QBinDiff : A modular differ to enhance binary diffing and graph alignment

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Binary Diffing

Introduction

Goal is **comparing** two (or more) binaries to analyze their differences. It usually done using functions with a 1-to-1 mapping computation.

(which can be problematic when functions are merged or split)

Use-cases:

- → malware diffing (analysing updates, or common components between two variants)
- → patch analysis / 1-day analysis (understanding if patch is correct, or what is 1-day about)
- \rightarrow anti-plagiarism
- → statically linked libraries identification (static binary against some libs)
- → symbol porting (e.g: IDA annotations to a new version of a binary)
- → backdoor detection (legitimate binary against a modified version)
- → cross-architecture diffing (for symbol porting etc..)

Impact of optimization & obfuscation





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Motivation: Our use-case

Edge-cases

- > Two banks (area) in the same binary
- Specified subset of functions
- > Obfuscated binaries

Core Ideas:

- <u>Observation</u>: Multiple obfuscations alters function contents but not the overall program call graph (because harder to put in practice)
- <u>Need</u>: We want to diff/relates/compare obfuscated binaries **without** having to deobfuscate them first.
- <u>Wish</u>: We want to bring manually acquired knowledge for the diff e.g: anchors, specific features etc.
- ⇒ Can improve diff using **resilient** features, <u>analyst knowledge</u>

Diffing ain't Similarity



(from similarity scores, create an assignment...)

QBinDiff





QBindiff



Key Features:

- Disassembler agnostic (use exported representation)
- Standalone program
- Python API (to be used programmatically)
- Two APIs:
 - High-level for binary diffing
 - Low-level for arbitrary diffing (matrices as input)
- Designed to be **modular**!



Blog ∕

TL;DR: Anything that can be encoded as features and a graph can be diffed!

Diffing Landscape

✓ × ✓ ×	decompiler exporter precision recall			fast no API (not modular) now OSS disass agnos	itic	× × ×	modular memory & time power-user generic API
		Diaphora (🗑	Bindiff (*)	Radiff2	QBindiff (*)	Ghidriff (*)	
	Language	Python	Java	С	Python	Python	
ler	IDA	V	V	×	 ✓ 	×	
dme	Ghidra	×	V	×	v	 ✓ 	
asse	Binja	×	 ✓ 	×	 ✓ 	×	In-house
Dis	Radare2	×	×	v	×	×	<u>exporter</u>
	Exporter	SQLite	Binexport	n/c	Binexport Quokka	n/c	
	Scripting API	 	×	n/c	v	n/c	*•••••*
	Use decompiler	V	×	×	×	n/c	0





 f_1'





Similarity (weight matrix)



 f_3

Sample 1 (#M nodes)

 f_1

 f_4

Ν

 f_2'

. 4

.0

.2

 f_2

 f'_4

1

1

 f_5

. . .

٠.





Similarity (weight vector)

12





Goal: Arbitrate between function similarity and call-graph topology to be more resilient if one of them is altered (+ still use imported functions as anchors)

We said Modular ?

General Parameters

- > features: 27 functions features (some taken from diaphora / bindiff)
- > distance: cosine, euclidean, haussmann (custom one)
- > tradeoff: cursor on function similarity or call graph topology
- > sparsity ratio: percentage of candidate matches to keep in similarity matrix
- > epsilon: Relaxation parameter (helps converging faster)
- > iterations: max number of belief propagation steps
- ⇒ We provide "best" default values for each of them

Developers Modularity

- custom executable format (to load arbitrary file)
- can diff anything by providing low-level matrices
- can develop custom features

"e.g: compilation unit aware feature where functions from the same CU, shall be close to their sibling in terms of addresses or order in the binary"

\Rightarrow Obtaining a good diff might require fine tuning parameters.

QBinDiff Usage

	Com	mand line
\$ qbindiff pr:	imary.BinExport \	
sec	condary.BinExport \	
-f:	f bindiff -o result.Bi	nDiff \ # output in bindiff format
-a2	L CS_ARCH_ARM:CS_MODE_	THUMB $\ \#$ with .BinExport better to
-a2	CS_ARCH_ARM:CS_MODE_	THUMB # specify arch in capstone
File loading		
Initialization		
Matching		
Saving Results	s	
[1
Score	206.0000	
Similarity	108.0000	
Squares	98	1
Nb matches	108	1
		1
Node cover	100.000% / 100.000%	
Edge cover	100.000% / 100.000%	



from qbindiff import QBinDiff, Program
from qbindiff.features import CyclomaticComplexity # etc

```
p1 = Program("primary.BinExport")
p2 = Program("secondary.BinExport")
```

```
differ = QBinDiff(p1, p2)
differ.register_feature_extractor(CyclomaticComplexity, 1.0)
# register your features
```

differ.process()
mapping = differ.compute_matching()
do anything you want if the result

⇒ Output is either a CSV or a .BinDiff file (to open it with bindiff)



Diffing Evaluation

How can we compare the functions pair that should be matched (*Ground-Truth*) and the functions that are matched by a differ on stripped binaries ?

True Positives

good match correctly identified

False Positives wrong match

identified

True Negative Not a match considered as-is

False Negative Good match not identified



		BinDiff	Diaphora3 Ql	BinDiff (BinExport) QBinDiff (Quokka)
zlib	libz.so.1.2.11	0.85	0.65	0.82	0.88
	libssl.so.3	0.81	0.64	0.83	0.86
openssl	openssl	0.95	0.68	0.92	0.98
	libcrypto.so.3	0.76	0.78	0.67	0.82
	nping	0.59	0.52	0.73	0.77
nmap	ncat	0.73	0.58	0.86	0.92
	nmap	0.8	0.8	0.73	0.82
clamav	libclamav	0.58	0.46	0.76	0.81
curl		0.65	0.56	0.83	0.88
unrar		0.68	0.62	0.81	0.87
Averaged		0.74	0.63	0.80	0.86

Standard differ f1-score comparison in a cross-optimizer/optimization setting (differ robustness against compilation variation)



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nmap	nping ncat nmap	$0.59 \\ 0.73 \\ 0.8$	$0.52 \\ 0.58 \\ 0.8$	0.73 0.86 0.73	0.77 0.92 0.82	Quokka is than Bing	bette Expor
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Glimpse of Obfuscation (results)





QBinDiff feature impact : stable, full and unstable features (Control-Flow Graph Flattening f1-score evolution)

What about diffing other things ?



Smart Contracts

⇒ Diffing two closed-source smart contracts using pyevmasm for disassembly, EtherSolve for CFG and call graph reconstruction.

 \Rightarrow Low-level API diffing with Qbindiff !



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 \Rightarrow Low-Level API enables diffing anything, inputs are similarity matrix and relationship graphs.

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Bioinformatics: Protein-protein interactions (node proteins, edge interactions between them)

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Bioinformatics: Protein-protein interactions (node proteins, edge interactions between them)

Matching fingerprints using Minutiae (Data from <u>NIST dataset 302</u>)

⇒ Generic optimization algorithms (binary diffing just a reification of the problem)

Conclusion



Binary Diffing

On common cases standard differs do the job great ! For more specific use-cases Qbindiff is more adapted !

General Diffing

QbinDiff can diff anything (as long as you can compute similarity between objects and determine relationships between objects)

Notes:

- \$ pip install qbindiff
- Platform for experiments
- Actively maintained & answer questions

Huge Thanks:

- current contributors
- past contributors (Alexis Challande, Elie Mengin)

To contribute..



https://github.com/quarkslab/qbindiff/

Thank you

Contact information:

Quarkslab

