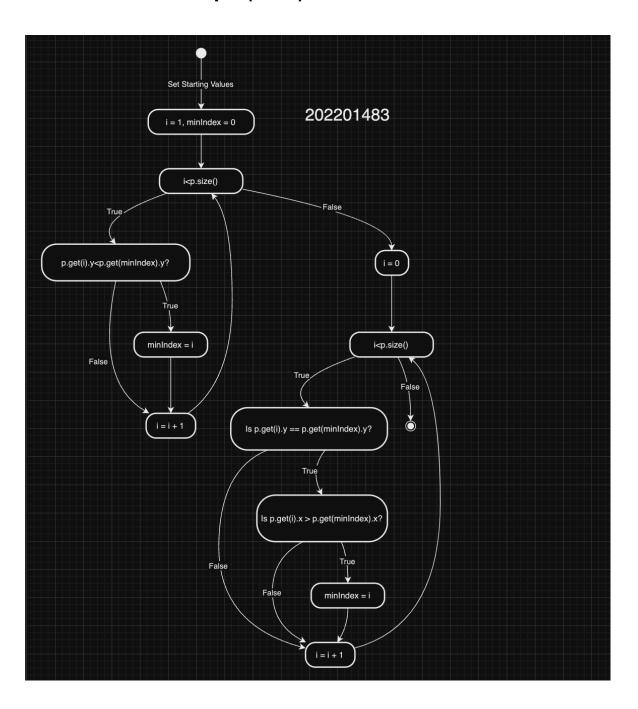
LAB 9: Mutation Testing

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1.Control Flow Graph (CFG)



Executable Java Code:

```
import java.util.Vector;
class Point {
   public String toString() {
public class ConvexHull {
   public static void doGraham(Vector<Point> p) {
        System.out.println("Searching for the minimum
        for (i = 1; i < p.size(); ++i) {
            System.out.println("Comparing " + p.get(i) + " with " +
p.get(min));
            if (p.get(i).y < p.get(min).y) {</pre>
                System.out.println("New minimum found: " +
p.get(min));
        System.out.println("Searching for the leftmost point with
```

a) Statement Coverage:

Test Case 1:

- Input: p = [(0, 1), (1, 2), (2, 3)]
- Explanation: This input ensures we go through both loops and perform minimum checks in both y and x comparisons.
- Expected Outcome: index 2

b) Branch Coverage:

Test Case 2:

• Input: p = [(1, 3), (2, 1), (3, 3)]

- Explanation: This input allows the code to take both paths in p.get(i).y <
 p.get(min).y and p.get(i).y == p.get(min).y. The x-comparison will also be
 tested when y values are equal.
- Expected Outcome: index 2

Test Case 3:

- Input: p = [(0,3),(1,3),(2,3)]
- Explanation: Ensures the code covers cases where multiple points have the same y value and tests the branch where x values are compared.
- Expected Outcome: Index 2

c) Basic Condition Coverage:

Test case 4:

- Input: p = [(2, 2), (1, 1), (0, 3)]
- Explanation: This set allows for basic condition testing where each part of p.get(i).y < p.get(min).y, p.get(i).y == p.get(min).y, and p.get(i).x > p.get(min).x evaluates as both true and false.
- Expected Outcome: index 2

Test Case 5:

- Input: p = [(1, 1), (1, 1), (2, 2)]
- Explanation: This input tests both true and false branches of each condition in isolation.
- Expected Outcome: Since the first two points are identical, the second loop tests the y equality and x comparison in a controlled manner. Min should be updated to reflect the highest x among points with the smallest y.

Identifying Undetected Code Mutations

For the test suite you have recently analyzed, can you pinpoint a mutation in the code (such as a deletion, alteration, or addition) that would result in a failure but is not captured by your current tests? This task should be performed using a mutation testing tool.

Types of Possible Mutations

Several common mutation types can be applied, including:

- Changes to Relational Operators: Modify <= to < or switch == to != in conditional statements.
- Logic Modifications: Remove or invert branches in if-statements.
- **Statement Adjustments:** Alter assignments or statements to see if the outcome goes unnoticed.

Potential Mutations and Their Consequences

- 1. Modifying the Comparison for the Leftmost Point:
 - Mutation: In the second loop, change p.get(i).x < p.get(min).x to p.get(i).x <= p.get(min).x.
 - Consequence: This change could lead to the selection of points sharing the same x-coordinate as the leftmost point, undermining the uniqueness of the minimum point.
- 2. **Undetected by Current Tests:** The existing test cases do not address situations where multiple points have identical x and y values, which would highlight if the function mistakenly includes such points as the leftmost.
- 3. Changing the y-Coordinate Comparison to <= in the First Loop:
 - Mutation: Alter p.get(i).y < p.get(min).y to p.get(i).y <= p.get(min).y in the first loop.
 - Consequence: This could allow points with the same y-coordinate but different x-coordinates to overwrite the minimum, potentially selecting a non-leftmost minimum point.
- 4. **Undetected by Current Tests:** The current test set lacks scenarios with multiple points sharing the same y-coordinate, which could cause this mutation to remain undetected. To expose this issue, a test with points having the same y but different x values is necessary.
- 5. Eliminating the x-coordinate Check in the Second Loop:

- Mutation: Remove the condition p.get(i).x < p.get(min).x from the second loop.
- Consequence: This would permit the selection of any point with the minimum y-coordinate as the "leftmost," irrespective of its x-coordinate.
- 6. **Undetected by Current Tests:** The existing tests do not verify whether the correct leftmost point is selected when multiple points share the same y-coordinate but have different x values.

Additional Test Cases to Identify These Mutations

To effectively detect these mutations, consider implementing the following test cases:

1. Test Case for Mutation 1:

- o **Input:** [(0, 1), (0, 1), (1, 1)]
- Expected Outcome: The leftmost minimum should remain (0, 1) despite duplicates. This case will check if the x <= mutation incorrectly includes duplicate points.

2. Test Case for Mutation 2:

- o Input: [(1, 2), (0, 2), (3, 1)]
- Expected Outcome: The function should identify (3, 1) as the minimum point based on the y-coordinate. This test will confirm whether using <= for y comparisons erroneously overwrites the minimum point.

3. Test Case for Mutation 3:

- o Input: [(2, 1), (1, 1), (0, 1)]
- Expected Outcome: The leftmost point should be (0, 1). This case will help determine if the x-coordinate check was incorrectly removed.

By adding these specific test cases, you can strengthen the test suite to ensure that these mutations are effectively caught.

• Python Code for Mutation:-

```
from math import atan2
class Point:
    def __init__(self, x, y):
       self.x = x
       self.y = y
    def __repr__(self):
       return f"({self.x}, {self.y})"
def orientation(p, q, r):
    # Cross product to find orientation
    val = (q.y - p.y) * (r.x - q.x) - (q.x - p.x) * (r.y - q.y)
    if val == 0:
        return 0 # Collinear
    elif val > 0:
       return 1 # Clockwise
    else:
       return 2 # Counterclockwise
def distance_squared(p1, p2):
```

```
return (p1.x - p2.x) ** 2 + (p1.y - p2.y) ** 2
def do_graham(points):
    # Step 1: Find the bottom-most point (or leftmost in case of a tie)
    n = len(points)
    min_y_index = 0
    for i in range(1, n):
                  if (points[i].y < points[min_y_index].y) or \</pre>
              (points[i].y == points[min_y_index].y and points[i].x <
points[min_y_index].x):
               min_y_index = i
    points[0], points[min_y_index] = points[min_y_index], points[0] p0 = points[0]
    # Step 2: Sort the points based on polar angle with respect to
0a
    points[1:] = sorted(points[1:], key=lambda p: (atan2(p.y - p0.y, p.x - p0.x),
distance_squared(p0, p)))
    # Step 3: Initialize the convex hull with the first three points hull = [points[0],
    points[1], points[2]]
    # Step 4: Process the remaining points for i in
     range(3, n):
```

```
# Mutation introduced here: instead of checking `!= 2`, we
incorrectly use `== 1`
        while len(hull) > 1 and orientation(hull[-2], hull[-1],
points[i]) == 1:
            hull.pop()
        hull.append(points[i])
    return hull
# Sample test to observe behavior with the mutation
points = [Point(0, 3), Point(1, 1), Point(2, 2), Point(4, 4),
          Point(0, 0), Point(1, 2), Point(3, 1), Point(3, 3)]
hull = do_graham(points)
print("Convex Hull:", hull)
```