

A New Bioinformatics-Inspired and Binary Analysis: Coding Style/Motif Identification

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For that B guy

Summary

After drawing an analog from computer binary analysis to a similar analysis problem in Biology, a useful technique modeled after BLAST was developed. This technique has been implemented with the binBLAST tool suite, a collection of command line tools with an optional web interface. This tool suite allows consideration of binary executables on a per-instruction level that does not require executables to follow any coding or interface standards. Of particular interest, this technique seems sensitive to coding and interface standards and creates the potential for automatic code/style identification.

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Overview

- Concept
- binBLAST program suite
- Application: Version analysis
- Work-in-progress

Motivation System Defense

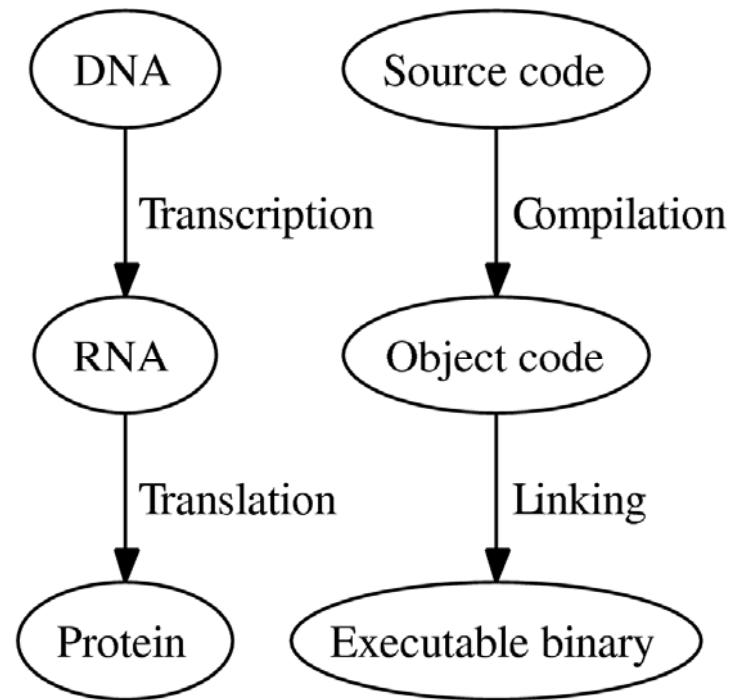
Current defense: policy, software, hardware

- New threats necessarily require patches
- Patches require verification
- Time available for verification is decreasing

The very tools we use to defend ourselves are contributing to the problem.

Bioinformatics Analogy

Functional analysis from code is not new...



Technique

Alignment Scoring Example

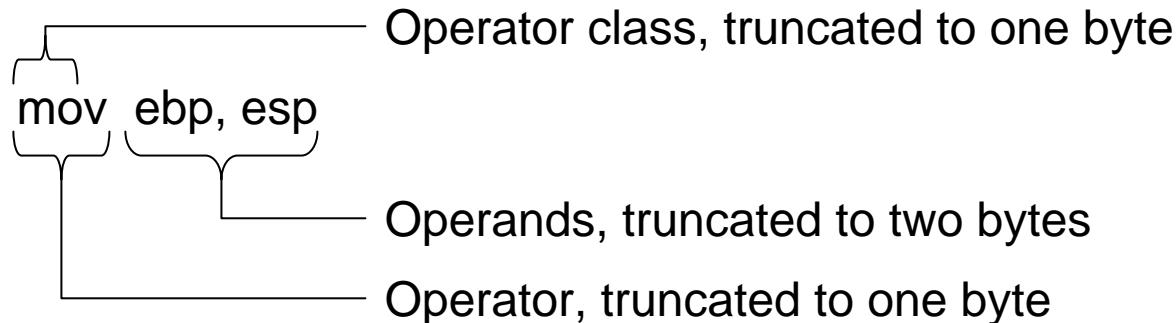
- Same concept as BLAST
- Scored string matching
 - Match adds one (+1)
 - Difference subtracts one (-1)
 - Actual scoring constants determined using Karlin-Altschul analysis

Align #1	T	H	E	S	E	
Align #2	T	H	E	S	I	S
Score	0 1 2 3 4					3 2 3

Technique

Scoring for Binaries

- Modified BLAST approach
- Karlin-Altschul analysis on over 553,901,654 instructions
- Instructions reduced to 4-byte format



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binBLAST Suite

- Major analysis tools
 - ❑ `mklib.py` – builds disassembly library/index
 - ❑ `bincompare` – comparison engine
 - ❑ `filterbincompare.py` – output filter to clean/to refactor
 - ❑ `matchoutput.py` – visualization tools
- Auxiliary tools
 - ❑ `binblast_html.cgi` – web-based interface
 - ❑ `objdumputil.py` – debugger interface

binBLAST Suite

mklab.py

```
$ ./mklab.py --help  
usage: mklab.py [options]
```

options:

- h, --help show this help message and exit
- i FILE, --iso=FILE Use an ISO file as the distribution source
- d DIR, --dir=DIR Use a directory tree as the distribution source
- n MY_LINUX_X.X, --name=MY_LINUX_X.X A unique identifier for this distribution
- b, --bin Produce binary output, name.dat and name.idx
- v, --verbose Produce verbose status information
- o, --no-db Do not produce the default database output, name.db

binBLAST suite

bincompare

```
$ ./bincompare --help
Usage: ./bincompare [options] fileA [offset [len]] fileB [offset
    [len]]
```

Options:

- h Print this help
- t=N: Set the threshold parameter to N, default is 10
- x1=N: Set scoring parameter x1 to N, default is 6
- x2=N: Set scoring parameter x2 to N, default is 5
- x3=N: Set scoring parameter x3 to N, default is 4
- x4=N: Set scoring parameter x4 to N, default is -4

Files:

name - The name of the comparison file, i.e. name.dat

offset - The start offset in quadwords
Relative to the start of the file
Defaults to 0

len - The length for comparison in quadwords
Defaults to the name's byte length / 4

The fileA length must be smaller (or the same size)
as fileB length.

binBLAST

filterbincompare.py

```
$ ./filterbincompare.py --help  
usage: filterbincompare.py [options]
```

options:

- h, --help show this help message and exit
- d, --no-dirout Do not correct dirout relative offsets to absolute offsets
- n, --nosort Don't sort results (reduces memory usage)
- t MINSCORE, --threshold=MINSCORE Threshold minimum score, if score is above Karlin-Altschul threshold
- l MINLEN, --minlen=MINLEN Minimum match length
- a, --filea Reduce results into matches covering only fileA

binBLAST

matchoutput.py

```
$ ./matchoutput.py --help  
usage: matchoutput.py [options]
```

options:

- h, --help show this help message and exit
- s, --similarity Create a similarity table (LaTeX format)
- d, --distance Create a distance table (PHYLIP format)
- m, --motifs Create motif groups in graph
- g, --graph Create a graph of the matches (graphviz dot format)
- a, --assembly Print aligned assembly (requires IDXFILEA STARTA,LENA IDXFILEB STARTB,LENB as arguments)

binBLAST Suite

Process Overview/Demo

- Add programs using `mklib.py`
- Perform comparison using `bincompare`
- Pipe output of `bincompare` through `filterbincompare.py`
- Pipe output of `filterbincompare.py` through `matchoutput.py`

Except for `mklib.py`, tools use `stdin/stdout` for data passing

binBLAST

Web Interface

The screenshot displays two Mozilla Firefox browser windows side-by-side, both showing results from a binBLAST query against the file `knoppix-finger-cygwin-file.out`.

Left Window (Coverage):

- Header: binBLAST - Display query - knoppix-finger-cygwin-file.out - Coverage - Mozilla Firefox
- Toolbar: File, Edit, View, Go, Bookmarks, Tools, Help.
- Address Bar: http://169.254.10.192/cgi-bin/binblast_html.cgi?act=
- Content:
 - binBLAST - Display query - knoppix-finger-cygwin-file.out - Coverage**
 - Add a file - Run a query - View results
 - /usr/bin/file.exe - /var/www/workdir/cygwin.tgz - /var/www/workdir/uploads
 - Match coverage: 0.963743
 - Sim File Archive Distro
 - 0.963743 /usr/bin/finger /var/www/workdir/knoppix.tgz /var/www/workdir/uploads
- Bottom: binBLAST
- Find Bar: Find: [] Find Next [] Find Previous [] Highlight [] Match case
- Status: Done

Right Window (Matches):

- Header: binBLAST - Display query - knoppix-finger-cygwin-file.out - Matches - Mozilla Firefox
- Toolbar: File, Edit, View, Go, Bookmarks, Tools, Help.
- Address Bar: http://169.254.10.192/cgi-bin/binblast_html.cgi?act=
- Content:
 - binBLAST - Display query - knoppix-finger-cygwin-file.out - Matches**
 - Add a file - Run a query - View results
 - FileA FileB
 - Score Len Name Offset Name Offset
 - 105 39 /usr/bin/file.exe 741 /usr/bin/finger 1133
 - 104 27 /usr/bin/file.exe 354 /usr/bin/finger 2867
 - 100 47 /usr/bin/file.exe 736 /usr/bin/finger 1127
 - 99 45 /usr/bin/file.exe 739 /usr/bin/finger 1127
 - 99 36 /usr/bin/file.exe 739 /usr/bin/finger 1116
 - 99 26 /usr/bin/file.exe 356 /usr/bin/finger 814
 - 98 41 /usr/bin/file.exe 724 /usr/bin/finger 1866
 - 96 48 /usr/bin/file.exe 736 /usr/bin/finger 1117
 - 95 28 /usr/bin/file.exe 746 /usr/bin/finger 1875
- Bottom: Done siteadvisor

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Application: Version Analysis

Sendmail

Program	Distribution	Date released	Likely compiler
postfix-2.2.8	SUSE (i386)	1/7/2006	gcc 3.4.5
chromium-0.9.12	SUSE (i386)	9/13/2005	gcc 3.4.4
sendmail-8.13.5	SUSE (i386)	9/16/2005	gcc 3.4.4
sendmail-8.13.4	Fedora (i386)	3/27/2005	gcc 3.3.6
sendmail-8.12.9	Mandrake (i586)	3/29/2003	gcc 3.2.2
sendmail-8.9.1	Redhat (i386)	7/7/1998	gcc 2.8.1

Application: Version Analysis

Raw Results

Score	Len	File A			File B		
		Name	Section	Off	Name	Section	Off
5095	899	sendmail-8.13.5	_init	0	sendmail-8.13.4	_init	0
4829	905	sendmail-8.12.9	_init	0	sendmail-8.13.4	_init	0
4797	899	sendmail-8.12.9	_init	0	sendmail-8.13.5	_init	0
4588	931	sendmail-8.13.5	_init	5	sendmail-8.13.4	(_init)	11
4488	907	sendmail-8.12.9	(_init)	32	sendmail-8.13.4	_init	5
...

Top results are associated with GCC-3 automatic code templates

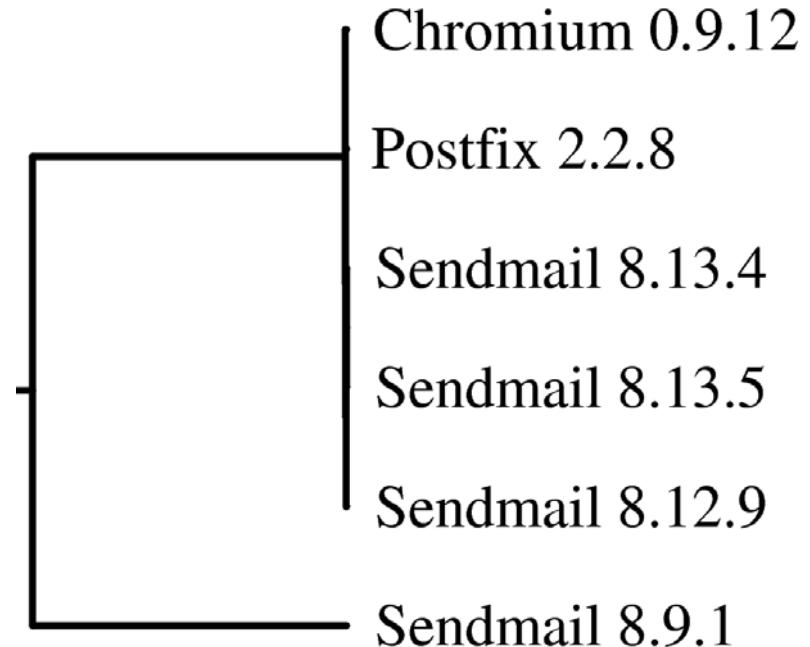
Code templates common in GCC-3

		sendmail-8.13.5-1.i386.rpm	sendmail-8.13.4-2.i386.rpm
Typical GCC-3 entry point	_init:	<pre>push ebp mov ebp,esp sub esp,0x8 call 9f08 (chroot@plt+0x4c) call 9f88 (chroot@plt+0xcc) call 991bc (sleep+0x2b82) leave ret</pre>	<pre>push ebp mov ebp,esp sub esp,0x8 call 9f08 (__memmove_chk@plt+0x48) call 9f88 (__memmove_chk@plt+0xc8) call 9a048 (sleep+0x2b96) leave ret</pre>
GCC-3 external symbol resolutions	SSL_CTX_set_tmp_ rsa_callback@plt-0x10:	<pre>push DWORD PTR [ebx+4] jmp DWORD PTR [ebx+8] add BYTE PTR [eax],al SSL_CTX_set_tmp_ rsa_callback@plt:</pre>	<pre>push DWORD PTR [ebx+4] jmp DWORD PTR [ebx+8] add BYTE PTR [eax],al SSL_CTX_set_tmp_ rsa_callback@plt:</pre>
Most common GCC-3 external call invocation	jmp DWORD PTR [ebx+12] push 0x0 jmp 8c3c (_init+0x18)	<pre>jmp DWORD PTR [ebx+12] push 0x0 jmp 8c20 (_init+0x18)</pre>	<pre>...</pre>

Application: Version Analysis

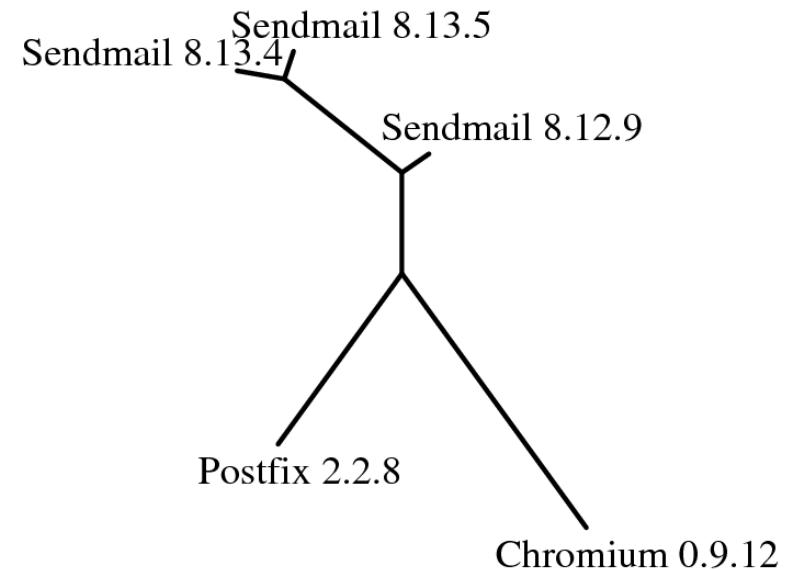
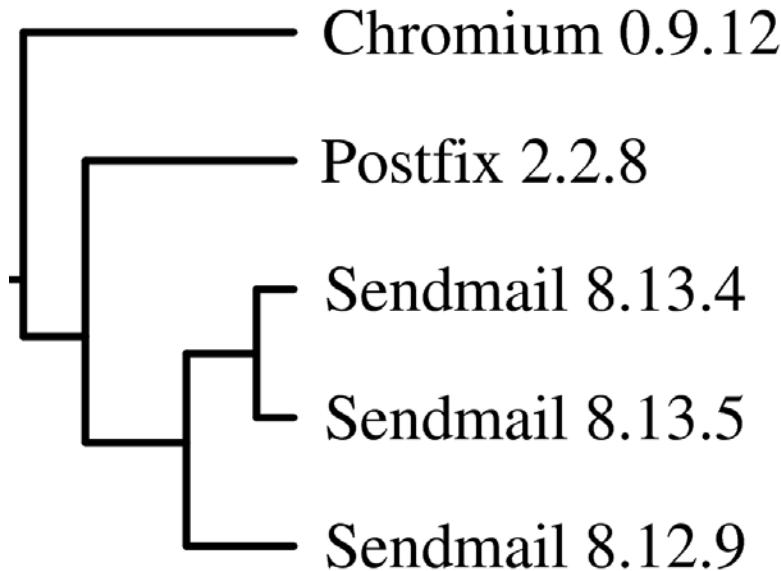
Phylogenetic Analysis

- PHYLIP Unweighted Pair Group Method with Arithmetic mean (UPGMA)
- Sendmail 8.9.1 distant because of use of GCC-2 compiler instead of GCC-3



Application: Version Analysis

Phylogenetic Analysis



Both the UPGMA (left) and Nearest-Neighbor (right) methods generate similar phylogenograms that reflect known relationships.

Review

- BLAST technique can be used on binaries
- binBLAST: an open-source analysis suite
- Sensitive to compiler code generation
- Detected relationships that mirror known relationships

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Work in Progress

- Improved web interface
- Automatic malware classification
- Automatic antivirus signature generation
- Motif identification/sub-alignment match removal
- Wiki-type collaborative RE environment

Suite available at

<http://www.offensivecomputing.net>

Selected References

- BLAST: S. Altschul et al., *Basic Local Alignment Search Tool*, 1990
- Malware genomics: E. Carrera et al., *Digital Genome Mapping - Advanced Binary Malware Analysis*, 2004
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- Alias analysis: S. Debray et al., *Alias Analysis of Executable Code*, 1998
- Structural analysis: H. Flake, *Structural Comparison of Executable Objects*, 2004
- PHYLIP: J. Felsenstein, *PHYLIP*, 2005
- `Packers': M. Oberhumer et al., *The Ultimate Packer for eXecutables*, 2004.