Software Engineering(IT-314)
LAB 10 MUTATION TESTING

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Q.1. The code below is part of a method in the ConvexHull class in the VMAP system. The following is a small fragment of a method in the ConvexHull class. For the purposes of this exercise, you do not need to know the intended function of the method. The parameter p is a Vector of Point objects, p.size() is the size of the vector p, (p.get(i)).x is the x component of the i^{th} point appearing in p, similarly for (p.get(i)).y. This exercise is concerned with structural testing of code, so the focus is on creating test sets that satisfy some particular coverage criteria.

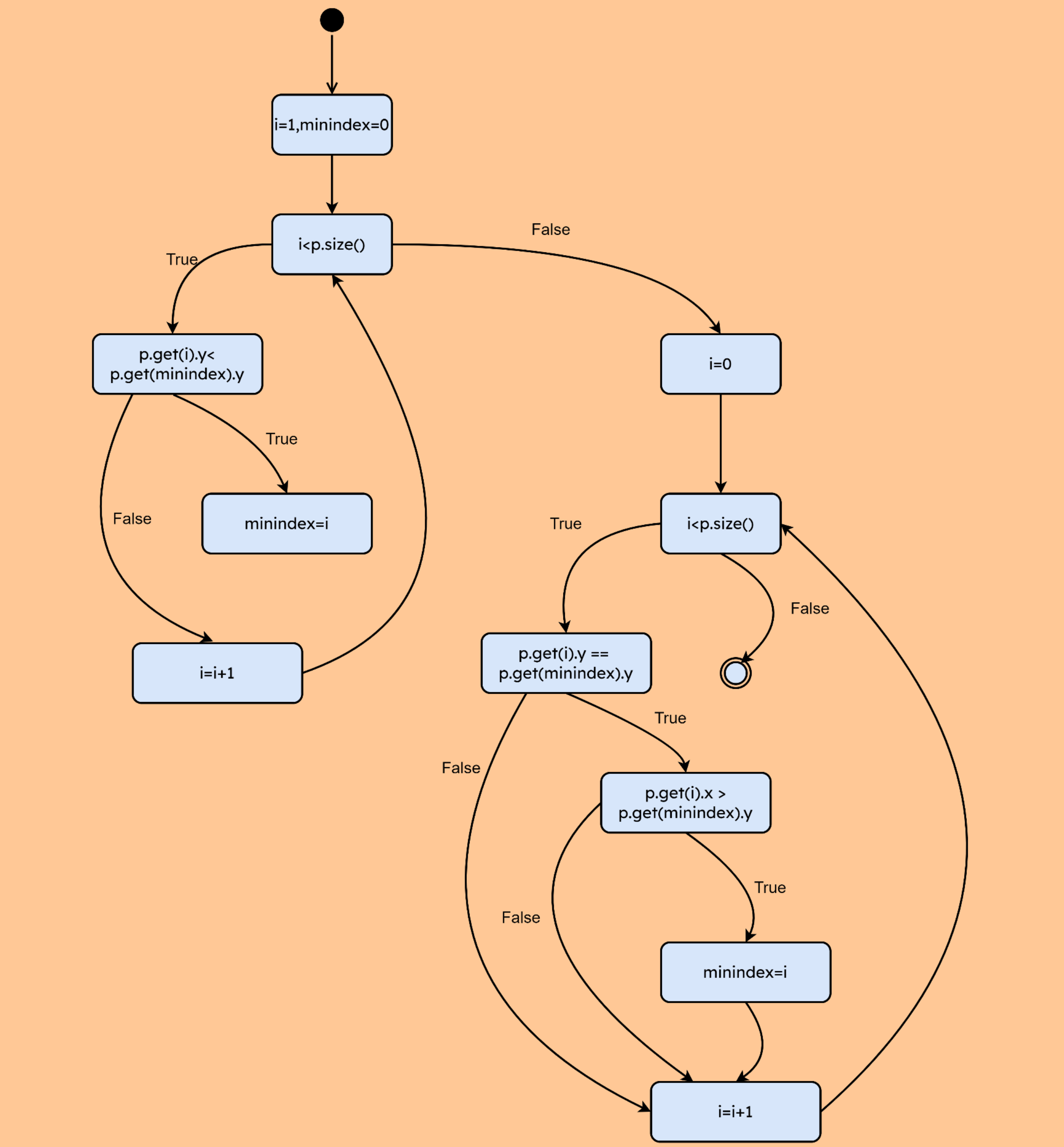
```
Vector doGraham(Vector p) {
        int i,j,min,M;

        Point t;
        min = 0;

        // search for minimum:
        for(i=1; i < p.size(); ++i) {
            if( ((Point) p.get(i)).y <
                          ((Point) p.get(min)).y )
            {
                min = i;
            }
        }

        // continue along the values with same y component
        for(i=0; i < p.size(); ++i) {
            if(( ((Point) p.get(i)).y ==
                          ((Point) p.get(min)).y ) &&
                 (((Point) p.get(i)).x >
                          ((Point) p.get(min)).x ))
            {
                 min = i;
            }
        }
```

For the given code fragment, you should carry out the following activities.

1. Convert the code comprising the beginning of the doGraham method into a control flow graph (CFG).

You are free to write the code in any programming language.

Control Flow Graph - doGraham



Java code - doGraham

```java
import java.util.Vector;

public class ConvexHull {

    public void doGraham(Vector<Point> p) {
        int i, min = 0;

        for (i = 1; i < p.size(); i++) {
            if (((Point) p.get(i)).y < ((Point) p.get(min)).y) {
                min = i;
            }
        }

        for (i = 0; i < p.size(); i++) {
            if (((Point) p.get(i)).y == ((Point) p.get(min)).y &&
                ((Point) p.get(i)).x > ((Point) p.get(min)).x) {
                min = i;
            }
        }
    }

    public static class Point {
        public int x;
        public int y;

        public Point(int x, int y) {
            this.x = x;
            this.y = y;
        }
    }

    public static void main(String[] args) {
        Vector<Point> points = new Vector<>();
        points.add(new Point(0, 0));
        points.add(new Point(1, 1));
        points.add(new Point(2, 2));
        points.add(new Point(1, 0));

        ConvexHull convexHull = new ConvexHull();
        convexHull.doGraham(points);

    }
}
```

Control Flow Graph Factory Tool YES
Eclipse flow graph generator YES

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), (: 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:

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.

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.

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.

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.

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.

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:

Test Case for Mutation 1:

- **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.

Test Case for Mutation 2:

- **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.

Test Case for Mutation 3:

- **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 Mutation CODE

```python
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 \

            (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
p0

    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)
```