



# INTRODUCTION TO SOFTWARE TESTING FOR THE SCIENTIFIC COMMUNITY

Myra Cohen, BSSw Fellow

<https://www.cs.iastate.edu/~mcohen>

[mcohen@iastate.edu](mailto:mcohen@iastate.edu)



IOWA STATE UNIVERSITY  
OF SCIENCE AND TECHNOLOGY

Laboratory for Variability-Aware Assurance and  
Testing of Organic Programs



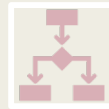
# Module I: Overview (cont.)



Motivation



What to test



Types of  
Testing



Models



Coverage



Oracles

# Types of Testing



Unit Testing



Integration Testing



System Testing



Configuration Testing



User Interface Testing



Regression Testing

# Models



Provide an **abstraction** of the software we are testing



Can be **for different dimensions** of the software (specifications, interface, code)



Allow us to reason about **how much** we have tested



The foundation for **automated test generation**

# Example Models

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Graphs

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Tabular

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Relational

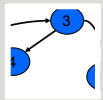
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Grammar based

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Logic based

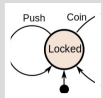
# Graph Models



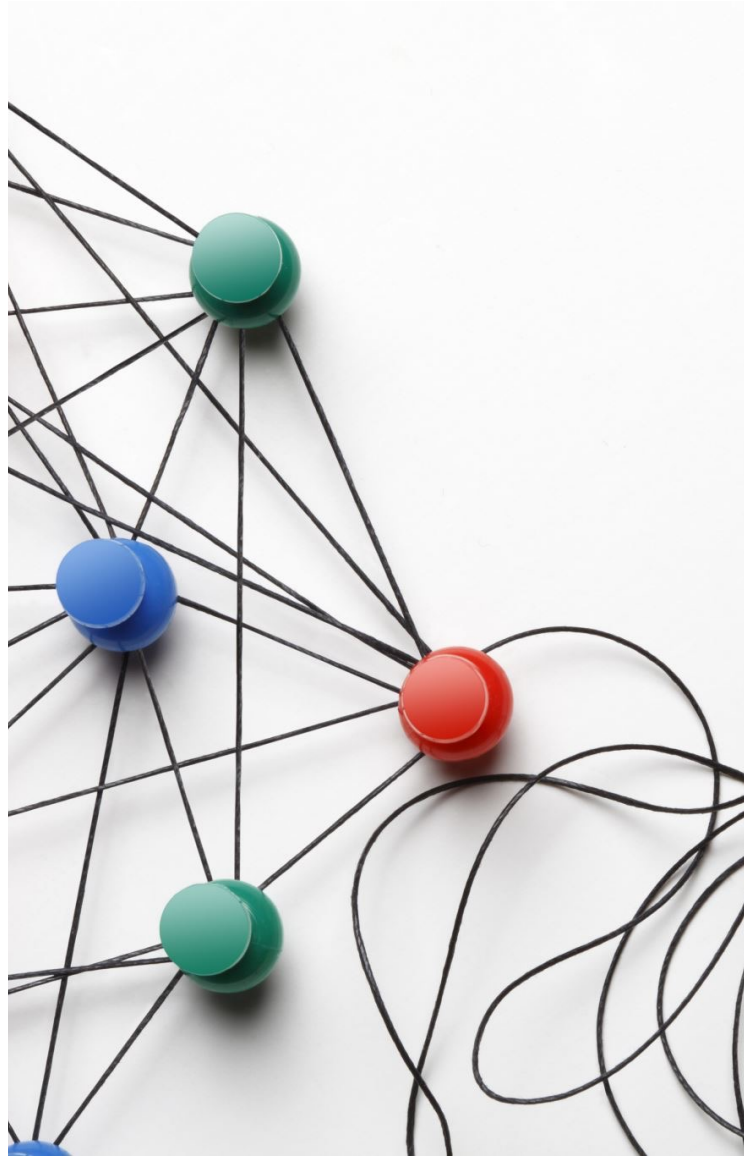
Program control flow graph



User interface



Program state machine

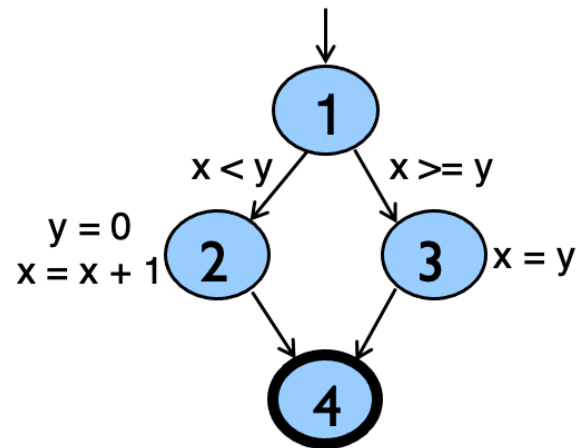


# Types of Graph Coverage

- All **nodes**
- All **edges** (pairs of nodes)
- All **length N** paths
- **M random** length N paths

# Program Code Coverage

```
if (x < y)
{
    y = 0;
    x = x + 1;
}
else
{
    x = y;
}
```



Control flow graph



# Program Code Coverage

Cog coverage: 38.75%

coverage.py v7.2.7, created at 2023-05-29 15:26 -0400

Module	statements	missing	excluded	branches	partial	coverage
cogapp/__init__.py	1	0	0	0	0	100.00%
cogapp/__main__.py	3	3	0	0	0	0.00%
cogapp/cogapp.py	500	224	1	210	30	49.01%
cogapp/makefiles.py	22	18	0	14	0	11.11%
cogapp/test_cogapp.py	845	591	2	24	1	29.57%
cogapp/test_makefiles.py	70	53	0	6	0	22.37%
cogapp/test_whiteutils.py	68	50	0	0	0	26.47%
cogapp/whiteutils.py	43	5	0	34	4	88.31%
<b>Total</b>	<b>1552</b>	<b>944</b>	<b>3</b>	<b>288</b>	<b>35</b>	<b>38.75%</b>

coverage.py v7.2.7, created at 2023-05-29 15:26 -0400

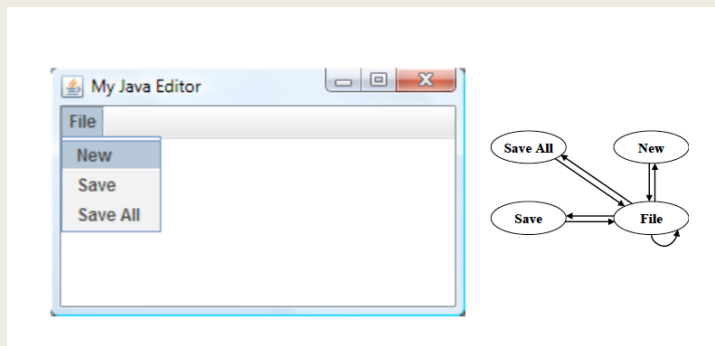
Example tools: jacoco, coverage.py, gcov

## Triangle.java

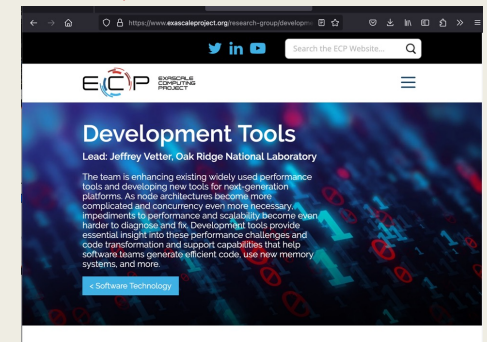
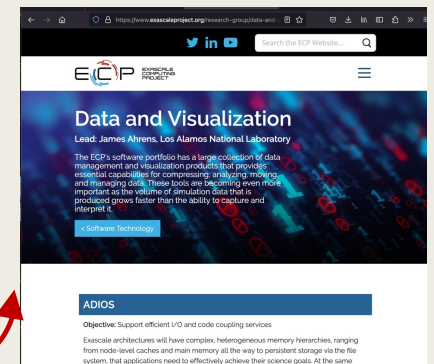
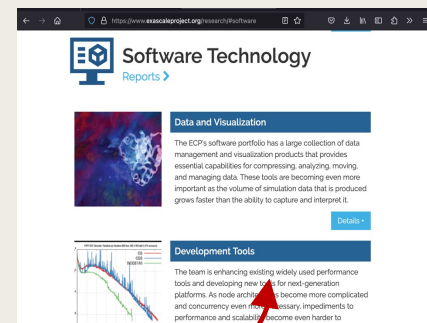
```
1. public class Triangle {
2.
3.     public enum TriangleType {
4.         INVALID, SCALENE, EQUILATERAL, ISOSCELES
5.     }
6.
7.     public static TriangleType classifyTriangle(int a, int b, int c) {
8.         if (a > b) {
9.             int tmp = a;
10.            a = b;
11.            b = tmp;
12.        }
13.
14.        if (a > c) {
15.            int tmp = c; // original: int tmp = a;
16.            a = c;
17.            c = tmp;
18.        }
19.
20.        if (b > c) {
21.            int tmp = b;
22.            b = c;
23.            c = tmp;
24.        }
25.
26.        if (a + b <= c) {
27.            return TriangleType.INVALID;
28.        } else if (a == b && b == c) {
29.            return TriangleType.EQUILATERAL;
30.        } else if (a == b || b == c) {
31.            return TriangleType.ISOSCELES;
32.        } else {
33.            return TriangleType.SCALENE;
34.        }
35.    }
36.
37. }
```

# Interface (graph) Coverage

Web



GUI



# Other Coverage

## Specification coverage

- Cover the system requirements

## Interaction coverage

- Measure interactions between components
  - Pairs, n-way coverage

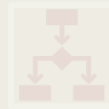
# Module I: Overview



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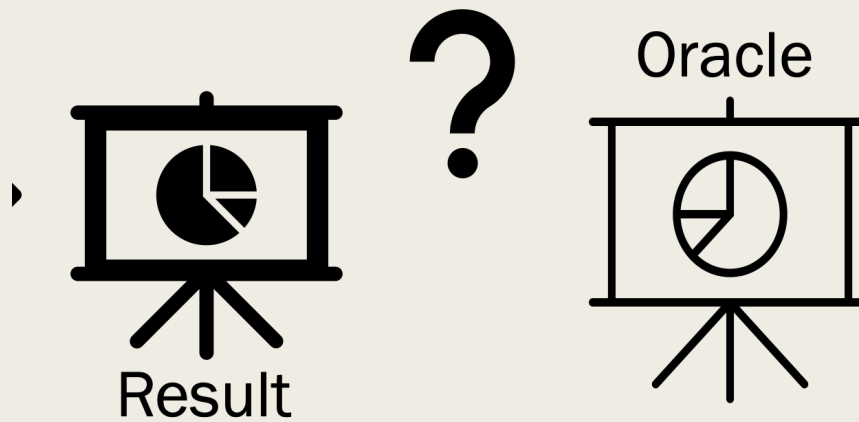


Coverage



Oracles

# What is the Correct Answer?



# Trivial Oracles

---

Program crashes

---

Core dump

---

Segmentation error

---

Overflow

---

Program hangs

# Trivial Oracles

- Good when we don't have a known result
- **Weakest oracle** since it only shows that the program fails/not that the result is incorrect
- Exact oracles are easy to compute in some programs

```
def classify_triangle(a, b, c):  
    # Sort the sides so that a <= b <= c  
    if a > b:  
        tmp = a  
        a = tmp #fault should be a=b  
        b = tmp  
  
    if a > c:  
        tmp = a  
        a = c  
        c = tmp  
  
    if b > c:  
        tmp = b  
        b = c  
        c = tmp  
  
    if a + b <= c:  
        return TriangleType.INVALID  
    elif a == b and b == c:  
        return TriangleType.EQUILATERAL  
    elif a == b or b == c:  
        return TriangleType.ISOSCELES  
    else:  
        return TriangleType.SCALENE
```

# Harder Oracles

**MEGA HIT** Assemble Reads with MEGAHIT v1.1.1  
Assemble metagenomic reads using the MEGAHIT assembler.

Run Configure Job Status Result

**Input Objects**

Read Library rhodo.art.q20.PE.reads

**Parameters (5 advanced parameters showing) hide advanced**

Parameter preset

--min-count

--k-min 1 ≤ ≤127

--k-max 1 ≤ ≤255

--k-step 1 ≤ ≤28

--k-list +

--min-contig-len 300 ≤ 2000

**Output Objects**

Output Assembly name





# Making Oracles Hard

- Results may **differ by small epsilons** (due to rounding)
- Expected result **may not be computable** without program
- May have **time series** results
- Takes a long time to manually compute each oracle (even when we can)
- Programs may be **stochastic** (or flaky)

# Examples

## Python docs

**Note:** The behavior of `round()` for floats can be surprising: for example, `round(2.675, 2)` gives 2.67 instead of the expected 2.68. This is not a bug: it's a result of the fact that most decimal fractions can't be represented exactly as a float. See [Floating Point Arithmetic: Issues and Limitations](#) for more information.

## Same growth values?

Expected:	0.35695124
Observed:	0.35695122

## Correct hits?

Descriptions	Graphic Summary	Alignments	Taxonomy					
Sequences producing significant alignments								
Download			Select columns					
Show			100					
<input checked="" type="checkbox"/> select all 100 sequences selected								
<a href="#">GenBank</a> <a href="#">Graphics</a> <a href="#">Distance tree of results</a> <a href="#">MSA Viewer</a>								
Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/> <a href="#">Saccharomyces pastorianus strain CBS 1483 chromosome ScXII</a>	<a href="#">Saccharomyc...</a>	1040	1040	100%	0.0	100.00%	1135585	<a href="#">CP048993.1</a>
<input checked="" type="checkbox"/> <a href="#">Saccharomyces cerevisiae strain CEN.PK113-7D chromosome XII</a>	<a href="#">Saccharomyc...</a>	1040	1040	100%	0.0	100.00%	1032974	<a href="#">CP046092.1</a>
<input checked="" type="checkbox"/> <a href="#">Saccharomyces cerevisiae strain ySR128 chromosome XII, complete sequence</a>	<a href="#">Saccharomyc...</a>	1040	1040	100%	0.0	100.00%	1076801	<a href="#">CP036478.1</a>
<input checked="" type="checkbox"/> <a href="#">Saccharomyces cerevisiae strain Y169 chromosome 12</a>	<a href="#">Saccharomyc...</a>	1040	1040	100%	0.0	100.00%	1061690	<a href="#">CP033481.1</a>

## Some Techniques



Differential testing



Metamorphic testing

# Some Techniques



*Run same tests using different programs  
that have the same functionality*

## Differential testing

# Some Techniques



## Metamorphic testing

*Define relations on sets of tests:*

*e.g. (subtraction)*

$A - B = C$

*Create  $A'$  (greater than  $A$ )*

*Then*

$A' - B = C'$  means  $C'$  is greater than  $C$

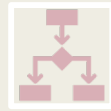
# Summary of Module I: Overview



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# Future Modules

Unit Testing and integrating with continuous integration

Testing configurations and combinatorial testing

Using differential and metamorphic testing

Regression testing - prioritization and test selection

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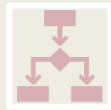
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