# Python Competitive Programming Notebook

PyCPBook Community

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**Abstract**

This document is a reference notebook for competitive programming in Python. It contains a collection of curated algorithms and data structures, complete with explanations and optimized, copy-pasteable code.

# Contents

# Chapter 1

# Contest & Setup

## Debugging Tricks

Author: PyCPBook Community Source: Collective experience from competitive programmers. Description: This section outlines common debugging techniques and tricks useful in a competitive programming context. Since standard debuggers are often unavailable or too slow on online judges, these methods are invaluable.

1. Debug Printing to stderr: - The most common technique is to print variable states at different points in the code. - Always print to standard error (`sys.stderr`) instead of standard output (`sys.stdout`). The online judge ignores `stderr`, so your debug messages won't interfere with the actual output and cause a "Wrong Answer" verdict. - Example: `print(f"DEBUG: Current value of x is {x}", file=sys.stderr)`

2. Test with Edge Cases: - Before submitting, always test your code with edge cases. - Minimum constraints: e.g., N=0, N=1, empty list. - Maximum constraints: e.g., N=10^5. (Check for TLE - Time Limit Exceeded). - Special values: e.g., zeros, negative numbers, duplicates. - A single off-by-one error can often be caught by testing N=1 or N=2.

3. Assertions: - Use `assert` to check for invariants in your code. An invariant is a condition that should always be true at a certain point. - For example, if a variable `idx` should always be non-negative, you can add `assert idx >= 0`. - If the assertion fails, your program will crash with an `AssertionError`, immediately showing you where the logic went wrong. - Assertions are automatically disabled in Python's optimized mode (`python -O`), so they have no performance penalty on the judge if it runs in that mode.

4. Naive Solution Comparison: - If you have a complex, optimized algorithm, write a simple, brute-force (naive) solution that is obviously correct but slow. - Generate a large number of small, random test cases. - Run both your optimized solution and the naive solution on each test case and assert that their outputs are identical. - If they differ, print the failing test case. This is the core idea behind the stress tests used in this project.

5. Rubber Duck Debugging: - Explain your code, line by line, to someone else or even an inanimate object (like a rubber duck). - The act of verbalizing your logic often helps you spot the flaw yourself. Time: N/A Space: N/A Status: Not applicable (Informational)

```python
import sys


def example_debug_print():
    """
    A simple example demonstrating how to print debug information
    to stderr without affecting the program's actual output.
    """
    data = [10, 20, 30]

    # This is the actual output that the judge will see.
    print("Processing started.")

    total = 0
    for i, item in enumerate(data):
        # This is a debug message. It goes to stderr and is ignored by the judge.
        print(f"DEBUG: Processing item {i} with value {item}", file=sys.stderr)
        total += item

    # This is the final output.
    print(f"The final total is: {total}")

```

## Template

Author: PyCPBook Community Source: Various competitive programming resources Description: A standard template for Python in programming contests. It provides fast I/O, increased recursion limit, and common helper functions to accelerate development under time constraints.

Fast I/O: Standard `input()` can be slow. This template redefines `input` to use `sys.stdin.readline()`, which is significantly faster for large inputs. Helper functions like `get_int()` and `get_ints()` are provided for convenience. For output, printing with `\n` is generally fast enough, but for a huge number of output operations, `sys.stdout.write()` can be used.

Recursion Limit: Python's default recursion limit (often 1000) is too low for problems involving deep recursion, such as tree/graph traversals on large datasets. `sys.setrecursionlimit(10**6)` increases this limit to avoid `RecursionError`.

Usage: Place your problem-solving logic inside the `solve()` function. The main execution block is set up to call this function. If the problem has multiple test cases, you can use the commented-out loop in the `main` function. Time: N/A Space: N/A Status: Not applicable (Utility)

```python
import sys
import math
import os

sys.setrecursionlimit(10**6)

input = sys.stdin.readline


def get_int():
    """Reads a single integer from a line."""
    return int(input())


def get_ints():
    """Reads a list of space-separated integers from a line."""
    return list(map(int, input().split()))


def get_str():
    """Reads a single string from a line, stripping trailing whitespace."""
    return input().strip()


def get_strs():
    """Reads a list of space-separated strings from a line."""
    return input().strip().split()


def solve():
    """
    This is the main function where the solution logic for a single
    test case should be implemented.
    """
    try:
        n, m = get_ints()
        print(n + m)
    except (IOError, ValueError):
        pass


def main():
    """
    Main execution function.
    Handles multiple test cases if required.
    """
    # t = get_int()
    # for _ in range(t):
    #     solve()
    solve()


if __name__ == "__main__":
    main()

```

# Chapter 2

# Data Structures

## Fenwick Tree

Author: PyCPBook Community Source: Based on common implementations in competitive programming resources Description: Implements a 1D Fenwick Tree, also known as a Binary Indexed Tree (BIT). This data structure is used to efficiently calculate prefix sums (or any other associative and invertible operation) on an array while supporting point updates.

A Fenwick Tree of size N allows for two main operations, both in logarithmic time: 1. add(idx, delta): Adds `delta` to the element at index `idx`. 2. query(right): Computes the sum of the elements in the range [0, right).

The core idea is that any integer can be represented as a sum of powers of two. Similarly, a prefix sum can be represented as a sum of sums over certain sub-ranges, where the size of these sub-ranges are powers of two. The tree stores these precomputed sub-range sums.

This implementation is 0-indexed for user-facing operations, which is a common convention in Python. The internal logic is adapted to work with this indexing. - To find the next index to update in `add`, we use `idx |= idx + 1`. - To find the next index to sum in `query`, we use `idx = (idx & (idx + 1)) - 1`.

Time: $O(\log N)$ for both `add` (point update) and `query` (prefix sum). Space: $O(N)$ to store the tree array. Status: Stress-tested

```python
class FenwickTree:
    """
    A class that implements a 1D Fenwick Tree (Binary Indexed Tree).
    This implementation uses 0-based indexing for its public methods.
    """

    def __init__(self, size):
        """
        Initializes the Fenwick Tree for an array of a given size.
        All elements are initially zero.

        Args:
            size (int): The number of elements the tree will support.
        """
        self.tree = [0] * size

    def add(self, idx, delta):
        """
        Adds a delta value to the element at a specific index.
        This operation updates all prefix sums that include this index.

        Args:
            idx (int): The 0-based index of the element to update.
            delta (int): The value to add to the element at `idx`.
        """
        while idx < len(self.tree):
            self.tree[idx] += delta
            idx |= idx + 1

    def query(self, right):
        """
        Computes the prefix sum of elements up to (but not including) `right`.
        This is the sum of the range [0, right-1].

        Args:
            right (int): The 0-based exclusive upper bound of the query range.

        Returns:
            int: The sum of elements in the prefix `[0, right-1]`.
        """
        idx = right - 1
        total_sum = 0
        while idx >= 0:
            total_sum += self.tree[idx]
            idx = (idx & (idx + 1)) - 1
        return total_sum

    def query_range(self, left, right):
        """
        Computes the sum of elements in the range [left, right-1].

        Args:
            left (int): The 0-based inclusive lower bound of the query range.
            right (int): The 0-based exclusive upper bound of the query range.

        Returns:
            int: The sum of elements in the specified range.
        """
        if left >= right:
            return 0
        return self.query(right) - self.query(left)
```

## Fenwick Tree 2D

Author: PyCPBook Community Source: KACTL, TopCoder tutorials Description: Implements a 2D Fenwick Tree (Binary Indexed Tree). This data structure extends the 1D Fenwick Tree to support point updates and prefix rectangle sum queries on a 2D grid.

The primary operations are: 1. add(r, c, delta): Adds `delta` to the element at grid cell (r, c). 2. query(r, c): Computes the sum of the rectangle from (0, 0) to (r-1, c-1).

A 2D Fenwick Tree can be conceptualized as a Fenwick Tree where each element is itself another Fenwick Tree. The `add` and `query` operations therefore involve traversing the tree structure in both dimensions, resulting in a time complexity that is the product of the logarithmic complexities of each dimension.

The `query_range` method uses the principle of inclusion-exclusion on the prefix rectangle sums to calculate the sum of any arbitrary sub-rectangle. Given a rectangle defined by top-left (r1, c1) and bottom-right (r2-1, c2-1), the sum is: Sum(r2, c2) - Sum(r1, c2) - Sum(r2, c1) + Sum(r1, c1), where Sum(r, c) is the prefix sum from (0,0) to (r-1, c-1).

Time: $O(\log R \cdot \log C)$ for `add` and `query` on an $R \times C$ grid. Space: $O(R \cdot C)$ to store the 2D tree. Status: Stress-tested

```python
class FenwickTree2D:
    """
    A class that implements a 2D Fenwick Tree using
    ↪ 0-based indexing.
    """

    def __init__(self, rows, cols):
        """
        Initializes the 2D Fenwick Tree for a grid
        ↪ of a given size.
        All elements are initially zero.

        Args:
            rows (int): The number of rows in the
            ↪ grid.
            cols (int): The number of columns in
            ↪ the grid.
        """
        self.rows = rows
        self.cols = cols
        self.tree = [[0] * cols for _ in
        ↪ range(rows)]

    def add(self, r, c, delta):
        """
        Adds a delta value to the element at grid
        ↪ cell (r, c).

        Args:
            r (int): The 0-based row index of the
            ↪ element to update.
            c (int): The 0-based column index of
            ↪ the element to update.
            delta (int): The value to add.
        """
        i = r
        while i < self.rows:
            j = c
            while j < self.cols:
                self.tree[i][j] += delta
                j |= j + 1
            i |= i + 1

    def query(self, r, c):
        """
        Computes the prefix sum of the rectangle
        ↪ from (0, 0) to (r-1, c-1).

        Args:
            r (int): The 0-based exclusive row
            ↪ bound of the query rectangle.
            c (int): The 0-based exclusive column
            ↪ bound of the query rectangle.

        Returns:
            int: The sum of the elements in the
            ↪ rectangle [0..r-1, 0..c-1].
        """
        total_sum = 0
        i = r - 1
        while i >= 0:
            j = c - 1
            while j >= 0:
                total_sum += self.tree[i][j]
                j = (j & (j + 1)) - 1
            i = (i & (i + 1)) - 1
        return total_sum

    def query_range(self, r1, c1, r2, c2):
        """
        Computes the sum of the rectangle from (r1,
        ↪ c1) to (r2-1, c2-1).

        Args:
            r1, c1 (int): The 0-based inclusive
            ↪ top-left coordinates.
            r2, c2 (int): The 0-based exclusive
            ↪ bottom-right coordinates.

        Returns:
            int: The sum of elements in the
            ↪ specified rectangular range.
        """
        if r1 >= r2 or c1 >= c2:
            return 0

        total = self.query(r2, c2)
        total -= self.query(r1, c2)
        total -= self.query(r2, c1)
        total += self.query(r1, c1)
        return total
```

## Hash Map Custom

Author: PyCPBook Community Source: KACTL, neal wu's blog Description: Provides an explanation and an example of a custom hash for Python's dictionaries and sets to prevent slowdowns from anti-hash tests. In competitive programming, some problems use test cases specifically designed to cause many collisions in standard hash table implementations (like Python's dict), degrading their performance from average $O(1)$ to worst-case $O(N)$.

This can be mitigated by using a hash function with a randomized component, so that the hash values are unpredictable to an adversary. A common technique is to XOR the object's standard hash with a fixed, randomly generated constant.

The `splitmix64` function shown below is a high-quality hash function that can be used for this purpose. It's simple, fast, and provides good distribution.

To use a custom hash, you can wrap integer or tuple keys in a custom class that overrides the `__hash__` and `__eq__` methods.

Example usage with a dictionary: `my_map = {}` `my_map[CustomHash(123)] = "value"`

This forces Python's `dict` to use your `CustomHash` object's `__hash__` method, thus using the randomized hash function. This is particularly useful in problems involving hashing of tuples, such as coordinates or polynomial hash values. Time: The hash computation is $O(1)$. Dictionary operations remain amortized $O(1)$. Space: Adds a small constant overhead per key for the wrapper object. Status: Not applicable (Utility/Informational)

```python
import time

# A fixed random seed ensures the same hash function for each run,
# but it's generated based on time to be unpredictable.
SPLITMIX64_SEED = int(time.time()) ^ 0x9E3779B97F4A7C15


def splitmix64(x):
    """A fast, high-quality hash function for 64-bit integers."""
    x += 0x9E3779B97F4A7C15
    x = (x ^ (x >> 30)) * 0xBF58476D1CE4E5B9
    x = (x ^ (x >> 27)) * 0x94D049BB133111EB
    return x ^ (x >> 31)


class CustomHash:
    """
    A wrapper class for hashable objects to use a custom hash function.
    This helps prevent collisions from anti-hash test cases.
    """

    def __init__(self, obj):
        self.obj = obj

    def __hash__(self):
        # Combine the object's hash with a fixed random seed using a robust function.
        return splitmix64(hash(self.obj) + SPLITMIX64_SEED)

    def __eq__(self, other):
        # The wrapped objects must still be comparable.
        return self.obj == other.obj

    def __repr__(self):
        return f"CustomHash({self.obj})"


# Example of how to use it
def custom_hash_example():
    # Standard dictionary, potentially vulnerable
    standard_dict = {}
    # Dictionary with custom hash, much more robust
    custom_dict = {}

    key = (12345, 67890)  # A tuple key, common in geometry or hashing problems

    # Using the standard hash
    standard_dict[key] = "some value"

    # Using the custom hash
    custom_key = CustomHash(key)
    custom_dict[custom_key] = "some value"

    print(f"Standard hash for {key}: {hash(key)}")
    print(f"Custom hash for {key}: {hash(custom_key)}")

    # Verifying that it works
    assert custom_key in custom_dict
    assert CustomHash(key) in custom_dict
    assert CustomHash((0, 0)) not in custom_dict

```

## Line Container

Author: PyCPBook Community Source: KACTL, CP-Algorithms Description: Implements a Line Container for the Convex Hull Trick. This data structure maintains a set of lines of the form `y = mx + c` and allows for efficiently querying the minimum `y` value for a given `x`. This is a key component in optimizing certain dynamic programming problems.

This implementation is specialized for the following common case: - Queries ask for the minimum value. - The slopes `m` of the lines added are monotonically decreasing.

The lines are stored in a deque, which acts as the lower convex hull. When a new line is added, we maintain the convexity of the hull by removing any lines from the back that become redundant. A line becomes redundant if the intersection point of its neighbors moves left, violating the convexity property. This check is done using cross-products to avoid floating-point arithmetic.

Queries are performed using a binary search on the hull to find the optimal line for the given `x`. If the `x` values for queries are also monotonic, the query time can be improved to amortized $O(1)$ by using a pointer instead of a binary search.

To adapt for maximum value queries, change the inequalities in `add` and `query`. To handle monotonically increasing slopes, add lines to the front of the deque and adjust the `add` method's popping logic accordingly.

Time: $O(\log N)$ for `query` due to binary search. Amortized $O(1)$ for `add` because each line is added and removed at most once. Space: $O(N)$ to store the lines on the convex hull. Status: Stress-tested

```python
class LineContainer:
    """
    A data structure for the Convex Hull Trick,
    ↪ optimized for minimum queries
    and monotonically decreasing slopes.
    """

    def __init__(self):
        # Each line is stored as a tuple (m, c)
        ↪ representing y = mx + c.
        self.hull = []

    def _is_redundant(self, l1, l2, l3):
        """
        Checks if line l2 is redundant given its
        ↪ neighbors l1 and l3.
        l2 is redundant if the intersection of l1
        ↪ and l3 is to the left of
        the intersection of l1 and l2.
        Intersection of (m1, c1) and (m2, c2) is x
        ↪ = (c2 - c1) / (m1 - m2).
        We check if (c3-c1)/(m1-m3) <=
        ↪ (c2-c1)/(m1-m2).
        To avoid floating point, we use
        ↪ cross-multiplication.
        Since slopes are decreasing, m1 > m2 > m3,
        ↪ so (m1-m3) and (m1-m2) are positive.
        The inequality becomes (c3-c1)*(m1-m2) <=
        ↪ (c2-c1)*(m1-m3).
        """
        m1, c1 = l1
        m2, c2 = l2
        m3, c3 = l3
        # Note the direction of inequality might
        ↪ change based on max/min query
        # and increasing/decreasing slopes. This is
        ↪ for min query, decr. slopes.
        return (c3 - c1) * (m1 - m2) <= (c2 - c1) *
        ↪ (m1 - m3)

    def add(self, m, c):
        """
        Adds a new line y = mx + c to the
        ↪ container.
        Assumes that m is less than the slope of
        ↪ any previously added line.
        """
        new_line = (m, c)
        while len(self.hull) >= 2 and
        ↪ self._is_redundant(
            self.hull[-2], self.hull[-1], new_line
        ):
            self.hull.pop()
        self.hull.append(new_line)

    def query(self, x):
        """
        Finds the minimum value of y = mx + c for a
        ↪ given x among all lines.
        """
        if not self.hull:
            return float("inf")

        # Binary search for the optimal line.
        # The function `f(i) = m_i * x + c_i` is
        ↪ not monotonic, but the
        # optimal line index is. Specifically, the
        ↪ function `f(i+1) - f(i)`
        # is monotonic. We are looking for the
        ↪ point where the function
        # transitions from decreasing to
        ↪ increasing.
        low, high = 0, len(self.hull) - 1
        res_idx = 0

        while low <= high:
            mid = (low + high) // 2
            # Check if mid is better than mid+1
            if mid + 1 < len(self.hull):
                val_mid = self.hull[mid][0] * x +
                ↪ self.hull[mid][1]
                val_next = self.hull[mid + 1][0] *
                ↪ x + self.hull[mid + 1][1]
                if val_mid > val_next:
                    low = mid + 1
                else:
                    res_idx = mid
                    high = mid - 1
            else:
                res_idx = mid
                high = mid - 1

        m, c = self.hull[res_idx]
        return m * x + c
```

## Ordered Set

Author: PyCPBook Community Source: KACTL, CP-Algorithms (adapted from Treap) Description: Implements an Ordered Set data structure using a randomized balanced binary search tree (Treap). An Ordered Set supports all the standard operations of a balanced BST (insert, delete, search) and two additional powerful operations: 1. `find_by_order(k)`: Finds the k-th smallest element in the set (0-indexed). 2. `order_of_key(key)`: Finds the number of elements in the set that are strictly smaller than the given key (i.e., its rank).

To achieve this, each node in the underlying Treap is augmented to store the size of the subtree rooted at that node. This `size` information is updated during insertions and deletions. The ordered set operations then use these sizes to navigate the tree efficiently. For example, to find the k-th element, we can compare `k` with the size of the left subtree to decide whether to go left, right, or stop at the current node.

The implementation is based on the elegant `split` and `merge` operations, which are modified to maintain the subtree size property.

Time: $O(\log N)$ on average for `insert`, `delete`, `search`, `find_by_order`, and `order_of_key` operations, where $N$ is the number of elements in the set. Space: $O(N)$ to store the nodes of the set. Status: Stress-tested

```python
import random


class Node:
    """Represents a single node in the Ordered Set's underlying Treap."""

    def __init__(self, key):
        self.key = key
        self.priority = random.random()
        self.size = 1
        self.left = None
        self.right = None


def _get_size(t):
    return t.size if t else 0


def _update_size(t):
    if t:
        t.size = 1 + _get_size(t.left) + _get_size(t.right)


def _split(t, key):
    """
    Splits the tree `t` into two trees: one with keys < `key` (l)
    and one with keys >= `key` (r).
    """
    if not t:
        return None, None
    if t.key < key:
        l, r = _split(t.right, key)
        t.right = l
        _update_size(t)
        return t, r
    else:
        l, r = _split(t.left, key)
        t.left = r
        _update_size(t)
        return l, t


def _merge(t1, t2):
    """Merges two trees `t1` and `t2`, assuming keys in `t1` < keys in `t2`."""
    if not t1:
        return t2
    if not t2:
        return t1
    if t1.priority > t2.priority:
        t1.right = _merge(t1.right, t2)
        _update_size(t1)
        return t1
    else:
        t2.left = _merge(t1, t2.left)
        _update_size(t2)
        return t2


class OrderedSet:
    """
    An Ordered Set implementation using a Treap.
    Supports finding the k-th element and the rank of an element.
    """

    def __init__(self):
        self.root = None

    def search(self, key):
        node = self.root
        while node:
            if node.key == key:
                return True
            node = node.left if key < node.key else node.right
        return False

    def insert(self, key):
        if self.search(key):
            return
        new_node = Node(key)
        l, r = _split(self.root, key)
        self.root = _merge(_merge(l, new_node), r)

    def delete(self, key):
        if not self.search(key):
            return
        l, r = _split(self.root, key)
        _, r_prime = _split(r, key + 1)
        self.root = _merge(l, r_prime)

    def find_by_order(self, k):
        """Finds the k-th smallest element (0-indexed)."""
        node = self.root
        while node:
            left_size = _get_size(node.left)
            if left_size == k:
                return node.key
            elif k < left_size:
                node = node.left
            else:
                k -= left_size + 1
                node = node.right
        return None

    def order_of_key(self, key):
        """Finds the number of elements strictly smaller than key."""
        count = 0
        node = self.root
        while node:
            if key == node.key:
                count += _get_size(node.left)
                break
            elif key < node.key:
                node = node.left
            else:
                count += _get_size(node.left) + 1
                node = node.right
        return count
```

```python

    def __len__(self):
        return _get_size(self.root)

```

## Segment Tree Lazy

Author: PyCPBook Community Source: CP-Algorithms, various competitive programming tutorials Description: Implements a Segment Tree with lazy propagation. This powerful data structure is designed to handle range updates and range queries efficiently. While a standard Segment Tree can perform range queries in $O(\log N)$ time, updates are limited to single points. Lazy propagation extends this capability to allow range updates (e.g., adding a value to all elements in a range) to also be performed in $O(\log N)$ time.

The core idea is to postpone updates to tree nodes and apply them only when necessary. When an update is requested for a range `[l, r]`, we traverse the tree. If a node's range is fully contained within `[l, r]`, instead of updating all its children, we store the pending update value in a `lazy` array for that node and update the node's main value. We then stop traversing down that path. This pending update is "pushed" down to its children only when a future query or update needs to access one of the children.

This implementation supports range addition updates and range sum queries. The logic can be adapted for other associative operations like range minimum/maximum and range assignment.

Time: $O(\log N)$ for both `update` (range update) and `query` (range query). The initial `build` operation takes $O(N)$ time. Space: $O(N)$ to store the tree and lazy arrays. A size of $4N$ is allocated to be safe for a complete binary tree representation. Status: Stress-tested

```python
class SegmentTree:
    def __init__(self, arr):
        self.n = len(arr)
        self.tree = [0] * (4 * self.n)
        self.lazy = [0] * (4 * self.n)
        self.arr = arr
        self._build(1, 0, self.n - 1)

    def _build(self, v, tl, tr):
        if tl == tr:
            self.tree[v] = self.arr[tl]
        else:
            tm = (tl + tr) // 2
            self._build(2 * v, tl, tm)
            self._build(2 * v + 1, tm + 1, tr)
            self.tree[v] = self.tree[2 * v] + self.tree[2 * v + 1]

    def _push(self, v, tl, tr):
        if self.lazy[v] == 0:
            return

        range_len = tr - tl + 1
        self.tree[v] += self.lazy[v] * range_len

        if tl != tr:
            self.lazy[2 * v] += self.lazy[v]
            self.lazy[2 * v + 1] += self.lazy[v]

        self.lazy[v] = 0

    def _update(self, v, tl, tr, l, r, addval):
        self._push(v, tl, tr)
        if l > r:
            return
        if l == tl and r == tr:
            self.lazy[v] += addval
            self._push(v, tl, tr)
        else:
            tm = (tl + tr) // 2
            self._update(2 * v, tl, tm, l, min(r, tm), addval)
            self._update(2 * v + 1, tm + 1, tr, max(l, tm + 1), r, addval)

            # After children are updated, update self based on pushed children
            self._push(2 * v, tl, tm)
            self._push(2 * v + 1, tm + 1, tr)
            self.tree[v] = self.tree[2 * v] + self.tree[2 * v + 1]

    def _query(self, v, tl, tr, l, r):
        if l > r:
            return 0
        self._push(v, tl, tr)
        if l == tl and r == tr:
            return self.tree[v]

        tm = (tl + tr) // 2
        left_sum = self._query(2 * v, tl, tm, l, min(r, tm))
        right_sum = self._query(2 * v + 1, tm + 1, tr, max(l, tm + 1), r)
        return left_sum + right_sum

    def update(self, l, r, addval):
        # Updates range [l, r] (inclusive)
        if l > r:
            return
        self._update(1, 0, self.n - 1, l, r, addval)

    def query(self, l, r):
        # Queries range [l, r] (inclusive)
        if l > r:
            return 0
        return self._query(1, 0, self.n - 1, l, r)

```

## Sparse Table

Author: PyCPBook Community Source: CP-Algorithms, USACO Guide Description: Implements a Sparse Table for fast Range Minimum Queries (RMQ). This data structure is ideal for answering range queries on a static array for idempotent functions like min, max, or gcd.

The core idea is to precompute the answers for all ranges that have a length that is a power of two. The table `st[k][i]` stores the minimum value in the range `[i, i + 2^k - 1]`. This precomputation takes $O(N \log N)$ time.

Once the table is built, a query for any arbitrary range `[l, r]` can be answered in $O(1)$ time. This is achieved by finding the largest power of two, `2^k`, that is less than or equal to the range length `r - l + 1`. The query then returns the minimum of two overlapping ranges: `[l, l + 2^k - 1]` and `[r - 2^k + 1, r]`. Because `min` is an idempotent function, the overlap does not affect the result.

This implementation is for range minimum, but can be easily adapted for range maximum by changing `min` to `max`.

Time: Precomputation is $O(N \log N)$. Each query is $O(1)$. Space: $O(N \log N)$ to store the sparse table. Status: Stress-tested

```python
import math


class SparseTable:
    """
    A class that implements a Sparse Table for efficient Range Minimum Queries.
    This implementation assumes 0-based indexing for the input array and queries.
    """

    def __init__(self, arr):
        """
        Initializes the Sparse Table from an input array.

        Args:
            arr (list[int]): The static list of numbers to be queried.
        """
        self.n = len(arr)
        if self.n == 0:
            return

        self.max_log = self.n.bit_length() - 1
        self.st = [[0] * self.n for _ in range(self.max_log + 1)]
        self.st[0] = list(arr)

        for k in range(1, self.max_log + 1):
            for i in range(self.n - (1 << k) + 1):
                self.st[k][i] = min(
                    self.st[k - 1][i], self.st[k - 1][i + (1 << (k - 1))]
                )

        self.log_table = [0] * (self.n + 1)
        for i in range(2, self.n + 1):
            self.log_table[i] = self.log_table[i >> 1] + 1

    def query(self, l, r):
        """
        Queries the minimum value in the inclusive range [l, r].

        Args:
            l (int): The 0-based inclusive starting index of the range.
            r (int): The 0-based inclusive ending index of the range.

        Returns:
            int: The minimum value in the range [l, r]. Returns infinity
                if the table is empty or the range is invalid.
        """
        if self.n == 0 or l > r:
            return float("inf")

        length = r - l + 1
        k = self.log_table[length]
        return min(self.st[k][l], self.st[k][r - (1 << k) + 1])

```

## Treap

Author: PyCPBook Community Source: KACTL, CP-Algorithms Description: Implements a Treap, a randomized balanced binary search tree. A Treap is a data structure that combines the properties of a binary search tree and a heap. Each node in the Treap has both a key and a randomly assigned priority. The keys follow the binary search tree property (left child's key < parent's key < right child's key), while the priorities follow the max-heap property (parent's priority > children's priorities).

The random assignment of priorities ensures that, with high probability, the tree remains balanced, leading to logarithmic time complexity for standard operations. This implementation uses `split` and `merge` operations, which are a clean and powerful way to handle insertions and deletions.

- `split(key)`: Splits the tree into two separate trees: one containing all keys less than `key`, and another containing all keys greater than or equal to `key`. - `merge(left, right)`: Merges two trees, `left` and `right`, under the assumption that all keys in `left` are smaller than all keys in `right`.

Using these, `insert` and `delete` can be implemented elegantly.

Time: $O(\log N)$ on average for `insert`, `delete`, and `search` operations, where $N$ is the number of nodes in the Treap. The performance depends on the randomness of the priorities. Space: $O(N)$ to store the nodes of the Treap. Status: Stress-tested

```python
import random


class Node:
    """
    Represents a single node in the Treap.
    Each node contains a key, a randomly generated priority, and left/right children.
    """
```

```python

    def __init__(self, key):
        self.key = key
        self.priority = random.random()
        self.left = None
        self.right = None


def _split(t, key):
    """
    Splits the tree rooted at `t` into two trees based on `key`.
    Returns a tuple (left_tree, right_tree), where left_tree contains all keys
    from `t` that are less than `key`, and right_tree contains all keys that are
    greater than or equal to `key`.
    """
    if not t:
        return None, None
    if t.key < key:
        l, r = _split(t.right, key)
        t.right = l
        return t, r
    else:
        l, r = _split(t.left, key)
        t.left = r
        return l, t


def _merge(t1, t2):
    """
    Merges two trees `t1` and `t2`.
    Assumes all keys in `t1` are less than all keys in `t2`.
    The merge is performed based on node priorities to maintain the heap property.
    """
    if not t1:
        return t2
    if not t2:
        return t1
    if t1.priority > t2.priority:
        t1.right = _merge(t1.right, t2)
        return t1
    else:
        t2.left = _merge(t1, t2.left)
        return t2


class Treap:
    """
    The Treap class providing a public API for balanced BST operations.
    """

    def __init__(self):
        """Initializes an empty Treap."""
        self.root = None

    def search(self, key):
        """
        Searches for a key in the Treap.
        Returns True if the key is found, otherwise False.
        """
        node = self.root
        while node:
            if node.key == key:
                return True
            elif key < node.key:
                node = node.left
            else:
                node = node.right
        return False

    def insert(self, key):
        """
        Inserts a key into the Treap. If the key already exists, the tree is unchanged.
        """
        if self.search(key):
            return  # Don't insert duplicates

        new_node = Node(key)
        l, r = _split(self.root, key)
        # l has keys < key, r has keys >= key.
        # Merge new_node with r first, then merge l with the result.
        self.root = _merge(l, _merge(new_node, r))

    def delete(self, key):
        """
        Deletes a key from the Treap. If the key is not found, the tree is unchanged.
        """
        if not self.search(key):
            return

        # Split to isolate the node to be deleted.
        l, r = _split(self.root, key)  # l has keys < key, r has keys >= key
        _, r_prime = _split(r, key + 1)  # r_prime has keys > key

        # Merge the remaining parts back together.
        self.root = _merge(l, r_prime)

```

## Union Find

Author: PyCPBook Community Source: Based on common implementations in competitive programming resources Description: Implements the Union-Find data structure, also known as Disjoint Set Union (DSU). It is used to keep track of a partition of a set of elements into a number of disjoint, non-overlapping subsets. The two primary operations are finding the representative (or root) of a set and merging two sets.

This implementation includes two key optimizations: 1. Path Compression: During a `find` operation, it makes every node on the path from the query node to the root point directly to the root. This dramatically flattens the tree structure. 2. Union by Size: During a `union` operation, it always attaches the root of the smaller tree to the root of the larger tree. This helps in keeping the trees shallow, which speeds up future `find` operations.

The combination of these two techniques makes the amortized time complexity of both `find` and `union` operations nearly constant. Time: $O(\alpha(N))$ on average for both find and union operations, where *alpha* is the extremely slow-growing inverse Ackermann function. For all practical purposes, this is considered constant time. Space: $O(N)$ to store the parent and size arrays for N elements. Status: Stress-tested

```python
class UnionFind:
    """
    A class that implements the Union-Find data
    ↪  structure with path compression
    and union by size optimizations.
    """

    def __init__(self, n):
        """
        Initializes the Union-Find structure for n
        ↪  elements, where each element
        is initially in its own set.
        Args:
            n (int): The number of elements.
        """
        self.parent = list(range(n))
        self.size = [1] * n

    def find(self, i):
        """
        Finds the representative (root) of the set
        ↪  containing element i.
        Applies path compression along the way.
        Args:
            i (int): The element to find.
        Returns:
            int: The representative of the set
            ↪  containing i.
        """
        if self.parent[i] == i:
            return i
        self.parent[i] = self.find(self.parent[i])
        return self.parent[i]

    def union(self, i, j):
        """
        Merges the sets containing elements i and
        ↪  j.
        Applies union by size.
        Args:
            i (int): An element in the first set.
            j (int): An element in the second set.
        Returns:
            bool: True if the sets were merged,
            ↪  False if they were already in the
            ↪  same set.
        """
        root_i = self.find(i)
        root_j = self.find(j)
        if root_i != root_j:
            if self.size[root_i] <
            ↪  self.size[root_j]:
                root_i, root_j = root_j, root_i
            self.parent[root_j] = root_i
            self.size[root_i] += self.size[root_j]
            return True
        return False

```

# Chapter 3

# Graph Algorithms

## Bellman Ford

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS) Description: Implements the Bellman-Ford algorithm for finding the single-source shortest paths in a weighted graph. Unlike Dijkstra's algorithm, Bellman-Ford can handle graphs with negative edge weights.

The algorithm works by iteratively relaxing edges. It repeats a relaxation step $V-1$ times, where $V$ is the number of vertices. In each relaxation step, it iterates through all edges `(u, v)` and updates the distance to `v` if a shorter path is found through `u`. After $V-1$ iterations, the shortest paths are guaranteed to be found, provided there are no negative-weight cycles reachable from the source.

A final, $V$-th iteration is performed to detect negative-weight cycles. If any distance can still be improved during this iteration, it means a negative-weight cycle exists, and the shortest paths are not well-defined (they can be infinitely small).

This implementation takes an edge list as input, which is a common and convenient representation for this algorithm.

Time: $O(V \cdot E)$, where $V$ is the number of vertices and $E$ is the number of edges. The algorithm iterates through all edges $V$ times. Space: $O(V+E)$ to store the edge list and the distances array. Status: Stress-tested

```python
def bellman_ford(edges, start_node, n):
    """
    Finds shortest paths from a start node,
    ↪  handling negative weights and
    detecting negative cycles.

    Args:
        edges (list[tuple[int, int, int]]): A list
        ↪  of all edges in the graph,
            where each tuple is (u, v, weight) for
            ↪  an edge u -> v.
        start_node (int): The node from which to
        ↪  start the search.
        n (int): The total number of nodes in the
        ↪  graph.

    Returns:
        tuple[list[float], bool]: A tuple
        ↪  containing:
            - A list of shortest distances.
            ↪  `float('inf')` for unreachable
            ↪  nodes.
            - A boolean that is True if a negative
            ↪  cycle is detected, False otherwise.
    """
    if not (0 <= start_node < n):
        return [float("inf")] * n, False

    dist = [float("inf")] * n
    dist[start_node] = 0

    for i in range(n - 1):
        updated = False
        for u, v, w in edges:
            if dist[u] != float("inf") and dist[u]
            ↪  + w < dist[v]:
                dist[v] = dist[u] + w
                updated = True
        if not updated:
            break

    for u, v, w in edges:
        if dist[u] != float("inf") and dist[u] + w
        ↪  < dist[v]:
            return dist, True

    return dist, False
```

## Bipartite Matching

Author: PyCPBook Community Source: CP-Algorithms, USACO Guide Description: Implements an algorithm to find the maximum matching in a bipartite graph. A bipartite graph is one whose vertices can be divided into two disjoint and independent sets, U and V, such that every edge connects a vertex in U to one in V. A matching is a set of edges without common vertices. The goal is to find a matching with the maximum possible number of edges.

This implementation uses the augmenting path algorithm, a common approach based on Ford-Fulkerson. It works by repeatedly finding "augmenting paths" in the graph. An augmenting path is a path that starts from an unmatched vertex in the left partition (U), ends at an unmatched vertex in the right partition (V), and alternates between edges that are not in the current matching and edges that are.

The algorithm proceeds as follows: 1. Initialize an empty matching. 2. For each vertex `u` in the left partition U: a. Try to find an augmenting path starting from `u` using a Depth-First Search (DFS). b. The DFS explores neighbors `v` of `u`. If `v` is unmatched, we have found an augmenting path of length 1. We match `u` with `v`. c. If `v` is already matched with some vertex `u'`, the DFS recursively tries to find an alternative match for `u'`. If it succeeds, we can then match `u` with `v`. 3. If an augmenting path is found, the size of the matching increases by one. The edges in the matching are updated by "flipping" the status of edges along the path. 4. The process continues until no more augmenting paths can be found. The size of the resulting matching is the maximum possible.

Time: $O(E \cdot V)$, where $V = |U| + |V|$ is the total number of vertices and $E$ is the number of edges. For each vertex in U, we may perform a DFS that traverses the entire graph. Space: $O(V)$ to store the matching and visited arrays for the DFS. Status: Stress-tested

```python
def bipartite_matching(adj, n1, n2):
    """
    Finds the maximum matching in a bipartite graph.

    Args:
        adj (list[list[int]]): Adjacency list for the left partition.
            `adj[u]` contains a list of neighbors of node `u` (from the left set)
            in the right set. Nodes in the left set are indexed 0 to n1-1.
            Nodes in the right set are indexed 0 to n2-1.
        n1 (int): The number of vertices in the left partition.
        n2 (int): The number of vertices in the right partition.

    Returns:
        int: The size of the maximum matching.
    """
    match_right = [-1] * n2
    matching_size = 0

    def dfs(u, visited):
        for v in adj[u]:
            if not visited[v]:
                visited[v] = True
                if match_right[v] < 0 or dfs(match_right[v], visited):
                    match_right[v] = u
                    return True
        return False

    for u in range(n1):
        visited = [False] * n2
        if dfs(u, visited):
            matching_size += 1

    return matching_size
```

## Dijkstra

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS) Description: Implements Dijkstra's algorithm for finding the single-source shortest paths in a weighted graph with non-negative edge weights.

Dijkstra's algorithm maintains a set of visited vertices and finds the shortest path from a source vertex to all other vertices in the graph. It uses a priority queue to greedily select the unvisited vertex with the smallest distance from the source.

The algorithm proceeds as follows: 1. Initialize a distances array with infinity for all vertices except the source, which is set to 0. 2. Initialize a priority queue and add the source vertex with a distance of 0. 3. While the priority queue is not empty, extract the vertex `u` with the smallest distance. 4. If `u` has already been processed with a shorter path, skip it. 5. For each neighbor `v` of `u`, calculate the distance through `u`. If this new path is shorter than the known distance to `v`, update the distance and add `v` to the priority queue with its new, shorter distance.

This implementation uses Python's `heapq` module as a min-priority queue. The graph is represented by an adjacency list where each entry is a tuple (neighbor, weight).

Time: $O(E \log V)$, where $V$ is the number of vertices and $E$ is the number of edges. The log factor comes from the priority queue operations. Space: $O(V + E)$ to store the adjacency list, distances array, and the priority queue. Status: Stress-tested

```python
import heapq


def dijkstra(adj, start_node, n):
    """
    Finds the shortest paths from a start node to all other nodes in a graph.

    Args:
        adj (list[list[tuple[int, int]]]): The adjacency list representation of
            the graph. adj[u] contains tuples (v, weight) for edges u -> v.
        start_node (int): The node from which to start the search.
        n (int): The total number of nodes in the graph.

    Returns:
        list[float]: A list of shortest distances from the start_node to each
                     node. `float('inf')` indicates an unreachable node.
    """
    if not (0 <= start_node < n):
        return [float("inf")] * n

    dist = [float("inf")] * n
    dist[start_node] = 0
    pq = [(0, start_node)]

    while pq:
        d, u = heapq.heappop(pq)

        if d > dist[u]:
            continue
```

```python
        for v, weight in adj[u]:
            if dist[u] + weight < dist[v]:
                dist[v] = dist[u] + weight
                heapq.heappush(pq, (dist[v], v))

    return dist

```

## Dinic

Author: PyCPBook Community Source: CP-Algorithms, KACTL Description: Implements Dinic's algorithm for computing the maximum flow in a flow network from a source `s` to a sink `t`. Dinic's is one of the most efficient algorithms for this problem.

The algorithm operates in phases. In each phase, it does the following: 1. Build a "level graph" using a Breadth-First Search (BFS) from the source `s` on the residual graph. The level of a vertex is its shortest distance from `s`. The level graph only contains edges `(u, v)` where `level[v] == level[u] + 1`. If the sink `t` is not reachable from `s` in the residual graph, the algorithm terminates. 2. Find a "blocking flow" in the level graph using a Depth-First Search (DFS) from `s`. A blocking flow is a flow where every path from `s` to `t` in the level graph has at least one saturated edge. The DFS pushes as much flow as possible along paths from `s` to `t`. Pointers are used to avoid re-exploring dead-end paths within the same phase. 3. Add the blocking flow found in the phase to the total maximum flow.

The process is repeated until the sink is no longer reachable from the source.

Time: $O(V^2E)$ in general graphs. It is much faster on certain types of graphs, such as $O(E\sqrt{V})$ for bipartite matching and $O(E\min(V^{2/3}, E^{1/2}))$ for unit-capacity networks. Space: $O(V + E)$ to store the graph, capacities, and level information. Status: Stress-tested

```python
from collections import deque


class Dinic:
    def __init__(self, n):
        self.n = n
        self.graph = [[] for _ in range(n)]
        self.level = [-1] * n
        self.ptr = [0] * n
        self.inf = float("inf")

    def add_edge(self, u, v, cap):
        # Forward edge
        self.graph[u].append([v, cap,
        ↪ len(self.graph[v])])
        # Backward edge
        self.graph[v].append([u, 0,
        ↪ len(self.graph[u]) - 1])

    def _bfs(self, s, t):
        self.level = [-1] * self.n
        self.level[s] = 0
        q = deque([s])
        while q:
            u = q.popleft()
            for i in range(len(self.graph[u])):
                v, cap, rev = self.graph[u][i]
                if cap > 0 and self.level[v] < 0:
                    self.level[v] = self.level[u] +
                    ↪ 1
                    q.append(v)
        return self.level[t] != -1

    def _dfs(self, u, t, pushed):
        if pushed == 0:
            return 0
        if u == t:
            return pushed

        while self.ptr[u] < len(self.graph[u]):
            edge_idx = self.ptr[u]
            v, cap, rev_idx =
            ↪ self.graph[u][edge_idx]

            if self.level[v] != self.level[u] + 1
            ↪ or cap == 0:
                self.ptr[u] += 1
                continue

            tr = self._dfs(v, t, min(pushed, cap))
            if tr == 0:
                self.ptr[u] += 1
                continue

            self.graph[u][edge_idx][1] -= tr
            self.graph[v][rev_idx][1] += tr
            return tr
        return 0

    def max_flow(self, s, t):
        if s == t:
            return 0
        total_flow = 0
        while self._bfs(s, t):
            self.ptr = [0] * self.n
            pushed = self._dfs(s, t, self.inf)
            while pushed > 0:
                total_flow += pushed
                pushed = self._dfs(s, t, self.inf)
        return total_flow

```

## Euler Path

Author: PyCPBook Community Source: CP-Algorithms, Wikipedia (Hierholzer's algorithm) Description: Implements Hierholzer's algorithm to find an Eulerian path or cycle in a graph. An Eulerian path visits every edge of a graph exactly once. An Eulerian cycle is an Eulerian path that starts and ends at the same vertex.

The existence of an Eulerian path/cycle depends on the degrees of the vertices:

For an undirected graph: - An Eulerian cycle exists if and only if every vertex has an even degree, and all vertices with a non-zero degree belong to a single connected component. - An Eulerian path exists if and only if there are zero or two vertices of odd degree, and all vertices with a non-zero degree belong to a single component. If there are two odd-degree vertices, the path must start at one and end at the other.

For a directed graph: - An Eulerian cycle exists if and only if for every vertex, the in-degree equals the out-degree, and the graph is strongly connected (ignoring isolated vertices). - An Eulerian path exists if and only if at most one vertex has `out-degree - in-degree = 1` (the start), at most one vertex has `in-degree - out-degree = 1` (the end), every other vertex has equal in- and out-degrees, and the underlying undirected graph is connected.

Hierholzer's algorithm finds the path by starting a traversal from a valid starting node. It follows edges until it gets stuck, and then backtracks, forming the path in reverse. This implementation uses an iterative approach with a stack.

Time: $O(V + E)$, as each edge and vertex is visited a constant number of times. Space: $O(V + E)$ to store the graph representation, degree counts, and the path. Status: Stress-tested

```python
from collections import Counter


def find_euler_path(adj, n, directed=False):
    """
    Finds an Eulerian path or cycle in a graph.

    Args:
        adj (list[list[int]]): The adjacency list representation of the graph.
            Handles multigraphs if neighbors are repeated.
        n (int): The total number of nodes in the graph.
        directed (bool): True if the graph is directed, False otherwise.

    Returns:
        list[int] | None: A list of nodes representing the Eulerian path,
                          or None if no such path exists.
    """
    if n == 0:
        return []

    num_edges = 0
    if directed:
        in_degree = [0] * n
        out_degree = [0] * n
        for u in range(n):
            out_degree[u] = len(adj[u])
            num_edges += len(adj[u])
            for v in adj[u]:
                in_degree[v] += 1

        start_node, end_node_count = -1, 0
        for i in range(n):
            if out_degree[i] - in_degree[i] == 1:
                if start_node != -1:
                    return None
                start_node = i
            elif in_degree[i] - out_degree[i] == 1:
                end_node_count += 1
                if end_node_count > 1:
                    return None
            elif in_degree[i] != out_degree[i]:
                return None

        if start_node == -1:
            for i in range(n):
                if out_degree[i] > 0:
                    start_node = i
                    break
            if start_node == -1:
                return [0] if n > 0 else []

    else:
        degree = [0] * n
        for u in range(n):
            degree[u] = len(adj[u])
            num_edges += len(adj[u])
        num_edges //= 2

        odd_degree_nodes = [i for i, d in enumerate(degree) if d % 2 != 0]
        if len(odd_degree_nodes) > 2:
            return None

        start_node = -1
        if odd_degree_nodes:
            start_node = odd_degree_nodes[0]
        else:
            for i in range(n):
                if degree[i] > 0:
                    start_node = i
                    break
            if start_node == -1:
                return [0] if n > 0 else []

    adj_counts = [Counter(neighbors) for neighbors in adj]
    path = []
    stack = [start_node]

    while stack:
        u = stack[-1]
        if adj_counts[u]:
            v = next(iter(adj_counts[u]))
            adj_counts[u][v] -= 1
            if adj_counts[u][v] == 0:
                del adj_counts[u][v]

            if not directed:
                adj_counts[v][u] -= 1
                if adj_counts[v][u] == 0:
                    del adj_counts[v][u]

            stack.append(v)
        else:
            path.append(stack.pop())

    path.reverse()

```

```python
    if len(path) == num_edges + 1:
        return path
    else:
        return None

```

## Floyd Warshall

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS) Description: Implements the Floyd-Warshall algorithm for finding all-pairs shortest paths in a weighted directed graph. This algorithm can handle graphs with negative edge weights.

The algorithm is based on a dynamic programming approach. It iteratively considers each vertex `k` and updates the shortest path between all pairs of vertices `(i, j)` to see if a path through `k` is shorter. The core recurrence is: `dist(i, j) = min(dist(i, j), dist(i, k) + dist(k, j))`

After running the algorithm with all vertices `k` from 0 to `V-1`, the resulting distance matrix contains the shortest paths between all pairs of vertices.

A key feature of Floyd-Warshall is its ability to detect negative-weight cycles. If, after the algorithm completes, the distance from any vertex `i` to itself (`dist[i][i]`) is negative, it indicates that there is a negative-weight cycle reachable from `i`.

This implementation takes an edge list as input, builds an adjacency matrix, runs the algorithm, and then checks for negative cycles.

Time: $O(V^3)$, where $V$ is the number of vertices. The three nested loops dominate the runtime. Space: $O(V^2)$ to store the distance matrix. Status: Stress-tested

```python
def floyd_warshall(edges, n):
    """
    Finds all-pairs shortest paths in a graph using the Floyd-Warshall algorithm.

    Args:
        edges (list[tuple[int, int, int]]): A list of all edges in the graph,
            where each tuple is (u, v, weight) for an edge u -> v.
        n (int): The total number of nodes in the graph.

    Returns:
        tuple[list[list[float]], bool]: A tuple containing:
            - A 2D list of shortest distances. `dist[i][j]` is the shortest
              distance from node `i` to node `j`. `float('inf')` for unreachable pairs.
            - A boolean that is True if a negative cycle is detected, False otherwise.
    """
    if n == 0:
        return [], False

    dist = [[float("inf")] * n for _ in range(n)]

    for i in range(n):
        dist[i][i] = 0

    for u, v, w in edges:
        dist[u][v] = min(dist[u][v], w)

    for k in range(n):
        for i in range(n):
            for j in range(n):
                if dist[i][k] != float("inf") and dist[k][j] != float("inf"):
                    dist[i][j] = min(dist[i][j], dist[i][k] + dist[k][j])

    has_negative_cycle = False
    for i in range(n):
        if dist[i][i] < 0:
            has_negative_cycle = True
            break

    return dist, has_negative_cycle

```

## Lca Binary Lifting

Author: PyCPBook Community Source: CP-Algorithms, USACO Guide Description: Implements Lowest Common Ancestor (LCA) queries on a tree using the binary lifting technique. This method allows for finding the LCA of any two nodes in logarithmic time after a precomputation step.

The algorithm consists of two main parts: 1. Precomputation: - A Depth-First Search (DFS) is performed from the root of the tree to calculate the depth of each node and to determine the immediate parent of each node. - A table `up[i][j]` is built, where `up[i][j]` stores the `2^j`-th ancestor of node `i`. This table is filled using dynamic programming: the `2^j`-th ancestor of `i` is the `2^(j-1)`-th ancestor of its `2^(j-1)`-th ancestor. `up[i][j] = up[up[i][j-1]][j-1]`.

2. Querying for LCA(u, v): - First, the depths of `u` and `v` are equalized by moving the deeper node upwards. This is done efficiently by "lifting" it in jumps of powers of two. - If `u` and `v` become the same node, that node is the LCA. - Otherwise, `u` and `v` are lifted upwards together, step by step, using the largest possible jumps (`2^j`) that keep them below their LCA (i.e., `up[u][j] != up[v][j]`). - After this process, `u` and `v` will be direct children of the LCA. The LCA is then the parent of `u` (or `v`), which is `up[u][0]`.

Time: Precomputation is $O(N \log N)$. Each query is $O(\log N)$. Space: $O(N \log N)$ to store the `up` table. Status: Stress-tested

```python
class LCA:
    def __init__(self, n, adj, root=0):
        self.n = n
```

```python
        self.adj = adj
        self.max_log = (n).bit_length()
        self.depth = [-1] * n
        self.up = [[-1] * self.max_log for _ in range(n)]
        self._dfs(root, -1, 0)
        self._precompute_ancestors()

    def _dfs(self, u, p, d):
        self.depth[u] = d
        self.up[u][0] = p
        for v in self.adj[u]:
            if v != p:
                self._dfs(v, u, d + 1)

    def _precompute_ancestors(self):
        for j in range(1, self.max_log):
            for i in range(self.n):
                if self.up[i][j - 1] != -1:
                    self.up[i][j] = self.up[self.up[i][j - 1]][j - 1]

    def query(self, u, v):
        if self.depth[u] < self.depth[v]:
            u, v = v, u

        for j in range(self.max_log - 1, -1, -1):
            if self.depth[u] - (1 << j) >= self.depth[v]:
                u = self.up[u][j]

        if u == v:
            return u

        for j in range(self.max_log - 1, -1, -1):
            if self.up[u][j] != -1 and self.up[u][j] != self.up[v][j]:
                u = self.up[u][j]
                v = self.up[v][j]

        return self.up[u][0]

```

## Prim Kruskal

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS) Description: This file implements two classic greedy algorithms for finding the Minimum Spanning Tree (MST) of an undirected, weighted graph: Kruskal's algorithm and Prim's algorithm. An MST is a subset of the edges of a connected, edge-weighted undirected graph that connects all the vertices together, without any cycles and with the minimum possible total edge weight.

Kruskal's Algorithm: This algorithm treats the graph as a forest and each node as an individual tree. It sorts all the edges by weight in non-decreasing order. Then, it iterates through the sorted edges, adding an edge to the MST if and only if it does not form a cycle with the edges already added. A Union-Find data structure is used to efficiently detect cycles. The algorithm terminates when V-1 edges have been added to the MST (for a connected graph).

Prim's Algorithm: This algorithm grows the MST from an arbitrary starting vertex. It maintains a set of vertices already in the MST. At each step, it finds the minimum-weight edge that connects a vertex in the MST to a vertex outside the MST and adds this edge and vertex to the tree. A priority queue is used to efficiently select this minimum-weight edge.

Time: - Kruskal's: $O(E \log E)$ or $O(E \log V)$, dominated by sorting the edges. - Prim's: $O(E \log V)$ using a binary heap as a priority queue. Space: - Kruskal's: $O(V + E)$ for the edge list and Union-Find structure. - Prim's: $O(V + E)$ for the adjacency list, priority queue, and visited array. Status: Stress-tested

```python
import heapq
import sys
import os

# Add content directory to path to import the solution
sys.path.append(
    os.path.join(os.path.dirname(__file__), "../../content/data_structures")
)
from union_find import UnionFind


def kruskal(edges, n):
    """
    Finds the MST of a graph using Kruskal's algorithm.

    Args:
        edges (list[tuple[int, int, int]]): A list of all edges in the graph,
          where each tuple is (u, v, weight).
        n (int): The total number of nodes in the graph.

    Returns:
        tuple[int, list[tuple[int, int, int]]]: A tuple containing:
          - The total weight of the MST.
          - A list of edges (u, v, weight) that form the MST.
          Returns (inf, []) if the graph is not connected and cannot form a single MST.
    """
    if n == 0:
        return 0, []

    sorted_edges = sorted([(w, u, v) for u, v, w in edges])
    uf = UnionFind(n)
    mst_weight = 0
    mst_edges = []

    for weight, u, v in sorted_edges:
        if uf.union(u, v):
            mst_weight += weight
```

```python
            mst_edges.append((u, v, weight))
            if len(mst_edges) == n - 1:
                break

    if len(mst_edges) < n - 1:
        # This indicates the graph is not connected.
        # The result is a minimum spanning forest.
        pass

    return mst_weight, mst_edges


def prim(adj, n, start_node=0):
    """
    Finds the MST of a graph using Prim's algorithm.

    Args:
        adj (list[list[tuple[int, int]]]): The adjacency list representation of
            the graph. adj[u] contains tuples (v, weight) for edges u -> v.
        n (int): The total number of nodes in the graph.
        start_node (int): The node to start building the MST from.

    Returns:
        tuple[int, list[tuple[int, int, int]]]: A tuple containing:
            - The total weight of the MST.
            - A list of edges (u, v, weight) that form the MST.
            Returns (inf, []) if the graph is not connected.
    """
    if n == 0:
        return 0, []
    if not (0 <= start_node < n):
        return float("inf"), []

    visited = [False] * n
    pq = [(0, start_node, -1)]  # (weight, current_node, previous_node)
    mst_weight = 0
    mst_edges = []
    edges_count = 0

    while pq and edges_count < n:
        weight, u, prev = heapq.heappop(pq)

        if visited[u]:
            continue

        visited[u] = True
        mst_weight += weight
        if prev != -1:
            mst_edges.append((prev, u, weight))
        edges_count += 1

        for v, w in adj[u]:
            if not visited[v]:
                heapq.heappush(pq, (w, v, u))

    if edges_count < n:
        # This indicates the graph is not connected.
        return float("inf"), []

    return mst_weight, mst_edges

```

## Scc

Author: PyCPBook Community Source: Based on Tarjan's algorithm from Introduction to Algorithms (CLRS) Description: Implements Tarjan's algorithm for finding Strongly Connected Components (SCCs) in a directed graph. An SCC is a maximal subgraph where for any two vertices u and v in the subgraph, there is a path from u to v and a path from v to u.

Tarjan's algorithm performs a single Depth-First Search (DFS) from an arbitrary start node. It maintains two key values for each vertex `u`: 1. `disc[u]`: The discovery time of `u`, which is the time (a counter) when `u` is first visited. 2. `low[u]`: The "low-link" value of `u`, which is the lowest discovery time reachable from `u` (including itself) through its DFS subtree, possibly including one back-edge.

The algorithm also uses a stack to keep track of the nodes in the current exploration path. A node `u` is the root of an SCC if its discovery time is equal to its low-link value (`disc[u] == low[u]`). When such a node is found, all nodes in its SCC are on the top of the stack and can be popped off until `u` is reached. These popped nodes form one complete SCC.

Time: $O(V + E)$, where $V$ is the number of vertices and $E$ is the number of edges, because the algorithm is based on a single DFS traversal. Space: $O(V)$ to store the discovery times, low-link values, the stack, and the recursion depth of the DFS. Status: Stress-tested

```python
def find_sccs(adj, n):
    """
    Finds all Strongly Connected Components of a directed graph using Tarjan's algorithm.

    Args:
        adj (list[list[int]]): The adjacency list representation of the graph.
        n (int): The total number of nodes in the graph.

    Returns:
        list[list[int]]: A list of lists, where each inner list contains the
                         nodes of a single Strongly Connected Component.
    """
    if n == 0:
        return []

    disc = [-1] * n
    low = [-1] * n
    on_stack = [False] * n
    stack = []
    time = 0
```

```python
    sccs = []

    def tarjan_dfs(u):
        nonlocal time
        disc[u] = low[u] = time
        time += 1
        stack.append(u)
        on_stack[u] = True

        for v in adj[u]:
            if disc[v] == -1:
                tarjan_dfs(v)
                low[u] = min(low[u], low[v])
            elif on_stack[v]:
                low[u] = min(low[u], disc[v])

        if low[u] == disc[u]:
            component = []
            while True:
                node = stack.pop()
                on_stack[node] = False
                component.append(node)
                if node == u:
                    break
            sccs.append(component)

    for i in range(n):
        if disc[i] == -1:
            tarjan_dfs(i)

    return sccs
```

## Topological Sort

Author: PyCPBook Community Source: Based on Kahn's Algorithm from Introduction to Algorithms (CLRS) Description: Implements Topological Sort for a Directed Acyclic Graph (DAG). A topological sort or topological ordering of a DAG is a linear ordering of its vertices such that for every directed edge from vertex `u` to vertex `v`, `u` comes before `v` in the ordering.

This implementation uses Kahn's algorithm, which is BFS-based. The algorithm proceeds as follows: 1. Compute the in-degree (number of incoming edges) for each vertex. 2. Initialize a queue with all vertices that have an in-degree of 0. These are the starting points of the graph. 3. While the queue is not empty, dequeue a vertex `u`. Add `u` to the result list. 4. For each neighbor `v` of `u`, decrement its in-degree. If the in-degree of `v` becomes 0, it means all its prerequisites have been met, so enqueue `v`. 5. After the loop, if the number of vertices in the result list is equal to the total number of vertices in the graph, the list represents a valid topological sort. If the count is less, it indicates that the graph contains at least one cycle, and a topological sort is not possible. In such a case, this function returns an empty list.

Time: $O(V+E)$, where $V$ is the number of vertices and $E$ is the number of edges. Each vertex is enqueued and dequeued once, and every edge is processed once. Space: $O(V+E)$ to store the adjacency list, in-degree array, and the queue. Status: Stress-tested

```python
from collections import deque


def topological_sort(adj, n):
    """
    Performs a topological sort on a directed graph.

    Args:
        adj (list[list[int]]): The adjacency list representation of the graph.
        n (int): The total number of nodes in the graph.

    Returns:
        list[int]: A list of nodes in topological order. Returns an empty list
                   if the graph contains a cycle.
    """
    if n == 0:
        return []

    in_degree = [0] * n
    for u in range(n):
        for v in adj[u]:
            in_degree[v] += 1

    q = deque([i for i in range(n) if in_degree[i] == 0])
    topo_order = []

    while q:
        u = q.popleft()
        topo_order.append(u)

        for v in adj[u]:
            in_degree[v] -= 1
            if in_degree[v] == 0:
                q.append(v)

    if len(topo_order) == n:
        return topo_order
    else:
        # Graph has a cycle
        return []
```

## Traversal

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS) Description: This file implements Breadth-First Search (BFS) and Depth-First Search (DFS), the two most fundamental graph traversal algorithms.

Breadth-First Search (BFS): BFS explores a graph layer by layer from a starting source node. It finds all nodes at a distance of 1 from the source, then all nodes at a distance of 2, and so on. It's guaranteed to find the shortest path from the source to any other node in an unweighted graph. The algorithm proceeds as follows: 1. Initialize a queue and add the `start_node` to it. 2. Initialize a `visited` array or set to keep track of visited nodes, marking the `start_node` as visited. 3. While the queue is not empty, dequeue a node `u`. 4. For each neighbor `v` of `u`, if `v` has not been visited, mark `v` as visited and enqueue it. 5. Repeat until the queue is empty. The collection of dequeued nodes forms the traversal order.

Depth-First Search (DFS): DFS explores a graph by traversing as far as possible along each branch before backtracking. It's commonly used for tasks like cycle detection, topological sorting, and finding connected components. The iterative algorithm is as follows: 1. Initialize a stack and push the `start_node` onto it. 2. Initialize a `visited` array or set, marking the `start_node` as visited. 3. While the stack is not empty, pop a node `u`. 4. For each neighbor `v` of `u`, if `v` has not been visited, mark `v` as visited and push it onto the stack. 5. Repeat until the stack is empty. The collection of popped nodes forms the traversal order.

Time: $O(V + E)$ for both BFS and DFS, where $V$ is the number of vertices and $E$ is the number of edges. Each vertex and edge is visited exactly once. Space: $O(V)$ in the worst case for storing the queue (BFS) or stack (DFS), and the visited array. Status: Stress-tested

```python
from collections import deque


def bfs(adj, start_node, n):
    """
    Performs a Breadth-First Search on a graph.

    Args:
        adj (list[list[int]]): The adjacency list representation of the graph.
        start_node (int): The node from which to start the traversal.
        n (int): The total number of nodes in the graph.

    Returns:
        list[int]: A list of nodes in the order they were visited.
    """
    if not (0 <= start_node < n):
        return []

    q = deque([start_node])
    visited = [False] * n
    visited[start_node] = True
    traversal_order = []

    while q:
        u = q.popleft()
        traversal_order.append(u)
        for v in adj[u]:
            if not visited[v]:
                visited[v] = True
                q.append(v)
    return traversal_order


def dfs(adj, start_node, n):
    """
    Performs a Depth-First Search on a graph.

    Args:
        adj (list[list[int]]): The adjacency list representation of the graph.
        start_node (int): The node from which to start the traversal.
        n (int): The total number of nodes in the graph.

    Returns:
        list[int]: A list of nodes in the order they were visited.
    """
    if not (0 <= start_node < n):
        return []

    stack = [start_node]
    visited = [False] * n
    # Mark as visited when pushed to stack to avoid re-adding
    visited[start_node] = True
    traversal_order = []

    # This loop produces a traversal order different from the recursive one.
    # To get a more standard pre-order traversal iteratively, we need a slight change.

    # Reset for a more standard iterative DFS traversal order
    visited = [False] * n
    stack = [start_node]

    while stack:
        u = stack.pop()

        if not visited[u]:
            visited[u] = True
            traversal_order.append(u)

            # Add neighbors to the stack in reverse order to process them in lexicographical order
            for v in reversed(adj[u]):
                if not visited[v]:
                    stack.append(v)

    return traversal_order
```

## Two Sat

Author: PyCPBook Community Source: CP-Algorithms, KACTL Description: Implements a solver for 2-Satisfiability (2-SAT) problems. A 2-SAT problem consists of a boolean formula in 2-Conjunctive Normal Form, which is a conjunction (AND) of clauses, where each clause is a disjunction

(OR) of two literals. The goal is to find a satisfying assignment of true/false values to the variables.

This problem can be solved in linear time by reducing it to a graph problem. The reduction works as follows: 1. Create an "implication graph" with `2N` vertices for `N` variables. For each variable `x_i`, there are two vertices: one for `x_i` and one for its negation `¬x_i`. 2. Each clause `(a OR b)` is equivalent to two implications: `(¬a => b)` and `(¬b => a)`. For each clause, add two directed edges to the graph representing these implications. 3. The original 2-SAT formula is unsatisfiable if and only if there exists a variable `x_i` such that `x_i` and `¬x_i` are in the same Strongly Connected Component (SCC) of the implication graph. This is because if they are in the same SCC, it means `x_i` implies `¬x_i` and `¬x_i` implies `x_i`, which is a contradiction. 4. If the formula is satisfiable, a valid assignment can be constructed from the SCCs. The SCCs form a Directed Acyclic Graph (DAG). We can find a reverse topological ordering of this "condensation graph". For each variable `x_i`, if the SCC containing `¬x_i` appears before the SCC containing `x_i` in this ordering, we must assign `x_i` to true. Otherwise, we assign it to false.

This implementation uses the `find_sccs` function (Tarjan's algorithm) to solve the problem.

Time: $O(V + E) = O(N + M)$, where $N$ is the number of variables and $M$ is the number of clauses. The graph has $2N$ vertices and $2M$ edges. Space: $O(N + M)$ to store the implication graph and SCC information. Status: Stress-tested

```python
import sys
import os

# The stress test runner adds the project root to the path.
# This allows importing other content modules using their full path.
from content.graph.scc import find_sccs


class TwoSAT:
    def __init__(self, n):
        self.n = n
        self.graph = [[] for _ in range(2 * n)]

    def _map_var(self, var):
        """Maps a 1-indexed variable to a 0-indexed graph node."""
        if var > 0:
            return var - 1
        return -var - 1 + self.n

    def add_clause(self, i, j):
        """
        Adds a clause (i OR j) to the formula.
        Variables are 1-indexed. A negative value -k denotes the negation of x_k.
        This adds two implications: (-i => j) and (-j => i).
        """
        # Add edge for (-i => j)
        self.graph[self._map_var(-i)].append(self._map_va
        # Add edge for (-j => i)
        self.graph[self._map_var(-j)].append(self._map_va

    def solve(self):
        """
        Solves the 2-SAT problem.

        Returns:
            tuple[bool, list[bool] | None]: A tuple where the first element is
            True if a solution exists, False otherwise. If a solution exists,
            the second element is a list of boolean values representing a
            satisfying assignment. Otherwise, it is None.
        """
        sccs = find_sccs(self.graph, 2 * self.n)
        component_id = [-1] * (2 * self.n)
        for idx, comp in enumerate(sccs):
            for node in comp:
                component_id[node] = idx

        for i in range(self.n):
            if component_id[i] == component_id[i + self.n]:
                return False, None

        assignment = [False] * self.n
        # sccs are returned in reverse topological order
        for i in range(self.n):
            # If component of x_i comes after component of not(x_i) in topo order
            # (i.e., has a smaller index in the reversed list), then x_i must be true.
            if component_id[i] < component_id[i + self.n]:
                assignment[i] = True

        return True, assignment

```

# Chapter 4

# String Algorithms

## Aho Corasick

Author: PyCPBook Community Source: CP-Algorithms, KACTL Description: Implements the Aho-Corasick algorithm for finding all occurrences of multiple patterns in a text simultaneously. This algorithm combines a trie (prefix tree) with failure links to achieve linear time complexity with respect to the sum of the text length and the total length of all patterns.

The algorithm works in two main stages: 1. Preprocessing (Building the Automaton): a. A trie is constructed from the set of all patterns. Each node in the trie represents a prefix of one or more patterns. b. An `output` list is associated with each node, storing the indices of patterns that end at that node. c. "Failure links" are computed for each node. The failure link of a node `u` points to the longest proper suffix of the string corresponding to `u` that is also a prefix of some pattern in the set. These links are computed using a Breadth-First Search (BFS) starting from the root.

2. Searching: a. The algorithm processes the text character by character, traversing the automaton. It starts at the root. b. For each character in the text, it transitions to the next state. If a direct child for the character does not exist, it follows failure links until a valid transition is found or it returns to the root. c. At each state, it collects all matches. This is done by checking the `output` of the current node and recursively following failure links to find all patterns that end as a suffix of the current prefix.

Time: Preprocessing is $O(L)$, where $L$ is the total length of all patterns. Searching is $O(N+Z)$, where $N$ is the length of the text and $Z$ is the total number of matches found. Space: $O(L)$ to store the trie and associated data. Status: Stress-tested

```python
from collections import deque


class AhoCorasick:
    def __init__(self, patterns):
        self.patterns = patterns
        self.trie = [{"children": {}, "output": [], "fail_link": 0}]
        self._build_trie()
        self._build_failure_links()

    def _build_trie(self):
        for i, pattern in enumerate(self.patterns):
            node_idx = 0
            for char in pattern:
                if char not in self.trie[node_idx]["children"]:
                    self.trie[node_idx]["children"][char] = len(self.trie)
                    self.trie.append({"children": {}, "output": [], "fail_link": 0})
                node_idx = self.trie[node_idx]["children"][char]
            self.trie[node_idx]["output"].append(i)

    def _build_failure_links(self):
        q = deque()
        for char, next_node_idx in self.trie[0]["children"].items():
            q.append(next_node_idx)

        while q:
            curr_node_idx = q.popleft()
            for char, next_node_idx in self.trie[curr_node_idx]["children"].items():
                fail_idx = self.trie[curr_node_idx]["fail_link"]
                while char not in self.trie[fail_idx]["children"] and fail_idx != 0:
                    fail_idx = self.trie[fail_idx]["fail_link"]

                if char in self.trie[fail_idx]["children"]:
                    self.trie[next_node_idx]["fail_link"] = self.trie[fail_idx][
                        "children"
                    ][char]
                else:
                    self.trie[next_node_idx]["fail_link"] = 0

                # Append outputs from the failure link node
                fail_output_idx = self.trie[next_node_idx]["fail_link"]
                self.trie[next_node_idx]["output"].extend(
                    self.trie[fail_output_idx]["output"]
                )
                q.append(next_node_idx)

    def search(self, text):
        """
        Finds all occurrences of the patterns in the given text.

        Args:
            text (str): The text to search within.
```

```python
        Returns:
            list[tuple[int, int]]: A list of tuples, where each tuple is
            (pattern_index, end_index_in_text). `end_index_in_text` is the
            index where the pattern ends.
        """
        matches = []
        curr_node_idx = 0
        for i, char in enumerate(text):
            while (
                char not in self.trie[curr_node_idx]["children"] and curr_node_idx != 0
            ):
                curr_node_idx = self.trie[curr_node_idx]["fail_link"]

            if char in self.trie[curr_node_idx]["children"]:
                curr_node_idx = self.trie[curr_node_idx]["children"][
            else:
                curr_node_idx = 0

            if self.trie[curr_node_idx]["output"]:
                for pattern_idx in self.trie[curr_node_idx]["output"]:
                    matches.append((pattern_idx, i))
        return matches
```

## Kmp

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS) Description: Implements the Knuth-Morris-Pratt (KMP) algorithm for efficient string searching. KMP finds all occurrences of a pattern `P` within a text `T` in linear time.

The core of the KMP algorithm is the precomputation of a "prefix function" or Longest Proper Prefix Suffix (LPS) array for the pattern. The LPS array, `lps`, for a pattern of length `M` stores at each index `i` the length of the longest proper prefix of `P[0...i]` that is also a suffix of `P[0...i]`. A "proper" prefix is one that is not equal to the entire string.

Example: For pattern `P = "ababa"`, the LPS array is `[0, 0, 1, 2, 3]`. - `lps[0]` is always 0. - `lps[1]` ("ab"): No proper prefix is a suffix. Length is 0. - `lps[2]` ("aba"): "a" is both a prefix and a suffix. Length is 1. - `lps[3]` ("abab"): "ab" is both a prefix and a suffix. Length is 2. - `lps[4]` ("ababa"): "aba" is both a prefix and a suffix. Length is 3.

During the search, when a mismatch occurs between the text and the pattern at `text[i]` and `pattern[j]`, the LPS array tells us how many characters of the pattern we can shift without re-checking previously matched characters. Specifically, if a mismatch occurs at `pattern[j]`, we know that the prefix `pattern[0...j-1]` matched the text. The value `lps[j-1]` gives the length of the longest prefix of `pattern[0...j-1]` that is also a suffix. This means we can shift the pattern and continue the comparison from `pattern[lps[j-1]]` without losing any potential matches.

Time: $O(N+M)$, where $N$ is the length of the text and $M$ is the length of the pattern. $O(M)$ for building the LPS array and $O(N)$ for the search. Space: $O(M)$ to store the LPS array for the pattern. Status: Stress-tested

```python
def compute_lps(pattern):
    """
    Computes the Longest Proper Prefix Suffix (LPS) array for the KMP algorithm.

    Args:
        pattern (str): The pattern string.

    Returns:
        list[int]: The LPS array for the pattern.
    """
    m = len(pattern)
    lps = [0] * m
    length = 0
    i = 1
    while i < m:
        if pattern[i] == pattern[length]:
            length += 1
            lps[i] = length
            i += 1
        else:
            if length != 0:
                length = lps[length - 1]
            else:
                lps[i] = 0
                i += 1
    return lps


def kmp_search(text, pattern):
    """
    Finds all occurrences of a pattern in a text using the KMP algorithm.

    Args:
        text (str): The text to search within.
        pattern (str): The pattern to search for.

    Returns:
        list[int]: A list of 0-based starting indices of all occurrences
                of the pattern in the text.
    """
    n = len(text)
    m = len(pattern)
    if m == 0:
        return list(range(n + 1))
    if n == 0 or m > n:
        return []

    lps = compute_lps(pattern)
    occurrences = []
    i = 0
    j = 0
    while i < n:
```

```python
        if pattern[j] == text[i]:
            i += 1
            j += 1
        if j == m:
            occurrences.append(i - j)
            j = lps[j - 1]
        elif i < n and pattern[j] != text[i]:
            if j != 0:
                j = lps[j - 1]
            else:
                i += 1
    return occurrences
```

## Manacher

Author: PyCPBook Community Source: CP-Algorithms, GeeksForGeeks Description: Implements Manacher's algorithm for finding the longest palindromic substring in a given string in linear time. Standard naive approaches take $O(N^2)$ or $O(N^3)$ time.

The algorithm cleverly handles both odd and even length palindromes by transforming the input string. A special character (e.g., '#') is inserted between each character and at the ends. For example, "aba" becomes "#a#b#a#" and "abba" becomes "#a#b#b#a#". In this new string, every palindrome, regardless of its original length, is of odd length and has a distinct center.

The core of the algorithm is to compute an array `p`, where `p[i]` stores the radius of the palindrome centered at index `i` in the transformed string. It does this efficiently by maintaining the center `c` and right boundary `r` of the palindrome that extends furthest to the right. When computing `p[i]`, it uses the information from the mirror position `i_mirror = 2*c - i` to get an initial guess for `p[i]`. It then expands from this guess, avoiding redundant character comparisons. This optimization is what brings the complexity down to linear time.

After computing the `p` array, the maximum value in `p` corresponds to the radius of the longest palindromic substring. From this radius and its center, the original substring can be reconstructed.

Time: $O(N)$, where $N$ is the length of the string. Space: $O(N)$ to store the transformed string and the palindrome radii array. Status: Stress-tested

```python
def manacher(s):
    """
    Finds the longest palindromic substring in a string using Manacher's algorithm.

    Args:
        s (str): The input string.

    Returns:
        str: The longest palindromic substring found in `s`. If there are
          multiple of the same maximum length, it returns the first one found.
    """
    if not s:
        return ""

    t = "#" + "#".join(s) + "#"
    n = len(t)
    p = [0] * n
    center, right = 0, 0
    max_len, max_center = 0, 0

    for i in range(n):
        mirror = 2 * center - i

        if i < right:
            p[i] = min(right - i, p[mirror])

        while (
            i - (p[i] + 1) >= 0
            and i + (p[i] + 1) < n
            and t[i - (p[i] + 1)] == t[i + (p[i] + 1)]
        ):
            p[i] += 1

        if i + p[i] > right:
            center = i
            right = i + p[i]

        if p[i] > max_len:
            max_len = p[i]
            max_center = i

    start = (max_center - max_len) // 2
    end = start + max_len
    return s[start:end]
```

## Polynomial Hashing

Author: PyCPBook Community Source: CP-Algorithms, KACTL Description: Implements a string hashing class using the polynomial rolling hash technique. This allows for efficient comparison of substrings. After an initial $O(N)$ precomputation on a string of length $N$, the hash of any substring can be calculated in $O(1)$ time.

The hash of a string $s = s_0 s_1 ... s_{k-1}$ is defined as: $H(s) = (s_0 p^0 + s_1 p^1 + ... + s_{k-1} p^{k-1}) \mod m$ where `p` is a base and `m` is a large prime modulus.

To prevent collisions, especially against adversarial test cases, this implementation uses two key techniques: 1. Randomized Base: The base `p` is chosen randomly at runtime. It should be larger than the size of the character set. 2. Multiple Moduli: Hashing is performed with two different large prime moduli (`m1`, `m2`). Two substrings are considered equal only if their hash values match for both moduli. This drastically reduces the probability of collisions.

The `query(l, r)` method calculates the hash of the substring `s[l...r-1]` by using precomputed prefix hashes and powers of `p`.

Time: Precomputation is $O(N)$. Each query is $O(1)$. Space: $O(N)$ to store precomputed prefix hashes and powers of the base. Status: Stress-tested

```python
import random


class StringHasher:
    def __init__(self, s):
        self.s = s
        self.n = len(s)

        self.m1 = 10**9 + 7
        self.m2 = 10**9 + 9

        self.p = random.randint(257, self.m1 - 1)

        self.p_powers1 = [1] * (self.n + 1)
        self.p_powers2 = [1] * (self.n + 1)
        for i in range(1, self.n + 1):
            self.p_powers1[i] = (self.p_powers1[i -
            ↪ 1] * self.p) % self.m1
            self.p_powers2[i] = (self.p_powers2[i -
            ↪ 1] * self.p) % self.m2

        self.h1 = [0] * (self.n + 1)
        self.h2 = [0] * (self.n + 1)
        for i in range(self.n):
            self.h1[i + 1] = (self.h1[i] * self.p +
            ↪ ord(self.s[i])) % self.m1
            self.h2[i + 1] = (self.h2[i] * self.p +
            ↪ ord(self.s[i])) % self.m2

    def query(self, l, r):
        """
        Computes the hash of the substring
        ↪ s[l...r-1].

        Args:
            l (int): The 0-based inclusive starting
            ↪ index.
            r (int): The 0-based exclusive ending
            ↪ index.

        Returns:
            tuple[int, int]: A tuple containing the
            ↪ two hash values for the substring.
        """
        if l >= r:
            return 0, 0

        len_sub = r - l
        hash1 = (
            self.h1[r] - (self.h1[l] *
            ↪ self.p_powers1[len_sub]) % self.m1
            ↪ + self.m1
        ) % self.m1
        hash2 = (
            self.h2[r] - (self.h2[l] *
            ↪ self.p_powers2[len_sub]) % self.m2
            ↪ + self.m2
        ) % self.m2
        return hash1, hash2

```

## Suffix Array

Author: PyCPBook Community Source: CP-Algorithms, GeeksForGeeks Description: Implements the construction of a Suffix Array and a Longest Common Prefix (LCP) Array. A suffix array is a sorted array of all suffixes of a given string. The LCP array stores the length of the longest common prefix between adjacent suffixes in the sorted suffix array.

Suffix Array Construction ($O(N \log^2 N)$): The algorithm works by repeatedly sorting the suffixes based on prefixes of increasing lengths that are powers of two. 1. Initially, suffixes are sorted based on their first character. 2. In the k-th iteration, suffixes are sorted based on their first $2^k$ characters. This is done efficiently by using the ranks from the previous iteration. Each suffix `s[i:]` is represented by a pair of ranks: the rank of its first $2^{k-1}$ characters and the rank of the next $2^{k-1}$ characters (starting at `s[i + 2^{k-1}:]`). 3. This process continues for $\log N$ iterations, with each sort taking $O(N \log N)$ time, leading to an overall complexity of $O(N \log^2 N)$.

LCP Array Construction (Kasai's Algorithm, $O(N)$): After the suffix array `sa` is built, the LCP array can be constructed in linear time using Kasai's algorithm. The algorithm utilizes the observation that the LCP of two suffixes `s[i:]` and `s[j:]` is related to the LCP of `s[i-1:]` and `s[j-1:]`. It processes the suffixes in their original order in the string, not the sorted order, which allows it to compute the LCP values efficiently.

Time: $O(N \log^2 N)$ for building the suffix array and $O(N)$ for the LCP array. Total time complexity is dominated by the suffix array construction. Space: $O(N)$ to store the suffix array, LCP array, and auxiliary arrays for sorting. Status: Stress-tested

```python
def build_suffix_array(s):
    """
    Builds the suffix array for a string using an
    ↪ O(N log^2 N) sorting-based approach.

    Args:
        s (str): The input string.

    Returns:
        list[int]: The suffix array, containing
        ↪ starting indices of suffixes in
                   lexicographically sorted order.
    """
    n = len(s)
    sa = list(range(n))
    rank = [ord(c) for c in s]
    k = 1
    while k < n:
        sa.sort(key=lambda i: (rank[i], rank[i + k]
        ↪ if i + k < n else -1))
        new_rank = [0] * n
        new_rank[sa[0]] = 0
        for i in range(1, n):
```

```python
            prev, curr = sa[i - 1], sa[i]
            r_prev = (rank[prev], rank[prev + k] if prev + k < n else -1)
            r_curr = (rank[curr], rank[curr + k] if curr + k < n else -1)
            if r_curr == r_prev:
                new_rank[curr] = new_rank[prev]
            else:
                new_rank[curr] = new_rank[prev] + 1
        rank = new_rank
        if rank[sa[-1]] == n - 1:
            break
        k *= 2
    return sa


def build_lcp_array(s, sa):
    """
    Builds the LCP array using Kasai's algorithm in O(N) time.

    Args:
        s (str): The input string.
        sa (list[int]): The suffix array for the string `s`.

    Returns:
        list[int]: The LCP array. `lcp[i]` is the LCP of suffixes `sa[i-1]` and `sa[i]`.
                   `lcp[0]` is conventionally 0.
    """
    n = len(s)
    if n == 0:
        return []

    rank = [0] * n
    for i in range(n):
        rank[sa[i]] = i

    lcp = [0] * n
    h = 0
    for i in range(n):
        if rank[i] == 0:
            continue
        j = sa[rank[i] - 1]
        if h > 0:
            h -= 1
        while i + h < n and j + h < n and s[i + h] == s[j + h]:
            h += 1
        lcp[rank[i]] = h
    return lcp
```

## Z Algorithm

Author: PyCPBook Community Source: CP-Algorithms, USACO Guide Description: Implements the Z-algorithm, which computes the Z-array for a given string `s` of length `N`. The Z-array `z` is an array of length `N` where `z[i]` is the length of the longest common prefix (LCP) between the original string `s` and the suffix of `s` starting at index `i`. By convention, `z[0]` is usually set to 0 or `N`; here it is set to 0.

The algorithm computes the Z-array in linear time. It does this by maintaining the bounds of the rightmost substring that is also a prefix of `s`. This is called the "Z-box", denoted by `[l, r]`.

The algorithm iterates from `i = 1` to `N-1`: 1. If `i` is outside the current Z-box (`i > r`), it computes `z[i]` naively by comparing characters from the start of the string and from index `i`. It then updates the Z-box `[l, r]` if a new rightmost one is found. 2. If `i` is inside the current Z-box (`i <= r`), it can use previously computed Z-values to initialize `z[i]`. Let `k = i - l`. `z[i]` can be at least `min(z[k], r - i + 1)`. - If `z[k] < r - i + 1`, then `z[i]` is exactly `z[k]`, and the Z-box does not change. - If `z[k] >= r - i + 1`, it means `z[i]` might be even longer. The algorithm then continues comparing characters from `r+1` onwards to extend the match and updates the Z-box `[l, r]`.

The Z-algorithm is very powerful for pattern matching. To find a pattern `P` in a text `T`, one can compute the Z-array for the concatenated string `P + '$' + T`, where `$` is a character not in `P` or `T`. Any `z[i]` equal to the length of `P` indicates an occurrence of `P` in `T`.

Time: $O(N)$, where $N$ is the length of the string. Space: $O(N)$ to store the Z-array. Status: Stress-tested

```python
def z_function(s):
    """
    Computes the Z-array for a given string.

    Args:
        s (str): The input string.

    Returns:
        list[int]: The Z-array for the string `s`.
    """
    n = len(s)
    if n == 0:
        return []

    z = [0] * n
    l, r = 0, 0
    for i in range(1, n):
        if i <= r:
            z[i] = min(r - i + 1, z[i - l])
        while i + z[i] < n and s[z[i]] == s[i + z[i]]:
            z[i] += 1
        if i + z[i] - 1 > r:
            l, r = i, i + z[i] - 1
    return z
```

# Chapter 5

# Mathematics & Number Theory

## Chinese Remainder Theorem

Author: PyCPBook Community Source: CP-Algorithms Description: Implements a solver for a system of linear congruences using the Chinese Remainder Theorem (CRT). Given a system of congruences: $x \equiv a_1 \pmod{n_1}$ $x \equiv a_2 \pmod{n_2}$ ... $x \equiv a_k \pmod{n_k}$ the algorithm finds a solution `x` that satisfies all of them. This implementation handles the general case where the moduli `n_i` are not necessarily pairwise coprime.

The algorithm works by iteratively combining pairs of congruences. Given a solution for the first `i-1` congruences, `x \equiv a_{res} (mod n_{res})`, it combines this with the i-th congruence `x \equiv a_i (mod n_i)`.

This requires solving a linear congruence of the form `k * n_{res} \equiv a_i - a_{res} (mod n_i)`. A solution exists if and only if `(a_i - a_{res})` is divisible by `g = gcd(n_{res}, n_i)`. If a solution exists, the two congruences are merged into a new one: `x \equiv a_{new} (mod n_{new})`, where `n_{new} = lcm(n_{res}, n_i)`. This process is repeated for all congruences. If at any step a solution does not exist, the entire system has no solution.

Time: $O(K \cdot \log(\max(n_i)))$, where $K$ is the number of congruences. Each merge step involves `extended_gcd`, which is logarithmic. Space: $O(1)$ Status: Stress-tested

```python
from content.math.modular_arithmetic import extended_gcd


def chinese_remainder_theorem(remainders, moduli):
    """
    Solves a system of linear congruences.
    `x \equiv remainders[i] (mod moduli[i])` for all i.

    Args:
        remainders (list[int]): A list of remainders (a_i).
        moduli (list[int]): A list of moduli (n_i).

    Returns:
        tuple[int, int] | None: A tuple `(result, lcm)` representing the solution
        `x \equiv result (mod lcm)`, or None if no solution exists.
    """
    if not remainders or not moduli or len(remainders) != len(moduli):
        return 0, 1

    a1 = remainders[0]
    n1 = moduli[0]

    for i in range(1, len(remainders)):
        a2 = remainders[i]
        n2 = moduli[i]

        g, x, _ = extended_gcd(n1, n2)

        if (a1 - a2) % g != 0:
            return None

        # Solve k * n1 \equiv a2 - a1 (mod n2)
        # k * (n1/g) \equiv (a2 - a1)/g (mod n2/g)
        # k \equiv ((a2 - a1)/g) * inv(n1/g) (mod n2/g)
        # inv(n1/g) mod (n2/g) is x from extended_gcd(n1, n2)
        k0 = (x * ((a2 - a1) // g)) % (n2 // g)

        # New solution: x = a1 + k*n1. With k = k0 + t*(n2/g)
        # x = a1 + (k0 + t*(n2/g)) * n1 = (a1 + k0*n1) + t*lcm(n1, n2)
        a1 = a1 + k0 * n1
        n1 = n1 * (n2 // g)  # lcm(n1, n2)
        a1 %= n1

    return a1, n1
```

## Miller Rabin

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS), Wikipedia Description: Implements the Miller-Rabin primality test, a probabilistic algorithm for determining whether a given number is prime. It is highly efficient and is the standard method for primality testing in competitive programming for numbers that are too large for a sieve.

The algorithm is based on properties of square roots of unity modulo a prime number and Fermat's Little Theorem. For a number `n` to be tested, we first write `n - 1` as `2^s * d`, where `d` is odd. The test then proceeds: 1. Pick a base `a` (a "witness"). 2. Compute `x = a^d mod n`. 3. If `x == 1` or `x == n - 1`, `n` might be prime, and this test passes for this base. 4. Otherwise, for `s-1` times, compute `x = x^2 mod n`. If `x` becomes `n - 1`, the test passes for this base. 5. If after these steps, `x` is not `n - 1`, then `n` is definitely composite.

If `n` passes this test for multiple well-chosen bases a, it is prime with a very high probability. For 64-bit integers, a specific set of deterministic witnesses can be used to make the test 100% accurate. This implementation uses such a set, making it reliable for contest use.

Time: $O(k \cdot (\log n)^2)$, where $k$ is the number of witnesses. Space: $O(1)$ Status: Stress-tested

```python
from content.math.modular_arithmetic import power


def is_prime(n):
    """
    Checks if a number is prime using the Miller-Rabin primality test.
    This implementation is deterministic for all integers up to 2^64.

    Args:
        n (int): The number to test for primality.

    Returns:
        bool: True if n is prime, False otherwise.
    """
    if n < 2:
        return False
    if n == 2 or n == 3:
        return True
    if n % 2 == 0 or n % 3 == 0:
        return False

    d = n - 1
    s = 0
    while d % 2 == 0:
        d //= 2
        s += 1

    # A set of witnesses that is deterministic for all 64-bit integers.
    witnesses = [2, 3, 5, 7, 11, 13, 17, 19, 23, 29, 31, 37]

    for a in witnesses:
        if a >= n:
            break
        x = power(a, d, n)
        if x == 1 or x == n - 1:
            continue

        is_composite = True
        for _ in range(s - 1):
            x = power(x, 2, n)
            if x == n - 1:
                is_composite = False
                break
        if is_composite:
            return False

    return True

```

## Modular Arithmetic

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS), CP-Algorithms Description: This module provides essential functions for modular arithmetic, a cornerstone of number theory in competitive programming. It includes modular exponentiation, the Extended Euclidean Algorithm, and modular multiplicative inverse.

Modular Exponentiation: The `power` function computes $(base^{exp}) \pmod{mod}$ efficiently using the binary exponentiation (also known as exponentiation by squaring) method. This avoids the massive intermediate numbers that would result from calculating $base^{exp}$ directly. The time complexity is logarithmic in the exponent.

Extended Euclidean Algorithm: The `extended_gcd` function computes the greatest common divisor (GCD) of two integers `a` and `b`. In addition, it finds two integer coefficients, `x` and `y`, that satisfy Bezout's identity: $a \cdot x + b \cdot y = \gcd(a, b)$. This is fundamental for many number-theoretic calculations.

Modular Multiplicative Inverse: The `mod_inverse` function finds a number `x` such that $(a \cdot x) \equiv 1 \pmod{m}$. This `x` is the modular multiplicative inverse of `a` modulo `m`. An inverse exists if and only if `a` and `m` are coprime (i.e., $\gcd(a, m) = 1$). This implementation uses the Extended Euclidean Algorithm. From $a \cdot x + m \cdot y = 1$, taking the equation modulo `m` gives $a \cdot x \equiv 1 \pmod{m}$. Thus, the coefficient `x` is the desired inverse.

Time: - `power`: $O($ $log(exp))$ - `extended_gcd`: $O($ $log($ $min(a,b)))$ - `mod_inverse`: $O($ $logm)$ Space: - All functions use $O(1)$ extra space for iterative versions. Status: Stress-tested

```python
def power(base, exp, mod):
    """
    Computes (base^exp) % mod using binary exponentiation.
    """
    res = 1
    base %= mod
    while exp > 0:
        if exp % 2 == 1:
            res = (res * base) % mod
        base = (base * base) % mod
        exp //= 2
    return res


def extended_gcd(a, b):
    """
    Returns (gcd, x, y) such that a*x + b*y = gcd(a, b).
    """
    if a == 0:
        return b, 0, 1
    gcd, x1, y1 = extended_gcd(b % a, a)
    x = y1 - (b // a) * x1
    y = x1
```

```python
    return gcd, x, y


def mod_inverse(a, m):
    """
    Computes the modular multiplicative inverse of a modulo m.
    Returns None if the inverse does not exist.
    """
    gcd, x, y = extended_gcd(a, m)
    if gcd != 1:
        return None
    else:
        return (x % m + m) % m
```

## Ntt

Author: PyCPBook Community Source: CP-Algorithms, KACTL Description: Implements the Number Theoretic Transform (NTT) for fast polynomial multiplication over a finite field. NTT is an adaptation of the Fast Fourier Transform (FFT) for modular arithmetic, avoiding floating-point precision issues. It is commonly used in problems involving polynomial convolution, such as multiplying large numbers or finding the number of ways to form a sum.

The algorithm works by: 1. Choosing a prime modulus `MOD` of the form `c * 2^k + 1` and a primitive root `ROOT` of `MOD`. 2. Evaluating the input polynomials at the powers of `ROOT` (the "roots of unity"). This is the forward NTT, which transforms the polynomials from coefficient representation to point-value representation in $O(N \log N)$ time. 3. Multiplying the resulting point-value representations element-wise in $O(N)$ time. 4. Interpolating the resulting polynomial back to coefficient representation using the inverse NTT in $O(N \log N)$ time.

This implementation uses the prime `MOD = 998244353`, which is a standard choice in competitive programming.

Time: $O(N \log N)$ for multiplying two polynomials of degree up to $N$. Space: $O(N)$ to store the polynomials and intermediate values. Status: Stress-tested

```python
from content.math.modular_arithmetic import power

MOD = 998244353
ROOT = 3
ROOT_PW = 1 << 23
ROOT_INV = power(ROOT, MOD - 2, MOD)


def ntt(a, invert):
    n = len(a)
    j = 0
    for i in range(1, n):
        bit = n >> 1
        while j & bit:
            j ^= bit
            bit >>= 1
        j ^= bit
        if i < j:
            a[i], a[j] = a[j], a[i]

    length = 2
    while length <= n:
        wlen = power(ROOT_INV if invert else ROOT, (MOD - 1) // length, MOD)
        i = 0
        while i < n:
            w = 1
            for j in range(length // 2):
                u = a[i + j]
                v = (a[i + j + length // 2] * w) % MOD
                a[i + j] = (u + v) % MOD
                a[i + j + length // 2] = (u - v + MOD) % MOD
                w = (w * wlen) % MOD
            i += length
        length <<= 1

    if invert:
        n_inv = power(n, MOD - 2, MOD)
        for i in range(n):
            a[i] = (a[i] * n_inv) % MOD


def multiply(a, b):
    if not a or not b:
        return []

    res_len = len(a) + len(b) - 1
    n = 1
    while n < res_len:
        n <<= 1

    fa = a[:] + [0] * (n - len(a))
    fb = b[:] + [0] * (n - len(b))

    ntt(fa, False)
    ntt(fb, False)

    for i in range(n):
        fa[i] = (fa[i] * fb[i]) % MOD

    ntt(fa, True)

    return fa[:res_len]
```

## Pollard Rho

Author: PyCPBook Team Source: CP-Algorithms, Wikipedia Description: Implements Pollard's Rho algorithm for integer factorization, combined with Miller-Rabin primality test for a complete factorization routine. Pollard's Rho is a probabilistic algorithm to find a non-trivial factor of a composite number `n`. It's particularly efficient at finding small factors. The algorithm uses Floyd's cycle-detection algorithm on a sequence of pseudorandom numbers modulo `n`, defined by $x_{i+1} = (x_i^2 + c)$

*modn*. A factor is likely found when `\\text{gcd}(|x_j - x_i|, n) > 1`. The `factorize` function returns a sorted list of prime factors of a given number `n`. It first checks for primality using Miller-Rabin. If `n` is composite, it uses Pollard's Rho to find one factor `d`, and then recursively factorizes `d` and `n/d`. Time: The complexity is heuristic. Finding a factor `p` takes roughly $O(p^{1/2})$ with trial division, but Pollard's Rho takes about $O(p^{1/4})$ or $O(n^{1/4})$ on average. The overall factorization time depends on the size of the prime factors of `n`. Space: $O($ *logn*$)$ for recursion depth in factorization. Status: Stress-tested

```python
import math
import random
from content.math.miller_rabin import is_prime


def _pollard_rho_factor(n):
    """Finds a non-trivial factor of n using Pollard's Rho. n must be composite."""
    if n % 2 == 0:
        return 2

    f = lambda val, c: (pow(val, 2, n) + c) % n

    while True:
        x = random.randint(1, n - 2)
        y = x
        c = random.randint(1, n - 1)
        d = 1

        while d == 1:
            x = f(x, c)
            y = f(f(y, c), c)
            d = math.gcd(abs(x - y), n)

        if d != n:
            return d


def factorize(n):
    if n <= 1:
        return []

    factors = []

    def get_factors(num):
        if num <= 1:
            return
        if is_prime(num):
            factors.append(num)
            return

        factor = _pollard_rho_factor(num)
        get_factors(factor)
        get_factors(num // factor)

    get_factors(n)
    factors.sort()
    return factors

```

## Sieve

Author: PyCPBook Community Source: CP-Algorithms, Wikipedia Description: Implements the Sieve of Eratosthenes, a highly efficient algorithm for finding all prime numbers up to a specified integer `n`.

The algorithm works by iteratively marking as composite (i.e., not prime) the multiples of each prime, starting with the first prime number, 2. 1. Create a boolean list `is_prime` of size `n+1`, initializing all entries to `True`. `is_prime[0]` and `is_prime[1]` are set to `False`. 2. Iterate from `p = 2` up to `sqrt(n)`. 3. If `is_prime[p]` is still `True`, then `p` is a prime number. 4. For this prime `p`, iterate through its multiples starting from `p*p` (i.e., `p*p`, `p*p + p`, `p*p + 2p`, ...) and mark them as not prime by setting `is_prime[multiple]` to `False`. We can start from `p*p` because any smaller multiple `k*p` where `k < p` would have already been marked by a smaller prime factor `k`. 5. After the loop, the `is_prime` array contains `True` at indices that are prime numbers and `False` otherwise.

This implementation returns the boolean array itself, which is often more versatile in contests than a list of primes (e.g., for quick primality checks). A list of primes can be easily generated from this array if needed.

Time: $O(N \log\log N)$, which is nearly linear. Space: $O(N)$ to store the boolean sieve array. Status: Stress-tested

```python
def sieve(n):
    """
    Generates a sieve of primes up to n using the Sieve of Eratosthenes.

    Args:
        n (int): The upper limit for the sieve (inclusive).

    Returns:
        list[bool]: A boolean list of size n+1 where is_prime[i] is True if i
                    is a prime number, and False otherwise.
    """
    if n < 2:
        return [False] * (n + 1)

    is_prime = [True] * (n + 1)
    is_prime[0] = is_prime[1] = False

    for p in range(2, int(n**0.5) + 1):
        if is_prime[p]:
            for multiple in range(p * p, n + 1, p):
                is_prime[multiple] = False

    return is_prime

```

# Chapter 6

# Geometry

## Convex Hull

Author: PyCPBook Community Source: CP-Algorithms (Monotone Chain Algorithm) Description: Implements the Monotone Chain algorithm (also known as Andrew's algorithm) to find the convex hull of a set of 2D points. The convex hull is the smallest convex polygon that contains all the given points.

The algorithm works as follows: 1. Sort all points lexicographically (first by x-coordinate, then by y-coordinate). This step takes $O(N \log N)$ time. 2. Build the lower hull of the polygon. Iterate through the sorted points and maintain a list representing the lower hull. For each point, check if adding it to the hull would create a non-left (i.e., clockwise or collinear) turn with the previous two points on the hull. If it does, pop the last point from the hull until the turn becomes counter-clockwise. This ensures the convexity of the lower hull. 3. Build the upper hull in a similar manner, but by iterating through the sorted points in reverse order. 4. Combine the lower and upper hulls to form the complete convex hull. The endpoints (the lexicographically smallest and largest points) will be included in both hulls, so they must be removed from one to avoid duplication.

This implementation relies on the `Point` class and `orientation` primitive from the `content.geometry.point` module. Time: $O(N \log N)$, dominated by the initial sorting of points. Space: $O(N)$ to store the points and the resulting hull. Status: Stress-tested

```python
from content.geometry.point import Point, orientation


def convex_hull(points):
    """
    Computes the convex hull of a set of points using the Monotone Chain algorithm.

    Args:
        points (list[Point]): A list of Point objects.

    Returns:
        list[Point]: A list of Point objects representing the vertices of the
                     convex hull in
                     counter-clockwise order. Returns an empty
                     list if fewer than 3 points are provided.
    """
    n = len(points)
    if n <= 2:
        return points

    # Sort points lexicographically
    points.sort()

    # Build lower hull
    lower_hull = []
    for p in points:
        while (
            len(lower_hull) >= 2 and orientation(lower_hull[-2], lower_hull[-1], p) <= 0
        ):
            lower_hull.pop()
        lower_hull.append(p)

    # Build upper hull
    upper_hull = []
    for p in reversed(points):
        while (
            len(upper_hull) >= 2 and orientation(upper_hull[-2], upper_hull[-1], p) <= 0
        ):
            upper_hull.pop()
        upper_hull.append(p)

    # Combine the hulls, removing duplicate start/end points
    return lower_hull[:-1] + upper_hull[:-1]

```

## Line Intersection

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS), CP-Algorithms Description: Provides functions for detecting and calculating intersections between lines and line segments in 2D space. This is a fundamental component for many geometric algorithms.

The module includes: - `segments_intersect(p1, q1, p2, q2)`: Determines if two line segments intersect. It uses orientation tests to handle the general case where segments cross each other. If the orientations of the endpoints of one segment with respect to the other segment are different, they intersect. Special handling is required for collinear cases, where we check if the segments overlap. - `line_line_intersection(p1, p2, p3, p4)`: Finds the intersection point of two infinite lines defined by pairs of points `(p1, p2)` and `(p3, p4)`. It uses a formula based on cross products to solve the system of linear equations representing the lines. This method returns `None` if the lines are parallel or collinear, as there is no unique intersection point.

All functions rely on the `Point` class and `orientation` primitive from `content.geometry.point`. Time: All functions are $O(1)$. Space: All functions are $O(1)$. Status: Stress-tested

```python
from content.geometry.point import Point, orientation


def on_segment(p, q, r):
    """
    Given three collinear points p, q, r, the function checks if point q
    lies on line segment 'pr'.
    """
    return (
        q.x <= max(p.x, r.x)
        and q.x >= min(p.x, r.x)
        and q.y <= max(p.y, r.y)
        and q.y >= min(p.y, r.y)
    )


def segments_intersect(p1, q1, p2, q2):
    """
    Checks if line segment 'p1q1' and 'p2q2' intersect.
    """
    o1 = orientation(p1, q1, p2)
    o2 = orientation(p1, q1, q2)
    o3 = orientation(p2, q2, p1)
    o4 = orientation(p2, q2, q1)

    if o1 != 0 and o2 != 0 and o3 != 0 and o4 != 0:
        if o1 != o2 and o3 != o4:
            return True
        return False

    if o1 == 0 and on_segment(p1, p2, q1):
        return True
    if o2 == 0 and on_segment(p1, q2, q1):
        return True
    if o3 == 0 and on_segment(p2, p1, q2):
        return True
    if o4 == 0 and on_segment(p2, q1, q2):
        return True

    return False


def line_line_intersection(p1, p2, p3, p4):
    """
    Finds the intersection point of two infinite lines defined by (p1, p2) and (p3, p4).
    Returns the intersection point as a Point object with float coordinates,
    or None if the lines are parallel or collinear.
    """
    v1 = p2 - p1
    v2 = p4 - p3
    denominator = v1.cross(v2)

    if abs(denominator) < 1e-9:
        return None

    t = (p3 - p1).cross(v2) / denominator
    return p1 + v1 * t

```

## Point

Author: PyCPBook Community Source: KACTL, CP-Algorithms, standard geometry texts Description: Implements a foundational Point class for 2D geometry problems. The class supports standard vector operations through overloaded operators, making geometric calculations intuitive and clean. It can handle both integer and floating-point coordinates.

Operations supported: - Addition/Subtraction: `p1 + p2`, `p1 - p2` - Scalar Multiplication/Division: `p * scalar`, `p / scalar` - Dot Product: `p1.dot(p2)` - Cross Product: `p1.cross(p2)` (returns the 2D magnitude) - Squared Euclidean Distance: `p1.dist_sq(p2)` - Comparison: `p1 == p2`, `p1 < p2` (lexicographical)

A standalone `orientation` function is also provided to determine the orientation of three ordered points (collinear, clockwise, or counter-clockwise), which is a fundamental primitive for many geometric algorithms. Time: All Point methods and the `orientation` function are $O(1)$. Space: $O(1)$ per Point object. Status: Stress-tested

```python
import math


class Point:
    def __init__(self, x, y):
        self.x = x
        self.y = y

    def __repr__(self):
        return f"Point({self.x}, {self.y})"

    def __eq__(self, other):
        return self.x == other.x and self.y == other.y

    def __lt__(self, other):
        if self.x != other.x:
            return self.x < other.x
        return self.y < other.y

    def __add__(self, other):
        return Point(self.x + other.x, self.y + other.y)

    def __sub__(self, other):
        return Point(self.x - other.x, self.y - other.y)

```

```python
    def __mul__(self, scalar):
        return Point(self.x * scalar, self.y * scalar)

    def __truediv__(self, scalar):
        return Point(self.x / scalar, self.y / scalar)

    def dot(self, other):
        return self.x * other.x + self.y * other.y

    def cross(self, other):
        return self.x * other.y - self.y * other.x

    def dist_sq(self, other):
        dx = self.x - other.x
        dy = self.y - other.y
        return dx * dx + dy * dy


def orientation(p, q, r):
    """
    Determines the orientation of the ordered triplet (p, q, r).

    Returns:
        int: > 0 for counter-clockwise, < 0 for clockwise, 0 for collinear.
    """
    val = (q.x - p.x) * (r.y - q.y) - (q.y - p.y) * (r.x - q.x)
    if val == 0:
        return 0
    return 1 if val > 0 else -1

```

## Polygon Area

Author: PyCPBook Community Source: Wikipedia (Shoelace formula), CP-Algorithms Description: Implements functions to calculate the area and centroid of a simple (non-self-intersecting) polygon. The area is calculated using the Shoelace formula, which computes the signed area based on the cross products of adjacent vertices. The absolute value of this result gives the geometric area. The centroid calculation uses a related formula derived from the shoelace principle. Both functions assume the polygon vertices are provided in a consistent order (either clockwise or counter-clockwise). Time: $O(N)$ for both area and centroid calculation, where $N$ is the number of vertices. Space: $O(1)$ Status: Stress-tested

```python
from content.geometry.point import Point


def polygon_area(vertices):
    """
    Calculates the area of a simple polygon using the Shoelace formula.

    Args:
        vertices (list[Point]): A list of Point objects representing the
                                vertices of the polygon in order.

    Returns:
        float: The area of the polygon.
    """
    n = len(vertices)
    if n < 3:
        return 0.0

    area = 0.0
    for i in range(n):
        p1 = vertices[i]
        p2 = vertices[(i + 1) % n]
        area += p1.cross(p2)

    return abs(area) / 2.0


def polygon_centroid(vertices):
    """
    Calculates the centroid of a simple polygon.

    Args:
        vertices (list[Point]): A list of Point objects representing the
                                vertices of the polygon in order.

    Returns:
        Point | None: A Point object representing the centroid, or None if the
                      polygon's area is zero.
    """
    n = len(vertices)
    if n < 3:
        return None

    signed_area = 0.0
    centroid_x = 0.0
    centroid_y = 0.0

    for i in range(n):
        p1 = vertices[i]
        p2 = vertices[(i + 1) % n]
        cross_product = p1.cross(p2)

        signed_area += cross_product
        centroid_x += (p1.x + p2.x) * cross_product
        centroid_y += (p1.y + p2.y) * cross_product

    if abs(signed_area) < 1e-9:
        return None

    area = signed_area / 2.0
    centroid_x /= 6.0 * area
    centroid_y /= 6.0 * area

    return Point(centroid_x, centroid_y)

```

# Chapter 7

# Dynamic Programming

## Common Patterns

Author: PyCPBook Community Source: Introduction to Algorithms (CLRS), CP-Algorithms Description: This file provides implementations for three classic dynamic programming patterns that are foundational in competitive programming: Longest Increasing Subsequence (LIS), Longest Common Subsequence (LCS), and the 0/1 Knapsack problem.

Longest Increasing Subsequence (LIS): Given a sequence of numbers, the goal is to find the length of the longest subsequence that is strictly increasing. The standard DP approach takes $O(N^2)$ time. This file implements a more efficient $O(N \log N)$ solution. The algorithm maintains an auxiliary array (e.g., `tails`) where `tails[i]` stores the smallest tail of all increasing subsequences of length `i+1`. When processing a new number `x`, we find the smallest tail that is greater than or equal to `x`. If `x` is larger than all tails, it extends the LIS. Otherwise, it replaces the tail it was compared against, potentially allowing for a better solution later. This search and replacement is done using binary search.

Longest Common Subsequence (LCS): Given two sequences, the goal is to find the length of the longest subsequence present in both of them. The standard DP solution uses a 2D table `dp[i][j]` which stores the length of the LCS of the prefixes `s1[0...i-1]` and `s2[0...j-1]`. The recurrence relation is: - If `s1[i-1] == s2[j-1]`, then `dp[i][j] = 1 + dp[i-1][j-1]`. - Otherwise, `dp[i][j] = max(dp[i-1][j], dp[i][j-1])`.

0/1 Knapsack Problem: Given a set of items, each with a weight and a value, determine the number of each item to include in a collection so that the total weight is less than or equal to a given limit and the total value is as large as possible. In the 0/1 version, you can either take an item or leave it. The standard solution uses a DP table `dp[i][w]` representing the maximum value using items up to `i` with a weight limit of `w`. This can be optimized in space to a 1D array where `dp[w]` is the maximum value for a capacity of `w`.

Time: - LIS: $O(N \log N)$ - LCS: $O(N \cdot M)$ where N and M are the lengths of the sequences. - 0/1 Knapsack: $O(N \cdot W)$ where N is number of items, W is capacity. Space: - LIS: $O(N)$ - LCS: $O(N \cdot M)$ - 0/1 Knapsack: $O(W)$ (space-optimized) Status: Stress-tested

```python
import bisect


def longest_increasing_subsequence(arr):
    """
    Finds the length of the longest increasing subsequence in O(N log N).
    """
    if not arr:
        return 0

    tails = []
    for num in arr:
        idx = bisect.bisect_left(tails, num)
        if idx == len(tails):
            tails.append(num)
        else:
            tails[idx] = num
    return len(tails)


def longest_common_subsequence(s1, s2):
    """
    Finds the length of the longest common subsequence in O(N*M).
    """
    n, m = len(s1), len(s2)
    dp = [[0] * (m + 1) for _ in range(n + 1)]

    for i in range(1, n + 1):
        for j in range(1, m + 1):
            if s1[i - 1] == s2[j - 1]:
                dp[i][j] = 1 + dp[i - 1][j - 1]
            else:
                dp[i][j] = max(dp[i - 1][j], dp[i][j - 1])
    return dp[n][m]


def knapsack_01(weights, values, capacity):
    """
    Solves the 0/1 Knapsack problem with space optimization.
    """
    n = len(weights)
    dp = [0] * (capacity + 1)

    for i in range(n):
        for w in range(capacity, weights[i] - 1, -1):
            dp[w] = max(dp[w], values[i] + dp[w - weights[i]])

    return dp[capacity]
```

## Dp Optimizations

Author: PyCPBook Community Source: CP-Algorithms, USACO Guide Description: This file explains and demonstrates several advanced dynamic programming optimizations. The primary focus is the Convex Hull Trick, with conceptual explanations for Knuth-Yao Speedup and Divide and Conquer Optimization.

Convex Hull Trick (CHT): This optimization applies to DP recurrences of the form: `dp[i] = min_{j<i} (dp[j] + b[j] * a[i])` (or similar). For a fixed `i`, each `j` defines a line `y = m*x + c`, where `m = b[j]`, `x = a[i]`, and `c = dp[j]`. The problem then becomes finding the minimum value among a set of lines for a given x-coordinate `a[i]`. A `LineContainer` data structure is used to maintain the lower envelope (convex hull) of these lines, allowing for efficient queries. The example below solves a problem with the recurrence `dp[i] = C + min_{j<i} (dp[j] + (p[i] - p[j])^2)`, which can be rearranged into the required line form. This works efficiently if the slopes of the lines being added are monotonic.

Knuth-Yao Speedup: This optimization applies to recurrences of the form `dp[i][j] = C[i][j] + min_{i<=k<j} (dp[i][k] + dp[k+1][j])`, such as in the optimal binary search tree problem. It can be used if the cost function `C` satisfies the quadrangle inequality (`C[a][c] + C[b][d] <= C[a][d] + C[b][c]` for `a <= b <= c <= d`). The key insight is that the optimal splitting point `k` for `dp[i][j]`, denoted `opt[i][j]`, is monotonic: `opt[i][j-1] <= opt[i][j] <= opt[i+1][j]`. This property allows us to reduce the search space for `k` from `O(j-i)` to `opt[i+1][j] - opt[i][j-1]`, improving the total time complexity from $O(N^3)$ to $O(N^2)$.

Divide and Conquer Optimization: This technique applies to recurrences of the form `dp[i][j] = min_{0<=k<j} (dp[i-1][k] + C[k][j])`. A naive computation would take $O(N^2)$ for each `i`, leading to $O(K * N^2)$ total time for `K` states. The optimization is based on the observation that if the cost function `C` has certain properties (often related to the quadrangle inequality), the optimal choice of `k` for `dp[i][j]` is monotonic with `j`. We can compute all `dp[i][j]` values for a fixed `i` and `j` in a range `[l, r]` by first finding the optimal `k` for the midpoint `mid = (l+r)/2`. Then, recursively, the optimal `k` for the left half `[l, mid-1]` must be in a smaller range, and similarly for the right half. This divide and conquer approach computes all `dp[i][j]` for a fixed `i` in $O(N \log N)$ time.

Time: Varies by optimization. CHT: $O(N \log N)$ or $O(N)$ amortized. Space: Varies. Status: Conceptual (Knuth-Yao, D&C), Stress-tested (CHT example).

```python
import sys
import os

# The stress test runner adds the project root to the path.
sys.path.append(os.path.abspath(os.path.join(os.path.dirname(
    "../../")))
from content.data_structures.line_container import LineContainer


def convex_hull_trick_example(p, C):
    """
    Solves an example problem using the Convex Hull Trick.
    Problem: Given n points on a line with increasing coordinates p[0]...p[n-1],
    find the minimum cost to travel from point 0 to point n-1. The cost of
    jumping from point i to point j is (p[j] - p[i])^2 + C.

    DP recurrence: dp[i] = min_{j<i} (dp[j] + (p[i] - p[j])^2 + C)
    This can be rewritten as:
    dp[i] = p[i]^2 + C + min_{j<i} (-2*p[j]*p[i] + dp[j] + p[j]^2)
    This fits the form y = mx + c, where:
    - x = p[i]
    - m_j = -2 * p[j]
    - c_j = dp[j] + p[j]^2
    Since p is increasing, the slopes m_j are decreasing, matching the
    `LineContainer`'s requirement.

    Args:
        p (list[int]): A list of increasing integer coordinates.
        C (int): A constant cost for each jump.

    Returns:
        int: The minimum cost to reach the last point.
    """
    n = len(p)
    if n <= 1:
        return 0

    dp = [0] * n
    lc = LineContainer()

    # Base case: dp[0] = 0. Add the first line to the container.
    # m_0 = -2*p[0], c_0 = dp[0] + p[0]^2 = p[0]^2
    lc.add(-2 * p[0], p[0] ** 2)

    for i in range(1, n):
        # Query for the minimum value at x = p[i]
        min_val = lc.query(p[i])
        dp[i] = p[i] ** 2 + C + min_val

        # Add the new line corresponding to state i to the container
        # m_i = -2*p[i], c_i = dp[i] + p[i]^2
        lc.add(-2 * p[i], dp[i] + p[i] ** 2)

    return dp[n - 1]

```