



A new dating service matches singles using major histocompatibility complex genes



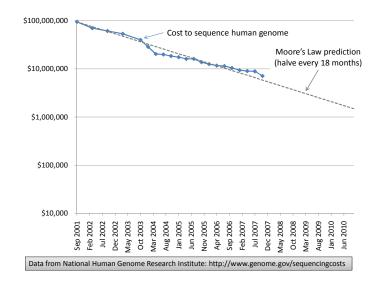
Genome Sequencing

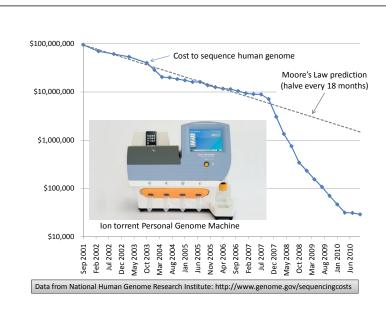
1990: Human Genome Project starts, estimate \$3B to sequence one genome (\$0.50/base)

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



Whitehead Institute, MIT







cost per 40-fold consumables coverage \$10,000,000 \$57,000,000 \$1,000,000 \$5,700,000 \$250,000 \$330,000 \$48,000 \$69,000 \$8,005 \$3,700 \$3,451 \$2,200 \$1.726 \$1.500

ling DNA Nanoarrays. Radoje L Burns, Bahram G. Kermani, Paolo undres Fernandez, Bryan Staker, Ryan Cedeno, Linsu Chen, Dan t, Coleen R. Hacker, Robert Hartlage, Ivin Kong, Tom Landers, Catherine Le, Helena Perazich, Kimberly Perry, Brock

A. Peters, Joe Peterson, Charit L. Pethiyagoda, Kaliprasad Pothuraju, Claudia Richter, Abraham M. Rosenbaum, Shaunak Roy, Jay Shaffo, Uladzislau Sharanhovich, 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 ETHAN HAWKE UMA THURMAN GATTACA HUMBONICA WAY OF DE HE BOARDET!

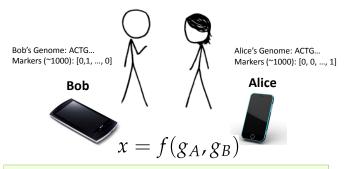






Personalized Medicine

Secure Two-Party Computation



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)

Bob (circuit evaluator)

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

Agree on $f(a,b) \rightarrow x$

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

Garbled Circuit Protocol

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

Andrew Yao, 1982/1986

Computing with Lookup Tables

Inputs		Output	
а	b	x	
0	0	0	
0	1	0	
1	0	0	
1	1	1	



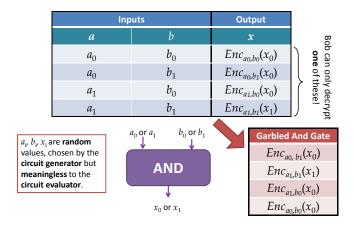
Computing with Meaningless Values?

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

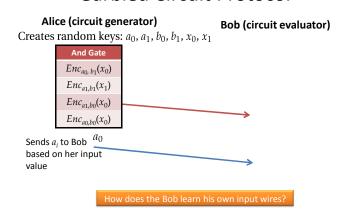
 a_{ν} b_{ν} $x_{\rm i}$ are random values, chosen by the circuit generator but meaningless to the circuit evaluator.



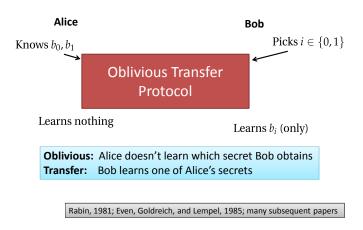
Computing with Garbled Tables



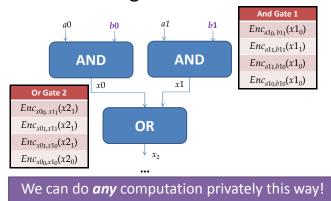
Garbled Circuit Protocol



Primitive: Oblivious Transfer

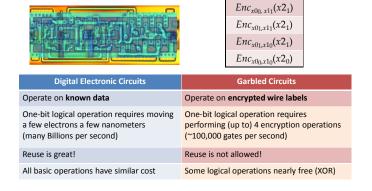


Chaining Garbled Circuits

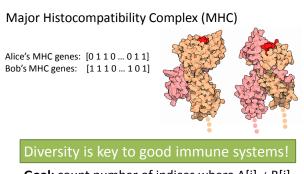


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Building Computing Systems



Offspring Immune System Test



Goal: count number of indices where $A[i] \neq B[i]$

1

XOR Every Cryptographer's Favorite Function



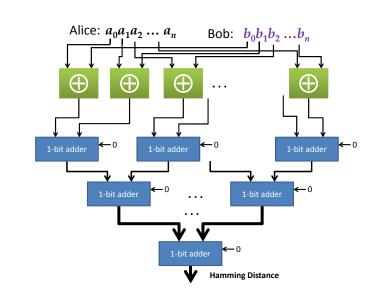
 $a \oplus a = 0$

 $a \oplus r$ is uniformly random

 $a \oplus r \oplus r = a$

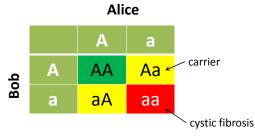
0 0 1

Can compute $a \oplus b$ on garbled inputs without and encryptions ("free").



Alice: $a_0 a_1 a_2 \dots a_n$ Bob: $b_0 b_1 b_2 ... b_n$ \oplus **Hamming Distance** Your offspring will have good immune systems! $H(r_0)$, $H(r_1)$

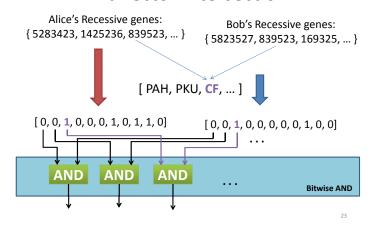
Heterozygous Recessive Risk



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



Scaling

What if there are millions of possible diseases? Length of bit vector:

number of possible values

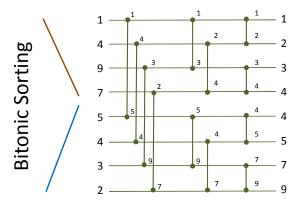
(2^L where L is number of bits for each value)

Pairwise Comparison

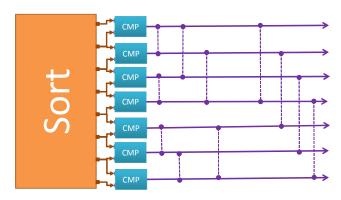
for i in range(0, n-1): for j in range(0, n-1): if A[i] = B[j] output A[i]



Sort-Compare-Shuffle Problem: the position where a matching element is revealed



(Imperfect) Shuffling



Some Results

Problem	Best Previous Result	Our Result	Speedup
Hamming Distance (Face Recognition, Genetic Dating) – two 900-bit vectors	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
Fingerprint Matching (1024- entry database, 640x8bit vectors)	~83s [Barni, 2010]	18 s	4.6

Scalable: 1 Billion gates evaluated at ~100,000 gates/second on laptop



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