \frac{t_{\mathcal{S}}(n)}{\text{work}_{\mathcal{P}}(n)}.$$

Observe that the speedup $S_{\mathcal{P}}(n)$ is asymptotically bounded by p and hence the efficiency $E_{\mathcal{P}}(n)$ is asymptotically at most one.

Exercise 43
You must clean the parking space of your car from snow. The parking space already contains n cubic meters of snow. One person can remove snow at the rate of x cubic meters per second. Unfortunately, snow is still falling at the rate of y cubic meters per second ($y < x$). But you may

[1] This statement is false, if the sequential algorithm has insufficient main memory and hence is forced to access external memory. Observe that the size of the main memory of the parallel system exceeds the size of the sequential system by the factor p.

ask some of your friends to help. Let $T(n,1)$ be the time taken by one person to clean the parking space, and let $T(n,p)$ be the time taken by p persons.

Compute the speedup $s(p)$ and show that superlinear speedup is achieved, i.e. $s(p) > p$. Why is this possible? Explain.

Exercise 44
In the n-body problem we are given the initial positions, masses, and velocities of n particles. We have to determine their subsequent motions as determined by classical mechanics.

We assume the following simplified setup. The force f_i acting on particle i is defined by

$$f_i = \sum_{j=1, j\neq i}^{n} F(x_i, x_j),$$

where x_i describes the position, mass and velocity of particle i. Design a parallel algorithm with $p \leq n$ processors which determines all f_i with efficiency $\Theta(1)$ and speedup $\Omega(p)$. You may assume that any sequential algorithm runs in time $\Omega(n^2)$.

Assume that we plan on solving the problem $\mathcal{A}$ with a parallel algorithm $\mathcal{P}$ which performs some fraction of its work sequentially. What is the best achievable speedup?

Theorem 3.2 *Let $\mathcal{P}$ be a parallel algorithm that uses p processors.*
(a) Amdahl's Law: Let $f \in [0,1]$ be given. If $\mathcal{P}$ performs $f \cdot t_{\mathcal{S}}(n)$ steps of $\mathcal{S}$ sequentially, then

$$S_{\mathcal{P}}(n) \leq \frac{1}{f + (1-f)/p}.$$

In particular, the speedup is always bounded by $1/f$.
(b) Gustafson-Barsis Law: If $\mathcal{P}$ computes sequentially for $f \cdot t_{\mathcal{P}}(n)$ steps, then

$$S_{\mathcal{P}}(n) \leq p - f \cdot (p-1).$$

Proof: (a) At best $t_{\mathcal{P}}(n) = f \cdot t_{\mathcal{S}}(n) + (1-f) \cdot t_{\mathcal{S}}(n)/p$ and hence

$$S_{\mathcal{P}}(n) = \frac{t_{\mathcal{S}}(n)}{t_{\mathcal{P}}(n)} \leq \frac{t_{\mathcal{S}}(n)}{f \cdot t_{\mathcal{S}}(n) + (1-f) \cdot t_{\mathcal{S}}(n)/p} = \frac{1}{f + (1-f)/p}$$

follows. For (b) we observe that at worst $\mathcal{S}$ runs for $f \cdot t_{\mathcal{P}}(n) + p \cdot (1-f) \cdot t_{\mathcal{P}}(n)$ steps and hence

$$S_{\mathcal{P}}(n) = \frac{t_{\mathcal{S}}(n)}{t_{\mathcal{P}}(n)} \leq \frac{f \cdot t_{\mathcal{P}}(n) + p \cdot (1-f) \cdot t_{\mathcal{P}}(n)}{t_{\mathcal{P}}(n)} = f + p \cdot (1-f) = p - f \cdot (p-1)$$

follows. □

Observe however that the estimates of both laws for the best-case speedup are overly optimistic, since we do not account for the communication overhead.

3.2.1 Varying the Number of Processors

Can we **scale down** the parallel algorithm $\mathcal{P}$, that is can we come up with an equivalent parallel algorithm $\mathcal{Q}$ which runs on q ($q < p$) processors and still at least roughly maintains the efficiency of $\mathcal{P}$? Assume $\mathcal{P}$ performs a total of $\mathrm{op}_i(n)$ operations in step i, where each individual operation is weighted by its execution time. Then the simulation of the ith step requires $\lceil \frac{\mathrm{op}_i(n)}{q} \rceil$ steps with q processors, provided the processors can solve the scheduling problem

determine which processor is to perform which operation

instantaneously. Hence, if the scheduling problem is solvable instantaneously, we get

$$\sum_{i=1}^{t_{\mathcal{P}}(n)} \left\lceil \frac{\mathrm{op}_i(n)}{q} \right\rceil \leq \sum_{i=1}^{t_{\mathcal{P}}(n)} \left(\frac{\mathrm{op}_i(n)}{q} + 1 \right) \leq \frac{\mathrm{work}_{\mathcal{P}}(n)}{q} + t_{\mathcal{P}}(n)$$

as the new running time. Thus the efficiency of $\mathcal{Q}$ is at least

$$\frac{E_{\mathcal{Q}}(n)}{E_{\mathcal{P}}(n)} \geq \frac{\mathrm{work}_{\mathcal{P}}(n)}{q \cdot (\frac{\mathrm{work}_{\mathcal{P}}(n)}{q} + t_{\mathcal{P}}(n))} = \frac{\mathrm{work}_{\mathcal{P}}(n)}{\mathrm{work}_{\mathcal{P}}(n) + q \cdot t_{\mathcal{P}}(n)} = \frac{1}{1 + \frac{q \cdot t_{\mathcal{P}}(n)}{\mathrm{work}_{\mathcal{P}}(n)}} = \frac{1}{1 + q/p}$$

and at least efficiency does not decrease considerably.

Theorem 3.3 *Let $\mathcal{S}$ be a sequential algorithm and let $\mathcal{P}$ be a parallelization of $\mathcal{S}$.*

(a) Assume that $q < p$. If the scheduling problem is solvable instantaneously, then there is an equivalent parallel algorithm $\mathcal{Q}$, which runs in time $O(\frac{t_{\mathcal{S}}(n)}{q} + t_{\mathcal{P}}(n))$ with q processors. Moreover $E_{\mathcal{Q}}(n) \geq \frac{1}{1+q/p} \cdot E_{\mathcal{P}}(n)$ and the efficiency of $\mathcal{Q}$ is almost as high as the efficiency of $\mathcal{P}$.
(b) If we increase (resp. decrease) the number of processors, but keep input size fixed, then efficiency and speedup tend to decrease (resp. increase).

Proof: (b) If we increase the number of processors, then we may scale down again and at worst efficiency stays about the same. □

Exercise 45
Determine the maximal efficiency when computing the Boolean OR with $p = n$ respectively with $p \leq \frac{n}{\log_2 n}$ processors.

We have just seen that a parallel algorithm $\mathcal{P}$ can be scaled down and at least (almost) maintains its efficiency. What happens if we increase input size, but keep the number of processors p fixed? If $N > n$, then we get

$$\frac{E_{\mathcal{P}}(N)}{E_{\mathcal{P}}(n)} = \frac{t_{\mathcal{S}}(N)}{t_{\mathcal{S}}(n)} \,/\, \frac{t_{\mathcal{P}}(N)}{t_{\mathcal{P}}(n)}.$$

Therefore we should expect efficiency to increase, since the sequential running time is faster growing than the parallel running time. We summarize the previous observations:

- If we keep input size fixed, but reduce the number of processors (i.e. if we scale down), then efficiency tends to increase. If we however increase the number of processors (i.e. if we scale up), then efficiency tends to decrease.

- efficiency tends to increase when we increase input size, but keep the number of processors fixed.

Our goal is to design parallel algorithms with high efficiency and as many processors as possible, since then we have also high efficiency for smaller numbers of processors. A good parallel algorithm should scale well, in other words it should reach high efficiency already for moderate input sizes.

Definition 3.4 A parallel algorithm $\mathcal{P}$ is **scalable** with efficiency E, if for every number p of processors there is an input size N_p such that $E_{\mathcal{P}}(n) \geq E$ whenever $n \geq N_p$. The **isoefficiency function** f_E with respect to E assigns the smallest input size $f_E(p)$ to $p \in \mathbb{N}$ such that $E_{\mathcal{P}}(n) \geq E$ whenever $n \geq f_E(p)$.

Example 3.2 In Section 2.1 we have introduce a parallel algorithm $\mathcal{P}$ for the prefix problem. If the operation $*$ can be evaluated in constant time, then time $t_{\mathcal{P}}(n) = O(\frac{n}{p} + \log_2 p)$ suffices for p processors. Observe that this approach achieves $\text{work}_{\mathcal{P}}(n) = \Theta(p \cdot (\frac{n}{p} + \log_2 p)) = \Theta(n + p \log_2 p)$ and hence $E_{\mathcal{P}}(n) = \Theta(\frac{n}{n+p\log_2 p})$. Thus, for $E = \Theta(1)$, we get the isoefficiency function $f_E(p) = \Omega(p \cdot \log_2 p)$.

Example 3.3 The Odd-Even Transposition Sort sorts n keys in time $\Theta(\frac{n}{p} \log_2 \frac{n}{p} + n)$ with p processors and hence $\text{work}_{\mathcal{P}}(n) = \Theta(p \cdot (\frac{n}{p} \log_2 \frac{n}{p} + n)) = \Theta(n \log_2 \frac{n}{p} + p \cdot n)$ follows. As a consequence $E_{\mathcal{P}}(n) = \frac{n \cdot \log_2 n}{n \log_2 \frac{n}{p} + p \cdot n}$ and we obtain constant efficiency iff $p = O(\log_2 n)$. Thus, for $E = \Theta(1)$, we get the isoefficiency function $f_E(p) = 2^{\Theta(p)}$.

Example 3.4 In the exercises of Section 2.2 we have descibed a recursive algorithm which sorts $n = m^2$ keys in time $O(\sqrt{n})$ with n processors. If we scale down and reduce the number of processors to p, then we should assign $\frac{n}{p}$ keys per processor. We start by sequentially sorting the keys for every processor. In the remaining $O(\sqrt{p})$ steps we perform a merging step with running time $\Theta(\frac{n}{p})$ and hence the parallel running time $t_{\mathcal{P}}(n)$ is bounded by $t_{\mathcal{P}}(n) = \Theta(\frac{n}{p} \log_2 \frac{n}{p} + \sqrt{p} \cdot \frac{n}{p})$. Thus $\text{work}_{\mathcal{P}}(n) = \Theta(p \cdot (\frac{n}{p} \log_2 \frac{n}{p} + \frac{n}{\sqrt{p}})) = \Theta(n \log_2 \frac{n}{p} + \sqrt{p} \cdot n)$ and as a consequence we achieve constant efficiency $E = \Theta(1)$ for $p = O(\log_2^2 n)$. In summary: we get the isoefficiency function $f_E(p) = 2^{\Theta(\sqrt{p})}$.

Of particular interest is the isoefficiency function f_E for the largest efficiency $E = \Theta(1)$. We should prefer algorithms whose isoefficiency function f_E grows as slow as possible since then the required input size for optimal efficiency is small. Thus the prefix algorithm has the most satisfying performance among the three examples.

3.3 Partitioning and Mapping

The design process of a parallel algorithm can be broken into the partitioning and mapping phase. The algorithm has to find a good compromise between computation and communication. Moreover the solution has to be scalable, that is its isoefficiency function should grow as slow as possible.

- In the **partitioning** phase we decompose the data (domain decomposition) and/or a specification of the computation (functional decomposition). The domain decomposition partitions the data into fragments and associates primitive tasks (i.e., parts of the computations) with the fragments. The functional decomposition breaks the computation into primitive tasks and subsequently associates data fragments with the primitive tasks

  As a rule of thumb the number of primitive tasks should be orders of magnitude larger than the targeted number of processors. If moreover primitive tasks have roughly same size, then good load balancing may be possible.

- **Mapping**. We have to combine primitive tasks into p larger tasks. The combination or mapping should preserve locality: tasks which communicate which each other, respectively tasks that depend on each other are good candidates for merging.

- **Computation and Communication**. Thus the partitioning phase has to define primitive tasks such that their communication pattern supports locality preserving mapping. In particular the resources required to communicate with other combined tasks should be dominated by the computing resources required for the combined task and moreover communication should be overlapped with computation whenever possible. If support for long messages is available, then replace many short messages by few (and correspondingly longer) messages and thereby save on the startup cost of communication.

- **Scalability**. The algorithm should be portable to systems with various numbers of processors. Its isoefficiency function should grow as slow as possible.

As an example we consider the prefix problem for operation $*$ and n elements $x_1, \ldots, x_n$. We decide in domain decomposition to associate primitive tasks with each element x_i. To minimize communication it is advisable to map disjoint intervals of n/p elements to the p processors. Thus we are led to the algorithm of Section 2.1. Observe that the computation resources per processor far outweighs the communication resources per processor.

Chapter 4

Parallel Linear Algebra

4.1 Matrix-Vector Multiplication

We are given a matrix A with m rows and n columns as well as a vector x with n components. Our goal is to compare the matrix-vector product $y = A \cdot x$ with

$$y_i = \sum_{j=1}^{n} A[i,j] \cdot x_j.$$

(We assume that addition and multiplication is defined by some field F such as the field of rationals, reals or the field of complex numbers.) The straightforward sequential algorithm computes $y_1, \ldots, y_m$ in consecutive steps. To compute y_i we have to perform n multiplications and $n-1$ additions. Thus overall $m \cdot n$ multiplications and $m \cdot (n-1)$ additions suffice.

We assume for the following that p divides m as well as n. To arrive at a good parallel algorithm with p processes we begin with data decomposition and mapping. We consider the following options.

- Rowwise decomposition: each process is responsible for m/p contiguous rows.
- Columnwise decomposition: each process is responsible for n/p contiguous columns.
- Checkerboard decomposition: Assume that k divides m and that l divides n. Imagine that the processes form a $k \times l$ mesh. Process (i,j) obtains the submatrix of A consisting of the ith row interval of length m/k and the jth column interval of length n/l. We demand that all submatrices have size $\Theta(m \cdot n/p)$ and hence $k \cdot l = p$.

We assume the following input/output conventions: each process knows the submatrix of A that it is responsible for; in particular we do not charge for redistributing A.[1] Process

[1] If we redistribute the matrix sequentially, then we may need time $\Omega(m \cdot n)$ and we could as well try to compute the matrix-vector product sequentially.

1 knows x and has to determine y. In all three options we distribute the $m \cdot n$ entries of matrix A evenly among the p processes.

For the rowwise decomposition we replicate x, that is we broadcast x to all processes in time $O(n \cdot \log_2 p)$. At the end of the computation process 1 performs a Gather operation in time $O(m)$, since $p-1$ messages of length m/p are involved. Thus the required communication time is proportional to $n \cdot \log_2 p + m$ and the rowwise decomposition requires time $\Theta(m \cdot n/p + n \cdot \log_2 p + m)$. Its efficiency is $\Theta(m \cdot n/(m \cdot n + p \cdot (n \cdot \log_2 p + m)))$ and constant efficiency follows for $n = \Omega(p)$ and $m = \Omega(p \cdot \log_2 p)$.

For the columnwise decomposition process 1 applies a Scatter operation to distribute the blocks of x to "their" processes. Since this involves $p-1$ messages of length n/p, time $O(n)$ is sufficient. Then process i computes the matrix-vector product $y^i = A^i \cdot x^i$ for its block A^i of columns and process 1 applies a Reduce operation to sum up $y^1, y^2, \ldots, y^p$. Thus the total communication time is $O(n + m \cdot \log_2 p)$ and the total running time is $O(m \cdot n/p + n + m \cdot \log_2 p)$. Hence it suffices to demand $m = \Omega(p)$ and $n = \Omega(p \cdot \log_2 p)$ to obtain constant efficiency.

For the checkerboard decomposition process 1 applies a Scatter operation addressed to the l processes of row 1 of the process mesh. This takes time $O(l \cdot n/l) = O(n)$. Then each process of row 1 broadcasts its block of x to the k processes in its column: time $O(n/l \cdot \log_2 k)$ suffices. At the end of the computation the processes in column 1 of the process mesh apply a Reduce operation for their row to sum up the l vectors of length m/k: time $O(m/k \cdot \log_2 l)$ is sufficient. Finally process 1 gathers the remaining $k-1$ vectors of length m/k in time $O(m)$. If $\log_2 k \leq l$ and $\log_2 l \leq k$, then the total communication time is bounded by $O(n+m)$ and we obtain constant efficiency, if $n = \Omega(p)$ and $m = \Omega(p)$.

Theorem 4.1 *The algorithms based on the rowwise, columnwise and checkerborad decomposition all determine the matrix-vector product $A \cdot x$ for an $m \times n$ matrix A in computing time $O(\frac{m \cdot n}{p})$ with p processors. Their communication times are bounded by $O(n \cdot \log_2 p + m)$, $O(n + m \cdot \log_2 p)$ and $O(n+m)$ –if $\log_2 k \leq l$ and $\log_2 l \leq k$– respectively.*

Observe that the checkerboard decomposition has the smallest communication time among all three decompositions, if $m \approx n$. What is the reason? Its messages have the smallest length!

Exercise 46
Determine the isoefficiency function for all three decompositions, provided $m = \alpha \cdot n$ with $0 < \alpha$. As usual we require efficiency $E = \Theta(1)$,

In many applications it is important to quickly compute the matrix-vector product $A \cdot x$ whenever the matrix A is *sparse*, i.e., whenever A has only few nonzero entries.

Exercise 47
Let A be an $m \times n$ matrix with N nonzero coefficients. For which input representation can we obtain a parallel algorithm that computes $A \cdot x$ in time $O(\frac{N}{p})$ with p processors?

4.2 Matrix Multiplication

We are given the $n \times n$ matrices A and B and have to compute the $n \times n$ product matrix $C = A \cdot B$. $C[i,j]$ is the inner product of row i of A and column j of B and hence $C[i,j] = \sum_{k=1}^{n} A[i,k] \cdot B[k,j]$. A sequential algorithm may compute $C[i,j]$ with n multiplications and $n-1$ additions and hence C can be computed sequentially with n^3 multiplications and $n^2 \cdot (n-1)$ additions. Alltogether running time $\Theta(n^3)$ is required.

We describe three parallel algorithms. Our first algorithm uses the **rowwise decomposition**: all rows of A and B with indices belonging to the interval $\{(i-1)\cdot n/p+1, \ldots, i\cdot n/p\}$ are assigned to process i. Thus process i receives the submatrices A^i of A and B^i of B. We further subdivide A^i and B^i into the square submatrices $A^{i,1}, \ldots, A^{i,p}$ and $B^{i,1}, \ldots, B^{i,p}$, where $A^{i,j}$ and $B^{i,j}$ consist of all columns of A^i and B^i whose indices belong to the interval $\{(j-1)\cdot n/p+1, \ldots, j\cdot n/p\}$. We define $C^{i,j}$ analogously and observe that

$$C^{i,j} = \sum_{k=1}^{p} A^{i,k} \cdot B^{k,j}$$

holds. We compute $C^{i,j}$ in p phases. In phase 1 process i computes the products $A^{i,i} \cdot B^{i,j}$ for $j = 1, \ldots, p$. Time $O(p \cdot \frac{n}{p} \cdot \frac{n}{p} \cdot \frac{n}{p}) = \frac{n^3}{p^2}$ suffices, since process i multiplies the $\frac{n}{p} \times \frac{n}{p}$ matrix $A^{i,i}$ with the p $\frac{n}{p} \times \frac{n}{p}$ matrices $B^{i,j}$. Afterwards we use a cyclic linear array as communication pattern. In particular process i sends B^i to process $j = (i+1) \mod p$ and hence receives B^{i-1}. (We work with residues $1, \ldots, p$.) Observe that the communication time is proportional to $\frac{n}{p} \cdot n = \frac{n^2}{p}$, the size of a matrix B^i. We repeat these pairs of compute and communications steps: in the kth phase process i computes the products $A^{i,i-k+1 \mod p} \cdot B^{i-k+1 \mod p,j}$ for $j = 1, \ldots, p$, sends $B^{i-k+1 \mod p}$ and receives $B^{i-k \mod p}$.

We have p phases with compute time $\frac{n^3}{p^2}$ and communication time $\frac{n^2}{p}$ per phase. Thus the running time is at most $O(\frac{n^3}{p} + n^2)$ and we achieve constant efficiency iff $n = \Omega(p)$. We can further obtain a speedup by overlapping the communication of the submatrix B^j with computation by initiating a non-blocking send/receive operation sufficiently early. Nevertheless we achieve a compute/communicate ratio of only $O(\frac{n^3}{p^2}/\frac{n^2}{p}) = O(\frac{n}{p})$ per phase.

The next two approaches use the **checkerboard decomposition**. Let $A^{i,j}, B^{i,j}$ and $C^{i,j}$ be the submatrix of A, B and C respectively, where we choose all rows with indices from the interval $\{(i-1)\cdot n/\sqrt{p}+1, \ldots, i\cdot n/\sqrt{p}\}$ and all columns with indices from the interval $\{(j-1)\cdot n/\sqrt{p}+1, \ldots, j\cdot n/\sqrt{p}\}$. We assume a $\sqrt{p} \times \sqrt{p}$ mesh of processes in which process (i,j) initially holds $A^{i,j}$ and $B^{i,j}$ and is required to finally hold $C^{i,j}$. Observe that

$$C^{i,j} = \sum_{k=1}^{\sqrt{p}} A^{i,k} \cdot B^{k,j}$$

holds. **Fox's algorithm** is composed of $\sqrt{p}$ phases. In the first phase process (i,i) broadcasts its submatrix $A^{i,i}$ to all processes of row i and, subsequently, any process (i,j) of

row i computes the matrix product $A^{i,i} \cdot B^{i,j}$. Our goal for process (i,j) in phase two is to compute the product $A^{i,i+1 \mod \sqrt{p}} \cdot B^{i+1 \mod \sqrt{p},j}$ and hence the first phase should conclude with process (i,j) sending $B^{i,j}$ to its neighbor $(i-1 \mod \sqrt{p}\ , j)$ on top and receiving $B^{i+1 \mod \sqrt{p},j}$ from its neighbor $(i+1 \mod \sqrt{p}\ , j)$ below. The general phase k has then the following form:

- Process $(i, i+k-1 \mod \sqrt{p})$ broadcasts its submatrix $A^{i,i+k-1 \mod \sqrt{p}}$ to all processors of row i.
- Any process (i,j) computes the product $A^{i,i+k-1 \mod \sqrt{p}} \cdot B^{i+k-1 \mod \sqrt{p},j}$ and
- sends $B^{i+k-1 \mod \sqrt{p},j}$ to its neighbor on top and receives $B^{i+k \mod \sqrt{p},j}$ from its neighbor below.

Our third approach, **Cannon's algorithm**, follows the approach of Fox's algorithm, but it replaces each broadcast by a simple send and hence is more efficient. In particular, the first step of Cannon's algorithm redistributes the submatrices such that afterwards

$$\text{process } (i,j) \text{ holds } A^{i,i+j \mod \sqrt{p}} \text{ and } B^{i+j \mod \sqrt{p},j}.$$

In its first phase

- process (i,j) first multiplies $A^{i,i+j \mod \sqrt{p}}$ and $B^{i+j \mod \sqrt{p},j}$,
- passes $A^{i,i+j \mod \sqrt{p}}$ to its left neighbor and $B^{i+j \mod \sqrt{p},j}$ to its neighbor above and
- receives $A^{i,i+j+1 \mod \sqrt{p}}$ from its right neighbor and $B^{i+1+j \mod \sqrt{p},j}$ from its neighbor below.

In subsequent phases processes continue to compute the respective product, send their A-matrix to the left neighbor and their B-matrix to the neighbor above. After $\sqrt{p}$ phases each process (i,j) has computed its matrix $C^{i,j}$ and, per phase, computing time $O(\frac{n^3}{(\sqrt{p})^3})$ and communication time $O(\frac{n^2}{p})$ suffice. Hence the total running time is at most $O(\frac{n^3}{p} + \frac{n^2}{\sqrt{p}} + \sqrt{p})$ and we achieve constant efficiency iff $\sqrt{p} \cdot n^2 + p^{3/2} = O(n^3)$, respectively iff $n = \Omega(\sqrt{p})$. Moreover we can proceed as for the rowwise decomposition and overlap communication with computation. This time however we achieve the far better compute/communicate ratio of $\Theta(\frac{n^3}{(\sqrt{p})^3} / \frac{n^2}{p}) = \Theta(\frac{n}{\sqrt{p}})$ and Cannon's algorithm is the better the larger the number p is.

Finally we describe the algorithm of Dekel, Nassimi and Sahni, the **DNS algorithm**, which uses a **three dimensional decomposition**. We describe the DNS algorithm first for n^3 processes and then show how to implement it with a given number p of processes. We imagine the n^3 processes to be arranged in a three-dimensional mesh of processes. Initially process $(i,j,1)$ stores $A[i,j]$ and $B[i,j]$ and is responsible to output $C[i,j]$.

In its first phase the DNS algorithm replicates data such that process (i,j,k) holds $A[i,k]$ and $B[k,j]$. If this is achieved, then (i,j,k) computes the product $A[i,k] \cdot B[k,j]$. Finally process $(i,j,1)$ applies a Reduce operation to compute $\sum_{k=1}^{n} A[i,k] \cdot B[k,j]$. All steps with the exception of the replication steps can be readily implemented. To implement the replication step process $(i,j,1)$ sends $A[i,j]$ to process (i,j,j) and $B[i,j]$ to process (i,j,i). Finally (i,j,j) broadcasts $A[i,j]$ to all processes $(i,*,j)$ and (i,j,i) broadcasts $B[i,j]$ to all processes $(*,j,i)$.

Thus the broadcast dominates during replication and hence replication takes time $O(\log_2 n)$. The multiplication step runs in constant time and the Reduce operation runs in logarithmic time. Thus the DNS algorithm has running time $O(\log_2 n)$ with n^3 processes and its efficiency $\Theta(1/\log_2 n)$ is rather small. However we can increase efficiency, if we scale down the number of processes to p.

Set $q = p^{1/3}$. We arrange the p processes in a three-dimensional mesh. Process $(i,j,1)$ receives the submatrices $A^{i,j}, B^{i,j}$ of A and B respectively, where $A^{i,j}$ as well as $B^{i,j}$ consists of all rows with indices in the interval $\{(i-1) \cdot n/q + 1, \ldots, i \cdot n/q\}$ and of all columns with indices in the interval $\{(j-1) \cdot n/q + 1, \ldots, j \cdot n/q\}$. We now mimic the approach with n^3 processes by replacing entries $A[i,j]$ and $B[i,j]$ by submatrices $A^{i,j}$ and $B^{i,j}$. In the replication step the $n/q \times n/q$ submatrices $A^{i,j}$ and $B^{i,j}$ have to be broadcast to all processes $(i,*,j)$ and $(*,j,i)$ respectively and hence the communication cost is bounded by $O(\frac{n^2}{q^2} \log_2 q)$. The multiplication step is expensive and requires time $O(\frac{n^3}{q^3})$. Finally the Reduce operation involves $\frac{n}{q} \times \frac{n}{q}$ submatrices and hence takes time $O(\frac{n^2}{q^2} \cdot \log_2 q)$. Thus the running time of the DNS algorithm is bounded by $O(\frac{n^3}{q^3} + \frac{n^2}{q^2} \log_2 q) = O(\frac{n^3}{p} + \frac{n^2}{p^{2/3}} \cdot \log_2 p)$. We achieve constant efficiency iff $\frac{n^3}{p} = \Omega(\frac{n^2}{p^{2/3}} \cdot \log_2 p)$ or equivalently iff $n^3 = \Omega(p \cdot \log_2^3 p)$.

Finally the compute/communicate ratio is $\Theta(\frac{n^3}{p} / \frac{n^2 \cdot \log_2 p}{p^{2/3}}) = \Theta(\frac{n}{p^{1/3} \cdot \log_2 p})$ and the DNS algorithm is superior, *provided* the number of processors is sufficiently large.

Theorem 4.2 *The algorithm based on the rowwise decomposition, Cannon's algorithm as well as the DNS algorithm all multiply two $n \times n$ matrices in computing time $O(\frac{n^3}{p} + n^2)$, $O(\frac{n^3}{p} + \sqrt{p})$ and $O(\frac{n^3}{p} + \frac{n^2}{p^{2/3}} \cdot \log_2 p)$ respectively with p processors. Their communication times are $O(n^2)$, $O(\frac{n^2}{\sqrt{p}} + \sqrt{p})$ and $O(\frac{n^2}{p^{2/3}} \cdot \log_2 p)$ respectively.*

Remark 4.1 A main ingredient of all three algorithms is a sequential algorithm to multiply matrices. At first the multiplication problem seems trivial. However we have to exert some care. Assume that we compute $A \cdot B$ sequentially with the three nested for-loops:

```
for i=1 to n do
     for j=1 to n do
          C[i,j] = 0;
          for k=1 to n do
```

```
C[i,j] = C[i,j] + A[i,k]*B[k,j];
```

Consider the outer i-loop and observe that performance is considerably improved, if we can keep the ith row of A and all of B within the cache. If B is too large, then we should instead use a checkerboard approach also sequentially, where block sizes should "just" fit into the cache.

Exercise 48
Assume that matrix multiplication of two $n \times n$ matrices runs in time $t_p(n)$ on p processors.

(a) Show how to compute the power A^k of an $n \times n$ matrix A in time $O(t_p(n) \cdot \log_2 k)$ with p processors.

(b) The sequence $(x_n \mid n \in \mathbb{N})$ is described by the recurrence

$$x_m = a_1 \cdot x_{m-1} + a_2 \cdot x_{m-2} + \cdots + a_r \cdot x_{m-r}.$$

Show how to determine x_n in time $O(t_p(r) \cdot \log_2 n + r/p + \log_2 p)$ with p processors. Which efficiency is obtainable, if we assume that the sequential complexity of determining x_n is $\Theta(n)$?

Exercise 49
In matrix multiplication entries are computed according to the formula $c_{i,j} = \sum_k a_{i,k} \cdot b_{k,j}$. In some applications similar expressions appear, but with addition and multiplication replaced by other operations.

(a) The transitive closure of a directed graph $G = (V, E)$ is the directed graph $G^* = (V, E^*)$, where we insert an edge (i, j) into E^* whenever there is a path in G from i to j. Show how to determine the transitive closure with the help of matrix multiplication.

Hint: Assume that G has n vertices and let A be the adjacency matrix of G. Interpret the power A^{n-1} after replacing addition by $\vee$ and multiplication by $\wedge$.

(b) In the shortest path problem we are given a directed graph and non-negative weights on its edges. We have to determine the length of a shortest path for any pair of vertices. Reduce the shortest path problem to matrix multiplication.

(c) We are given p processors. Implement your solutions for (a) and (b), assuming that p processors are available. Determine running time and efficiency, if the sequential time complexity is $\Theta(n^3)$ for graphs with n vertices.

Exercise 50
A $n \times n$ matrix X is called banded with half-bandwidth b, provided $X[i, j] = 0$ whenever $|i - j| > b$. Assume that the $n \times n$ banded matrices A and B have half-bandwidth b_A and b_B respectively.

(a) Show that $C = A \cdot B$ has half-bandwidth $b_A + b_B$ and that C can be computed sequentially in time $O(n \cdot (b_A + b_B))$.

(b) Assume that the $n \times n$ banded matrix X has half-bandwidth b_X. We represent X by the matrix X' with $X'[i, j] = X[i, i - b_X + j]$, if $0 < i - b_X + j \leq n$, and $X'[i, j] = 0$ otherwise.

Assume that A and B are presented by A' and B'. Design a parallel algorithm to determine C' where $C = A \cdot B$. We work with p processors. The matrices A' and B' are partitioned according to the checkerboard decomposition.

4.3 Solving Linear Systems

We are given a matrix A and a right-hand side b and would like to solve the linear system $A \cdot x = b$. We begin by investigating lower triangular matrices A and describe back substitution in Section 4.3.1. When dealing with arbitrary matrices we have to apply Gaussian elimination and we describe efficient parallelizations in Section 4.3.2. We consider iterative methods (Jacobi relaxation, Gauss-Seidel algorithm, the conjugate gradient approach and the Newton method) in Section 4.3.3. These methods work very fast for important classes of matrices and are in particular capable of exploiting sparsity. As an application we show how to approximately solve linear partial differential equations.

4.3.1 Back Substitution

We assume that A is a $n \times n$ invertible lower triangular matrix and we wish to solve the system $A \cdot x = b$ of linear equations. Since A is a lower triangular matrix

$$A[i,1] \cdot x_1 + \cdots + A[i,i] \cdot x_i = b_i$$

is the ith linear equation. A sequential solution is easy to obtain, if we first determine x_1 from the first equation. Assuming that we already know $x_1, \ldots, x_{i-1}$, we utilize the ith equation to determine x_i. Since an evaluation of the ith equation requires time $O(i)$, the sequential solution requires overall time $O(n^2)$.

Our goal is to solve $A \cdot x = b$ with $p \leq n$ processors in time $O(\frac{n^2}{p})$. Our first solution assumes the **off-diagonal decomposition** of matrix A: process 1 knows the main diagonal and process i (for $i \geq 2$) knows the $i-1$st offdiagonal $A[i,1], A[i+1,2], \ldots, A[n,n-i+1]$. We use the linear array as communication pattern and start with the case of $p = n$ processes.

Process 1 successively determines $x_1, \ldots, x_n$ and passes x_i, immediately after computing it, to process 2. From that point on x_i is sent thru the linear array. How can we solve the ith equation $A[i,1] \cdot x_1 + \cdots + A[i,i] \cdot x_i = b_i$ as fast as possible? After receiving x_1, process i computes $A[i,1] \cdot x_1$, passes $A[i,1] \cdot x_1$ to process $i-1$ and x_1 to process $i+1$. In the next step process $i-1$ receives x_2 from process $i-2$, computes the product $A[i,2] \cdot x_2$, sends the sum $A[i,1] \cdot x_1 + A[i,2] \cdot x_2$ to process $i-2$ and x_2 to process i. Thus, following the principle of "just in time production", process 1 obtains $A[i,1] \cdot x_1 + A[i,2] \cdot x_2 + \cdots + A[i,i-1] \cdot x_{i-1}$, determines x_i and passes it on to process 2. The communication pattern when determining x_1, x_2, x_3, x_4 is shown in Figure 4.3. Now let p be arbitrary. In the off-diagonal decomposition we assign the off-diagonals $(A[j,1], \ldots, A[n,n-j+1])$ for $j \in \{(i-1) \cdot n/p + 1, \ldots, i \cdot n/p\}$ to process i. The computing time *per unknown* increases from $O(1)$ to $O(\frac{n}{p})$, whereas the communication time per unknown remains constant. We have n unknowns and our running time is therefore bounded by $O(\frac{n^2}{p} + n)$. We achieve constant efficiency whenever $n = \Omega(p)$.

Now let us consider the **rowwise decomposition**. When determining x_i from the ith equation we face the problem that processes $1, \ldots, i-1$ do not know the ith row of A. But

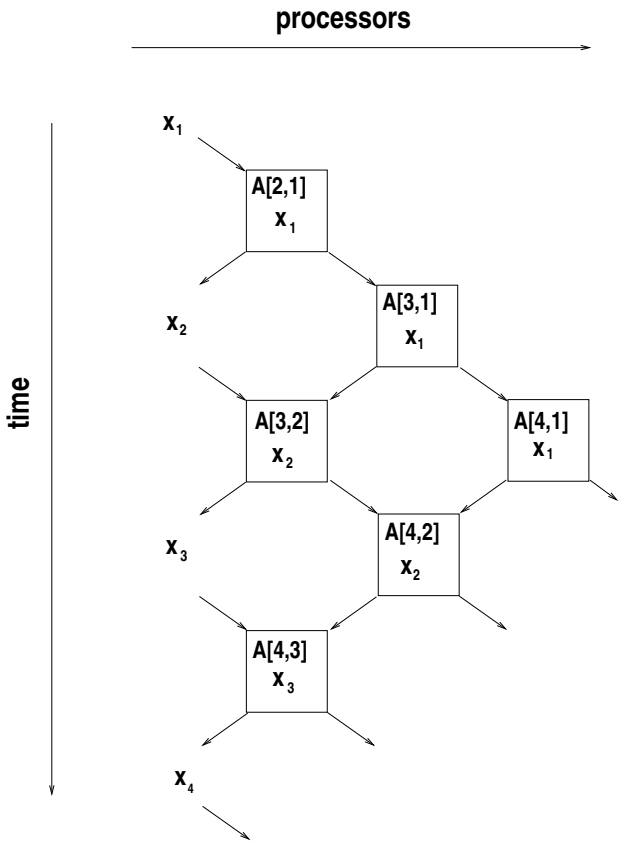


Figure 4.1: Solving a lower triangular system of equations.

process i can supply this information by sending $A[i,j]$ to process $i-j+1$ just in time. However computations do not dominate communications anymore and we therefore change our approach. Once x_j is determined, process j broadcasts x_j to processes $j+1,\ldots,n$. When working with an arbitrary number p of processes, we have one broadcast per unknown as well as computing time $O(\frac{n}{p})$. Now the running time is bounded by $O(\frac{n^2}{p}+n\cdot\log_2 p)$ and we achieve constant efficiency whenever $n=\Omega(p\cdot\log_2 p)$.

Theorem 4.3 *Let A be a $n\times n$ invertible lower triangular matrix. Then the linear system $A\cdot x=b$ can be solved in computing time $O(\frac{n^2}{p})$ for the off-diagonal as well as the rowwise decomposition. The off-diagonal decomposition has communication time $O(n)$, whereas communication time $O(n\cdot\log_2 p)$ suffices for the rowwise decomposition.*
A can be inverted in computing time $O(\frac{n^3}{p})$ and communication time $O(n^2)$.

Exercise 51
Show how to invert a nonsingular lower triangular matrix A within the resources stated in Theorem 4.3.

Exercise 52
In the interleaved row decomposition of A process i receives all rows with indices in the set $\{j\cdot p+$

$i \mid j = 0, \ldots, n/p - 1\}$. Why is the interleaved row decomposition a better choice than the row decomposition?

4.3.2 Gaussian Elimination

Again let A be an $n \times n$ matrix and let b be vector with n coordinates. Our goal is to solve the system $A \cdot x = b$ with Gaussian elimination. What is the sequential performance of Gaussian elimination? If we start with row 1 as pivot row, then we can eliminate the nonzeroes below $A[1,1]$ in column 1 by setting

$$\text{row}_j = \text{row}_j - \frac{A[j,1]}{A[1,1]} \cdot \text{row}_1$$

for $j > 1$. In general, if we have already eliminated nonzeroes below the diagonals in columns $1, \ldots, i-1$, then we eliminate nonzeroes below $A[i,i]$ in column i by setting

$$\text{row}_j = \text{row}_j - \frac{A[j,i]}{A[i,i]} \cdot \text{row}_i$$

for $j > i$. The elimination step for row i involves $n - i$ other rows j. Since any such row j requires $2 \cdot (n - i + 1)$ arithmetic operations, the elimination step for row i involves at most $2 \cdot (n-i+1)^2$ arithmetic operations. Thus the total number of arithmetic operations is bounded by

$$\sum_{i=1}^{n-1} 2 \cdot (n - i + 1)^2 = O(n^3).$$

However our procedure is not numerically stable, if the pivot $A[i,i]$ is very small: $\frac{A[j,i]}{A[i,i]}$ can grow correspondingly large and significant roundoff errors result. Hence we apply Gaussian elimination with **partial pivoting** and use as pivot the largest entry in column i among rows $i, i+1, \ldots, n$. If the largest entry sits in row j, then we swap rows i and j and compute as before.

Finally all elimination steps have to be simultaneously performed for the right-hand side b. We can take care of b by including b as the $n+1$st column of A. Thus we replace A by the augmented matrix A'.

We describe a parallelization of Gaussian elimination with partial pivoting and assume a rowwise decomposition of the augmented matrix A'. As usual we work with p processes, where process i knows all rows with indices in the interval $\{(i-1) \cdot n/p + 1, \ldots, i \cdot n/p\}$. Our approach is to keep the sequential structure of pivoting steps and to parallelize each pivoting step instead. Assume that we have reached row i.

How can we determine the largest entry in column i among rows $i, \ldots, n$? Each process i begins by determining the largest entry M_i among the rows it knows. As a first option we could apply MPI_Allreduce with Max as operation and values $M_1, \ldots, M_p$. Afterwards each

process knows the value M of the largest entry. If $M_i = M$, then process i submits i and otherwise submits zero to a second MPI_Allreduce with Max as operation. Thus, after two Allreduce operations the pivot is determined. Fortunately MPI supplies the by far more appropriate operation MPI_Maxloc which determines for a set of pairs $(M_1, 1), \ldots, (M_p, p)$ a largest M_i and returns (M_i, i). Determining all local winners $M_1, \ldots, M_p$ takes computing time $O(n/p)$. The call of MPI_Maxloc requires communication time $O(\log_2 p)$.

Now that the pivot is known, the winning process broadcasts the relevant portion of the winning row to the remaining processes and does so in time $O(n \cdot \log_2 p)$. All processes can now simultaneously perform their respective elimination steps in time at most $O(\frac{n^2}{p})$. Over all n pivoting steps computing time $O(\frac{n^3}{p})$ and communication time $O(n^2 \log_2 p)$ suffice. Thus we reach constant efficiency, whenever $n = \Omega(p \cdot \log_2 p)$ holds.

The weak spot of our approach is the broadcast which dominates the communication costs with communication time $O(n \log_2 p)$. Moreover it brings the entire computation to a screeching halt and does not allow to overlap communication with computation. Thus we change our pivoting strategy, select the largest entry not in column i, but in row i instead. If process j knows row i, it computes the largest entry $A[i, k]$ of row i and all non-zeroes in row i are to be eliminated next. We use column k as pivot column and hence process j determines the vector m_i of coefficients required to eliminate all non-zeroes in row i.

However, instead of broadcasting m_i and pivot position k, process j only sends m_i and k to its neighbor process $j+1$. Whereas process j is now free to compute, process $j+1$ has to immediately propagate the pivoting information to its neighbor process $j + 2$, but can directly afterwards begin its part of the elimination work. Thus we replace the broadcast of (m_i, k) by *pipelining* and "cover" communication with computation.

But now distant processes are delayed and pipelining seems to slow down the computation. Observe however that the pipelined communication can start right after m_i is recomputed. Thus, when performing the elimination step for pivot row i, the process holding row $i + 1$ recomputes row $i + 1$ as its first task, determines the maximal entry and the corresponding vector r_{i+1} of coefficients and sends the new pivot information before returning to its elimination work for the current pivot. No delay is incurred when working with pivot row $i + 1$, provided the compute time $\Theta(\frac{n^2}{p})$ per pivoting steps dominates the maximal delay $p \cdot n$. Thus, if $n = \Omega(p^2)$ and hence if n is sufficiently large, pipelining is delay-free except for the first row.

Theorem 4.4 *The pipelined algorithm works with the row decomposition of the augmented matrix A'. If $n = \Omega(p^2)$, then it performs Gaussian elimination with partial pivoting in computing time $O(\frac{n^3}{p})$ using p processors.*

4.3.3 Iterative Methods

In an *iterative method* an approximate solution of a linear system $A \cdot x = b$ is successively improved. One starts with an initial "guess" $x(0)$ and then replaces $x(t)$ by a presumably better solution $x(t+1)$. Iterative methods are particularly well-suited for parallel algorithms whenever they are based on matrix-vector products. As a consequence this type of iterative methods can exploit sparse linear systems. We describe the Jacobi relaxation and its variants as well as the conjugate gradient method for solving linear systems. Finally we present the Newton method to approximately compute the inverse of a matrix.

Jacobi Relaxation.

We assume again that a linear system $A \cdot x = b$ with nonzero diagonal is to be solved. A solution x satisfies

$$x_i = \frac{1}{A[i,i]} \cdot \left(b_i - \sum_{j \neq i} A[i,j] \cdot x_j \right).$$

Hence, if we assume that we already know an approximate solution $x_i(t)$, then the Jacobi iteration

$$x_i(t+1) = \frac{1}{A[i,i]} \cdot \left(b_i - \sum_{j \neq i} A[i,j] \cdot x_j(t) \right) \tag{4.1}$$

"could be" a better approximation and this is indeed the case, provided the matrices M^t, with the iteration matrix $M = D^{-1} \cdot (D - A)$, converge to zero with t approaching infinity. (D is the diagonal matrix with $D[i,i] = A[i,i]$.)

Exercise 53
Assume that the matrix A is invertible and let x be the unique solution of the linear system $A \cdot x = b$. Show that

$$x(t+1) - x = M \cdot (x(t) - x)$$

holds and consequently $x(t) - x = M^t \cdot (x(0) - x)$ follows for all t.

Each Jacobi iteration (4.1) corresponds to a matrix-vector product which we already know how to parallelize in time $O(\frac{n^2}{p})$. Thus we obtain an extremely fast approximation, whenever few iterations suffice. Few iterations suffice for instance for the important class of diagonally dominant matrices:

Exercise 54
(a) Assume that A is invertible and that the vectors $x(t)$ converge to a vector x^*. Show that $A \cdot x^* = b$ holds.

(b) Assume that the matrix A is row diagonally dominant, i.e., $|A[i,i]| > \sum_{j \neq i} |A[i,j]|$ holds for all i. Show that the Jacobi Relaxation converges. What can you say about the rate of convergence?

In many practical applications the **Jacobi overrelaxation** converges faster: for a suitable choice of the coefficient γ we apply the iteration

$$x_i(t+1) = (1-\gamma) \cdot x_i(t) + \frac{\gamma}{A[i,i]} \cdot \left(b_i - \sum_{j \neq i} A[i,j] \cdot x_j(t) \right).$$

Observe that we obtain the Jacobi relaxation (4.1) as a special case by setting $\gamma = 1$. Another extension of the Jacobi relaxation is the **Gauss-Seidel algorithm** which incorporates already recomputed values of x_j (i.e., it replaces $x_j(t)$ by $x_j(t+1)$). An example is the rule

$$x_i(t+1) = \frac{1}{A[i,i]} \cdot \left(b_i - \sum_{j<i} A[i,j] \cdot x_j(t+1) - \sum_{j>i} A[i,j] \cdot x_j(t) \right). \tag{4.2}$$

Observe however that the Gauss-Seidel algorithm looks inherently sequential. Finally we can also apply overrelaxation to the Gauss-Seidel algorithm and obtain one of the fastest iterative methods.

The Conjugate Gradient Method.

We have to require that A is symmetric and positive definite[2]. We describe the conjugate gradient method which turns out to be faster than the Jacobi Relaxation in many cases.

Exercise 55
Assume that $A = B^T \cdot B$ for some invertible matrix B.

(a) Show that $x^T A x \geq 0$ for all x and $x^T A x = 0 \Leftrightarrow x = 0$.

(b) Let z be an arbitrary vector. Show that $q_z(x) = \frac{1}{2}(x-z)^T A (x-z)$ is a convex function. Hint: show first that $\frac{1}{2} x^T A x$ is convex. Then utilize that $r \cdot f(x+z)$ is a convex function of x, whenever $r \geq 0$ and z is arbitrary.

(c) Show that $\nabla q_z(x) = Ax - Az$, where ∇q_z is the gradient of q_z.

(d) Set $z = x^*$ where $A \cdot x^* = b$. Then $\nabla q_z(x) = Ax - b$ and q_z has a unique minimum for $x = x^*$.

Thus it suffices to minimize q_z. An iteration of the conjugate gradient method has the form

$$x(t+1) = x(t) + \gamma(t) \cdot \text{direction}(t),$$

where the vector direction(t) is the direction of update and the scalar step size $\gamma(t)$ is determined by

$$q_z\left(x(t) + \gamma(t) \cdot \text{direction}(t)\right) = \min_{\gamma} q_z\left(x(t) + \gamma \cdot \text{direction}(t)\right). \tag{4.3}$$

[2] A is symmetric and positive definite iff $A = B^T \cdot B$ for some invertible matrix B.

The choice of direction is the novel feature of this method, since the vectors direction(t) are chosen to be "A-conjugate", namely

$$\text{direction}(r)^T \cdot A \cdot \text{direction}(t) = 0$$

holds, whenever $r \neq t$.

Exercise 56
Assume that direction$(0), \ldots,$ direction$(n-1)$ are indeed A-conjugates.

(a) Show that the vectors direction$(0), \ldots,$ direction$(n-1)$ are linearly independent.

(b) Use (4.3) to show that $\nabla q_z(x(k+1))^T \cdot \text{direction}(k) = 0$ holds. Then infer $\nabla q_z(x(k+1))^T \cdot \text{direction}(i) = 0$ for all i $(0 \leq i \leq k)$.

(c) $x(k+1)$ minimizes q, when we restrict q to $x(0) + V_k$, where V_k is the vector space spanned by direction$(0), \ldots,$ direction(k).

As a consequence $x(n)$ minimizes q_z and hence all we have to do is to guarantee that the vectors direction(t) are A-conjugates. We choose $x(0)$ arbitrarily and set direction$(0) = -(A \cdot x_0 - b)$. Since $\nabla q_z(x_0) = A \cdot x_0 - b$, we initially search in the direction of the negative gradient. For $t > 0$ we set

$$\begin{aligned} \text{direction}'(t) &= A \cdot x(t-1) - b \text{ and} \\ \text{direction}(t) &= -\text{direction}'(t) + \frac{||\text{direction}'(t)||^2}{||\text{direction}'(t-1)||^2} \cdot \text{direction}(t-1). \end{aligned}$$

Finally we choose

$$\gamma(t) = \frac{\text{direction}(t)^T \cdot \text{direction}'(t)}{\text{direction}(t)^T \cdot A \cdot \text{direction}(t)}$$

as step size.

Exercise 57
Show that the vectors direction(t) are A-conjugates.

Our parallel algorithm computes the sequence $x(t)$ and utilizes that the matrix-vector products $A \cdot \text{direction}(t)$ can be computed in time $O(\frac{n^2}{p})$ with p processes.

Inversion by Newton Iteration.

We assume that A is an invertible matrix and that X_t is an approximate inverse of A. The Newton iteration

$$X_{t+1} = 2 \cdot X_t - X_t \cdot A \cdot X_t$$

determines for many important classes of matrices a better approximation of A^{-1}. To see why consider the residual matrix

$$R_t = I - A \cdot X_t$$

which measures the "distance" between A^{-1} and X_t. We observe

$$\begin{aligned} R_{t+1} &= I - A \cdot X_{t+1} \\ &= I - A \cdot (2 \cdot X_t - X_t \cdot A \cdot X_t) \\ &= (I - A \cdot X_t)^2 = R_t^2 \end{aligned}$$

and R_t converges rapidly towards the 0-matrix, whenever X_0 is a good approximation of A^{-1}. For well conditioned matrices such a good initial approximation is obtained with[3]

$$X_0 = \frac{A^T}{\text{trace}(A^T \cdot A)}.$$

Since the Newton iteration is based on matrix-matrix products, each iteration is easily parallelized. In [BT89] it is shown that $O(\log_2 n)$ iterations suffice for a large class of matrices.

4.3.4 Finite Difference Methods

We describe the finite difference method as a method to approximately solve partial differential equations (PDEs).[4] We restrict ourselves to the **Poisson equation $\mathbf{u_{xx} + u_{yy} = H}$**, but our approach can also be applied to the large class of linear PDEs. (A linear second-order PDE has the form

$$A \cdot u_{xx} + 2B \cdot u_{xy} + C \cdot u_{yy} + E \cdot u_x + F \cdot u_y + G \cdot u = H,$$

with functions $A, \ldots, H$ depending on x and y only. Observe that neither u nor any of its partial derivatives is allowed to appear as a coefficient. Linear PDEs of higher degree are defined analogously.) We will see that the finite difference method leads to a sparse linear system, which is solvable with the help of the iterative methods of Section 4.3.3.

Our goal is to find a function $u : [0,1]^2 \to \mathbb{R}$ which satisfies the Poisson equation and which has prescribed values on the boundary of the unit square. If the solution u is sufficiently smooth and if Δ is sufficiently small, then we may approximate $u_x(x,y)$ by

$$u_x(x,y) \approx \frac{u(x+\Delta, y) - u(x,y)}{\Delta}$$

and $u_{xx}(x,y)$ by

$$\begin{aligned} u_{xx}(x,y) &\approx \frac{\frac{u(x+\Delta,y)-u(x,y)}{\Delta} - \frac{u(x,y)-u(x-\Delta,y)}{\Delta}}{\Delta} \\ &= \frac{u(x+\Delta,y) - 2u(x,y) + u(x-\Delta,y)}{\Delta^2}. \end{aligned}$$

[3] The trace of a square $n \times n$ matrix M is defined by $\text{trace}(M) = \sum_{i=1}^{n} M[i,i]$.

[4] We refer to the finite element method as another successful technique to solve PDEs numerically.

We approximate u_{yy} analogously and hence we get

$$\frac{u(x+\Delta,y)+u(x-\Delta,y)+u(x,y+\Delta)+u(x,y-\Delta)-4u(x,y)}{\Delta^2} \approx H(x,y) \tag{4.4}$$

as a consequence of the Poisson equation. To apply the finite difference method we choose a sufficiently large integer N with $\Delta = \frac{1}{N}$ and set

$$u_{i,j} = u(\frac{i}{N}, \frac{j}{N}) \text{ as well as } H_{i,j} = H(\frac{i}{N}, \frac{j}{N}).$$

If we replace approximate equality in (4.4) by exact equality and choose (x, y) be one of the grid points $\{(\frac{i}{N}, \frac{j}{N}) \mid 0 < i, j < N\}$, then we obtain the linear system

$$-4u_{i,j} + u_{i+1,j} + u_{i-1,j} + u_{i,j+1} + u_{i,j-1} = \frac{H_{i,j}}{N^2}$$

with $(N-1)^2$ equations in $(N-1)^2$ unknowns. (Remember that the values of u at the boundary are prescribed.) The system is extremely large, since it has $(N-1)^4$ entries. However it is sparse, since any equation has at most five nonzero coefficients. We utilize sparsity by processing the system beginning with the lower boundary and working upwards. In other words we utilize the presentation

$$u_{i+1,j} = 4u_{i,j} - (u_{i-1,j} + u_{i,j+1} + u_{i,j-1}) + \frac{H_{i,j}}{N^2}. \tag{4.5}$$

After starting from an initial solution $u_{i,j}(0)$, we can solve this system with the Jacobi relaxation

$$u_{i+1,j}(t+1) = 4u_{i,j}(t) - (u_{i-1,j}(t) + u_{i,j+1}(t) + u_{i,j-1}(t)) + \frac{H_{i,j}}{N^2}\ , \tag{4.6}$$

the Gauss-Seidel algorithm or apply an overrelaxation. We utilize the sparsity of the matrix A of the system and observe that one iteration runs in sequential time $O(N^2)$ for either method. (Remember that A is a $(N-1)^2 \times (N-1)^2$ matrix and arbitrary matrices of this dimension require up to $\Theta(N^4)$ operations!)

How can we obtain an efficient parallelization of one iteration? We assume a checkerboard decomposition of A in the following sense. We partition the $N-1$ rows of the grid $\{\frac{1}{N}, \ldots, \frac{N-1}{N}\}^2$ into $\sqrt{p}$ intervals $I_1, I_2, \ldots$ as well as the $N-1$ columns into $\sqrt{p}$ intervals $J_1, J_2, \ldots$. We imagine the p processes to be arranged in a $\sqrt{p} \times \sqrt{p}$ mesh and assign the vector $(u_{i,j} \mid (i,j) \in I_r \times J_s)$ to process (r,s). The process responsible for determining $u_{i+1,j}(t+1)$ has to know $u_{i-1,j}(t), u_{i,j+1}(t), u_{i,j-1}(t)$ and $u_{i,j}(t)$. It can perform the update without communication unless one or more of the required values belongs to one of its three neighbors –the neighbor to the left, right or the neighbor on top–. In either case the missing values belong to the neighbor's boundary with the exception of $u_{i-1,j}(t)$ which may have distance one from the boundary. Thus after each process sends the $O(\frac{N}{\sqrt{p}})$ values

to its left, right and upper neighbor and receives values in return, it can recompute its values without communication. The computation time is bounded by $O(\frac{N^2}{p})$, since each recomputation only involves $O(1)$ values and $\frac{N^2}{p}$ values have to be recomputed, and the communication time is bounded by $O(\frac{N}{\sqrt{p}})$. Therefore running time $O(\frac{N^2}{p} + \frac{N}{\sqrt{p}})$ suffices and we achieve constant efficiency whenever $N = \Omega(\sqrt{p})$.

Theorem 4.5 *Assume that p processors are available to approximate a solution of the Poisson equation. For one iteration of the Jacoby with or without overrelaxation computing time $O(\frac{N^2}{p})$ and communication time $O(\frac{N}{\sqrt{p}})$ suffices.*

Exercise 58
Assume a column decomposition instead of a checkerboard decomposition. Analyze the computation and communication time.

Remark 4.2 It can be shown that the matrix of the linear system (4.5) is symmetric and positive definite [BT89]. As a consequence one can show that the Jacoby algorithm, the Gauss-Seidel algorithm as well as the conjugate gradient method converge. Moreover the overrelaxation variants converge as well whenever $\gamma \in]0, 2[$.

Remark 4.3 **Trading communications against computations**.
Assume that communication costs dominate computation costs and assume that slightly longer messages result in almost unchanged communication costs. To utilize these assumptions we let neighbor processes exchange more values, namely all values of grid points within distance at most k from the respective boundary. The receiving process duplicates the computation of its neighbor on the received values and thus, at the expense of redundant computations, the next $k-1$ iterations can run without communication.

We already mentioned that the Gauss-Seidel algorithm converges, but the update rule (4.2) is in general inherently sequential. In our application however we obtain an efficient parallelization if we proceed as follows. Label the grid point (i, j) white iff $i + j$ is even and black otherwise. Instead of rule (4.6) we use the update

$$u_{i,j}(t+1) = \frac{u_{i+1,j}(t) + u_{i-1,j}(t) + u_{i,j+1}(t) + u_{i,j-1}(t)}{4} - \frac{H_{i,j}}{4N^2} \tag{4.7}$$

and in this perspective white grid points are updated with the help of black grid points only. Thus we may execute one iteration of the Gauss-Seidel algorithm by first updating black grid points conventionally with the Jacobi relaxation (4.7). Then we apply the Gauss-Seidel algorithm to update white grid points for iteration $t+1$ by using the already updated black grid points.

Observe that we may need black grid points of iteration $t + 1$ which belong to neighbors. If neighbors have communicated the values of grid points within distance at least two, then the process responsible for (i, j) can perform the update of white grid points without communication. Thus redundant computations help in this particular case to reduce communications as well as to implement the Gauss-Seidel algorithm.

Exercise 59
We consider the linear second-order PDE $A \cdot u_{xx} + 2B \cdot u_{xy} + C \cdot u_{yy} + E \cdot u_x + F \cdot u_y + G \cdot u = H$ which is to be solved on the square $[0,1]^2$. We demand the boundary conditions $u(0,y) = K_1(y), u(1,y) = K_2(y), u(x,0) = K_3(x)$ and $u_y(x,0) = K_4(x)$. Compare the finite difference method for this class of PDEs to the finite difference method for the Poisson equation. Which input decomposition do you choose?

4.4 The Discrete Fourier Transform

Let F be a field. We say that $\omega_n \in F$ is an *nth root of unity* iff $\omega_n^n = 1$. If moreover

$$|\{\omega_n, \omega_n^2 \ldots, \omega_n^{n-1}, \omega_n^n\}| = n \text{ and } \omega_n^n = 1,$$

then we say that ω_n is a *primitive nth root of unity.*

Example 4.1 We consider the field $F = \mathbb{Z}_5$ of all residues modulo 5. Then 2 is a primitive fourth root of unity, since $2^2 \equiv 4 \bmod 5$, $2^3 \equiv 3 \bmod 5$ and $2^4 \equiv 1 \bmod 5$.

Example 4.2 The field of real numbers has only ± 1 as roots of unity, since they are the only real roots of the polynomial equation $x^n = 1$. Why? If $x^n = 1$, then the absolute value of x must be one! But $x^n = 1$ has n roots over the complex numbers. We represent a complex number z by its polar coordinates $|z|$ and angle ϕ with

$$z = |z| \cdot (\cos 2\pi\phi + i \cdot \sin 2\pi\phi) = |z| \cdot e^{2\pi i \cdot \phi}.$$

Hence, when multiplying complex numbers z_1 and z_2, we have to multiply lengths and add angles:

$$z_1 = |z_1| \cdot e^{2\pi i \cdot \phi_1}, z_2 = |z_2| \cdot e^{2\pi i \cdot \phi_2} \Rightarrow z_1 \cdot z_2 = |z_1| \cdot |z_2| \cdot e^{2\pi i \cdot (\phi_1 + \phi_2)}.$$

Define

$$\omega_n = e^{2\pi i/n} \tag{4.8}$$

and we obtain $\omega_n^k = e^{2\pi i \cdot k/n}$: powers of ω_n are numbers of length 1 and their angles increase by multiples of $\frac{1}{n}$. Since $\omega_n^n = 1$ and since all powers ω_n^k $(1 \leq k \leq n)$ have distinct angles, we have shown that ω_n is an nth root of unity.

Exercise 60
Let w be an nth root of unity.

(a) Show that $\sum_{k=0}^{n-1} w^k = 0$ holds.

(b) Assume that n is even. Show that $w^{n/2} = -1$ holds, provided w is a primitive root of unity.

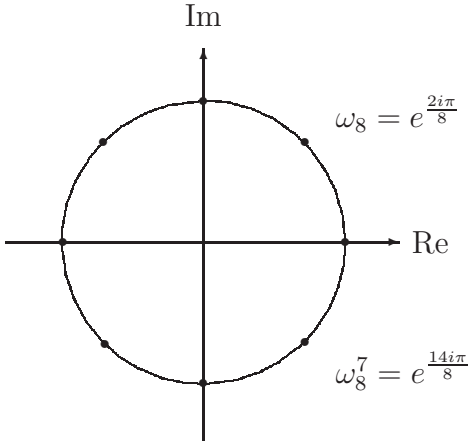


Figure 4.2: Primitive 8-th root of unity $\omega_8 = e^{\frac{2i\pi}{8}}$ and its powers.

Let ω_n be a primitive nth root of unity over some fixed field F. We observe that each power ω_n^i is a root of $x^n = 1$ (and hence deserves the name "root of unity"), since $(\omega_n^i)^n = (\omega_n^n)^i = 1$. Thus, since polynomials of degree n have at most n different roots, the powers $\omega_n, \omega_n^2, \ldots, \omega_n^n$ are all the n different roots of $x^n = 1$.

Definition 4.6 **The Discrete Fourier Transform**

Let F be a field. The discrete Fourier transform of a vector $\vec{x} \in F^n$ is the matrix-vector product

$$\mathrm{DFT}_n \cdot \vec{x} = (\sum_{k=0}^{n-1} \omega_n^{j \cdot k} \cdot x_k \mid 0 \leq j < n) = (\sum_{k=0}^{n-1} x_k (\omega_n^j)^k \mid 0 \leq j < n).$$

$\mathrm{DFT}_n = (\omega_n^{j \cdot k})_{0 \leq j,k < n}$ is the matrix of the discrete Fourier transform.

Thus the discrete Fourier Transform evaluates the degree $n-1$ polynomial with coefficients $(x_0, \ldots, x_{n-1})$ at all roots of unity.

Why would we want to compute the DFT matrix-vector product? The continuous Fourier transform decomposes a signal $x(t)$ into its spectrum of frequency components

$$X(w) = \frac{1}{\sqrt{2\pi}} \cdot \int_{\infty}^{\infty} e^{-iwt} \cdot x(t) dt.$$

The discrete Fourier transform for the complex root of unity $\omega_n^{-1} = e^{-2\pi i/n}$ is applied to a discrete sample of the continuous signal and it approximates the continuous transform if n is sufficiently large, i.e., if the time intervals used for sampling are sufficiently small. Thus for instance in lossy data compression, a discrete signal is decomposed into its frequency

components and high frequency components are dropped. In decompression the inverse transform is applied to the modified frequency components.

Besides the many applications in signal processing, there are further applications in solving differential equations, multiplying integers and polynomials to name only a few. All these applications are based on the Fast Fourier Transform, namely fast algorithms computing the discrete Fourier Transform.

We begin by showing how to multiply polynomials with the help of the discrete Fourier transform. The crucial observation is that the inverse transform is the original transform in disguise, and hence can be computed fast. Moreover the inverse transform can be interpreted as interpolating a polynomial at the roots of unity.

Lemma 4.7 ***The inverse transform***

(a) $DFT_n^{-1} = (\frac{\omega_n^{-j\cdot k}}{n})_{0\le j,k<n}$.

(b) $\vec{y} = DFT_n \cdot \vec{x}$ *is the result after evaluating the polynomial with coefficients* x *at all* n*th roots of unity.*

(c) $\vec{x} = DFT_n^{-1} \cdot \vec{y}$ *is the result of interpolating given the values at the* n*th roots of unity.*

Proof (a): We multiply the jth row of DFT_n with the kth column of DFT_n^{-1} and obtain the inner product

$$\sum_{l=0}^{n-1} \omega_n^{j\cdot l} \cdot \frac{\omega_n^{-l\cdot k}}{n} = \frac{1}{n} \cdot \sum_{l=0}^{n-1} \omega_n^{(j-k)\cdot l}.$$

If $j = k$, then the inner product is the same as adding $\frac{1}{n}$ n times and we obtain the value one as required. If $j \neq k$, then we observe the identity $1 + u + \cdots u^{n-1} = (u^n - 1)/(u - 1)$ and can hence conclude

$$\frac{1}{n} \cdot \sum_{l=0}^{n-1} \omega_n^{(j-k)\cdot l} = \frac{1}{n} \cdot \frac{\omega_n^{(j-k)\cdot n} - 1}{\omega_n^{j-k} - 1} = \frac{1}{n} \cdot \frac{(\omega_n^n)^{(j-k)} - 1}{\omega_n^{j-k} - 1} = 0.$$

(b) We already observed that $\vec{y} = \mathrm{DFT}_n \cdot \vec{x}$ is the result after *evaluating* the polynomial with coefficients x at all roots of unity. To show **(c)** we utilize that DFT_n^{-1} is the inverse of DFT_n. Hence

$$\mathrm{DFT}_n^{-1} \cdot \vec{y} = \mathrm{DFT}_n^{-1} \cdot \mathrm{DFT}_n \cdot \vec{x} = \vec{x}.$$

Thus $\vec{x} = \mathrm{DFT}_n^{-1} \cdot \vec{y}$ is the result of *interpolating* given the values at the roots of unity. □

The following algorithm determines the vector of coefficients of the product polynomial $r = p \cdot q$, where p and q are polynomials of degree at most $n - 1$.

Algorithm 4.8 **Determining the coefficients for the product polynomial** $r = p \cdot q$**.**

/* p and q are polynomials of degree at most $n-1$. x_p is the vector of coefficients of p and x_q is the vector of coefficients of q. */

(1) Compute $\vec{y_p} = \mathrm{DFT}_{2n} \cdot (0, \vec{x_p})$ and $y_q = \mathrm{DFT}_{2n} \cdot (0, \vec{x_q})$;

/* Hence the degree $n-1$ polynomials p and q are evaluated at the $2n$th roots of unity. To achieve this, we have augmented the vectors of coefficients by n zeroes. */

(2) for $j = 0$ to $2n-1$ do

$z_j = (y_p)_j \cdot (y_q)_j$;

/* Observe that z is the result of evaluating the product polynomial r at the $2n$th roots of unity. */

(3) $\vec{x} = \mathrm{DFT}_{2n}^{-1}(\vec{z})$ is the vector of coefficients of the product polynomial $r = p \cdot q$.

Lemma 4.9 *Algorithm 4.8 is correct. Its running time for degree n polynomials is proportional to the time required to perform the $2n$th discrete Fourier transform.*

Proof: In step (1) we evaluate the degree $n-1$ polynomials at the $2n$th roots of unity and in step (2) evaluate the product polynomial r at the $2n$th roots of unity. Since the degree of r is $2n-2$, we determine the vector of coefficients of r when applying the inverse transform in step (3). □

Now we come to the crucial question: how fast can $\mathrm{DFT}_n \vec{x}$ and $\mathrm{DFT}_n^{-1} \vec{y}$ be computed?

Algorithm 4.10 **The Fast Fourier Transform**
/* We assume that n is a power of two. */

(1) Let $x_{\mathrm{even}} = (x_0, x_2, \ldots, x_{n-2})$ be the vector of even coordinates and $x_{\mathrm{odd}} = (x_1, x_3, \ldots, x_{n-1})$ be the vector of odd coordinates of x.

(2) pardo

recursively determine $u = (\mathrm{DFT}_{n/2}) \cdot x_{\mathrm{even}}$ and $v = (\mathrm{DFT}_{n/2}) \cdot x_{\mathrm{odd}}$

with ω_n^2 as primitive $\frac{n}{2}$th root of unity;

(3) for $j = 0$ to $n-1$ pardo

$$y_j = \begin{cases} u_j + \omega_n^j \cdot v_j & 0 \le j < \frac{n}{2} \\ u_{j-n/2} + \omega_n^j \cdot v_{j-n/2} & \frac{n}{2} \le j < n. \end{cases}$$

Let $T(n)$ be the running time of this "idealized" parallel program for sequences x of length n. We observe that step (3) "should" run in constant time with n processors and hence we obtain the recurrence

$$T(n) = T(\frac{n}{2}) + O(1)$$

with solution $T(n) = O(\log_2 n)$. (If we implement algorithm 4.10 as a sequential algorithm, then we obtain the recurrence $T(n) = 2 \cdot T(\frac{n}{2}) + O(n)$ with solution $T(n) = O(n \cdot \log_2 n)$. In particular, we can determine the vector of coefficients of a product polynomial in time $O(n \cdot \log_2 n)$ and thus considerably faster than time $O(n^2)$ with the school method.)

Why does Algorithm 4.10 work correctly? Is ω_n^2 indeed a primitive $\frac{n}{2}$th root of unity?

Exercise 61
Show that ω_n^2 is a primitive $\frac{n}{2}$th root of unity.

Did we choose the right values for y_j? We start with $0 \leq j < \frac{n}{2}$.

$$\begin{aligned}
y_j = \sum_{k=0}^{n-1} \omega_n^{j\cdot k} \cdot x_k &= \sum_{k=0,k \text{ even}}^{n-1} \omega_n^{j\cdot k} \cdot x_k + \sum_{k=0,k \text{ odd}}^{n-1} \omega_n^{j\cdot k} \cdot x_k \\
&= \sum_{k=0}^{n/2-1} \omega_n^{j\cdot(2k)} \cdot x_{2k} + \sum_{k=0}^{n/2-1} \omega_n^{j\cdot(2k+1)} \cdot x_{2k+1} \\
&= \sum_{k=0}^{n/2-1} (\omega_n^2)^{j\cdot k} \cdot x_{2k} + \omega_n^j \cdot \sum_{k=0}^{n/2-1} (\omega_n^2)^{j\cdot k} \cdot x_{2k+1} \\
&= (\mathrm{DFT}_{n/2} \cdot x_{\text{even}})_j + \omega_n^j \cdot (\mathrm{DFT}_{n/2} \cdot x_{\text{odd}})_j
\end{aligned}$$

and this was to be shown.

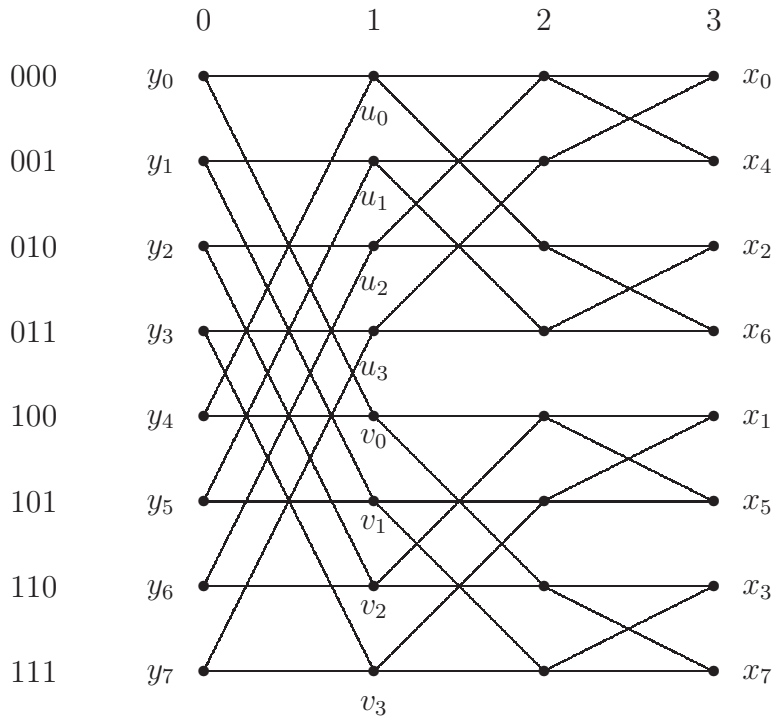
Exercise 62
Show that $(\mathrm{DFT}_n \cdot x)_i = (\mathrm{DFT}_{n/2} \cdot x_{\text{even}})_{i-n/2} + \omega_n^i \cdot (\mathrm{DFT}_{n/2} \cdot x_{\text{odd}})_{i-n/2}$ holds for $\frac{n}{2} \leq i < n$.

Exercise 63
A Hadamard matrix is a square matrix H with $H[i,j] \in \{-1, 1\}$. Moreover any two rows of H have be orthogonal. The following recursive definition describes the specific Hadamard matrix H_n with n rows and columns:

$$H_2 = \begin{pmatrix} 1 & 1 \\ 1 & -1 \end{pmatrix}, \qquad H_n = \begin{pmatrix} H_{n/2} & H_{n/2} \\ H_{n/2} & -H_{n/2} \end{pmatrix}.$$

Show how to compute the matrix-vector product $y = H_n \cdot x$ with n processes in time $O(\log_2 n)$.

Next we implement Algorithm 4.10 on the butterfly network B_d where $n = 2^d$. The input x is split into the subsequences x_{even} and x_{odd} and we interpret this step as reorganizing x to obtain the new sequence $(x_{\text{even}}, x_{\text{odd}})$. In other words, $x_{b_1 \cdots b_k}$ now ends up in position $b_k b_1 \cdots b_{k-1}$. The next recursion step repeats the partition into even and components, but



restricted to x_{even} and x_{odd}: hence $x_{b_1 \cdots b_k}$ is in position $b_k b_{k-1} b_1 \cdots b_{k-2}$ after two recursion steps and in position $\text{rev}(b_1 \cdots b_k) = b_k b_{k-1} \cdots b_2 b_1$ at the end of the recursion. Thus we should input x in "bit reversal order" in column d of B_d. Observe that u_i and v_i determine y_i as well as $y_{i+n/2}$ and these computations can be carried out by communicating between columns 0 and 1. Finally, u_i and v_i are the result of recursive calls and their computation succeeds by communicating between columns 1 and 2 and so forth.

Thus the Fast Fourier Transform, when applied to sequences of length $n = 2^d$, uses the butterfly network B_d as communication pattern. We work with n processes with one process per row of B_d. Activity begins in column d and then moves left with only one column being active at a time.

Thus our algorithm runs in time $O(d)$ with $n = 2^d$ processors and we have achieved an optimal parallelization, since the Fast Fourier Transform runs in time $O(n \cdot \log_2 n)$ and our implementation produces work $O(d \cdot 2^d) = O(n \cdot \log_2 n)$. We now have to discuss implementations for an arbitrary number of p processors.

4.4.1 The Binary Exchange Algorithm

In the binary exchange algorithm we assign disjoint intervals of 2^{d-k} x-inputs to the $p = 2^k$ processes. (The intervals are chosen relative to the bit reversal order. In particular, for $k = 2$ and $d = 3$ assign x_0 and x_4 to process 1, x_2 and x_6 to process 2, x_1 and x_5 to process

3 and x_3 and x_7 to process 4.)

Exercise 64
Assume that an algorithm $\mathcal{A}$, running on B_d, uses only columns $C_k, \ldots, C_d$ in some order.

Show how to simulate $\mathcal{A}$ with $p = 2^k$ processes such that no communication is required. (The ith process receives the ith interval of 2^{d-k} numbers.)

There is no need to communicate for the first $d-k$ iterations, but in each of the remaining k iterations each process executes a point-to-point send/receive operation at a communication cost of $O(\frac{n}{p})$. Moreover the computing time during the first $d-k = \log_2(\frac{n}{p})$ iterations is $O(\frac{n}{p}\log_2\frac{n}{p})$. In the remaining $k = \log_2 p$ iterations the computing time is $O(\frac{n}{p})$ per iteration and we obtain the total computing time

$$O(\frac{n}{p}\log_2\frac{n}{p} + \frac{n}{p}\cdot\log_2 p) = O(\frac{n}{p}\cdot\log_2 n).$$

The total communication time is bounded by $O(\frac{n}{p}\cdot\log_2 p)$ and hence is only marginally smaller than the computing time. Thus we obtain constant efficiency, provided $\log_2 n = \Omega(\log_2 p)$. Since the asymptotic analysis of the communication time hides large constants, we consider also other solutions.

4.4.2 The Transpose Algorithms

We try to reduce the communication cost by applying the following observation.

Exercise 65
Let $\mathcal{A}$ be an algorithm on Q_d with 2^d processes where process $u \in \{0,1\}^d$ receives the input x_u. Firstly $\mathcal{A}$ uses only edges of dimensions $\frac{d}{2}+1, \ldots, d$. From time t onwards only edges of dimensions $1, \ldots, \frac{d}{2}$ are used.

We would like to simulate $\mathcal{A}$ by an algorithm $\mathcal{B}$ with $2^{d/2}$ processes, where process $u \in \{0,1\}^{d/2}$ receives the set of all inputs x_{uv} with $v \in \{0,1\}^{d/2}$. Show that there is an algorithm $\mathcal{B}$ which simulates $\mathcal{A}$ with one all-to-all personalized broadcast as the only communication step. Moreover $\mathcal{B}$ is slowed down by at most the factor $O(2^{d/2})$.

Imagine that the input sequence x is arranged into a $\sqrt{n}\times\sqrt{n}$ mesh such that all communications of the first $\log_2\sqrt{n}$ steps of the FFT butterfly algorithm are between sequence elements of a column and hence all communications of the last $\log_2\sqrt{n}$ steps are between sequence elements of a row. We assign $\sqrt{n}/p$ columns to each process and then work in three phases: at first each process implements the fast Fourier transform within its columns, then an all-to-all personalized broadcast is executed and finally, as the last and third phase, each process implements the fast Fourier transform again within its columns. This perspective is the reason why this approach is called the *two-dimensional* transpose algorithm.

Algorithm 4.11 **The two-dimensional transpose algorithm.**
/* $p = 2^k$ processes (with $p \leq 2^{d/2}$) are available to determine the discrete Fourier transform for a sequence of length $2^d = n$. Process $u^1 = u_1 \cdots u_k \in \{0,1\}^k$ receives all numbers $x_{u_1 \cdots u_k **}$. */

(1) Perform the first $d/2$ iterations of the FFT butterfly algorithm without any communication.

(2) Determine the transpose by an all-to-all personalized broadcast, i.e., process $u^1 = u_1 \cdots u_k$ sends the data of butterfly node $(u^1 u^2 v^2 v^1, \frac{d}{2})$ (for $v^1 \in \{0,1\}^k$ and $u^2, v^2 \in \{0,1\}^{d/2-k}$) to process v^1.

(3) Perform the last $d/2$ iterations of the FFT butterfly algorithm without any communication: process v^1 simulates all butterfly nodes $** v_1 \cdots v_k$.

In the general case of $p = 2^k \leq 2^{d/2}$ processes, Algorithm 4.11 assigns $2^{d-k} = \frac{n}{p}$ numbers to any process. The all-to-all personalized broadcast sends p messages of length $\frac{1}{p} \cdot \frac{n}{p} = \frac{n}{p^2}$ each from one process to the remaining p processes. Thus the communication cost is proportional to $O(\frac{n}{p})$ whereas the computing time of $O(\frac{n \cdot \log_2 n}{p})$ is unchanged. We reach constant efficiency assuming $n = \Omega(p^2)$. If we compare the binary exchange and the transpose algorithm, then the transpose algorithm reduces the combined message length by the factor $\log_2 p$, however the cheap send/receive is replaced by the expensive all-to-all personalized broadcast and we have to expect larger constant factors.

The *three-dimensional* transpose algorithm is a compromise between the binary exchange and the two-dimensional transpose algorithm. Instead of three phases we now work with five phases. In phase one we perform the first $\frac{1}{3} \cdot \log_2 n$ steps of the fast Fourier transform without communication. A "restricted" all-to-all broadcast (within the sub-butterfly on the last $\frac{2 \log_2 n}{3}$ dimensions) guarantees that the next $\frac{1}{3} \cdot \log_2 n$ steps of the fast Fourier transform run again without communication. After a final all-to-all broadcast the final $\frac{1}{3} \cdot \log_2 n$ steps run again without communication. Observe that each all-to-all broadcast exchanges messages of length $\frac{n}{p}$ within groups of $p^{2/3}$ processes. In comparison with the two-dimensional transpose algorithm, the combined message length doubles, but the all-to-all broadcasts apply to smaller groups.

Theorem 4.12 *Let n be a power of two.*

(a) The binary exchange algorithm runs in time $O(\frac{n \cdot \log_2 n}{p})$ and spends $O(\frac{n \cdot \log_2 p}{p})$ steps on communication.

(b) The two- and three-dimensional transpose algorithms run in time $O(\frac{n \cdot \log_2 n}{p})$ and spend $O(\frac{n}{p})$ steps on communication.

4.5 Conclusion

We have parallelized the matrix-vector and the matrix-matrix product for various input partitions and obtained optimal parallel algorithms.

Then we have turned our attention to solving linear systems of equations. We have developed back substitution to solve lower triangular systems and then parallelized Gaussian elimination with partial pivoting. Iterative methods are particularly well suited for sparse linear systems. We have discussed the Jacobi relaxation and overrelaxation, the Gauss-Seidel algorithm and the conjugate gradient method. We then have applied iterative methods to solve linear partial differential equations.

With the binary exchange algorithm and the transpose algorithm we have presented optimal parallelizations of the discrete Fourier transform.

Chapter 5

Algorithms for Hard Problems

We survey Monte Carlo and Markov chain Monte Carlo methods, backtracking, branch & bound and alpha-beta pruning as general techniques to solve computationally hard search and optimization problems. All these methods immediately profit from parallelization. Monte Carlo methods give better results when more more trials are performed and Backtracking, branch & bound and alpha-beta pruning require only very little interaction when partitioning their search efforts among several processes.

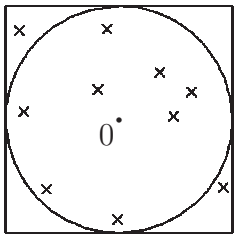
We do not attempt to give an in depth discussion, but rather restrict ourselves to a survey emphasizing aspects of parallelization. Most of these approaches are trivially parallelizable, however issues such as dynamic load balancing and termination detection have to be dealt with.

5.1 Monte Carlo Methods

The Monte Carlo method encompasses any technique of statistical sampling employed to approximate solutions to quantitative computational problems.[1] An important application area is to simulate the behavior of various physical and mathematical systems.

Example 5.1 **Approximating** π
We show how to approximate π. Observe that the area of the circle C with radius one equals π, whereas the area of the square $S = [-1, +1]^2$ equals four. Hence if we randomly draw p points from S and if $p(C)$ is the number of points which already belong to the circle C, then the ratio $\frac{p(C)}{p}$ converges to $\frac{\pi}{4}$.

[1] With computer science terminology one would speak of randomized algorithms for computational problems.



Exercise 66
Assume that we draw n points from the square S at random. Use the Chebycheff inequality to bound the error $\frac{|\text{estimate}-\pi/4|}{\pi/4}$.

Example 5.2 **Evaluating Multi-Dimensional Integrals**
Many deterministic methods of numerical integration such as the Newton-Coles formulas (rectangle and trapezoidal rule, Simpson's rule) and Gaussian quadrature operate by taking a number of samples from a function. In general, this works very well for functions of few variables. However, for high dimensional functions deterministic integration methods tend to be inefficient. For instance, if we distribute points in the interval $[0,1]$ with distance at most $\frac{1}{N}$ between neighboring points, then N points are required. To obtain a similar spacing for the cube $[0,1]^k$, N^k grid points are required.

To numerically integrate a function of a single variable, N equally spaced points for a sufficiently small step size $1/N$ are required. If we integrate a function depending on a k-dimensional vector, then for large k the same spacing on a k-dimensional grid requires the inordinately large number of N^k grid points.

The Monte Carlo method interpretes an integral $\int_{x\in\Omega} f(x)d^kx$ as the product $V(\Omega)\cdot E_\Omega(f)$, where $V(\Omega)$ is the volume of the integration region Ω and $E_\Omega(f)$ is the expected value of f restricted to $\Omega \subseteq \mathbb{R}^k$. As long as the function f in question is reasonably well-behaved, its integral $\int_{x\in\Omega} f(x)d^kx$ is estimated by randomly selecting points $x_1,\ldots,x_M \in \Omega$ and returning the estimate $\frac{V(\Omega)}{M}\cdot\sum_{i=1}^M f(x_i)$. To bound the error of this estimate we use the Chebycheff inequality

$$\text{prob}\left[|Y - \text{E}\left[Y\right]| > t\right] \leq \frac{\text{Var}\left[Y\right]}{t^2}$$

and apply it to the random variable $Y = \frac{1}{M}\cdot\sum_{i=1}^M X_i$, where $X_i = f(x_i)$ is the result of the ith random experiment. We interpret X_i as the ith repetition of the experiment X and observe that $\text{E}\left[Y\right] = E[\frac{1}{M}\cdot\sum_{i=1}^M X_i] = \frac{M}{M}E[X] = E[X]$. But the random experiments $X_1,\ldots,X_M$ are independent and in particular

$$\text{Var}\left[Y\right] = \frac{1}{M^2}\cdot\sum_{i=1}^M \text{Var}\left[X_i\right] = \frac{1}{M^2}\cdot\sum_{i=1}^M \text{Var}\left[X\right] = \frac{1}{M}\cdot\text{Var}\left[X\right]$$

holds. We have reduced variance by the factor M and hence the Chebycheff inequality

implies the inequality

$$\begin{aligned}\text{prob}\left[\left|\frac{1}{M}\cdot\sum_{i=1}^{M} f(x_i) - \frac{1}{V(\Omega)}\int_{x\in\Omega} f(x)d^k x\right| > t\right] &= \text{prob}\left[|Y - \mathrm{E}[Y]| > t\right] \\ &\leq \frac{\mathrm{Var}[Y]}{t^2} = \frac{\mathrm{Var}[X]}{M\cdot t^2}.\end{aligned}$$

Thus as a consequence,

$$|\frac{V(\Omega)}{M}\cdot\sum_{i=1}^{M} f(x_i) - \int_{x\in\Omega} f(x)d^k x| > t\cdot V(\Omega)$$

holds with probability at most $\frac{\mathrm{Var}[X]}{M\cdot t^2}$. We set $t = c\cdot\frac{\sqrt{\mathrm{Var}[X]}}{\sqrt{M}}$ and the approximation error is larger than $t\cdot V(\Omega)$ with probability at most $\frac{1}{c^2}$. Observe that an s^2-fold increase in the number of sample points is required, if we want to reduce the error by a factor of s.

This simple approach however converges only very slowly if the function is very complex and for instance has small islands of high activity. A refinement of this method is to somehow make the points random, but more likely to come from regions of high contribution to the integral than from regions of low contribution. In other words, the points should be drawn from a distribution similar in form to the integrand. Understandably, doing this precisely is just as difficult as solving the integral in the first place, but there are approximate methods available such as Markov Chain Monte Carlo methods (see Section 5.1.1).

In the above two examples we get more accurate answers the more trials we perform. Here we have the opportunity to profit from parallel computation by sampling with p processes instead of using just one process. Observe that this "embarrassingly parallel" approach requires no communication whatsoever with the exceptions of the last step of averaging individual results.

Good pseudo random numbers suffice for Monte Carlo methods and we discuss some important generators in Section 5.1.2. Finally in Section 5.1.1 we describe Markov chain Monte Carlo methods and in particular the Metropolis and Simulated Annealing algorithms as two prominent Monte Carlo optimization methods.

5.1.1 Markov Chain Monte Carlo Methods

We begin with a few basic facts on finite Markov chains.

Definition 5.1 A finite Markov chain $\mathcal{M} = (\Omega, P)$ is described by a finite set Ω of states and by a matrix P of transition probabilities between states in Ω. In particular, $P[u, v]$ is the probability to visit $v \in \Omega$, given that $u \in \Omega$ is currently visited. We demand that $\sum_{v\in\Omega} P[u, v] = 1$ holds for all states u.

Exercise 67
Let $\mathcal{M} = (\Omega, P)$ be a Markov chain. Show that $P^t[u, v]$ is the probability that the random walk reaches state v after t steps provided the walk begins in state u.

If there is a path with positive probability between any two states in Ω and if $P[x, x] > 0$ holds for all states x, then the following fundamental properties hold:

(a) $\mathcal{M}$ has a unique **stationary distribution** π, i.e., $\pi^T \cdot P = \pi^T$ holds. (Assume that π is a stationary distribution. If $\mathcal{M}$ is in state u with probability $\pi(u)$, then after one step $\mathcal{M}$ is in state v with probability

$$\sum_{u \in \Omega} \pi(u) P[u, v] = (\pi^T \cdot P)(v) = \pi(v)$$

and $\mathcal{M}$ stays in the stationary distribution π.)

(b) $\lim_{t \to \infty} P^t[u, v] = \pi(v)$ holds and the frequency with which v is visited does not depend on the starting state u.

Exercise 68
Show property (b).

Markov chain Monte Carlo (MCMC) methods (also called random walk Monte Carlo methods) construct a Markov chain that has a target distribution as its stationary distribution. The state of the chain after a large number of steps is then used as a sample from the target distribution. The quality of the sample improves with time, however the number of steps required to converge to the stationary distribution within an acceptable error, may be quite large. We say that a chain **rapidly mixes** if it reaches the stationary distribution quickly from any other distribution.

Exercise 69
(a) We consider a Markov chain with state set $\{0, 1, \ldots, n\}$ and transition probabilities $P[i, i+1] = P[i+1, i] = 1/2$ for $1 \leq i \leq n-1$ and $P[0, 0] = P[n, n-1] = 1$. Determine the expected time $T(i)$ for each state i in which state 0 is reached.

(b) We have to determine whether a formula α in conjunctive normalform with at most two literals per clause is satisfiable. Our algorithm first chooses an arbitrary assignment x. Then it repeats the following steps *sufficiently often*: if the current assignment is satisfying, the algorithm halts. Otherwise determine an arbitrary clause which is not satisfied and flip the value of a randomly selected variable appearing in the clause. If no satisfying assignment is found, declare α to be not satisfiable.

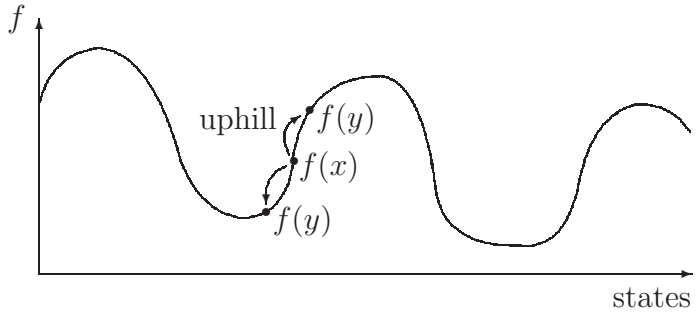
Use part (a) to determine the number of iterations sufficient to find a satisfying assignment with probability at least $1/2$, provided α is satisfiable.

Example 5.3 Multi-Dimensional Integrals
A first important application of MCMC methods is the approximation of a multi-dimensional integral $\int_{x \in \Omega} f(x) d^k x$. In these methods, an ensemble of "walkers" moves around

the integration region randomly in the search of "high-activity" areas. A walker checks its current area to determine a point with a considerable contribution towards the integral respectively to determine the next area to walk into. In particular, a Markov chain is constructed for which the integrand corresponds to its stationary distribution.

Example 5.4 **MCMC optimization methods**
A second important application concerns the approximation of optimization problems. Assume that we have to minimize a multi-dimensional function f over some finite domain Ω. For any point $x \in \Omega$ let $N(x) \subseteq \Omega$ be the neighborhood of x. We interpret the points in Ω as states of a Markov chain.

The **Metropolis algorithm** starts at some initial point $x \in \Omega$. If the algorithm is currently visiting point x, then it randomly chooses a neighbor $y \in N(x)$ and continues with y as long as y is at least as good as x, i.e., $f(y) \leq f(x)$. The case $f(y) > f(x)$ is crucial. Since we would like to minimize f we should be reluctant to continue with y, however if we do not tolerate a worse solution, then we get stuck in local minima.



The Metropolis algorithm proposes a compromise and accepts an uphill move with probability $e^{-\frac{f(y)-f(x)}{T}}$: the larger the "temperature" T the higher the probability that a bad neighbor is accepted. Assume that the algorithm continues its walk for a fixed, but sufficiently long time and reaches a solution $x \in \Omega$. Since the walk has been long and since we only reluctantly accept an uphill move, the probability of a good solution x (i.e., $f(x)$ is relatively small) should be relatively high. Indeed it turns out that the probability of x tends to the probability

$$q_T(x) = \frac{1}{N_T} \cdot e^{-\frac{f(x)}{T}} \quad \text{with} \quad N_T = \sum_{x \in \Omega} e^{-\frac{f(x)}{T}}.$$

Exercise 70
Assume that the neighborhoods are symmetric (i.e., $x \in U(x)$ for all $x \in \Omega$, $y \in N(x)$ whenever $x \in N(y)$ and $|U(x)| = |U(y)|$ for all $x, y \in \Omega$). Moreover assume that there is a path from x to y for any pair $(x, y) \in \Omega^2$. We fix the temperature T. Then the Markov chain (Ω, P_T) has a unique stationary distribution π.

(a) Show that q_T is reversible, i.e., $q_T(x) \cdot P_T[x, y] = q_T(y) \cdot P_T[y, x]$ holds.

(b) Show that any reversible distribution ρ coincides with the stationary distribution. Thus q_T coincides with the stationary distribution π.

The next example shows that we should incorporate a mechanism to reduce the temperature T.

Example 5.5 In the Vertex Cover problem we are given an undirected graph $G = (V, E)$ and we are looking for a cover, i.e., a subset $C \subseteq V$ of minimal size such that each edge has at least one endpoint in C. We say that subsets $U_1, U_2 \subseteq V$ are neighbors iff U_2 results from U_1 after inserting a node or removing a node from U_1.

We apply the Metropolis algorithm to the empty graph, i.e., $E = \emptyset$. Obviously the empty set is a minimal cover. Assume we start with the cover $x = V$. Initially the Metropolis algorithm removes elements from its current solution. But if its current solution x has only few elements, then there are far more larger than smaller neighbors: the Metropolis algorithm begins to add nodes!

Observe that the smaller we choose T the higher will be the probability of global minima and it is to be expected that the time to converge increases sharply with decreasing temperature. **Simulated Annealing**[2] (SA), an extension of the Metropolis algorithm, tries to reduce the convergence time by proposing a cooling schedule. SA starts a random walk with a fixed temperature $T = T_0$ where T_0 has to be sufficiently large. After "*sufficiently many*" steps the temperature T will be cooled down geometrically by setting $T = \alpha \cdot T$ with $0 < \alpha < 1$ and a new random walk is started.

Algorithm 5.2 **Metropolis and Simulated Annealing**

(1) Set $x = x_0$ for some initial solution $x_0 \in \Omega$. Choose a temperature T.
/* The larger T the more likely are uphill moves. */

(2) Repeat sufficiently often:

(a) Choose a neighbor y of x with probability $P[x, y]$.

(b) IF $f(y) \leq f(x)$ THEN set $x = y$ ELSE set $x = y$ with probability $e^{-\frac{f(y)-f(x)}{T}}$.

(3) Whereas the Metropolis algorithm now terminates, Simulated Annealing may choose a lower temperature T and return to step (2).

We choose the problem of graph partition as an application of SA. We are given an undirected graph $G = (V, E)$ and look for a subset $W \subseteq V$ with $\mid W \mid = \frac{1}{2} \cdot \mid V \mid$ such that the number of crossing edges, i.e., $\mid \{e \in E \ : \mid e \cap W \mid = 1\} \mid$ is minimal. The minimization

[2]Simulated Annealing has received its name in analogy with physical annealing in which a material is first heated and atoms can rearrange freely. When slowly cooling down, the movement of atoms is more and more restricted until the material reaches a minimum energy state: hopefully a perfect crystal with regular structure has formed.

problem is $\mathcal{NP}$-complete and no efficient solutions are to be expected. As solutions we accept arbitrary partitions $(W, V \setminus W)$ and choose

$$f(W) := \mid \{e \in E \ : \ \mid e \cap W \mid = 1\} \mid + \underbrace{\alpha \cdot (\mid W \mid - \mid V \setminus W \mid)^2}_{\text{penalty term}}$$

as objective function, where the penalty term tries to enforce a balanced partition. The neighborhood $N(W)$ consists of all subsets $W' \subseteq V$ with $\mid W \oplus W' \mid \leq 1$. SA starts with a randomly chosen partition $(W, V \setminus W)$ with $\mid W \mid = \frac{1}{2} \cdot \mid V \mid$ and then tries to find better partitions by successively inserting, resp. removing nodes.

[JAGS89] proposes to determine the initial temperature T_0 such that 40% of all neighbors are accepted. Furthermore they keep the temperature constant over a period of $16 \cdot \mid V \mid$ steps and then cool it down by the factor $\alpha = 0,95$. If G is randomly generated, then SA is more successful than tailor-made heuristics and this phenomenon occurs even if we allot the same time that SA consumes. Further experiments are run on structured graphs by choosing between 500 and 1000 points from the square $[0,1]^2$ and connecting two points whenever they are sufficiently close. For this class of "geometric random" graphs the performance of SA collapses and tailor-made heuristics turn out to be far superior even if SA is given significantly more time.

In other words one should not expects miracles from either Metropolis or Simulated Annealing. However if problem-specific algorithms are not available, then both algorithms are excellent starting points. Performing p random walks in parallel is easily achieved without any communication.

So far we have considered Markov chains whose set of states is so huge that a direct computation of the stationary distribution is completely out of question. The next example shows that parallel algorithms are of central importance when the set of states is of barely manageable size.

Example 5.6 **Google**
The search engine Google assigns a *page rank* $\mathrm{pr}(w)$ to a website w, where $\mathrm{pr}(w)$ is evaluated by a peer review: $\mathrm{pr}(w)$ "should" be the higher the more websites with high page rank point to w. To define the page rank Google sets up a Markov chain (W, P) where W is the set of all websites. Moreover, if $\mathrm{fanout}(w)$ is the number of pages that w points to, then Google defines

$$P[w_1, w_2] = \begin{cases} 0 & w_1 \text{ does not point to } w_2, \\ \frac{1}{\mathrm{fanout}(w_1)} & \text{otherwise.} \end{cases}$$

Imagine that a "random surfer" begins at some website v and jumps at random from one page to the next. Then we would like to define $\mathrm{pr}(w)$ as the probability that w is reached after a fixed, but sufficiently large number of steps. We have to require that $\mathrm{pr}(w)$ does not depend on the starting part, however we face a problem for instance if we start from a

dead end. Therefore Google inserts new low-probability links and connects each page w_1 with any other page w_2. The probability to reach a given website w is now independent of the starting point and coincides with $\pi(w)$, where π is the stationary distribution.

To compute page ranks one has to determine the stationary distribution, a daunting task involving a transition matrix with several billions of rows and columns. Google chooses a parallel solution employing several thousand PC's. We begin with the uniform distribution π_0 and, if π_i is determined, set $\pi_{i+1}^T = \pi_i^T \cdot P$. Two facts help. First of all the transition matrix P is sparse and hence the total work per iteration is "only" bounded by a few ten billions. Secondly the web chain is rapidly mixing and we obtain a good approximation of the stationary distribution after relatively few iterations. Thus ultimately the success of Google is based on the fact that the matrix-vector product is highly parallelizable.

5.1.2 Pseudo Random Number Generators

A generator G is a deterministic algorithm which produces a string $y = G(x) \in \{0,1\}^{p(n)}$ given a seed $x \in \{0,1\}^n$. Moreover we require $p(n) > n$ and hence G has to stretch its seed x into a longer string y. A **statistical test** $\mathcal{T}$ is a randomized algorithm which either outputs zero or one and runs on inputs of length n in time polynomial in n. One says that a generator G **passes the test** $\mathcal{T}$ if the acceptance probability r_n of $\mathcal{T}$, given a truly random string of length $p(n)$, is not observably different from the acceptance probability g_n of $\mathcal{T}$, given a string $G(x)$.[3] (The acceptance probability is determined by running $\mathcal{T}$ on all strings of length $p(n)$, respectively on all strings $G(x)$ for $x \in \{01,\}^n$.) Finally we say that G is a **crytographically secure pseudo random generator**, provided G passes all statistical tests.

Example 5.7 **The Blum-Blum-Shub (BBS) Generator**
For a seed s_0 determine the sequence $s_{i+1} = s_i^2 \bmod N$, where $N = p \cdot q$ with primes $p \equiv q \equiv 3 \mod 4$. The BBS generator produces the pseudo-random string $G(s_0) = (s_1 \bmod 2, \ldots, s_m \bmod 2)$ with, say, $m = (\lceil \log_2 s_0 \rceil)^k$ for a constant k. One can show that the BBS generator is cryptographically secure, *provided* factoring of most numbers $N = p \cdot q$ —with primes $p \equiv q \equiv 3 \mod 4$ — is computationally hard. Observe however that the BBS generator is quite expensive since we have to square in order to get one random bit.

The remaining prominent generators trade cryptographical security against speed of evaluation.

Example 5.8 **The Linear Congruential Generator**
The linear congruential generator (LC) is defined by its modulus m, its coefficient a and its offset b. We generate a sequence x_i by starting with a seed x_0 and setting

$$x_{i+1} = a \cdot x_i + b \mod m.$$

[3] r_n is not observably different from g_n iff for all $k \in \mathbb{N}$ there is a bound N_k such that $|g_n - r_n| \leq n^{-k}$ for all $n \geq N_k$.

One can show that the LC generator is cryptographically *insecure*, however it is fast and has large periods, if m is a sufficiently large prime number.

Exercise 71
We consider the linear congruential generator

$$x_{i+1} = ax_i + b \bmod m.$$

(a) Show that

$$x_i = a^i x_0 + b \cdot (1 + a + \cdots + a^{i-1}) \bmod m$$

holds.

(b) Suppose that m is a prime. Show: if $x_{i+j} = x_i$, then $x_0 = x_j$.

(c) Suppose that m is a prime and that $|\{a^i \mod m \mid i\}| = m - 1$ holds. How many initial values x_0 have period length at most K? (x_0 has period length at least K iff $x_0, \ldots, x_{K-1}$ are pairwise distinct.)

Example 5.9 **The Mersenne Twister**
The Mersenne twister MT 19937 is a very fast generator with the gigantic period length $2^{19937}-1$. Its period length is a Mersenne prime, explaining its name. The Mersenne twister is based on the technique of generalized linear feedback shift registers. Its recurrence is of the form

$$x_n = x_{n-227} \oplus (x^U_{n-624} \circ x^L_{623}) \cdot A$$

All sequence numbers x_n are 32-bit words. x^U_m is the leading bit of x_m and x^L_m is the string consisting of the trailing 31 bits of x_m. A is a 32×32 bit matrix with a 31×31 identity matrix in the upper left. The first column of A is zero with the exception of the entry in row 32. Its last row is 9908B0DF in hexadecimal. MT 19937 requires a seed of $19937 = 32 \cdot 623 + 1$ bits, namely 623 strings of length 32 plus the leading bit of x_0. The recurrence expands the seed each time by 32 bits.

The notion for cryptographical security requires an infinite family of generators and hence cannot be applied to the Mersenne twister. The Mersenne twister does pass for instance the Diehard tests[4], but there is no strong mathematical theory in support. The twister has become increasingly popular for Monte Carlo methods due to its speed and its extremely large period length. It is now part of the GNU scientific library.

Example 5.10 **The Lagged Fibonacci Generator**
The lagged Fibonacci generator uses the recurrence

$$S_n = S_{n-j} * S_{n-k} \mod M$$

for $0 < j < k$. (This generalizes the recurrence $S_n = S_{n-1} + S_{n-2}$ defining the Fibonacci sequence.) The operation $*$ may either be addition, subtraction, multiplication or bitwise xor. Its advantages are speed and long period lengths, however the generators are mathematically only incompletely understood and their speed and period length are inferior in comparison to the Mersenne twister.

[4]See `http://random.com.hr/products/random/manual/html/Diehard.html`

When running a randomized parallel algorithm, a master process should assign different seeds to the processes, since we would like the processes to compute independently. This can be done by creating a pseudo random sequence sequentially and by assigning subsequences to the processes.

5.2 Backtracking

In a decision problem we are given a set U of *potential* solutions and we have to determine whether U contains a *true* solution. For instance let α be a conjunction of disjunctions. α describes the set U of all truth assignments to the variables of α and we have to determine whether U contains a true solution, namely an assignment satisfying α.

Backtracking searches for a solution by trying to construct a true solution step by step from *partial* solutions. Backtracking begins with the partial solution $r = U$, which corresponds to the set of all potential solutions. It then applies a branching operator B to r which returns a partition $r_1 \cup \cdots \cup r_k$ of r. The branching operator B defines the backtracking tree $\mathcal{T}$: initially $\mathcal{T}$ consists only of the root r. Then we attach children $r_1, \ldots, r_k$ to r to mimic the partition $r = r_1 \cup \cdots \cup r_k$. In general, if $\mathcal{B}$ has a node v which is not a singleton set, then we apply B to v to obtain a partition $v = v_1 \cup \cdots \cup v_l$ and correspondingly we make $v_1, \ldots, v_l$ children of v.

Backtracking tries to generate only a very small portion $\mathcal{B}^*$ of $\mathcal{B}$. Namely, whenever it finds that a node v does not have a true solution, it disqualifies v and v will not be expanded any further. Often backtracking generates $\mathcal{B}^*$ in a depth first search manner:

> if it currently inspects v and if v can be disqualified, then it "backs up" and continues with the parent of v. Otherwise it continues recursively with a not yet inspected child of v.

Example 5.11 Assume that $\alpha(x_1, \ldots, x_n)$ is a conjunction of disjunctions. We would like to determine whether α is satisfiable, i.e., whether α has a satisfying assignment (of truth values to propositional variables).

In our approach partial solutions correspond to partial assignments. To be specific, assume that we already have assigned truth value to all variables x_j for $j \in J$. We determine a disjunction d of *minimal* size and choose an arbitrary variable x_i appearing in d. The branching operator B then produces two partial solutions by additionally setting $x_i = 0$ respectively $x_i = 1$.

Why do we define a truth value for a variable appearing in a disjunction of minimal size? Our hope is that this allows us to faster falsify partial assignments. In particular, we run the following test after fixing the value of x_i: we look for any disjunction with exactly one unspecified variable, fix the variable appropriately and continue looking for disjunctions with exactly one unspecified variable. If some disjunction is falsified during this process, then the partial assignment is doomed and we disqualify it.

Exercise 72
Can we refine the satisfiability test for partial assignments by inspecting any disjunction with at most two unspecified variables, setting one of the variables arbitrarily and checking the consequences?

Of course, the satisfiability test should be efficient.

Backtracking uses depth-first search to minimize the required memory resources. When implementing parallel Backtracking with p processes it is advisable that first each process generates the same top portion of the search tree such that the number of nodes is at least proportional to p. If that is done, each process starts to search within the subtrees of "its" nodes. Observe that so far no communication is required. However this changes when a process runs out of work and hence we encounter a problem of dynamic load balancing. We discuss load balancing schemes in Section 6.1.

After deciding which load balancing scheme to use we still have to take care of an apparently innocent problem: how to decide when to terminate? Observe that a process cannot assume that it is done just because it currently does not have work to do. Even asking the remaining processes is no good idea: if a process replies that it is idle, then this process may receive a work assignment soon afterwards. We describe **Dijkstra's token termination detection algorithm** for the general termination problem in chapter 7.

5.3 Branch & Bound

Our goal is to minimize a function f over a finite domain Ω. Branch & Bound again utilizes the branching operator B, but does not differentiate between potential and true solutions. As for backtracking the branching operator defines a tree $\mathcal{T}$, which this time we call the branch & bound tree. The crucial requirement of Branch & Bound is the existence of a lower bound α with

$$\alpha(v) \leq \min\{f(x) \mid x \in \Omega \text{ is a leaf in the subtree of } \mathcal{T} \text{ with root } v\}.$$

Example 5.12 In the traveling salesman problem (TSP) we are given a set of nodes in the plane and are asked to compute a tour of shortest length traversing all nodes. (Observe that we do not require the tour to return to its origin.) TSP leads to an $\mathcal{NP}$-complete problem and is therefore in all likelihood a computationally hard problem. A somewhat related, but computationally far easier problem is the minimum spanning tree problem (MST) in which we look for a spanning tree[5] with minimal weight, i.e., minimal sum of edge lengths. What is the relation between TSP and MST? If a path P of length L traverses all nodes, then we have found a spanning tree of weight L, namely the path P. In other words, we have found a lower bound for TSP which is computable within reasonable resources.

Branch & Bound begins by constructing a "good" initial solution x with the help of a heuristic and sets $\beta = f(x)$. Initially only the root of T is unexplored. In its general step

[5]A spanning tree connects all nodes.

Branch & Bound has computed a set U of unexplored nodes and it chooses an unexplored node $v \in U$ to explore. If $\alpha(v) \geq \beta$, then the best solution in the subtree of v is not any better than the best solution found so far and Branch & Bound considers the entire subtree with root v to be explored. If v is a leaf corresponding to a solution x, then β is updated by $\beta = \min\{\beta, f(x)\}$. Otherwise Branch & Bound generates all children of v and add them to its set U of unexplored nodes. It terminates with the optimal value β if all nodes are explored.

There are various heuristics to select an unexplored node from the set U, among them versions and combinations of depth-first and best-first search. In best-first search an unexplored node v with smallest lower bound $\alpha(v)$ is selected. If several choices remain, then the deepest node and hence the most constrained node is selected.

A Parallel Branch & Bound Implementation

We let all processes simultaneously determine the top portion of the Branch & Bound tree. Afterwards processes determine, according to some predefined procedure, "their" subproblems. Each process i works on its subproblem by representing its set U_i of unexplored nodes by its own private priority queue. Up to this point no communication is required and communication becomes necessary only

- if a process runs out of work and has to request work using some dynamic load balancing scheme or
- if a process has found a better upper bound.

Branch & Bound is the more successful the better the lower and upper bounds are. Therefore, to obtain good upper bounds as fast as possible, some parallel implementations let processes also exchange promising unexplored nodes.

5.4 Alpha-Beta Pruning

Assume that we have to find a winning move in a two-player game with players Alice and Bob. Alice begins and the two players alternate. We require the game to be finite and that it ends with a payment to Alice: If the payment is $-1, 0$ or 1, then Alice wins, if she receives a payment of 1 and Bob wins, if she receives a payment of -1. Our goal is to determine a winning strategy for Alice, that is a strategy that guarantees the highest possible payment to Alice.

Any such game has a game tree $\mathcal{B}$. The root r corresponds to the initial configuration and it is marked with Alice, who starts the game. If a node v of $\mathcal{B}$ corresponds to the configuration c_v, then we generate a child w of v for any possible move: the child w is marked with the opposing player and it corresponds to the configuration c_v as altered by

the current move. If however the game is decided in v, then v becomes a leaf and we mark v with the payment $A(v)$ to Alice.

We can determine the highest possible payment to Alice with the **minimax** evaluation of $\mathcal{B}$, an application of depth-first search. We say that a node v of $\mathcal{B}$ is a max-node, if v is marked with Alice and otherwise that v is min-node.

Algorithm 5.3 The function Minimax(v)

(1) If v is a leaf, then return $A(v)$.

(2) If v is a max-node, then // Alice makes a move.

- Max $= -\infty$,
- traverse all children w of v and set Max $= \max\{\text{Max}, \text{Minimax}(w)\}$.
  // Alice makes her best move.
- Return Max.

(3) If v is a min-node, then // Bob makes a move.

- Min $= \infty$,
- traverse all children w of v and set Min $= \min\{\text{Min}, \text{Minimax}(w)\}$.
  // Bob makes his best move.
- Return Min.

Indeed the minimax evaluation can be significantly accelerated. Namely, let us have a look at the minimax evaluation of a max-node v and let us assume that the min-node u is an ancestor of v. Moreover assume that the Min-variable of u, when visiting v, equals β. To evaluate the max-node v we have to consider all children w of v, that is we have to consider all possible moves of Alice. If Alice can enforce, for some child w, a payment of at least β, then Bob can prevent Alice from reaching v without increasing her payment: for instance he can make a move in u to exclude v, but to still limit Alice to payments of at most β. The evaluation of v can be stopped!

Of course a similar argument applies to the evaluation of a min-node v: Let the max-node u be an ancestor of v and assume that the Max-variable of u currently equals α. If Bob has a particularly clever move (v, w), which bounds the payment of Alice to at most α, then Alice can move in u as to make v unreachable and still receive payment α. How should we define α and β when evaluating a min-node, resp. a max-node v?

> α should be the maximal value of a Max-Variable of a "max-ancestor" of v and β should be the minimal value of a Min-variable of a "min-ancestor" of v.

If we implement these ideas, then we are led to the alpha-beta algorithm, which again searches the game tree via depth-first search, but accelerates the search by using parameters α and β.

Algorithm 5.4 The function alpha-beta (v, α, β).

/* The first call uses parameters $\alpha = -\infty, \beta = +\infty$ and $v = r$. */

(1) If v is a leaf, then return $A(v)$.

(2) Otherwise traverse all children w of v:

- If v is a max-node, then set $\alpha = \max\{\ \alpha,\ \text{alpha-beta}(w, \alpha, \beta)\ \}$;
  /* If α equals the maximal value of a Max-variable of a max-ancestor before evaluating v, then we make sure that this property also holds for the children w of v: If $\alpha <$ alpha-beta(w, α, β), then (v, w) is a better move for Alice. */
  If $\alpha \geq \beta$, then stop and return α.
  /* Bob can prevent Alice from reaching v . */
- If v is a min-node, then set $\beta = \min\{\ \beta,\ \text{alpha-beta}(w, \alpha, \beta)\ \}$;
  /* If β equals the minimal value of a Min-variable of a min-ancestor before evaluating v, then we make sure that this property also holds for the children w of v: If $\beta >$ alpha-beta(w, α, β), then (v, w) is a better move for Bob. */
  If $\alpha \geq \beta$, then stop and return β.
  /* Alice can prevent Bob from reaching v . */

(3) Return α, if v is a max-node and return β otherwise.

What is the result of Alpha-Beta(v, α, β)?

Lemma 5.5 *For the subtree with root v, let A be the largest payment reachable by Alice.*

(a) If v is max-node, then $\max\{\alpha, A\}$ *is returned, provided $A \leq \beta$.*

(b) If v is a min-node, then $\min\{\beta, A\}$ *is returned, provided $\alpha \leq A$.*

Exercise 73
Show Lemma 5.5.

How should we choose the parametres of the first call? Certainly we should start the evaluation of $\mathcal{B}$ at the root r. If we set $\alpha = -\infty$ and $\beta = \infty$, then Lemma 5.5 guarantees, that the maximally reachable payment to Alice is returned. The first call has therefore the form

$$\text{Alpha-Beta}(r, -\infty, \infty).$$

Exercise 74
(a) What is the final value of β, when Alpha-Beta $(r, -\infty, \infty)$ terminates?

(b) How can one determine an optimal first move of Alice?

The next problem shows that the alpha-beta algorithm visits only $\Theta(\sqrt{N})$ vertices in the best case, if N is the number of vertices of $\mathcal{B}$.

Exercise 75
Let $\mathcal{B}$ be a complete b-ary tree of depth d, whose leaves are labeled with arbitrary real-valued scores.

(a) Show: $\mathcal{B}$ has a path, called a principal variation, which corresponds to a game played optimally by both players.

(b) Show: there is an evaluation of $\lfloor$ by alpha-beta in which at most $\mathrm{opt} = b^{\lceil d/2 \rceil} + b^{\lfloor d/2 \rfloor} - 1$ nodes have to be traversed. Moreover any evaluation of $\mathcal{B}$ by alpha-beta pruning has to traverse at least opt nodes.

Hence, in the best case, alpha-beta reduces the search effort from $\Theta(b^d)$ to $\Theta(\sqrt{b^d})$. Hence, in comparison with the minimax evaluation the number of simulated moves can be doubled.

The experimental experience for instance for chess programs shows that the best case is indeed almost reached. To see why we consider the typical structure of a chess program, which consists of an *evaluation procedure*, which assigns a score to a configuration, and a *search procedure* which evaluates a move with as high a lookahead as possible. The search procedure is mostly based on variants of the alpha-beta algorithm, such that a heuristic powers the depth-first search component: depth-first search continues its search with the highest rated successor configuration. Thus, if the evaluation procedure is good, then it is not that surprising that the best case is reached.

However also alpha-beta search finds optimal moves only for trivial games. For instance one assumes that there are about 38^{84} different configurations in chess and even a reduction to 38^{42} is not going to help much. Therefore chess programs try to achieve as high a lookahead as possible to judge a move; the evaluation procedure is used to obtain a score for the obtained final configurations. The true power of alpha-beta search, in comparison with the minimax evaluation is the doubled lookahead.

There are many heuristic modifications on top of the alpha-beta pruning paradigm. We mention the two most important ones.

- **Aspiration search**: we start conventional alpha-beta pruning with the "search window" $[-\infty, \infty]$, i.e., we set $\alpha = -\infty$ and $\beta = +\infty$. If we have evidence that the minimax value lies in the search window $[\alpha, \beta]$ with $-\infty < \alpha \leq \beta < \infty$, then it is advisable to start with the smaller search window, since then the number of explored nodes might decrease considerably.

- **Iterative deepening**: assume that heuristic evaluations are available for all nodes of the game tree and assume that we have already explored all nodes up to depth

d. As a consequence we already know a principal variation PV_d for depth d. When trying to *deepen* our search *iteratively* to say depth $d+1$, then it is reasonable to conjecture that a principle variation PV_{d+1} for depth $d+1$ is "close" to PV_d and hence it makes sense to begin alpha-beta pruning with the nodes of PV_d. If our conjecture is correct, then correspondingly many nodes can be pruned.

We may also combine aspiration search with iterative deepening. If m_d is the minimax value for depth d, then m_{d+1} "should" not differ that much from m_d and a small search window around m_d "should" suffice.

Exercise 76
We consider a complete binary tree T of depth $2d$ whose leaves are labelled with 0 (corresponding to a lost game for Alice) or 1 (corresponding to a won game for Alice). We have to determine whether Alice has a winning strategy.

(a) Show that any deterministic algorithm has to inspect all 4^d leaves in the worst case.

(b) Now consider the following randomized algorithm. To evaluate an inner node v of T randomly select a child and evaluate the child recursively. If the evaluation of the child already determines v, then the evaluation of v terminates. Otherwise the remaining child is evaluated as well.

Show: if the algorithm is started at the root, then it inspects on the average at most $O(3^d)$ leaves.

Alpha-Beta Pruning, a Parallel Implementation

Certainly we could proceed as for Backtracking and Branch & Bound and, for instance, if the number of first moves of Alice exceeds the number of processes, partition the children of the root among the processes. But this strategy will blow up the **search overhead**, namely the increase in the number of traversed nodes in comparison with a sequential implementation. Observe that we have to battle search overhead with **communication overhead** and finding the right compromise is the main challenge in the design of parallel implementations of alpha-beta pruning.

In particular let us assume that the game tree $\mathcal{G}$ is the complete b-ary tree of depth d. Then we know that $\text{opt}_d = b^{\lceil d/2 \rceil} + b^{\lfloor d/2 \rfloor} - 1$ nodes of $\mathcal{G}$ are inspected in the best case. If a parallel alpha-beta pruning implementation with $p = b$ decides to evaluate all children of the root in parallel, then each process has to inspect $\text{opt}_{d-1} = b^{\lceil (d-1)/2 \rceil} + b^{\lfloor (d-1)/2 \rfloor} - 1$ nodes of its subtree. If d is even, then $\text{opt}_{d-1} = b^{\lceil d/2 \rceil} + b^{\lfloor d/2 \rfloor}/b - 1 \geq b^{\lceil d/2 \rceil} \geq \text{opt}_d/2$ and the best achievable speedup is two! Observe that in this particular case the search overhead is $p \cdot \text{opt}_{d-1} - \text{opt}_d \geq p \cdot \text{opt}_d/2 - \text{opt}_d = (p/2 - 1) \cdot \text{opt}_d$.

More or less all parallel implementations of alpha-beta pruning try to mimic a depth-first traversal to various degrees. In particular, the **young brothers wait concept (YBWC)** is emphasized: the leftmost child (i.e., the eldest brother) has to be evaluated before processes work on the remaining siblings (i.e., the younger brothers).[6] Even if

[6]Observe that this concept does *not* enforce a depth-first traversal, since the number of siblings is large. We may evaluate siblings in parallel and hence by a breadth-first search.

the leftmost child is not optimal, its minimax value may help to narrow the search windows for its siblings. For instance, assume that alpha-beta pruning has determined the minimax value m_w of the leftmost child w of the MAX node v. If we now explore the remaining children w' of v in parallel, then it suffices to find a move of B in w' with final minimax score at most m_w to prune the subtree of w'. Thus in a setting where good moves are explored first, it pays to throw all computing power at the subtree of the leftmost child and then to process siblings in parallel.

We describe two approaches based on YBWC. The first approach uses "synchronization nodes" whereas the second approach uses asynchronous parallelism.

- **Partial synchronization**: A leftmost child v is a **synchronization nodes**, whenever a parallel implementation enforces YBWC by exploring v before its siblings. In many implementations all nodes of the leftmost path p of $\mathcal{G}$ are synchronization nodes. Consequences are at least initially dramatic. For instance only one process is at work when the deepest node of p is evaluated and more processes enter only after higher nodes of p are reached. Thus a strict enforcement of YBWC keeps the search overhead low at the expense of unbalanced work loads.

  If the computation progresses there is sufficient work and load balancing becomes an important issue. Idle processes send work requests via random polling. If a process q receives such a request from process p, it checks its current depth-first path p_d and chooses a sibling s of a node of p_d. It sends s to p and enters a master-slave relationship with slave p. The slave p may become a master after receiving a work request. When finishing its task and when all of its slaves have terminated as well, the slave p becomes idle. In this case p either asks its master q for more work or it launches a work request and terminates the old master-slave relationship with q.

  The chess program Zugzwang of the university of Paderborn applies partial synchronization. It became vice champion in the 1992 Word Computer Chess Championships. However partial synchronization seems not adequate in workstation clusters where typically processors are powerful and links are slow.

- **Asynchronous parallel hierarchical iterative deepening (APHID)** uses fixed master-slave relationships [B98]. If the first d levels of the game tree $\mathcal{G}$ have to be explored, then the master first evaluates the top $d' < d$ levels. Whenever the master encounters a node of depth d' for the first time it assigns the evaluation task to a slave while trying to balance the work load.

  The master continuously repeats his evaluations of the top d' levels, accepting updates from the slaves, performing heuristic evaluations of *uncertain leaves*[7], informing slaves to terminate a task, performing load balancing by reallocating tasks from overworked to moderately busy processes, respectively informing a slave about the (changed)

[7] A leaf is uncertain, if the responsible slave did not yet report its final result. The slave however may report preliminary results which are then part of a new heuristic estimate of the corresponding leaf.

relevance of its leaves. The relevance of a leaf is determined for instance by YBWC and the search depth achieved so far for the leaf: the smaller the search depth the higher the priority, thus allowing the leaf to catch up.

Slaves use iterative deepening to work on their assigned tasks completely independent of other slaves and hence work asynchronously. They also work with aspiration search, centered around the hypothetical minimax value of the root. The master may update the hypothetical value after computing better heuristic estimates due to preliminary results obtained from the slaves.

It may seem that the master is a communication bottleneck. This can certainly be the case, but a fixed master-slave hierarchy alleviates this problem.

The approach of APHID seems to be more adequate for workstation clusters. However, since slaves are working asynchronously, APHID has a considerable search overhead which it tries to reduce by firstly controlling the top d' levels through a single process and secondly by assigning higher relevance for leftmost leaves. In [B98] at least competitive performance in comparison with partially synchronous alpha-beta search is claimed.

5.5 Conclusion

Monte Carlo methods are prime examples of embarrassingly parallel algorithms and are responsible for consuming a substantial percentage of supercomputer cycles. We have considered applications such as approximating multi-dimensional integrals and optimization by Markov chain Monte Carlo methods (i.e., the Metropolis and simulated annealing algorithm). Finally we have discussed pseudo-random generators to supply randomness deterministically.

Backtracking (for solving search problems) and alpha-beta pruning (for solving optimization problems) require the parallelization of sequential tree traversals. Important side issues were load balancing, a subject that we consider in the next chapter in more detail, and termination detection.

Chapter 6

Load Balancing

We have encountered load balancing problems when performing backtracking, branch & bound and alpha-beta pruning. But load balancing is a problem occurring frequently whenever processors have different amounts of work or have different speed. As an example we consider the embarrassingly parallel problem of computing an approximation of the Mandelbrot set.

Example 6.1 **Approximating the Mandelbrot Set**.
Let c be a complex number and consider the iteration

$$z_0(c) = 0, \quad z_{k+1}(c) = z_k^2(c) + c.$$

Then the Mandelbrot set $\mathcal{M}$ is defined as the set of all complex numbers c such that $z_k(c)$ remains bounded, i.e., $|z_k(c)| \leq M(c)$ for a suitable constant $M(c)$ and all k.

> **Exercise 77**
> Show that c belongs to $\mathcal{M}$ iff $|z_k(c)| < 2$ for all k.

To display the Mandelbrot set we use a regular grid of pixels and color a pixel $c \notin \mathcal{M}$ with a color which depends on the smallest k with $|z_k(c)| \geq 2$. There are faster methods, but for the purpose of this example we restrict ourselves to using the recurrence when determining membership in $\mathcal{M}$. Certainly we may bound the number of iterations (and possibly incorrectly claim that a pixel belongs to $\mathcal{M}$, if we did not reach 2 within the bound), however still different pixels present radically different work loads, if the bound is sufficiently large.

There are different load balancing techniques such as *static load balancing*, where pixels are assigned to processes ahead of time, or *dynamic load balancing*, where idle processes receive pixel groups during run time. A good static load balancing scheme is to randomly assign pixels to processes and this approach is in our application superior to dynamic load balancing, since the load will be partitioned into approximately equal-sized shares and no more communication is required.

However if we utilize that $\mathcal{M}$ and $\overline{\mathcal{M}}$ are connected and if we only want to display $\mathcal{M}$ without coloring its complement, then a dynamic load balancing scheme wins: we work with a master-slave architecture and begin with a single slave. Initially the slave receives a rectangle within the complex plane on which $\mathcal{M}$ is to be displayed. If the slave finds that all boundary pixels belong to $\mathcal{M}$, then it "claims" that the rectangle is a subset of $\mathcal{M}$. Otherwise the rectangle is returned to the master who partitions it into two rectangles and assigns one slave for each new rectangle. This procedure continues until all slaves are busy.

The static load balancing problem in the Mandelbrot example was easy, since the tasks –determining membership for pixels– are completely independent. However, in general, tasks depend on each other and we have to work with the task graph $\mathcal{T} = (T, E)$. The nodes of $\mathcal{T}$ correspond to the tasks and we have a directed edge (s, t) from task s to task t whenever task s has to complete before task t can be dealt with. We assume an ideal situation in which we know the duration w_t for each task t. Then we should try to partition T into p disjoints subsets $T_1, \ldots, T_p$ such that processes

- carry essentially the same load, i.e., $\sum_{t \in T_i} w_t \approx (\sum_{t \in T} w_t)/p$, and
- communicate as little as possible, i.e., the number of edges connecting two tasks in different classes of the partition is as small as possible.

For $p = 2$ we have already encountered this problem as the problem of graph partition (GP) in Section 5.1.1. GP is $\mathcal{NP}$-complete and hence we cannot expect to find efficient algorithms which determine perfect assignments. However there are heuristics such as simulated annealing or the Kernighan-Lin heuristic which often give decent approximative results.

But often, as in our discussion of search problems, we do not even know the tasks, let alone their duration, and we have to come up with solutions on the fly. We distinguish the following scenarios for load balancing.

- **static** or **semi-static load balancing**: the task graph and the duration of tasks is known beforehand or at well-defined time steps. In all algorithms of Chapter 4 the duration of tasks was known beforehand and we have applied static load balancing by using a rowwise decomposition or checkerboard decomposition.

  We have encountered a simple version of static load balancing when approximating the Mandelbrot set. Here we have utilized that the tasks are independent. Difficult instances are solved by applying heuristics for GP.

- **dynamic load balancing**: the available information on the task graph is insufficient and task assignments have to be determined during execution. There are two major approaches.

- In **centralized load balancing** there is a centralized priority queue of tasks, which is administered by one or more masters assigning tasks to slaves (cp. the chess program APHID in Section 5.4). This approach normally assumes a small number of processes. Rules of thumb: use larger tasks at the beginning to avoid excessive overhead and smaller tasks near the end to even out the finish times; take different processor speeds into account.
- In **distributed dynamic load balancing** one distinguishes methods based on work stealing or task pulling (i.e., idle processes request work) and work sharing or task pushing (i.e., overworked processes assign work).

We concentrate on distributed dynamic load balancing, the most important scheduling problem in parallel computation, and describe work stealing as well as work sharing in some detail.

6.1 Work Stealing

We discuss the following three methods.

- **Random Polling**: If a process runs out of work, it requests work from a randomly chosen process.
- **Global Round Robin**: Whenever a process requests work, it accesses a *global* target variable and requests work from the specified process.
- **Asynchronous Round Robin**: Whenever a process requests work, it accesses its *local* target variable, requests work from the specified process and then increments its target variable by one modulo p, where p is the number of processes.

To compare the three methods we make the following simplifying assumptions. We assume that the total work W is initially assigned to process 1. Whenever process i requests work from process j, then process j donates half of its current load and keeps the remaining half. Finally we assume that p processes participate.

Our goal is to determine the number of rounds, when trying to achieve a perfect parallelization, i.e., work $O(W/p)$ for all processes.

Random Polling. We define $V(p)$ to be the expected number of work requests such that each process has *received* at least one work request after $V(p)$ requests have been issued. Since the load of a process is reduced by at least the factor $1-\alpha$ after a request is served, after $V(p)$ requests the peak load is reduced by at least the factor $1-\alpha$. Hence the total number of requests is bounded by $O(V(p) \cdot \log_2 p)$ and $V(p) \cdot \log_2 p$ is the communication overhead.

How large is $V(p)$? To model random polling we assume that we start with a collection of p boxes which are initially empty. In one trial we randomly select a box and insert a ball. We would like to determine the expected number of balls until each box hat at least one ball. More generally let $f(i,p)$ be the expected number of required balls to fill all boxes assuming that we start with exactly i filled boxes. Then our goal is to determine $f(0,p)$ and we first claim

$$f(i,p) = \frac{i}{p} \cdot (1 + f(i,p)) + \frac{p-i}{p} \cdot (1 + f(i+1,p)).$$

This relation is indeed true, since with probability i/p we fill an already filled box, whereas with probability $1 - i/p = (p-1)/p$ we fill an empty box. Thus we get

$$\frac{p-i}{p} \cdot f(i,p) = 1 + \frac{p-i}{p} \cdot f(i+1,p) \text{ and hence } f(i,p) = \frac{p}{p-i} + f(i+1,p).$$

In particular we have $f(0,p) = \frac{p}{p-1} + \cdots + \frac{p}{p-i} + f(i+1,p)$ and hence

$$f(0,p) = p \cdot \sum_{i=0}^{p-1} \frac{1}{p-i} = p \cdot \sum_{i=1}^{p} \frac{1}{i} = \Theta(p \cdot \ln(p))$$

follows. When does random polling achieve constant efficiency?

Exercise 78
Assume that the expected communication time of some load balancing scheme is $C_p(W)$. Then show that the expected running time is bounded by $O(\frac{W}{p} + C_p(W))$.

Random polling reduces the peak load to below $O(W/p)$ after at most $O(V(p)/p \cdot \log_2 p) = O(\log_2^2 p)$ rounds[1]. We obtain constant efficiency, if the computing time $O(W/p)$ dominates and this is the case for

$$W = \Omega(p \cdot \log_2^2(p)).$$

Global Round Robin. To obtain a computing time of at most $O(W/p)$, the global target variable has to be accessed at least $\Omega(p)$ times. But then, to obtain constant efficiency, we have to demand that $\frac{W}{p} = \Omega(p)$ and equivalently that $W = \Omega(p^2)$ holds.

Asynchronous Round Robin. In the best case only $\log_2 p$ rounds suffice and the requirement $\frac{W}{p} = \Omega(\log_2 p)$ or $W = \Omega(p \cdot \log_2 p)$ guarantees constant efficiency.

Exercise 79
Show that $\Theta(p)$ rounds may be required in the worst case until $\Omega(p)$ processes have work. Thus constant efficiency only holds for $W = \Omega(p^2)$.

[1]Our analysis can be improved to show that a peak load of $O(W/p)$ can be reached after an expected number $O(\log_2 p)$ of rounds

The performance of asynchronous Round Robin is in general better than global Round Robin, since it avoids the bottleneck of a global target variable. However, to avoid its worst case, randomization and therefore random polling is preferable. We now show that random polling gives a provably good speedup for backtracking. In particular we describe which tasks a donating process should hand over to the requesting process.

The Speedup of Random Polling for Backtracking

We analyze random polling for backtracking under the following assumptions. An instance of backtracking generates a tree T of height h with N nodes and degree d. We assume that the entire tree is to be searched with p processes.

- In the beginning only process 1 is active and it inserts the root of T into its initially empty stack.
- If at any time an active process takes the topmost node v off its stack, then it *expands* v and pushes all children of v onto the stack. Thus the stack of a process is composed of generations with the current generation on top of the stack and the oldest generation at the bottom.
- An idle process p uses random polling to request work from a randomly chosen process q: if q itself is idle, then the request fails, otherwise q serves an arbitrarily chosen request and **sends one half of its oldest generation**.

The following observation shows that this work transfer pays off, since nodes are only moved rarely.

Remark 6.1 Whenever a node v is donated, then it migrates together with one half of its current siblings. Hence the generation of v is halved in each donation step involving v. Since v is immediately expanded if it is the only received node, v participates in at most $\lceil \log_2 d \rceil$ donation steps, where d is the degree of T.

> **Exercise 80**
> Show that any parallel algorithm that traverses T by a depth-first traversal has to spend at least $\max\{N/p, h\}$ steps, where N is the number of nodes of T and h the height of T.

We show that our implementation of random polling almost, namely up to the factor $\log_2 d$, reaches the lower time bound. Since nodes are moved only rarely, we only have to show that most of the time sufficiently many processes are busy or, equivalently, that work requests are answered with sufficient high probability.

Theorem 6.1 *With probability at least* $1 - N \cdot d^{-\Omega(h+N/p)}$*, random polling runs for at most*

$$O(\log_2 d \cdot \max\{N/p, h\})$$

steps and hence its speedup is at least $\Omega(\frac{p}{\log_2 d})$*, whenever* $h \leq N/p$.

Proof. If less than $p/2$ processes are idle in some given step, then we say that the step succeeds and otherwise that it fails. If a process is busy, then it participates in expanding a node or fulfilling a work request. However there are at most $O(\log_2 d \cdot N)$ such operations and hence there are at most $O(\log_2 d \cdot N/p)$ successful steps. Thus it suffices to show that there are at most $O(\log_2 d \cdot h)$ failing steps.

We fix an arbitrary node v of T. In any step there is a unique process which stores v or the lowest, already expanded ancestor of v in its stack. We say that v *receives a request*, if "its" process receives a request for work. After at most $\lceil \log_2 d \rceil \cdot h$ requests for work, v belongs to the oldest generation of its process and v, from this point on, continues to belong to the oldest generation until it is expanded. Hence v is expanded after at most $\lceil \log_2 d \rceil$ further requests. After how many failing steps does v receive $\lceil \log_2 d \rceil \cdot (h+1)$ requests?

We determine the probability q that v receives a request in a failing step. In a failing step there are exactly k idle processes with $k \geq p/2$. The probability that none of them requests node v is therefore

$$(1 - \frac{1}{p})^k \leq (1 - \frac{1}{p})^{p/2} \leq e^{-1/2},$$

if we apply Lemma 1.2. But $q \geq 1 - e^{-1/2} \geq 1/3$. Therefore random polling performs in each failing step a random trial with success probability at least $1/3$ and the expected number of successes in t trials is at least $t/3$. We apply the Chernoff bound of Theorem 1.8 and obtain

$$\text{prob}[\ \sum_{i=1}^{t} X_i < (1-\beta) \cdot t/3\ ] \leq e^{-(t/3)\cdot\beta^2/2}.$$

In particular, for $\beta = 1/2$, random polling has less than half the number of expected successes, namely less than $t/6$ successes in t trials with probability at most $e^{-t/24}$. Set $t = 6\lceil \log_2 d \rceil \cdot (h + 1 + N/p)$ and there are less than $\lceil \log_2 d \rceil \cdot (h+1)$ requests for v with probability at most $e^{-\Omega(\log_2 d \cdot (h+1+N/p))} = d^{-\Omega(h+N/p)}$. We arrive at the claimed failure probability, since we have considered only a fixed node v, but have to consider all N nodes. □

Remark 6.2 In [BL94] random polling is shown to work almost optimally for a larger class of computing problems.

6.2 Work Sharing

We compare work stealing and work sharing assuming that work assignments are determined by random strategies in both cases, i.e., that random polling is employed for work stealing and that in work sharing a busy process assigns work to a randomly chosen process.

- The more processes are busy the higher the probability that a busy process receives more work in work sharing. Even if a busy process may deny the work assignment its load increases due to the communication task. In work stealing however a busy process profits, since it gets rid of part of its work with high probability.
- The less processes are busy the higher the probability that a busy process assigns work to an idle process. With only few processes busy work sharing is more efficient in reducing peak loads.

Since normally only a minority of processes is idle, work stealing is preferable. However if urgent work is to be done and no volunteers are available, then work sharing is required. "Extreme work sharing", i.e., assigning any subsequent task to other processors increases the communication overhead, but evens out the work load as the following example shows.

Remark 6.3 [CRY94] consider tree-structured computations. A tree-structured computation begins with a root task. In general, the time to expand a node requires an unknown amount of time. If a node is expanded, a possibly empty set of children is generated. Load balancing is achieved by work sharing in the following way:

> any process has its own pool of tasks. Whenever a process needs more work it picks a task from its pool. Any children of the currently expanded task are assigned to pools of randomly chosen processes.

Thus [CRY94] follow a "work rejection" strategy in which a process only performs the task of expanding a node, but assigns any subsequent task, i.e., children tasks to other processes. This strategy increases the communication overhead, but it guarantees with high probability that processes receive a uniform load even in the presence of tasks of different duration.

In particular, [CRY94] show that with high probability the run time with p processors is proportional to $\frac{W}{p} + h \cdot T$, where W is the total work (i.e., the time of a sequential algorithm for the tree-structured computation), h is the depth of the tree and $T = \max_v D(v) / \min_v D(v)$ is the ratio of longest and shortest duration of a node. Observe that this bound is better than the bound of Theorem 6.1 for random polling!

We begin by studying the following model scenario. We observe p clients, where the ith client assigns its task at time i to one of p servers. We assume that all tasks require the same run time, but to complicate matters we assume that the clients do not know of each others actions. We are looking for an assignment strategy that keeps the maximum load of a server as low as possible.

A first attempt, in analogy to random polling, is to randomly choose a server for each task. What is the probability q_k that *some* server receives k tasks? If k is not too large, then

$$\binom{p}{k} \cdot (\frac{1}{p})^k \cdot (1 - \frac{1}{p})^{p-k} \approx \binom{p}{k} \cdot (\frac{1}{p})^k \approx (\frac{p}{k} \cdot \frac{1}{p})^{\Theta(k)} = (\frac{1}{k})^{\Theta(k)}$$

is the probability that a *fixed* server receives exactly k tasks. Thus $q_k \leq p \cdot k^{-\Theta(k)}$ and our analysis shows that q_k is small whenever $k = \alpha \cdot \frac{\log_2 p}{\log_2 \log_2 p}$ for a sufficiently large constant α. The surprising fact is that our estimate is asymptotically tight and the server with the heaviest burden will have $\Theta(\frac{\log_2 p}{\log_2 \log_2 p})$ tasks with high probability and our load balancing attempt was not very successful.

Let d be a natural number. Surprisingly we can drastically reduce the maximum load with the following *uniform allocation scheme*:

> Whenever a task is to be assigned, then choose d servers at random, enquire their respective load and assign the task to the server with smallest load. If several servers have the same minimal load, then choose a server at random.

Theorem 6.2 *There is $\alpha > 0$ such that, with probability at least $1 - p^{-\alpha}$, the maximum load of the uniform allocation scheme is bounded by*

$$\frac{\log_2 \log_2(p)}{\log_2(d)} \pm \Theta(1).$$

As a consequence, whenever we ask two servers at random ($d = 2$), then we reduce the maximum load from $\Theta(\frac{\log_2(p)}{\log_2 \log_2(p)})$ to now $\Theta(\log_2 \log_2(p))$. This case is also called the **two-choice paradigm**.

Remark 6.4 [ACMR98] investigate when many clients submit their tasks simultaneously. Assume that each client selects two servers at random and that a server replies with the number of requests it has served so far. A client then chooses a server with the least number of requests. It is shown that the maximum load is bounded by $O(\sqrt{\frac{\log_2 p}{\log_2 \log_2 p}})$ with high probability. Thus the two choice paradigm still reduces the maximum load substantially, however not as strongly as in the sequential setup.

What is "behind" Theorem 6.2 for $d = 2$? We define β_i as the number of servers with at least i tasks. Then it turns out that the β_i decrease quadratically, that is, $\beta_{i+1}^2 \approx \beta_i$ holds and hence $\beta_{\log_2 \log_2(n)} \approx 1$ follows. The two-choice paradigm is successful, since there are only very few servers with high load and the choice of two servers with high load is therefore correspondingly small.

Can we further decrease the load with other allocation schemes? In *non-uniform* allocation we partition the servers into d groups of same size and assign tasks according to the "always-go-left" principle:

> Choose one server at random from each group and assign a task to the server with minimal load. If several servers have the same minimal load, then choose the leftmost one.

To analyze non-uniform allocation we introduce the sequence $F_d(k)$ recursively. We set $F_d(k) = 0$ for $k \leq 0$, $F_d(1) = 1, F_d(k) = \sum_{i=1}^{d} F_d(k-i)$ for $k > 0$ and set

$$\phi_d = \lim_{k \to \infty} (F_d(k))^{\frac{1}{k}}.$$

Exercise 81
(a) Show $\phi_1 = 1$, $\phi_2 \approx 1,61, \phi_3 \approx 1,83$ and $\phi_4 \approx 1,92$.

(b) Show that $2^{(d-1)/d} < \phi_d < 2$ holds.

Theorem 6.3 *If we assign p tasks to p servers according to non-uniform allocation, then, with probability at least $1 - p^{-\alpha}$, the maximum load is bounded by*

$$\frac{\log_2 \log_2(p)}{d \cdot \log_2(\phi_d)} \pm \Theta(1).$$

α is a positive constant.

Non-uniform allocation seems nonsensical, since servers in left groups are handicapped, but we obtain nonetheless a significant load reduction even for $d = 2$. What is the reason? If we randomly choose a server from among several servers of same minimal load and omit the always-go-left rule, then the load increases to the load of Theorem 6.2. If we select d servers at random, and hence omit the group structure, than random tie breaking turns out to be optimal and again the load increases to the load of Theorem 6.2. Thus the combination of the group concept with the always-go-left rule does the trick.

Image the assignment of tasks over time. At any moment in time one has to expect that servers in left groups have to carry a larger load than servers in right groups. But then, in subsequent attempts, servers in right groups will win the new tasks and their load follows the load of servers in right groups. The combination of the group approach with always-go-left enforces therefore on one hand a larger load of left servers with the consequence that right servers have to follow suit. The preferential treatment of right groups enforces a more uniform load distribution.

Proof of Theorem 6.2 Assume that a server carries a too high load. In the first part of our analysis we try to figure out the reason for this high load and introduce a witness tree. In particular, the probability that some server is overloaded will coincide with the probability that a witness tree of high depth exists. We then show in the second part of our analysis how to bound the probability that a witness tree of high depth exists.

Part I: the Witness Tree. A witness tree W of depth L has to show why a server carries at least $L + 4$ tasks. Suppose that server s has at least $L + 4$ tasks. We then construct a witness tree W recursively as follows. The root of W represents the last task t assigned to x. Any of the d servers $s_1, \ldots, s_d$, chosen as potential servers for t has already

received at least $L+3$ tasks, since server $s \in \{s_1, \ldots, s_d\}$ carries $L+4$ tasks including task t. We generate d children of the root and let the ith child represent the last task assigned to s_i. We continue this construction recursively until all nodes correspond to leaves. Since we only expand down to depth L each leaf has at least has at least four tasks.

The witness tree W is completely defined once we label each node with the task it represents. We have obtained the complete d-ary tree of depth L, whose nodes are labeled with tasks. We say that the above task assignment *activates* W.

Part II: the Probability of Activating a Witness Tree. We first determine the number of different witness trees and then bound the probability that a particular tree of large depth has been activated. Let v be an arbitrary node of the complete d-ary tree of depth L. We have to assign p tasks and hence there are most p choices for the task represented by v. Thus there are at most p^m different witness trees, where $m = \sum_{i=0}^{L} d^i$ is the number of nodes.

Let W be a fixed witness tree. We have to bound the probability that W is activated. If u is a child of v, then the server receiving the task of u also competes for the task of v. But a fixed server competes for a particular task with probability $\binom{p-1}{d-1}/\binom{p}{d} = \frac{d}{p}$. The "edge experiments" are independent and hence

$$\left(\frac{d}{p}\right)^{m-1}$$

is the probability that all $m-1$ edges are "activated".

When is leaf b activated? Each of the d servers competing for the task represented by b has to have at least three tasks. But at any time there are at most $p/3$ servers with at least three tasks and hence b is activated with probability at most 3^{-d}. The probability of leaf activation does not increase, if other leaves have already been activated, and hence the probability that all leaves are activated is bounded by

$$3^{-d \cdot d^L}$$

from above. But then the probability that some witness tree of depth L is activated is at most

$$\begin{aligned} p^m \cdot \left(\frac{d}{p}\right)^{m-1} \cdot 3^{-d \cdot d^L} &\leq p \cdot d^{2 \cdot d^L} \cdot 3^{-d \cdot d^L} \\ &\leq p \cdot 2^{-d^L}. \end{aligned}$$

In the first inequality we bound the number $m-1$ of edges by twice the number d^L of leaves. The second inequality follows, since $2 \cdot d^2 \leq 3^d$ holds. For

$$L \geq \log_d \log_2 p + \log_d(1+\alpha) = \frac{\log_2 \log_2 p}{\log_2 d} + \log_d(1+\alpha)$$

we get

$$d^L \geq (1+\alpha) \cdot \log_2 p \quad \text{und} \quad 2^{-d^L} \leq p^{-(1+\alpha)}.$$

But then the probability that some witness tree of depth L has been activated is at most $p^{-\alpha}$ and hence the probability that some server receives at least

$$L + 4 \geq \frac{\log_2 \log_2 p}{\log_2 d} \pm \Theta(1)$$

tasks is at most $p^{-\alpha}$. □

6.3 Conclusion

Load balancing, the task to evenly distribute work among all processes, is a fundamental problem. In static load balancing the task assignment is determined before the computation starts. Even if the duration of tasks is known beforehand, dependencies among tasks make the load balancing non-trivial and in general the load balancing problem is computationally as hard as the $\mathcal{NP}$-complete problem of graph partition.

For dynamic load balancing, tasks are assigned during run time. Random polling, i.e., requesting work from a randomly chosen process is the most successful work stealing method. Dynamic load balancing via work sharing proceeds by pushing tasks, i.e., processes with many tasks send some of their tasks to other processes. In uniform allocation a task is pushed to a process of minimum load chosen from a random sample of d processes, ties are broken arbitrarily. The two-choice paradigm, i.e., setting $d = 2$, leads to a significant reduction of the maximum load and in particular the maximum load is reduced exponentially when distributing p tasks among p processes. A further reduction can be achieved when ties are broken non-uniformly.

Work stealing is appropriate, if relatively few processes are idle, whereas work sharing has the edge, if relatively few processes are busy.

Chapter 7

Termination Detection

The Termination Detection Problem For Active And Inactive Processes

We assume the following model: a process is either active or inactive. Whereas an active process may turn inactive, an inactive process cannot send messages and stays inactive unless it receives a message. How can we determine whether all tasks have been completed?

Observe that our load balancing schemes force idle processes to ask for work and hence these schemes do not meet the above requirements. However, if we do not consider a request for work to be a message, then the specifications of the model are met, provided an inactive process requesting work turns only active when receiving a message.

We begin with the additional assumption that messages are *delivered in-order*: if a process p first sends a message M_1 directly to another process q and later sends a message M_2 to another process which triggers a sequence of messages ending in q, then M_1 arrives at q before the last message of the triggered sequence arrives at q. Later we describe a solution without any assumptions. Other than that we assume an asynchronous system without any restrictions. In particular, if an active process does not have a task to work on, it may or may not request a task from a colleague. A busy process on the other hand may ask a colleague to accept a subtask and suddenly new tasks may pop up.

It is not sufficient if, say, process 1 asks each process whether it is inactive, since right after a positive answer the queried process might receive a message containing a new task. In Dijkstra's solution a token is passed around the ring of processes starting with process 1 and traveling from process i to process $i+1$ and from process p back to process 1. The token only leaves a process if the process turns inactive and our goal is therefore to return the token to process 1 who then should determine whether all processes are inactive. However an inactive process, and hence an already visited process, may turn active whenever it receives a message. Our algorithm has to detect the (possible) reactivation, but how?

The observation that the reactivation must have been, at least indirectly, initiated by an active and hence unvisited process is crucial: Dijkstra's algorithm equips all processes

with a color which is initially set to white. Any process i which sends a message to process j with $j < i$ is a suspect for reactivating a process and it turns black. If a black process receives a token, it colors the token black and hence process 1 is not forced into the wrong conclusion that all of his colleagues terminated.

Algorithm 7.1 **Dijkstra's Token Termination Detection Algorithm I**

(1) When process 1 turns inactive, it initiates an attempt to detect termination. Process 1 turns white and sends a white token to process 2.

/* The next step is the only step that colors a process black. */

(2) If process i sends a message to process j and $i > j$, then i turns black.

/* We demand in step (3) that a black process colors the token black and a white process does not change the color of the token. Now assume that process k is a rightmost process which changes its state from inactive to active after the token left and assume that the token is white when it left k.

Why does process k change its state? k passes on a white token and hence all processes to the left of k did not send messages to their left *before* passing on the token. Since messages and token are delivered in order, process k can only change its state due to a sequence of messages originating in a process l to its right. When process l sends its (possibly indirect) wake-up call, then l has not yet forwarded the token: remember that k is the rightmost process changing its state. But then l is black before it passes the token and hence it passes on a black token. Consequently process 1 does not incorrectly decide upon termination. */

(3) Assume that process $i > 1$ has just received the token. It keeps the token as long as it is active. If it turns inactive, it colors the token:

> If i is black, then the token turns black. Otherwise, if i is white, the color of the token is unchanged.

Process i passes the token along to process $i + 1$, respectively to process 1, if $i = p$. Afterwards it turns white.

/* The process turns white to get ready for the next round. */

Theorem 7.2 *Assume that messages are delivered in order. If process 1 receives a white token from process p, then all processes are inactive.*

Exercise 82
Verify Theorem 7.2.

Assume that all processes are inactive before the token is inserted into the ring and no messages are pending. Then it may still be the case that a process is colored black, but all processes are colored white after one round and only an additional round determines termination.

Observe that the token might be on its way for an unpredictable length of time, however the token itself consumes at most time $O(p)$ due to the "handshakes" (send/receive operations) between adjacent processes on the ring. Moreover, process 1 does not have to wait for the token to return, but may turn active again when receiving a message. Thus the token is nothing else but an inexpensive background process which guarantees that termination is quickly recognized.

Now assume that process 1 recognizes that all processes are inactive. Does it suffice to broadcast a shutdown message and execute MPI_Finalize? It does suffice provided all messages sent to process 1 have been delivered. If, say, process i has sent a message to process 1, then i turns black and will color the token black. When the token arrives at process 1 the message sent by process i must have arrived as well, *provided messages are delivered in order*. With the same reasoning any process i may execute MPI_Finalize after receiving the shutdown broadcast from process 1, *provided messages are delivered in order*.

MPI guarantees that messages are *non-overtaking*: if a process sends two messages to another process, namely first message M_1 and subsequently message M_2, then M_1 will be received before M_2 is received. However observe that MPI does not guarantee that messages are delivered in-order. Thus Algorithm 7.1 is inadequate, since undelivered messages may describe new tasks. In our new approach we equip all processes additionally with a message count. Initially all processes are white and their message count is zero. Whenever a process receives a message it decrements its message count and increments its count if it sends a message. We utilize that the sum of message counts is zero iff all messages have been delivered and use the token to sum message counts. But we do not have access to all message counts simultaneously and we have to worry that an already processed message count might not be accurate.

Algorithm 7.3 Dijkstra's Token Termination Detection Algorithm II

(1) When process 1 becomes inactive and when the token has returned, the process initiates an attempt to detect termination. Process 1 turns white and sends a white token with message count zero to process 2.

/* Our goal is to enforce that all processes are inactive and no messages are pending provided the token is white and its message count is zero. */

(2) If a process i sends or receives a message, then i turns black.

/* If the token is white when finally reaching process 1, then the token has passed only white processes and neither process has sent or received a message between the last two successive visits of the token. Thus message counts did not change! It may

however happen that messages are still in flight, but then the token's message count will be non-zero. */

(3) Assume that process $i > 1$ has just received the token. If i is black, then the token turns black. Otherwise, if i is white, the color of the token is unchanged.

Process i keeps the token as long as it is active. If it turns inactive, process i adds its message count to the message field and passes the token along to process $i + 1$, respectively to process 1, if $i = p$. Afterwards process i turns white.

Theorem 7.4 *Assume that process 1 is white, when it receives a white token from process p and that the count field of the token plus the message count of process 1 is zero. Then all processes are inactive and there are no more messages in the system. Hence process 1 may send a shut down message to all processes.*

Exercise 83
Verify Theorem 7.4.

Exercise 84
Consider Algorithm 7.3.

(a) Does it suffice in step (2) that a process i is colored black only if it sends a message to a process j with $j < i$?

(b) Does it suffice in step (2) that a process i is colored black only if it sends a message?

Termination Detection In Dynamic Load Balancing

We **first** try a simple, but incorrect approach. If a process A finds a solution during Backtracking, then it broadcasts a shutdown message to all of its colleagues and executes MPI_Finalize. To halt computation as soon as possible, each process periodically checks with MPI_Iprobe whether it has received a shutdown message and if so, executes MPI_Finalize. If process B, before receiving the shutdown message from A, detects a solution by itself, then it broadcasts its own stop message. This message cannot be delivered to process A resulting in a run-time error.

Our **second** successful approach utilizes that we perform dynamic load balancing by requesting work. Process 1 is distinguished as the process which initially carries the entire load. We initially assign weight 1 to process 1 and weight 0 to the remaining processes. Whenever process i requests and receives work from process j, it also receives the weight $w_j/2$ from process j, where w_j is the current weight of process j. Thus, after this transfer, we set $w_i = w_j/2$ and $w_j = w_j/2$. Finally, whenever a process finishes its (current) task *and* the entire weight it handed out during execution of the task has been returned, it hands its weight back to the donating process. The donor then adds the received weight to its current weight. If process 1 has received weight 1 again, it knows that all tasks have completed. To terminate the computation, process 1 sends a "a shutdown token" into the

process ring and determines the difference between sent and received requests. The token is recycled for so long until difference zero is determined: at this time all processes are inactive and all messages are delivered.

Observe that only powers 2^{-k} change hands and if k is too large, then the weight may be identified as zero. There is however no problem, if the power k is exchanged instead of 2^{-k}.

Our **third** approach uses Dijkstra's algorithm. We say that a process is active if it has a task to work on and inactive otherwise. Only assignments of work are considered to be messages; in particular requests for work are not considered messages. We now may use Algorithm 7.3, since an inactive process stays inactive unless receiving a message. When process 1 receives an OK to terminate it knows that all processes are inactive and hence all work has been completed. Now the shutdown token prepares the actual shutdown.

Exercise 85
Here are two more procedures to detect termination. Are they correct?

(a) Process 1 inserts a token into the process ring. A process keeps the token as long as it has work to do and passes it along otherwise. Process 1 prepares the shutdown whenever receiving the token from process p.

(b) Process 1 inserts a white token into the process ring. A process colors the token black if it has work to do and passes it along. An idle process passes the token along without changing its color. Process 1 prepares the shutdown whenever receiving a white token from process p.

Exercise 86
(a) The weight procedure for termination detection in dynamic load balancing has to be modified to allow early termination when a process finds a solution. How should that be done?

(b) Does the adaption of Dijkstra's algorithm has to be modified?

Chapter 8

Divide & Conquer and Dynamic Programming

In an application of divide & conquer to solve a problem P, we have to solve a hierarchy of subproblems. This hierarchy corresponds to a tree T_P of subproblems: the root represents P and a node u is a child of v iff the subproblem of u is used when solving the subproblem of v. Finally leaves are directly solvable subproblems.

Observe that the subproblems represented by children of a node v can be solved independently. Therefore we obtain a parallelization of a sequential divide & conquer algorithm whenever the task of solving the subproblem of a node v, given solutions for the subproblems of its children, can be parallelized. We have already seen a first example when parallelizing the fast Fourier transform. Mergesort and quicksort turn out to be two further examples.

8.1 Sorting

We assume throughout that n keys are equally distributed among p processes. We could have required that all keys initially belong to one process who is then supposed to distribute the keys among its colleagues. However this convention does not allow to show the difference in speed between different sorting procedures, since the distribution task is inherently sequential and requires linear time $\Omega(n)$. With the same argumentation we do not require to output the sorted sequence to a distinguished process, but instead that the keys within each process are sorted and that all keys of process i are not larger than any key for process $i+1$.

We have already discussed odd-even transposition sort (OETS) which sorts n keys with p processes in time $O(\frac{n}{p} \cdot \log \frac{n}{p} + n)$. The performance is not convincing, since the compute/communicate ratio is very poor in each phase and communication dominates each merging effort. Moreover, OETS is efficient only if we have few, i.e., $p = O(\log_2 n)$

processors. Parallelizations of quicksort turn out to be superior.

8.1.1 Parallelizing Quicksort

The sequential quicksort determines a splitter (or pivot) x_i, rearranges the input sequence into a subsequence of keys x_j with $x_j \leq x_i$ and into a subsequence of keys x_j with $x_j > x_i$ and then applies quicksort recursively to both subsequences. Thus we have to pay particular attention to the rearrangement step, since the two recursive calls can be parallelized.

Algorithm 8.1 **A parallel quicksort.**
/* We sort the sequence x of n pairwise distinct keys with p processes. Processor i receives the ith interval of X of length $\frac{n}{p}$. */

if $n = 1$ then stop; else

(1) Each process determines a local (approximate) median. Processor 1 executes a Gather operation, determines a global approximate median M and broadcasts M to its colleagues.
/* Time $O(\frac{n}{p})$ and communication $O(p + \log_2 p) = O(p)$ suffice. */

(2) for $i = 1$ to p pardo: process i partitions its sequence according to M;
/* Time $O(\frac{n}{p})$ without any communication is sufficient. */

(3) Apply MPI_Scan to determine the two prefix sums $\sum_{j=1}^{i} \text{smaller}_j$ and $\sum_{j=1}^{i} \text{larger}_j$, where smaller_j (resp. larger_j) is the number of keys of process j which are smaller (resp. larger) than M.
/* The communication cost is bounded by $O(\log_2 p)$. */

(4) The number k of keys smaller than M is broadcasted. The "first" $\frac{p \cdot k}{n-1}$ processes will be responsible to recursively sort the smaller keys, the remaining processes are responsible to recursively sort the larger keys.
Determine the new key positions and send the keys to their new process;
/* The local computation time is $O(\frac{n}{p})$. The communication is bounded by $O(\frac{n}{p})$, since each process has to send up to $\frac{n}{p}$ keys. */

(5) Apply the sequential quicksort whenever only one process is assigned. Otherwise recursively sort the first $k - 1$ keys and the last $n - k$ keys in parallel.

If we determine exact local medians in step (1), then the approximate median M is larger than one half of all local medians. Therefore, by definition of a local median, M is larger than one fourth of all keys and, with the same argument, smaller than one fourth of all keys. Since we stop the recursion when only one process is responsible, Algorithm 8.1 requires at most $\log_{4/3} p$ iterations. Finally observe that the time for computation as well as communication is bounded by $O(\frac{n}{p} + p)$.

We maintain throughout with the help of step (4) that a process is responsible for roughly $\frac{n}{p}$ keys, since keys are evenly distributed among available processes. All in all we have a computing time of

$$O((\frac{n}{p}+p)\cdot\log_{4/3}p+\frac{n}{p}\cdot\log_2\frac{n}{p})=O(\frac{n}{p}\cdot\log_2 n+p\cdot\log_2 p),$$

since $O(\frac{n}{p}\cdot\log_2\frac{n}{p})$ is the time to sort sequentially when recursion is stopped in step (6).

The contribution of $p\log_2 p$ is used when processes send their local medians to process 1 in step (1). If we only perform random splitter selection, then the communication cost of p per round can be replaced by the communication cost of $\log_2 p$ per round (for broadcasting splitter M and for performing MPI_Scan in step (3)).

Theorem 8.2 *Parallel quicksort sorts n keys in time $O(\frac{n\cdot\log_2 n}{p}+p\cdot\log_2 p)$. The randomized version sorts n keys in expected time $O(\frac{n\cdot\log_2 n}{p}+\log_2^2 p)$.*

Hence the deterministic quicksort achieves constant efficiency whenever $p\leq\sqrt{n}$, whereas the randomized quicksort is already optimal whenever $p\leq n/\log_2 n$. However we should not be satisfied, since the compute/communicate ratio per iteration is constant and hence too large.

Remark 8.1 **Hyperquicksort**
Here we do not attack the real problem of extensive communication, but discuss some potential computational improvements. In particular, we study the effect of the following modifications:

- Now we require that all processes initially sort their $\frac{n}{p}$ keys. This action has two consequences. The first positive consequence is that determining the local splitter has become trivial. Moreover, and this is the second positive consequence, *if* we require that all processes finish an iteration by sorting their keys again, then there is no need for the sequential sort in step (5) of the parallel quicksort. Certainly the main question is the computational cost of sorting in each iteration.

- Steps (3) and (4) implement the rearranging step and simultaneously perform some load balancing. Instead we completely give up on load balancing. Imagine that p is a power of two and that the p processes form a hypercube. Then it is natural to demand that all processes $0w$ (resp. $1w$) are responsible to work on all elements smaller (resp. larger) than the first splitter M. Hence if process $0w$ receives the splitter M, it sends its keys larger than M to process $1w$ and receives keys smaller than M in return. Thus rearrangement is performed by a single communication step on the hypercube, explaining the name hyperquicksort. As an additional profit each process can apply a single merging step to sort the sorted subsequence of its remaining keys and the received sorted subsequence in linear time.

In effect a process in hyperquicksort trades the time to compute a local median and to rearrange its keys against sorting its keys all the time, but gives up on any serious load balancing. Thus hyperquicksort is easier to implement than the parallel quicksort of Algorithm 8.1. However, the missing load balancing significantly degrades its performance and it does not attack the real problem of extensive communication.

Hyperquicksort has been used for the Intel iPSC and the nCUBE/ten which organize processors in a hypercube architecture.

8.1.2 Sample Sort

Our goal is to compress the $O(\log_2 p)$ iterations of quicksort into essentially one phase. This is accomplished by selecting a sample of $p-1$ splitters.

Algorithm 8.3 **Sample sort.**
/* We sort the sequence x of n pairwise distinct keys with p processes. Processor i receives the ith interval of X of length $\frac{n}{p}$. */

(1) each process sorts its $\frac{n}{p}$ keys sequentially and determines a sample of size s that it sends to process 1, who then executes a Gather operation.

/* Time $O(\frac{n}{p}\log_2 \frac{n}{p})$ and communication $O(p \cdot s)$ suffice. */

(2) Processor 1 sorts the received $(p-1)\cdot s$ keys and computes the final sample S of size $p-1$ with the help of its keys. Finally it broadcasts S.

/* $O(ps \log_2 ps)$ computing steps and $O(p \log_2 p)$ communication steps suffice. */

(3) each process partitions its keys according to the sample S. Then an all-to-all personalized broadcast is applied in which a process earmarks each of its $p-1$ sorted subsequences for a particular colleague.

/* Time $O(p \cdot \log_2 \frac{n}{p})$ suffices. The communication cost is bounded by $O(\frac{n}{p})$ in the best case: if the length of subsequences is not asymptotically related, then the all-to-all broadcast may take longer. */

(4) Each process merges the p sorted sequences and is done.

/* Time $O(\frac{n}{p} \cdot \log_2 p)$ is enough. Why? */

The computing time is at most $O(\frac{n}{p} \cdot \log_2 \frac{n}{p} + p \cdot \log_2 \frac{n}{p} + \frac{n}{p} \cdot \log_2 p) = O(\frac{n}{p} \log_2 n + p \cdot \log_2 \frac{n}{p})$ steps. (Here we assume that $p \cdot s \leq n/p$ and equivalently that $s \leq n/p^2$ holds.) The time for communication is bounded by $O(p \cdot s + p \cdot \log_2 p + \frac{n}{p}) = O(p \cdot \log_2 p + \frac{n}{p})$, again since $p \cdot s \leq n/p$.

Theorem 8.4 *Sample sort runs in time* $O(\frac{n}{p} \cdot \log_2 n + p \cdot \log_2 \frac{n}{p})$ *and with communication cost at most* $O(p \cdot \log_2 p + \frac{n}{p})$*, when sorting* n *keys with* p *processors. If* $p \leq \sqrt{\frac{n}{\log_2 n}}$*, then computing time is bounded by* $O(\frac{n}{p} \cdot \log_2 n)$ *and communication time is bounded by* $O(\frac{n}{p})$*.*

Exercise 87
We consider the following procedure to determine a set of $p-1$ good splitters. After sorting its $\frac{n}{p}$ keys a process selects keys in position $i \cdot \frac{n}{p^2}$ for $i = 0, \ldots p-1$ as its sample and sends this sample to process 1, who then sorts all p^2 keys. Then process 1 computes the final sample S by selecting all keys in positions $i \cdot p$ for $i = 1, \ldots, p-1$ and broadcasts S. Determine the maximal number of keys received by a process in step (4) of sample sort.

Hence sample sort performs successful load balancing if we set $s = p$. In this case one should demand $n = \Omega(p^3)$, since otherwise sorting all samples dominates the run time.

Sample sort has the least communication if we use parallel quicksort and hyperquicksort as a comparison. If the all-to-all broadcast in step (3) runs in time $O(\frac{n}{p})$, then sample sort is the superior sorting procedure. In a sense, the algorithms for the fast Fourier transform respectively for parallel quicksort seems comparable with parallel quicksort playing the role of the binary exchange algorithm and sample sort playing the role of the transpose algorithm.

8.1.3 Parallelizing Mergesort

Let n be a power of two. The sequential, non-recursive mergesort works in $\log_2 n$ phases where within phase i it merges consecutive intervals of length 2^i.

Algorithm 8.5 **The sequential, non-recursive mergesort.**

/* The sequence $x = (x_0, \ldots, x_{n-1})$ is to be sorted. */

for $i = 0$ to $\log_2 n - 1$ do
  for $j = 0$ to $\frac{n}{2^{i+1}} - 1$ pardo
    merge $(x_{j \cdot 2^i}, \ldots, x_{(j+1) \cdot 2^i - 1})$ and $(x_{(j+1) \cdot 2^i}, \ldots, x_{(j+2) \cdot 2^i - 1})$;

In our parallel implementation we work with p processes who start by sorting their n/p keys. Then the final $\log_2 p$ merging phases have to be parallelized and the crucial question is therefore the performance of merging in parallel. We first describe **odd-even merging**.

Exercise 88
Let m be a power of two. For a sequence $x = (x_0, \ldots, x_{m-1})$ let $\text{even}(x) = (x_0, x_2, x_4, \ldots, x_{m-2})$ and $\text{odd}(x) = (x_1, x_3, x_5, \ldots, x_{m-1})$ be the subsequences of even- and odd-numbered components of x.

Assume that x and y are sorted sequences of length m each. To merge x and y, odd-even Merge recursively merges

- even(x) and odd(y) to obtain the sorted sequence $u = (u_0, u_1, \ldots, u_{m-1})$ and
- odd(x) and even(y) to obtain the sorted sequence $v = (v_0, v_1, \ldots, v_{m-1})$.

Finally odd-even merge computes the output sequence $w = (w_0, \ldots, w_{2m-1})$ from u and v as follows: in parallel for $0 \leq i \leq m-1$, if $u_i \leq v_i$ then set $w_{2i} = u_i, w_{2i+1} = v_i$ and otherwise $w_{2i} = v_i, w_{2i+1} = u_i$.

(a) Show with the 0-1 principle that odd-even merge works correctly.

(b) Assume that consecutive intervals of x and y –of length $m/2q$ each– are distributed among q processes. Show how to implement odd-even merge in computing time $O(\frac{m}{q} \cdot \log_2 2q)$ and communication time $O(\frac{m}{q} \cdot \log_2 q)$.

Thus, after sorting n/p keys sequentially in time $O(\frac{n}{p} \cdot \log_2 \frac{n}{p})$ without communication, sorted sequences of length n/p are merged. This phase is followed by merging sorted sequences of length $2n/p$ and in general by merging sorted sequences of length $2^k \cdot n/p$ for $k = 0, \ldots, \log_2 p - 1$. If we fix k, then we have to solve $p/2^{k+1}$ merging problems involving sorted sequences of length $m = 2^k \cdot n/p$. In any such merging problems $q = 2^{k+1}$ processes participate and hence computing time $O(\frac{m}{q} \cdot \log_2 2q) = O(\frac{n}{p} \cdot (k+1))$ and communication time $O(\frac{m}{q} \cdot \log_2 q) = O(\frac{n}{p} \cdot (k+1))$ suffice. All in all,

Theorem 8.6 *Odd-even mergesort runs in time $O(\frac{n}{p} \cdot \log_2^2 p + \frac{n}{p} \cdot \log_2 \frac{n}{p})$ and its communication cost is bounded by $O(\frac{n}{p} \cdot \log_2^2 p)$.*

Thus we cannot expect good performance, unless communication is dominated by computation, and hence $\log_2^2 p << \log_2 \frac{n}{p}$ is required. In conclusion, if the number of processors is too large, the performance of the parallel mergesort breaks down due to extensive communication requirements. If the number of processors is sufficiently small, the parallel mergesort is doing ok, but is in now way better than a parallel quicksort with similar resources. We make a second attempt and change our merging approach. The next problem proposes the **bitonic merge** algorithm.

Exercise 89

Let m be a power of two. A sequence $(x_0, \ldots, x_{m-1})$ is called bitonic iff there is a position i such that $(x_0, \ldots, x_i)$ is monotonically increasing and $(x_{i+1}, \ldots, x_{m-1})$ is monotonically decreasing.

We describe bitonic merge to merge an increasing sequence $(x_0, \ldots, x_{m-1})$ with a decreasing sequence $(x_m, \ldots, x_{2m})$ A single comparison suffices for $m = 1$. In the general case compare x_i with x_{i+m} in parallel for all $1 \leq i \leq m$. After switching keys between the two halves if necessary, bitonic merge merges the first and the second half recursively.

(a) Show that bitonic merge works correctly.

(b) Show that we obtain a sorting algorithm as follows: recursively sort the first half of all keys increasingly and the second half decreasingly. Merge the two sequences with bitonic merge. Determine the computing time and the communication cost when sorting a sequence of m keys with q processors.

(c) Is there a performance difference between sorting with odd-even merging and sorting with bitonic merging?

Thus odd-even merge and bitonic merge behave more or less identically and, as a consequence of Theorems 8.2, 8.4 and 8.6, our implementations of parallel quicksort are superior to our parallel implementations of mergesort.

8.2 Dynamic Programming

Dynamic programming is a generalization of divide & conquer in which the hierarchy of subproblems corresponds to a directed graph without cycles. Typically, subproblems have few different degrees of complexity and subproblems of same complexity can be solved independently. Thus, as for divide & conquer, a successful parallelization of a sequential dynamic programming algorithm normally depends only on parallelizing the task of solving the subproblem of a node from solutions to subproblems of its immediate ancestors.

Dynamic programming has gained importance due to many applications within bioinformatics.

8.2.1 Transitive Closure and Shortest Paths

In the **transitive closure problem** we are given a directed graph $G = (V, E)$ with node set $V = \{1, \ldots, n\}$. Our goal is to determine the transitive closure graph $\overline{G} = (V, \overline{E})$, where the edge (i, j) belongs to $\overline{E}$ iff there is a path in G starting in i and ending in j. Warshall's algorithm determines the transitive closure graph with the help of the adjacency matrix A, where A is defined by

$$A[i,j] = \begin{cases} 1 & (i,j) \in E \\ 0 & \text{otherwise.} \end{cases}$$

Warshall's Algorithm

```
for k=1 to n do
      for i=1 to n do
        for j=1 to n do
          A[i,j] = A[i,j] or ( A[i,k] and A[k,j]);
```

Why is Warshall's algorithm correct? An inductive argument shows that, when the iteration for k terminates,

$$A[i,j] = 1 \;\Leftrightarrow\; \text{there is a path in } G \text{ from } i \text{ to } j \text{ whose intermediate nodes all belong to } \{1, \ldots, k\}.$$

Observe that Warshall's algorithm consists of three nested for-loops and hence runs in time $O(n^3)$.

We describe a parallel algorithm which maintains the sequential outer k-loop, but parallelizes the inner i, j-loops. We work with the rowwise decomposition of A and assume that all rows with indices in the interval $\{(i-1) \cdot n/p + 1, \ldots, i \cdot n/p\}$ are assigned to process i. Assume that we have reached k. All updates $A[i,j] = A[i,j] \vee (A[i,k] \wedge A[k,j])$ have to be performed in parallel. If a process knows the ith row, then it is responsible for the update of $A[i,j]$. The process does know $A[i,k]$, but it may have no information on $A[k,j]$. Thus the the process holding row k should broadcast it. Observe that the iteration for k requires computing time $O(\frac{n^2}{p})$ and broadcast time $O(n \cdot \log_2 p)$. The overall running time is therefore bounded by $O(\frac{n^3}{p} + n^2 \log_2 p)$ and we reach constant efficiency, if $n = \Omega(p \cdot \log_2 p)$ holds.

Let us also try the checkerboard decomposition, where processes form a $\sqrt{p} \times \sqrt{p}$ mesh and each process holds a submatrix with $n/\sqrt{p}$ rows and $n/\sqrt{p}$ columns. The process responsible for $A[i,j]$ may not know $A[i,k]$ or $A[k,j]$. Thus the process holding $A[i,k]$ (resp. $A[k,j]$) has to broadcast its values in its row (resp. column) of the mesh of processes. The communication time per k-iteration is bounded by $O(\frac{n}{\sqrt{p}} \log_2 \sqrt{p})$, whereas the computation time stays at $O(\frac{n^2}{p})$. We have n k-iterations and the performance has improved to running time $O(\frac{n^3}{p} + \frac{n^2}{\sqrt{p}} \log_2 \sqrt{p})$. Constant efficiency is reached, whenever $n = \Omega(\sqrt{p} \cdot \log_2 \sqrt{p})$.

Theorem 8.7 *Assume that p processors utilize the checkerboard decomposition. Then the transitive closure of a given directed graph with n nodes can be determined in computing time $O(\frac{n^3}{p} + \frac{n^2}{\sqrt{p}} \log_2 \sqrt{p} + n)$ and communication time $O(\frac{n^2}{\sqrt{p}} \log_2 \sqrt{p})$.*

In the **all-pairs-shortest-path problem** we are given a directed graph $G = (V, E)$ with node set $V = \{1, \ldots, n\}$. We assign weights $w(e)$ to the edges $e \in E$ and would like to determine the length of a shortest path from i to j for any pair (i, j) of nodes. Floyd's algorithm solves the all-pairs-shortest-path problem with the help of the weighted adjacency matrix

$$B[i,j] = \begin{cases} w(i,j) & (i,j) \in E \\ \infty & \text{otherwise.} \end{cases}$$

Floyd's Algorithm

```
for k=1 to n do
      for i=1 to n do
        for j=1 to n do
          B[i,j] = min ( B[i,j], B[i,k] + B[k,j] );
```

As for Warshall's algorithm one shows with an inductive argument that, when the iteration for k terminates,

$$B[i,j] = \text{the length of a shortest path in } G \text{ from } i \text{ to } j \text{ whose intermediate nodes all belong to } \{1, \ldots, k\}.$$

Since Floyd's algorithm also consists of three nested for-loops, it runs in time $O(n^3)$ as well. Observe that we can apply the parallelization of Warshall's algorithm with the obvious changes and obtain a parallelization of Floyd's algorithm.

Theorem 8.8 *Assume that p processors utilize the checkerboard decomposition. Then the all-pairs-shortest-path problem of a given directed graph with n nodes can be solved in computing time $O(\frac{n^3}{p} + \frac{n^2}{\sqrt{p}} \log_2 \sqrt{p} + n)$ and communication time $O(\frac{n^2}{\sqrt{p}} \log_2 \sqrt{p})$.*

Remark 8.2 Thus we have obtained efficient parallelizations for Warshall's and Floyd's algorithm. These solutions are satisfying for dense graphs with $\Omega(n^2)$ edges. For sparse graphs however we obtain a faster transitive closure computation, if we run a depth-first search beginning in each node (running time $O(n^2+n\cdot|E|)))$, and a faster all-pairs shortest path solution, if we run Dijkstra's single-source-shortest-path algorithm for each node in V (running time $O((n^2 + n \cdot |E|) \cdot \log_2 n))$. Efficient parallelizations are neither known for depth-first search nor for Dijkstra's algorithm!

Exercise 90

Assume we are given an $n \times n$ matrix (or image) M of zeroes and ones. If (i, j), (k, l) are neighbors in $M_2(n)$ or if (i, j), (k, l) are neighbors via diagonal edges, then we say that (i, j), (k, l) are *connected*, whenever $M[i, j] = M[k, l] = 1$. The connected component of (i, j) consists of all pairs (r, s) which are connected with (i, j). Observe that an image decomposes into disjoint connected components.

We describe an algorithm to determine all connected components of a given image. Only processes (i, j) with $M[i, j] = 1$ are active. First any active process (i, j) determines the label $n \cdot i + j$ as well as the set of neighbors that it is connected to. In subsequent steps active processes reset their label to the smallest label among active processes that they are connected to and repeat this procedure "sufficiently long".

Show that the minimization step may have to be repeated $\Omega(n^2)$ times.

We say that an image is convex iff M, when restricted to rows or columns, has the form $0^* \cdot 1^* \cdot 0^*$. Show that the algorithm runs for at most $O(n)$ steps whenever the image is convex.

Exercise 91

We describe an algorithm for determining all connected components of a two-dimensional $n \times n$ grid of zeroes and ones. We say that two grid points (i, j) and (k, l) with label one are connected iff $|i - k| + |j - l| \leq 1$ or if (i, j) and (k, l) are neighbors via diagonal edges. We allow ones to change to zeroes and vice versa according to the following transition rules for the upper left cell:

$$\begin{array}{c|c} 1 & 0 \\ \hline 0 & 0 \end{array} \implies \begin{array}{c|c} 0 & * \\ \hline * & * \end{array} \quad \text{and} \quad \begin{array}{c|c} 0 & 1 \\ \hline 1 & * \end{array} \implies \begin{array}{c|c} 1 & * \\ \hline * & * \end{array}$$

(Cells beyond the boundary are set to zero by default.) Show the following properties for the transition from the image at time t to the image at time $t + 1$:

(a) A connected component never decomposes into two or more connected components.

(b) Two or more components are never merged into one component.

(c) No ones exist after $2n$ steps.

(d) Just before extinction a connected component consists of exactly one cell.

Show how to determine all connected components of an image in time $O(n)$.

8.2.2 The Global Pairwise Alignment Problem

Quite often similarities of DNA, RNA sequences or proteins imply functional similarity. However point mutations such as insertions deletions or substitution of nucleotides makes a direct comparison of such sequences an apparently complex problem.

Let's have a more detailed look. We view a DNA sequence as a word over the alphabet $\Sigma = \{\text{adenine, cytosine, guanine, thymine}\}$. We would like to determine how many insertions, deletions or substitutions of letters are necessary to obtain sequence v from sequence u. Instead of tackling this problem right away we choose a slightly different perspective and imagine a blank symbol "$-$" inserted in several positions of u as well as v. The new, longer strings u^* and v^* are required to have same length and the blank symbol is not allowed to appear in the same position for u as well as for v. Is this the case, then u^* and v^* are called an *alignment* of u and v.

If $u_i^* = -$, then we imagine v_i^* as inserted into u, and if $v_i^* = -$, then we imagine that u_i^* has been deleted. Finally, if both $u_i^* \neq v_i^*$ are different from the blank symbol, then we say that u_i^* has been substituted by v_i^*. Of course we are looking for an alignment which verifies a maximal similarity between u and v.

Definition 8.9 The similarity of an alignment u^*, v^* of u and v is defined by

$$s(u^*, v^*) = \sum_i d(u_i^*, v_i^*),$$

where the function $d : (\Sigma \cup \{-\}) \times (\Sigma \cup \{-\}) \to \mathbb{R}$ penalizes a disagreement with a low or negative score.

The algorithm of Needleman-Wunsch determines an alignment of maximum score for two strings u and v of length n and m respectively. It does so by computing a maximum alignment for the prefixes $u_1 \cdots u_i$ of u and $v_1 \cdots v_j$ of v. Here is the crucial observation: if $D(i, j)$ is the maximum score, then

$$D(i,j) = \max\{D(i, j-1) + d(-, v_j), D(i-1, j) + d(u_i, -), D(i-1, j-1) + d(u_i, v_j)\}.$$

Why? An optimal alignment may match match v_j with a blank, u_i with a blank or match u_i and v_j. In either case the alignment of the remaining strings has to be optimal.

Algorithm 8.10 **Global Pairwise Alignment**

(1) // Initialization starts.
$D(0, 0) = 0$;
for $(i = 1;\ i <= n;\ i++)$
$D(i, 0) = \sum_{k=1}^{i} d(u_k, -)$;
for $(j = 1;\ j <= m;\ j++)$
$D(0, j) = \sum_{k=1}^{j} d(-, v_k)$;

(2) for $(i = 1;\ i <= n;\ i++)$

for $(j = 1;\ j <= m;\ j++)$ // The subproblem to determine $D(i,j)$ is solved:

$D(i,j) = \max\{D(i,j-1)+d(-,v_j), D(i-1,j)+d(u_i,-), D(i-1,j-1)+d(u_i,v_j)\}$.

The run time of algorithm 8.10 is dominated by the two nested for-loops and hence is proportional to $O(n \cdot m)$. Observe that to determine $D(i,j)$ we only need to know $D(i',j')$ for $i' + j' < i + j$. Hence we reorganize step (2) of algorithm 8.10 by working with an outer k-loop and compute $D(i, k-i)$ with an inner i-loop. Thus our parallelization works sequentially on the outer k-loop and parallelizes the inner loop.

In a typical application for the global alignment problem both strings u and v have approximately the same length. To simplify the exposition we assume that both strings have identical length n. We choose the rowwise decomposition of the score matrix D. Our parallel implementation works in $2n$ phases and computes in phase k all entries $D(i, k-i)$.

If a process becomes active, it evaluates its portion of the score matrix D. The process begins with boundary pairs $(i, k-i)$ whose solution it immediately communicates to the respective neighbor process and finishes with interior pairs. Each phase requires the communication of two boundary pairs and can be completed in time $O(\frac{n}{p})$. Hence the total run time is bounded by $O(\frac{n^2}{p} + n)$.

Exercise 92
What is the run time when choosing the checkerboard decomposition?

8.2.3 RNA Secondary Structure Prediction

RNA (ribonucleic acid) is involved in the production of proteins either as information carrier (mRNA) or by translating this information into proteins (rRNA, tRNA). Unlike DNA molecules which are composed of two strands of complementary nucleotides, most RNA molecules possess only a single strand. RNA is made up of four bases, namely the complementary pairs adenine and uracil as well as cytosine and guanine; thus uracil replaces thymine in comparison to DNA molecules.

The RNA secondary structure consists of all hydrogen bonds between complementary bases within the molecule. This two-dimensional folding pattern is of particular importance for the functionality of an RNA molecule.

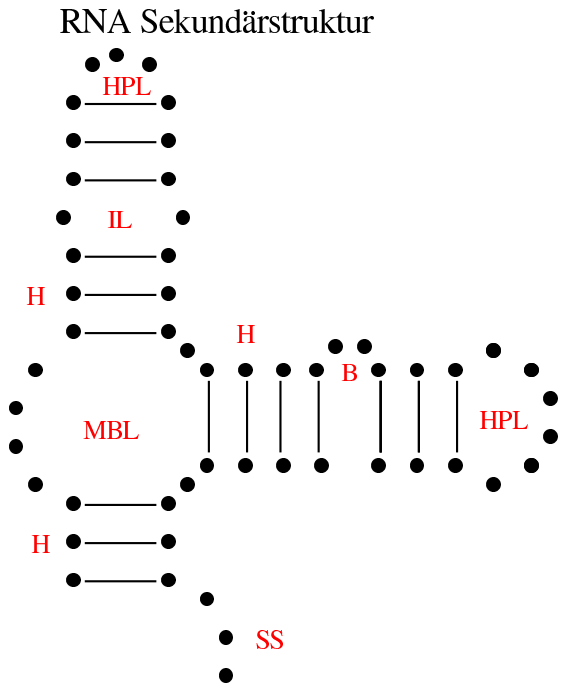
Definition 8.11 Let $R \in \{A, C, G, U\}^n$ be the primary structure of an RNA molecule. Its secondary structure is described by a set $P \subseteq \{\ \{i,j\} \mid 1 \leq i \neq j \leq n\}\ \}$ of pairs satisfying the following conditions:

(a) For any pair $\{i,j\} \in P$ the property $|i-j| \geq 5$ holds. Thus bonds are only possible between bases in distance at least five.

(b) The pairs in P form a matching: each position $i \in \{1, \ldots, n\}$ belongs to at most one pair in P.

(c) Pairs in P correspond to complementary bases and we have either $\{R_i, R_j\} = \{A, U\}$ or $\{R_i, R_j\} = \{C, G\}$ for any pair $(i, j) \in P$.

(d) The folding may not cross itself: if $\{i, j\}$ and $\{k, l\}$ belong to P and if $i < j, k < l$ hold, then $i < k < j < l$ is excluded.



[1]

To predict the secondary structure from its primary structure we assume that the folding minimizes its free energy by maximizing the number of bonds. Under this assumptions we have to solve the following problem:

> A string $R \in \{A, C, G, U\}^n$ is given. Determine an RNA secondary structure which maximizes $|P|$.

Property (4) is of great help when trying to compute an optimal secondary structure P_{opt}, namely if P_{opt} contains the pair $\{k, n\}$, then P_{opt} decomposes into the optimal secondary structures for the prefix $R_1 \cdots R_{k-1}$ and for the suffix $R_{k+1} \cdots R_{n-1}$ of R. Therefore our dynamic programming algorithm solves the subproblems "determine $D(i, j)$", where

$D(i, j) =$ The number of bonds in an optimal secondary structure for $R_i \cdots R_j$.

[1] Aus: www.zib.de/MDGroup/temp/lecture/l5/p_secondary/rna_second.pdf

To determine $D(i,j)$ we differentiate two cases. Firstly, if j is not involved in a match, then we have $D(i,j) = D(i,j-1)$. Secondly, if P_{opt} contains the *legal* pair (k,j), then $D(i,j) = D(i,k-1) + D(k+1,j-1) + 1$. (The pair (k,j) is legal, if $i \leq k \leq j-5$ and $\{R_k, R_j\} = \{A,U\}$ or $\{R_k, R_j\} = \{C,G\}$ holds. Thus we enforce properties (a) and (c) of Definition 8.11. By decomposing (i,j) into $(i,k-1)$ and $(k+1,j-1)$ we guarantee that property (b) is satisfied, since neither k nor j can appear in another pair.) Thus we obtain the **recurrence**

$$D(i,j) = \max_{k,(k,j) \text{ ist legal}} \{D(i,k-1) + D(k+1,j-1) + 1, D(i,j-1)\} \tag{8.1}$$

which is implemented by the following program.

Algorithm 8.12 **RNA Secondary Structure Prediction**

(1) for $(l = 1;\ l <= 4;\ l{+}{+})$
  for $(i = 1;\ i <= n-l;\ i{+}{+})$
    Set $D(i, i+l) = 0$;

(2) for $(l = 5;\ l <= n-1;\ l{+}{+})$
  for $(i = 1;\ i <= n-l;\ i{+}{+})$
    Determine $D(i, i+l)$ with recurrence (8.1).

We have to solve a total of $\binom{n}{2}$ subproblems $D(i,j)$. Since each subproblem is solved in time $O(n)$, our program runs in cubic time $O(n^3)$.

The parallel implementation maintains the outer l-loop and parallelizes the inner loop. When computing $D(i, i+l)$ we only need to know $D(i, i+l')$ and $D(i+l'+1, i+l-1)$ for $l'+1 < l-1$. We choose the rowwise decomposition of the matrix D and hence we have to guarantee only that the process responsible for computing $D(i, i+l)$ has access to all values $D(i+l'+1, i+l-1)$ for $l'+1 < l-1$. Assume that a process needs access to an unknown value $D(i+l'+1, i+l-1)$ for the first time. If $D(i+l'+1, i+l-1)$ is required for some row r, then r is its "largest row" or ($r = i+l'$ and $l' = 0$). Thus any process needs at most $O(n)$ unknown values for any iteration of the l-loop. Moreover at most $\frac{n}{p}$ values come from a particular process.

Thus before an iteration of the l-loop we have to perform an all-to-all personalized broadcast in which each process sends personalized messages of length $O(\frac{n}{p})$. Since the compute time per iteration is bounded by $O(\frac{n^2}{p})$, the run time per iteration is bounded by $O(\frac{n^2}{p} + n)$ and the total run time is $O(\frac{n^3}{p} + n^2)$. We reach constant efficiency whenever $p \leq n$.

Theorem 8.13 *An optimal RNA secondary structure according to Definition 8.11 can be determined sequentially in time $O(n^3)$ for a string of length n. With $p \leq n$ processes compute time $O(\frac{n^3}{p})$ and communication time $O(n^2)$ is sufficient.*

8.3 Conclusion

Divide & conquer algorithms are prime candidates for parallelization, since subproblems can be solved independently. We have parallelized quicksort and mergesort, but obtained faster solutions for quicksort. However sample sort is the fastest solution, provided the all-to-all personalized broadcast is efficiently supported.

Dynamic programming algorithms have the advantage that subproblems of same complexity can be solved independently. For example we have obtained almost optimal parallel algorithms for the all-pairs-shortest path problem and the transitive closure problem. Finally we have obtained efficient parallel algorithms the pairwise alignment problem as well as for the RNA secondary structure prediction.

Chapter 9

A Complexity Theory for Parallel Computation

What are "reasonable" parallel computation models? Is it possible that we overlooked reasonable parallel computation models that allow even faster parallel computations for important problems? What are limits of parallel computations: are there problems with efficient sequential computations which are hard to parallelize? Is it possible to relate parallel computations to sequential computations?

The next sections try to give some answers. In particular, we relate parallel time and sequential space and define the notion of $\mathcal{P}$-completeness which allows to identify problems which are (apparently) hard to parallelize. We begin by introducing the space complexity of problems.

9.1 Space Complexity

We consider off-line Turing machines to define the space complexity of problems. An off-line Turing machine consists of

- an input tape which stores the input $\$w_1 \cdots w_n\$$ for letters $w_1, \ldots, w_n$ belonging to the input alphabet Σ. The dollar symbol is used as an end marker.
- a working tape which is infinite to the left and to the right. The tape alphabet is binary.
- an output tape which is infinite to the right. Cells store letters from an out alphabet Γ.

The input tape has a read-only head which can move to the left or right neighbor neighbor of a cell. At the beginning of the computation the head visits the cell storing the leftmost

letter of the input word. The working tape has a read/write head with identical movement options. At the beginning of the computation all cells store the blank symbol B. Finally the output tape has a write-only head which can move to the right only.

An off-line Turing machine computes by reading its input, performing computations on its working tape and printing onto its output tape. If the machine stops with output 1, then we say that the machine accepts the input; the machine rejects the input, if it writes a 0. For Turing machine M and input alphabet Σ, let

$$L(M) = \{w \in \Sigma^* \mid M \text{ accepts } w\}$$

be the language accepted by M.

Off-line Turing machines are ideally suited to define the space complexity of a sequential computation. For Turing machine M let $\text{space}_M(w)$ be the number of different cells of the working tape which are visited during the computation of M on input w. We define the space consumption of M on input length n and input alphabet Σ as the worst-case over all inputs $w \in \Sigma^n$, i.e.,

$$\text{space}_M(n) := \max_{w \in \Sigma^n} \text{space}_M(w).$$

We can now introduce the space complexity classes.

Definition 9.1

(a) Let $s : \mathbb{N} \to \mathbb{N}$ be a function. Then

$$\text{DSPACE}(s) = \{L \subseteq \{0,1\}^* \mid \begin{array}{l} L = L(M) \text{ for a Turing machine } M \\ \text{with } \text{space}_M(n) = O(s(n)) \end{array} \}$$

is the complexity class of all languages computable in (deterministic) space s.

(b) Instead of $\text{DSPACE}(\log_2 n)$ we use the abbreviation DL, deterministic logarithmic space.

DL is the smallest non-trivial space complexity class, since we need logarithmic space to remember a single position within the input.

We are interested as well in the space complexity of nondeterministic Turing machines. For a nondeterministic Turing machine M we define $L(M)$ as the set of inputs for which there is an accepting computation of M and set

$$\text{nspace}_M(w) = \left\{ \begin{array}{l} \text{the maximal number of cells of the working tape, which are} \\ \text{visited during an accepting computation on input } w. \end{array} \right.$$

as the nondeterministic space complexity of M on w. The space consumption of M on input length n and input alphabet Σ is then

$$\text{nspace}_M(n) := \max_{w \in \Sigma^n \cap L(M)} \text{nspace}_M(w).$$

Definition 9.2 (b) Let $s : \mathbb{N} \to \mathbb{N}$ be a function. Then

$$\mathrm{NSPACE}(s) := \{L \subseteq \{0,1\}^* \mid \begin{array}{l} L = L(M) \text{ for a nondeterministic Turing} \\ \text{machine with } \mathrm{nspace}_M(n) = O(s(n)) \end{array} \}.$$

(b) $\mathrm{NSPACE}(\log_2 n)$ is abbreviated by NL.

Is there a relationship between DL, NL and Nick's class $\mathcal{NC}$? We answer this question by first defining the computation graph of an off-line Turing machine.

Definition 9.3 Let M be a nondeterministic off-line Turing machine with space complexity at most s. For an input w we define the computation graph $G_M(w)$ as follows. The configurations[1] of M on input w are the nodes of $G_M(w)$. An edge leads from configuration k_1 to configuration k_2 iff k_2 is a potential immediate successor of k_1. An additional node yes is added and each accepting configuration k sends an edge into yes.

Lemma 9.4 *Let M be a nondeterministic off-line Turing machine.*

(a) Let k_0 be the initial configuration of M. Then

$$M \text{ accepts } w \;\Leftrightarrow\; \text{there is a path from } k_0 \text{ to yes in } G_M(w).$$

(b) If M has space complexity $s(n) = \Omega(\log_2 n)$, then $G_M(w)$ has at most $2^{O(s(n))}$ nodes and edges.

Exercise 93
Prove Lemma 9.4 (a).

How large is $G_M(w)$, if w has length n and if M has space complexity s? If M has Q as its set of states, then $G_M(w)$ has at most

$$|Q| \cdot (n+2) \cdot s(n) \cdot 2^{s(n)}$$

nodes, since there are $n+2$ positions of the input head, $s(n)$ positions of the working tape head and $2^{s(n)}$ possible contents of the working tape. Thus, if $s(n) = \Omega(\log_2 n)$, then $G_M(w)$ has at most $2^{O(s(n))}$ nodes and edges. □

Theorem 9.5

(a) DL $\subseteq$ NL.

[1] A configuration consists of the contents of the working tape, the current state and the positions of the input and working tape heads.

(b) Any language in NL can be accepted in time $O(\log_2^2 n)$ with a polynomial number of processors.

Proof: The inclusion DL $\subseteq$ NL is obvious, since a nondeterministic machine, given the same resources, is at least as powerful a deterministic machine. Hence it suffices to show **(b)**. Let M be a nondeterministic off-line Turing machine working in logarithmic space. If $|w| = n$, then $G_M(w)$ has poly(n) nodes. We construct the computation graph $G_M(w)$ in logarithmic time with a polynomial number of processors: reserve one processor for any pair of configurations and let this processor check, whether the pair corresponds to a transition.

To determine whether M accepts w, all we have to do is to check whether there is a path from k_0 to yes in $G_M(w)$. Our parallelization of Warshall's algorithm (Theorem 8.7) is not fast enough. Instead we use matrix multiplication to obtain a faster solution. Moreover we even work with a conventional $\{\neg, \wedge, \vee\}$-circuit.

Lemma 9.6 *The transitive closure of a graph directed G with n nodes can be computed by a circuit in depth $O(\log_2^2 n)$ and size $O(n^3 \cdot \log_2 n)$.*

Proof: Let A be the adjacency matrix of G, i.e.,

$$A[k_1, k_2] = \begin{cases} 1 & (k_1, k_2) \text{ is an edge of } G, \\ 0 & \text{otherwise.} \end{cases}$$

We also set the diagonal to one (i.e., insert self loops (k, k) for all configurations k) and call the new matrix B. Let B^r denote the rth power of B, where the logical OR replaces addition and the logical AND replaces multiplication. Then

$$B^r[k_1, k_2] = 1 \Leftrightarrow \text{there is a path in } G \text{ from } k_1 \text{ to } k_2 \text{ of length at most } r \ .$$

This equivalence is shown inductively. First observe that it is true for $r = 1$ due to the definition of B. Assume the equivalence holds for r. Then $B^{r+1}[k_1, k_2] = \bigvee_k B^r[k_1, k] \wedge B[k, k_2]$ by definition of the boolean matrix product. We apply the induction hypothesis and obtain

$$\begin{aligned} B^{r+1}[k_1, k_2] = 1 \quad \Leftrightarrow \quad & \text{there is } k \text{ and a path in } G \text{ from } k_1 \text{ to } k \text{ of length} \\ & \text{at most } r. \text{ Moreover } (k, k_2) \text{ is an edge of } G. \end{aligned}$$

This establishes the claim. But G has n nodes and hence $B^{n-1}[k_1, k_2] = 1$ iff G has a path from k_1 to k_2. Thus it suffices to successively compute the matrix powers $B^2, B^4, \ldots, B^{2^t}$ with $t = \lceil \log_2 n \rceil$.

Each matrix product $B^{2^{i+1}}$ can be computed very fast: first compute all conjunctions $B^{2^i}[k_1, k] \wedge B^{2^i}[k, k_2]$ in parallel and then "sum up" conjunctions with a tree of OR's. The summation step involves n operands and therefore runs in time $\log_2 n$ with $O(n^3)$ gates. Thus one matrix multiplication requires $O(\log_2 n)$ steps and all matrix products can be computed in time $O(\log_2^2 n)$. $\square$

9.2 Circuit Depth Versus Space

We work with $\{\wedge, \vee, \neg\}$-circuits of fan-in two. We are particularly interested in the complexity parameters *size* and *depth* of the circuit. The size of S is the number of nodes of S and its depth is the length of the longest path. Thus depth is the appropriate parameter to measure the parallel computing time of S.

A circuit family $(S_n \mid n \in \mathbb{N})$ specifies one circuit for each input size $n \in \mathbb{N}$. We require that the description of the family is only moderately complex. In particular, we say that the circuit family is uniform if its circuits can be described by off-line Turing machines whose space complexity is logarithmic in the size of the circuit.

Definition 9.7 Set $S = (S_n \mid n \in \mathbb{N})$ be a family of circuits, where S_n is a circuit with n inputs and size $s(n)$. We say that S is a uniform circuit family iff there is a deterministic off-line Turing machine M which, on input 1^n, eventually prints all edges of S_n onto its output tape as well as all nodes with their assigned operation, respectively with their assigned input bit. M has to have space complexity at most $O(\log_2(n \cdot s(n)))$.

Observe that an off-line Turing machine M with space complexity $t(n) \geq \log_2 n$ runs for at most $2^{O(t(n))}$ steps, since otherwise M has to enter a configuration twice and thus enters a loop. Hence M can describe circuits of size at most $2^{O(t(n))}$ and our definition of uniformity is quite restrictive, since we only allow the minimal space complexity. Is there a connection between circuit depth and space complexity?

Theorem 9.8 *Assume that $s(n) = \Omega(\log_2 n)$. If M is a nondeterministic off-line Turing machine with space complexity $s(n)$, then there is a uniform circuit family $(S_n \mid n \in \mathbb{N})$ with depth $O(s^2(n))$ recognizing $L(M)$.*

Proof: We know that an input w belongs to $L(M)$ iff there is a path in $G_M(w)$ from the initial configuration k_0 to yes. We compute the transitive closure of $G_M(w)$ with the help of Lemma 9.6 in depth $O(\log_2^2 N)$, where $N = 2^{O(s(n))}$ is the number of nodes of $G_M(w)$.

We are required to build a uniform circuit family. But configurations have length $O(\log_2 n + s(n))$ and hence space $O(\log_2(n) + s(n))$ is sufficient to output all valid transitions between configurations on input 1^n. □

But we can also simulate circuits of small depth by off-line Turing machines of small space.

Theorem 9.9 *If the uniform family $(S_n \mid n \in \mathbb{N})$ consists of circuits of depth $s(n)$, then there is a deterministic off-line Turing machine with space complexity $O(s^2(n))$ which accepts exactly those words which are accepted by the circuit family.*

Proof: We describe an off-line Turing machine M which accepts exactly those inputs w which are accepted by $S_{|w|}$. Set $n = |w|$. Since S_n has depth $s(n)$, the circuit has at most $2^{s(n)+1} - 1$ nodes. But we may evaluate S_n with depth-first search using a stack of height $O(s(n))$. Since the stack holds nodes from the circuit, all we need is space complexity $O(s^2(n))$. □

Exercise 94
Show that the space complexity of the simulating Turing machine of Lemma 9.9 can be improved to $O(s(n))$.

9.2.1 The Parallel Computation Thesis

By Lemma 9.8 and Lemma 9.9 we have a quadratic relationship between the depth of circuits and the space complexity of Turing machines. One can also show that circuit families and MPI algorithms, resp. parallel register machines are polynomially related, when comparing depth and parallel time, and the conjecture is natural that

> parallel time for any *reasonable* parallel computing model is polynomially related to the space complexity for sequential computations.

This conjecture is exactly the contents of the *parallel computation thesis* which classifies any parallel computing model violating the thesis as unreasonable.

Observe however that the parallel computation thesis does not restrict the "size" of a parallel machine and the polynomial relationship between space and parallel time can in general only be achieved with parallel machines of exponential size.

9.3 $\mathcal{P}$-completeness

We remember that all languages in $\mathcal{NC}$ can be accepted efficiently by a sequential computation.

Lemma 9.10 $\mathcal{NC} \subseteq \mathcal{P}$.

Which languages in $\mathcal{P}$ are hard to parallelize? We are not able to answer this question, however we can show that there are languages which are the hardest to parallelize: if any such language belongs to $\mathcal{NC}$, then $\mathcal{NC}$ equals $\mathcal{P}$. Since $\mathcal{NC} \neq \mathcal{P}$ holds in all likelihood, we have strong evidence that a hardest language does not belong to $\mathcal{NC}$. To compare the hardness of languages we define a reduction between languages.

Definition 9.11 We say that language L_1 is reducible to language L_2 ($L_1 \leq_{\text{par}} L_2$), iff there is a "translation" T such that

$$w \in L_1 \Leftrightarrow T(w) \in L_2.$$

Moreover we demand that T is computable in poly-logarithmic time by an MPI algorithm with a polynomial number of processors.

Which languages are the hardest languages?

Definition 9.12 A language K is called $\mathcal{P}$-hard iff $L \leq_{\text{par}} K$ for all languages $L \in \mathcal{P}$. K is called $\mathcal{P}$-complete iff K is $\mathcal{P}$-hard and K belongs to $\mathcal{P}$.

We summarize the most important properties of our reduction.

Lemma 9.13

(a) If $L_1 \leq_{\text{par}} L_2$ and $L_2 \leq_{\text{par}} L_3$, then $L_1 \leq_{\text{par}} L_3$.

(b) Assume that K is $\mathcal{P}$-hard and that $K \leq_{\text{par}} L$ holds. Then L is $\mathcal{P}$-hard.

(c) Assume that $K \leq_{\text{par}} L$ holds. Then, if L belongs to $\mathcal{NC}$, so does K.

(d) Assume that language L is $\mathcal{P}$-hard. If L belongs to $\mathcal{NC}$, then $\mathcal{NC} = \mathcal{P}$.

Proof (a): is obvious. **(b)** Let M be an arbitrary language in $\mathcal{P}$. We know that $M \leq_{\text{par}} K$, since K is $\mathcal{P}$-hard. But $K \leq_{\text{par}} L$ by assumption and we conclude $M \leq_{\text{par}} L$ with part (a). Since M is an arbitrary language in $\mathcal{P}$, this shows that L is $\mathcal{P}$-hard.

(c) Since $K \leq_{\text{par}} L$ holds, there is a translation T with $w \in K \Leftrightarrow T(w) \in L$. Moreover the translation T can be implemented by an MPI algorithm in poly-logarithmic time with a polynomial number of processors. We also know that L belongs to $\mathcal{NC}$ and hence L can be accepted by an MPI algorithm T_L in poly-logarithmic time with a polynomial number of processors. Now to decide, whether an input w belongs to K, we first run T on w, pipe the result into T_L and output the verdict of T_L. Hence $K \in \mathcal{NC}$.

(d) Since L is $\mathcal{P}$-hard, we have $K \leq_{\text{par}} L$ for an arbitrary language K in $\mathcal{P}$. If however L belongs to $\mathcal{NC}$, then K also belongs to $\mathcal{NC}$ with part (b). Thus in this case $\mathcal{P} \subseteq \mathcal{NC}$ and the claim $\mathcal{P} = \mathcal{NC}$ follows with Lemma 9.10. □

Exercise 95
We say that language K is reducible to language L with respect to constant depth ($K \leq_C L$) iff there is a uniform family S_n of unbounded fan-in circuits of constant depth and polynomial size which accepts K. Moreover S_n may have oracle gates which accept input z iff $z \in L$.

(a) Show that $\leq_C$ is transitive.

(b) If $K \leq_C L$ holds, then L requires asymptotically the same depth as K, provided only circuits of polynomial size are considered.

Exercise 96
We consider the following problems.

- MULTIPLICATION: determine the product of two n-Bit numbers.
- SUM: determine the sum of n n-Bit numbers.
- BINARY COUNTING: determine the binary representation of $\sum_{i=1}^{n} x_i$ when summing n bits.
- UNARY COUNTING: determine the unary representation of $\sum_{i=1}^{n} x_i$ when summing n bits.
- SORTING: sorting n n-bit numbers.
- MAJORITY: determine if $x = (x_1, \ldots, x_n)$ has at least as many ones as zeroes.

Show the following reductions:

(a) MULTIPLICATION $\leq_C$ SUM.
(b) SUM $\leq_C$ BINARY COUNTING.
(c) BINARY COUNTING $\leq_C$ UNARY COUNTING.
(d) UNARY COUNTING $\leq_C$ SORTING.
(e) SORTING $\leq_C$ MAJORITY.
(e) MAJORITY $\leq_C$ MULTIPLICATION.

Thus all problems are equivalent.

Exercise 97
We consider the following problems:

- UR: for a given undirected graph and two nodes u and v, decide whether u and v belong to the same connected component of G.
- UCON: decide if a given undirected graph is connected.
- DR: for a given directed graph G and two nodes u and v, decide whether there is a path in G from u to v.
- DCON: decide if a given directed graph is strongly connected.

Show the following reducibilities:

(a) UCON $\leq_C$ UR.
(b) UR $\leq_C$ DR.
(c) DCON $\leq_C$ DR and DR $\leq_C$ DCON.
(d) PARITY $\leq_C$ UCON.
(e) DR $\leq_C$ 2-SAT.

9.3.1 The Circuit Value Problem

The input of the Circuit Value problem (CVP) consists of a circuit S and an input w of S. The pair (S, w) belongs to CVP iff the circuit S accepts w. (Hence we assume that S has a single output node.)

Observe that CVP is a very easy problem for sequential computation, since circuit evaluation is immediate with graph traversals such as depth-first search. However a parallel evaluation in poly-logarithmic time seems hard for circuits of large depth.

Theorem 9.14 *CVP is $\mathcal{P}$-complete.*

Proof: We already observed that CVP belongs to $\mathcal{P}$ and it suffices to show that CVP is $\mathcal{P}$-hard. Thus we pick an arbitrary language L in $\mathcal{P}$ and have to show that $L \leq_{\text{par}}$ CVP holds. What do we know about L? There is a Turing machine M with a single tape which computes in polynomial time and accepts exactly the words in L. Hence

$$w \in L \Leftrightarrow M \text{ accepts } w.$$

Let us assume that M runs in time $t(n)$. Our goal is to simulate M by a *uniform* circuit family $(S_n \mid n \in \mathbb{N})$ of polynomial size such that

$$M \text{ accepts } w \Leftrightarrow S_{|w|} \text{ accepts } w$$

holds. Why does this suffice? We define the translation T by $T(w) = (S_{|w|}, w)$ and

$$w \in L \Leftrightarrow S_{|w|} \text{ accepts } w$$

follows. Can we compute $T(w)$ in poly-logarithmic time? Since we assume that the circuit family is uniform and of polynomial size, there is an off-line Turing machine M^* which writes the description of circuit $S_{|w|}$ onto its output tape and uses not more than logarithmic space. Thus the question, whether a pair of nodes is an edge, can be answered in logarithmic space. But DL $\subseteq \mathcal{NC}$ with Theorem 9.5 and hence the translation can be computed within $\mathcal{NC}$.

Assume that input w has length n. Since M runs in time $t(n)$, it visits only the cells with addresses

$$-t(n), -t(n)+1, \cdots, -1, 0, +1, \cdots, t(n).$$

Here we assume that letter w_i is written on the cell with address i and that the read/write head of M initially "sits" on the cell with address 0. We simulate M on input w with a circuit S_n which is built like a two-dimensional mesh. The ith "row" of S_n is supposed to reflect the configuration of M on input w at time i and hence its nodes correspond to the tape cells, express the current state of M, respectively indicate the current position of the read/write head. Indeed we have to block the nodes into small groups $S_{i,j}$ $(-t(n) \leq j \leq t(n))$ of constant size to enable the required coding.

How does row $i+1$ depend on row i and in particular, how are the groups $S_{i+1,j}$ working? If cell j is not visited at time i, then its contents has to remain unchanged. Obviously this can be easily enforced, since group $S_{i+1,j}$ just has to "ask" group $S_{i,j}$, whether the head was visiting. Since we assume here a negative answer, group $S_{i+1,j}$ assigns the letter remembered by group $S_{i,j}$ to cell j.

If however cell j is visited at time i, then this is reported by group $S_{i,j}$. We assume in this case that $S_{i,j}$ also stores the current state which it transmits together with the current contents of cell j to group $S_{i+1,j}$. Now group $S_{i+1,j}$ can determine the new contents of cell j, the new state and the neighbor which will be scanned at time $i+1$.

Observe that all groups $S_{i,j}$ are identical for $i \geq 1$. Only the groups $S_{0,j}$ vary, since cell j stores w_j for $1 \leq j \leq n$ and the blank symbol otherwise. Finally we have to add a binary tree on top of row $t(n)$ which checks whether the final state is accepting. Due to its easy structure we can construct S_n with an off-line Turing machine within logarithmic space and the family $(S_n \mid n \in \mathbb{N})$ is therefore universal. □

For later application we introduce variants of CVP. In *M-CVP* we assume a monotone circuit S and ask whether S accepts input w. (A circuit is monotone, if it does not have negations.) *M_2-CVP* is defined as M-CVP, however the circuit is required to have fan-out at most two. Finally we investigate *NOR-CVP*, a variant of CVP, in which we assume that the circuit is built from NOR-gates only. (Remember that $\mathrm{NOR}(u,v) = \neg(u \vee v)$.)

We will reduce CVP to M-CVP and need to push negations of a given circuit down to the input bits.

Lemma 9.15 *Let S be a circuit. Then there is an equivalent circuit S' which uses negations only for inputs and which can be constructed in logarithmic space from S. The size of S' at most doubles in comparison to S.*

Proof: We push negations in S to the inputs using the De Morgan rules

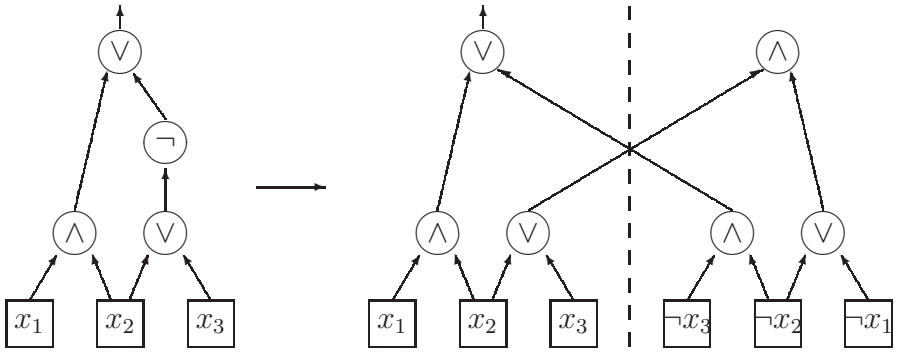
$$\neg(x \wedge y) \equiv \neg x \vee \neg y \quad \text{and} \quad \neg(x \vee y) \equiv \neg x \wedge \neg y.$$

However there is a problem, since the result of a gate may be needed in its negated as well as in its pure form. The equivalent circuit S' should therefore also provide both forms. In particular, the circuit S' has two gates u_{pos} and u_{neg} for any gate u of S.

- If u is an input bit x_i, then $u_{\mathrm{pos}} = x_i$ and $u_{\mathrm{neg}} = \neg x_i$.

- for an interior gate u of S, u_{pos} keeps the functionality of u, whereas u_{neg} interchanges $\wedge$ and $\vee$.

For any edge (u,v) of S, the equivalent circuit S' has two edges, namely $(u_{\mathrm{pos}}, v_{\mathrm{pos}})$ and $(u_{\mathrm{neg}}, v_{\mathrm{neg}})$. On the other hand, for any path $u \to \neg \to v$ in S, we insert the edges $(u_{\mathrm{pos}}, v_{\mathrm{neg}})$ and $(u_{\mathrm{neg}}, v_{\mathrm{pos}})$ into S'.



Obviously S' can be constructed from S in logarithmic space. Since the number of nodes doubles, the claim follows. □

Theorem 9.16

(a) M-CVP is $\mathcal{P}$-complete.

(b) M_2-CVP is $\mathcal{P}$-complete.

(c) NOR-CVP is $\mathcal{P}$-complete.

Proof: All three problems obviously belong to $\mathcal{P}$ and it suffices to show $\mathcal{P}$-hardness in each case. **(a)** Assume that (S, w) is an input of CVP. By Lemma 9.15 there is an equivalent circuit S' with negations only at the input bits such that the transformation $S \mapsto S'$ is computable by an off-line Turing machine in logarithmic space.

We define an input w_m which agrees with w on all not negated sources and disagrees with w on all negated sources. Finally we remove all negations from S' and obtain the monotone circuit S_m. Observe that the function computed by S on w coincides with the function computed by the new monotone circuit S_m on input w_m. Hence

$$(S, w) \in \text{CVP} \Leftrightarrow S \text{ accepts } w \Leftrightarrow S_m \text{ accepts } w_m \Leftrightarrow (S_m, w_m) \in \text{M-CVP}.$$

Therefore the translation $(S, w) \to (S_m, w_m)$ has the required properties and we have verified the reduction CVP $\leq_{\text{par}}$ M-CVP.

(b) It suffices to show the reduction M-CVP $\leq_{\text{par}}$ M_2-CVP. Assume that (S, w) is an input for M-CVP. We have to transform the monotone circuit S into an equivalent monotone circuit S^* such that no node has fan-out larger than two.

> **Exercise 98**
> Show that such a circuit S^* can be constructed by an MPI algorithm in poly-logarithmic time with a polynomial number of processors.

The translation $(S, w) \mapsto (S^*, w)$ establishes the reduction M-CVP $\leq_{\text{par}}$ M_2-CVP.

(c) We verify the reduction CVP $\leq_{\text{par}}$ NOR-CVP. We observe first that

$$\begin{aligned} \neg u &\equiv \text{NOR}(u,u), \\ u \wedge v &\equiv \text{NOR}(\neg u, \neg v) \text{ and} \\ u \vee v &\equiv \text{NOR}(\text{NOR}(u,v), \text{NOR}(u,v)) \end{aligned}$$

holds. Thus, if (S,w) is an input of CVP, then replace all gates by small NOR-circuits to obtain an equivalent NOR-circuit S^*. The translation $(S,w) \mapsto (S^*,w)$ establishes the wanted reduction to NOR-CVP. □

Exercise 99
In the emptiness problem for context-free grammars (ECFG) we are given a context-free grammar G and we have to check whether the generated language $L(G)$ is non-empty.

Show that ECFG is P-complete. Hint: verify the reduction M-CVP $\leq_{\text{par}}$ ECFG.

9.3.2 Network Flow

We describe the Flow problem (FP). An input for FP consists of

- a directed graph $G = (V,E)$,
- two distinguished nodes, the source $s \in V$ and the sink $t \in V$
- and a capacity function $c : E \to \mathbb{R}$.

We call a function $f : E \to \mathbb{R}$ a flow, if $0 \leq f(e) \leq c(e)$ for all edges $e \in E$ and if *flow conservation*

$$\sum_{u \in V,(u,v) \in E} f(u,v) = \sum_{u \in V,(v,u) \in E} f(v,u)$$

holds for any node $v \in V \setminus \{s,t\}$: the amount of flow entering v has to coincide with the amount of flow leaving f. Observe that flow conservation is not required for the source and the sink. In the optimization version of the flow problem a *maximal flow* f is to be determined: we say that a flow f is maximal, if f maximizes

$$|f| = \sum_{u \in V,(s,u) \in E} f(s,u) - \sum_{u \in V,(u,s) \in E} f(u,s),$$

i.e., if the net flow pumped out of s is maximal.

We say that input (G,s,t,c) belongs to FP iff all capacities are natural numbers and the maximal flow is odd. It turns out that the flow problem, even as an optimization problem can be solved with the help of linear programming and hence FP is certainly not harder than LIP or LPP. However FP is still $\mathcal{P}$-complete.

Theorem 9.17 *FP is $\mathcal{P}$-complete.*

Proof: We mention without proof that FP belongs to $\mathcal{P}$ and hence it suffices to show that FP is $\mathcal{P}$-hard. We claim that the reduction M_2-CVP $\leq_{\text{par}}$ FP holds.

Let (S, w) be an input for M_2-CVP and let $G = (V, E)$ be the directed graph of circuit S. We may assume that the output gate of S is an OR-gate: if not, then replace S by two copies of S which are fed into an OR-gate. We know that the fan-out of G is at most two. Moreover we may assume that each input node of G has fan-out one: if an input node has two outgoing edges, then add a copy and distribute the two edges among the original and its copy.

To translate (S, w) into an equivalent input for FP, we define a new graph G^* by adding two new nodes s and t to G. s will be the unique source of G^* and we add connections from s to all sources of G. (The sources of G correspond to the inputs of S.) t will be the unique sink of G^* and we add one connection from the old sink t_G of G to t. (t_G computes the output of the circuit.) Finally we add edges from OR-gates to s and from AND-gates to t.

To define capacities, we first compute a topological sort $\text{nr} : V \to \{1, \ldots, |V|\}$ of G. Assume that G has exactly n nodes. We say that an edge of G is an *internal* edge of G^*. The fanout of a node z of G only counts internal edges leaving z except for the old sink t_G: we set $\text{fanout}(t_G) = 1$ to account for the edge (t_g, s).

- If z is an input node for variable x_i, then set

$$c(s, z) = \begin{cases} 2^{n-\text{nr}(z)} & w_i = 1, \\ 0 & \text{otherwise.} \end{cases}$$

- If z is not an input node, then z receives edges from exactly two nodes x and y. We define

$$c(x, z) = 2^{n-\text{nr}(x)} \text{ and } c(y, z) = 2^{n-\text{nr}(y)}.$$

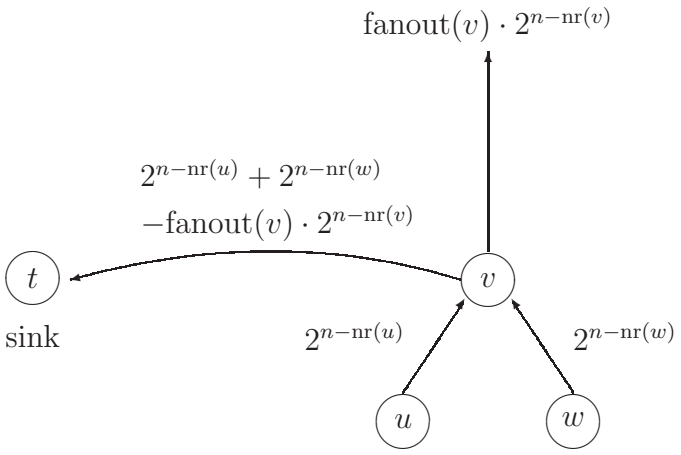
  If z is an AND-gate, then set

$$c(z, t) = 2^{n-\text{nr}(x)} + 2^{n-\text{nr}(y)} - \text{fanout}(z) \cdot 2^{n-\text{nr}(z)},$$

  respectively if z is an OR-gate, then

$$c(z, s) = 2^{n-\text{nr}(x)} + 2^{n-\text{nr}(y)} - \text{fanout}(z) \cdot 2^{n-\text{nr}(z)}.$$

- If $z = t_G$, then $c(t_G, s) = 2^{n-\text{nr}(x)} + 2^{n-\text{nr}(y)} - 1$. We set $c(s_g, t) = 1$ and hence, if t_G receives the maximal possible flow $2^{n-\text{nr}(x)} + 2^{n-\text{nr}(y)}$, the edge (t_G, t) can transport the remaining flow of one to t. Observe that all other nodes have links to t of even capacity.



AND-gates and capacities of incident edges.

We claim that the translation $(S, w) \mapsto (G^*, s, t, c)$ establishes a reduction from M_2-CVP to FP.

As a first step we determine a maximal flow f^*. We set $f^*(s, z) = c(s, z)$ and hence we pump a flow of $2^{n-\mathrm{nr}(z)}$ into z whenever the input bit of gate z is one. Observe that only one edge is leaving z. This edge has capacity $2^{n-\mathrm{nr}(z)}$ and will be completely filled by f^*. If however the input bit of z is zero, then we just move flow zero across the one edge leaving z. We maintain the following policy for all other nodes z of G:

(1) if z evaluates to one, then fill its fan-out(z) many internal edges to capacity and push the excess flow to s respectively to t. If $z = t_g$, then push flow one along edge (t_G, t).

(2) if z evaluates to zero, then push zero flow along its fan-out(z) many internal edges and any excess flow to s respectively to t.

Exercise 100
Show that f^* is a flow.

To show that f^* is a maximal flow, we define the node sets

$$\begin{aligned} V_1 &= \{s\} \cup \{z \in G \mid \text{the gate } z \text{ evaluates to one }\} \\ V_0 &= \{t\} \cup \{z \in G \mid \text{the gate } z \text{ evaluates to zero }\}. \end{aligned}$$

By property (1) of f^*, all internal edges from a node in V_1 to a node in V_0 are filled to capacity. Edges from AND-gates in V_1 to t are also filled to capacity, whereas edges from OR-gates in V_1 stay in V_1. The edge (s_g, t) is filled to capacity as well, provided t_G evaluates to one. Hence all edges from a node in V_1 to a node in V_0 are filled to capacity.

By property (2) f^* pushes zero flow across all internal edges from a node in V_0 to a node in V_1. Edges from AND-gates in V_0 to t stay within V_0. An OR-gate in V_0 receives zero flow along its two internal edges and hence an OR-gate in V_0 has no flow to distribute.

Since the edge (t_G, t) stays inside V_0 if $t_G \in V_0$, all edges from a node in V_0 to a node in V_1 receive zero flow.

But then f^* maximizes

$$\text{value}(g) = \sum_{x \in V_1, y \in V_0, (x,y) \in E} g(x,y) - \sum_{x \in V_0, y \in V_1, (x,y) \in E} g(x,y)$$

among all flows g.

Exercise 101
Show that value$(g) = |g|$ holds for any flow g.

Thus f^* is a maximal flow. We are done, if we can show

Claim 9.1 *$|f^*|$ is odd iff S accepts w.*

Remember that the old sink t_G is the only node which may push a flow of one to t, whereas all other nodes push either zero flow or even flow to t. But t_G pushes flow one iff it evaluates to one, that is iff the circuit accepts the input w. □

Exercise 102
Why do we leak out excess flow of AND-gates to t and excess flow of OR-gates to s?

Exercise 103
Let $G = (V_1 \cup V_2, E)$ be a bipartite graph with $n = |V_1| = |V_2|$, i.e., all edges are incident with a node in V_1 and a node of V_2. We associate a matrix $A = (A_{i,j})$ of indeterminantes with G by setting

$$A_{i,j} := \begin{cases} X_{i,j} & (v_i, v_j) \in E, \\ 0 & \text{otherwise.} \end{cases}$$

Show that G has a perfect matching iff the determinant of A is not the zero-polynomial. (A matching is a set of node-disjoint edges. A matching M is perfect, if all nodes are endpoint of some edge of M.)

Exercise 104
Decide whether a given bipartite graph has a perfect matching. You may use a randomized MPI algorithm with poly-logarithmic run time and polynomially many processors.

Hint: the determinant can be computed in poly-logarithmic run time by an MPI algorithm with polynomially many processors. Moreover you may utilize that a polynomial $p \not\equiv 0$ (with n indeterminants) of degree d does not vanish on an input from $\{-d, \ldots, d\}^n$ with probability at least $\frac{1}{2}$.

Exercise 105
Show with the help of the constant depth reduction $\leq_C$ that

- MATCHING: Does the bipartite graph G have a matching of size at least k?
- NETZWORK-FLOW: Does a network have a flow of at least k? (We require that all capacities are polynomially bounded (in $|V|$) natural numbers.)

possess also randomized $\mathcal{NC}$ algorithms.

Hence by checking all flow-values we can determine in randomized $\mathcal{NC}$, if the maximal flow is even or odd, *provided* capacities are polynomially bounded. Our negative result on network flow suggests that the polynomial bound is crucial.

9.3.3 Parallelizing Sequential Programs

When is it possible to parallelize sequential programs? We first consider the simple greedy heuristic for the independent set problem of Section 13.3 and ask whether we can find a fast parallel program with identical output.

Algorithm 9.18 **A simple heuristic**

$I := \emptyset$;

for $v = 1$ to n do

If (v is not connected with a node from I) then

$I = I \cup \{v\}$;

In the Lexicographically First Maximal Independent Set problem (LFMIS) we are given an undirected graph $G = (\{1, \ldots, n\}, E)$ and a node v. The pair (G, v) belongs to LFMIS iff v belongs to the set I computed by Algorithm 9.18.

Before showing that LFMIS is $\mathcal{P}$-complete we determine longest paths in a directed acyclic graph $G = (V, E)$.

Lemma 9.19 *The all-pairs-longest path problem for a directed acyclic graph G with n nodes can be solved in time $O(\log_2^2 n)$ with n^3 processors.*

Proof: We proceed as in Lemma 9.6 and reduce the all-pairs-longest-path problem to a problem in matrix multiplication. In particular, for $n \times n$ matrices X and Y we introduce a non-standard matrix multiplication by setting

$$X * Y[u, v] = \max_{w \in V} X[u, w] + Y[w, v].$$

Let A be the adjacency matrix of G and assume that the diagonal of A is zero, i.e., G has no self-loops. Then

$$A^k[u, v] = \max_{w_1, \ldots, w_{k-1}} A[u, w_1] + A[w_1, w_2] + \cdots + A[w_{k-1}, v]$$

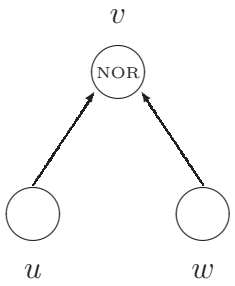
and hence $A^k[u, v]$ is the length of a longest path $u \xrightarrow{*} v$, among all paths $u \xrightarrow{*} v$ of length at most k. In particular $A^{n-1}[u, v]$ is the length of a longest path from u to v.

We may compute A^{n-1} by computing the matrix powers $A^2, \ldots, A^{2^i}, A^{2^{i+1}}, \ldots, A^{2^t}$ for $t = \lceil \log_2 n \rceil$ and hence time $O(\log_2^2 n)$ with n^3 processors is sufficient. Observe that the matrix product allows to traverse nodes multiple times and hence we have to require G to be acyclic. □

Theorem 9.20 *LFMIS is $\mathcal{P}$-complete.*

Proof: It is obvious that LFMIS belongs to $\mathcal{P}$. We show that LFMIS is $\mathcal{P}$-hard, by showing the reduction NOR-CVP $\leq_{\text{par}}$ LFMIS.

The idea of the reduction is simple. Let (S, w) be an input for NOR-CVP and let G be the directed graph for circuit S. A NOR gate



"fires", if both u and w evaluate to zero. Thus all nodes that evaluate to one form an independent set I. However how to make sure that Algorithm 9.18 picks I? We modify G and change the names of nodes.

We first determine a topological sort of G, that is a bijection $\pi : V \to \{1, \ldots n\}$ such that $\pi(u) < \pi(v)$ for any edge (u, v). Let length(v) be the length of a longest path ending in v. To determine a topological sort we replace each node v by the pair (length$(v), v)$ and sort all pairs. Since length(v) can be determined fast with Lemma 9.19, a topological sort can be computed fast.

Now replace the name of a node by its rank within the topological sort. Thus the smallest number is given to a source which may however evaluate to zero. Since the node with smallest number will belong to the independent set, we invent a new node 0 and connect 0 with all sources which evaluate to 0. We call the new (undirected) graph G^*.

Claim 9.2 *Algorithm 9.18 determines for G^* the independent set*

$$I = 0 \cup \{z \mid z \text{ evaluates to one }\}.$$

Observe that we are done, if claim 9.2 holds: we define the translation $(S, w) \mapsto (G^*, n)$ and S accepts w iff the sink n of G evaluates to one.

Proof of Claim 9.2: Certainly 0 is chosen, since it has the smallest number. The remaining nodes of G are processed by Algorithm 9.18 according to their topological number and we therefore argue inductively.

Case 1: z is an input node of G. Then z is either a source, which is equivalent to z evaluating to one, or z receives an edge from 0. In the first case z will be inserted into I and in the second case 0 prevents an insertion of z.

Case 2: z is not a source and z fires. We already observed that a NOR gate fires, if its two immediate predecessors evaluate to zero. By induction hypothesis the two predecessors have not been chosen and thus z is included into I.

Case 2: z is not a source and z does not fire. Then at least one immediate predecessor of z fires and hence has been included into I. Thus z is not chosen. □

The depth-first search algorithm is another famous sequential algorithm which is notoriously hard to parallelize. In the Ordered Depth-First Search problem (ODFS), the input consists of a directed graph $G = (V, E)$ and the three nodes $s, u, v \in V$. The quadruple (G, s, u, v) belongs to ODFS iff node u is visited before node v in the depth-first search started in node s. (Observe that the depth-first search traversal is uniquely defined, once we specify the adjacency list representation of the graph.)

Theorem 9.21 *ODFS is $\mathcal{P}$-complete.*

Proof: See [Ja92]. □

9.4 Conclusion

We have introduced the space complexity of sequential computations with the help of off-line Turing machines and have observed that all languages recognizable by a nondeterministic off-line Turing machine within logarithmic space are parallelizable. Moreover it turns out that circuit depth and space are polynomially related, provided we consider only uniform circuits, i.e., circuit families whose circuits are easy to construct. This observation is evidence for the parallel computation thesis which calls a parallel model of computation unreasonable, if its parallel time is not polynomially related to space complexity. There is further evidence for the parallel computation thesis, since all known "reasonable" models of parallel computation such as MPI algorithms, parallel register machines or circuits satisfy the polynomial relationship.

The "parallel reducibility" $\leq_{\text{par}}$ allows us to compare two languages with respect to their complexity for parallel algorithms. We have defined $\mathcal{P}$-complete languages as those languages in $\mathcal{P}$ which are at least as hard to parallelize as any other problem in $\mathcal{P}$. We have seen that the Circuit Value problem is a generic $\mathcal{P}$-complete problem which for instance allows us to show that Linear Programming and Network Flow are $\mathcal{P}$-complete. We

also considered the problem of parallelizing sequential programs and have shown that the Lexicographically First Maximal Independent Set problem and the Ordered Depth-First Search problem are in all likelihood not parallelizable. Further $\mathcal{P}$-complete problems can be found in [GHR95].

Chapter 10

Linear Programming

In linear programming a linear objective function

$$\sum_{i=1}^{n} c_i x_i$$

is to be minimized subject to linear constraints $\sum_{j=1}^{n} A[i,j] \cdot x_j \geq b_i$ for $j = 1, \ldots, m$ and to non-negativity constraints $x_1 \geq 0, \ldots, x_n \geq 0$. The vector $x = (x_1, \ldots, x_n)$ is a vector of real numbers. Thus, if A is the $m \times n$ matrix with $A = (A[i,j])_{1 \leq i \leq m, 1 \leq j \leq n}$, $c = (c_1, \ldots, c_n)$ and $b = (b_1, \ldots, b_m)$ is the vector of right hand sides, then we have to solve the minimization problem

$$\min c^T \cdot x \text{ s.t. } A \cdot x \geq b \text{ and } x \geq 0. \tag{10.1}$$

Linear programs have many important applications in computer science (flow problems, matching, scheduling) and business (logistics). Moreover, efficient sequential algorithms such as interior point methods exist and, in a sense, linear programming is the most powerful class of optimization problems with efficient algorithmic solutions. Thus the main question is the existence of parallel algorithms with substantial speedups, but, as we see in section 10.1, substantial speedups cannot be expected in general and therefore we consider the restricted class of *positive linear programs* in section 10.2.

10.1 Linear Programming

In the Linear Inequalities problem (LIP) we are given an $m \times n$ matrix $A \in \mathbb{Z}^{m \cdot n}$ and a vector $b \in \mathbb{Z}^m$. The pair (A, b) belongs to LIP iff the system $A \cdot x \geq b$ of linear inequalities has a solution.

In the Linear Programming Problem LPP we receive the same input as in LIP, but obtain additionally a vector $c \in \mathbb{Z}^n$ and a rational number α. The quadruple (A, b, c, α)

belongs to LPP iff there is a vector x that solves the linear system $A \cdot x \geq b$ and also satisfies $c^T x \leq \alpha$. Thus LPP is the language version of Linear Programming.

Theorem 10.1

(a) LIP is $\mathcal{P}$-complete, even if all parameters are either $-1, 0$ or 1.

(b) LPP is $\mathcal{P}$-complete, even if all parameters are either $-1, 0$ or 1.

Proof: Both LIP and LPP belong to $\mathcal{P}$ due to efficient algorithms by Karmarkar [Ka84] and Khachiyan [Kh79] and hence it suffices to show $\mathcal{P}$-hardness. **(a)** We verify the reduction M-CVP $\leq_{\text{par}}$ LIP. Let (S, w) be an input of M-CVP. We assign linear inequalities to any node c of the monotone circuit S.

Case 1: c is a source storing the ith input bit. Use the inequalities

$$\begin{array}{ll} x_c \geq 0,\ -x_c \geq 0 & \text{if } w_i = 0, \\ x_c \geq 1,\ -x_c \geq -1 & \text{if } w_i = 1. \end{array}$$

Case 2: $c \equiv a \wedge b$ is an AND-gate. This time we use the inequalities

$$x_a - x_c \geq 0,\ x_b - x_c \geq 0,\ x_c - x_a - x_b \geq -1,\ x_c \geq 0.$$

Case 3: $c \equiv a \vee b$ is an OR-gate. Now we choose

$$x_c - x_a \geq 0,\ x_c - x_b \geq 0,\ x_a + x_b - x_c \geq 0,\ -x_c \geq -1.$$

We show inductively that x_c coincides with the value of gate c, if w is the input for S. We observe that the variables x_c for sources c are forced in Case 1 to take on the value of the corresponding input bit. If $c \equiv a \wedge v$, then we already know that x_a and x_b coincide with the values of gates a and b respectively. Thus $x_a, x_b \in \{0, 1\}$ and an inspection of Case 2 shows that x_c has to coincide with the value of gate c. The argument for $c \equiv a \wedge v$ is similar.

Finally, if t is the output gate of the circuit, then we add the inequality $x_t \geq 1$ to the system. The claimed reduction of M-CVP to LIP follows, since the translation from (S, w) to the system of inequalities is computable in poly-logarithmic time with a polynomial number of processors.

(b) The reduction LIP $\leq_{\text{par}}$ LPP is immediate, if we choose the translation $(A, b) \mapsto (A, b, \vec{0}, 0)$, since the existence of a solution x with $A \cdot x \geq b$ and $0^T \cdot x \geq 0$ is equivalent to the existence of a solution of $A \cdot x \geq b$. □

10.2 Positive Linear Programs

Definition 10.2 The linear program (10.1) is called positive iff $A[i.j] \geq 0, b_i \geq 0$ and $c_i \geq 0$ for all i and j. A positive linear program is also called a *covering problem*.

Example 10.1 Assume we are given the universe $U = \{1, \ldots, n\}$ and subsets $S_1, \ldots, S_k \subseteq U$ with weights $c_1, \ldots, c_k$. The *SET COVER* problem asks to determine a cover $S_{i_1}, \ldots, S_{i_r}$ of the universe U (i.e., $\bigcup_{j=1}^{r} S_{i_j} = U$) of minimal weight $\sum_{j=1}^{r} c_{i_j}$. We translate SET COVER into the positive linear program

$$\min \sum_{i=1}^{k} c_i \cdot x_i \text{ s.t. } A \cdot x \geq 1 \text{ and } x \geq 0,$$

where A is an $n \times k$ matrix with a row for every element $u \in U$ and a column for every subset S_i such that $A[u, i] = 1$, if u belongs to subset S_i, and $A[u, i] = 0$ otherwise. No integral solution my be optimal, but one can show that the best fractional and the best integral solutions are by at most a factor of $O(\log_2 n)$ apart.

We say that the linear program

$$\max b^T \cdot y \text{ s.t. } A^T \cdot y \leq c \text{ and } y \geq 0 \tag{10.2}$$

is the dual program of the primal problem (10.1). The dual of a positive linear program is also called a *packing problem*. The Duality Theorem captures the important property of linear programs, namely that primal and dual program have identical optimal values.

Fact 10.1 *Duality Theorem.*

If the primal or the dual program have solutions, then

$$\max b^T \cdot y \ (s.t.\ A^T \cdot y \leq c, y \geq 0) \ = \ \min c^T \cdot x \ (s.t.\ A \cdot x \geq b, x \geq 0).$$

The weak duality theorem, namely the statement

$$\max b^T \cdot y \ (\text{s.t. } A^T \cdot y \leq c, y \geq 0) \ \leq \ \min c^T \cdot x \ (\text{s.t. } A \cdot x \geq b, x \geq 0)$$

can be verified easily, since

$$b^T \cdot y \leq (A \cdot x)^T \cdot y = x^T \cdot (A^T \cdot y) \leq x^T \cdot c = c^T \cdot x.$$

Example 10.2 In the *MATCHING* problem we are given a bipartite graph $G = (V_0 \cup V_1, E)$ and our goal is to find a matching[1] of maximal size. (We assume that all edges have exactly

[1] A matching $M \subseteq E$ is a collection of edges such that no two edges have an endpoint in common.

one endpoint in common with V_0 and one endpoint in common with V_1.) We formalize MATCHING as the maximization problem

$$\max \sum_{e \in E} y_e \text{ s.t. } A_G \cdot y \leq 1 \text{ and } y \geq 0$$

with unknowns y_e for every edge $e \in E$. The incidence matrix A_G of G has a row for every node $u \in V_0 \cup V_1$ and a column for every edge $e \in E$; in particular $A_G[u, e] = 1$ iff node u is an endpoint of edge e and $A_G[u, e] = 0$ otherwise. Although we allow fractional values y_e, it can be shown that an optimal solution y with $y_e \in \{0, 1\}$ for all edges $e \in E$ exists. Let us have a look at the primal problem

$$\min \sum_{v \in V_0 \cup V_1} x_v \text{ s.t. } A_G^T \cdot x \geq 1, x \geq 0.$$

Again one can show that optimal solutions x with $x_v \in \{0, 1\}$ for all nodes $v \in V_0 \cup V_1$ exist and we can translate the primal problem as follows: determine a subset $W \subseteq V_0 \cup V_1$ of minimal size such that all edges in E have at least one endpoint in W. Thus we are looking for a vertex cover of minimal size. Observe that the primal problem is a positive linear program.

Example 10.3 In the *INDEPENDENT SET* problem we are given an undirected graph $G = (V, E)$. Our goal is to determine an independent set[2] of maximal size. We translate INDEPENDENT SET into the following linear program:

$$\max \sum_{v \in V} x_v \text{ s.t. } x_u + x_v \leq 1 \text{ for every edge } e = \{u, v\} \text{ and } x \geq 0.$$

The dual problem has one dual variable y_e for every primal constraint. Thus we get the positive linear program

$$\min \sum_{e \in E} y_e \text{ s.t. } \sum_{e, v \in e} y_e \geq 1 \text{ for every node } v \text{ and } y \geq 0.$$

If all variables have only values in $\{0, 1\}$, then we are looking for a subset of edges of minimal size such that all nodes are covered by at least one edge.

The independent set problem is very hard to approximate and consequently the gaps between integral and fractional solutions may be large: observe that the vector $(1/2, \ldots, 1/2)$ is a solution of the fractional program and hence the fractional optimum is at least $\frac{|V|}{2}$. However the complete graph with V as its set of nodes has only independent sets of size 1.

[2] $I \subseteq V$ is an independent set iff no two nodes in I are connected by an edge.

10.2.1 A Parallel Algorithm

We assume that the constraint matrix A in (10.1) has m rows and n columns. Our goal is to compute an almost optimal solution of the positive linear program.

$$\min c^T \cdot x \text{ s.t. } A \cdot x \geq b \text{ and } x \geq 0.$$

We work with p processes which use a $\sqrt{p} \times \sqrt{p}$ mesh of processes. In particular, process (i, j) is responsible for all constraints u with $u \in R_i = \{(i-1) \cdot \frac{m}{\sqrt{p}} + 1, \ldots i \cdot \frac{m}{\sqrt{p}}\}$ and for all components x_v with $v \in C_j = \{(j-1) \cdot \frac{n}{\sqrt{p}} + 1, \ldots j \cdot \frac{n}{\sqrt{p}}\}$. We say that the submatrix $A^{(i,j)}$ consisting of all rows in R_i and all columns in C_j belongs to process (i, j).

Claim 10.1 *We may assume $b_u = 1$ for $u = 1, \ldots, m$ and $A[u, v] = 0$ or $A[u, v] \geq 1$. Moreover $\max_v c_v = 1$ without loss of generality.*

Proof: First divide each primal constraint $\sum_{v=1}^{n} A[u, v] \cdot x_v \geq b_u$ by its right hand side b_u. (If $b_u = 0$, then the constraint can be dropped.) Thus, in particular, each entry $A[u, v]$ is to be replaced by $A[u, v]/b_u$ and b_u is to be replaced by 1. We now assume that $b_u = 1$ holds for all u.

Next divide $A[u, v]$ as well as c_v by $\lambda_v = \min\{A[u', v] \mid A[u', v] > 0 \text{ and } 1 \leq u' \leq m\}$. In other words, we divide $A[u, v]$ and c_v by the smallest non-zero entry in column v. To verify that this transformation does not change the optimal value, observe that the previous jth dual constraint $\sum_{u=1}^{m} A[u, v] \cdot y_u \leq c_v$ is replaced by the equivalent constraint $\sum_{u=1}^{m} A[u, v] \cdot y_u/\lambda_v \leq c_v/\lambda_v$.

Finally replace each c_v by $\frac{c_v}{\max_v c_v}$ and the new and old objective function have identical optimal solutions. □

Exercise 106
Assume that x and y are optimal primal and dual solutions after applying the two transformations. How do obtain optimal solutions for the original parameters A, b and c?

Claim 10.2 *Assume that the matrix A has only a single row. If $\frac{A[1,v]}{c_v} = \max_w\{\frac{A[1,w]}{c_w}\}$, then $\sum_{v=1}^{n} c_v \cdot x_v$, subject to $\sum_{v=1}^{n} A[1, v] \cdot x_v \geq 1$, is minimized by setting all variables, except for x_v, to zero.*

Proof: We interpret c_v as the price of item v and $A[1, v]$ as its value. Thus in the single-row minimization problem we have to buy items of value at least one as cheaply as possible. Intuitively we should choose the item with the largest "value-per-cost" ratio. Indeed, if we replace x_v by $z_v = c_v \cdot x_v$, then we have to minimize $\sum_{v=1}^{n} z_v$ subject to $\sum_{v=1}^{n} \frac{A[1,v]}{c_v} \cdot z_v \geq 1$ and we should choose the required quantity of the item v maximizing $\frac{A[1,v]}{c_v}$. □

If A has many rows, then we follow a greedy approach. In particular, we define the value-per-cost ratio

$$\gamma_v = \sum_{u=1}^{m} \frac{A[u,v]}{c_v} \cdot r_u,$$

where $r_u = 1$ holds initially for all u. Thus initially we assign relevance $r_u = 1$ to all constraints u and try to satisfy as many constraints as possible as cheaply as possible by incrementing only variables x_v with large value-per-cost ratio γ_v. We start from $x_v = 0$ and increment x_v by using the geometrically increasing sequence $1/\lambda^L, 1/\lambda^{L-1}, \ldots, 1/\lambda^{L-L} = 1$ of increments; the parameters $\lambda > 1$ and L will be determined later.

However we have to be prepared to adjust our approach during the computation. Whenever a primal constraint u is satisfied, then all value-per-cost ratios of primal variables x_v with $A[u,v] > 0$ should be recomputed, since we should increase x_v only due to unsatisfied constraints w with $A[w,v] > 0$. Therefore we introduce new parameters r'_u with $r'_u = r_u$ for not yet satisfied constraints, $r'_u = 0$ for satisfied constraints and recompute γ_v with r'_u replacing r_u.

The following incrementation procedure is called several times. Before the first call we have $r_u = 1$ for all constraints u and $x_v = 0 = y_u$ for the dual variable y_u. Moreover we set $W_u = w_u = 0$, where W_u is the total value of constraint u and w_u is the value of constraint u restricted to the current phase. W_u, w_u and y_u are determined with the help of parameters $w_{u,j}$ and $y_{u,j}$.

Algorithm 10.3 Increment(i, j, κ, k)

// We describe process (i,j). Set $r'_u = r_u$ for all constraints u.

for $l = 1$ to L do

(1) Set $w_{u,j} = y_{u,j} = 0$ for all $u \in R_i$.

(2) // Process (i,j) increments x_v if its value-per-cost ratio is sufficiently large.
for all $v \in C_j$ do
if $\gamma_v \geq \kappa^k$ then

$$\begin{aligned} x_v &= x_v + \frac{1}{\lambda^{L-l}} \text{ and for any } u \in R_i \\ w_{u,j} &= w_{u,j} + A[u,v] \cdot \frac{1}{\lambda^{L-l}}, \quad y_{u,j} = y_{u,j} + r'_u \cdot A[u,v] \cdot \frac{1}{\lambda^{L-l}} / \gamma_v. \end{aligned}$$

(3) Results are communicated:

(a) process (i,j) participates in an MPI_Allreduce restricted to its row of processes and sends $w_{u,j}$. Upon completion it knows $w_u = w_u + \sum_j w_{u,j}$, the value of constraint u when restricted to increments of the current phase.

(b) $W_u = W_u + \sum_j w_{u,j}$ is the total value of constraint u over all calls of Increment.

(c) With the same procedure $y_u = y_u + \sum_j y_{u,j}$ is determined.

(d) If $w_u \geq 1$ for $u \in R_i$, then process (i,j) sets $r'_u = 0$. It then determines the vector $\gamma^{(i,j)}$ of value-per-cost ratios for all of its variables x_v with $v \in C_j$, restricted to constraints $u \in R_i$:

$$\gamma_v^{(i,j)} = \sum_{u \in R_i} \frac{A[u,v]}{c_v} \cdot r'_u.$$

(d) Process (i,j) sends $\gamma^{(i,j)}$ in another MPI_Allreduce restricted to its column of processes. Now each process knows γ_v for all its primal variables x_v.

1. Dual Variables

We do not need the dual variables y_u when computing the primal variables, however we need them when analyzing the approximation performance. Therefore we motivate the update of y_u in step (2) first. Remember that all right hand sides b_u equal one and hence the objective function of the dual maximization problem is the sum of the dual variables.

Claim 10.3

(a) After incrementing y_u in step (2), $\sum_u y_u = \sum_u y_u + \sum_{v,\gamma_v \geq \kappa^k} c_v \cdot \frac{1}{\lambda^{L-l}}$.

(b) At all times $\sum_u y_u = \sum_v c_v \cdot x_v$.

Proof: (b) follows immediately from (a) and we restrict ourselves to (a).

$$\begin{aligned}
\sum_u y_u &= \sum_u y_u + \sum_u r'_u \cdot \sum_{v,\gamma_v \geq \kappa^k} A[u,v] \cdot \frac{1}{\lambda^{L-l}} / \gamma_v \\
&= \sum_u y_u + \sum_{v,\gamma_v \geq \kappa^k} \frac{1}{\lambda^{L-l}} \cdot \sum_u A[u,v] \cdot r'_u / \gamma_v \\
&= \sum_u y_u + \sum_{v,\gamma_v \geq \kappa^k} \frac{1}{\lambda^{L-l}} \cdot \sum_u A[u,v] \cdot r'_u / \sum_u \frac{A[u,v]}{c_v} \cdot r'_u \\
&= \sum_u y_u + \sum_{v,\gamma_v \geq \kappa^k} c_v \cdot \frac{1}{\lambda^{L-l}}.
\end{aligned}$$

Thus step (2) enforces that each incrementation step has identical primal and dual contributions. *If* our primal and dual vectors are feasible solutions after a call of "Increment", then we have found an optimal solution as a consequence of the duality theorem.

2. More Calls of Increment

We cannot expect x to be a feasible solution after the first call of "Increment", since constraints with too few primal variables of high relevance remain unsatisfied. Moreover, even if we have satisfied all constraints, we cannot be sure that our solution is approximately optimal. Therefore we make a second attempt and call "Increment" again. However we first recompute r_u to reflect the need of satisfying constraint u: decrease r_u whenever $w_u \geq 1$ and hence whenever the total value W_u of constraint u has increased by at least one. Hence the value-per-cost ratio γ_v decreases and we therefore lower the hurdle κ^k as well.

We continue calling "Increment" and incrementing x until we can be sure that all constraints are satisfied at least f times where f will be defined later. Finally we rescale x_v by setting $x_v = x_v / \min_u\{W_u \mid A[u,v] > 0\}$. Observe that for any u'

$$\sum_v A[u',v] \cdot \frac{x_v}{\min_u\{W_u \mid A[u,v] > 0\}} \geq \sum_v A[u',v] \cdot \frac{x_v}{W_{u'}} = 1$$

and we obtain a feasible solution which hopefully approximates well. Dual variables are treated analogously: set $y_u = y_u / \max_v\{\sum_{u'} A[u',v] \cdot y_{u'}/c_v \mid A[u,v] > 0\}$ and for any v'

$$\begin{aligned} & \sum_u A[u,v'] \cdot \frac{y_u}{\max_v\{\sum_{u'} A[u',v] \cdot y_{u'}/c_v \mid A[u,v] > 0\}} \\ \leq & \sum_u A[u,v'] \cdot \frac{y_u}{\sum_{u'} A[u',v'] \cdot y_{u'}/c_{v'}} = c_{v'}. \end{aligned}$$

Here is the global structure of our approach.

Algorithm 10.4 A description of process (i,j).

(0) Initially $r_u = 1$, $x_v = y_u = 0$ as well as $W_u = w_u = 0$.

(1) for $k = K$ down to $-f+1$ do

Repeat until $\gamma_v \leq \kappa^{k+1}$ for all $v \in C_j$

(a) Set $r'_u = r_u$ for all constraints u and call Increment(i,j,κ,k).

(b) If $W_u \geq f$, then set $r_u = 0$. // We disregard constraint u from now on. Otherwise $r_u = r_u/\kappa^{\lfloor w_u \rfloor}$. // r_u is decreased iff $w_u \geq 1$.

(b) $w_u = w_u - \lfloor w_u \rfloor$.
// Show $W_u = \lfloor W_u \rfloor + w_u$ by induction. Observe that $r_u = 1/\kappa^{\lfloor W_u \rfloor}$.

(3) For any $v \in C_j$, divide x_v by $\min_u\{W_u \mid A[u,v] > 0\}$. For any $u \in R_i$ divide y_u by $\max_v\{\sum_{u'} A[u',v] \cdot y_{u'}/c_v \mid A[u,v] > 0\}$.

3. Analyzing the Approximation Performance

Assume that each primal constraint has value at least f and each dual constraint has value at most g. Then $\frac{1}{g} \cdot \sum_u y_u \leq \text{opt} \leq \frac{1}{f} \cdot \sum_v c_v \cdot x_v$ with the weak duality theorem. By Claim 10.3 we know that $\sum_v c_v \cdot x_v = \sum_u y_u$ before rescaling primal and dual variables in step (3) and consequently

$$\frac{1}{g} \cdot \sum_v c_v \cdot x_v \leq \text{opt} \leq \frac{1}{f} \cdot \sum_v c_v \cdot x_v.$$

Thus $\frac{f}{g}(\frac{1}{f} \cdot \sum_v c_v \cdot x_v) = \frac{1}{g} \cdot \sum_v c_v \cdot x_v \leq \text{opt}$ and we have shown:

Claim 10.4 *If each primal constraint has value at least f and each dual constraint has value at most g, then the approximation factor is at most $\frac{g}{f}$.*

But is the value of each primal constraint indeed at least f?

Claim 10.5 *If algorithm 10.4 stops, then $W_u \geq f$ for every constraint u.*

Proof: We pick a constraint u arbitrarily and consider an arbitrary variable x_v appearing in u, i.e., $A[u, v] > 0$. We have $\gamma_v = \sum_w \frac{A[w,v]}{c_v} \cdot r'_w \geq \frac{A[u,v]}{c_v} \cdot r'_u \geq r'_u$, since $A[u, v]/c_v \geq 1$ by Claim 10.1.

Assume that constraint u is *not* satisfied when calling "Increment" for hurdle κ^k with $-f+1 \leq k \leq 0$. Then, after "Increment" terminates, $r'_u = r_u$, since u is not satisfied during the call, and $r_u < \kappa^k$, since otherwise $\gamma_v \geq r'_u = r_u \geq \kappa^k$ and x_v is finally incremented by $1/\lambda^{L-L} = 1$ satisfying constraint u after all. But $r_u = 1/\kappa^{\lfloor W_u \rfloor}$ and hence $\lfloor W_u \rfloor \geq -k + 1$. Thus for any call of "Increment" for k with $-f + 1 \leq k \leq 0$ we have $\lfloor W_u \rfloor \geq -k + 1$ or constraint u will be satisfied. But then $\lfloor W_u \rfloor \geq 1$ for $k = 0$ as well as $\lfloor W_u \rfloor \geq -k + 1$ by an inductive argument. The claim follows. □

4. Bounding Dual Variables

To obtain a good upper bound on g we have to bound the dual variables y_u. We observe the growth of y_u at the at most f time steps $t_1, \ldots, t_f$ at which constraint u is satisfied. Assume that constraint u has been satisfied at time t_i after calling Increment with parameter k in step (1a) and let y_u^+ be the increment of y_u obtained during the time interval $]t_{i-1}, t_i]$. We now restrict our attention to this time interval.

Whenever the primal variable x_v is incremented in step (2) of Increment(i, j, κ, k), y_u^+ increases by

$$r'_u \cdot A[u, v] \cdot \frac{1}{\lambda^{L-l}}/\gamma_v \leq r_u \cdot A[u, v] \cdot \frac{1}{\lambda^{L-l}}/\gamma_v \leq r_u \cdot A[u, v] \cdot \frac{1}{\lambda^{L-l}}/\kappa^k,$$

since $\gamma_v \geq \kappa^k$ has to hold. But then

$$y_u^+ \leq r_u \cdot (w_u - w'_u)/\kappa^k, \tag{10.3}$$

where w'_u is the initial value of w_u in the current call of Increment. Observe that w'_u is the fractional part of w_u when the previous call terminates at time t_{i-1}. It may happen that we do not account for all of y_u at time t_{i-1}, but omit an amount $s \leq r_u \cdot w'_u/\kappa^k$. However we still get

$$y_u^+ + s \leq r_u \cdot w_u/\kappa^k$$

and can "account" for s during time interval $[t_{i-1}, t_i]$. Whenever u is satisfied we set $r'_u = 0$ in step (3d) of Increment(i, j, κ, k) and hence y_u^+ is not increased any further. We assume that we just satisfied constraint u and moreover assume first that u is satisfied in the very first incrementation step. Remember that Increment(i, j, κ, k) starts with the initial value w'_u for $0 \leq w'_u < 1$. Then $\sum_{v,\gamma_v \geq \kappa^k} A[u, v] \cdot \frac{1}{\lambda^{L-1}}$ is added to w'_u. We would like to show that

$$w'_u + \sum_{v,\gamma_v \geq \kappa^k} A[u, v] \cdot \frac{1}{\lambda^{L-1}} \leq 1 + \lambda$$

holds. Since $w'_u \leq 1$, it suffices to demand

$$\sum_{v,\gamma_v \geq \kappa^k} A[u, v] \leq \lambda^L.$$

The inequality follows, if we choose λ and L such that $\lambda^L \geq \max_u \sum_v A[u, v]$ holds. In general, after satisfying u, its new value is at most "previous value" $+\lambda\cdot$ "previous value" due to step (2) of Increment. Since the previous value is less than one, the new value of constraint u is also in the general case at most $1 + \lambda$ and

$$y_u^+ \leq r_u \cdot (1 + \lambda)/\kappa^k$$

follows throughout.

Now consider the special case that $1 \leq w_u < 2$ holds *after* step (1a). The next call of Increment works with the fractional part $w'_u = w_u - \lfloor w_u \rfloor$ and with $r_u = r_u/\kappa$. We count the contribution $y_u^+ - r_u \cdot w'_u/\kappa^{k+1} \leq r_u \cdot (w_u - w'_u/\kappa)/\kappa^k$ and account for the remaining contribution $s \leq \frac{r_u}{\kappa} \cdot w'_u/\kappa^k$ in the next time interval. We claim $r_u \cdot (w_u - w'_u/\kappa)/\kappa^k \leq r_u \cdot \kappa/\kappa^k$: the inequality is equivalent with $w_u - w'_u/\kappa \leq \kappa$. Maximize the left hand side by setting $w_u = 2$ and verify that $2 - 1/\kappa \leq \kappa$ holds. We summarize:

Claim 10.6 *Assume that $\lambda^L \geq \max_u \sum_v A[u, v]$ holds. If constraint u is satisfied when calling Increment(i, j, κ, k), then*

$$y_u^+ \leq \ r_u \cdot (1 + \lambda)/\kappa^k.$$

Moreover, if $1 \leq w_u < 2$ after the call, then $y_u^+ \leq r_u \cdot \kappa/\kappa^k + r_u \cdot (w_u - \lfloor w_u \rfloor)/\kappa^{k+1}$.

In step (1b) either r_u is unchanged ($w_u < 1$), reduced by the factor $\kappa^{-\lfloor w_u \rfloor}$ or else set to zero ($W_u \geq f$). Since we assume that we just satisfied constraint u, we only have to deal with the last two cases. r_u will be decreased in these two cases and we have to follow its effect on the the upper bound of Claim 10.6. In particular we express the upper bound in dependence of r_u^-, where r_u^- is the reduction of r_u after step (1b).

Case 1: $1 \leq w_u < 2$. We have to account for at most the amount $\beta_u = r_u \cdot \kappa/\kappa^k$ of y_u^+. In step (1b) we set $r_u = r_u/\kappa$ and hence $r_u^- = r_u - r_u/\kappa = r_u(\kappa-1)/\kappa$. As a consequence of Claim 10.6

$$\beta_u = r_u \cdot \kappa/\kappa^k = \frac{\kappa}{\kappa-1} \cdot r_u^- \cdot \kappa/\kappa^k \leq \frac{\kappa \cdot \max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot r_u^-.$$

Case 2: $w_u \geq 2$. We account for $\beta_u = y_u^+$. In step (1b) r_u is divided by at least κ^2 and hence $r_u^- \geq r_u - r_u/\kappa^2 = r_u \cdot (\kappa^2-1)/\kappa^2$. As a consequence of Claim 10.6

$$\begin{aligned}
\beta_u &= y_u^+ \leq r_u \cdot (1+\lambda)/\kappa^k \\
&\leq \frac{\kappa^2}{\kappa^2-1} \cdot r_u^- \cdot (1+\lambda)/\kappa^k \\
&\leq \frac{(1+\kappa)\cdot\kappa\cdot\max\{\kappa,\lambda\}}{(\kappa+1)\cdot(\kappa-1)\cdot\kappa^k} \cdot r_u^- = \frac{\kappa\cdot\max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot r_u^-.
\end{aligned}$$

Case 3: $W_u \geq f$. We again account for $\beta_u = y_u^+$. In step (1b) we set $r_u = 0$ and hence $r_u^- = r_u$. We apply Claim 10.6 again and get

$$\begin{aligned}
\beta_u &= r_u \cdot (1+\lambda)/\kappa^k = r_u^- \cdot (1+\lambda)/\kappa^k \leq \frac{\kappa^2}{\kappa^2-1} \cdot r_u^- \cdot (1+\lambda)/\kappa^k \\
&\leq \frac{(1+\kappa)\cdot\kappa\cdot\max\{\kappa,\lambda\}}{(\kappa+1)\cdot(\kappa-1)\cdot\kappa^k} \cdot r_u^- = \frac{\kappa\cdot\max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot r_u^-.
\end{aligned}$$

We have shown

Claim 10.7 *If constraint u is satisfied when calling Increment(i,j,κ,k) in step (1a), then after step (1b),*

$$\beta_u \leq \frac{\kappa\cdot\max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot r_u^-.$$

5. The Growth of Dual Constraints

We continue our "accounting procedure" for controlling the growth of y_u respectively of the dual constraints by counting an increase only, when constraint u is satisfied. Hence we evaluate the dual constraint v for the increments β_u after step (1b) and get with Claim 10.7

$$\sum_u A[u,v]\cdot\beta_u = c_v \cdot \sum_u \frac{A[u,v]}{c_v}\cdot\beta_u \leq c_v \cdot \frac{\kappa\cdot\max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot \sum_u \frac{A[u,v]}{c_v}\cdot r_u^-$$

Remember that $\gamma_v = \sum_u \frac{A[u,v]}{c_v} \cdot r_u$. We set γ_v^- to be the reduction of γ_v after step (1b). How does γ_v^- behave? r_u decreases only if constraint u has just been satisfied and if so, then $r_u = r_u - r_u^-$. Thus $\gamma^- = \sum_u \frac{A[u,v]}{c_v} \cdot r_u^-$ and hence

$$\sum_u A[u,v] \cdot \beta_u \leq c_v \cdot \frac{\kappa \cdot \max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot \sum_u \frac{A[u,v]}{c_v} \cdot r_u^- \leq c_v \cdot \frac{\kappa \cdot \max\{\kappa,\lambda\}}{(\kappa-1)\cdot\kappa^k} \cdot \gamma_v^-.$$

Choose κ and K such that $\gamma_v \leq \kappa^{K+2}$ holds initially for all v. Then the repeat-loop in algorithm 10.4 guarantees that $\gamma_v \leq \kappa^{k+2}$ holds for all k with $k \leq K$ and hence

$$\sum_u A[u,v] \cdot \beta_u \leq c_v \cdot \frac{\kappa^3 \cdot \max\{\kappa,\lambda\}}{\kappa-1} \cdot \frac{\gamma_v^-}{\gamma_v}.$$

Remember that each y_u is the sum of β_u's. Since $\beta_u = 0$, whenever constraint u is not satisfied, we may sum over all times at which step (1b) is executed. We begin algorithm 10.4 with $\gamma_v \leq \kappa^{K+2}$ and end up with $\gamma_v = 0$. In between we produce the sequence $\kappa^{K+2} \geq \gamma_v(0) \geq \gamma_v(1) \geq \cdots \geq \gamma_v(t) \geq \kappa^{-f+1} > \gamma_v(t+1) = 0$. We set $\gamma_v^-(i) = \gamma_v(i) - \gamma_v(i+1)$ and hence

$$\sum_u A[u,v] \cdot y_u \leq c_v \cdot \frac{\kappa^3 \cdot \max\{\kappa,\lambda\}}{\kappa-1} \cdot \sum_{i=0}^{t} \frac{\gamma_v^-(i)}{\gamma_v(i)}.$$

Exercise 107
Show $\sum_{i=0}^{t} \frac{\gamma_v^-(i)}{\gamma_v(i)} \leq \int_{\kappa^{-f+1}}^{\kappa^{K+2}} \frac{dx}{x} = (K+f+1)\cdot\ln\kappa$.

As a consequence of the exercise we obtain

$$\begin{aligned}\sum_u A[u,v]\cdot y_u &\leq c_v \cdot \frac{\kappa^3\cdot\max\{\kappa,\lambda\}}{\kappa-1}\cdot(K+f+1)\cdot\ln\kappa \\ &\leq c_v\cdot\kappa^3\cdot\max\{\kappa,\lambda\}\cdot(K+f+1),\end{aligned}$$

since $\ln\kappa = \ln(\kappa-1+1) \leq \kappa-1$ with Lemma 1.2.

6. Approximation Performance

Thus, if we divide all dual variables by $g = \kappa^3\cdot\max\{\kappa,\lambda\}\cdot(K+f+1)$, then we have determined a feasible dual solution. We apply Claim 10.4 and conclude that the primal solution x/f is $\frac{g}{f}$-approximate. **We set** $f = \frac{K+1}{\kappa-1}$ and obtain

$$\begin{aligned}\frac{g}{f} &= \frac{\kappa^3\cdot\max\{\kappa,\lambda\}\cdot(K+f+1)}{f} \\ &= \frac{\kappa^3\cdot\max\{\kappa,\lambda\}\cdot(K+\frac{K+1}{\kappa-1}+1)}{\frac{K+1}{\kappa-1}} \\ &= \kappa^4\cdot\max\{\kappa,\lambda\}.\end{aligned}$$

We now have to decide how to set the remaining unspecified parameters κ, K and λ, L. Certainly κ and λ should be chosen as small as possible to keep the approximation factor small. **We set** $\kappa = \lambda = 1 + \varepsilon$ and the approximation factor is bounded by

$$(1+\varepsilon)^5 = 1 + 5 \cdot \varepsilon + O(\varepsilon^2).$$

7. The Number of Rounds

Finally we determine the number of rounds. We require that $\gamma_v \leq \kappa^{K+2}$ holds initially for all v and hence $K = \log_{1+\varepsilon}(\max_v \sum_u \frac{A[u,v]}{c_v}) - 2$.

Exercise 108
Show $\log_{1+\varepsilon} N = (\log_{1+\varepsilon} 2) \cdot \log_2 N$ and $\log_{1+\varepsilon} 2 = \Theta(\frac{1}{\varepsilon})$.

Set $P = \log_2(\max_v \sum_u \frac{A[u,v]}{c_v}) - 2$ and $\gamma_v \leq \kappa^{K+2}$ holds initially for all v, provided $K = \Theta(\log_2(P)/\varepsilon) - 2$. For Claim 10.6 to hold we have demanded $\lambda^L \geq \max_u \sum_v A[u,v]$ and hence we set $L = \log_{1+\varepsilon}(\max_u \sum_v A[u,v]) = \Theta(\log_2(D)/\varepsilon)$, where $D = \max_u \sum_v A[u,v]$.

Exercise 109
Show that the "repeat-until" statement of algorithm 10.4 requires at most

$$\lceil 1 + \frac{K+2}{\kappa \cdot \ln \kappa^K} \rceil = O(1 + \frac{1}{\varepsilon})$$

iterations.

We are particularly interested in tight approximations and hence require $\varepsilon \leq 1$. Then the number of rounds is bounded by

$$\begin{aligned} O((K+f) \cdot (1+\frac{1}{\varepsilon}) \cdot L) &= O((K + \frac{K+1}{\kappa - 1})(1+\frac{1}{\varepsilon}) \cdot L) = O(\frac{K}{\varepsilon} \cdot \frac{1}{\varepsilon} \cdot L) \\ &= O(\frac{P \cdot D}{\varepsilon^4}). \end{aligned}$$

Theorem 10.5 *[KMW06] Assume that* $0 < \varepsilon \leq 1$ *holds.*
Set $\kappa = \lambda = 1+\varepsilon$ *as well as* $K = \log_{1+\varepsilon}(\max_v \sum_u \frac{A[u,v]}{c_v}) - 2$ *and* $L = \log_{1+\varepsilon}(\max_u \sum_v A[u,v])$.
If $P = \log_2(\max_v \sum_u \frac{A[u,v]}{c_v}) - 2$ *and* $D = \max_u \sum_v A[u,v]$, *then*

algorithm 10.4 determines a $(1+\varepsilon)$*-approximate solution in* $O(\frac{\log_2 P \cdot \log_2 D}{\varepsilon^4})$ *rounds.*

Thus the outer k-loop of Algorithm 10.4 with $f = O(\frac{\log_2 P}{\varepsilon^2})$ rounds is particularly expensive. The repeat-until loop of algorithm 10.4 as well as the l-loop of Increment(i, j, κ, K) run for $O(\frac{1}{\varepsilon})$, resp. $O(\frac{\log_2 P}{\varepsilon})$ rounds.

8. Andere Wahl von r_u

(0) Obtaining good approximate solutions fast: a sequence of approximations for $1+\varepsilon_k$ with $\varepsilon_k = 2^{-k}$. How to profit from the previous approximation for $1+\varepsilon_k$ when aiming for $1+\varepsilon_{k+1}$?

(1) $\gamma_v = \sum_{u=1}^{m} \frac{A[u,v]}{c_v} \cdot r_u$ is the value of dual constraint v when evaluated at r_u.

(2) Duality is used only for the analysis but not for the algorithm. As a consequence primal constraints are satisfied (at least) f times, whereas dual constraints may be satisfied up to $K+f$ times: $f = K/\varepsilon$ follows.

- Assume $\gamma_v = \sum_{u=1}^{m} \frac{A[u,v]}{c_v} \cdot y_u$. According to linear complementarity, $x_v = 0$ if dual constraint v is not tight, resp. if γ_v is small.
- Constraint u has to be satisfied f times: $\gamma_v \geq y_u$ whenever $A[u,v] > 0$. If $y_u \geq \kappa^k$, then $\gamma_v \geq y_u$ and u will be satisfied during Increment(κ, k) by x_v-increments.
- The ratio $\max_{u,w} \frac{y_w}{y_u}$ should be decreased to say $(1+\varepsilon)^{\log_2 n}$ by rescaling.
- Crucial question: how fast are the dual variables growing?
-

Part II

Parallel Random Access Machines

Chapter 11

Introduction

11.1 Shared Memory

Since parallel machines are built from sequential machines we begin with a description of random access machines (RAM), a formal model of a von Neumann machine. Its architecture consists of

- an *input device*,
- a *CPU* which stores the program as well as a label referring to the current command,
- a storage of an unbounded number of *registers*,
- an *accumulator* which may access a register directly by its address or indirectly by an address stored ina register. The accumulator is also capable of performing arithmetic or boolean operations.
- And an *output device*.

For simplicity we assume that input and output device correspond to a sequentially from left to right readable, resp. writable tape, which is partitioned into cells. These cells, as well as the accumulator and the registers can store an integer. Registers have natural numbers as addresses; the address 0 is reserved for the accumulator. We specify the value of register i by $v(i)$ and hence $v(0)$ is the value of the accumulator. A RAM can execute the following commands:

- direct and indirect loading:

load	i	$v(0) := v(i)$
load	$*i$	$v(0) := v\,(v(i))$

- direct and indirect storing:

$$\begin{array}{lll} \text{store} & i & v(i) := v(0) \\ \text{store} & *i & v\left(v(i)\right) := v(0) \end{array}$$

- arithmetic operations:

$$\begin{array}{lll} \text{add} & i & v(0) := v(0) + v(i) \\ \text{sub} & i & v(0) := v(0) - v(i) \\ \text{mult} & i & v(0) := v(0) * v(i) \\ \text{div} & i & v(0) := \lfloor v(0)/v(i) \rfloor \end{array}$$

  Moreover, we may use the indirect variants add $*i$, sub $*i$, mult $*i$ and div $*i$.

- Comparisons have the form:

$$\text{if } \textit{Test} \text{ then } \textit{command}$$

  We may use "end-of-file" as a test as well as comparisons of the form

$$v(0) \left\{ \begin{array}{c} = \\ \geq \\ \leq \end{array} \right\} v(i).$$

- A goto has the form "goto label", where label is the unique identifier of a command.

- The input command "read" has as consequence that the currently read integer is written into the accumulator and the input head is advanced by one position to the right. The input command "write" has as consequence that the value of the accumulator is written onto the output tape. The output head is advanced by one position to the right.

- The computation halts, if the command "stop" is executed.

To measure the running time of a program we consider *uniform running time* and *logarithmic running time*. The uniform running time is the number of executed operations, whereas the logarithmic running time is proportional to the binary length of the operands and proportional to the binary length of memory locations involved in the computation. Logarithmic running time is more realistic, since it considers the size of the operands. We will however use uniform running time which is far easier to analyze. Moreover our algorithms will only work on relatively small operands and hence uniform and logarithmic running time are strongly related.

We define PRAMs as a powerful multiprocessor model with a shared memory and synchronous computation. Thus we demand the best of all worlds and can concentrate purely on algorithmic questions.

Definition 11.1 A PRAM with p processors consists of

- p random access machines which we also call processors. Each processor has its own name which is an integer.
- A shared memory of an unbounded number of registers. Each register has its own unique address, a natural number, and is capable of storing an integer.

A PRAM is computing in a synchronous manner, i.e., all processors are following a global clock. An input $x_1, \ldots, x_n$ of n integers is stored in the first n registers of the shared memory and each processor receives the input length n as well as the number of processors in a special local register. All processors work according to the same RAM-program, but we also assume that a processor has its own set of local data (such as its name) stored in its local registers as a priori information. All other local and global registers are initialized to be zero. Read- and write-commands have to be adjusted as follows.

- read*: if i is the contents of the first local register of the processor, then the contents of the ith register from the shared memory is written into the accumulator
- write*: if i is the contents of the first local register of the processor, then write the contents of the accumulator into the ith register from the shared memory.

Thus each processor uses its first local register as an address register. If m outputs have to be determined, then they have to be stored in the first m global registers at the end of the computation. We say that an input is accepted (resp. rejected) iff the first register receives the value 1 (resp. 0) at the end of the computation.

We still have to clarify how to deal with read and write conflicts. We have a read-conflict (resp. write conflict) iff at some time at least two processors try to read from (resp. write into) the same register.

Definition 11.2 Let P be a PRAM program.

(a) P is a EREW-PRAM (exclusive read exclusive write PRAM) iff there are neither read nor write conflicts.

(b) P is a CREW-PRAM (concurrent read exclusive write PRAM) iff there are no write conflicts.

(c) ERCW-PRAM and CRCW-PRAM algorithms are defined analogously.

How to deal with write conflicts, in particular if different processors try to write different values into the same register at the same time?

Definition 11.3 (a) The *common model* demands that all processors writing into the same register at the same time write the same value.

(b) The *arbitrary model* writes an arbitrary value (from among the values to be written) into the register. It is demanded that the PRAM program works for all choices correctly.

(c) In the *priority model* the processor with the smallest address wins and its value is written.

Observe that the common model provides the most restrictive conflict resolution scheme, since any PRAM algorithm for the common model also works in the arbitrary and in the priority model. Finally, the arbitrary model is more restrictive than the priority model.

When should we call a problem parallelizable? We require a super-fast parallel algorithm which runs in at most poly-logarithmic time and uses at most a polynomial number of processors.

Definition 11.4 The functions $p, t : \mathbb{N} \to \mathbb{N}$ are given. We define $\mathrm{EREW}(p(n), t(n))$ as the class of languages $L \subseteq \{0,1\}^*$ which are recognizable with a uniform EREW-PRAM algorithm in time $O(t(n))$ using not more than $O(p(n))$ processors. The classes $\mathrm{ERCW}(p(n), t(n))$, $\mathrm{CREW}(p(n), t(n))$ and $\mathrm{CRCW}(p(n), t(n))$ are defined analogously.

We set $\mathcal{NC} = \bigcup_{k,l \in \mathbb{N}} \mathrm{CRCW}(n^k, (\log_2 n)^l)$. Thus the complexity class $\mathcal{NC}$ consists of all languages $L \subseteq \{0,1\}^*$ such that L can be recognized by a CRCW-PRAM algorithm in poly-logarithmic time with a polynomial number of processors.

$\mathcal{NC}$ is shorthand for Nick's Class, since Nick Pippenger has proposed the class to capture all problems in $\mathcal{P}$ which are parallelizable.[1]

Exercise 110
Show that $\mathcal{NC} \subseteq \mathcal{P}$.

Open Problem 1
Show that $\mathcal{NC}$ is a proper subset of $\mathcal{P}$.

The concurrent access to cells from shared memory is unrealistic from a hardware point of view. However we may simulate even CRCW-PRAM's by message passing algorithms with relatively small delay. In particular, assume that we are given a CRCW-PRAM P with $p(n)$ processors which runs in time $t(n)$. We simulate P by a message passing algorithm with $p(n)$ processors arranged in a hypercube network.

Each processor ρ of P is simulated by exactly one node of the hypercube, namely node $v(\rho)$. Moreover we distribute cells of the shared memory among the nodes of the hypercube

[1] $\mathcal{P}$ is the class of all languages which are recognizable by Turing machines within polynomial time.

and achieve a "randomly behaving" distribution with the help of a good hash function. When simulating a particular processor ρ we have to differentiate two cases.

Case 1: Processor ρ is executing a local operation, that is, it neither executes a read nor a write statement. This case is easy, since node $v(\rho)$ may perform the operation with the information it already knows.

Case 2. Processor ρ executes a read or write statement and node $v(\rho)$ will have to fetch the required information from one of its colleagues. Thus we are faced with a routing problem, which we know how to solve on the hypercube. The distribution of the shared memory via hashing implies that, with high probability, no bottlenecks arise. Ranade [R91] provides the details of this sketch. In particular he shows

Theorem 11.5 *A CRCW-PRAM algorithm which runs in time $t(n)$ with $p(n)$ processors can be simulated by a message passing algorithm with $p(n)$ processors in time $O(t(n) \cdot \log_2 p(n)))$ with high probability.*

Exercise 111
Design a parallel algorithm in pseudo code for the the prefix problem. The algorithm should run in time $O(\frac{n}{p(n)} + \log_2 n)$ on a EREW-PRAM with $p(n)$ processors, provided the associative operation can be evaluated in constant time.

11.2 Comparing PRAMs of Different Types

Our first result shows a simple hierarchy of the different parallel computation modes.

Lemma 11.6 *Let* RAM(t) *be the class of all languages which can be recognized by a (sequential) random access machine in time $t(n)$ for inputs of length n. Then*

$$\mathrm{EREW}(p(n), t(n)) \subseteq \mathrm{CREW}(p(n), t(n)) \subseteq \mathrm{CRCW}(p(n), t(n)) \subseteq \mathrm{RAM}(p(n) \cdot t(n)).$$

Exercise 112
Verify Lemma 11.6.

What are the known limitations of the various PRAM models? We mention the following results, which are shown in [Ja92].

Fact 11.1 *(a) The input for the **zero-counting problem** is a sorted 0/1 sequence A. We have to determine the position i with $A[i] = 0$ and $A[i+1] = 1$. Then any EREW-PRAM algorithm for the zero-counting problem requires time $\Omega(\log_2 \frac{n}{p})$ with p processors.*

*(b) Any CREW-PRAM algorithm requires time $\Omega(\log_2 n)$ to compute the **Boolean OR** of n bits, even if there is an unlimited number of processors.*

*(c) The problem of computing the **parity function** on n bits requires time $\Omega(\frac{\log_2 n}{\log_2 \log_2 n})$ on a priority CRCW-PRAM with a polynomial number of processors.*

We use Fact 11.1 to separate the different PRAM modes.

Exercise 113
A summation CRCW-PRAM solves a write conflict by summing all values requesting the same register and assigning the sum to the register.

(a) Show that the parity function of n bits can be computed with n processors in constant time.

(b) Show that n keys can be sorted in constant time with n^2 processors.

I: Exclusive Reads Versus Concurrent Reads

Are concurrent reads more powerful that exclusive reads? The answer is yes as shown by the following **parallel search problem**. The input consists of a sorted array X of n keys and an additional key y.

Definition 11.7 Set $X[0] = -\infty$ and $X[n+1] = +\infty$. We define $\text{rank}(y \mid X)$ to be the position j with $X[j] < y \leq X[j+1]$.

Our goal is to determine $\text{rank}(y \mid X)$, i.e., the number of elements of X which are smaller than y.

Algorithm 11.8 **Solving the parallel search problem with a CREW PRAM**

(1) p processors are available.

(2) $m = n+1$; $l = 0$; $X[0] = -\infty$, $X[m] = +\infty$;

/* y belongs to the interval $[X[0], X[m]]$, since $[X[0], X[m]] = [-\infty, +\infty]$. This property will be maintained as an invariant. */

(3) repeat $\lceil \log_p(n+2) \rceil$ times

for $i = 1$ to p pardo

if $X[l + (i-1) \cdot \frac{m}{p}] \leq y \leq X[l + i \cdot \frac{m}{p} - 1]$ then

$l = l + (i-1) \cdot \frac{m}{p}$; $m = \frac{m}{p}$;

if $X[l + i \cdot \frac{m}{p} - 1] < y < X[l + i \cdot \frac{m}{p}]$ then

$\text{rank}(y \mid X) = l + i \cdot \frac{m}{p} - 1$; stop;

/* There are no write conflicts. However there are read conflicts, since y and l have to be known to all processors. */

Algorithm 11.8 performs a parallel search by partitioning the sorted sequence into p intervals of same size. Within constant time the interval containing key y is determined. Thus time

$$\lceil \log_p(n+2) \rceil = \Theta(\log_p n) = \Theta(\frac{\log_2 n}{\log_2 p}).$$

is sufficient.

Theorem 11.9 *(a) Algorithm 11.8 determines rank$(y \mid X)$ for a sorted sequence X of size n on a CREW PRAM. Thus it solves the parallel search problem with p processors in time $O(\frac{\log_2 n}{\log_2 p})$.*
(b) Each EREW-PRAM with p processors requires at least $\Omega(\log_2 \frac{n}{p})$ steps to determine rank$(y \mid X)$ and hence concurrent reads are provably more powerful than exclusive reads.

Proof (b) follows from Fact 11.1 (a). □

Exercise 114
We would like to solve the all-to-all broadcasting problem, assuming that one processor sends a message to n other processors.

(a) Show how to solve the one-to-all broadcasting problem in time $O(1)$ on a CREW PRAM with n processors.

(b) Show that time $\Theta(\log_2 n)$ is sufficient and necessary, if we work with an EREW PRAM with n processors.

II: Exclusive Writes Versus Concurrent Writes

Example 11.1 We want to compute the Boolean OR of n Bits $x_1, \ldots, x_n$ with n processors. We assume that x_i is initially stored in register i. Processor i reads x_i from the shared memory. If $x_i = 1$, then processor i writes a 1 into register 1 of the shared memory. The computation stops immediately with the output stored in register 1.

Alternatively we could have described our algorithm as follows.

Algorithm 11.10 **An ERCW-Algorithm for the Boolean OR**

(1) n is the number of input bits. x is a shared array variable storing n bits.

(2) Set $N = n$;

(3) for $p = 1$ to N pardo
    if $x[p]$ then $x[1] =$ true;

Algorithm 11.10 is an ERCW-Algorithm, since we have write conflicts when several processors try to write into register 1. But processors always write the same value 1 and hence Algorithm 11.10 works in the common model.

Thus ERCW-PRAMs and hence also CRCW-PRAMs are provably more powerful than CREW-PRAMs. On the positive side, EREW-PRAMs and hence also CREW-PRAMs are successful, if time $O(\log_2 n)$ is allowed. To achieve this result we design an EREW-algorithm which evaluates $x_1 \vee \cdots \vee x_n$ on a binary tree with n leaves.

Algorithm 11.11 **An EREW-Algorithm for the Boolean OR**

(1) n is the number of input bits. x is a shared array variable storing n bits.

(2) $N = \lfloor n/2 \rfloor$;
for $p = 1$ to N pardo
$r = n$;
while $r > 1$ do
$m = r$; $r = \lceil r/2 \rceil$;
if $(p \leq m) \wedge (p + r \leq m)$ then
$x[p] = x[p] \vee x[p + r]$;

Thus initially the or's $x[p] = x[p] \vee x[p + \lceil n/2 \rceil]$ are computed simultaneously for $p \leq n - \lceil n/2 \rceil = \lfloor n/2 \rfloor$. It remains to determine $x[1] \vee \cdots \vee x[\lfloor n/2 \rfloor]$ recursively. Hence this EREW-algorithm determines the Boolean OR in time $\log_2 n$ with $\lfloor n/2 \rfloor$ processors.

Example 11.2 We want to find the minimum of n integers $x_1, \ldots x_n \in \{1, \ldots, n\}$ using the priority model.

Algorithm 11.12 **An ERCW-Algorithm to determine the minimum**

(1) n numbers are stored in the shared array x.

(2) for $p = 1$ to n pardo
$x[x[p]] = 0$;
if $x[p] = 0$ then $x[1] = p$;

We utilize the priority model in the last step. Register 1 contains the minimal value, since the processor with the smallest name is allowed to write. But processor p is only allowed to compete if p is among the n input numbers. Observe that we use n processors and work in two steps.

This is another example for the power of concurrent writes over exclusive writes: Assume that the input sequence is a sequence of zeroes and ones and assume that a CREW-PRAM algorithm can find a minimal element in time $o(\log_2 n)$. We design another CREW-PRAM algorithm that computes an n-bit OR in time $o(\log_2 n)$, contradicting Fact 11.1 (b). In its first step the CREW-PRAM changes each one into a zero and each zero into a one. Then it determines the minimal element. The minimal element is a one iff the OR of the original bits evaluates to zero.

Exercise 115
We are given a binary sequence $x = (x_0, \ldots, x_n)$, which is stored in the first n registers of the shared memory. Show how to determine the position of the first one in time $O(1)$ with n processors on a CRCW PRAM.

Hint: Partition the sequence into $\sqrt{n}$ intervals of length $\sqrt{n}$ and determine for each interval, if it contains a one. Can you determine the smallest interval with a one in time $O(1)$?

We have seen already that ERCW-PRAMs are more powerful that CREW-PRAMs when computing an n-bit OR. Here we show as a consequence of Theorem 11.5 that EREW-PRAMs can catch up to CRCW-PRAMs, if given a little more time.

Theorem 11.13 $\mathrm{CRCW}(p,t) \subseteq \mathrm{EREW}(p, t \cdot \log_2 p)$*, if we assume the priority mode for CRCW algorithms and allow randomized EREW computations.*

Exercise 116
Verify Theorem 11.13.

III: Comparing Write Resolution Schemes

First we compare the powerful "priority" resolution scheme with the weak "common" resolution scheme.

Theorem 11.14 *Any priority-CRCW PRAM P with p processors and time t can be simulated by a common-CRCW PRAM Q with $O(p \cdot \log_2 p)$ processors in time $O(t)$.*

Proof: The two models differ only in their write statement and we have to find the processor with smallest address among all processors trying to write into the same shared memory location.

We reserve for each register of P a block of $2 \cdot p - 1$ registers within the shared memory of Q. We demand that the blocks of different registers are disjoint and all cells are initialized to be zero.

Processor i_Q of Q will simulate processor i_P of P with the help of $\log_2 p$ assistants. If i_P tries to write into memory location r_i, then i_Q writes a one into the ith cell of the block of register r_i. We can use the $2 \cdot p - 1$ cells of a block to implement a binary tree of depth $\log_2 p$ with the first p cells as its leaves. Thus at this moment the leaves that correspond to processors with a write request receive a one and the rest is labeled by a zero. Processor i_Q uses its assistants to enforce the write request of processor i_P: the assistants write a one in each predecessor of its leaf for which the leaf belongs to a left subtree. Observe that all writes are according to the common model, since all processors write a one.

After writing into the nodes of the tree, each processor i_Q determines with the help of its assistants, whether there is a predecessor with a one for which its leaf belongs to the

right subtree. If this is the case, then i_Q has to give up the write request. If this is not the case, then i_Q can execute the desired write. □

How big is the computing power of CRCW-PRAMs? The XOR of n bits turns out to be a tough problem.

Theorem 11.15 *Let P be a priority CRCW PRAM. Then P requires at least $\Omega(\frac{\log_2 n}{\log\log n})$ steps to compute the XOR $x_1 \oplus \cdots \oplus x_n$ with a polynomial number of processors.*

Proof: This is a consequence of Fact 11.1 (c). □

Observe that $\oplus$ is an associative operation and hence Theorem 11.15 shows that the prefix problem has no solutions with running time $o(\frac{\log_2 n}{\log\log n})$ and a polynomial number of processors.

11.3 Conclusion

We have introduced PRAMs as a synchronous parallel computing model with a shared memory and have distinguished exclusive and concurrent read/write resolution schemes. We have defined the complexity class $\mathcal{NC}$ as the class of all *parallelizable* problems in $\mathcal{P}$, that is as the class of problems in $\mathcal{P}$ with PRAM algorithms running in poly-logarithmic time with a polynomial number of processors.

Finally we have compared PRAM algorithms with message passing algorithms and have compared the various conflict resolution schemes.

Chapter 12

Linked Lists and Trees

We describe a collection of methods which are of great help in designing parallel algorithms for graph problems. In particular we discuss the doubling technique, Euler tours and tree contraction.

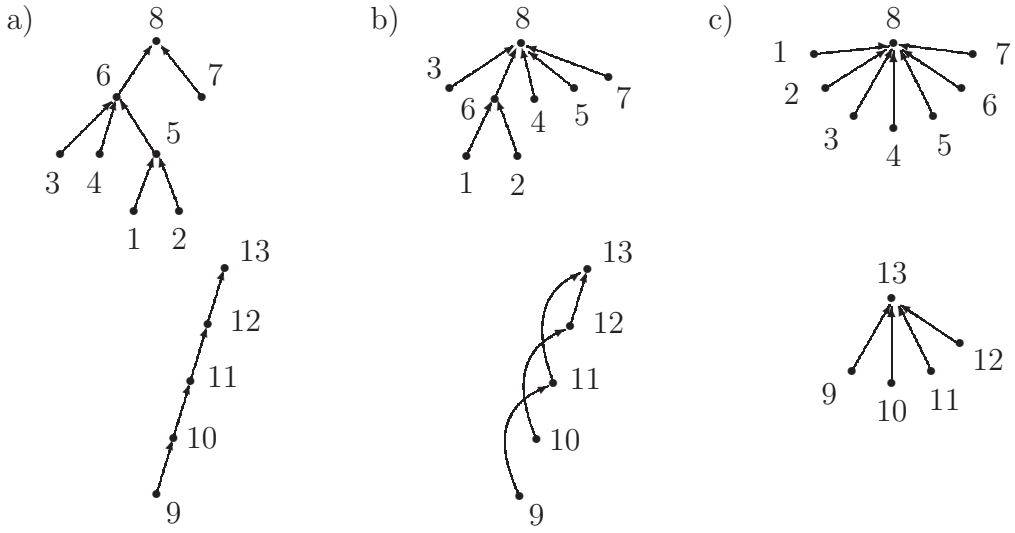
12.1 The Doubling Technique

We describe the **pointer jumping** technique, a method which allows a fast traversal of trees and linked lists in particular. A forest F is represented by its set $V = \{1, \ldots, n\}$ of n nodes and by an array parent, where parent$[i]$ is the parent of node i. (If i is a root, then parent$[i] = i$.) Our goal is to determine the respective root for all nodes in parallel.

Algorithm 12.1 **Finding the root via pointer jumping**

for $i = 1$ to n pardo
  while parent$[i] \neq$ parent$\big[$parent$[i]\big]$ do
    parent$[i] =$ parent$\big[$parent$[i]\big]$;
  Output (i,parent$[i]$);

Algorithm 12.1 works with n processors, where processor i is responsible for node i. Node i advances to become a child of its current grandfather unless its parent is a root. Observe that the edges "double in length".



Example for Algorithm 12.1

Theorem 12.2 *Algorithm 12.1 is a CREW-PRAM algorithm working with n processors. If F is a forest with n nodes and if d is the depth of F, then algorithm 12.1 determines a root for all nodes of F in time $O(\log_2 d)$.*

Proof: The shared array "parent" is concurrently read, but only exclusively written and hence Algorithm 12.1 is a CREW-PRAM algorithm. We still have to determine the running time. We claim inductively that if node i becomes a child of node j in round t, then i and j have distance 2^t in the original forest, provided j is not a root.

The claim is true for $t = 0$. If i is a child of k in round t and becomes a child of j in round $t + 1$, then, by induction hypothesis i and k as well as k and j have distance 2^t in F and hence i and j have distance 2^{t+1} in F. □

Exercise 117
Show that time $\Omega(\log_2 n)$ is required for an EREW PRAM with n processors. This statement holds, even if we work with forests of depth two.

Exercise 118
A tree T is given by parent pointers. Moreover we assign a real number x_v to each node v. Show how to determine, in parallel for all nodes v, the sum of all values which are assigned to nodes on the path from v to the root. You may work with CREW-PRAM in time $O(\log_2 n)$ with n processors, provided T has n nodes.

In our second application of pointer jumping we consider the **list ranking** problem:

Given is a singly linked list of n nodes. The linked list is represented by a shared array S, where $S[i]$ is the successor of i within the linked list. (If i is the end of the list, we set $S[i] = 0$.) Each node i has also a value $V[i] = a_i$ and the problem is to

determine the n suffix sums

$$\begin{array}{ccccccccc} & & & & & & & & a_n \\ & & & & & & a_{n-1} & * & a_n \\ & & & & & & \vdots & & \\ a_1 & * & a_2 & * & \ldots & * & a_{n-1} & * & a_n \end{array}$$

for an associative operation $*$.

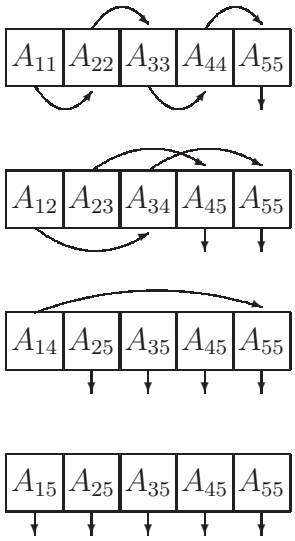
If we set for instance $V[i] = 1$ for all i, then the output for list element i is its distance (plus one) from the end of the list. There is a strong similarity to the prefix problem. Whereas we are now interested in suffix sums, we had to compute prefix sums in the prefix problem, however this difference is not substantial. The crucial difference is that we had random access to elements in the prefix problem and are now restricted to a list access only.

Algorithm 12.3 **List ranking via pointer jumping**

for $i = 1$ to n pardo

$W[i] = V[i]$; $T[i] = S[i]$;
while $(T[i] \neq 0)$ do
$W[i] = W[i] * W[T[i]]$;
$T[i] = T[T[i]]$;

Exercise 119
Verify Algorithm 12.3 and show that it runs on an EREW-PRAM.



Change of the successor array in Algorithm 12.3.

Theorem 12.4 *Assume that the operation $*$ can be evaluated sequentially in time T. Then Algorithm 12.3 solves the list ranking problem for n elements and can be implemented on a EREW-PRAM in time $\Theta(T \cdot \log_2 n)$ with n processors.*

Algorithm 12.3 is simple and fast, but not efficient since the total work is $\Theta(T \cdot n \cdot \log_2 n)$ whereas a sequential algorithm just requires time $\Theta(T \cdot n)$. Efficient algorithms with $O(\frac{n}{\log_2 n})$ processors and running time $O(T \cdot \log_2 n)$ are known.

12.2 Euler Tours and Tree Contraction

Traversing a graph is a fundamental method in many graph algorithms and depth-first search is a very fast sequential graph traversal.

Algorithm 12.5 **Depth-first search**

(1) Depth-first search is a recursive procedure which is started at node v. We assume that initially no node is marked as "visited".

(2) Depth-first-search(v)

```
Mark v as visited;
Let u be the first node on the adjacency list of v;
while u ≠ nil do
    if u is not marked visited then
        depth-first-search(u);
    Replace u by the next node on the adjacency list of v;
```

However an efficient parallel implementation of depth-first search is not known. In this chapter we describe a fast parallel implementations of depth-first search for trees which are known beforehand and show how to use this method to determine a preorder, postorder or breadth first search traversal for trees. (Observe that our parallel backtracking algorithm for implicitly defined trees –see Section 6.1– does not produce a depth-first search traversal.)

How does depth-first search work when applied to trees? Starting at the root it follows the tree edges to reach a leaf. After reaching a leaf, the traversed edges are traversed in backwards direction. Depth-first search stops, when all edges are traversed exactly once in either direction.

Definition 12.6 Let $T = (V, E)$ be an undirected tree. We set $E^* = \{(i, j) \mid \{i, j\} \in E\}$ and define the "Euler graph"

$$\text{Euler}(T) := (V, E^*)\,.$$

An *Euler tour* is a path in Euler(T) which traverses all edges of Euler(T) exactly once and returns to its starting point.

Exercise 120
Show that an Euler tour of a tree T corresponds to a depth-first search traversal of T.

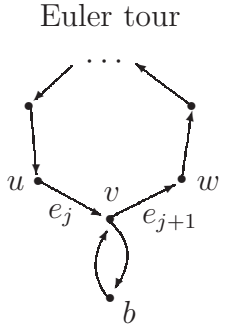
Thus it suffices to come up with a fast algorithm that determines an Euler tour. Assume that T is given by its adjacency list representation. Hence all neighbors of a node $v \in V$ are collected in a linked list $N[v]$ and the linked list orders neighbors according to their position within the list. Which edge should follow after edge (u, v) on the Euler tour?

$$\text{If } N[v] = (\ldots, u, w, \ldots,), \text{ then continue with edge } (v, w).$$

Moreover, if u is the last node in $N[v]$, then we continue with edge (v, w), where w is the first node in $N[v]$. We call (v, w) the successor of edge (u, v).

Lemma 12.7 *If we always select the successor of the last edge as the next edge, then we obtain an Euler tour in Euler(T).*

Proof: We give an inductive proof on the number n of nodes of T. If $n = 1$, then T and thus Euler(T) has no edges. Now assume that T is a tree with $n + 1$ nodes. If $l \in V$ is a leaf, then l its adjacency list consists only of its parent v. We remove l (from T and Euler(T)) and our "recipe" produces an Euler tour $(e_1, \ldots e_{n-1})$.



Assume that leaf l is the right neighbor of u in list $N[v]$ and that w is the right neighbor of l; in particular $N[v] = (\ldots, u, l, w, \ldots)$. Now consider the edge $\mathbf{e_j} = (\mathbf{u}, \mathbf{v})$. Our recipe for the original graph requires that, after traversing edge (u, v), we continue with edge $(\mathbf{v}, \mathbf{l})$. Parent v is its own right neighbor in list $N[l]$ and we continue with edge $(\mathbf{l}, \mathbf{v})$. But w is the right neighbor of l in list $N[v]$ and $\mathbf{e_{j+1}} = (\mathbf{v}, \mathbf{w})$ is the next edge. The recipe works, since

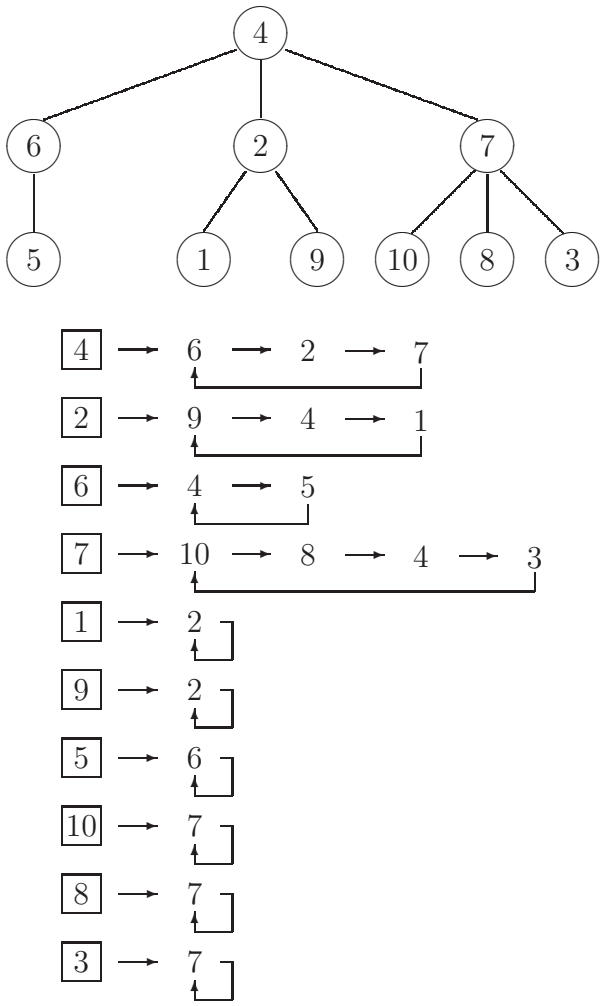
$$(e_1, e_2, \ldots, e_j, (v, l), (l, v), e_{j+1}, e_{j+2}, \ldots, e_{n-1}).$$

is an Euler tour. □

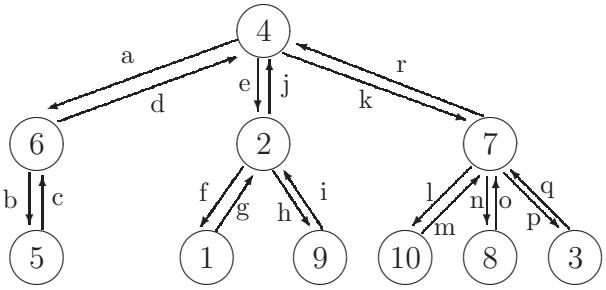
To come up with fast implementation for finding Euler tours we have to figure out how to compute the successor $e' = (v, w)$ of an edge $e = (u, v)$. We simplify this problem by demanding that T is given as an adjacency list with cross references. In particular we require that

- the adjacency list $N[v]$ is given as a circular list and
- for any element w in $N(v)$ there is a link to element v in $N(w)$.

Example 12.1 We consider the following tree:



The circular adjacency lists without cross references.



The Euler tour which begins in edge $(4, 6)$.

If we start with the edge $(4,6)$, then we obtain the Euler tour

$$\begin{array}{llllllll} (4,6), & (6,5), & (5,6), & (6,4), & & & & \\ (4,2), & (2,1), & (1,2), & (2,9), & (9,2), & (2,4), & & \\ (4,7), & (7,3), & (3,7), & (7,10), & (10,7), & (7,8), & (8,7), & (7,4). \end{array}$$

Theorem 12.8 *Assume that a tree $T = (V, E)$ is given as an adjacency list with cross references. Then we can find the successors of all edges in parallel in time $O(1)$ with $2(|V| - 1)$ processors on an EREW-PRAM. Hence an Euler tour, represented as a linked list, can be constructed in time $O(1)$ with $|V|$ processors on an EREW-PRAM as well.*

We now bring in the harvest. Postorder(v) and preorder(v) are recursive procedures according to the following recipes

- Postorder(v): first the descendants of a node v are traversed and then v.
- Preorder(v): first v is traversed and then its descendants.

The *numbering of a traversal* assigns the time to each node at which it is traversed. The level-order numbering assigns the depth, that is the length of the path from the root, to a node.

Theorem 12.9 *Let $T = (V, E)$ be an undirected rooted tree which is presented as an adjacency list with cross references. Then the following problems are solvable on an EREW-PRAM in time $O(\log_2 |V|)$ with $\frac{|V|}{\log_2 |V|}$ processors:*

(a) determine the parent parent(v) for each node $v \in V$,

(b) determine a postorder numbering,

(c) determine a preorder numbering,

(d) determine a level-order numbering and

(e) determine the number of descendants for every node $v \in V$.

Proof: All our solutions compute an Euler tour, assign weights to the edges and compute prefix sums. (Since we apply list ranking and thus are only able to compute suffix sums, we have to reverse edge directions.)

Algorithm 12.10 **The Euler tour algorithm**

(1) A tree is given as an adjacency list with cross references.

(2) Assign weights "weight(e)" to edges e of Euler(T).
// The weight assignment has to be done in a problem dependent way.

(3) Determine an Euler tour beginning in the root.

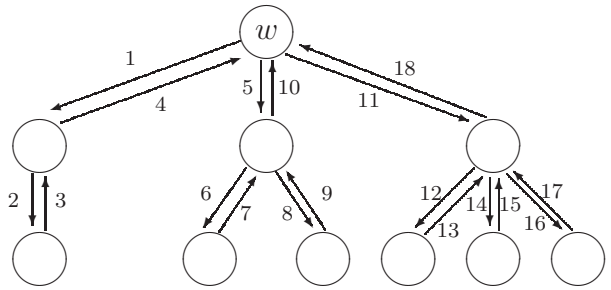
(4) Apply list ranking, with addition as operation, to the reversed list of the Euler tour.

(5) Evaluate the sums in a problem specific way.

(a) We have to determine parents in parallel and set weight(e) = 1 for all edges e. Let value(e) be the sum computed by list ranking for edge e. We can now characterize the parent of a node v by

$$u \text{ is parent of } v \;\Leftrightarrow\; \text{value}(u,v) < \text{value}(v,u).$$

Why? value(u,v) is the position in which (u,v) appears within the Euler tour. value$(u,v) <$ value(v,u) implies that the Euler tour has a segment of the form $u \to v \to \cdots \to v \to u$. But then v has to belong to the subtree of u and hence u is the parent of v.



List ranking when determining parents. (See example 12.1.)

(b) To determine the postorder numbering we first determine parents and set

$$\text{weight}(u, \text{parent}(u)) = 1, \quad \text{weight}(\text{parent}(u), u) = 0.$$

We claim that

$$\text{post}(v) = \begin{cases} n & v \text{ is the root,} \\ \text{value}(v, \text{parent}(v)) & \text{otherwise} \end{cases}$$

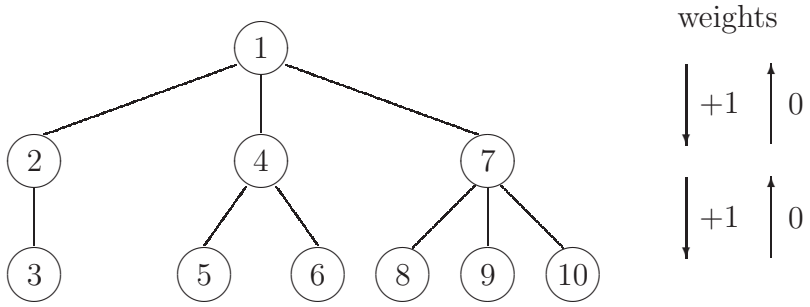
is a postorder numbering. This is indeed true, since we assign to node v the moment in time at which v was visited the last time. **(c)** As for postorder we first determine parents and then set

$$\text{weight}(u, \text{parent}(u)) = 0, \quad \text{weight}(\text{parent}(u), u) = 1.$$

This time we claim that

$$\text{post}(v) = \begin{cases} 1 & v \text{ is the root,} \\ \text{value}(\text{parent}(v), v) + 1 & \text{otherwise} \end{cases}$$

is a preorder numbering. Also this claim holds, since we assign the moment in time at which node v is visited for the first time.



Preorder numbering with Euler tours.

(d) The level-order is also easy to determine. We set weight(parent(v), v) = 1 to capture that depth increases by one and weight(v, parent(v)) = -1 to capture that we move back up to decrease depth by one. Thus

$$\text{level}(v) = \begin{cases} 0 & v \text{ is the root,} \\ \text{value}(\text{parent}(v), v) & \text{otherwise} \end{cases}$$

is a level-order numbering.

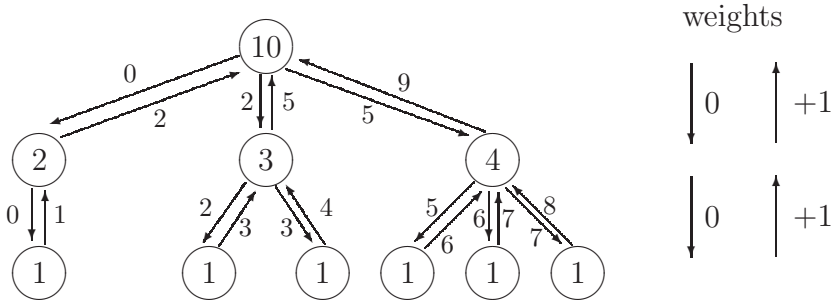
(e) The task is to determine the number of descendants in parallel for all nodes v. (We count a node as its own descendant.) Set

$$\text{weight}(v, \text{parent}(v)) = 1, \quad \text{weight}(\text{parent}(v), v) = 0$$

and

$$\text{value}(v, \text{parent}[v]) - \text{value}(\text{parent}[v], v)$$

is the the number of descendants of v, provided v is different from the root, since each descendant is counted once by counting its "back edge". Obviously the root has n descendants.



Determining the number of descendants with the help of Euler tours.

We conclude the argument with a running time analysis. List ranking dominates the running time and we utilize that list ranking can be supported in time $O(\log_2 n)$ with $\frac{n}{\log_2 n}$ processors. □

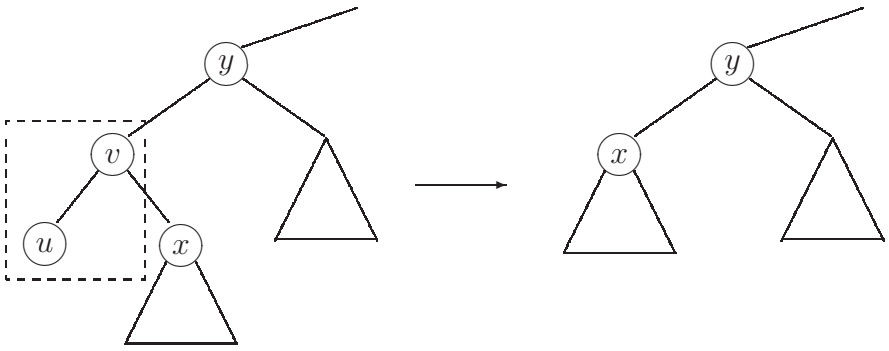
Exercise 121
Determine an inorder numbering of a binary tree which is given as an adjacency list with cross references. Your algorithm should run on an EREW-PRAM with $\frac{n}{\log_2 n}$ processors in time $O(\log_2 n)$.

Hint: an interior node v is traversed by inorder after crossing the edge (u, v), where u is the left child of v. Therefore it seems natural to assign weights different from zero only to these edges (u, v). However how should we proceed, if v is a leaf?

Exercise 122
A tree is given as an adjacency list with cross references. Determine the least common ancestor of a given pair (u, v) of nodes in time $O(\log_2 n)$ with $\frac{n}{\log_2 n}$ processors on a EREW-PRAM.

We describe another important application of Euler tours, the *evaluation of arithmetic expressions*. Let $T = (V, E)$ be an *expression tree*, i.e., a tree all of whose inner nodes have degree two and are labeled with either $+, -, \cdot$ or $/$. Leaves are labeled by real numbers and our goal is to evaluate the corresponding arithmetic expression. We again assume that the tree is represented as an adjacency list with cross references.

We apply $O(\log_2 n)$ iterations to T, where each iteration *contracts* T until at most three leaves "survive" and we can evaluate immediately. We have to combine contraction with evaluation, but restrict ourselves first to describing the contraction process. Let's assume that our current tree has the structure of the left hand side tree in the following figure.

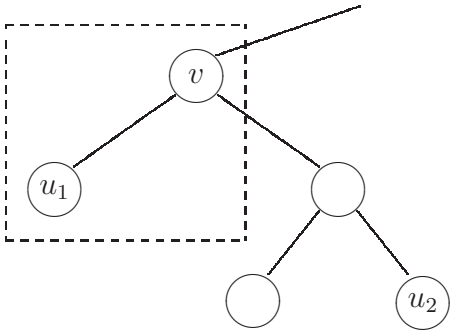


Locally, a contraction step consists in removing leaf u as well as its parent v and making the sibling x of u a child of the grandparent y. (When evaluating we have to partially evaluate v excluding the contribution of x. The partial result is stored in the grandparent y.)

However, globally, many contraction steps have to be performed in parallel without collisions: If leaf u is supposed to be removed, then we have to guarantee that

- neither the sibling x of u nor
- the grandparent y of u is removed by other contraction steps.

Our first approach is to remove only every second leaf, that is all leaves in an odd position relative to the preorder numbering restricted to leaves. But this is not sufficient:



Collisions when removing leaves in odd positions only.

The grandparent v of u_2 is removed when we remove the leaf u_1, but v has to survive if we also remove u_2. Therefore we impose a further restriction and remove in a first subphase only *left leaves in an odd position* followed by a second subphase where right leaves in odd position are removed. (Hence, in the above example, we first remove the left leaf u_1 and subsequently the right leaf u_2. How to determine leaves in odd position?

Algorithm 12.11 **The selection process: finding leaves in odd position**

(1) Determine an Euler tour of Euler(T).

(2) A node is a leaf iff it has exactly one neighbor.

(3) Set weight$(e) = \begin{cases} 1 & e = (u, l) \text{ for a leaf } l, \\ 0 & \text{otherwise;} \end{cases}$

(4) Determine the prefix sums value(parent$[l], l)$ for all leaves l via list ranking.
// value(parent$[l], l)$ is the number of leaves "to the left" of l.

The contraction process consists of a logarithmic number of iterations where we first eliminate left leaves in odd position followed by eliminating right leaves in odd position.

Algorithm 12.12 **The contraction process.**

(1) Perform the selection process of Algorithm 12.11;

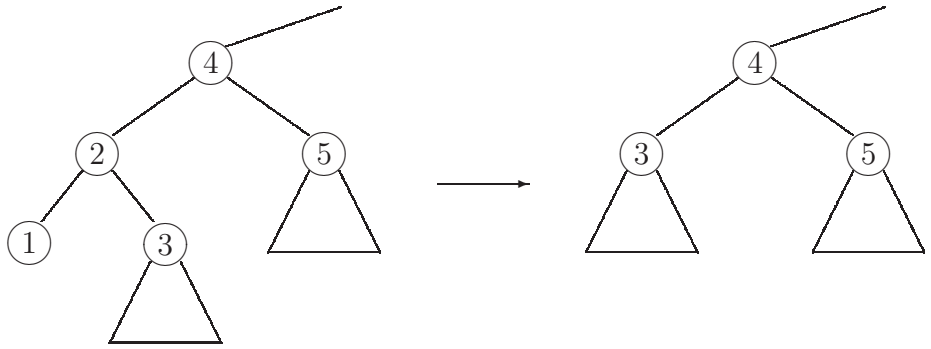
(2) while there are more than three leaves do

- Remove all left leaves in odd position;
- Remove all right leaves in odd position;
  /* Now only leaves in even position remain. All positions are divided by two and hence the new leaves in odd positions can be determined in time $O(1)$. */

Theorem 12.13 *Assume that a given binary tree is represented by an adjacency list with cross references. Then Algorithm 12.12 performs the contraction process in time $O(\log_2 n)$ on an EREW-PRAM with $\frac{n}{\log_2 n}$ processors, where n is the number of nodes.*

Proof: The selection process runs in time $O(\log_2 n)$ on an EREW-PRAM with $\frac{n}{\log_2 n}$ processors. Now observe that we half the number of leaves after one iteration and hence only a logarithmic number of iterations are performed. We are done, since each iterations runs in constant time. □

We still have to combine contraction and evaluation. Consider a local contraction step



We have to remove node 2, although we do not know its value. We do know however that nodes are computing rational functions and hence we represent all values as rational functions

$$\frac{ax_v + b}{cx_v + d},$$

where x_v is the (possibly unknown) value computed by the subtree with root v and parameters a, b, c and d are to be determined during contraction. We begin by choosing $a = d = 1$, $b = c = 0$ for all nodes v.

In the above example of removing node 2 the function typ of node 3 has to be recomputed. We assume that node 3 is currently computing the function $\frac{ax_3+b}{cx_3+d}$ and let e be the result of node 1. If node 2 is performing a division, then $\frac{e}{\frac{ax_3+b}{cx_3+d}} = \frac{(ec)x_3+(de)}{ax_3+b}$ is the new function of node 3. In case of an addition, the new value is $e + \frac{ax_3+b}{cx_3+d} = \frac{(a+ec)x_3+(b+ed)}{cx_3+d}$. The cases of node 2 performing a subtraction or multiplication are similar. We can now conclude

Theorem 12.14 *Let T be an expression tree which is represented as an adjacency list with cross references. Then the arithmetic expression of T can be evaluated in time $O(\log_2 n)$ with $O(\frac{n}{\log_2 n})$ by an EREW-PRAM algorithm, where n is the number of nodes.*

Exercise 123
We are given a rooted binary tree T via parent and child pointers. Moreover each node v is labelled

with the real number x_v. Show how to determine, in parallel for all nodes v, the minimal value in the subtree with root v. If T has n nodes, then your algorithm should run in time $O(\log_2 n)$ on an EREW PRAM with $3n$ processors.

Exercise 124
Show how to derive an expression tree from a fully bracketed arithmetic expression. You may assume that the input is given as an array with the following structure:

$$A: \quad \texttt{array}\ [1 \ldots n]\ \texttt{of}\ \{\,'(', ')', '+', '-', '*', '/', '0', '1', \ldots, '9'\,\}$$

12.3 Conclusion

We have solved the list ranking problem, a version of the prefix problem for singly linked lists, with pointer jumping. Pointer jumping is an instance of the doubling technique.

The method of Euler tours allows to parallelize many tree traversals such as preorder, postorder, inorder and level-order. Another important application is the evaluation of arithmetic expressions, which was achieved by also applying the method of tree contraction. In each of these applications list ranking was a central tool.

In all cases we obtained optimal parallel algorithms with running time $O(\log_2 n)$ by utilizing optimal algorithms for list ranking. Is it possible to reduce the running time even further? The prefix problem is not harder than the list ranking problem and an "easy" instance is to determine all prefix sums of $x_1 \oplus \cdots \oplus x_n$. However we have shown in Theorem 11.15 that any reduction below time $\Omega(\frac{\log_2 n}{\log_2 \log_2 n})$ will force a super-polynomial number of processors and hence $\Omega(\frac{\log_2 n}{\log_2 \log_2 n})$ is also a lower bound for the list ranking problem.

Open Problem 2
Determine the smallest running time for CRCW-PRAM algorithms, which solve the list ranking problem with a polynomial number of processors.

Chapter 13

Algorithms for Graphs

We have already solved the all-pairs-shortest path problem with a message passing algorithm in computing time $O(\frac{n^3}{p} + \frac{n^2}{\sqrt{p}} \log_2 \sqrt{p} + n)$ and communication time $O(\frac{n^2}{\sqrt{p}} \log_2 \sqrt{p})$. We can utilize its solution to determine a breadth-first search tree in parallel, but this solution will be quite expensive for sparse graphs.

Exercise 125
Determine a breadth-first search tree for a given directed graph $G = (V, E)$. What is the total work and the running time of your solution?

The situation for depth-first search trees is even more complex, since deterministic solutions with poly-logarithmic time and polynomially many processors are not known. (In [AAK90] a randomized algorithm with poly-logarithmic time and polynomially many processors is described. The solution is however not efficient.) Our goal is nevertheless to obtain almost optimal parallel algorithms for fundamental graph problems such as determining connected components, computing minimal spanning trees, coloring graphs and determining minimal independent sets. In all these cases we have to work without graph traversals.

Many important graph problems have almost optimal parallel algorithms with fast running time, with the single-source-shortest-path problem as the most prominent graph problem that is missing from this list.

13.1 Connected Components

Let $G = (V, E)$ be an undirected graph with n nodes and m edges. Our goal is to determine the connected components[1] of G. Our algorithm begins by forming singleton loops, i.e., by connecting each node to itself. Singleton loops are trivial example of stars, which consist

[1] A subset $C \subseteq V$ is a connected component of G iff any two nodes of C are connected by a path and there is no node in $V \setminus C$ which is connected to a node in C.

of a distinguished node, the root, and other nodes; all nodes of a star, including the root, are connected with the root.

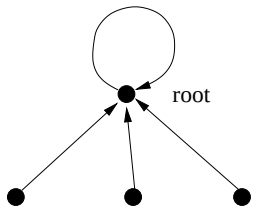


Figure 13.1: A star.

Subsequent steps of our algorithm merge stars. Our hope is that we can represent connected components as stars after relatively few merging steps. In particular our implementation has to organize the merging step and we have to tackle the following issues.

- Each merging step (or "hooking step") attaches some star below others. This process destroys the star-property.
- A merging schedule has to be determined such that merging loops (i.e., attach star s_1 below star s_2 and star s_2 below s_1) are impossible.

Algorithm 13.1 **Determining connected components.**

/* The undirected graph $G = (V, E)$ with $|V| = n$ and $|E| = m$ is given. We work with $n + m$ processors, i.e., we have one processor per node and one processor per edge. */

(1) for $i = 1$ to n pardo parent$[i] = i$;

/* The parent-array defines n stars where each star consists of the root only. An edge $\{u, v\} \in E$ is called alive, if u and v belong to different stars. Observe that initially all edges are alive. */

(2) while (at least one edge of G is alive) do

(a) each root w (i.e., each node w with parent$(w) = w$) chooses a gender $g(w) \in \{0, 1\}$ *at random* and assigns its gender to its children. We interpret gender 0 as male and gender 1 as female;

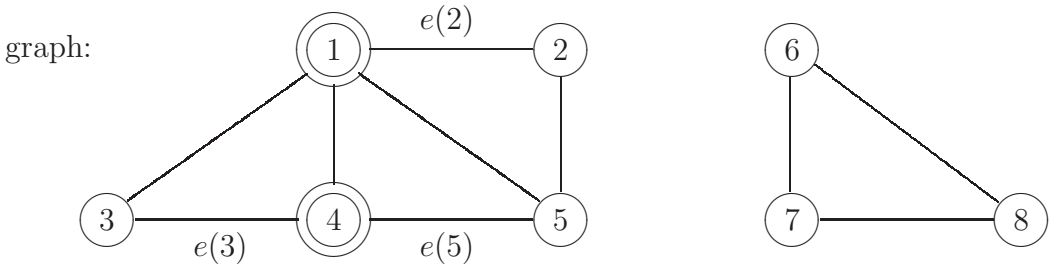
/* We apply the method of *symmetry breaking* by randomization. Symmetry breaking allows to assign different tasks to different processors. */

(b) each processor responsible for connecting a male star m with a female star f tries to write f into the register of m.

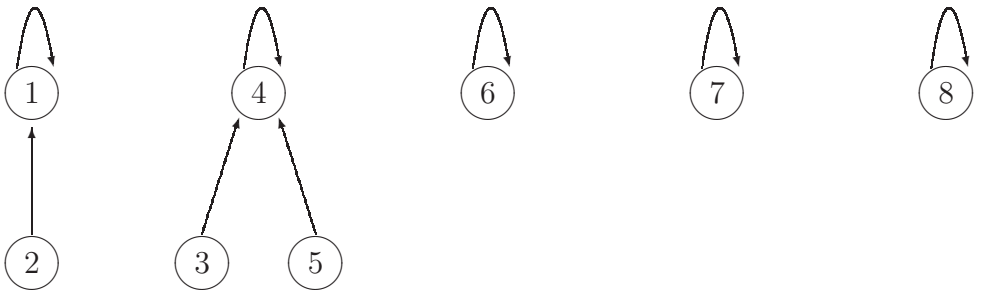
(c) The arbitrary-write resolution scheme assigns a female star $f(m)$ to any male star m. The root of m is made to point to the root of $f(m)$.

(d) for $i = 1$ to n pardo parent[i] = parent[parent[i]];
// One round of pointer jumping repairs the star property.

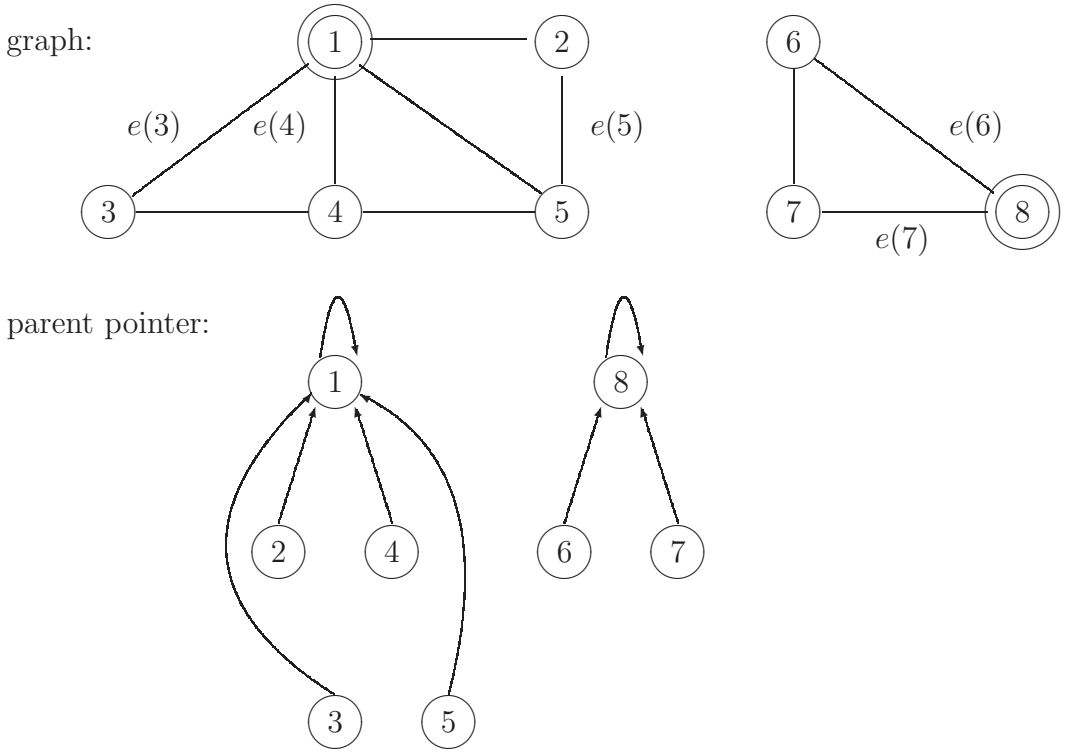
Example 13.1 We show the result of the first iteration for a graph on eight nodes. Female nodes are distinguished by two circles and edges chosen by male nodes are marked.



parent pointer:



Thus we have obtained five stars. For the second iteration we assume that the stars of nodes 1 and 8 are female and that all other stars are male.



and $\{1,2,3,4,5\}$, $\{6,7,8\}$ are the connected components of G.

We begin the analysis with the following immediate observations.

Lemma 13.2 *(a) One round of pointer jumping suffices to repair the star property.*

(b) At all times do the nodes of a star belong to the same connected component.

(c) Each iteration of the while-loop runs in time $O(1)$ on a CRCW-PRAM with $n+m$ processors. The arbitrary mode is used.

We say that a star is *alive*, if one of its nodes is endpoint of an alive edge. We say that the root of a star *disappears* if its star is attached below another star.

Lemma 13.3 *The root of a fixed alive star disappears with probability at least $\frac{1}{4}$.*

Proof: Consider an alive edge $\{u,v\}$, where u belongs to the fixed star. With probability $\frac{1}{4}$ the star of u will be male and the star of v will be female. Hence the root of the star of u disappears with probability $\frac{1}{4}$. □

Theorem 13.4 *Algorithm 13.1 runs in expected time $O(\log_2 n)$ with $n+m$ processors on a CRCW-PRAM in the arbitrary mode. In particular $5 \cdot \log_2 n$ iterations of the while-loop suffice with probability at least $1 - \frac{1}{n}$.*

Proof: It suffices to show that $5 \cdot \log_2 n$ iterations of the while-loop suffice with probability at least $1 - \frac{1}{n}$. We fix some node w and determine the probability p_w that w does not disappear as root after $5 \cdot \log_2 n$ iterations:

$$p_w \leq \left(1 - \frac{1}{4}\right)^{5 \cdot \log_2 n} = \left(\frac{3}{4}\right)^{5 \cdot \log_2 n} = \left(\frac{243}{1024}\right)^{\log_2 n} \leq \left(\frac{1}{4}\right)^{\log_2 n} = 2^{-2 \cdot \log_2 n} = n^{-2}.$$

But at most n nodes can be a root and hence the probability that at least two roots of a connected component do not disappear is at most $\frac{1}{n}$ and this was to be shown. □

Algorithm 13.1 is efficient, but not optimal, since a sequential algorithm can determine connected components in time $O(n+m)$. An optimal probabilistic algorithm can be found in [Ga86].

Exercise 126
Show that Algorithm 13.1 runs in expected time $O(\log_2 n)$.

Exercise 127
(a) Modify Algorithm 13.1 so that the determined spanning forest is given as an adjacency list with cross references.

(b) Show how to determine in time $O(\log_2 n)$ with $n + m$ processors, whether an undirected graph G with n nodes and m edges is bipartite. You may use a CRCW-PRAM with the arbitrary mode.

Exercise 128
Our goal is determine all bridges of an undirected graph $G = (V, E)$. A bridge is an edge whose removal leaves its endpoints in two different connected components. Begin by computing a spanning forest and a preorder numbering.

(a) Show that only edges of the spanning forest can be bridges.

(b) Show how to determine all bridges in time $O(\log_2 |V|)$ with $|V| + |E|$ processors on a CRCW PRAM with the arbitrary mode. You may assume that minimal (resp. maximal) keys can be determined in time $O(\log_2 |V|)$ with $|V|$ processors in parallel for all subtrees of the spanning forest.

Hint: for any edge e of the forest consider the preorder numbers of nodes appearing below edge e.

Exercise 129
We want to solve the 2-SAT problem: determine, if existing, a satisfying assignment for a formula F in conjunctive normal form with at most two literals per clause. (Observe that the corresponding problems for three literals is $\mathcal{NP}$-complete.)

Consider the directed graph G, which contains a node for every positive and a node for every negative occurrence of a variable. Moreover there is are two edges $\neg L_1 \rightarrow L_2$ and $\neg L_2 \rightarrow L_1$ for every clause $L_1 \vee L_2$. Thus we interpret clauses as edges.

(a) Show that F is satisfiable iff L and $\neg L$ belong to different strongly connected components for all literals L.

(b) Determine in time $O(\log_2 n)$ on a CRCW-PRAM with polynomially many processors, if a satisfying assignment exists.

(c) All literals belonging to the same connected component are forced to obtain the same truth value in a satisfying assignment.

(d) Determine a satisfying assignment in time $O(\log_2 n)$ on a CRCW-PRAM with polynomially many processors.

13.2 Minimum Spanning Trees

We are given an undirected connected graph $G = (V, E)$ and a function weight: $E \to \mathbb{R}$, assigning real numbers to edges. We look for a spanning tree[2] $T = (V, E_T)$ of G such that

$$\text{weight}(T) = \sum_{e \in E_T} \text{weight}(e)$$

is minimal among all spanning trees for G. The sequential algorithms of Kruskal and Prim are not suitable for parallelization. Instead we choose the algorithm of Boruvka:

- begin with a forest of singleton trees.
- as long as the forest F contains more than one tree:

  determine for each tree T of F an edge e_T with minimal weight connecting a node of T with a node outside of T. Insert e_T.

We verify Boruvka's algorithm by induction on the number of iterations. We assume that edges have pairwise distinct weights; we can enforce this, if we replace weight(e) by $n^2 \cdot \text{weight}(e) + n \cdot u + v$, provided $e = \{u, v\}$. (We assume that $V = \{0, \ldots, n-1\}$ is the set of nodes.)

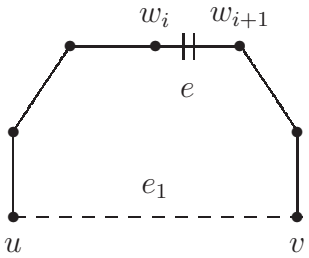
Let $(T_1, \ldots, T_k)$ be the trees in the current forest F. Hence, if V_i is the set of nodes of T_i, then we obtain the partition $V = \bigcup_{i=1}^{k} V_i$. By induction hypothesis we may assume that any minimum spanning tree contains each T_i as a subtree. Boruvka's algorithm determines edges $(e_1, \ldots, e_k)$, such that e_i is the edge of minimal weight connecting a node in T_i with a node outside of T_i.

Lemma 13.5 *Any minimum spanning tree contains all edges in* $\{e_1, \ldots, e_k\}$.

Proof: We assume otherwise and obtain a minimal spanning tree T which does not, say, contain the edge $e_1 = \{u, v\}$ with $u \in V_1$ und $v \in V \setminus V_1$. We know that there is a path

$$w_0 = u \longrightarrow w_1 \longrightarrow w_2 \longrightarrow \ldots \longrightarrow w_r \longrightarrow v = w_{r+1}$$

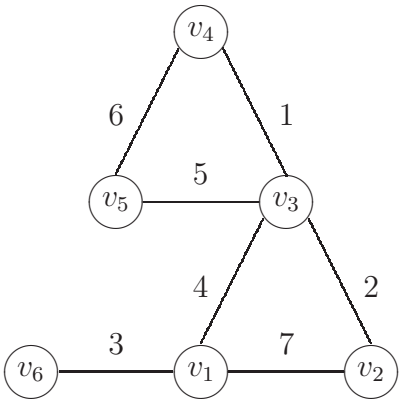
in T. Let $e = \{w_i, w_{i+1}\}$ be the first edge of this path, which connects a node in V_1 with a node in $V \setminus V_1$.



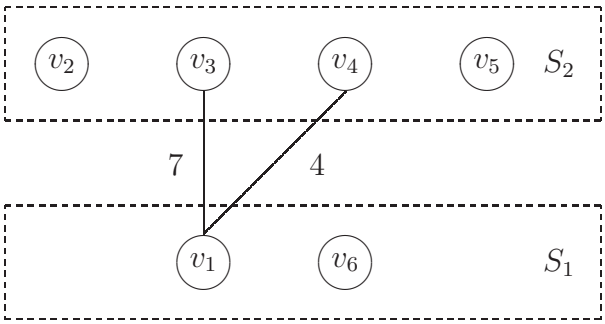
[2] T is a spanning tree of G, if T is a tree containing all nodes of G.

We remove e and insert e_1 instead. Observe that we have again obtained a tree, but with smaller weight than T, a contradiction. □

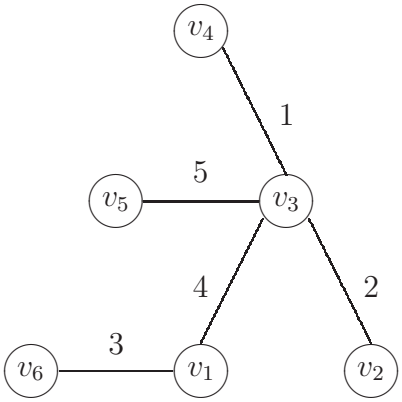
Example 13.2 We run an ideal parallel version of Boruvka's algorithm on the graph



and obtain two super nodes after merging singleton trees in the first phase of Boruvka's algorithm.



The first super node consists of the set $S_1 = \{v_2, v_3, v_4, v_5\}$ of nodes and the second super node consists of the set $S_2 = \{v_1, v_6\}$. In the second iteration we choose the edge with weight 4 connecting the two super nodes which we can subsequently merge to obtain the minimum spanning tree



We still have to organize the merging step and do so by utilizing the ideas of Algorithm 13.1. We determine a minimal weight external edge for each tree in the current forest and assign genders to all trees. Any male tree, which is linked to a female tree by its minimal weight external edge is then attached as a subtree of the female tree. In order for any node to recognize its current tree as fast as possible we again use the star representation of forests. Finally we choose the *extended priority mode* of a CRCW-PRAM to determine a minimal weight external edge: the processor trying to write the smallest value wins.

Algorithm 13.6 **Computing a minimum spanning tree.**

/* The undirected, connected graph $G = (V, E)$ with $|E| = m$ is given. We work with m processors, i.e., we have one processor per edge. */

(1) for $i = 1$ to n pardo parent$[i] = i$;

/* We initialize the collection of singleton stars. Again we call an edge alive, if its two endpoints belong to different stars. */

(2) while (at least one edge of G is alive) do

(a) for (all edges $e = \{u, v\}$) pardo

The processor assigned to e checks if the endpoints of e belong to different stars. If this is the case, then it writes weight(e) into the register of its root via the priority mode.
The processor then checks the register of the root to determine if it has won, i.e., if the weight stored in the register coincides with the weight $w(e)$ of its edge. If this is the case, then it write the edge e into the register.

(b) each root w chooses a gender $g(w) \in \{0, 1\}$ at random. If its gender is male, then it checks whether the external endpoint of the winning edge e is female and discards e otherwise.

/* We again apply the method of symmetry breaking, but *after* determining shortest crossing edges. */

(c) for $i = 1$ to n pardo
parent$[i]$ = parent[parent$[i]$];
/* One round of pointer jumping repairs the star property. */

Theorem 13.7 *Algorithm 13.6 determines a minimal spanning tree on a CRCW-PRAM in extended priority mode. m processors suffice and its running time is bounded by $O(\log_2 n)$ with probability at least $1 - \frac{1}{n}$.*

Exercise 130
A connected undirected graph $G = (V, E)$ is given as well as weights on its edges. In the all-pairs-most shallow path problem we have to determine for each pair of nodes $u, v \in V$ a path from u to v whose maximal weight edge is as small as possible.

(a) Show that there is a tree such that the unique path between any two nodes u and v is the most shallow path between u and v.

(b) Solve the all-pairs-most shallow path problem in time $O(\log_2 |V|)$ with $|V| + |E|$ processors on a CRCW PRAM with priority mode.

Exercise 131
We are given a complete undirected graph $C_n = (V, E)$ with n nodes and a weight function weight: $E \to \mathbb{R}_{\geq 0}$. We require that the triangle inequality

$$\text{weight}(u, v) \leq \text{weight}(u, w) + \text{weight}(w, v)$$

is satisfied for all nodes u, v and w. Our goal is to determine a tour which visits all nodes exactly once and whose length is at most twice as large as the minimal tour. Your solution should run on a EREW-PRAM with $|V|^2$ processors in time $O(\log_2^2(|V|))$.

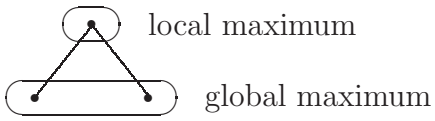
Hint: Show that the weight of a minimum spanning tree is less than or equal to the length of a minimal tour. How do you transform a spanning tree into a not much longer tour? Note that the *traveling salesman problem*, namely to determine a tour of minimal length, is $\mathcal{NP}$-complete.

13.3 Maximal Independent Sets

We say that I is an independent set, if no two nodes of I are connected by an edge Determining a *largest* independent set is a hard problem. In particular it is known that the language

$$\{(G, k) \mid G \text{ has an independent set of size at least } k \}$$

is $\mathcal{NP}$-complete. We say that I is a *maximal* independent set, if I is not contained in a larger independent set, i.e., each node in $V \setminus I$ is connected to a node in I. Thus whereas a largest independent set corresponds to a global maximum, a maximal independent set corresponds to a local maximum.



Sequential solutions are trivial as the following program shows.

Algorithm 13.8 **A simple heuristic**

$I := \emptyset$;

for $v = 1$ to n do

If (v is not connected with a node from I) then

$I = I \cup \{v\}$;

Algorithm 13.8 is trivial, but seems to be inherently sequential, since we cannot predict in early stages if a node is eventually included into I. Indeed, we show in Section 9.3.3 that the for-loop of Algorithm 13.8 cannot be parallelized: the problem to determine whether a node v of G belongs to I has no fast parallel algorithms even if we are allowed to compute with a polynomial number of processors. But is it at least possible to compute *some* maximal independent set? We define

$$N(u) := \{v \in V \mid \{v, u\} \in E\}$$

as the set of neighbors of node u and extend this notion to subsets $X \subseteq V$ by defining

$$N(X) := \bigcup_{u \in X} N(u)$$

as the set of neighbors of X. $d(u) = \mid N(u) \mid$ is the degree of node u.

Algorithm 13.9 **A parallel Independent Set Algorithm.**

(1) Set $I = \emptyset$;

(2) while $V \neq \emptyset$ do

(2a) for $v \in V$ pardo
if (v is isolated) then
$I = I \cup \{v\}$; $V = V \setminus \{v\}$;
else mark v with probability $\frac{1}{2 \cdot d(v)}$;

(2b) for $\{u, v\} \in E$ pardo
if (u and v are both marked) then
unmark the node of smaller degree, resp. unmark both nodes if their degrees coincide;

(2c) /* Let X be the set of nodes which are still marked. */
Set $I = I \cup X$; $V = V \setminus \big(X \cup N(X)\big)$;
/* The set I is independent, but possibly not maximal. We have removed X and the set of its neighbors to prepare the next iteration. Observe that degrees have to be recomputed after any iteration. */

Algorithm 13.9 performs symmetry breaking by randomly selecting nodes. The selection probability of a node is inversely proportional to its degree and we hope of course that the set X of step (2c) is almost independent.

Example 13.3 Let G be a cycle of length n. Then each node has degree 2 and we mark nodes with probability $\frac{1}{4}$. Observe that a node i is inserted into X iff neither $i-1$ nor $i+1$ is marked and this happens with probability $(\frac{3}{4})^2$. Thus we expect $|I| = \frac{1}{4} \cdot (\frac{3}{4})^2 \cdot n \geq \frac{n}{8}$ to hold after the first round.

Exercise 132
Determine the expected number of iterations for the cycle of length n.

If marked nodes are connected to each other, then we remove the node of small degree. Why not remove the node of large degree? If a node of high degree survives, then we can eliminate all of their many neighbors in step (2c) and thus considerably reduce the number of nodes we have to consider.

Example 13.4 This hope is deceptive. We consider a complete bipartite graph with $n^{1/4}$ nodes in the first layer and $n - n^{1/4}$ nodes in the second layer. It is highly probable that Algorithm 13.9 does not choose any high-degree node from the first layer and about $\frac{n^{3/4}}{2}$ nodes from the second layer. In this case only the $n^{1/4}$ nodes of the first layer will be removed from X.

This is bad news, however the bad news turn into good news if we observe that we have removed all edges by removing all layer 1 nodes.

We now show that the above examples are quite characteristic, namely that we can expect

(1) about 50% of all marked nodes to survive

(2) and to remove a constant percentage of all edges per iteration.

Observe that property (2) guarantees an expected number of logarithmically many iterations and Algorithm 13.9 would serve its purpose.

Lemma 13.10 *Any marked node v is inserted into I with probability at least $\frac{1}{2}$.*

Proof: A marked node v is not inserted into I, if a neighbor is marked, whose degree is at least as high as v. Let p be the probability of such an event and set

$$\text{dangerous}(v) = \{\, u \in N(v) \mid d(u) \geq d(v)\}.$$

Then we get

$$\begin{aligned} p &\leq \sum_{u \in \text{ dangerous}(v)} \text{prob}\,[u \text{ is marked}] = \sum_{u \in \text{ dangerous}(v)} \frac{1}{2 \cdot d(u)} \\ &\leq \sum_{u \in \text{ dangerous}(v)} \frac{1}{2 \cdot d(v)} \leq \frac{d(v)}{2 \cdot d(v)} = \frac{1}{2} \end{aligned}$$

and this was to be shown. □

The notion of good nodes and good edges are crucial.

Definition 13.11 A node v is called good iff at least one third of its neighbors have a degree of at most $d(v)$. An edge is good, if at least one endpoint is good.

Example 13.4 shows that there are graphs with only very few good nodes. However we will show later that most edges are good. Thus we have made substantial progress, if we can show that a large proportion of good nodes is removed from V and this is what we show next. If v is good, then v has $d(v)/3$ neighbors of degree at most $d(v)$ and with probability at most

$$p = (1 - \frac{1}{2 \cdot d(v)})^{d(v)/3}$$

none of these neighbors is marked. We apply Lemma 1.2 and obtain

$$p \leq e^{-1/6}.$$

Thus, with probability at least $1 - e^{-1/6}$, at least one such neighbor w is marked. We already know with Lemma 13.10 that a marked node is inserted into I with probability at least $\frac{1}{2}$ and hence the good node v is removed from V with probability at least $\frac{1-e^{-1/6}}{2}$.

Lemma 13.12 *Let v be a good node with at least one neighbor. Then v is removed from V after one iteration with probability at least $\frac{1-e^{-1/6}}{2}$.*

Thus we expect to lose a constant fraction of all good nodes. Our next goal is therefore to show that most edges are good, i.e., are incident to at least one good node.

Lemma 13.13 *At least one half of all edges is good.*

Proof: A bad node v has by definition fewer than $d(v)/3$ neighbors of degree not exceeding its own degree and hence such a node has at least twice the number of higher-degree than lower-degree neighbors.

We direct edges from a low-degree to a high-degree endpoint. If a (now directed) edge $e = (u, v)$ is bad, then we can assign injectively two further edges (v, u_1), (v, u_2) to e, since the bad node v has double the number of higher-degree neighbors.

Thus we have constructed an injection g from the set of bad edges into the set of all pairs of edges and g assigns two edges to any bad edge. But this is only possible, if there are at most $\frac{|E|}{2}$ bad edges. □

Let F be the set of all edges before an iteration (2) in Algorithm 13.9 and let F' be the set of edges which still belong to the graph after the iteration. At least one half of all edges in F has a good node as endpoint. But a good node is eliminated in one iteration with probability at least $c = \frac{1-e^{-1/6}}{2}$ and hence we get $\mathrm{E}\left[|F'|\right] \leq (1 - c) \cdot |F|$.

Exercise 133
Show that Algorithm 13.9 stops after an expected number of logarithmically many iterations.

Theorem 13.14 *Algorithm 13.9 determines a maximal independent set with an expected number of $O(\log_2 n)$ iterations for graphs with n nodes and m edges. $n+m$ processors on a CRCW-PRAM are used.*

Exercise 134
Let G be an undirected graph with n nodes and m edges. A matching of is a subset $M \subseteq E$ of node-disjoint edges. We say that a matching M is *locally optimal*, if no proper superset $M \cup \{e\}$ is a matching. A matching is called *optimal*, if M is a matching with a maximal number of edges.

(a) Let M be a locally optimal matching and let M' be an optimal matching. Show $|M'| \leq 2 \cdot |M|$.

(b) In a group of n people each person knows at least one and at most two persons. Each person decides at random to shake hands with a person she knows. However, a hand shake only counts, if both involved persons choose each other. Show that the expected number of hand shakes is at least $n/4$.

(c) We again consider a group of n people, but now assume no upper bound on the number of acquaintances per person. This time a person first offers her *left* hand to a randomly chosen acquaintance, and in a second step, shakes a randomly chosen left hand offered to her with her *right* hand. In the third and last step each person which is involved in two handshakes withdraws one of her hands at random.

Now we have formed couples which remain stable. We iterate this procedure until no more new couples can be formed. Show that this procedure determines at least opt/2 couples, where opt is the optimal number of couples that can conceivably be formed.

(d) The procedure from part (c) can be implemented on a randomized CRCW PRAM to determine a locally optimal matching with $n+m$ processors. Thus the implementation extends the current matching in each iteration by a matching M. Show for a good node (see Definition 13.11), that

$$\text{prob}[\ v \text{ is endpoint of an edge from } M\ ] \geq 1/4$$

holds.

(e) Show that the expected time of the CRCW PRAM implementation is bounded by $O(\log_2 n)$.

13.4 Coloring

Our goal is to color nodes of an undirected graph with as few colors as possible such that no two adjacent nodes share the same color. We start with coloring very simple graphs, namely cycles which we interpret as circular lists.

13.4.1 List Coloring

In the *list coloring problem*, we have to color a singly linked, circular list with three colors such that neighboring list elements receive different colors. (Observe that there is no coloring with two colors, if the list has an odd number of elements.) The list coloring problem appears to be simple, but our goal is to achieve an almost constant running time.

We assume that the singly linked, circular list is represented by a successor array S, where $S[i]$ specifies the successor of i in the list. Our first goal is to find a coloring with

few colors such that adjacent list elements receive different colors. Assume that the list consists of n elements. We start with an n-coloring by assigning color i to element i and set color$[i] = i$.

Algorithm 13.15 **Reducing the number of colors**

for $i = 1$ to n pardo

Determine a bit position k in which color$[i]$ and color$[S[i]]$ differ. Let b be the kth bit in the binary representation of color$[i]$, where we count bit positions starting from the *least* significant bit.

Set color$^*[i] = 2 \cdot (k-1) + b$.

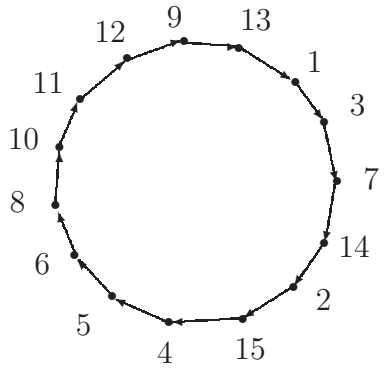
Lemma 13.16 *Assume that the list has n elements which are legally colored with D colors from the set $\{0, \ldots, D-1\}$. Then Algorithm 13.15 finds a legal coloring with at most $d = 2 \cdot \lceil \log_2 D \rceil$ colors from the set $\{0, \ldots, d-1\}$. It runs on a EREW-PRAM in constant time with n processors. Here we assume that a differing bit position can be found in time $O(1)$.*

Proof: We show by contradiction that the new coloring is legal. Assume that there is a list element i with color$^*[i]$ =color$^*[S[i]]$. By definition of color*, there are k and l with

$$\text{color}^*[i] = 2(k-1) + b \quad \text{and} \quad \text{color}^*[S[i]] = 2(l-1) + c.$$

Since $b, c \in \{0, 1\}$, we have $b = c$ and consequently $k = l$. But color$[i]$ and color$[S[i]]$ differ in their kth bit. We have $k = l$ and color$[i]$, color$[S[i]]$ agree in their kth bit position after all.

How many colors are used? The original colors have binary representations of length at most $\lceil \log_2 D \rceil$ and hence we use at most $2 \cdot (\lceil \log_2 D \rceil - 1) + 2 = 2 \cdot \lceil \log_2 D \rceil$ new colors. An EREW implementation is obvious, since each processor just has to read the color of his right neighbor. □



v	color[v]	$k-1$	color*[v]
1	0001	1	2
3	0011	2	4
7	0111	0	1
14	1110	2	5
2	0010	0	0
15	1111	0	1
4	0100	0	0
5	0101	0	1
6	0110	1	3
8	1000	1	2
10	1010	0	0
11	1011	0	1
12	1100	0	0
9	1001	2	4
13	1101	2	5

Example for Algorithm 13.15

To come up with a 3-coloring, we repeatedly apply Algorithm 13.15. Observe however that we reduce the number of colors only if $2 \cdot \lceil \log_2 D \rceil < D$ and this is the case for $D \geq 7$.

Algorithm 13.17 **Determining a 3-coloring**

(1) Set color$[i] = i$;

(2) Apply Algorithm 13.15 as long as at least seven colors are used.

(3) /* Each list element is now colored with a color from the set $\{0, \ldots, 5\}$. Next we remove the colors $3, 4$ and 5. */

for $f = 3$ to 5 do

for $i = 1$ to n pardo
if color$[i] = f$ then
choose a color $f^* \in \{0, 1, 2\}$ which is not used by a neighbor and
set color$[i] = f^*$.

Definition 13.18 For $x > 1$ we set $\log^{(1)}(x) := \log_2 x$ and $\log^{(k)}(x) := \log_2 \left(\log^{(k-1)}(x) \right)$ for $k > 1$. Finally set $\log^*(x) := \min\{i \in \mathbb{N} \mid \log^{(i)}(x) \leq 1\}$.

$\log^*(x)$ is an extremely slow growing function: We have $\log^*(2) = 1$, $\log^*(2^2) = 2$, $\log^* \left(2^{2^2} \right) = 3$ and $\log^* \left(2^{2^{2^2}} \right) = 4 \geq \log^*(64.000)$. Hence we have $\log^*(x) < 5$, whenever $x \leq 2^{64.000}$, and the $\log^*$ function is for all practical purposes bounded by 5.

Theorem 13.19 *Algorithm 13.17 determines a legal 3-coloring for a list of n elements in time $O(\log^* n)$ with n processors. It can be implemented on an EREW-PRAM.*

Proof: In step (3) we also need to know the color of our left neighbor. This is easily achieved, if each processor communicates its color to its right neighbor.

Algorithm 13.17 is obviously correct and we only have to determine the running time. The number of colors is reduced from D to $2 \cdot \lceil \log_2 D \rceil \leq 2\,(\log_2 D + 1) = 2\log_2(2D)$. Applying Algorithm 13.15 twice brings a reduction to at most

$$2 \cdot \log_2\,(4 \cdot \log_2(2D)) \leq 2 \cdot \log_2 \log_2(2D) + 4 \leq \log_2 D \text{ for } D \geq 2^{12}.$$

Hence Algorithm 13.15 is applied at most $(2\log^* n)$ times until $D \leq 2^{12}$ is reached. Then a constant number of applications suffices. □

We now show how to obtain an optimal 3-coloring algorithm, if we allow time $O(\log_2 n)$. We apply Algorithm 13.15 only once to obtain a legal coloring with $O(\log_2 n)$ colors and then construct a 3-coloring by sequentially replacing all colors from 3 onwards.

Algorithm 13.20 **An optimal 3-coloring**

(1) Set color$[(i)] = i$. We work with $p = \frac{n}{\log_2 n}$ processors.

(2) Apply Algorithm 13.15 once.

(3) Sort the list elements according to their color in time $O(\log_2 n)$ with an EREW-PRAM algorithm.

(4) for $f = 3$ to $2 \cdot \lceil \log_2 n \rceil$ do

Distribute the elements with color f evenly among the p processors.

for $i = 1$ to p pardo

Processor i inspects all of its elements sequentially and chooses each time a color different from the color of the two neighbors.

We show in section 13.4.3 how to implement step (3) with $\frac{n}{\log_2 n}$ processors. Thus we obtain

Theorem 13.21 *Algorithm 13.20 determines a 3-coloring for a singly linked, circular list in time $O(\log_2 n)$ with $\frac{n}{\log_2 n}$ processors on an EREW-PRAM.*

13.4.2 Coloring Graphs

The coloring problem for graphs $G = (V, E)$ is hard, since it is known that the language

$$\{(G, k) \mid G \text{ can be colored with at most } k \text{ colors } \}$$

is $\mathcal{NP}$-complete. However, we are content with good and not necessarily optimal solutions and aim at coloring graphs of maximal degree d with at most $d+1$ colors. It is known that such a coloring always exists and can be found by a simple greedy algorithm. (Observe that $d+1$ colors are also required in some cases, since a clique[3] on d nodes has degree $d-1$ and requires d colors.)

Example 13.5 Assume that we have a collection of n processes which compete for resources such as printers or disk accesses. We connect two processes by an edge, if both require the same resource. Assume now that we have found a coloring with c colors. All nodes with the same color form an independent set and hence can be executed in parallel. Thus all processes can be executed within c scheduling steps.

Our algorithmic solution is based on Algorithm 13.17 which 3-colors a cycle of n nodes in time $O(\log^* n)$ with n processors (see Theorem 13.19). In particular we proceed now as follows.

- We direct all edges in an arbitrary way and label all edges leaving a node with numbers from $\{1, \ldots, d\}$.
- The subgraph of all edges with the same fixed label is a "pseudo-forest", i.e., a directed graph of fan-out one. Show that any pseudo-forest can be 3-colored with a modified version of Algorithm 13.17.
- Thus the graph is now decomposed into d pseudo-forests, each of which has been 3-colored. Show how to obtain a $d+1$-coloring by suitably compressing the $3 \cdot d$ colors.

We assume that edges are directed and try to color a pseudo-forest with 3-colors. As for Algorithm 13.17 we start with a coloring which assigns color i to node i and then subsequently reduce the number of colors radically. First we adapt the reduction procedure used by Algorithm 13.17 as follows.

Algorithm 13.22 **Coloring pseudo-forests: Reducing the number of colors.**

for $i = 1$ to n pardo

[3] A clique is an undirected graph such that any two nodes are connected by an edge.

if (i has no successor) then

set color$[i] = \begin{cases} 0 & \text{color(i) is even,} \\ 1 & \text{otherwise;} \end{cases}$

else

/* Let j be the unique successor of i. Determine a bit position k in which color$[i]$ and color$[j]$ differ. Let b be the kth bit in the binary representation of color$[i]$, where we count bit positions starting from the least significant bit. */

set color$^*[i] = 2 \cdot (k-1) + b$;

Exercise 135
Assume that we start with a k-coloring. Show that algorithm 13.22 determines a new coloring with $2 \cdot \lceil \log_2 k \rceil$ colors.

Thus we have obtained the radically reduced coloring as promised and can color pseudo-forests after $O(\log^* n)$ rounds of reducing the number of colors. All we have to do is to run Algorithm 13.17, where we replace calls of Algorithm 13.15 by calls of Algorithm 13.22 and adjust the final compression to three colors.

Algorithm 13.23 **A 3-coloring for pseudo-forests**

(1) Set color$[i] = i$;

(2) Apply Algorithm 13.22 as long as at least seven colors are used.

(3) /* Each node is now colored with a color from the set $\{0, \ldots, 5\}$. Next we remove the colors $3, 4$ and 5. */

for $i = 1$ to n pardo

if (i has no successor) then color$[i] = 5 -$ color$[i]$;

else color$[i]$ = color$[S[i]]$;

/* $S[i]$ is the unique successor of i. We have chosen a new legal coloring such that all immediate predecessors of a node have the same color. If i has no successor, then we have assigned a new color guaranteeing that our revised coloring stays legal. */

for $f = 3$ to 5 do

for $i = 1$ to n pardo

if color$[i] = f$ then

set color$[i] = f^*$, where color $f^* \in \{0, 1, 2\}$ is not used by some neighbor;

We can now formulate the coloring algorithm for graphs.

Algorithm 13.24 **Coloring graphs of degree d with $d+1$ colors.**

/* $G = (V, E)$ is a graph of degree at most d. */

(1) for all edges $\{u, v\} \in E$ pardo

direct $\{u, v\}$ arbitrarily;

for all $v \in V$ pardo

label all edges leaving v injectively with numbers from $\{1, \ldots, d\}$;

(2) for $f = 1$ to d do

color the pseudo-forest of f-edges with three colors

from $\{3 \cdot (f-1), 3 \cdot (f-1) + 1, 3 \cdot (f-1) + 2\}$.

// We have computed a $3d$-coloring, which we now compress into a $d+1$ coloring.

(3) Sort nodes according to their color.

(4) for $f = d + 1$ to $3d$ do

distribute nodes with color f evenly among processors and

replace their color with a new legal color in $\{0, \ldots, d\}$.

We work with n processors, where n is the number of nodes. Step (1) runs in time $O(d)$, since up to $d \cdot n$ edges have to be processed. Step (2) runs in time $O(d \cdot \log n)$, since d pseudo-forests have to be 3-colored. Step (3) is cheap as we will see in section 13.4.3: time $O(\log_2 n)$ suffices.

Exercise 136
Show how to implement step (4) in time $O(d)$ using the priority write resolution scheme. You may assume that the elements of the adjacency list of a node v are stored in an interval of consecutive registers and that the length of this interval is known.

Theorem 13.25 *Algorithm 13.24 colors a graph G of n nodes and maximal degree d with $d+1$ colors. It runs in time $O(\log_2 n + d)$ on an ERCW-PRAM with n processors.*

Exercise 137
Determine a good implementation of step (4) for an EREW-PRAM.

13.4.3 A Parallel Counting Sort

The sequential algorithm Counting Sort sorts an array A of n keys from the set $\{0, \ldots, n-1\}$ in linear time. First the number Count[i] of occurrences of key i is determined. Then we sort A by writing Count[0] zeroes, followed by Count[1] ones etc.

```
void counting_sort ( )
  {
    int Count[m]; int where = 0;
    for (int i = 0; i < m; i++)  //  Initializing Count.
```

```
    Count[i] = 0;
  for (int j = 1; j <= n; j++) //  Computing Count.
    Count[A[j]]++;
  for (i = 0; i < m; i++)  //
    {
     for (j = 1; j <= Count[i]; j++)
       A[where + j] = i;
     where += Count[i];
    }
}
```

Thus Counting Sort runs in time $O(n+m)$. We first describe an efficient parallelization for $m = \log_2 n$ and $p = \frac{n}{\log_2 n}$ processors.

Algorithm 13.26 **Stable Sorting of n numbers from $\{0, \ldots, \log_2 n - 1\}$.**

(1) for $i = 1$ to p pardo

processor i determines the frequency $f_{i,j}$ of value j in its subsequence $A[(i-1)\log_2(n)+1], \ldots, A[i \cdot \log_2 n]$. // Time $O(\log_2 n)$ and p processors suffice.

(2) the processors determine all prefix sums for the following sequence in row-order

$$\begin{array}{llll} f_{1,0} & f_{2,0}, & \ldots, & f_{p,0}, \\ f_{1,1} & f_{2,1}, & \ldots, & f_{p,1}, \\ \cdots & \cdots & & \cdots \\ f_{1,\log_2(n)-1} & f_{2,\log_2(n)-1} & \ldots, & f_{p,\log_2(n)-1} \end{array}$$

This is done with the parallel prefix algorithm after writing $f_{i,j}$ into register $i + j \cdot p$. // Time $O(\log_2 n)$ and p processors suffice.

(3) /* register $i + j \cdot p$ stores now the number $s_{i,j}$ of elements less than j plus the number of elements with value j stored by processors $1, \ldots, i$. */

processor i writes j into the registers with addresses in $[s_{i-1,j} + 1, s_{i-1,j} + f_{i,j}]$.

Theorem 13.27 *Algorithm 13.26 sorts n numbers from the set $\{0, \ldots, \log_2 n - 1\}$ in time $O(\log_2 n)$ with $\frac{n}{\log_2 n}$ processors. It can be implemented as a stable[4] sorting algorithm.*

Hence we can sort n numbers from the set $\{0, \ldots, \log_2^k n - 1\}$ by running k phases. In the first phase we sort the n numbers, restricted to their least significant $\log_2 \log_2 n$ bits, with

[4]A sorting algorithm is stable, if in the sorted sequence the "information" attached to element $A[i]$ appears before the "information" attached to element $A[j]$, provided $A[i] \leq A[j]$ and $i < j$.

algorithm 13.26. We utilize its stability and run it a second time but now on the following $\log_2 \log_2 n$ bits. We can iterate this process k times and have successfully sorted n numbers with $\frac{n}{\log_2 n}$ processors in time $O(k \cdot \log_2 n)$.

Can we do better for n numbers from the set $\{0, \ldots, n-1\}$? We first assume an apparently unfair advantage, namely that we know upper bounds f_i on the number of times element i appears. We also demand that the upper bounds are quite good, namely we demand that

$$\sum_{i=0}^{n-1} f_i = O(n)$$

holds. The idea is now to reserve registers $1 + 2\sum_{i=1}^{k-1} f_i, \ldots, 2\sum_{i=1}^{k} f_i$ for value k: any processor storing an element $A[i]$ with $A[i] = k$ tries to write into one of the registers reserved for k by choosing such a register at random. We say that the processor is successful, if no one else tries to write into the same register. A successful processor is happy, failing processors have to try until they are successful. There seems to be a good chance that processors with value k will all succeed rather quickly, since we reserved twice as many registers as there are requests. Once all attempts have succeeded, all we have to do is to remove gaps with the parallel prefix algorithm and we have sorted.

Algorithm 13.28 **A parallel Counting Sort with upper bounds**

/* The array A is to be sorted. We assume that frequencies $f_0, \ldots f_{n-1}$ are known with $\sum_{i=0}^{n-1} f_i = O(n)$. Frequency f_i is an upper bound on the number of elements with value i, i.e., $|\{i \mid x_i = j\}| \leq f_j$. We work with $p = \frac{n}{\log_2 n}$ processors. */

(1) Compute all prefix sums $s_i = \sum_{i=0}^{n-1} f_i$.

(2) for $i = 1$ to p pardo

for $j = 1$ to $\log_2 n$ do /* sequential for */

processor i inspects $k = A[(i-1)\log_2(n) + j]$ and chooses a random number q with $q \in \{2s_{k-1} + 1, 2s_{k-1} + 2, \ldots, 2s_k\}$;

If the register stores a value different from a default value, then its attempt has failed. Otherwise it tries to write its address into register q and checks in the subsequent step whether its address is stored. If it is, it replaces its address by k and its attempt has been successful.

If the attempt failed, the processor has to try again.

(3) remove gaps with the parallel prefix algorithm.

How long does it take until each processor has successfully stored all of its $\log_2 n$ numbers?

Lemma 13.29 *Let $d \geq 4$ be arbitrary. Algorithm 13.28 solves the sorting problem with upper bounds in time $O(d \cdot \log_2 n)$ with $\frac{n}{\log_2 n}$ processors. This statement holds with probability at least*

$$1 - n \cdot e^{-\frac{d}{16} \cdot \log_2 n}.$$

Proof: We have to worry about using too many attempts. But we know that the success probability is at least $\frac{1}{2}$, since the number of registers is at least twice as large as the number of elements to be stored.

We define the 0-1 random variables $Y_1, Y_2, \ldots, Y_{d \cdot \log_2 n}$ by setting $Y_i = 1$, if processor 1 was successful during its ith attempt to write one of its numbers. We define P as the probability that *some processor* had to use more than $d \cdot \log_2 n$ attempts to successfully write all its $\log_2 n$ numbers. Define P_1 as the probability that processor 1 had to use more than $d \cdot \log_2 n$ attempts. Then

$$P \leq \frac{n}{\log_2 n} \cdot P_1$$

and we concentrate only on processor 1 from now on. Let's check the expected behavior. We have

$$\mathrm{E}\left[\sum_{j=1}^{d \cdot \log_2 n} Y_i\right] \geq \frac{d}{2} \cdot \log_2 n$$

and can apply the Chernoff bound (Theorem 1.8), observing $\frac{2}{d} \leq \frac{1}{2}$ since $d \geq 4$,

$$\begin{aligned} P_1 &\leq \mathrm{prob}\left[\sum_{j=1}^{d \cdot \log_2 n} Y_j < \log_2 n\right] \\ &\leq \mathrm{prob}\left[\sum_{j=1}^{d \cdot \log_2 n} Y_j \leq \frac{2}{d} \cdot \frac{d}{2} \cdot \log_2 n\right] \\ &\leq \mathrm{prob}\left[\sum_{j=1}^{d \cdot \log_2 n} Y_j \leq \left(1 - \frac{1}{2}\right) \cdot \frac{d}{2} \cdot \log_2 n\right] \\ &\leq e^{-\frac{1}{4} \cdot \frac{d}{4} \cdot \log_2 n}. \end{aligned}$$

Thus we can conclude $P \leq \frac{n}{\log_2 n} \cdot e^{-\frac{d}{16} \cdot \log_2 n} \leq n \cdot e^{-\frac{d}{16} \cdot \log_2 n}$ and this was to be shown. □

Our goal is to determine upper bounds for frequencies in expected time $O(\log_2^2 n)$ with $p = \frac{n}{\log_2^2 n}$ processors. We work probabilistically and draw a sample of $s = \frac{n}{\ln n}$ numbers from the array A. We then sort the sample with the randomized quicksort in expected time $O(\frac{s \cdot \log_2 s}{p} + \log_2^2 p) = O(\log_2^2 n)$. We will see that determining frequencies, restricted to the sample, is easy with a parallel prefix algorithm, since the sample is already sorted.

However it is quite likely that the sample frequencies are inaccurate and hence we take them only as a first rough guess and "round them up". However the rounding process may

make the sum of new frequencies too large. Therefore we restrict all values of A to belong to the set $\{0,\ldots,m-1\}$ and determine first for which values of m reliable upper bounds can be determined.

We fix the value of j. Let f_j be the observed frequency of j in the sample and let h_j be the true frequency in A. To investigate f_j we assume that the sample is determined by successively choosing s components from A with replacement. We therefore define random variables $X_1,\ldots,X_s$ with $X_i = 1$, iff j is chosen as the ith element of the sample, and $X_i = 0$ otherwise. Obviously we have

$$f_j = \sum_{i=1}^{s} X_i.$$

The next step is an application of the Chernoff bound, utilizing that $X_1,\ldots,X_s$ are independent random variables. We observe that $E[f_j] = \frac{h_j}{n}\cdot s$ is the expected value of the sample frequency f_j and obtain

$$\text{prob}[\ \sum_{i=1}^{s} X_i \leq (1-\beta)\cdot E[\sum_{i=1}^{s} X_i]\ ] \leq e^{-E[\sum_{i=1}^{s} X_i]\cdot\beta^2/2}.$$

We set $\beta = 1/2$, utilize that $f_j = \sum_{i=1}^{s} X_i$ as well as $E[\sum_{i=1}^{s} X_i] = E[f_j] = \frac{h_j}{n}\cdot s$ hold and obtain

$$\text{prob}[\ f_j \leq \frac{1}{2}\cdot\frac{h_j}{n}\cdot s\ ] \leq e^{-\frac{h_j}{n}\cdot s\cdot/8}.$$

The observed frequency f_j should be extrapolated as $f'_j = \frac{n}{s}\cdot f_j$ and we get prob$[\ f'_j \leq \frac{1}{2}\cdot h_j\ ] \leq e^{-\frac{h_j}{n}\cdot s\cdot/8} = e^{-\frac{h_j}{\ln n}/8}$. However the estimate f'_j is insufficient for instance if h_j is small: in this case j might not even occur in the sample. Moreover we have m experiments, one for each value in $\{0,\ldots,m-1\}$, and errors accumulate. We therefore "round up" and choose

$$f^*_j = 16\cdot\max\{f'_j, \ln^2 n\}$$

as upper bound.

- If $h_j \leq 16\ln^2 n$, then $h_j \leq f^*_j$ holds with certainty.
- If $h_j > 16\ln^2 n$, then $h_j > f^*_j$ holds with probability at most $e^{-2\ln n} = n^{-2}$. Thus $h_j \leq f^*_j$ holds for all values j with probability at least $1-\frac{1}{n}$.
- We have to bound the sum of upper bounds and get $\frac{1}{16}\cdot\sum_{j=0}^{m-1} f^*_j \leq m\cdot\ln^2 n + \sum_{j=0}^{m-1} f'_j = m\cdot\ln^2 n + \frac{n}{s}\cdot\sum_{j=0}^{m-1} f_j = m\cdot\ln^2 n + n$. We therefore choose $m = \frac{n}{\ln^2 n}$.

Algorithm 13.30 **Upper-bounding frequencies**

/* The array A has only elements from the set $\{0,\ldots,m-1\}$, where $m = \frac{n}{\ln^2 n}$. We work with $p = \frac{n}{\log_2^2 n}$ processors. */

(1) draw a sample of $s = \frac{n}{\ln n}$ elements from A;

(2) sort the sample with the randomized quicksort.

/* Time $O(\log_2^2 n)$ with $\frac{n}{\log_2^2 n}$ processors suffices. */

(3) to determine the frequency f_j^* of value j within the sample, apply the parallel prefix algorithm over the domain $\mathbb{N} \times \{0, \ldots, \frac{n}{\log_2^3 n} - 1\}$ and define the associative operation $*$ by

$$(i,j) * (k,l) = \begin{cases} (i+k, j) & j = l, \\ (k,l) & \text{otherwise.} \end{cases}$$

/* The pair (i,j) expresses that so far i elements with value j appeared. The operation $*$ is continuing the counting, as long as identical values meet and otherwise resets the counter. Before applying the parallel prefix algorithm, each element $A[i]$ of the sample has to be replaced by $(1, A[i])$. */

(4) Let $t_1, \ldots, t_s$ be the sequence of prefix sums.

for $j = 0$ to $m - 1$ pardo

$$f_j := \begin{cases} i & \exists k \text{ with } t_k = (i,j), t_{k+1} = (i',j') \text{ and } j < j', \\ 0 & \text{otherwise.} \end{cases}$$

(5) for $j = 0$ to $m - 1$ pardo

$f_j^* = 16 \cdot \max\{\frac{n}{s} \cdot f_j, \ln^2 n\}$.

We summarize.

Theorem 13.31 *Let $m = \frac{n}{\ln^2 n}$. Algorithm 13.30 sorts an array of length n with values in $\{0, \ldots, m-1\}$ with $\frac{n}{\log_2^2 n}$ processors in time $O(\log_2^2 n)$. This statement holds with probability at least $1 - \frac{1}{n}$.*

Finally we utilize that algorithm 13.30 is stable.

Algorithm 13.32 **A parallel Counting Sort for** $\{0, \ldots, n \cdot \log_2^k n\}$

(1) Sort the sequence, but restricted to the last $\log_2 n - \log_2 \ln^2 n$ least significant bits. In particular

determine upper bounds on frequencies with algorithm 13.30;

sort with algorithm 13.28;

(2) sort according to the remaining $O(k \cdot \log_2 \log_2 n)$ bits by applying the stable sorting algorithm 13.26 $O(k)$ times.

Theorem 13.33 *Algorithm 13.32 sorts n numbers from the set $\{0, \ldots, n \cdot \log_2^k n\}$ with $\frac{n}{\log_2^2 n}$ processors. With probability at least $1 - \frac{1}{n}$ time $O(k \cdot \log_2^2 n)$ is sufficient.*

Exercise 138
A summation CRCW-PRAM solves a write conflict by summing all values requesting the same register and assigning the sum to the register.

Show how to sort n keys from the set $\{0, \ldots, n^2 - 1\}$ in time $O(\log_2 n)$ with $\frac{n}{\log_2 n}$ processors.

13.5 Conclusion

We have seen crucial applications of symmetry breaking in all problems we discussed, emphasizing that symmetry-breaking may be one of the most important algorithmic methods for graph problems. In all applications, with the exception of graph coloring, we have used randomization as "symmetry-breaker".

Part III

Distributed Algorithms

Chapter 14

Introduction

We assume the model of asynchronous message passing within the framework of fixed connection networks: processors are interconnected by links and compute asynchronously by exchanging messages with their neighbors. Links are fixed once and for all and hence the computation proceeds on the undirected graph $G = (V, E)$, where V is the set of processors and E is the set of links between processors. We assume throughout that processors have only limited knowledge of the distributed system G, a realistic assumption for large distributed systems such as the Internet.

Asynchronous computations are nondeterministic, since message delays are unpredictable. Distributed algorithms have to cope with any potential delay scenario and are therefore in general far more difficult to design than parallel algorithms for synchronous computations.

Two complexity measures are of interest, namely the *message complexity* and the *time complexity* of a distributed algorithm. The message complexity of an algorithm is the maximum, over all possible delay scenarios, of the total number of messages sent. Since the time required for a basic communication between neighbors is by several orders of magnitude larger than the time to process elementary statements, we have to be interested in reducing the message complexity as far as possible.

The running time of a local computation is defined as for a sequential computation. Messages however may be delayed and we assume that any delay in the real-valued interval $[0, 1]$ can potentially occur. Our algorithms have to cope with unbounded delays: delays in the interval $[0, 1]$ are used for analyzing running time under "fair conditions" only. Certainly we should try to minimize running time.

In this chapter we introduce the echo algorithm and study different broadcasting services. In Chapter 15 we tackle the problem of selecting a leader, an innocent, but surprisingly nasty problem. As a consequence of our solution we will be able to determine spanning trees even without distinguished nodes. Distributed traversal algorithms are the next topic. We study depth-first and breadth-first search traversals and experience the

complexity of designing efficient distributed algorithms already for the "simple" breadth-first search traversal. We conclude with a distributed algorithm to determine minimum spanning trees. Chapter 16 deals with the problem of synchronizing distributed algorithms, a technique which allows to apply arbitrary algorithms to asynchronous computing models.

14.1 The Echo Algorithm

We describe the echo algorithm. If the echo algorithm is initiated by processor r, then it determines a spanning tree rooted in r

Algorithm 14.1 **The echo algorithm.**

/* Initially all nodes, except the root, are asleep. For each node w parent pointers and the sets Children_w are to be computed. Initially all parent pointers are set to be nil, the sets Children_w are empty and the local variables "received_w" is initialized to be zero. */

(1) the root r sends a wake-up call to all its neighbor;

(2) upon w receiving a wake-up call from node v;
    if (parent$[w]$ = `nil`) then
        parent$[w] = v$;
        send a wake-up call to all neighbors except v;
    else $\text{received}_w = \text{received}_w + 1$;

(3) upon w receiving a "child" message from node v;
    insert v into Children_w;
    $\text{received}_w = \text{received}_w + 1$;

(4) when ($w \neq r$ and received_w = number of neighbors of w -1)
    send a "child" message to parent$[w]$;

(5) when ($w = r$ and received_r = number of neighbors of r)
    the root has received all acknowledgements and the computation stops;

Theorem 14.2 *Let $G = (V, E)$ be a network with diameter D. The echo algorithm determines a spanning tree for G in time $O(D)$ by exchanging at most $O(|E|)$ messages.*

Assume that we are given an associative and commutative operation $\oplus$ such as addition, multiplication, minimum or maximum. If processor i stores the value x_i, then we can determine the "sum" $x_1 \oplus \cdots \oplus x_n$ by first computing a spanning tree with the help of the

echo algorithm. Then nodes recursively determine the sum of values within their subtree and report the value to their parents. Thus we may use the echo algorithm to evaluate sums.

Observe that the echo algorithm, when executed in a *synchronous* fashion, computes a breadth-first search tree. We show in Sections 15.1 and 15.2 how to compute a depth-first traversal respectively a breadth-first traversal in linear time asynchronously.

14.2 Broadcast Services

Our goal is to support a *broadcast service* and in particular to support the operations

- $\text{send}_i(m, \text{qos})$: processor i broadcasts message m and requires qos as quality of service.
- $\text{receive}_i(m, j, \text{qos})$: processor i receives the message m that was previously broadcast by processor j. Again, qos describes the desired quality of service.

We differentiate various quality measures. In the **basic quality of service** model (`basic`) the properties of *integrity* (every received message must have been previously broadcasted), *liveness* (every processor eventually receives every broadcast) and *no duplicates* (no broadcast is received more than once) are enforced.

The **single-source FIFO** (`ss-fifo`) model assumes the properties of the `basic` model, but additionally guarantees that all messages sent by the same source i are received in the order that they are sent[1].

The **total order** (`total`) model requires the `basic` model and it also guarantees that all processors receive messages in the same order. (Observe that the `total` model does not necessarily subsume the `ss-fifo` model.)

To introduce the next quality of service we first define the notion of an *event* as well as the *happen before* relation. (See also figure 14.1.)

Definition 14.3 A distributed algorithm generates events for each processor[2]. Events are **internal** computations or communication steps such as **send** or **receive** operations. We say that event E_1 **happens before** event E_2 iff

- E_1 and E_2 are events for the same processor and event E_1 occurs before E_2 or
- E_1 is a send event for a message m sent from a processor p to a processor q and E_2 is the corresponding receive event for message m or
- there is a sequence $D_1, \ldots, D_k$ of events with $D_1 = E_1$ and $D_k = E_2$ such that D_i happens before D_{i+1} for all $i < k$.

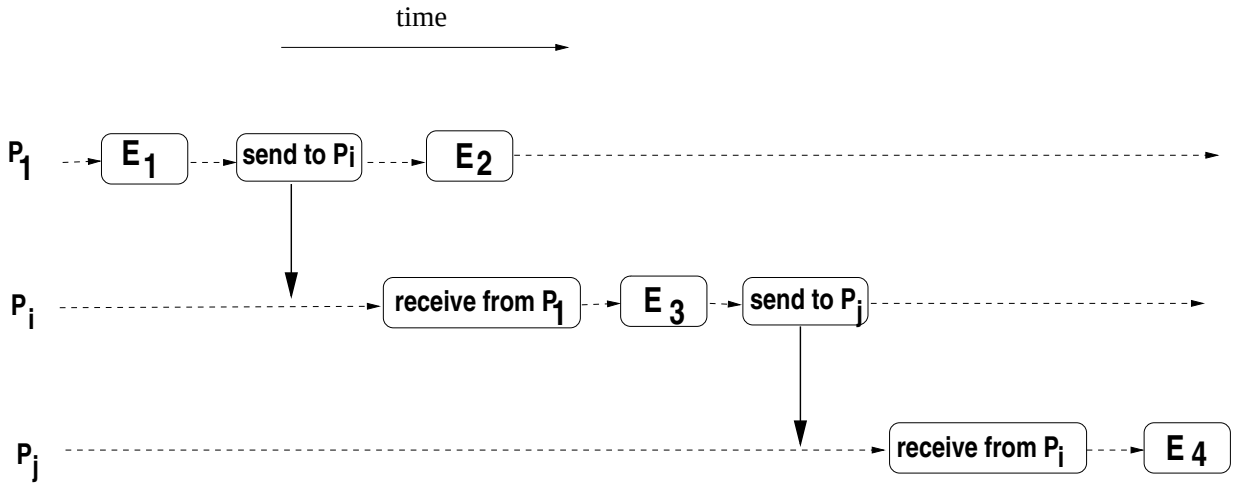


Figure 14.1: Event E_1 happens before E_2, E_3 and E_4. Event E_3 happens before E_4. Event "receive from P_1" happens before E_3 and E_4. But E_2 does not happen before E_3.

Finally we define the model of **causal ordering** (`causal`): for any two messages m_1 and m_2 and for any processor p, if m_1 happens before m_2, then p receives m_1 before m_2. Moreover we also require that the the `basic` model is subsumed. (Observe that the `causal` model subsumes the (`ss-fifo`) model, but the `causal` and `total` model may be incomparable.)

How can implement the various broadcast services? The `basic` model can be implemented by the echo algorithm. To implement the `ss-fifo` model we again use the echo algorithm, but append a sequence number to each message: if processor p sends a message with sequence number T, then a subsequent message is sent with sequence number $T+1$. If a processor q receives a message from processor p with sequence number T, then it "opens" the message only, if all messages with sequence numbers smaller than T have already been received. Appending sequence numbers is not necessary if each processor forwards messages in a first-in-first-out manner.

The echo algorithm is also the basic ingredient for an implementation of the more complicated `total` and `causal` model. The idea is as follows. Messages are appended by timestamps and a processor sends a message with a time stamp larger than any other timestamp it knows of. A processor opens a received message m only, if the timestamp of m is minimal among all unopened messages and if it knows that no messages with smaller timestamps are "on the way". But their knowledge is necessarily inaccurate and to obtain a better approximation of a global clock they inform each other whenever they see a message from a colleague with a timestamp larger than their current estimate for this colleague. This is done by a broadcast within the `ss-fifo` model.

[1]We assume that each processor executes at most one receive operation at any time.
[2]A more general definition allows to associate events with processes instead of processors.

Algorithm 14.4 **Broadcasting with timestamps.**

/* `qos` is either `total` or `causal`. */

(1) when executing a send$_i(m,$ `qos`$)$ operation;

BEGIN when

time$_i[i]$ = time$_i[i] + 1$;

send$_i((m,$time$_i[i]),$ `ss-fifo`$)$;

END when;

(2) when executing a receive$_i((m, T), j,$ `ss-fifo`$)$ operation;

BEGIN when

time$_i[j] = T$;

/* T is the largest timestamp from j, since send operations use `ss-fifo`. */

message (m, T, j) is inserted into Pending, but not opened;

if $T >$ time$_i[i]$ then

time$_i[i] = T$; send$_i((\text{update}, T),$ `ss-fifo`$)$;

/* Colleagues are informed that a new larger timestamp has been found. */

END when

(3) when executing a receive$_i((\text{update}, T), j,$ `ss-fifo`$)$ operation;

time$_i[j] = T$; /* Again we utilize the `ss-fifo` service. */

(4) when $((m, T, j) \in \text{Pending}) \wedge (\forall k : T \leq \text{time}_i[k]) \wedge ((T, j)$ is the lexicographically smallest pair in Pending)

execute a receive$_i(m, j,$ `qos`$)$ operation; /* (m, T, j) is opened. */

We verify that Algorithm 14.4 implements the `total` service. Integrity and no duplicates follows, since we are using the `ss-fifo` service. Is liveness satisfied, i.e., is each message received and opened? The `ss-fifo` service guarantees that each message is received and hence we have to ask whether a received message (m, T, j) is eventually opened. We assume by way of contradiction that (m, T, j) is stuck in the pending set of processor i and that (m, T, j) is the lexicographically smallest stuck message. Thus it is only possible to stop (m, T, j) by enforcing time$_i[k] < T$ for some k.

However the `ss-fifo` service satisfies liveness and processor k eventually receives message (m, T) from processor j. The message will force processor k to raise its timestamp to T and to broadcast its update (see step (2)). Processor i eventually receives the update and resets time$_i[k]$ in step (3), thus removing the lock on (m, T, j).

Finally we check that all processors open messages in identical order. Assume that processor p_i opens message (m_1, T_1, j_1) before message (m_2, T_2, j_2) is opened. Hence p_{j_1} has sent m_1 with timestamp T_1 and p_{j_2} has sent m_2 with timestamp T_2. It suffices to show that $(T_1, j_1) < (T_2, j_2)$ holds, since then each processor has to open messages in the same sequence.

Case 1: (m_2, T_2, j_2) is in the pending set of processor i, when (m_1, T_1, j_1) is opened. Hence $(T_1, j_1) < (T_2, j_2)$ follows.

Case 2: (m_2, T_2, j_2) is not in the pending set of processor i, when (m_1, T_1, j_1) is opened. At the time of opening (m_1, T_1, j_1) the inequality $T_1 \leq \text{time}_i[j_2]$ has to hold and processor i has received a message from processor j_2 with a timestamp of at least T_1. But (m_2, T_2, j_2) is received later and, due to the properties of a `ss-fifo` service, has been sent later. Therefore $T_1 < T_2$ follows as a consequence of timestamping in step (1).

Theorem 14.5 *Algorithm 14.4 implements a broadcast in the* `total` *model and in the* `causal` *model.*

Proof: We still have to verify that Algorithm 14.4 implements the `causal` service. We already know that $(T_1, j_1) < (T_2, j_2)$ holds, whenever some processor opens (m_1, T_1, j_1) before (m_2, T_2, j_2). Thus it suffices to show that $T_1 < T_2$ holds, whenever sending m_1 happens before sending m_2.

This is certainly the case, if m_1 and m_2 are sent by the same processor, since we are using the `ss-fifo` service. Hence we have to show that $T_1 < T_2$ holds, provided processor j_2 receives (m_1, T_1, j_1) before broadcasting (m_2, T_2). But $T_1 < T_2$ follows due to the way processor j_2 timestamps in steps (1) and (2). □

Chapter 15

Leader Election and Spanning Trees

In the *rooted spanning tree* problem we are given a network of processors and have to determine a parent pointer for each processor. In the *unrooted spanning tree* problem each processor has to determine its incident tree edges. Finally we also consider the problem of *electing a leader*, or in other words, to distinguish exactly one processor. (The leadership problem is solved, if each processor knows whether it is the leader.)

We will see that the unrooted spanning tree problem is equivalent to the leadership problem. But we have to start with a bad surprise, since the leadership problem (and hence the unrooted spanning tree problem) turns out to be unsolvable in anonymous systems!

Definition 15.1 A network is called anonymous iff all processors have initially identical information and start in the same initial state.

Lemma 15.2 *If all processors of an anonymous network have the same number of neighbors, then no deterministic algorithm can select a leader.*

Proof: Let D be a deterministic leader selection algorithm. We show that D fails even if processors compute in a synchronous manner. Initially all processors are in the same state and have identical information. Therefore we may assume inductively that all processors are in the same state after t steps and have received, respectively sent identical messages so far. Thus, in step $t+1$, all processors receive the same message from the same number of neighbors and, since all processors have an identical history, they act identically in step $t+1$. □

We have two options. Namely we can try randomized algorithms or equip each processor with a unique ID. We choose the second option.

Theorem 15.3 *Assume that the network $G = (V, E)$ has n processors with unique IDs.*

(a) If we are given an unrooted spanning tree T for the network, then we can determine a leader with n messages in time $O(H)$, where H is the height of T.

(b) If we are given a leader, then we can determine a (rooted) spanning tree with $O(|E|)$ messages in time $O(D)$, where D is the diameter of the network.

Proof (a): Observe that a node is a leaf iff it has exactly one neighbor. We send messages from the leaves upwards and observe that the messages converge in a node or an edge.

Algorithm 15.4 **Electing a leader on an unrooted spanning tree**

(1) processor i determines whether it is a leaf;

(2) if (i is a leaf) then

    i sends "elect" to its parent;

(3) upon receiving elect messages from all but one neighbor:

    send an elect message to the remaining neighbor;

    /* Either there is a node receiving elect messages from all of its neighbors before sending an elect message itself or there is an edge transporting elect messages in both directions. */

(4) upon receiving elect messages from all neighbors before sending an elect message itself:

    the processor is elected;

(5) upon receiving elect messages from a neighbor to which an elect message was sent:

    exchange IDs and elect the node with larger ID;

We call this procedure a *convergecast*, since the information from all nodes converges in a "reverse" *broadcast*.

Exercise 139
Modify Algorithm 15.4 such that each node can determine when to stop.

(b) We already know that we can use the echo algorithm to determine a spanning tree given a leader r. (See Theorem 14.2.) □

We now simultaneously determine a leader and build a spanning tree by building successively growing spanning forests[1]. Whenever two spanning trees meet, the two trees are merged and the root with larger ID is chosen as new root.

[1] A spanning forest is a subgraph without a cycle. Moreover all nodes have to belong to the subgraph.

However, since we are computing in a distributed fashion, the process of merging trees and choosing a new root is only eventually completing. Moreover, before completion a new merging step might have occurred which complicates things even further. But the conceptual approach is simple: all nodes *broadcast* their IDs, a process that we interpret as growing broadcast trees. As soon as a subtree has a confirmed leaf, this leaf participates in a *convergecast* in order to conclude the election. However, as soon as a larger ID is detected, links are reset and any convergecast is immediately halted upon detection. After a while we have new confirmed leaves and the whole process starts over again.

Algorithm 15.5 **Building a spanning tree and determining a leader.**

/* Each node w maintains the value $\mathrm{Max}(w)$, which stores the largest ID seen so far. Initially $\mathrm{Max}(w) = \mathrm{ID}_w$ and $\mathrm{parent}[w] = w$ for all nodes w. Finally each node w maintains counters "$\mathrm{received}_w$", "$\mathrm{acknowledged}_w$" with initial value zero. */

(1) each node w sends ID_w to all its neighbors;

(2) upon w receiving the message m from node v;

if $(m > \mathrm{Max}(w))$ then

BEGIN if /* Panic! Reinitialize parameters. */

$\mathrm{Max}(w) = m$; $\mathrm{parent}[w] = v$;

set $\mathrm{received}_w = 0$;

send the value m to all neighbors except v;

END if;

if $(m = \mathrm{Max}(w))$ then

$\mathrm{received}_w = \mathrm{received}_w + 1$;

/* Ignore any message m with $m < \mathrm{Max}(w)$. */

(3) when ($\mathrm{received}_w$ = number of neighbors of w-1)

if $(\mathrm{Max}(w) \neq \mathrm{ID}_w)$ then

send the message $\mathrm{Max}(w)$ to $\mathrm{parent}[w]$;

/* w reports to its parent that $\mathrm{Max}(w)$ is the largest ID in its subtree. */

(4) when ($\mathrm{received}_w$ = number of neighbors of w)

send "w is the leader" to all neighbors;

/* Only the root receives acknowledgements from all neighbors. All children of w have verified $\mathrm{Max}(w)$ as largest ID and w is elected. */

(5) upon w receiving a "u is the leader" or a "child" message from node v;
    if (acknowledged$_w = 0$ and w is not the leader) then
        send "u is the leader" to all neighbors except v;
    /* The first received message must be a leader message. */
    acknowledged$_w$ = acknowledged$_w + 1$;

(6) when (acknowledged$_w$ = number of neighbors of w);
    send a "child" message to parent[w] and stop working;

Theorem 15.6 *Algorithm 15.5 determines a leader and a spanning tree for an undirected graph $G = (V, E)$. It uses $O(|V| \cdot |E|)$ messages and runs in time $O(D)$, where D is the diameter of G.*

Exercise 140
Verify Theorem 15.6. Observe that a node with a self loop counts itself as a neighbor.

Hint: Why does a node inform its parent in step (3) only after consulting all other nodes? Is a leader message for node u always correct?

Exercise 141
Design a randomized algorithm to simultaneously determine a leader and build a spanning tree even for anonymous networks.

15.1 Depth-first Search

The sequential depth-first search traversal of a network $G = (V, E)$ leads to a running time of $O(|E|)$, provided G is connected. We show how to come up with a solution in linear time.

We imagine that a token is passed around and that its path describes the depth-first traversal. Our algorithm guarantees that the token moves only along tree edges and hence linear time is guaranteed. The basic idea is as follows. If a processor p receives the token for the very first time, p informs all neighbors except its father by sending a "visit" message. It then waits until all neighbors have acknowledged the message. Thus all neighbors know that p has been visited and will not attempt to visit p again, unless returning to p, since the subtree of p has been successfully traversed.

Algorithm 15.7 **Depth-first search in linear time**

/* Initially all parent pointers are defined to be nil. Each processor q is equipped with an array traversed$_p$ which has one entry for every neighbor of q. All cells of traversed$_p$ are initialized to be false. Processor p acts as an initiator. */

(1) for the initiator p only:

make yourself your own parent;

send the message (`visit`,p) to all neighbors;

wait until all messages have been acknowledged;

choose an arbitrary neighbor q; set traversed$_p[q]$ = true and send the token to q;

(2) upon q receiving a (`visit`, r) message;

acknowledge and set traversed$_q(r)$ = true;

(3) upon q receiving the token from processor q_0;

BEGIN upon

if (q is visited for the first time) then

BEGIN if

set q_0 to be your parent;

send the message (`visit`,q) to all neighbors except q_0;

wait until all messages have been acknowledged;

END if;

if (there is a neighbor r with traversed$_q[r]$ = false) then

set traversed$_q[r]$ = true and send the token to r;

else send the token to your father;

/* if q is the initiator, then q terminates. */

END upon;

The token passes each tree edge twice and waits at most one step before being passed onto the next node. (The delay is due to the period waiting for acknowledgments.) Hence the algorithm runs in linear time. Finally observe that each non-tree edge carries two `visit` messages and two acknowledgments and each tree edge carries one `visit` message (from the parent to the child), one acknowledgment (from the child to the parent) and two token messages.

Theorem 15.8 *Algorithm 15.7 determines a depth-first search traversal of an undirected network $G = (V, E)$ in time $O(|V|)$ by exchanging at most $4 \cdot |E|$ messages.*

We can slightly improve Algorithm 15.7 by not requesting acknowledgments and thus not requiring a one-step delay. However now it may happen that a processor p sends a `visit` message to all neighbors, passes the token along to neighbor q, but the `visit` message to a neighbor r is delayed for so long that r is traversed during the traversal of q. Thus

it may happen that r forwards the token back to p and the token is thus passed along a non-tree edge. However p expects the token to be handed back from q and knows that its `visit` message to r is delayed. It sets $\text{traversed}_p[r] = \text{true}$ and ignores the token. Processor r receives the (`visit`,p) message eventually and knows that it forwarded the token incorrectly. It sets $\text{traversed}_r[p] = \text{true}$ and continues.

15.2 Breadth-First Search and Single-Source-Shortest Paths

Our goal is to determine single-source shortest paths for undirected graphs. If Algorithm 14.1 computes in a synchronous fashion, then it computes a breadth-first search tree for the graph $G = (V, E)$. Moreover Algorithm 14.1 requires $O(|E|)$ messages and synchronous time $O(D)$, where D is the diameter of G. It turns out that asynchronous algorithms achieve only rather weak performances.

We first describe a distributed version of Dijkstra's algorithm for a distinguished source s. Our algorithm works in D phases. After phase d a tree T_d of shortest paths is constructed which covers all nodes within distance at most d from s. In phase $d+1$ we extend T_d to include all nodes within distance exactly $d+1$.

First the root of T_d sends a "pulse" message to the nodes of T_d. If a leaf receives the pulse, it sends an (explore,$d+1$) message to all those neighbors in G which are within distance at least d from s. If a node u outside of T_d receives its first (explore,$d+1$) message from a leaf v, it sends a positive acknowledgment to u and considers itself to be a child from v, whereas all subsequent (explore,$d+1$) messages are negatively acknowledged. A leaf waits until all of its neighbors within distance at least d have sent their acknowledgments. (We interpret receiving a (explore,$d+1$) message from a fellow leaf as a negative acknowledgment.) After receiving all desired acknowledgments the leaf sends a positive (negative) acknowledgment to its parent whenever it has received itself at least one positive (resp. no positive) acknowledgment. Acknowledgments are propagated back to the root following the procedure outlined for leaves. If the root receives at least one positive acknowledgment, it starts a new phase by sending another pulse message and otherwise broadcasts a "done" message.

Theorem 15.9 *Let $G = (V, E)$ be an undirected graph with edges of length one only. Let $s \in V$ be a distinguished node. The distributed version of Dijkstra's algorithm determines a tree of shortest paths with root s. It requires $O(|E| + D \cdot |V|)$ messages and runs in time $O(D^2)$, where D is the diameter of G.*

Proof: The algorithm runs in D phases and each phase requires time $O(D)$ to broadcast the pulse message and to collect acknowledgments. (The extension process of T_d is fast and requires only constant time.) Tree edges are used for communicating up to D times,

whereas non-tree edges are used only once. Hence at most $O(|E| + D \cdot |V|)$ messages are sent. □

The performance is not satisfactory, since the running time is quadratic when compared to the running time for synchronous computing. The reason is that the root enforces a quasi-synchronous computation by sending its pulse messages and this synchronization overhead dominates the message and running time complexity. In our next attempt we follow a truly distributed approach.

Algorithm 15.10 **The asynchronous Bellman Ford algorithm.**

/* Parent pointers are computed to define a shortest path tree for source s. Initially all parent pointers are defined to be nil and the variables distance(i) are initialized to be infinite for all nodes except s. We set distance(s) = 0. */

(1) the source s sends zero to all its neighbors;

(2) upon receiving a message from node v with value d;

```
if (d+ weight(v, i) < distance(i)) then
BEGIN if
    make v your parent;
    distance(i) = d+ weight(v, i);
    send a message with value distance(i) to all neighbors except v;
END if;
```

Exercise 142
Show that the tree as defined by the parent pointers eventually coincides with a tree of shortest paths.

Exercise 143
Assume that all weights are one. D denotes the diameter.

(a) Modify Algorithm 15.10 such that each processor can decide upon terminating.

(b) Show that at most $O(D \cdot |E|)$ messages are sent.

(c)Show that Algorithm 15.10 runs in time $O(|V|)$ and give an example in which time $\Omega(|V|)$ is required.

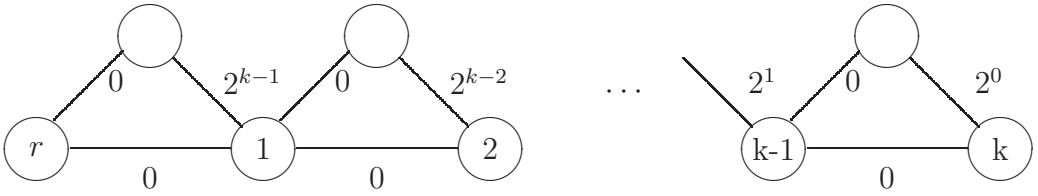
Exercise 144
Show that the algorithm of Bellman Ford runs in time $O(|V| \cdot |E|)$ when computing in a synchronous fashion with arbitrary edge lengths. (Even edges of negative length are allowed as long as no cycles of negative length exist.)

The performance of Algorithm 15.10 is mixed. It does eventually converge against a tree of shortest paths and does so reasonably fast in case all weights are one. For large diameter

$D = \Theta(n)$ and edge lengths one Bellman Ford is superior, whereas the distributed version of Dijkstra's algorithm is superior for small diameter $D = o(\sqrt{|V|})$.

However we show next that the performance of the asynchronous Bellman Ford algorithm for arbitrary non-negative weights may be disastrous. We define message delays such that the Bellman Ford algorithm is forced into exponential running time. To achieve this goal we make the realistic assumption that messages are transported according to the first-in-first-out principle.

We consider a rather simple input graph which results after gluing together 3-cycles. Assume that n is odd and let $n = 2 \cdot k + 1$.



Observe that the shortest path from source r to node k has length zero. However the longest path has length $2^k - 1$ and we schedule messages in such a way that all distances from the set $\{2^k - 1, 2^k - 2, \ldots, 2, 1, 0\}$ are eventually assumed. We begin by delaying messages along horizontal edges and processor k will therefore determine $2^{k-1} + 2^{k-2} + \cdots + 2 + 1 = 2^k - 1$ as its first distance estimate.

Then we allow the message from $k - 1$ to k to arrive and processor k decreases its estimate to $2^k - 2$. Next we allow the message from $k - 2$ to arrive in $k - 1$ and $k - 1$ will therefore update its own distance estimate from $2^k - 2$ to $2^k - 4$. Processor $k - 1$ sends its new estimate along both edges; we again delay the horizontal edge and processor k receives $2^k - 4$ via its expensive edge of length one and it updates its distance from $2^k - 2$ to $2^k - 3$. We release the message waiting for delivery along the horizontal edge between $k - 1$ and k and processor determines the new estimate $2^k - 4$.

We repeat this process of releasing messages waiting for transportation along horizontal edges, but immediately stopping progress by forcing the news of the shorter connection to travel along expensive edges. Observe that we simulate a binary counter and hence all intermediate estimates will be assumed: we have forced Algorithm 15.10 to run for $2^k = 2^{(n-1)/2}$ steps.

Theorem 15.11 *(a) Algorithm 15.10 eventually stabilizes and its parent pointers define a tree of shortest paths.*

(b) If all weights are one, then it computes with $O(n \cdot |E|)$ messages in time $O(D)$, where D is the diameter of the network.

(c) For arbitrary weights and synchronous computing, algorithm 15.10 requires at most $O(n \cdot |E|)$ edges and uses at most $n-1$ rounds.

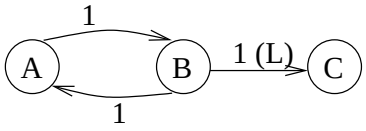
(d) For arbitrary weights and asynchronous computing, algorithm 15.10 requires at least $2^{(n-1)/2}$ steps for a graph with n nodes.

Proof. (a), (b) and (c) follow from the above problems, except that we have to do a performance analysis for the synchronized case. It suffices to show that Algorithm 15.10 terminates in time $O(n)$, since then not more than $O(n \cdot |E|)$ messages can be exchanged along the $|E|$ edges. We first observe inductively that after t rounds:

> distance(i) equals the length of a path from the source r to i. This path is shortest among all paths from r to i with at most t edges.

Thus after $n-1$ rounds the length of a shortest path is determined. □

Bellman Ford also adapts only slowly to changing link conditions as shown by the "Count-to-infinity" problem. We consider three nodes A, B and C, which are linked as follows.



Initially all links have the same speed 1, however after some time the link from B to C decreases from speed 1 to speed L. Accordingly node B increases its distance estimate to C from 1 to 3, since A claims distance 2 from C. Subsequently A increases its distance estimate to 4 and after i iterations, B (resp. A) estimates the C-distance to be $i+2$ (resp. $i+1$). Thus $\Theta(L)$ steps are required before the process stops. If the link between B and C crashes (and hence $L = \infty$), then the process even continues ad infinitum.

Nevertheless Bellman Ford is still used as a procedure for packet routing in the "Route Information Protocol" (RIP) which is employed for small nets.

Remark 15.1 The currently fastest distributed single-source-shortest paths algorithms are described in [A89]. In particular, for any $\varepsilon > 0$, $O(|E|^{1+\varepsilon})$ messages suffice when computing in time $O(D^{1+\varepsilon})$ for edge lengths one. For arbitrary edge length with largest length W running time $O(D^{1+\varepsilon} \cdot \log W)$ and $O(|E|^{1+\varepsilon} \cdot \log W)$ messages suffice.

We encounter another solution with running time $O(D)$ and $O(D \cdot |E|)$ messages in Chapter 16.

15.3 Multicast

Typical applications for multicast services include broadcast from arbitrary sources within multicast groups as well as Internet applications such as the delivery of multimedia datastreams (video on demand, interactive television, life events). Since huge sets of data have to be moved with a high quality of service in real time, special care has to be exercised.

We again assume the model of an undirected graph whose nodes correspond to (say) Internet routers as well as to sets of customers associated with the respective router. To avoid flooding the net, each multicast group g uses a tree T_g and transports the data stream along the edges of T_g: observe that each edge has to transport only a single packet, since routers will take care of delivering the desired number of copies to its customers.

A multicast service has to answer to the following questions:

- How are groups recognized?
- How is T_g determined?
- How are users dynamically added, respectively removed within a multicast group?

To recognize groups we have to enforce that customers submit registrations for multicast groups to their router and hence routers are aware of all multicast groups they have to support. Obviously we should choose T_g as a tree of shortest paths covering all routers that provide service to group g. However there are various ways of measuring distance. If distance is measured as the number of "hops" (i.e., path length is the number of edges), then we can apply the asynchronous Bellman Ford algorithm (Algorithm 15.10) respectively the distributed version of Dijkstra's algorithm. For general edge length synchronized versions of Dijkstra's algorithm have to be considered (see Chapter 16 and [A89]).

We describe Reverse Path Multicasting[2] (RPM). The source of a multicast group g broadcasts its multicast packet using the tree T_g. Whenever a router R finds out that no members of group g are associated with routers of its subtree it reports this fact to its parent. This message is moved up the tree until a router is found which has at least one group member in its subtree and all routers without group members in their subtrees are removed. On the other hand the tree T_g has to be updated whenever a customer registers for group g with a router that does not belong to T_g.

15.4 Minimum Cost Spanning Trees

Our goal is to determine the minimum cost spanning tree for the given network. Each edge of the network has a weight which is known to both endpoints; moreover processors have

[2]The multicast packet reverses the path it would use when travelling as a unicast packet from the receiving group member to the source.

unique IDs. We demand that each processor determines all incident edges of the spanning tree at the end of the computation. Our basic approach is as follows:

- We assume that the edges have pairwise different weights[3]. We start with a forest of singleton trees which we define to be of level zero. Finally we distinguish one node who sends a wake-up call to all its neighbors.

- We merge spanning trees of level k to obtain a spanning tree of level $k+1$ as follows:

  (0) In each spanning tree an edge, called the core, is distinguished. The endpoint of the core with higher ID is chosen as leader. We assume that all nodes of a spanning tree know the level of their tree as well as the core.

  (1) The leader broadcasts a request signal to all nodes of its tree. Upon receiving the request a node queries all its neighbors, beginning with a "minimum weight neighbor", and determines a EMW, an external edge of minimum weight, i.e., an edge of minimum weight connecting it with a node of a different tree.

  (2) The EMW and its weight are reported back by a convergecast such that the leader receives a single EMW of minimum weight. The convergecast has to make sure that all nodes report individual EMWs since otherwise a smallest EMW of the spanning tree cannot be determined.

  (3) Two spanning trees of same level are *merged*, provided their EMWs coincide. In this case the level increases by one and the EMW is the new core.

  /* We require identical EMW's to obtain disjoint pairs of merged trees. */

However, due to message delays, we cannot assume that always two spanning trees with same level and common EMW exist. Therefore we also allow to "absorb" a tree of smaller level into a tree of larger level.

(4) Assume that processor i is in the process of determining its EMW edge and that i belongs to the tree T_1. Moreover assume that i is connected to a processor j by an edge $e = \{i, j\} \in E$ and that j belongs to the tree T_2. Finally assume that i is in the process of determining its EMW edge and that it announces its level to j.

If the level of T_1 is larger than the level stored by j, then j waits with its answer until the level of j's tree reaches the level of T_1. Thus processor i is forced to wait as well.

/* Attention: the level reported by j may be outdated, i.e., too small. */

If the level of T_1 is smaller than or equal to the level of T_2, then processor i waits until it receives a message of its root reporting the EMW edge of tree T_1. If e is the EMW edge of T_1, then i reports this to j. Subsequently j broadcasts the level and core of T_2 into T_1: T_2 absorbs T_1, the merged tree retains the larger of the two levels

[3]For $i < j$ we change the weight w of the edge $\{i, j\}$ to $(n+1)^2 \cdot w + (n+1) \cdot j + i$.

and the core of T_2 is the core of the merged tree. If j is in the process of determining its EMW edge, then it takes over as leader of T_1 and requests the next EMW edge of T_1. If j has already concluded its EMW search, then e is not its EMW edge and hence *the absorption step does not interfere with the process of determining the EMW edge of* T_2.

/* If e is not the EMW edge of T_1, then i takes no further action. Processor j may be in the process of determining its EMW edge as well, but it has to wait until the tree of i reaches its level. */

Exercise 145
Show that the waiting strategy in step (4) does not produce a deadlock.

We have to address the major question, namely *can neighboring processors i and j determine reliably whether they belong to different trees?* Assume that processor i is in the process of determining its EMW edge and queries a neighbor j. If j has the same identifier (core and level), then i knows that j belongs to the same tree and edge $\{i, j\}$ is not external.

If however j has a different identifier, then it could happen that both belong to the same tree, but they developed with different speed. Here the level comes to the rescue.

If the level of j is at least as large as the level of i, but cores are different, then i and j belong to different trees.

This follows from the way identifiers are assigned when merging, since the core is identical as long as the level does not change. Hence, if the two levels agree, but cores are different, then the two trees have to be different. If the level of j is larger, then trees have to be different, since i is actively searching for an EMW and it knows that it is up-to-date. (Observe that j may be waiting for a message from its root informing it about its new level and core and hence its current knowledge may not be up to date.)

Hence we can determine whether an edge is external, provided the tree of the actively computing processor i has a level not larger than the tree of its neighbor j. Observe that we only allow a merging or an absorption step, if the level of i's tree is not larger, since i is forced to wait otherwise.

Theorem 15.12 *The minimum spanning tree can be determined with $O(n \cdot \log_2 n + |E|)$ messages in time $O(n \cdot \log_2 n)$.*

Proof: We have given already a sketch of correctness. To determine the number of messages observe that an edge is only tested if it is a possible minimum weight edge. If the test is negative, then both endpoints belong to the same spanning tree and the edge does not have to be tested again. Thus the number of negative tests is responsible for $|E|$ messages. All other messages concern positive tests. Since a node triggers a positive test

in at most one spanning tree of level k, each node is responsible for at most $\log_2 n$ messages related to a positive test. Hence we have at most $O(n \cdot \log_2 n)$ such messages. □

Exercise 146
Assume that all processors are awake immediately. Then show inductively that all processors reach a level of at least k after at most $O(k \cdot n)$ steps. Which maximal level can be reached?

15.5 Conclusion

We have seen that the problem of determining a spanning tree and the problem of electing a leader are equivalent. Both problems cannot be solved by a deterministic algorithm for anonymous networks, provided the network is regular[4]. We therefore had to assume that processors have a unique ID. The leadership problem and the spanning tree problem are solved simultaneously by starting parallel attempts of building a spanning tree. Whenever two spanning trees meet, the tree initiated by the the processor with larger ID wins and eventually the tree initiated by the processor with largest ID survives. We had to carefully employ sequences of pairs of broadcast and convergecast to make sure that all nodes of a tree know the ID of their root.

We have implemented a depth-first search traversal in linear time and observed that breadth-first search trees are easy to determine, if synchronous computing is guaranteed. The situation for asynchronous computing however is completely different and neither the Bellman Ford algorithms nor a distributed version of Dijkstra's shortest path algorithm came anywhere near the performance for synchronous computing. The situation for arbitrary weights turned out to be even more disastrous: we have shown that the Bellman Ford algorithm requires exponential running time, if a bad message schedule can be chosen. However we encounter a more efficient solution in Chapter 16.

When determining a minimum spanning tree we have again followed the old idea of growing trees along external edges of minimal weight. However we encountered two severe problems. Firstly trees may grow with different speeds: we therefore introduced the notion of a layer to merge trees of roughly same size and hence to cut down on excessive message exchanges. Secondly nodes of the same subtree may or may not know of their status: we use identifiers, composed of the core edge and the layer of the tree, to decide whether nodes belong to different trees.

[4]An undirected graph is regular iff all nodes have the same number of neighbors

Chapter 16

Synchronization

Is it possible to design a *synchronizer*, i.e., a simulation of an arbitrary synchronous algorithm by an asynchronous algorithm? The answer is positive and we will determine the cost of synchronizers in terms of running time and number of messages.

We begin by describing **synchronizer** α, a simple synchronizer which is very effective in minimizing running time. When simulating a send operation from processor p_i to processor p_j, processor p_i executes the same send event, but waits for an acknowledgment from p_j. If p_i receives acknowledgments from all neighbors, it considers itself `safe` and sends a "safe" message to all neighbors. The simulation terminates successful, if p_i receive "safe" messages from all neighbors.

Observe that if some neighbor p_j of p_i is not safe, then p_j has not received an acknowledgment from some neighbor p_k and p_j has to assume that p_k did not receive its message. If this is the case, then p_k is behind and p_j has to wait which in turn forces p_i to wait. The crucial observation is that the local requirement of waiting for "safe" messages from all neighbors suffices for a successful simulation!

Algorithm 16.1 **Synchronizer** α

/* We describe how to simulate one step of an arbitrary synchronous algorithm. The sets Ack_i and Safe_i are initially empty. We have to assume that each processor executes a synchronous send. (If this is not the case, enforce dummy sends.) */

(1) when an internal event E occurs;
    simulate E;

(2) when the event synchronous-send$_i(m, j)$ occurs;
    execute asynchronous-send$_i(m, j)$;

(3) upon p_j receiving message m from neighbor p_i;
    execute asynchronous-send$_j(\texttt{ack}, i)$;

(4) upon p_i receiving an acknowledgment from neighbor p_j;
BEGIN upon
insert j to Ack_i;
if ($|\text{Ack}_i|$ = number of neighbors of p_i) then
BEGIN if
set $\text{Ack}_i = \emptyset$;
send the message `safe` to all neighbors;
END if;
END upon;

(5) upon p_i receiving a "safe" message from p_j;
BEGIN upon
insert j to Safe_i;
if ($|\text{Safe}_i|$ = number of neighbors of p_i) then
BEGIN if
$\text{Safe}_i = \emptyset$;
begin simulation of the next step;
END if;
END upon;

First of all we observe that any step of a synchronous algorithm is simulated by the steps (2) - (5) and hence any step is simulated in time $O(1)$. We send messages, acknowledgments and safe messages over all edges and hence $O(|E|)$ messages are sent additionally.

Theorem 16.2 *Synchronizer α simulates each step of an arbitrary algorithm in time $O(1)$ with $O(|E|)$ messages.*

Exercise 147
Verify Theorem 16.4.

We now come to a first important application. We already observed that the echo algorithm computes a breadth-first spanning tree when computing in a synchronous environment. Hence, if we apply synchronizer α to the echo algorithm, we obtain an asynchronous algorithm computing a breadth-first search spanning tree.

Corollary 16.3 *Let $G = (V, E)$ be an undirected graph with diameter D. If synchronizer α is applied to the echo algorithm, then we obtain an asynchronous algorithm, which determines a breadth-first search tree in time $O(D)$ with $O(D \cdot |E|)$ messages.*

Observe that running time $O(D)$ is optimal and far better than running time $O(D^2)$ for the distributed version of Dijkstra's algorithm and $O(|V|)$ for Bellman Ford. The message complexity asymptotically coincides with the message complexity of Bellman Ford, but is larger than the message complexity $O(D \cdot |V|)$ of Dijkstra's algorithm.

Synchronizer β assumes that a spanning tree T has been determined. To simulate a synchronous send operation we use T to verify that all processors are safe. In particular leaves send a "safe" message to their parents. An arbitrary node sends a "safe" message to its parents, if it has received "safe" messages from all children and is safe itself. If the root is safe, it broadcasts a `go` message down the tree and the simulation of the next round can begin. If T is a breadth-first search tree and if the network has diameter D, then the running time has increased from constant time to $O(D)$, but message complexity has decreased from $O(|E|)$ to $O(|V|)$.

Theorem 16.4 *Assume that the network $G = (V, E)$ is given, where D is the diameter of G. Then synchronizer β simulates each step of an arbitrary algorithm in time $O(D)$ with $O(|V|)$ messages.*

Remark 16.1 We more or less obtain the distributed version of Dijkstra's algorithm when applying synchronizer β to the echo algorithm. (Synchronizer β is not applied when sending explore messages.)

We conclude with **synchronizer** γ which allows tradeoffs between synchronizers α and β and hence between running time and message complexity. Whereas we have assumed a spanning tree for synchronizer β, we now assume that a spanning forest F is given. We proceed as follows.

(1) Within each tree T of F synchronizer β is applied. If the root of T concludes that all nodes of T are safe, then it broadcasts a "your tree is safe" message within T.

(2) We say that trees T_1 and T_2 of F are neighbors, if there is an edge which connects a node of T_1 with a node of T_2. We assume that exactly one edge connecting T_1 and T_2, called a *connecting* edge, is chosen. Endpoints of connecting edges e send a "my tree is safe" message along e.

(3) Each tree collects safety messages of neighbor trees by moving these message towards the root. The respective root can then determine when all neighbor trees are safe and, if this is indeed the case, broadcasts a `go` message within its tree to simulate the next step.

Observe that we obtain synchronizer α, if we use a forest of singletons, and synchronizer β, if the forest consists of a single tree only.

Let H be the maximal height of a tree of F and let C be the number of connecting edges. Then each simulation step runs in time $O(H)$ and exchanges at most $O(|V| + C)$ messages. We next show how to obtain "good" forests.

Lemma 16.5 *The undirected graph $G = (V, E)$ is given. For each k there is a spanning forest F_k and a set C_k of connecting edges such that*

(a) all trees in F_k have height at most $\log_2 |V| / \log_2 k$

(b) and C_k has size at most $(k-1) \cdot |V|$.

Proof: We compute F_k by successively computing trees $T_1, T_2, \ldots$. Assume that trees $T_1, \ldots, T_i$ are already determined and assume that V' is the set of nodes which does not belong to any of the already constructed trees. We build a tree T_{i+1} by choosing an arbitrary node $v \in V'$ as root.

T_{i+1} will be a tree of shortest paths restricted to nodes of V' which we build level by level. We terminate the construction of T_{i+1}, if the number of nodes in a new level is less than $(k-1) \cdot$ old, where old is the total number of nodes included so far. Hence, if T_{i+1} has l levels, then it has at least k^{l-1} nodes and its height is bounded by $\log_2 |V| / \log_2 k$ as a consequence.

Thus we only have to worry about the number of connecting edges. If e is a connecting edge for trees T_i and T_j (for $i < j$), then we charge e to T_i. We stop the construction of T_i, when the number of nodes of the next level is too small, namely less than $(k-1) \cdot m$, where m is the number of nodes of T_i. Hence T_i has at most $(k-1) \cdot |T_i|$ neighbor trees and therefore at most $(k-1) \cdot |T_i|$ connecting edges are charged to T_i. □

Theorem 16.6 *Let $G = (V, E)$ be a network and let $k \in \mathbb{N}$ be arbitrary. Synchronizer γ simulates each step of an arbitrary algorithm in time $O(\frac{\log_2 |V|}{\log_2 k})$ with $O(k \cdot |V|)$ messages.*

Observe that synchronizer γ considerably improve on synchronizer β, since for $k = 2$ running time $O(\log_2 |V|)$ is guaranteed with $O(|V|)$ messages. This is to be compared to running time $O(\text{diameter})$ and $O(|V|)$ messages for synchronizer β. However the number of messages doubles and we have to precompute the spanning forest.

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