

# INTRODUCTION TO SOFTWARE TESTING FOR THE SCIENTIFIC COMMUNITY

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#### Module I: Overview













Motivation

What to test

Types of Testing

Models

Coverage

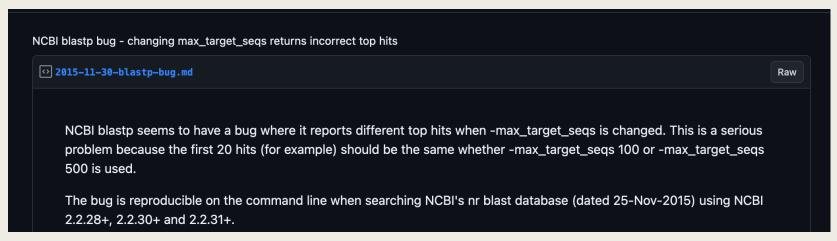
Oracles

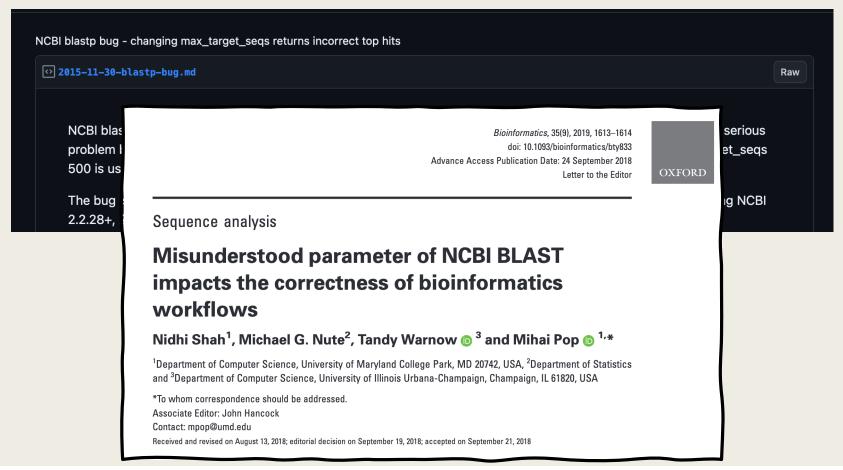
```
Error: NCBI C++ Exception:
T0 "/tmp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/objistrasnb.cpg
```

T0 "/tmp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/member.cpp", li

```
Error: NCBI C++ Exception:
T0 "/tmp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/objistrasnb.cp;
T0 "/tmp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/member.cpp", limp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/member.cpp", limp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/member.cpp", limp/BLAST/2.11.0/gompi-2020b/ncbi-blast-2.11.0+-src/c++/src/serial/member.cpp
```

```
ial/objistrasnb.cpp", line 499: Error: (CSerialException::e0verflow) byte 132: overf
ial/member.cpp", line 767: Error: (CSerialException::e0verflow) ncbi::CMemberInfoFur
```





Bioinformatics, 35(15), 2019, 2699–2700 doi: 10.1093/bioinformatics/bty1026 Advance Access Publication Date: 24 December 2018 Letter to the Editor



Sequence analysis

# Reply to the paper: Misunderstood parameters of NCBI BLAST impacts the correctness of bioinformatics workflows

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Associate Editor: John Hancock

Contact: madden@ncbi.nlm.nih.gov

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Dear Editor,

A recent letter by Shah et al. (2018) addressed the use of a command-line parameter in BLAST (Altschul et al., 1997; Camacho et al., 2009). BLAST is a very popular tool, so it is not surprising that this topic has provoked a great deal of interest. The authors have, however, conflated three different issues. One is a bug that will be fixed in the BLAST+ 2.8.1 release due out in December 2018, another is simply how BLAST works and the third might be viewed as a shortcoming of our implementation of composition-based statistics (CBS). Here, we address these issues and describe some new documentation about the BLAST process.

Shah et al. (2018) did not provide their own example in the letter, but later provided one at <a href="https://github.com/shahnidhi/BLAST\_maxtargetseq\_analysis">https://github.com/shahnidhi/BLAST\_maxtargetseq\_analysis</a>. At the NCBI, we examined the new example and it became clear that the demonstrated behavior was a bug, resulting from an overly aggressive optimization, introduced in 2012 for BLASTN and MegaBLAST (DNA–DNA alignments). This bug has been fixed in the BLAST+ 2.8.1 release, due out in December 2018. The aberrant behavior seems to occur only in alignments with an extremely large number of gaps, which is the case in the example provided by Shah and collaborators.

#### contributed articles



DOI:10.1145/3382037

An approach to reproducibility problems related to porting software across machines and compilers.

BY DONG H. AHN, ALLISON H. BAKER, MICHAEL BENTLEY, IAN BRIGGS, GANESH GOPALAKRISHNAN, DORIT M. HAMMERLING, IGNACIO LAGUNA, GREGORY L. LEE, DANIEL J. MILROY, AND MARIANA VERTENSTEIN

#### Keeping Science on Keel When Software Moves

the machine instructions that actually get executed. Unfortunately, such changes do affect the computed results to a significant (and often worrisome) extent. In a majority of cases, there are not easily definable a priori answers one can check against. A programmer ends up comparing the new answer against a trusted baseline previously established or checks for indirect confirmations such as whether physical properties such as energy are conserved. However, such non-systematic efforts might miss underlying issues, and the code may keep misbehaving until these are fixed.

In this article, we present real-world evidence to show that ignoring numerical result changes can lead to misleading scientific conclusions. We present techniques and tools that can help computational scientists understand and analyze compiler effects on their scientific code. These techniques are applicable across a wide range of examples to narrow down the root-causes to single files, functions within files, and even computational expressions that affect specific variables. The developer may then rewrite the code selectively and/or suppress the application of certain optimizations to regain more predictable behavior.

Going forward, the frequency of required ports of computational software will increase, given that performance gains can no longer be obtained by mere-

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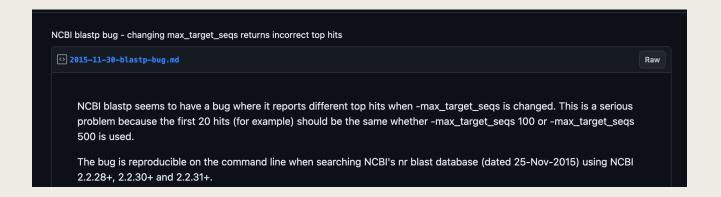
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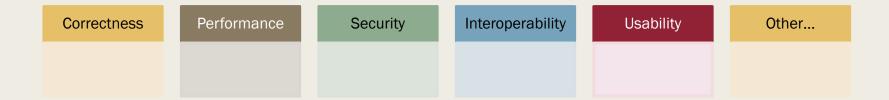


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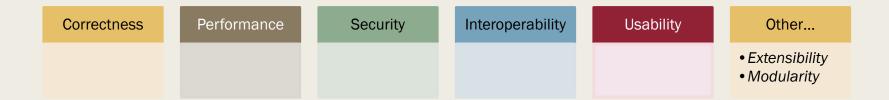
```
C:\lab>
f77 -0
data.exe
>
...ERROR
...why scientific programming does not compute
>
```

Merali, Zeeya. "Computational Science: ...Error." Nature 467, no. 7317 (Oct, 2010): 775–77

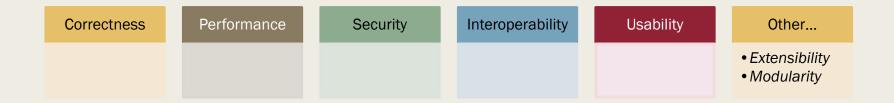
#### What Should We Test?



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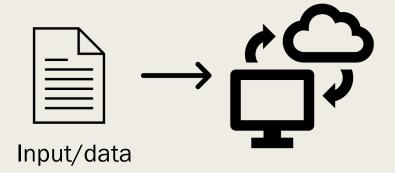
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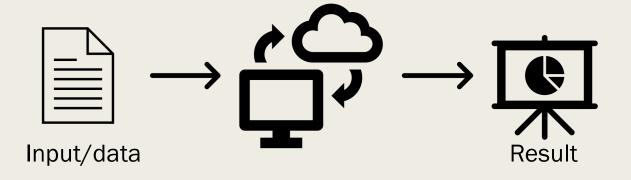


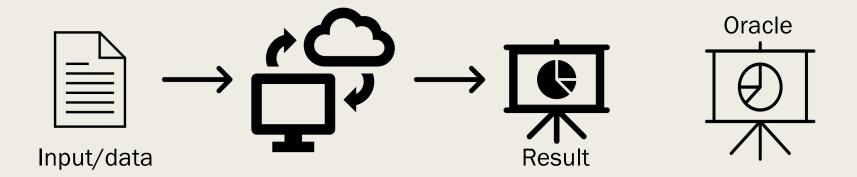
Our focus will be on correctness and interoperability

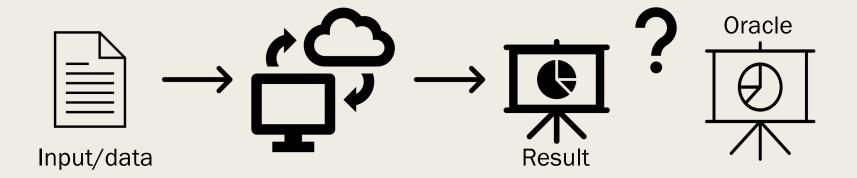


Input/data









#### Limitations

Testing can only show the presence of faults. It cannot determine their absence.

兴

Edsger W. Dijkstra

# Challenge

- To detect a program FAILURE we need to:
  - Reach a FAULT in the code
  - Infect the code (change to incorrect state) ERROR
  - Propagate the error out of program
  - Reveal (detect) the error (ORACLE)

RIPR model Ammann, Offutt (Introduction to Software Testing, 2016)

```
def classify_triangle(a, b, c):
   if a > b:
       tmp = a
                #fault should be a=b
       a = tmp
       p = 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
```

```
def classify_triangle(a, b, c):
   if a > b:
       tmp = a
                 #fault should be a=b
       a = tmp
       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
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       return TriangleType.ISOSCELES
   else:
       return TriangleType.SCALENE
```

- 1. Test Case 3, 4, 5 (scalene)
  - doesn't reach fault



```
def classify_triangle(a, b, c):
   if a > b:
       tmp = a
                 #fault should be a=b
       a = tmp
                    5,5,1
       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
```

- 1. Test Case 3, 4, 5 (scalene)
  - doesn't reach fault
- 2. Test Case 5, 1, 1 (invalid)
  - reaches fault and infects
  - reveals (returns isosceles)



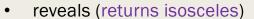


```
def classify_triangle(a, b, c):
   if a > b:
        tmp = a
                 #fault should be a=b
       a = tmp
       b = tmp
                     2.2.-1
    if a > c:
       tmp = a
       a = c
       c = tmp
   if b > c:
       tmp = b
       b = c
       c = tmp
   if a + b <= c:
        return TriangleType.INVALID
   elif a == b and b == c:
        return TriangleType.EQUILATERAL
   elif a == b or b == c:
       return TriangleType.ISOSCELES
   else:
       return TriangleType.SCALENE
```

- 1. Test Case 3, 4, 5 (scalene)
  - doesn't reach fault



- 2. Test Case 5, 1, 1 (invalid)
  - reaches fault and infects





- 3. Test Case 2, 1, -1 (invalid)
  - · reaches fault and infects
  - Doesn't propagate (2, 2,-1) is still INVALID



#### Software vs. Data



Scientific software is often data (or model driven)



Both software and data can lead to faults



We start by focusing on software

#### But I Have Unit Tests...

- These are an essential part of testing
- Focus is on individual modules
- Can be re-used each time system changes (regression testing)
- Can be packaged with software when released
- Other testing focuses on the system specifications and overall program behavior

#### Module I: Overview







What to test



Types of Testing



Models



Coverage



Oracles

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Any opinions, findings, and conclusions or recommendations expressed in this material are those of the author(s) and do not necessarily reflect the views of the DOE or NSF.