

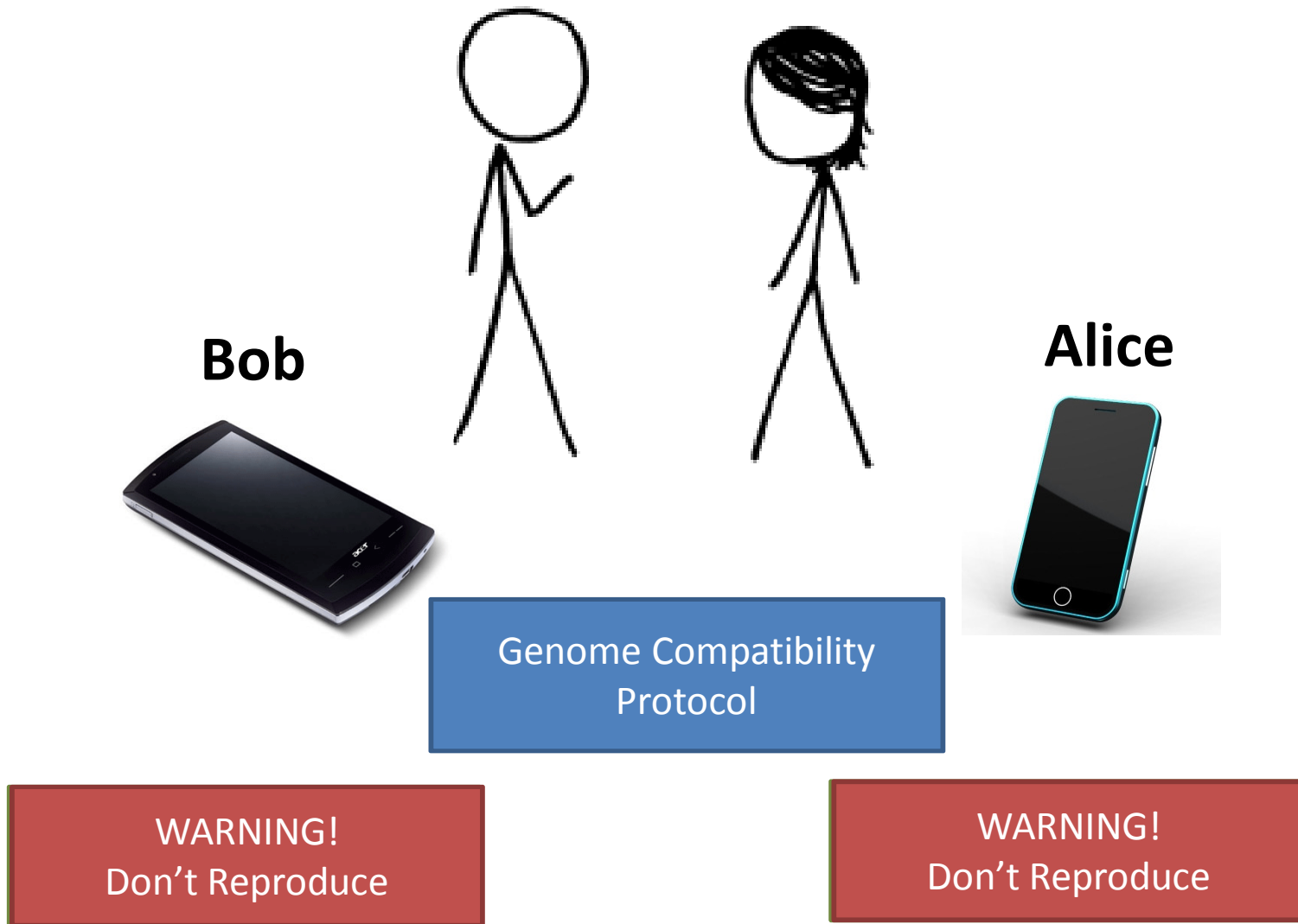


Computing Cooperatively with People You Don't Trust

University of Richmond
30 January 2012

David Evans
University of Virginia
<http://www.cs.virginia.edu/evans>
<http://MightBeEvil.com>

“Genetic Dating”





TheScientist [News](#) [Current Issue](#) [Archive](#) [Sun](#)

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By Kerry Grens

Forget mistletoe - what about DNA?

A new dating service matches singles using major histocompatibility complex genes



ScientificMatch.com
"The Science of Love"

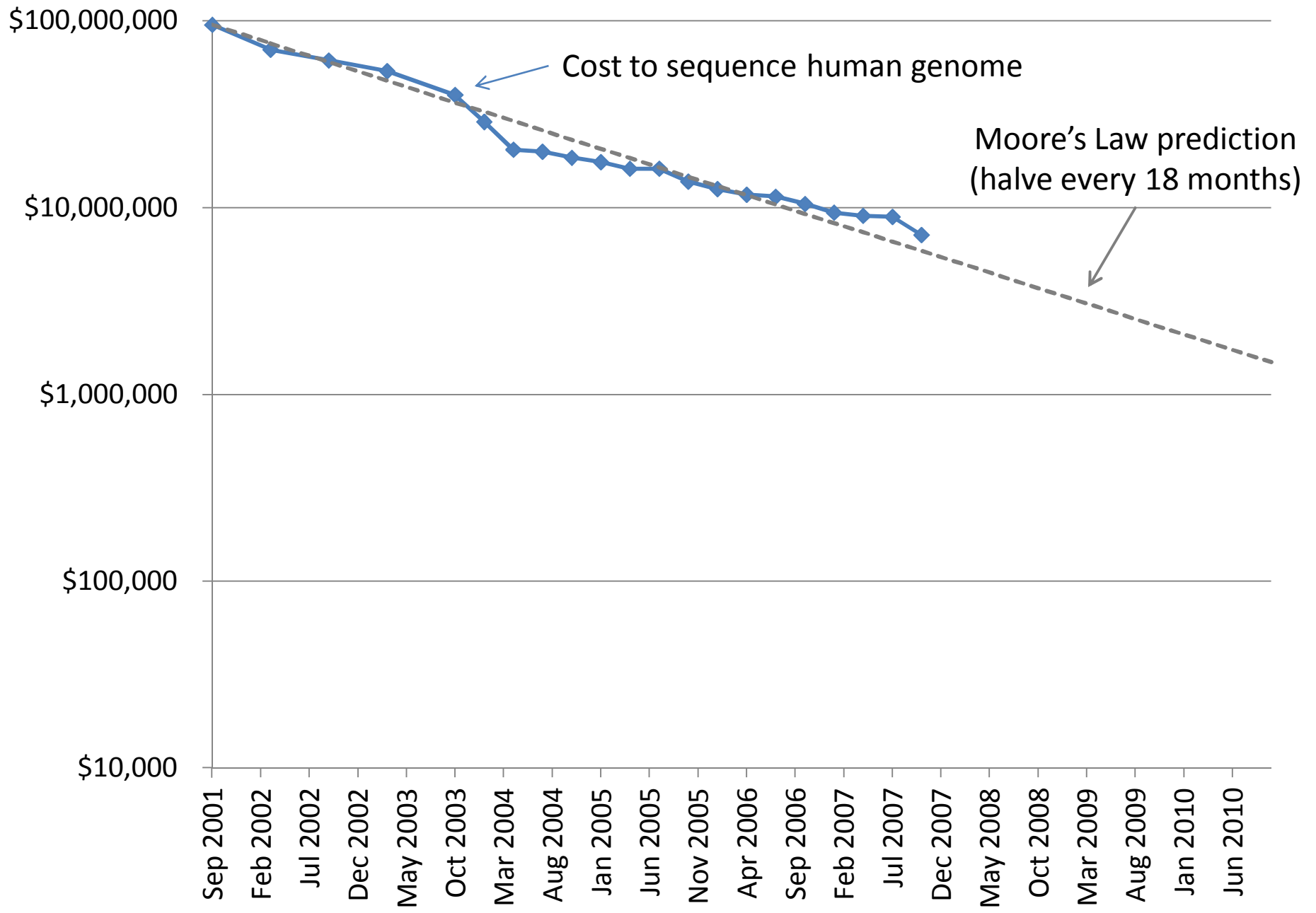
Genome Sequencing

1990: Human Genome Project starts, estimate \$3B to sequence one genome (\$0.50/base)

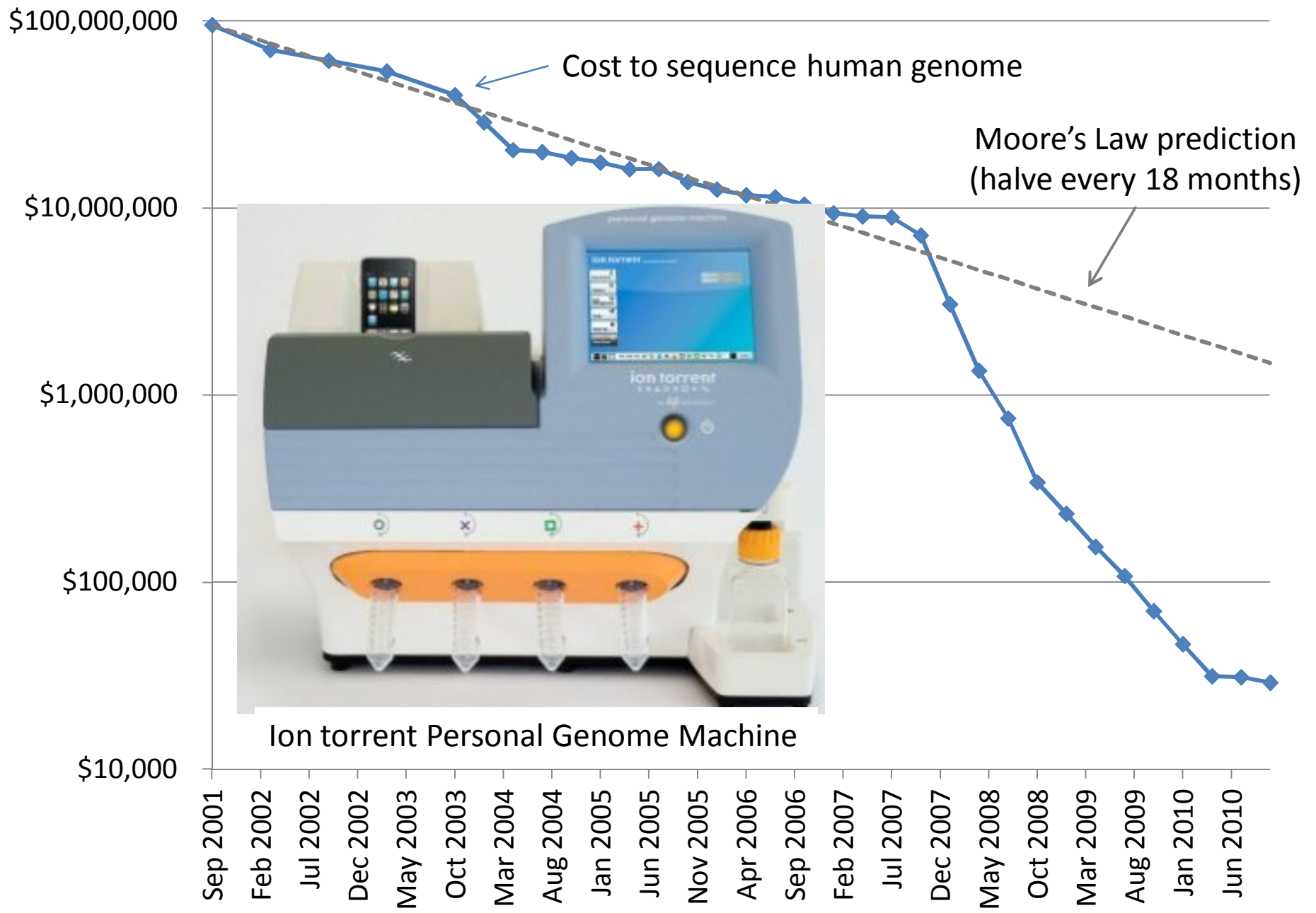
2000: Human Genome Project declared complete, cost ~\$300M



Whitehead Institute, MIT



Data from National Human Genome Research Institute: <http://www.genome.gov/sequencingcosts>

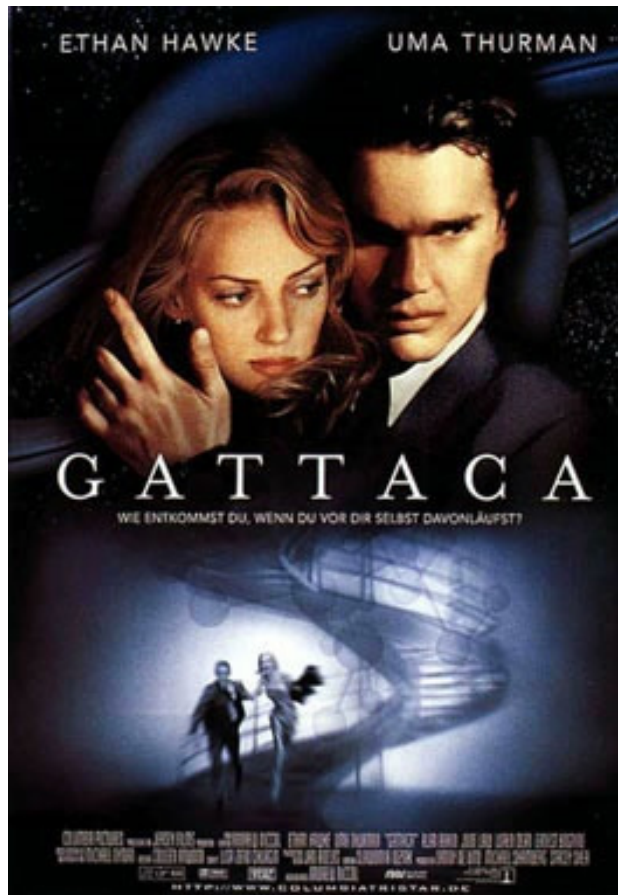


Data from National Human Genome Research Institute: <http://www.genome.gov/sequencingcosts>

Year	reference	Technology	Sample	Average Reported Coverage depth (fold)	Reported sequencing consumables cost	Estimated cost per 40-fold coverage
	S4	Sanger (ABI)	JCV	7	\$10,000,000	\$57,000,000
	S5	Roche(454)	JDW	7	\$1,000,000	\$5,700,000
	S6	Illumina	NA18507	30	\$250,000	\$330,000
	S7	Helicos	SRQ	28	\$48,000	\$69,000
2009	this work	this work	NA07022	87	\$8,005	\$3,700
2009	this work	this work	NA19240	63	\$3,451	\$2,200
2009	this work	this work	NA20431	45	\$1,726	\$1,500

[Human Genome Sequencing Using Unchained Base Reads on Self-Assembling DNA Nanoarrays.](#) Radoje Drmanac, Andrew B. Sparks, Matthew J. Callow, Aaron L. Halpern, Norman L. Burns, Bahram G. Kermani, Paolo Carnevali, Igor Nazarenko, Geoffrey B. Nilsen, George Yeung, Fredrik Dahl, Andres Fernandez, Bryan Staker, Krishna P. Pant, Jonathan Baccash, Adam P. Borcharding, Anushka Brownley, Ryan Cedeno, Linsu Chen, Dan Chernikoff, Alex Cheung, Razvan Chirita, Benjamin Curson, Jessica C. Ebert, Coleen R. Hacker, Robert Hartlage, Brian Hauser, Steve Huang, Yuan Jiang, Vitali Karpinchyk, Mark Koenig, Calvin Kong, Tom Landers, Catherine Le, Jia Liu, Celeste E. McBride, Matt Morenzoni, Robert E. Morey, Karl Mutch, Helena Perazich, Kimberly Perry, Brock A. Peters, Joe Peterson, Charit L. Pethiyagoda, Kaliprasad Pothuraju, Claudia Richter, Abraham M. Rosenbaum, Shaunak Roy, Jay Shafto, Uladzislau Sharanovich, Karen W. Shannon, Conrad G. Sheppy, Michel Sun, Joseph V. Thakuria, Anne Tran, Dylan Vu, Alexander Wait Zaranek, Xiaodi Wu, Snezana Drmanac, Arnold R. Oliphant, William C. Banyai, Bruce Martin, Dennis G. Ballinger, George M. Church, Clifford A. Reid. **Science, January 2010.**

Dystopia

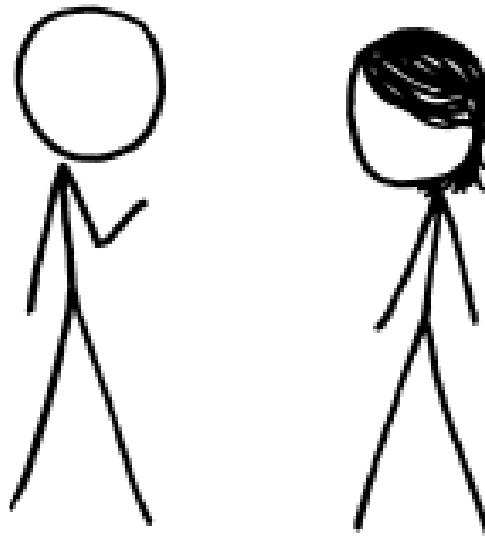


Personalized Medicine

Secure Two-Party Computation

Bob's Genome: ACTG...
Markers (~1000): [0,1, ..., 0]

Bob



Alice's Genome: ACTG...
Markers (~1000): [0, 0, ..., 1]

Alice



$$x = f(g_A, g_B)$$

Can Alice and Bob compute a function of their private data, without exposing anything about their data besides the result?

Secure Function Evaluation

Alice (circuit generator)

Picks $a \in \{0, 1\}^s$

Bob (circuit evaluator)

Picks $b \in \{0, 1\}^t$

Agree on

$f(a, b) \rightarrow x$

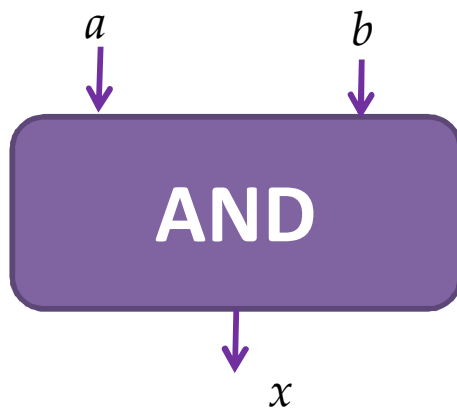
Garbled Circuit Protocol

Outputs $x = f(a, b)$
without revealing a
to Bob or b to Alice.

Andrew Yao, 1982/1986

Regular Logic

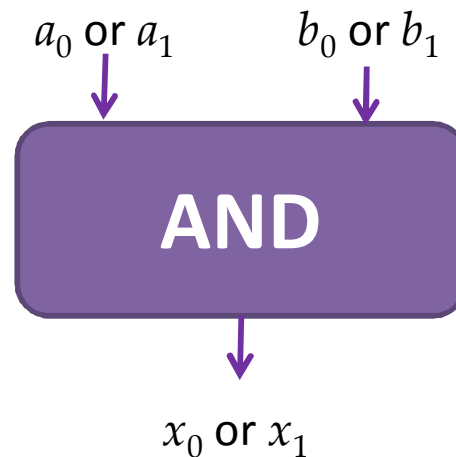
Inputs		Output
<i>a</i>	<i>b</i>	<i>x</i>
0	0	0
0	1	0
1	0	0
1	1	1



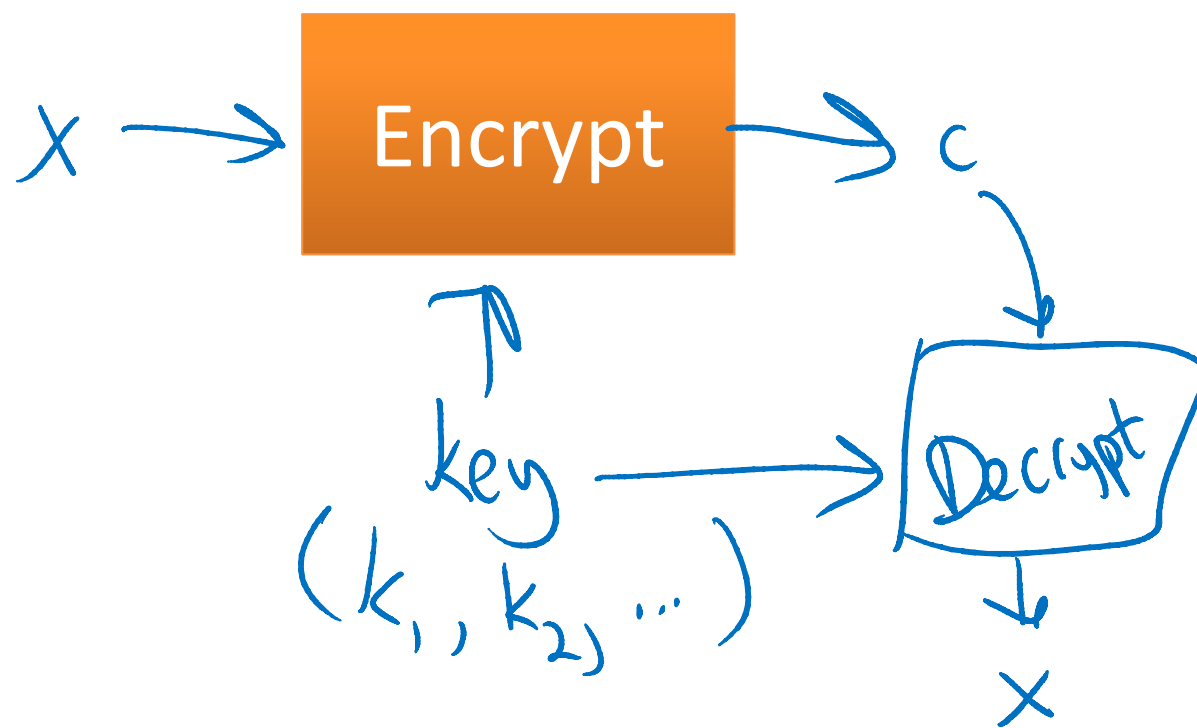
Computing with Meaningless Values?

Inputs		Output
a	b	x
a_0	b_0	x_0
a_0	b_1	x_0
a_1	b_0	x_0
a_1	b_1	x_1

a_i, b_i, x_i are **random** values, chosen by the **circuit generator** but **meaningless** to the **circuit evaluator**.

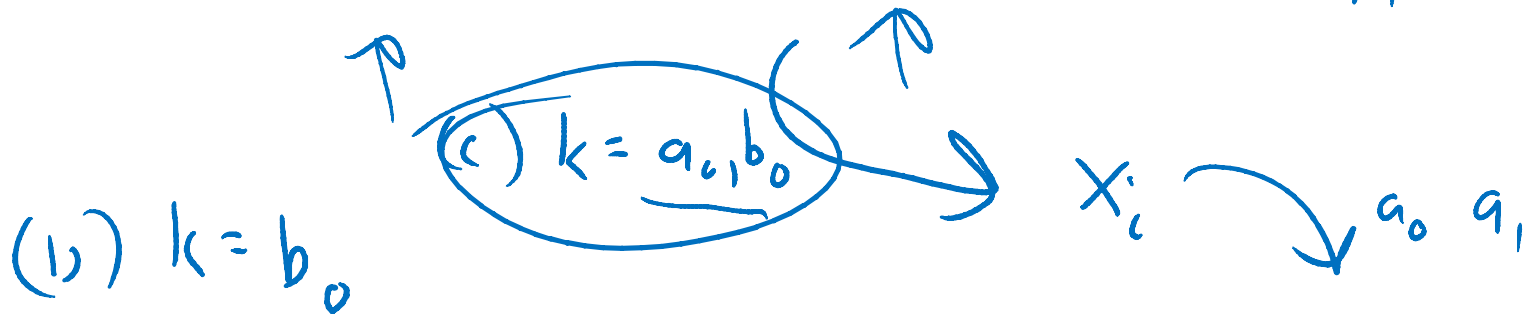


Encryption



Logic with Privacy

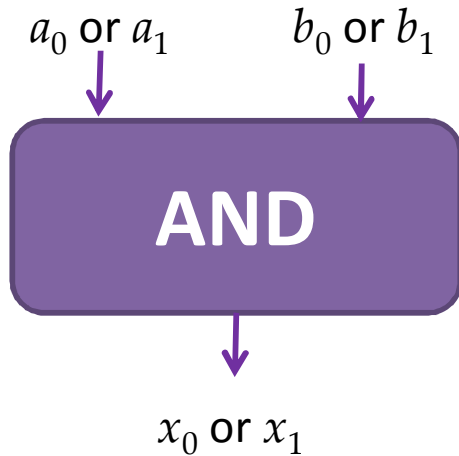
Inputs		Output
a	b	x
a_0	b_0	$Enc_{a_0, b_0}(x_0)$
a_0	b_1	$Enc_{a_0, b_1}(x_0)$
a_1	b_0	$Enc_{a_1, b_0}(x_0)$
a_1	b_1	$Enc_{a_1, b_1}(x_1)$



Computing with Garbled Tables

Inputs		Output
a	b	x
a_0	b_0	$Enc_{a_0,b_0}(x_0)$
a_0	b_1	$Enc_{a_0,b_1}(x_0)$
a_1	b_0	$Enc_{a_1,b_0}(x_0)$
a_1	b_1	$Enc_{a_1,b_1}(x_1)$

Bob can only decrypt
one of these!



Garbled And Gate
$Enc_{a_0,b_1}(x_0)$
$Enc_{a_1,b_1}(x_1)$
$Enc_{a_1,b_0}(x_0)$
$Enc_{a_0,b_0}(x_0)$



Garbled Circuit Protocol

Alice (circuit generator)

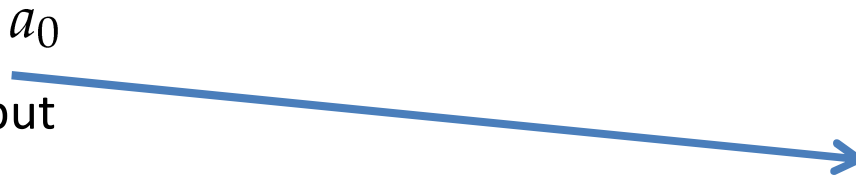
Creates random keys: $a_0, a_1, b_0, b_1, x_0, x_1$

Bob (circuit evaluator)

Garbled Gate
$Enc_{a_0, b_1}(x_0)$
$Enc_{a_1, b_1}(x_1)$
$Enc_{a_1, b_0}(x_0)$
$Enc_{a_0, b_0}(x_0)$



Sends a_i to Bob based on her input value



How does the Bob learn his own input wires?

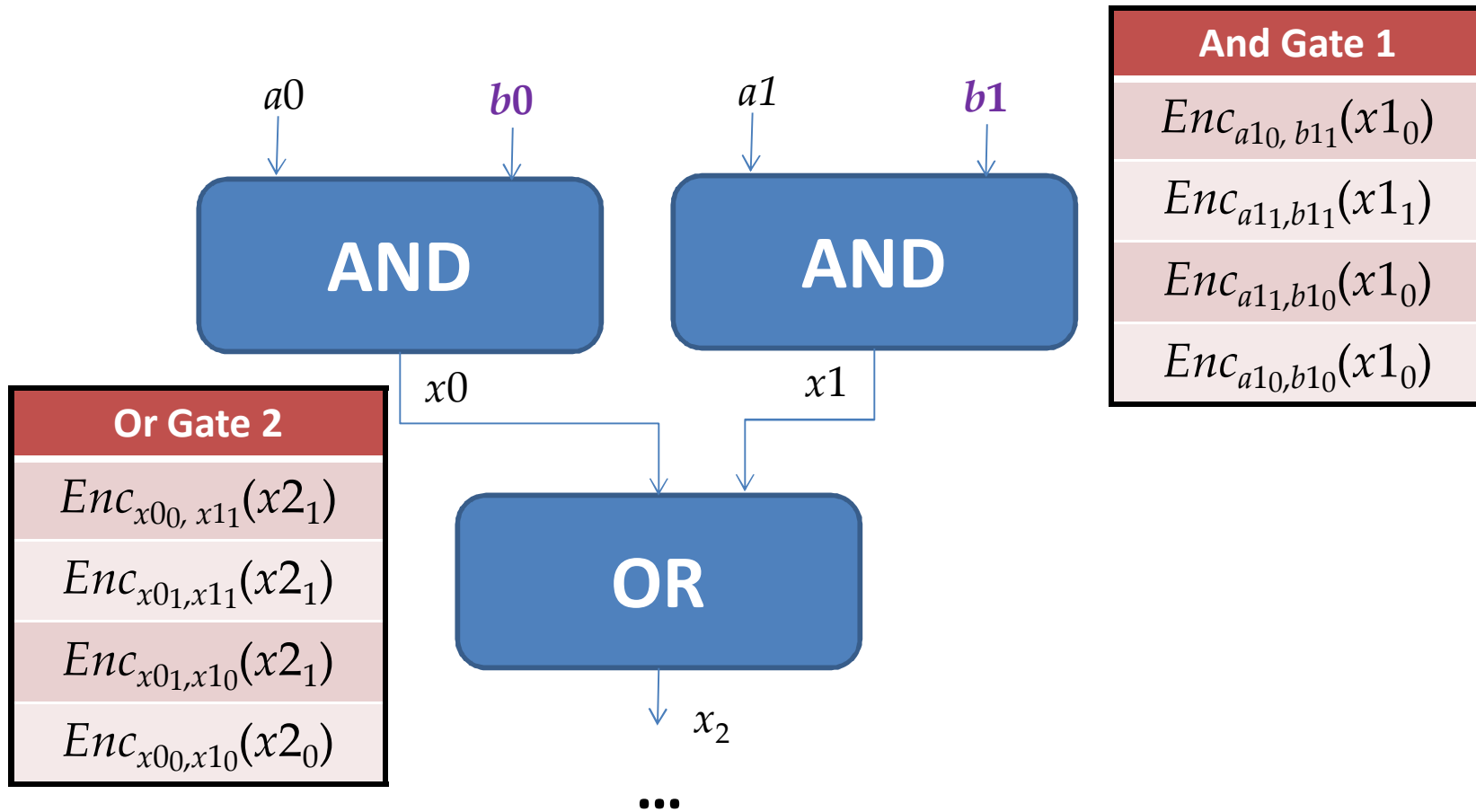
Primitive: Oblivious Transfer



Oblivious: Alice doesn't learn which secret Bob obtains
Transfer: Bob learns one of Alice's secrets

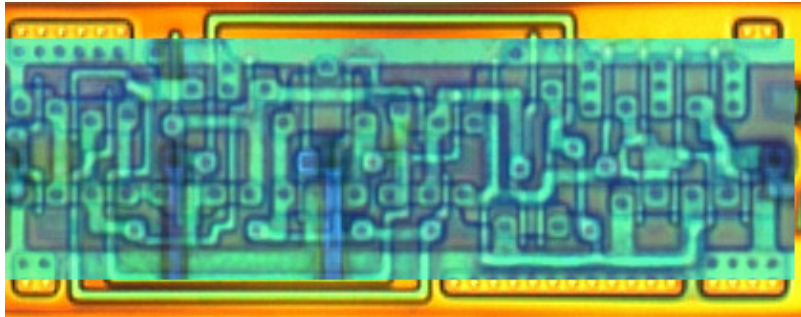
Rabin, 1981; Even, Goldreich, and Lempel, 1985; many subsequent papers

Chaining Garbled Circuits



We can do *any* computation privately this way!

Building Computing Systems



$Enc_{x_{00}, x_{11}}(x_{2_1})$
$Enc_{x_{01}, x_{11}}(x_{2_1})$
$Enc_{x_{01}, x_{10}}(x_{2_1})$
$Enc_{x_{00}, x_{10}}(x_{2_0})$

Digital Electronic Circuits	Garbled Circuits
Operate on known data	Operate on encrypted wire labels
One-bit logical operation requires moving a few electrons a few nanometers (hundreds of Billions per second)	One-bit logical operation requires performing (up to) 4 encryption operations: very slow execution
Reuse is great!	Reuse is not allowed for privacy: huge circuits needed

Fairplay

Alice

Bob

```
program Millionaires {  
  type int = Int<4>; // 4-bit integer  
  type AliceInput = int;  
  type BobInput = int;  
  type AliceOutput = Boolean;  
  type BobOutput = Boolean;  
  type Output = struct {  
    AliceOutput alice, BobOutput bob};  
  type Input = struct {  
    AliceInput alice, BobInput bob};  
  
  function Output out(Input inp) {  
    out.alice = inp.alice > inp.bob;  
    out.bob = inp.bob > inp.alice;  
  }  
}
```

SFDL Program

SFDL
Compiler

SFDL
Compiler

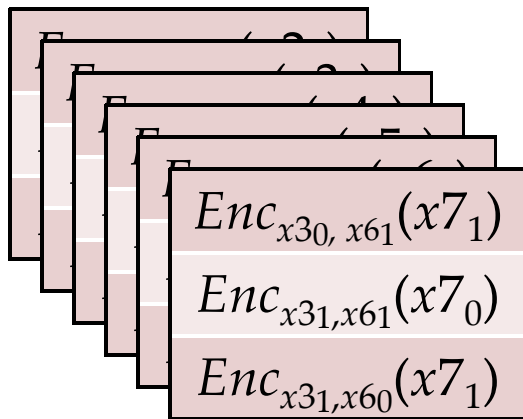
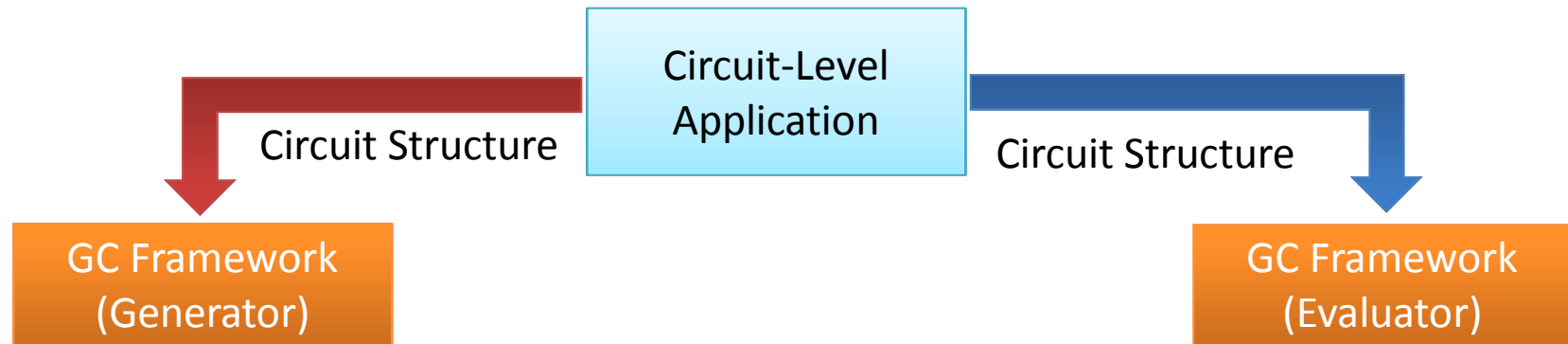
Circuit
(SHDL)

Garbled Tables
Generator

Garbled Tables
Evaluator

Dahlia Malkhi, Noam Nisan,
Benny Pinkas and Yaron Sella
[USENIX Sec 2004]

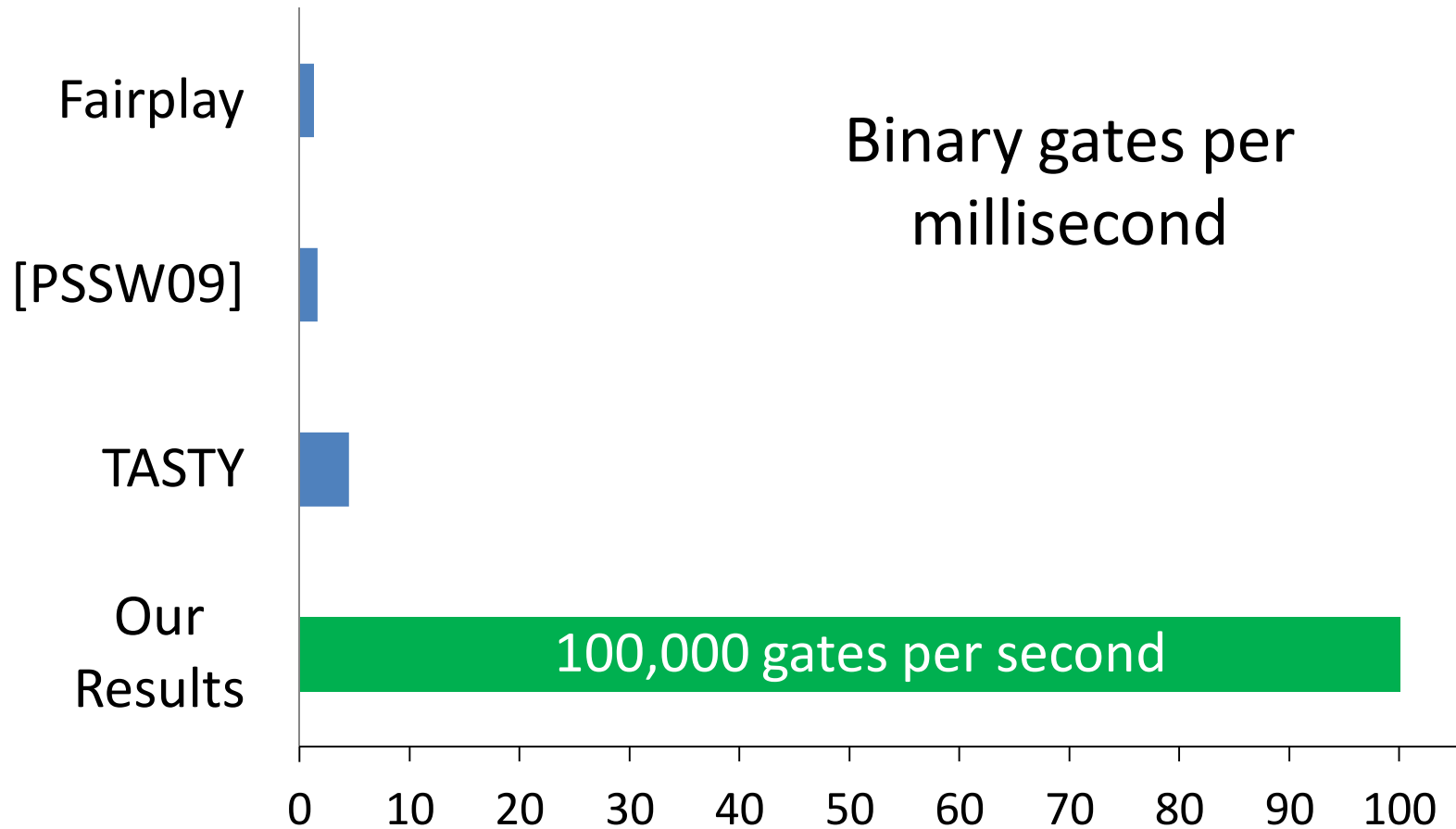
Faster Garbled Circuits



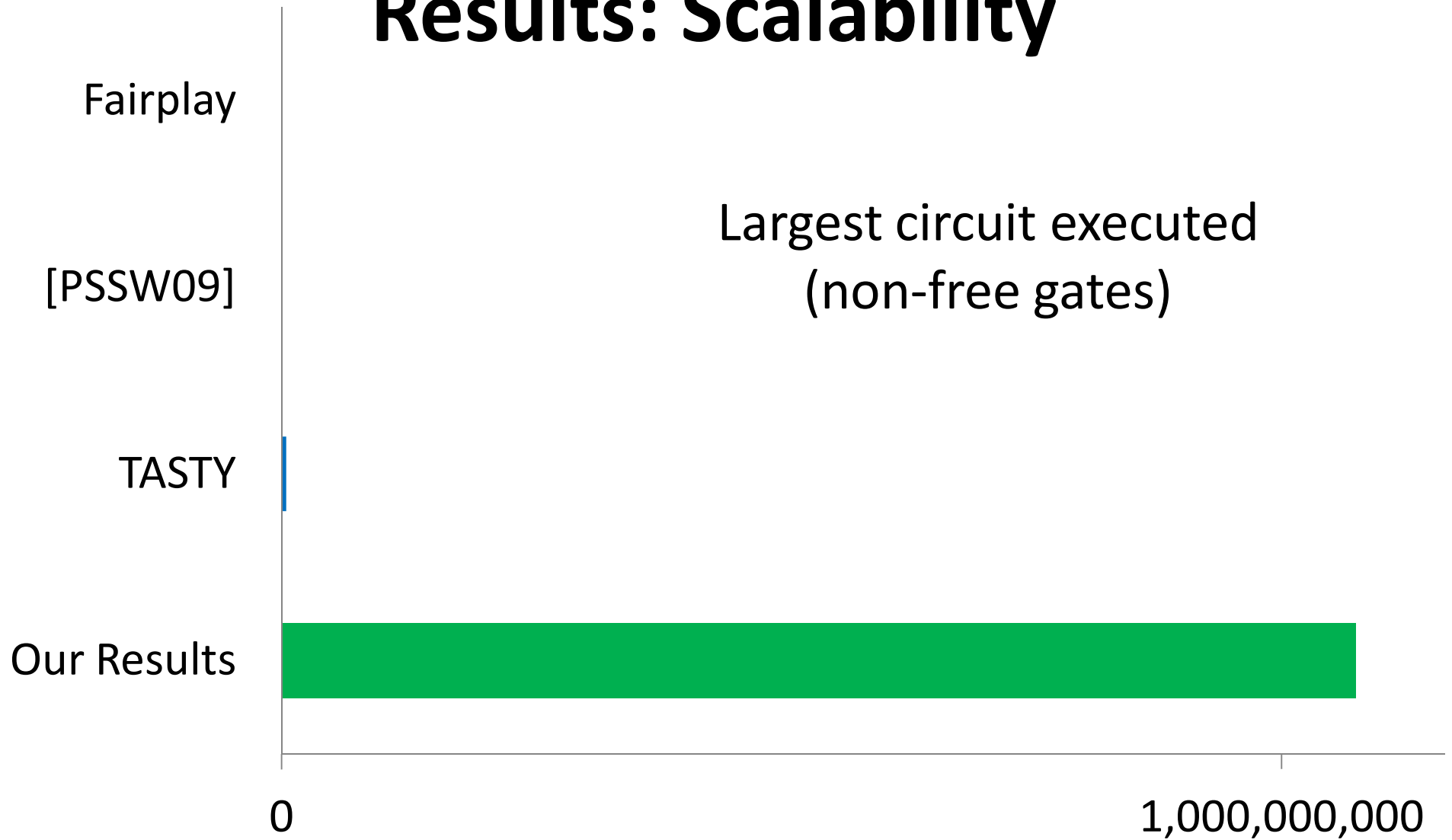
$x2_1$
 $x3_1$
 $x4_1$
 $x5_1$
 $x6_0$
 $x7_1$

Gates can be evaluated as they are generated: **pipelining**
Gates can be evaluated in any topological sort order: **parallelizing**
Garbled evaluation can be **combined with normal execution**

Results: Performance



Results: Scalability





Privacy-Preserving
Biometric Matching

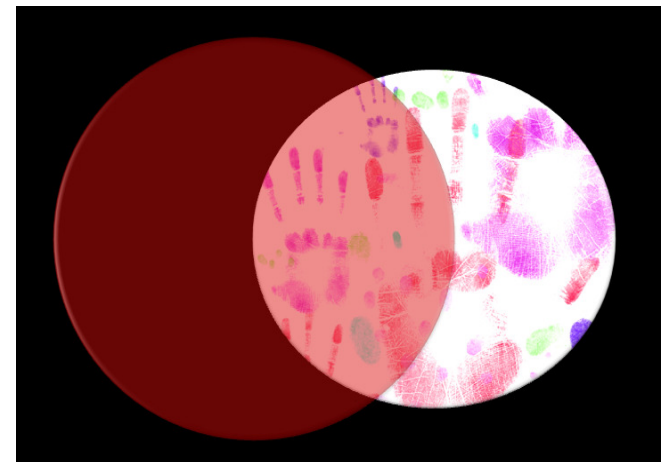


Private AES
Encryption

Private
Personal
Genomics



Applications



Private Set Intersection

Heterozygous Recessive Risk

Alice

		A	a
Bob	A	AA	Aa ← carrier
	a	aA	aa ← cystic fibrosis

Alice's Heterozygous Recessive genes: { 5283423, 1425236, 839523, ... }

Bob's Heterozygous Recessive genes: { 5823527, 839523, 169325, ... }

Goal: find the intersection of A and B

Bit Vector Intersection

Alice's Recessive genes:
{ 5283423, 1425236, 839523, ... }

Bob's Recessive genes:
{ 5823527, 839523, 169325, ... }

[PAH, PKU, **CF**, ...]

[0, 0, **1**, 0, 0, 0, 1, 0, 1, 1, 0]

[0, 0, **1**, 0, 0, 0, 0, 0, 0, 1, 0, 0]

...

AND

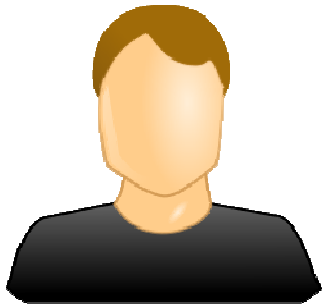
AND

AND

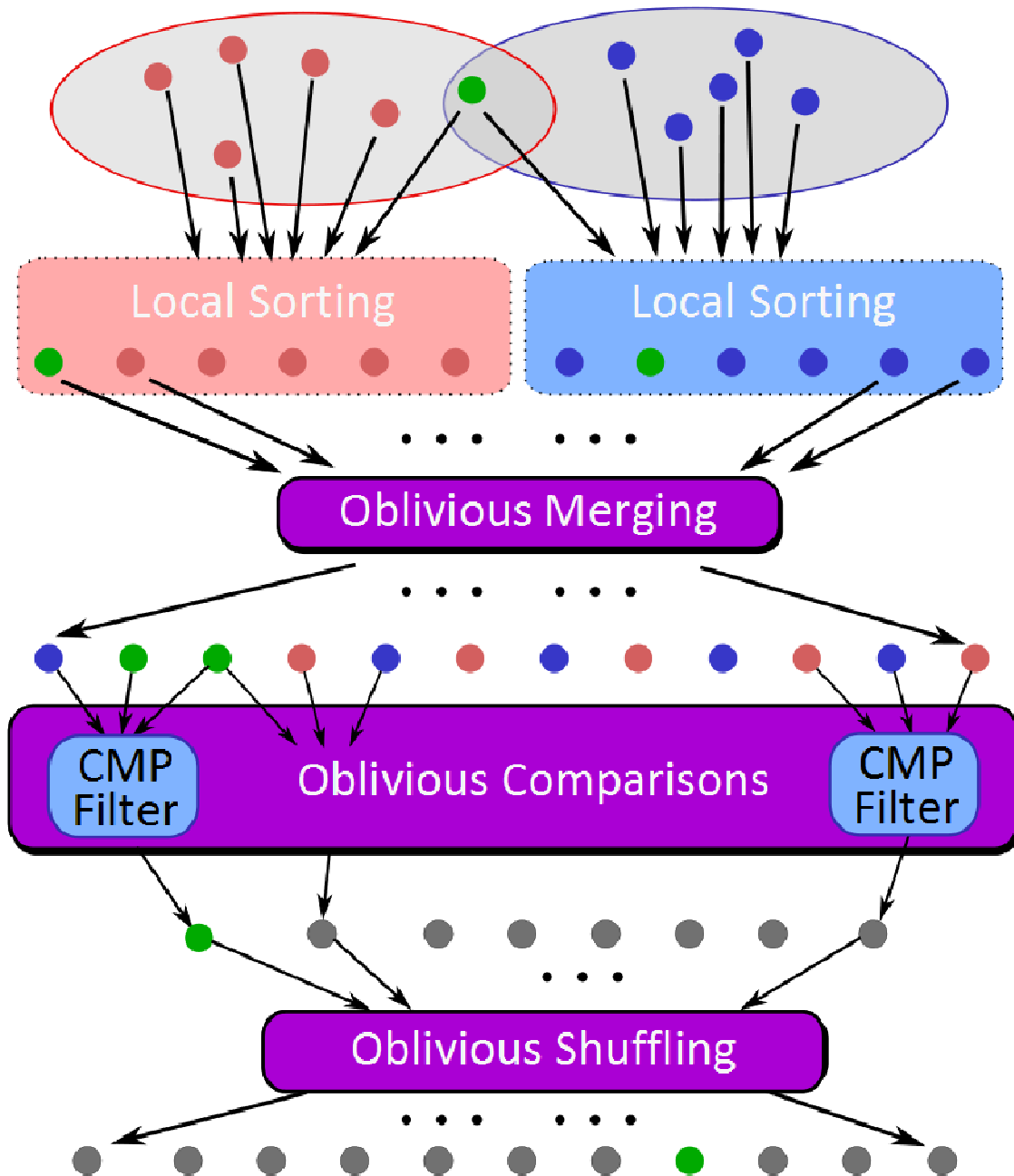
...

Bitwise AND

Common Contacts



Sort-Compare-Shuffle

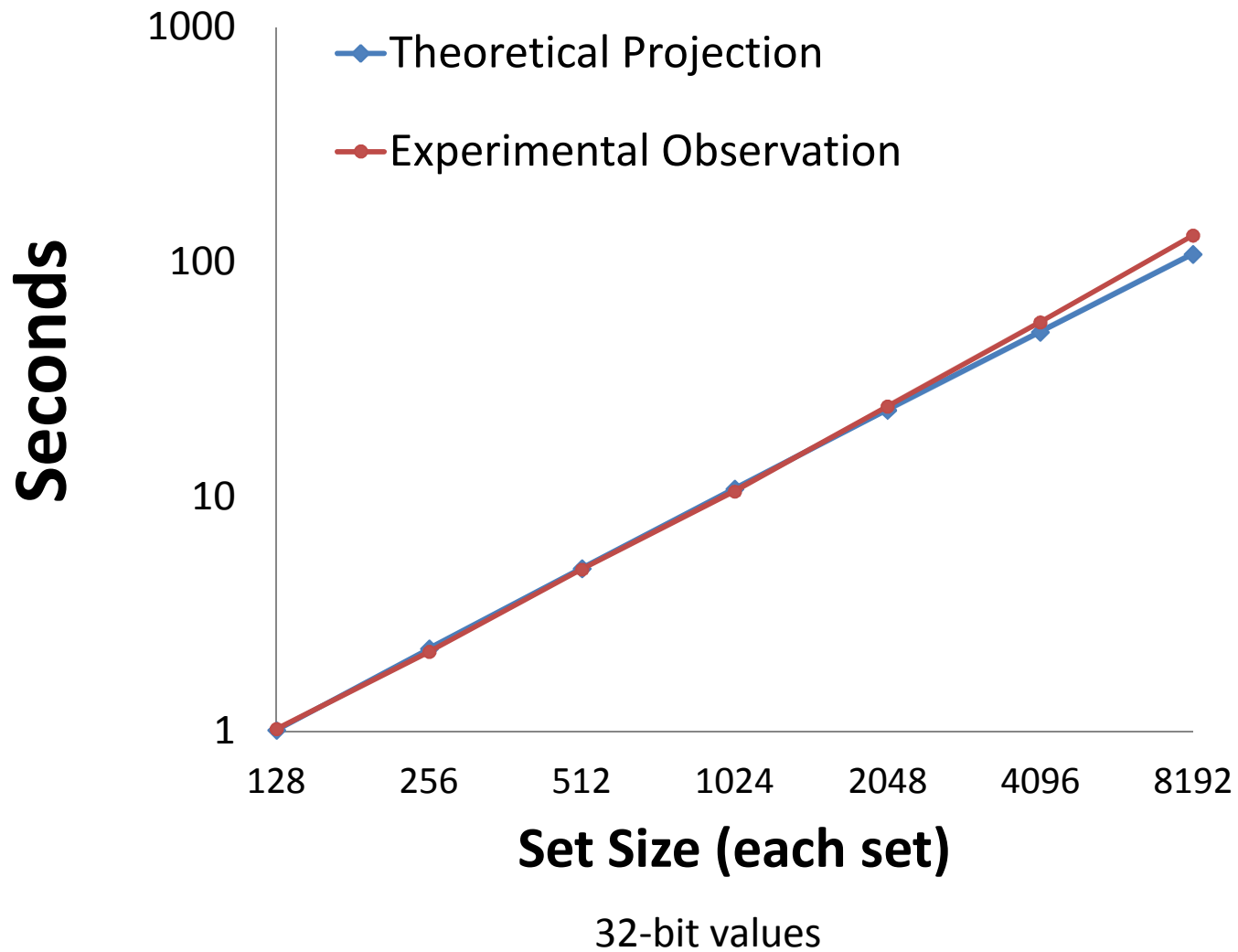


Sort: Take advantage of total order of elements

Compare adjacent elements

Shuffle to hide positions

SCS-WN Protocol Results



CommonContacts

UVa Secure Computation



- OVERVIEW
- USER REVIEWS (1)
- WHAT'S NEW
- PERMISSIONS

Description

CommonContacts allows two users to collaboratively discover common entries in their



User Reviews

5 star	3
4 star	0
3 star	0
2 star	0
1 star	0

Average rating:

5.0

★★★★★

3

David Evans on September 28, 2011 (Motorola XOOM with version 1.3)

★★★★★ **Best App Ever!**

This is the coolest secure computation application there is!

Yan on August 25, 2011 (HTC Nexus One with version 1.3)

★★★★★ **useful app**

good



Hatomico
EMPERATRIZ
★★★★★ (17)

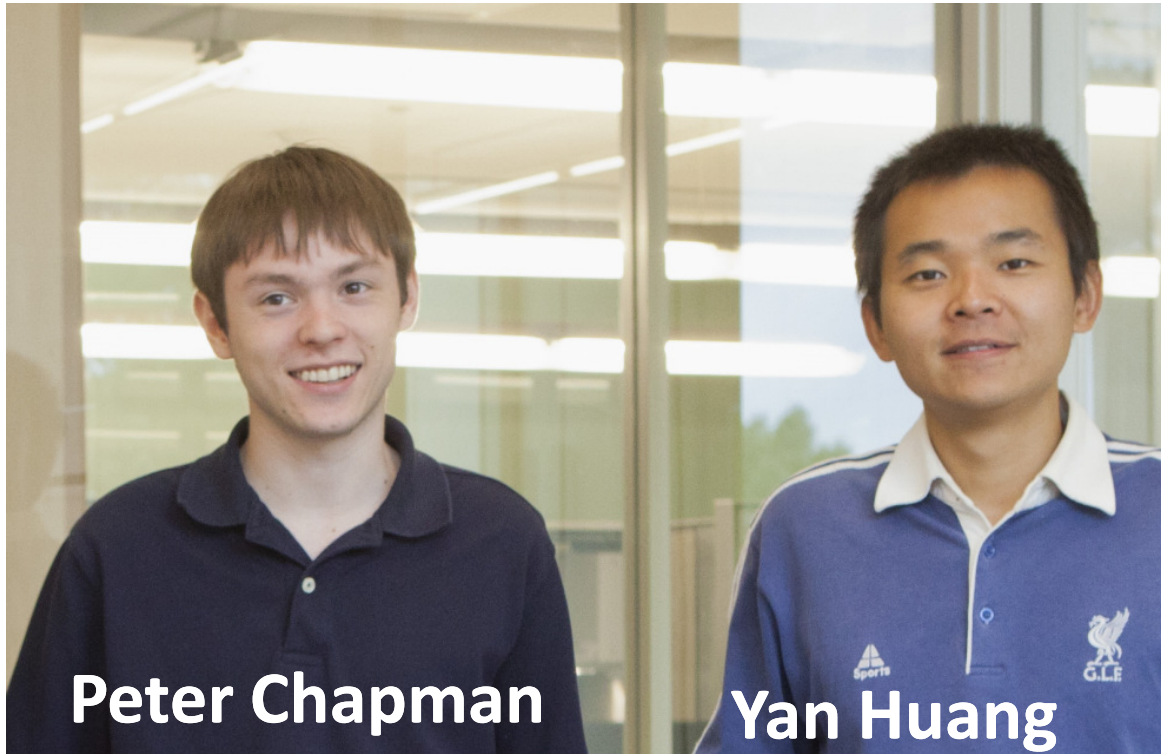
good



	Problem	Best Previous Result	Our Result	Speedup
NDSS 2012	Private Set Intersection (contact matching, common disease carrier)	Competitive with best custom protocols, scales to millions of 32-bit elements		
USENIX Security 2011	Hamming Distance (Face Recognition)	213s [SCiFI, 2010]	0.051s	4176
	Levenshtein Distance (genome, text comparison) – two 200-character inputs	534s [Jha+, 2008]	18.4s	29
	Smith-Waterman (genome alignment) – two 60-nucleotide sequences	[Not Implementable]	447s	-
	AES Encryption	3.3s [Henecka, 2010]	0.2s	16.5
NDSS 2011	Fingerprint Matching (1024-entry database, 640x8bit vectors)	~83s [Barni, 2010]	18s	4.6

Research Group and Alumni





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MightBeEvil.com

