Complexity

	$\mathbf{D}' \cdot \mathbf{O} \cdot 1 = 1$	ound, Big-Theta – exact bound
$B_1 \alpha_{-1} I = IIDDAT DOIIDA$	$Bid_limad_2 = low for b$	$\alpha_{11}\alpha_{11} = \alpha_{11}\alpha_{11} = \alpha_{11}\alpha_{11}\alpha_{11} = \alpha_{11}\alpha_{11}\alpha_{11} = \alpha_{11}\alpha_{11}\alpha_{11} = \alpha_{11}\alpha_{11}\alpha_{1$
Dig=0 = unner nound.	Dig = Oinega = iOwei D	

Sum [0,n]	Result			type of recurrence	big-O class
i	n(n-1)/2	T(n)		$T(n \operatorname{div} 2) + c$	$O(\log n)$
- ^ :	$(a^{(n+1)}, 1)/(a, 1)$	T(n)		T(n-1) + c	O(n)
a^i	(a^(n+1)-1)/(a-1)	T(n)		$2T(n \operatorname{div} 2) + c$	O(n)
i^2	(1/6)n(n+1)(2n+1)	T(n)	=	$T(n \operatorname{div} 2) + c_1 n + c_0$	O(n)
1.72	(1/0)11(11+1)(211+1)	T(n)	=	$2T(n \text{ div } 2) + c_1n + c_0$	$O(n \log n)$
ia^i	$a(na^{n+1})(n+1)(a^{n})+1)/(a-1)^{2}$	T(n)		$T(n-1) + c_1 n + c_0$	$O(n^2)$
		T(n)	=	$T(n-1) + c_2n^2 + c_1n + c_0$	$O(n^3)$
1/i	O(logn)	T(n)	=	2T(n-1)+c	$O(2^n)$

Probability/Randomization

<u>Markov's Inequality:</u> $Pr[X \ge aE[X]] \le 1/a$ OR $Pr[X \ge a] \le E[X]/a$

<u>Union Bound:</u> Pr[UA_i] <= sum of A_i

<u>Kth Smallest:</u> Quicksort, but only going down one branch. W is O(n), S is $O((\log^2)(n))$ <u>Quicksort:</u> Elements compared iff one of them is a pivot and they aren't split. The probability that element i and element j are compared is 2/(j-i+1). Summed, this predicts an overall work of O(nlogn)

BSTs & Treaps

Cost Specification 11.13 (BST's). The **BST** cost specification is defined as follows. The variables n and m are defined as $n = \max(|T_1|, |T_2|)$ and $m = \min(|T_1|, |T_2|)$ when applicable.

	Balanced BST			
	Work	Span		
empty	<i>O</i> (1)	O(1)		
singletonv	<i>O</i> (1)	<i>O</i> (1)		
find(T,k)	$O\left(1 + \lg T \right)$	$O\left(1 + \lg T \right)$		
insert(T,k)	$O\left(1 + \lg T \right)$	$O\left(1 + \lg T \right)$		
delete(T,k)	$O\left(1 + \lg T \right)$	$O\left(1 + \lg T \right)$		
$union(T_1, T_2)$	$O\left(m \cdot \lg \frac{n}{m}\right)$	$O\left(1+\lg n\right)$		
$intersect(T_1, T_2)$	$O\left(m \cdot \lg \frac{n}{m}\right)$	$O\left(1+\lg n\right)$		
$difference(T_1, T_2)$	$O\left(m \cdot \lg \frac{n}{m}\right)$	$O\left(1 + \lg n\right)$		
split(T,k)	$O\left(1 + \lg T \right)$	$O\left(1 + \lg T \right)$		
$join(T_1, T_2)$	$O(\lg(T_1 + T_2))$	$O(\lg(T_1 + T_2))$		

Treap: Satisfies BST property on keys, max-heap property on priorities

<u>Treap Height</u>: For a given S, the treap for S can be generated by Quicksort, indicating that the height of S is the same as the recursion depth for Quicksort which is O(logn) with high probability

Sets & Tables

Sets represented as BST

Graphs

Costs	Edge Set	<u>Adj Table</u>	<u>Adj Seq</u>
(u,v) in G	O(log E)	O(log V)	O(dG(u)))
Map over edges	O(E)	O(E)	O(E)
Find neighbors	O(E)	O(log V)	O(1)
Map over Ng(v)	O(dG(v))	O(dG(v))	O(dG(v))
<i>dG(v)</i>	O(E)	O(log V)	O(1)

DFS Numberings and DFS trees:

- *Tree edge*: (u,v) if v is discovered by u during DFS

$$- d(u) < d(v) < f(v) < f(u)$$

- Back edge: (u,v) if u is a descendant of v

- d(v) < d(u) < f(u) < f(v)

- Forward edge: (u,v) if u is an ancestor of v
 d(u) < d(v) < f(v) < f(u)
- Cross edge: (u,v) if an edge is not one of the other edges - d(u) < f(u) < d(v) < f(v)

Theorem: On a directed acyclic graph (DAG) when finishing a vertex v in DFS, all vertices reachable from v have already exited

Algorithm 14.33 (Directed cycles with generalized directed DFS).

$$\begin{split} \Sigma_0 &= (\{\}, false) : Set \times bool \\ revisit & ((S, fl), v, _) = (S, fl \lor (S[v])) \\ discover & ((S, fl), v, _) = (S \cup \{v\}, fl) \\ finish & ((S, _), (_, fl), v, _) = (S, fl) \end{split}$$

Algorithm 14.32 (Topological sort with generalized directed DFS).

$$\begin{split} \Sigma_0 &= [\]: \text{vertex list} \\ \text{revisit}(L, ., .) &= L \\ \text{discover}(L, ., .) &= L \\ \text{finish}(., L, v, .) &= v :: L \end{split}$$

Algorithm 14.31 (Undirected Cycles with generalized undirected DFS).

```
\begin{split} \Sigma_0 &= \mbox{ false : bool } \\ \mbox{revisit(_)} &= \mbox{true} \\ \mbox{discover(fl, \_, \_)} &= \mbox{fl} \\ \mbox{finish(\_, fl, \_, \_)} &= \mbox{fl} \end{split}
```

Shortest Paths

<u>Djikstra's Algorithm</u>: For a weighted graph G=(V,E,w) and a source s, Djikstra's algorithm is priority-first search on G starting at s with d(s)=0, using priority p(v) = min(d(x) + w(v)) and setting d(v)=p(v) when v is visited.

- Sequential, O(mlogn)

- Djikstra's Property: The overall shortest-path weight from s via a vertex in X directly to a neighbor in Y (the frontier) is as short as any path from s to any vertex in Y

Operation	Line	# of calls	PQ	Tree Table	Array	ST Array
deleteMin insert	Line 9 Line 17	O(m) O(m)	$\begin{array}{c} O(\log m) \\ O(\log m) \end{array}$	-	-	-
find insert	Line 12 Line 16	O(m) O(n)	-	$O(\log n)$ $O(\log n)$	O(1) O(n)	$O(1) \\ O(1)$
$N_G^+(v)$ iterate	Line 18 Line 18	O(n) O(m)	-	$O(\log n)$ O(1)	$O(1) \\ O(1)$	-

- Can fail on graphs with negative weights (cyclic w/ negative weights \rightarrow infinite length path)

Figure 15.1: The costs for the important steps in the algorithm dijkstraPQ.

Bellman-Ford

- Constructs path by adding edges when beneficial. Stops when more than |V| edges are used.

- At each step, distances updated by D' = { $v \rightarrow min(D[v],min(D[v] + w(u,v))$ for neighbors_ : v in V} - Cost

-Table: W = O(nmlogn), S = O(nlogn)

- Array sequence: W = O(nm), S = O(nlogn)

Graph Contraction

<u>Star contraction</u>: For example, to determine the centers, we can flip a coin for each vertex. If a vertex flips heads, then it becomes the center of a star. If a vertex flips tails, then it tries to become a satellite by finding a neighbor that is a center. If no such neighbor exists (all neighbors have flipped tails or the vertex is isolated), then the vertex becomes a center. If a vertex has multiple centers as neighbors, can pick one arbitrarily.

- Removes n/4 vertices in expectation

Minimum Spanning Trees

<u>Light-edge property</u>: Let G=(V,E,w) be a connected, undirected, weighted graph with distinct edge weights. For any cut of G, the minimum weight edge that crosses the cut is in the minimum spanning tree of G

<u>Kruskal's Algorithm</u>: At each step, choose the minimum weight edge which does not form a cycle - Cost: W = S = O(mlogn)

<u>Prim's Algorithm</u>: Priority-first search on G starting at an arbitrary vertex s using priority p(v) = min w(x,v) for x in X and setting T = T U P(u,v)} when visiting v where w(u,v) = p(v).

- Cost: W = S = O(mlogn)

<u>Boruvka's Algorithm:</u> At each step, select the minimum edge incident on each vertex and contract these edges. Remove self edges and keep the minimum-weight redundant edges. Add selected edges to MST. Rinse and repeat.

- Cost:

- Tree contraction: W = O(mlogn), $S = O((log^3)(n))$

- Star contraction: W = O(mlogn), S = O((log^2)(n))

Dynamic Programming

<u>Top-down approach (memoization)</u>: The top-down approach is based on generating implicitly the recursion structure from the root of the DAG down to the leaves. Each time a solution to a smaller

instance is found for the first time it generates a mapping from the input argument to its solution. <u>Bottom-up approach</u>: One way to implement bottom-up dynamic programming is to do some form of systematic traversal of a DAG. We can start from the bottom of the graph and work our way back up towards subproblems that depend on the current subproblem.

Hashing

Load Factor: n/m where n is total number of keys, m is number of distinct hash values

<u>Collision Resolution</u>: Separate chaining, open addressing (linear probing, quadratic probing), perfect hashing, multiple choice hashing/cuckoo hashing

<u>Parallel hashing (with open addressing)</u>: To insert keys into a hash table in parallel, we perform multiple rounds of writings into the table in parallel. Any key that cannot be written because of a collection continues into next round until all keys have been written.

- Work: O(|K|) where K is the set of keys to be inserted

- Span: O(log|K|)

Priority Queues

Leftist property: For all node x in a leftist heap, $rank(L(x)) \ge rank(R(x))$

Implementation	insert	findMin	deleteMin	meld
(Unsorted) Sequence	O(n)	O(n)	O(n)	O(m+n)
Sorted Sequence	O(n)	O(1)	O(n)	O(m+n)
Balanced Trees (e.g. Treaps)	$O(\log n)$	$O(\log n)$	$O(\log n)$	$O(m\log(1+\frac{n}{m}))$
Leftist Heap	$O(\log n)$	O(1)	$O(\log n)$	$O(\log m + \log n)$

PASL

- <u>Compare and swap</u>: When executed with a 'target' atomic object and an 'expected' cell and a new value 'new', the following is done atomically:

1. Read contents of 'target'

2. If the contents equals the contents of 'expected', then write 'new' into the 'target' and return T

3. Otherwise, return F

<u>ABA Problem</u>: When multiple threads update a value such that it goes from a value A to B and then back to A, the compare-and-swap won't detect this change and will be oblivious to any side effects.
<u>Thread</u>: A maximal computation consisting of a sequence of instructions that do not contain calls to fork(2) except perhaps as its last action

- <u>Scheduling</u>: Assigning each thread a processor such that:

- 1. Each thread is assigned to a unique processor for as many consecutive steps as its weight
- 2. No thread is executed before its descendants in the DAG
- 3. No processor is assigned more than at most one thread at a time

- <u>Greedy Scheduling Principle</u>: If a computation is run on P processors using a perfect greedy scheduler that incurs no costs in creating, locating, and moving threads, then the total time (clock cycles) for running the computation Tp is bounded by Tp < (W/P) + S. Where W is the work of the computation and S is the span of the computation (in clock cycles)

- <u>P-processor speedup</u>: The speedup on P processors is the ratio Tb/Tp where the term Tb represents the run time of the sequential baseline program and the term Tp is the time measured for the P-processor run

- <u>Asymptotically work efficient</u>: If the work of the algorithm is the same as the work of the best known serial algorithm

- <u>Observed work efficiency</u>: A parallel algorithm that runs in time T1 on a single processor has *observed work efficient factor of r* if r = T1/Tseq where Tseq is the time taken by the fastest known sequential algorithm

- <u>Good parallel algorithm:</u>

- Asymptotically work efficient

- Observably work efficient (r < 1.5)

- It has low span

- <u>Granularity control/coarsening</u>: Switching to a sequential algorithm when the problem size falls below a certain threshold to avoid excessive parallel overhead

- <u>Parallel</u>: An algorithm or application that performs multiple computations at the same time for the purposes of improving the completion or run time

- <u>Concurrent</u>: A computation that involves independent agents which can be implemented with processes or threads, that communicate and coordinate to accomplish the intended result