IT313: Software Engineering

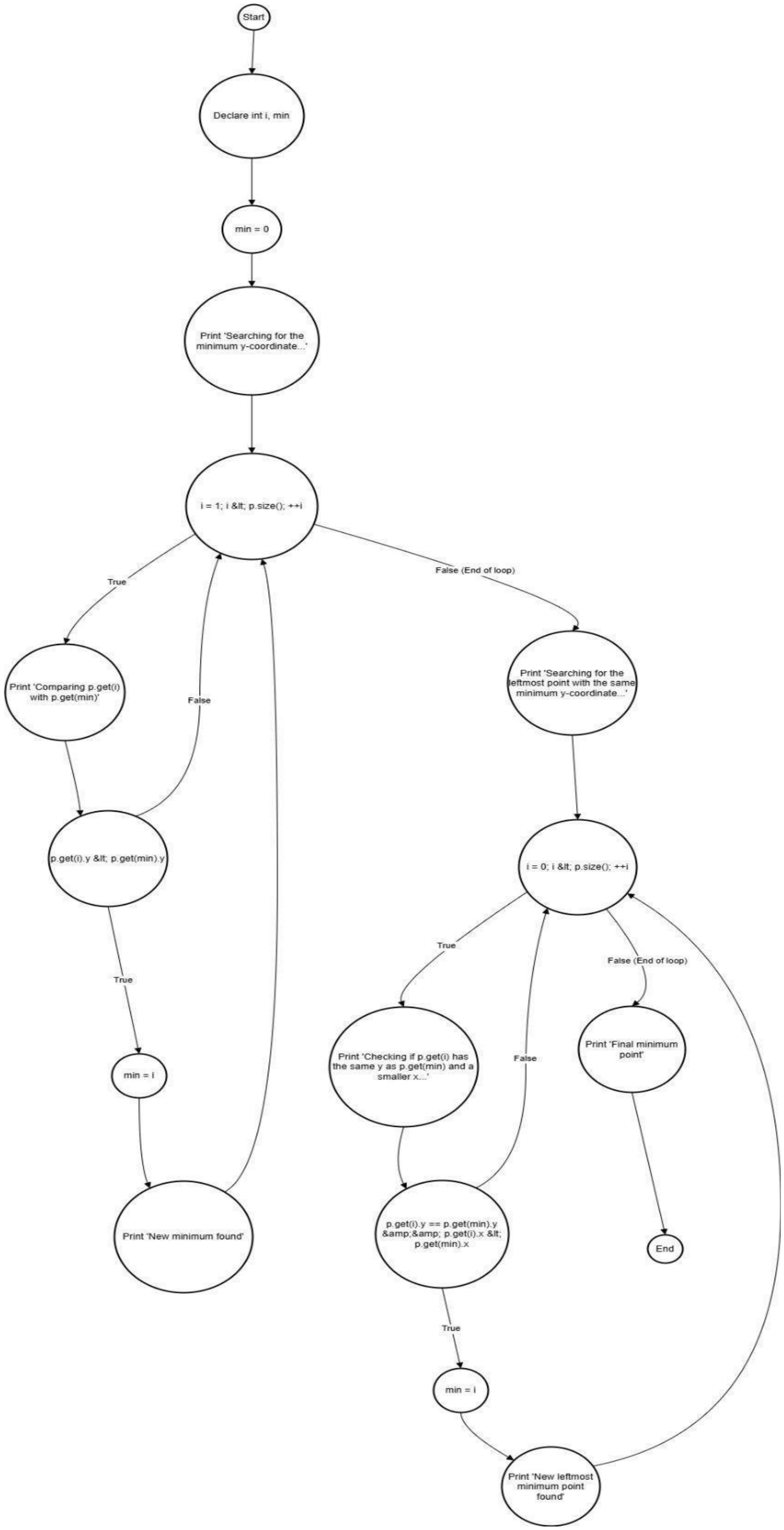
Lab 9 – Mutation Testing

Name – Mehul Vagh

ID - 202201251

Code :

```
class Point{
  double x, y;
  public Point(double x, double y) {
    this.x = x;
    this.y = y;
  }
}
// Vector class
class Vector {


    private
    java.util.ArrayList < Point > points;

    public Vector() {}
    points = new java.util.ArrayList < > ();

    public void add(Point p) {}
    points.add(p);

    public Point get(int index) {
    return points.get(index);
 }

 public int size() {}

 return points.size();
}
// Main class with doGraham method
public class GrahamScan {
public static int doGraham(Vector p) {
    int i, min;
    min = 0;

    // search for minimum
    for (i = 1; i < p.size(); ++i) {
        if (p.get(i).yp.get(min).y) {
        min = i;
        }
    }
// continue along the values with same y component
   for(i=0; i<p.size(); ++i) {
       if ((p.get(i).y == p.get(min).y) && (p.get(i).x > p.get(min).x)) {
       min = i;
       }
   }

   return min;
   }
}
```


Start
Declare int i, min
min = 0
Print 'Searching for the minimum y-coordinate...'
i = 1; i < p.size(); ++i
True
False (End of loop)
Print 'Comparing p.get(i) with p.get(min)'
False
p.get(i).y < p.get(min).y
True
min = i
Print 'New minimum found'
Print 'Searching for the leftmost point with the same minimum y-coordinate...'
i = 0; i < p.size(); ++i
True
False (End of loop)
Print 'Checking if p.get(i) has the same y as p.get(min) and a smaller x...'
False
Print 'Final minimum point'
p.get(i).y == p.get(min).y && p.get(i).x < p.get(min).x
True
End
min = i
Print 'New leftmost minimum point found'

Construct test sets for your flow graph that are adequate for the following criteria:

a. **Statement Coverage.**

b. **Branch Coverage.**

c. **Basic Condition Coverage.**

a. Statement Coverage

Objective: Ensure that each statement in the flow graph is executed at least once.

Test Set:

1. **Test Case 1:**
    - Inputs: Any list with more than one point (e.g., [(0, 1), (1, 2), (2, 0)])
    - This will traverse through the entire flow, covering statements related to finding the minimum y-coordinate and leftmost minimum point.
2. **Test Case 2:**
    - Inputs: [(2, 2), (2, 2), (3, 3)]
    - This checks for points with the same y-coordinate and ensures the leftmost point logic executes.

b. Branch Coverage

Objective: Ensure that each branch (true and false) from every decision point is executed.

Test Set:

1. **Test Case 1:**
    - Inputs: [(0, 1), (1, 2), (2, 0)]
    - This will take the true branch for finding the minimum y-coordinate.
2. **Test Case 2:**
    - Inputs: [(2, 2), (2, 2), (3, 3)]
    - This will test the scenario where y-coordinates are equal, triggering the branch for checking x-coordinates.
3. **Test Case 3:**
    - Inputs: [(1, 2), (1, 1), (2, 3)]
    - This ensures the flow takes the false branch when checking for new minimum y-coordinates and the leftmost check.

c. Basic Condition Coverage

Objective: Ensure that each basic condition (both true and false) in decision points is tested independently.

Test Set:

1. **Test Case 1:**
   - Inputs: [(1, 1), (2, 2), (3, 3)]
   - This will evaluate both conditions for the y-coordinate comparisons.
2. **Test Case 2:**
   - Inputs: [(1, 1), (1, 1), (1, 2)]
   - This checks the scenario where the y-coordinates are the same but evaluates the x-coordinate condition.
3. **Test Case 3:**
   - Inputs: [(3, 1), (2, 2), (1, 3)]
   - This ensures that both conditions in the loop are executed, confirming the function's logic is robust.

Using a mutation testing tool, identify any mutations of the code (such as deletions, modifications, or insertions) that would cause a failure but are not detected by your current test set.

Types of Possible Mutations :

We can apply typical mutation types, including:

- **Relational Operator Changes**: Modify <=to <or ==to !=in the conditions.
- **Logic Changes**: Remove or invert a branch in an if-statement.
- **Statement Changes**: Modify assignments or statements to see if the effect goes undetected.

Potential Mutations and Their Effects

1. **Changing the Comparison for 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**.

   - **Effect** : This could cause the function to select points that share the same x-coordinate as the leftmost point, potentially disrupting the uniqueness of the minimum point.

- **Not Detected by Current Tests** : The existing tests do not address the scenario where multiple points have the same x and y values, which would indicate whether the function incorrectly accepts such points as the leftmost.

2. **Altering the y-Coordinate Comparison to <=in the First Loop**:
   - **Mutation**: Change **p.get(i).y < p.get(min).y to p.get(i).y <= p.get(min).y** inthe first loop.
   - **Effect**: This would permit points with the same y-coordinate but different x-coordinates to overwrite the minimum, potentially resulting in the selection of a non-leftmost minimum point.
   - **Undetected by Current Tests**: The current test set does not include cases where multiple points share the same y-coordinate, allowing this mutation to remain undetected. To uncover this issue, we would need a test case where several points have the same y-coordinate but different x-coordinates.

3. **Removing the Check for x-coordinate in the Second Loop**:
   - **Mutation** : Remove the condition **p.get(i).x < p.get(min).x** in the second loop.
   - **Effect** : This would lead the function to choose any point that has the same minimum y-coordinate as the "leftmost," irrespective of its x-coordinate.
   - **Undetected by Current Tests**: The current tests do not explicitly verify whether the correct leftmost point is selected when multiple points have the same y value but different x values.

Additional Test Cases to Detect These Mutations

To detect these mutations, we can add the following test cases:

1. **Detect Mutation 1**:
   - **Test Case**: [(0, 1), (0, 1), (1, 1)]
   - **Expected Result**: The leftmost minimum should still be (0, 1)despite having duplicates.
   - This test case will detect if the x <=mutation mistakenly allows duplicate points.
2. **Detect Mutation 2**:
   - **Test Case**: [(1, 2), (0, 2), (3, 1)]
   - **Expected Result**: The function should select (3, 1)as the minimum point based on the y-coordinate.
   - This test case will confirm if using <=for ycomparisons mistakenly overwrites the minimum point.

3. **Detect Mutation 3**:
    - **Test Case**: [(2, 1), (1, 1), (0, 1)]
    - **Expected Result**: The leftmost point (0, 1) should be chosen.
    - This will reveal if the x-coordinate check was mistakenly remove

These additional test cases would help ensure that any such mutations do not survive undetected by the test suite, strengthening the coverag

Python Code for Mutation :-

```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)))
```

```python
# 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)
```