Hilfszettel zur Klausur
von Tim S., Seite 1 von 2

1 Recap

Abstract Data Type (ADT) an object with well-defined operations, e.g. a stack supports push() and pop() operations
can be implemented using different data structures, e.g. a stack can be implemented using a linked list or an array
Array a contiguous sequence of objects with the same size
close to how computers store data in their memory
can also be multi-dimensional
support fast access to their elements through indexing
resizing and inserting values in arbitrary locations are expensive
in python: no built-in data structure, lists are indexable, use numpy library for proper/faster arrays
Lists main operations: append/prepend, head/tail
typically implemented usingn linked lists (python lists are array-based)
Stacks last-in-first-out (LIFO) data structure
basic operations: push, pop
can be implemented using linked lists (or arrays)
Queues first-in-first-out (FIFO) data structure
basic operations: enqueue, dequeue
can be implemented using linked lists (or maybe arrays)
Strings often implemented based on character arrays
Maps/Dictionaries similar to arrays and lists, but allow indexing with (almost) arbitrary data types
maps generally implemented using hashing
Sets implement the mathematical (finite) sets, a collection of unique elements without order
Algorithms Desirable properties: correctness, robustness, efficiency, simplicity
Resursion have to define one or more base cases
each recursive step should approach the base case

2 Analysis of Algorithms

characterize running times of algorithms as a function of input size:

Family	Definition
Constant	$f(n) = c$
Logarithmic	$f(n) = \log_b n$
Linear	$f(n) = n$
N log N	$f(n) = n \log n$
Quadratic	$f(n) = n^2$
Cubic	$f(n) = n^3$
Other polynomials	$f(n) = n^k$, for $k > 3$
Exponential	$f(n) = b^n$, for $b > 1$
Factorial	$f(n) = n!$

Logarithm the inverse of exponentiation: x = logb n -> b**x = n
for us, no base means base-2
log xy = log x + log y
log (x/y) = log x - log y
log x**a = a log x
logb x = logk x / logk b
grow much slower than linear functions
Polynomials degree-0: f(n) = c
degree-1: f(n)=n+c
degree-2: f(n)=n**2+n+c
generally drop the lower order terms
1+2+3+...+n = n(n+1)/2
Permutations
n! = n*(n-1)*...*2*1
P(n,k) = n*(n-1)*...*(n-k-1) = n!/(n-k)!
Combinations
n choose k C(n,k) = P(n.k)/P(k,k) = n!/(n-k)!*k!
P(n,k) = n*(n-1)*...*(n-k-1) = n!/(n-k)!
Proof by induction
used for both proving the correctness and running times of algorithms
show that the base case holds
assume the result is correct for n, show that it also holds for n+1
Hardware independence characterized by random access memory (RAM)
the data and instructions are stored in the RAM
processing unit performs basic operations in constant time
any memory cell with an address can be accessed in equal (constant) time
the processor fetches them as needed and executes following the instruction
there may be other, specialized registers
modern processing units also employ a cache
Formal analysis of running time simply count the number of primitive operations
primitive operations include: assignment, arithmetic operations, compare primitive data types (in Java: boolean, byte, char, short, int, long, float and double), access a single memory location, function calls, return from functions
non-primitive operations: loops, recursion, compare sequences
Big-O notation used for indicating an upper bound of an algorithm as a function of running time
if running time of an algorithm is O(f(n)), its running time grows proportional to f(n) as the input size n grows
drop the constants and lower order terms
transitivity: if f(n)=O(g(n)), and g(n)=O(h(n)), then f(n)=O(h(n))
additivity: if both f(n) and g(n) are O(h(n)), f(n)+g(n)=O(h(n))
maximum problem size asymptotic analysis is important: assume we can solve a problem of size m in a given time on current hardware, when we get a better computer, we can calculate the new problem size we can solve in the same time
gap between polynomial and exponential algorithms: problem size for exponential algorithms does not scale with faster computers
worst case analysis
in most cases we are interested in the worst case analysis
average case analysis is also useful, but requires defining a distribution over possible inputs and is often more challenging
pro: easier, get a very strong guarantee that the algorithm won't perform worse than the bound
con: in some problems, worst case examples are very rare
asymptotic analysis
our analyses are based on asymptotic behavior
pro: correct for a 'large enough' input
con: constant or lower order factors are not always unimportant
Big-O relatives Big-O(upper bound): f(n) is O(g(n)) if f(n) is asymptotically less than or equal to g(n)
Big-Omega (lower bound): f(n) is Omega(g(n)) if f(n) is asymptotically greater than or equal to g(n)
Big-Theta (upper/lower bound): f(n) is Theta(g(n)) if f(n) is asymptotically equal to g(n): f(n) is O(g(n)) and f(n) is Omega(g(n))
Summary sublinear (e.g. logarithmic), linear, and nlogn algorithms are good
polynomial algorithms may be acceptable in many cases
exponential algorithms are bad

3 Algorithmic patterns

Recursion
recursion depth:
compilers/interpreters allocate space on a stack for the bookkeeping for each function call
most environments limit the number of recursive calls: long chains of recursion are likely to cause errors
tail recursion:
e.g. linear search
easy to convert to iteration
easy to optimize, and optimized by many compilers (not by the Python interpreter)
Brute force in some cases we may need to enumerate all possible cases (e.g. to find the best solution)
common in combinatorial problems
often intractable, practical only for small input sizes
the beginning of finding a more efficient approach
example: segmentation
Divide and conquer divide the problem into smaller parts until it becomes trivial to solve
once small parts are solved, results are combined
goes well with recursion
a particular flavor: binary search (sometimes called decrease and conquer)
example: nearest neighbors, merge sort, quick sort, integer multiplication, matrix multiplication, fast Furrier transform
not always yield good results, cost of merging should be less than the gain from the divisions
Greedy algorithm optimizes a local constraint
results in correct solutions for some problems, in others they may result in "good enoughßolutions
efficient if works
examples: graph algorithms (find shortest paths, scheduling)
e.g. produce minimum number of coins for a particular sum s (not correct for coins of 10, 30, 40 and sum value of 60)
Dynamic programming save earlier results to reduce computation
sometimes called memoization
examples: common parsing algorithms, Fibonacci
Others backtracking, branch-and-bound; randomized algorithms; distributed algorithms (sometimes called swarm optimization); transformation

4 Sorting

Bubble sort
compare first 2 elements, swap if not in order
shift and compare the next 2 elements, again swap if needed
when read the end, repeat the process from the beginning unless there were no swaps in the last iteration

```
swapped = True
n = len(seq)
while swapped:
  swapped = False
  for i in range(n - 1):
    if seq[i] > seq[i + 1]:
      seq[i], seq[i + 1]\
          = seq[i + 1], seq[i]
      swapped = True
```

concerns: many swaps, in-place
not practical, not used in practice

Insertion sort
assume the elements arrive one by one, and we have a sorted sequence
shift all elements larger than the new one to the right
put the new element in its correct place

```
for i in range(1, len(seq)):
  cur = seq[i]
  j = i
  while seq[j - 1] > cur\
           and j in range(1,i+1):
    seq[j] = seq[j - 1]
    j -= 1
  seq[j] = cur
```

performs reasonably fast for sorting short sequences, on longer sequences, performs worse than more advanced algorithms like merge sort or quick sort
in practice faster than bubble sort and selection sort
online: sort items as they arrive
stable: do not swap elements with equal keys
adaptive: faster if order of elements closer to sorted sequence

Merge sort
split the sequence
sort the subsequences
merge the sorted lists

```
# s1, s2: sequences to be merged
# s: target sequence
i, j = 0, 0
n = len(s1) + len(s2)
while i + j < n:
  if j == len(s2) or \
     i < len(s1) and s1[i] < s2[j]:
    s[i+j] = s1[i]
    i += 1
  else:
    s[i+j] = s2[j]
    j += 1
def merge_sort(s):
  n = len(s)
  if n <= 1: return
  s1, s2 = s[:n//2], s[n//2:]
  merge_sort(s1)
  merge_sort(s2)
  merge(s1, s2, s)
```

log n splits
particular useful for settings with low random-access memory, or sequential access
well-studied, many variants (in-place, non-recursive)

Quicksort
another popular divide-and-conquer sorting algorithm
the big part of the work is done before splitting
worst time complexity is O(n**2), but in practice performs better than merge sort on average
pick a pivot p, and divide the sequence into 3 parts:
L: smaller than p
G: larger than p
E: equal to p
sort L and G recursively
combination is simple concatenation

```
def qsort(seq):
  if len(seq <= 1): return seq
  return qsort([x for x in seq if x <  seq[-1]])\ # < p
      +        [x for x in seq if x == seq[-1]]\  # = p
      + qsort([x for x in seq if x >  seq[-1]])   # > p
```

similar to merge sort, performs O(n) operations at each level in recursion
overall complexity is proportional to n*depthOfTree
unlike merge sort, no balanced-tree guarantee, in the worst case the depth of the tree can be n, resulting in O(n**2) complexity
worst case: when input sequence is sorted
randomized quicksort: pick the pivot randomly
best case: pick the median of the sequence as pivot, but finding median requires O(nlogn)
common apprach: pick 3 values (typically first, middle, last) and select the median
can be easily implemented in-place

Algorithm	worst	average	best	memory	in-place	stable
Bubble sort	n^2	n^2	n	1	yes	yes
Insertion sort	n^2	n^2	n	1	yes	yes
Merge sort	$n \log n$	$n \log n$	$n \log n$	n	no	yes
Quicksort	n^2	$n \log n$	$n \log n$	$\log n$	yes	no

Bucket sort
puts elements of the input into a pre-defined number of ordered 'buckets'
elements in each bucket is sorted (typically using insertion sort, worst case O(n**2)
can retrieve the sorted elements by visiting each bucket
does not compare elements to each other when deciding which bucket to place them
in speical cases results in O(n) worst-case complexity (as many buckets as keys)

Radix sort
sort objects with multiple keys
define the order of key pairs as (k1,l1)<(k2,l2) if k1<k2, or k1=k2 and l1<l2, can be generalized to key tuples of any length
also known as lexicographic or dictionary order
use multiple stable bucket sorts for this purpose

5 Trees

a hierarchical, non-linear data structure
a graph with certain properties
in cl: parse trees, language trees, decision trees

Definitions
a set of nodes organized hierarchically with the following properties:
If a tree is non-empty, it has a special node root
Except the root node, every node in the tree has a unique parent (all nodes except the root are children of another node)
Alternatively, recursive definition:
the empty set of nodes is a tree
otherwise a tree contains a root with sub-trees as its children
siblings nodes with the same parent
internal nodes nodes with children
leaf nodes nodes without children
path sequence of connected nodes
ancestors/decendants any node in the path from the root to a particular node; a node is the descendant of its ancestors
internal nodes nodes with children
subtree a tree rooted by a non-root node
depth number of edges from root
height number of edges from the deepest descendant; the height of a tree is the height of its root

Ordered trees
if there is an odering between siblings, e.g. document (e.g. HTML) structure tree, parse trees, family tree
in many cases order is not important (e.g. class hierarchy in object-oriented program, file tree in computer)

Binary trees
nodes can have at most 2 children
have a natural order: left/right child
proper/full: if every node has either 2 children or none
complete: if every level except possibly the last is completely filled, all nodes at the last level is at the left
perfect: a full binary tree whose leaf nodes have the same depth
properties: for a binary tree with nl leaf nodes, ni internal nodes, n nodes and height h:
h+1 <= n <= 2**(h+1)-1
1 <= nl <= 2**h
h <= ni <= 2**h -1
log(n+1)-1 <= h <= n-1
for any proper binary tree: nl=ni+1

Implementation
general case: linked data structure
arrays: root stored at index 0, left child of the node at index i stored at 2i+1, right child at 2i+2, parent at (i-1)/2 (if the binary tree is complete, this representation does not waste (much) space

Breadth first traversal (level order)

```
def breadth_first(root):
  queue = []
  queue.append(root)
  while queue:
    node = queue.pop(0)
    # process the node
    print(node.data)
    for child in node.children:
      queue.append(child)
```

Pre-order traversal

```
def pre_order(node):
  # process the node
  print(node.data)
  for child in node.children:
    pre_order(child)
```

Post-order traversal

```
def post_order(node):
  for child in node.children:
    post_order(child)
  # process the node
  print(node.data)
```

In-order traversal

```
def in_order(node):
  in_order(node.left)
  # process the node
  print(node.data)
  in_order(node.right)
```

6 Priority Queues

a collection, an abstract data type, that stores items (key-value pairs)
key: priority of the item
value: actual data of interest
its interface similar to a standard queue, but the item with the highest priority (minimum or maximum key value) instead of the first item entered into the queue is removed
applications ranging from data compression to discrete optimization

Operations
insert(k,v): similar to enqueue(v)
remove(): similar to dequeue(), often called remove-min() or remove-max() depending on minimum or maximum key value that is considered having the highest priority

Implementation
unsorted list: insert O(1), remove O(n)
sorted list: insert O(n), remove O(1)
binary heap: insert O(logn), remove O(logn)
(some improvements:
d-ary heaps: insert O(logd n), remove O(dlogd n)
fibonacci heaps: insert O(1), remove O(logn)

Sorting with priority queues
implemented with sorted list: = insertion sort O(n**2)
use unsorted list: = selection sort O(n**2)
use binary heap: = heap sort O(nlogn) (not stable; not in-place: needs O(n) extra space
in-place heap sort:
1. bottom-up heap construction
2. iteratively remove the maximum element and place it at the end
efficiency: heap construction O(n) + n*remove-min O(nlogn) = O(nlogn)

7 Binary Heaps

a binary tree where the nodes store items with an ordering relation

Properties
shape: a complete binary tree (all levels of the tree, except possibly the last one, are full; all empty slots (if any) are to the right of the filled nodes at the lowest level)
heap order: max-heap: parents' keys larger than children's keys; min-heap: parents' keys smaller than children's keys
Height log n
at least 2**h nodes -> h<=logn
at most 2**(h+1)-1 nodes -> h>=log(n+1)-1
add new item
add to the first available slot
bubble up until the heap property is satisfied
at most h=logn comparisons/swaps
remove the min/max
item to be removed is at the root
replace root with the element at the last slot
bubble down until the heap property is satisfied
implementation can be stored efficiently using an array data structure (like any complete binary tree)
construction for n items, we can construct a heap by inserting each key in O(nlogn) time
Bottom-up construction (O(n) complexity) (if we have the complete list):
1. fill the leaf nodes (h=logn, num of internal nodes=2**h-1, num of leaf nodes=n-2**h-1
2. fill the next level, bubble down if necessary
3. repeat 2 until all elements are inserted and heap property is satisfied
Python standard heap implementation
heapq module
allows maintaining a list(array) based heap
heappush(h,e): insert e(a key-value tuple) into heap h
heappop(h): return the minimum value from heap h
heapify(h): construct a heap from given list heappos(h)

8 Graphs

collection of vertices(nodes) connected pairwise by edges(arcs)
edges can be directed (also called arcs, 2-tuples or ordered pairs) and undirected (unordered pairs, or pair sets)
applications
city maps, chemical formulas, neural networks, ANNs, electronic circuits, computer networks, infectious diseases, probability distributions, word semantics
food web, course dependencies, social media, scheduling, games, academic networks, inheritance relations in OOP, flow charts, financial transactions, world's languages, PageRank algorithm
types
directed graph: with only directed edges, e.g. course dependencies
undirected graph: with only undirected edges, e.g. transportation(e.g. railway) networks
mixed graph: contains both directed and undirected edges (e.g. city map)
simple: there is only a single edge between 2 nodes
weighted: the edges have associated weights
complete: contains edges from each node to every other node
bipartite: has 2 disjoint sets of nodes, where edges are always across the sets
multi-graph: there are multiple edges (with the same direction) between a pair of nodes
hyper-graph: a single edge can link more than 2 nodes
more definitions
endpoints: two nodes joined by that edge
incident: an edge is incident to a node if the node is one of its endpoints
adjacent/neighbors: two nodes are incident to the same edge
degree/valency: number of its incident edges
indegree: num of incoming edges
outdegree: num of outgoing edges
parallel: 2 edges whose both endpoints are the same; for directed graph parallel edges are ones with the same direction
self-loop: an edge from a node to itself
path: a sequence of alternating edges and nodes
cycle: a path that starts and ends at the same node
simple: a path/cycle in which every node is visited only once reachable: X is reachable from Y if there is a directed path from Y to X
connected: a graph is connected if all nodes are reachable from each other
strongly connected: a directed graph is strongly connected if all nodes are reachable from each other
subgraph: a graph formed by a subset of nodes and edges of a graph
connected components: its maximally connected subgraphs if a graph is not connected
spanning subgraph: a subgraph that includes all nodes of the graph
tree: a connected graph without cycles
spanning tree: a spanning subgraph which is a tree
forest: a disconnected acyclic graph
properties
for an undirected graph with m edges and set of nodes V: $\Sigma deg(v) = 2m$
for a directed graph: $\Sigma indeg(v) = \Sigma outdeg(v) = 2m$
for a single undirected graph: m<=(n(n-1))/2
for a directed graph: m<=n(n-1)
graph ADT
add_node(v), remove_node(v), adjacent(u,v), neighbors(v), remove_edge(u,v), add_edge(u,v), nodes(), edges()
edge list keep a simple list of edges (and possibly notes)
remove_node(v):O(m), adjacent(u,v):O(m), neighbors(v):O(m), remove_edge(u,v):O(m), add_edge(u,v):O(1)
adjacency list keep simple lists for nodes and edges
add_node(v):O(1), remove_node(v):O(deg(v)), adjacent(u,v):O(min(deg(u),deg(v))), neighbors(v):O(deg(v))
adjacency matrix keep simple lists for nodes and edges
add_node(v):O(n), remove_node(v):O(n), adjacent(u,v):O(1), neighbors(v):O(n)
interesting problems directed path, shortest path, cycle, Eulerian path(a cycle that uses each edge exactly once), Hamiltonian path(a cycle that uses each node exactly once), connected, node that breaks connectivity if removed, can it be drawn without crossing edges, are two graphs isomorphic, importance of a web page based on the links pointing to it

Graph traversal

DFS
easy with recursion
starts from a start node
marks each node it visits as visited (typically put in a set)
take an arbitrary unvisited neighbor, continue visiting the nodes recursively
terminates when backtracking leads to the start node with no unvisited nodes left

```
def dfs(start, visited=None):
  if visited is None:
    visited = {start: None}
  for node in start.neighbors():
    if node not in visited:
      visited[node] = start
      dfs(node, visited)
```

discovery edges: the edges that we take to discover a new node
non-tree edges: other edges
back edges: the edges to an ancestor in the DFS tree
forward edges: the edges to a descendant node in the DFS tree
cross edges: the edges to a non-ancestor/non-descendant node
properties: discovery edges form a spanning tree of the connected component; if a node v is connected to the start node, there is a path from the start node to v in the DFS tree; visits each node and check each edge once (twice for undirec-

ted graphs); complexity is O(n+m) for n nodes and m edges

BFS

explore all options in parallel, divides the nodes into level (starting node at level 0...)
typically implemented with a queue
if replace the queue with a stack, it is an iterative version of DFS

```
def bfs(start):
  queue = [start]
  visited = {start: None}
  while queue:
    current = queue.pop(0)
    for node in current.neighbors():
      if node not in visited:
        visited[node] = current
        queue.append(node)
```

shortest path: if a node v is reachable from the start node, BFS finds the shortest path from the start node to v
complexity: O(n+m)

find path

traverse the graph from the source code, record the discovery edges
start from the target node, trace the path back to the source
with BFS, we get the shortest path
running time is the length of the path O(n)

```
def find_path(source, target, visited):
  path = []
  if target in visited:
    path.append(target)
    current = target
    while current is not source:
      parent = visited[current]
      path.append(parent)
      current = parent
  return path.reverse()
```

test connectivity, find connected components, find cycle

connected: yes if the "visited"nodes have the same length as the graph nodes
find the connected components: run traversal multiple times until all nodes are visited
cyclic: yes if there is a back edge during graph traversal

Directed graphs

terminology

for any pair of nodes u and v, a directed graph is
strongly connected: if there is a directed path between u to v and v to u
semi-connected: if there is a directed path between u to v or v to u
weakly connected: if the undirected graph obtained by replacing all edges with undirected edges is a connected graph

check strong connectivity

naive attempt: traverse the graph independently from each node (strongly connected if all traversals visit all nodes)
time complexity O(n(n+m))
better:
1. traverse the graph from an arbitrary node
2. reverse all edges, traverse again
3. intuition: if there a reverse path from D to A, then D is reachable from A
time complexity: O(n+m)

transitive closure another graph where:
-the set of nodes are the same as the original graph
-there is an edge between two nodes u and v if v is reachable from u
for undirected graph, can be computed by computing the connected components
a straightforward algorithm:
1. run n graph traversals from each node in the graph
2. add an edge between the start node to any node discovered by the traversal
time complexity O(n(n+m))
(note: in a dense graph m is O(n**2))
Floyd-Warshall algorithm: efficient if graph is implemented with an adjacency matrix and is not sparse
1. setting transitive closure to the original graph
2. for k=1...n, add a directed edge (vi,vj) to transitive closure if it already contains both (vi,vk) and (vk,vj)

```
T = [row[:] for row in G]
for k in range(n):
  for i in range(n):
    if i == k: continue
    for j in range(n):
      if j == i or  j == k:
        continue
      T[i][j] = T[i][j] or \
                T[i][k] and T[k][j]
```

time complexity O(n**3)
a version of this is used for finding shortest paths in weighted graphs

Directed acyclic graphs(DAGs) directed graphs without cycles
applications: course dependence, class inheritance, scheduling constrains over tasks in a project, dependency parser output
topological order: a sequence of nodes such that for every directed edge (u,v) u is listed before v; there may be multiple topological orderings, e.g. any acceptable order that the courses can be taken
topological sort:
1. keep record of number of incoming edges
2. a node is ready to be placed in the sorted list if there are no unprocessed incoming edges
time complexity O(n+m)
if topological ordering does not contain all the edges, the graph includes a cycle

```
topo, ready = [], []
incount = {}
for u in nodes:
   incount[u] = u.indegree()
   if incount[u] == 0:
      ready.append(u)
while len(ready) > 0:
   u = ready.pop()
   topo.append(u)
   for v in u.neighbors():
      incount[v] -= 1
   if incount[v] == 0:
      ready.append(v)
```

Shortest Paths

weighted graph weights can be any numeric value, but some algorithms require non-negative weights or Euclidean weights (weights that are proper distance metrics)
weights often indicate distance or cost, but can also represent positive relations (e.g. affinity between nodes)
weight of a path: the sum of weights of the edges on the path

shorted paths

applications: navigation, routing in computer networks, optimal construction of electronic circuits, robotics, transportation, finance...
shortest path on unweighted graphs: a BFS search tree
shortest path on unweighted graphs: different versions of the problem, restrictions on weights

Dijkstra's algorithm a weighted version of BFS, finds shorted path from a single source node to all connected nodes
weights have to be non-negative
a greedy algorithm, grows a 'cloud' of nodes for which we know the shortest paths from the source node
new nodes are included in the cloud in order of their shortest paths from the source node
1. maintain a list D of minimum known distances to each node
2. at each step:
-take closest node out of Q
-update the distances of all nodes
3. can be more efficient if Q is implemented using a priority queue

```
1: $D[s] \leftarrow 0$
2: for each node $v \neq s$ do
3:     $D[v] \leftarrow \infty$
4: $Q \leftarrow$ nodes
5: while Q is not empty do
6:     Remove node u with min D[u] from Q
7:     for each edge $(u, v)$ do
8:         if $D[u] + w(u, v) < D[v]$ then
9:             $D[v] \leftarrow D[u] + w(u, v)$
10: D contains the shortest distances from s
```

complexity: in general $O(t_{find-min}n + t_{update-key}m)$
with list-based implementation of Q: O(m+n**2)=O(n**2)
with a priority queue: O((m+n)logn)
similar to traversal algorithms, does not give the shortest-path tree, but can be extracted from distances D, running time O(n**2) or O(n+m)

```
1: $T \leftarrow \varnothing$
2: for $u \in D - \{s\}$ do
3:     for each edge $(v, u)$ do
4:         if $D[v] == D[u] + w(v, u)$ then
5:             $T \leftarrow T \cup (v, u)$
```

Shortest paths on DAGs directed acyclic graphs
similar to Dijkstra's, but simpler and faster
only difference is to follow a topological order
will also work with negative edge weights

Bellman-Ford algorithm single-source shortest path problem for directed graph
include cycles, negative weights, exclude negative cycles
1. similar to earlier algorithms, initialize D[s]=0, D[v]=infinity
2. make n passes over the edges:
-update distances for each edge (relax edges)
-stop if there were no changes at the end of a pass

Minimum Spanning Tree

spanning tree

- spanning graph: includes all nodes
tree - acyclic, connected

minimum spanning tree

applications: network design, cluster analysis, traveling salesman problem, object/network recognition in images, avoidig cycles in broadcasting, dithering in images audio video, error correction codes, dna sequencing

'cut property'

a cut of a graph is a partition that divides its nodes into two disjoint (non-empty) sets
given any cut, the edge with the lowest weight across the cut is in the MST

Prim-Jarnik algorithm greedy algorithm, finding MST for weighted undirected graph
1. starts with a single 'start' node, grows the MST greedily
2. at each step:
-consider a cut between nodes visited and the rest of the nodes
-select the minimum edge across the cut
3. repeat the process until all nodes are visited

```
1: pick any node s
2: $C[s] \leftarrow 0$
3: for each node $v \neq s$ do
4:     $C[v] \leftarrow \infty$
5:     $E[v] \leftarrow$ None
6: $T \leftarrow \varnothing$
7: $Q \leftarrow$ nodes
8: while Q is not empty do
9:     Retrieve v with min C[v] from Q
10:    Connect v to T
11:    for edge $(v, w)$, where w is in Q do
12:        if $cost(v, w) < C[w]$ then
13:            $C[w] \leftarrow cost(v, w)$
14:            $E[w] \leftarrow v$
```

complexity: two loops over number of nodes, O(n**2) if we need to search
if use a priority queue for Q, O(mlogm)
with a priority queue: O((m+n)logn)

Kruskal's algorithm finding MST on undirected graphs
1. start with each node in its own partition
2. at each iteration, choose the edge with the minimum weight across any two clusters, and join them
3. terminates when there are no clusters to join

```
1: $T \leftarrow \varnothing$
2: for each node v do
3:     create_cluster(v)
4: for (u,v) in edges sorted by weight do
5:     if $cluster(u) \neq cluster(v)$ then
6:         $T \leftarrow T \cup \{(u, v)\}$
7:         union(cluster(u), cluster(v))
```

loop over edges, but beware of the sorting requirement
O(mlogm) with simple data strcutures

Directed trees

-rooted directed tree (arborescence): an acyclic directed graph where all nodes are reachable from the root node through a single directed path (what computational linguists simply calls a tree)
- anti-arborescence: a rooted directed tree where all edges are reversed
- polytree (a drected tree): a directed graph where undirected edges form a tree
finding an MST in a directed graph = finding a rooted directed tree

Chu-Liu/Edmonds algorithm

1. the MST for a directed graph has to start from a designated root node
- if selected node has any incoming edges, remove them
- common practice to introduce an artificial root node with equal-weight edges to all ndoes
2. for all non-root nodes, select the incoming edge with lowest weight, remove others
3. if the resulting graph has no cycles, it is an MST 4. if there are cycles, break them
- consider the cycle as a single node - select the incoming edge that yields the lowest cost if used for breaking the cycle 5. repeat until no cycles remain
generally defined recursively: at each step, create a new graph with a contracted cycle call the procedure with the new graph
at most n recursions: the cycle has to include more nodes at every step
at each call, m steps for finding minimum incoming edge (also finding a cycle with O(n), but m>=n)
the vanilla algorithm runs in O(mn), there are improved versions
in CL dependency parsing:
1. begin with fully connected weighted graph, except the root node has no incoming edges
2. weights are estimated from a treebank, typically determined by a machine learning method trained on a treebank
3. often use probabilities, i.e. maximize the weight of the tree
4. one of the most common (and successful) approaches to dependency parsing

9 Maps & Hash Tables

hash function

a one-way function that takes a variable-length object and turns it into a fixed-length bit string
most common application: set, map (associative array/dictionary/symbol table)
other applic.: database indexing, cache management, efficient duplicate detection, file signature verification against corrupt/tempered files, password storage, electronic signatures, part of many cryptographic algorithms/applications

set

abstract data type, unordered collection without duplicates
basic operations: x in s, s.add(x), s.remove(x)

map

abstract data type, a collection that allows indexing with almost any data type (Python dict require immutable data type)
basic operations: d[key], d[key]=val, del d[key]
implement sets and maps:

	Check/retrieve	Add	Remove
Sorted array:	$O(\log n)$	$O(n)$	$O(n)$
Unsorted array:	$O(n)$	$O(1)$	$O(n)$
Skip list:	$O(\log n)$	$O(\log n)$	$O(\log n)$
Balanced search trees:	$O(\log n)$	$O(\log n)$	$O(\log n)$
Hash tables:	$O(1)$	$O(1)$	$O(1)$

hash function

h() maps a key to an integer index between 0 and m(size of array)
we use h(k) as an index to an array(of size m)
collision: occurs if 2 different key values are mapped to the same integer
2 parts: map any object (variable bit string) to an integer (e.g., 32 or 64 bit); compress the range of integers to map size(m)
main challenge with implementing hash maps: avoid and handle the collisions

compress hash codes

easy way: use modulo m+1 to map any integer to range [0,m]
good hash functions minimize collisions, but collisions occur
2 common approaches to handle collisions: separate chaining, open addressing

separate chaining each array element keeps a pointer to a secondary container(typically a list); when an collision occurs, add the item to the list
complexity: all operations require locating the element first, cost include hashing(constant)+search in secondary data structure, worst-case O(n)
with a good hash function, the probability of collision is n/m, O(n/m)=O(1) (if m>n)
expected complexity for all operations is O(1)

load factor = num of entries/num of indices
low load factor: better run time (fewer collisions)/more memory usage
when load factor is over a threshold, the map is extended(needs rehash)
around 0.75 is considered optimal

open addressing(linear probing) during insertion, if there is a collision, look for the next empty slot and insert
during lookup, probe until there is an empty slot
when delete an element, insert a special value that is treated as full during lookup and empty during insertion
tends to create clusters of items, especially if load factor is high(>0.5)
quadratic probing provides some improvement

quadratic probing prob (h(k)+i**2) mod m for i=0,1,... until an empty slot is found
if m is prime and load factor is less than 0.5, guaranteed to find an empty slot
although better than linear probing, creates its own kind of clustering

double hashing prob (h(k)+i*h'(k)) mod m for i=0,1,..., where h'(k) is another hash function
common choice: h'(k)=q-(k mod q) for a prime number q<m

pseudo random number generator prob $(h(k) + i * r_i) mod m$ for i=0,1,..., where r_i is the i-th number generated by a peudo number generator
pseudo random number generators generate numbers that are close to uniform, given the same seed, the sequence is deterministic
the most common choice for modern programming languages, avoids problems with inputs that intentionally generate hash collisions

has DoS attachs

a denial-of-service(DoS) attach aims to break or slow down an internet site/service
input to a web-based program is passed as key-value pairs, which are typically stored in a dictionary
if one intentionally posts an input with large number of colliding keys, the hash table implementation needs to chain long sequences or probe large number of times and eventually re-hash
this increases expected to O(1) time to worst-case complexity

xor or add

hash codes must be consistent: if a==b, h(a)==h(b)
should minimize collisions, values for h should be uniformly distributed
should be fast to compute (or not if used for passwords
simple appraoch: bitwise add (or XOR) each k-bit segment of the memory representation of the object, ignoring the overflow
in practice create many collisions due to associativity (abc, bca and cba get the same hash code)

polynomial hash codes

multiply with powers of a constant, will produce different values with sequences with the same items in different order

$$h(x) = \sum_{i}^{n} x_i a^{n-i-1} = x_0 a^{n-1} + x_1 a^{n-2} + \ldots + x_{n-1}$$

cyclic-shift hash codes

shifts some bits from one end to the other at each step in the running sum
a fast way of obtaining a non-associative valid hash code since bitwise operations are simple

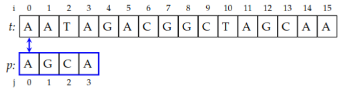
```
def cyclic_shift(s):
  mask = 0xffff
  h = 0
  for ch in s:
    h = (h << 5 & mask) | (h >> 11)
    h ^= ord(ch)
  return h
```

cryptographic hash functions in cryptography, it is important to have hash functions for which it is difficult to find two keys with the same hash value
well-known hash functions: MD5, SHA-1, RIPEMD-160, Whirlpool, SHA-2, SHA-3, BLACK2, BLACK3
designed for applications like digital fingerprinting, password storage
computationally inefficient for use in data structures

10 String Matching

find all occurrences of pattern p (length m) in text t (length n)
The size of the alphabet (q) is often an important factor
p occurs in t with shift s if p[0:m] == t[s:s+m]
A string x is a prefix/suffix of string y, if y=xw/ y=wx for a possibly empty string w

Brute-force string search


i 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
t: A A T A G A C G G C T A G C A A
p: A G C A
j 0 1 2 3

Start from the beginning, of i = 0 and j = 0
-if j == m, announce success with s = i
-if t[i]! = p[j]: shift p (increase i, set j = 0)
-otherwise: compare the next character (increase i and j, repeat)
worst case: t: AAAAAAAAC, p: AAC

Boyer-Moore algorithm

start comparing from the end of p
If t[i] does not occur in p, shift m steps
Otherwise, align the last occurrence of t[i] in p with t[i]

```
last = {}
for j in range(m):
  last[P[j]] = j
i,j = m-1, m-1
while i < n:
  if T[i] == P[j]:
    if j == 0:
      return i
    else:
      i -= 1
      j -= 1
  else:
    k = last.get(T[i], -1)
    i += m - min(j, k+1)
    j = m - 1
return None
```

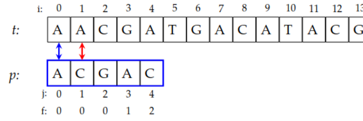
on average performs better than brute-force
wost case complexity O(nm), e.g. t=aaaaaaa, p=baa
faster version exists O(n+m+q)

FSA

1. start at state 0, switch states based on the input
2. all unspecified transitions go to state 0
3. when at the accepting state, announce success
naive attemp building automaton O(qm**3)
matching O(n)
space requirement O(qm) if stored in matrix
faster algorithms for construction exists

Knuth-Morris-Pratt (KMP) algorithm

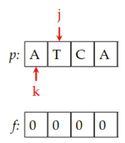
1. in case of a match, increment both i and j
2. on failure, or at the end of the pattern, decide which new p[j] compare with t[i] based on a function f
3. f[j-1] tells which j value to resume the comparisons from


i: 0 1 2 3 4 5 6 7 8 9 10 11 12 13
t: A A C G A T G A C A T A C G
p: A C G A C
j: 0 1 2 3 4
f: 0 0 0 1 2

```
i, j = 0, 0
while i < n:
  if T[i] == P[j]:
    if j == m - 1:
      return i - m + 1
    else:
      i += 1
      j += 1
  elif j > 0:
    j = f[k - 1]
  else:
    j += 1
return None
```

either increase i or shift the comparison
runs at most 2n times, complexity O(n)
build prefix/failure table

```
f = [0] * m
j, k = 1, 0
while j < m:
  if P[j] == P[k]:
    f[j] = k + 1
    j += 1
    k += 1
  elif k > 0:
    k = f[k - 1]
  else:
    j += 1
```



Robin-Karp algorithm

1. instead of matching the string itself, matching the hash of it (based on a hash function)
2. If a match found, we need to verify – the match may be because of a hash collision
3. Otherwise, the algorithm makes a single comparison for each position in the text
a hash should be computed for each position (size m) (rolling hash functions avoid this complication)

rolling hash function changes the hash value only based on the item coming in and going out of the window
to reduce collisions, better rolling-hash functions (e.g. polynomial hash functions) can be used

11 String Edit Distance

typically formulated as the (inverse) cost of obtaining one of the strings from the other through a number of edit operations
once we obtain the optimal edit operations, we may also be able to determine the optimal alignment between the strings

Hamming distance

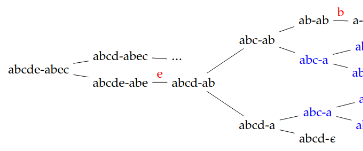
number of different symbols in the corresponding positions
easy calculation, but cannot handle sequences of different lengths

Longest common subsequence (LCS)

an order-preserving sequence of symbols from a string (solved by UNIX diff)
e.g. LCS(hygiene, hygeine) = hygine / hygene
naive solution:
1. Enumerate all subsequences of the first string (exponential)
2. Check if it is also a subsequence of the second string
O(m2**n) for strings of size n and m
recursive definition:

$$LCS(Xx, Yy) = \begin{cases} LCS(X, Y)x & \text{if } x = y \\ \text{longer of } LCS(Xx, Y) \text{ and } LCS(X, Yy) & \text{otherwis} \end{cases}$$

divide and conquer:



dynamic programming:

- In the standard dynamic programming algorithm, we store the LCS, in a matrix ℓ, where $\ell_{i,j}$ is the length of the LCS($X_{:i}, Y_{:j}$)
- Once we fill in the matrix, the $\ell_{n,m}$ is the length of the LCS
- We can trace back and recover the LCS using the dynamic prog matrix

```
l = np.zeros(shape=(n+1,m+1))
for i in range(1, n):
  for j in range(1, m):
    if X[i] == Y[j]:
      l[i, j] = l[i - 1, j - 1] + 1
    else:
      l[i, j] = max(l[i-1, j], l[i, j-1])
```

time complexity O(nm), space complexity O(nm)
back errors give a set of edit operations (assume original string is the vertical one):

Hilfszettel zur Klausur
von Tim S., Seite 3 von 2

		0	1	2	3	4	5	6	7	8
		ϵ	h	i	y	g	e	i	n	e
0	ϵ	0	0	0	0	0	0	0	0	0
1	h	0	1	1	1	1	1	1	1	1
2	y	0	1	1	2	2	2	2	2	2
3	g	0	1	1	2	3	3	3	3	3
4	i	0	1	2	2	3	3	4	4	4
5	e	0	1	2	2	3	4	4	4	5
6	n	0	1	2	2	3	4	4	5	5
7	e	0	1	2	2	3	4	4	5	6

Alignments:

```
h-yg-iene
ciccicdcc
hiygei-ne
```

```
h-ygie-ne
cicddcicc
hiyg-eine
```

- copy (diagonal arrows in the demonstration)
- insert (left arrows in the demo)
- delete (up arrows in the demo)

cost: copy 0, delete 1, insert 1

Levenshtein distance

the total cost of insertions, deletions and substitutions
naive recursion as in lcs with cost 1 for all operations
`d[i,j]= min(d[i-1,j]+1, d[i,j-1]+1, d[i-1,j-1])`

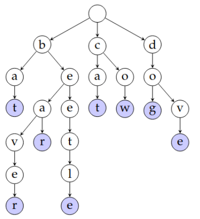
		0	1	2	3	4	5	6	7	8
		ϵ	h	i	y	g	e	i	n	e
0	ϵ	0	1	2	3	4	5	6	7	8
1	h	1	0	1	2	3	4	5	6	7
2	y	2	1	1	1	2	3	4	5	6
3	g	3	2	2	2	1	2	3	4	5
4	i	4	3	2	3	2	2	2	3	4
5	e	5	4	3	3	3	2	3	3	3
6	n	6	5	4	4	4	3	3	3	4
7	e	7	6	5	5	5	4	4	4	3

swap

useful for applications like spell checking

12 Tries

a trie (or prefix tree) is a tree-based data structure, particularly used for fast pattern matching



search

start from root, jump to node with current character
fail: if there is no character to follow/input ends in a non-leaf node
accpet if at a leaf node at the end of the input
to prevent that no string is a prefix of another: append a special end-of-string symbol/mark the nodes that correspond to ends of strings

complexity

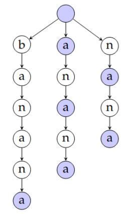
O(n) for search, insert or delete
a factor from the alphabet size q, but can be reduced to O(log q) with binary search, or O(1) if a method allowing direct addressing is used

properties

Internal nodes may have as many children as the number of symbols in the alphabet (in practice much smaller, average degree of nodes goes down as the depth increase)
height of the trie=longest string
num of leaves = num of strings
worst case num of nodes=total length of all strings

compress replace 'redundant' nodes with nodes labeled with substrings, saves space and may speed up operations

suffix tries tries that include all suffixes of a string, O(n) for substring search
if the search ends in a leaf node, the pattern is a suffix of the string



All suffixes:
#
a#
na#
ana#
nana#
anana#
banana#

Standard suffix tries use O(n**2) space, compression reduces space requirement to O(n), can be further reduced by keeping indexes to the string rather than the string itself in the (compressed) trie nodes
Iterative insertion of suffixes result in a quadratic (O(qn**2)) construction time complexity
there are linear time algorithms for constructing suffix tries
generalized suffix tries allow storing multiple strings(documents) in a single suffix trie (each string gets a special end-of-string marker)

13 Finite State Automata

Every regular language is generated/recognized by an FSA, every FSA generates/recognizes a regular language
One of the states is the initial state, some states are accepting states

Deterministic finite automata(DFA)

At any state and for any input, a DFA has a single well-defined action to take
we can add a sink(or error) state to make all transitions well-defined (for brevity skipped)

Non-deterministic finite automata(NFA)

transition table cells have sets of states

transition table

		symbol	
		a	b
state	→0	0,1	0,1
	1	1,2	1
	*2	0,2	0

NFA recognition(with backtracking)
1. start at q0
2. take the next input, place all possible actions to an agenda (state, character index)
3. get the next action from the agenda, act
4. at the end of input: accept-if in an accepting state; reject-not in accepting state & agenda empty; backtrack-otherwise

worst time complexity is exponential
depth-first search with stack as agenda, breath-first search with queue as agenda
machine learning methods to guide a best solution
NFA recognition(parallel version) 1. start at q0
2. take the next input, mark all possible next states
3. if an accepting state is marked at the end of the input, accept

note: the process is deterministic and finite-state

ϵ-NFA

allows moving without consuming an input symbol
any ϵ-NFA can be converted to an NFA

NFA-DFA equivalence

the set of DFA is a subset of the set of NFA(DFA is also an NFA)
NFA can automatically be converted to the equivalent DFA
DFA recognition is O(n), NFA recognition may be exponential
NFA are often easier to construct/may require less memory

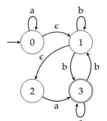
ϵ removal

1. start with finding the ϵ-closure of all states
2. replace each arc to each state with arc(s) to all states in the ϵ-closure

with transition table:

transition table

		symbol			
		a	b	ϵ	ϵ^*
state	→0	0	∅	1	0,1,2
	1	∅	1,3	2	1,2
	2	3	∅	∅	2
	*3	3	1	∅	3

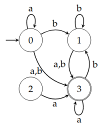


transition table

		symbol			
		a	b	ϵ	ϵ^*
state	→0	0	∅	1	0,1,2
	1	∅	1,3	2	1,2
	2	3	∅	∅	2
	*3	3	1	∅	3

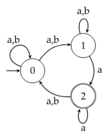
$\Rightarrow$

	symbol	
	a	b
→0	0,1,2	1,3
1	1,2,3	1,2,3
2	3	∅
*3	3	1,2



NFA Determinization

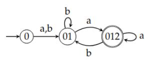
subset construction



transition table with subsets

	symbol	
	a	b
~~∅~~	~~∅~~	~~∅~~
→ {0}	{0, 1}	{0, 1}
~~{1}~~	~~{1, 2}~~	~~{1}~~
~~* {2}~~	~~{0, 2}~~	~~{0}~~
{0, 1}	{0, 1, 2}	{0, 1}
~~* {0, 2}~~	~~{0, 1, 2}~~	~~{0, 1}~~
~~* {1, 2}~~	~~{0, 1, 2}~~	~~{0, 1}~~
* {0, 1, 2}	{0, 1, 2}	{0, 1}

	symbol	
	a	b
→ {0}	{0, 1}	{0, 1}
{0, 1}	{0, 1, 2}	{0, 1}
* {0, 1, 2}	{0, 1, 2}	{0, 1}



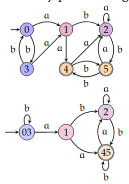
can skip the unreachable states during subset construction

FSA Minimization

for any regular language there is a unique minimal DFA
throw away unreachable states, merge equivalent states

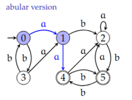
Hopcroft's algorithm

find and eliminate equivalent states by partitioning the set of states

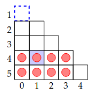


- Accepting & non-accepting states form a partition
  $Q_1 = \{0, 1, 2, 3\}$, $Q_2 = \{4, 5\}$
- If any two nodes go to different sets for any of the symbols split
- $Q_1 = \{0, 3\}$, $Q_3 = \{1\}$, $Q_4 = \{2\}$, $Q_2 = \{4, 5\}$
- Stop when we cannot split any of the sets, merge the indistinguishable states

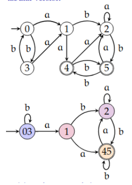
abular version



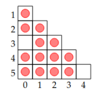
- Create a state-by-state table, mark *distinguishable* pairs: (q_1, q_2) such that $(\Delta(q_1, x), \Delta(q_2, x))$ is a distinguishable pair for any $x \in \Sigma$



tabular version



- Create a state-by-state table, mark *distinguishable* pairs: (q_1, q_2) such that $(\Delta(q_1, x), \Delta(q_2, x))$ is a distinguishable pair for any $x \in \Sigma$

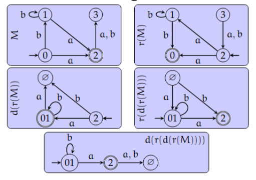


- Merge indistinguishable states
- The algorithm can be improved by choosing which cell to visit carefully

O(n log n) complexity

Brzozowski's algorithm

'double reversal'

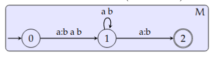


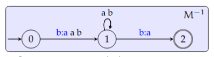
exponential worst-time complexity
can also be used with NFAs(resulting in the minimal equivalent DFA)

Finite State Transducers

The machine moves between the states based on an input symbol, while it outputs the corresponding output symbol
The relation defined by an FST is called a regular (or rational) relation
we treat an FSA as a simple FST that outputs its input
FST share many properties of FSAs, however:
- FSTs are not closed under intersection and complement
- we can compose(and invert) FSTs
- determinizing FSTs is not always possible

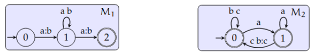
FST inversion (M**-1)





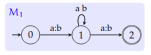
FST composition

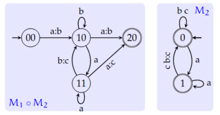
sequential application:



$$\xrightarrow{M_1 \circ M_2}$$

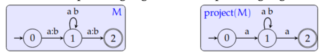
$$aa \xrightarrow{M_1} bb \xrightarrow{M_2} bb$$
$$bb \xrightarrow{M_1} \varnothing \xrightarrow{M_2} \varnothing$$
$$aaaa \xrightarrow{M_1} baab \xrightarrow{M_2} baac$$
$$abaa \xrightarrow{M_1} bbab \xrightarrow{M_2} bbac$$





FST projection

turns an FST into a FSA, accepting either the input language or the output language



FST determinization

means converting to a subsequential FST
can extend the subset construction to FSTs
not all FSTs can be determinized

sequential FSTs

has a single transition from each state on every input symbol
Output symbols can be strings, as well as ϵ
linear recognition time
do not allow ambiguity

subsequential FSTs

A k-subsequential FST is a sequential FST which can output up to k strings at an accepting state
allow limited ambiguity
linear recognition time