

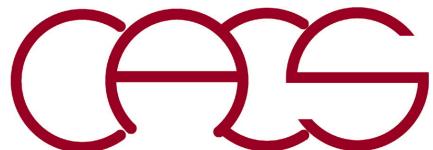
Molecular-Dynamics Machines

Aiichiro Nakano

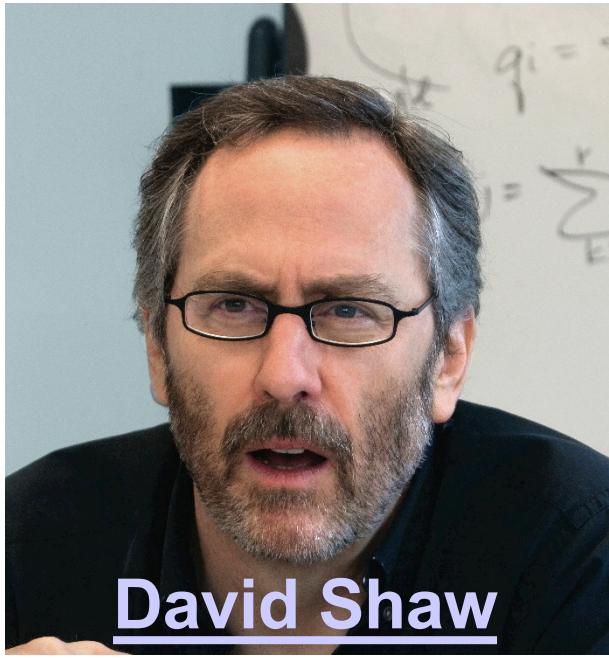
*Collaboratory for Advanced Computing & Simulations
Department of Computer Science
Department of Physics & Astronomy
Department of Quantitative & Computational Biology
University of Southern California*

Email: anakano@usc.edu

Why parallel MD? It's hot in computer science!



Anton: Computational Microscope



David Shaw

“... make all these discoveries because they were looking at the world in a different way.”

Named after Anton van Leeuwenhoek, who is often referred to as “the father of microscopy”

“... there’s still a lot of juicy, low-hanging fruit in this (molecular simulation) area ...”

16 μ s/day simulation on 512 nodes
(5 μ s/step execution time)



D E Shaw Research

A conversation with David E. Shaw, CACM 52(10), 49 ('09)

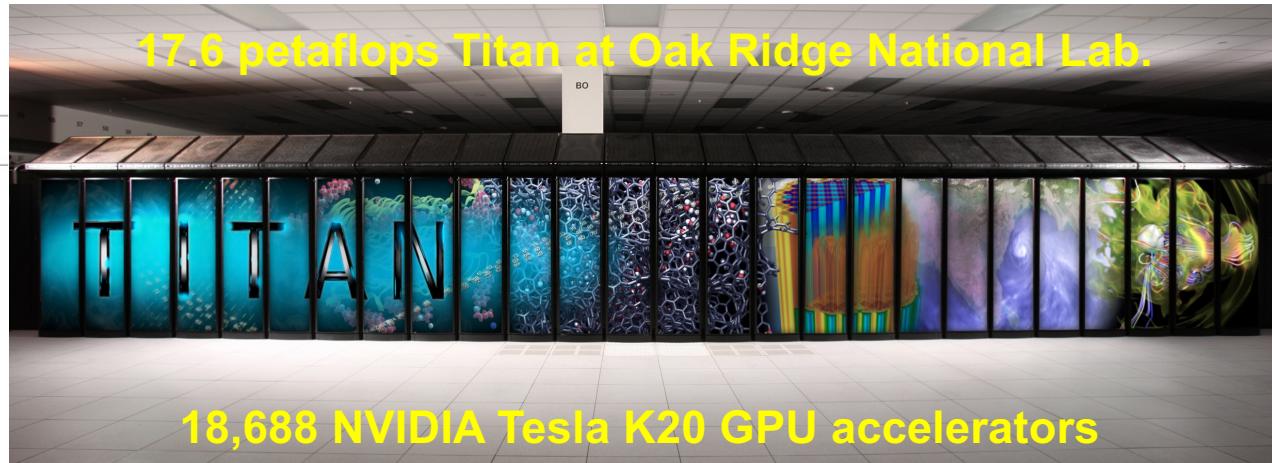
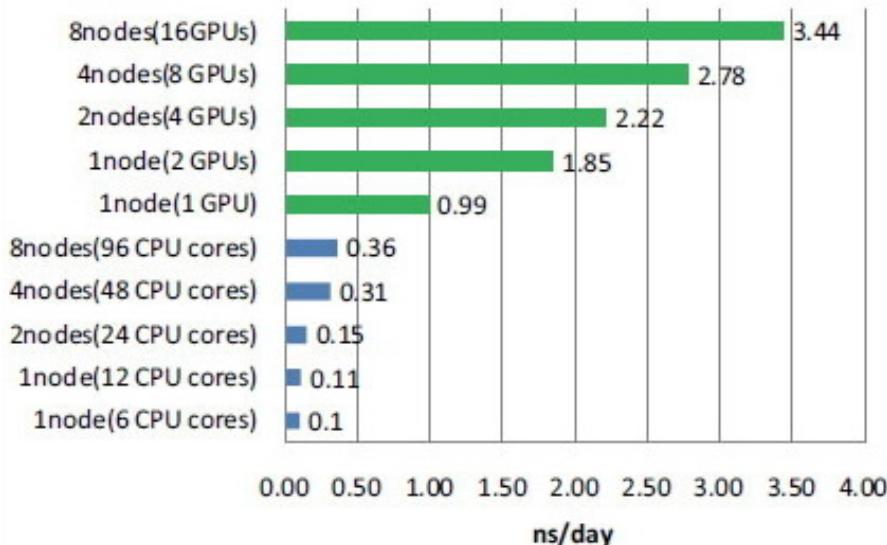
MD on GPU Clusters

GPU acceleration and other computer performance increases will offer critical benefits to biomedical science.

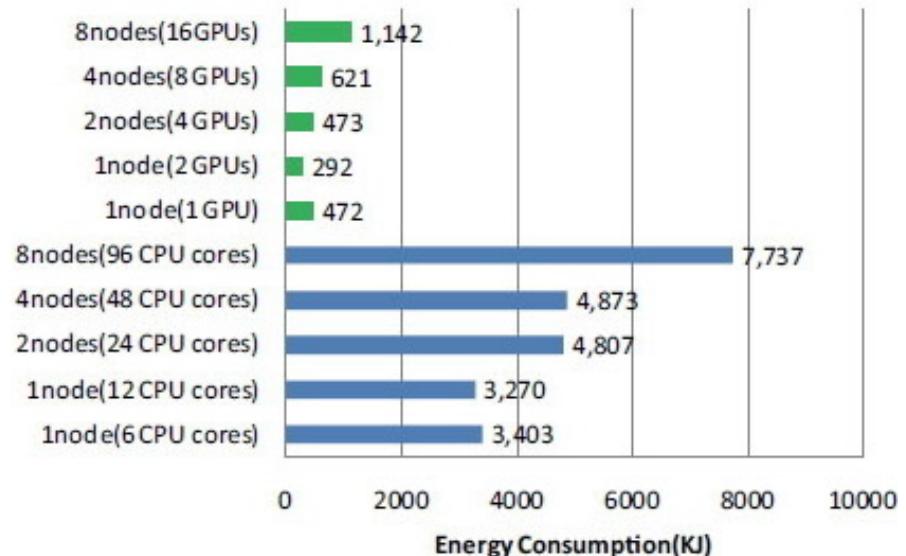
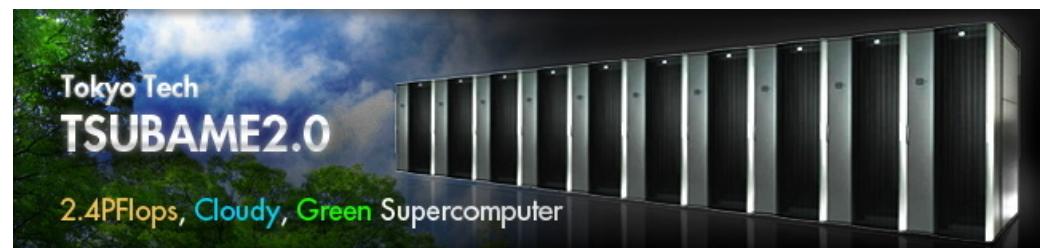
BY JAMES C. PHILLIPS AND JOHN E. STONE

Probing Biomolecular Machines with Graphics Processors

CACM 52(10), 34 ('09)

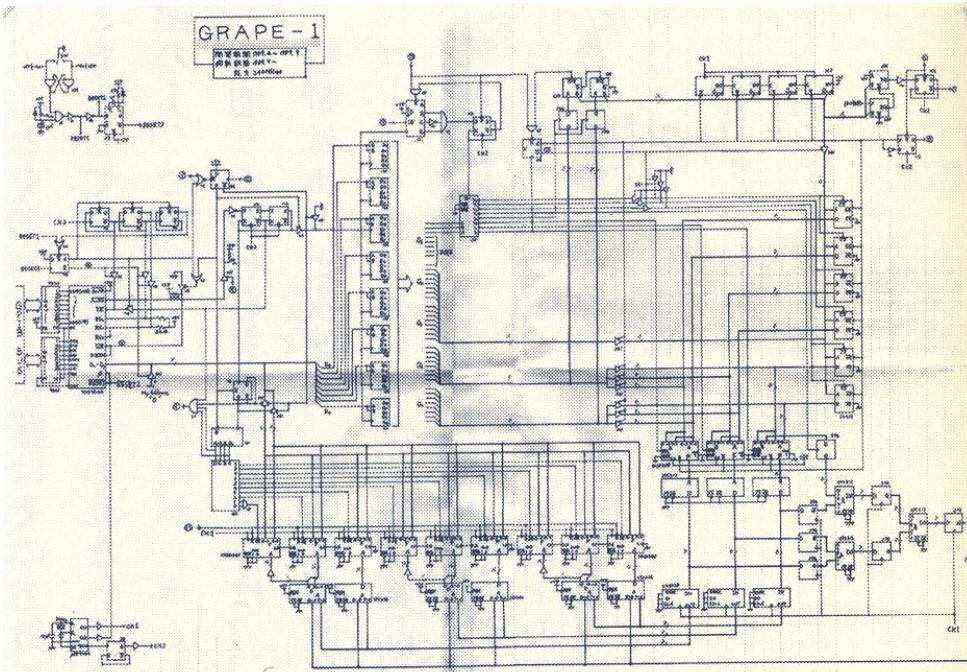


18,688 NVIDIA Tesla K20 GPU accelerators



Energy Consumption(kJ)

GRAPE 1 (\$2K, 1989)

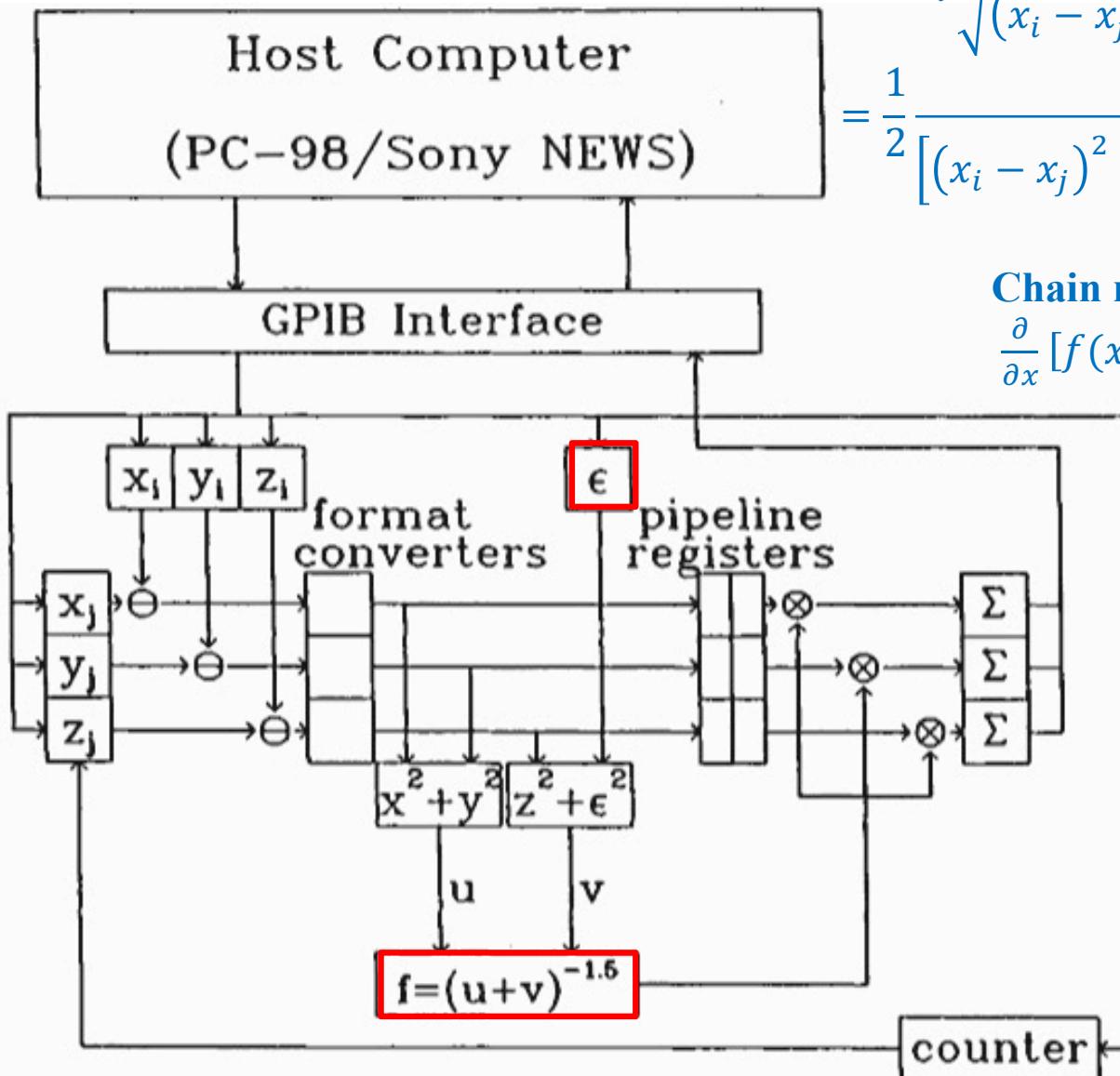


Tomoyoshi Ito & comics he authored

- **GRAPE (GRAvity PipE) = special-purpose computer for the gravitational N -body problem built by astrophysicists at Univ. of Tokyo**
- **GRAPE 1 designed by a 1st-year Ph.D. student (with \$140K/year income)**

Gravitational Pipeline

$$\frac{d^2 \mathbf{x}_i}{dt^2} = \mathbf{f}_i = \sum_j \frac{m_j (\mathbf{x}_j - \mathbf{x}_i)}{(r_{ij}^2 + \varepsilon^2)^{3/2}}$$



$$-\frac{\partial}{\partial x_i} \frac{1}{\sqrt{(x_i - x_j)^2 + (y_i - y_j)^2 + (z_i - z_j)^2 + \varepsilon^2}} \\ = \frac{1}{2} \frac{2(x_i - x_j)}{\left[(x_i - x_j)^2 + (y_i - y_j)^2 + (z_i - z_j)^2 + \varepsilon^2\right]^{3/2}}$$

Chain rule:

$$\frac{\partial}{\partial x} [f(x)]^{-1/2} = -\frac{1}{2} [f(x)]^{-3/2} \frac{\partial f}{\partial x}$$

- Small ε to avoid if $(i \neq j)$ & pipeline stall
- $x^{-3/2}$ was implemented as table look-up using read-only memory (ROM)

D. Sugimoto et al.,
Nature 345, 33 ('90)

GRAPE & Gordon Bell Prizes

SC2003 Gordon Bell Award

Junichiro Makino

University of Tokyo

Performance Evaluation and Tuning of
GRAPE-6—Towards 40 “Real” Tflops

SC2001
GORDON BELL PRIZE

Junichiro Makino

Winner, Peak Performance

A 11.55 Tflops Simulation of Black Holes
in a Galactic Center on GRAPE-6

SC2000
GORDON BELL PRIZE

Junichiro Makino

Winner, Peak Performance Category

A 1.349 Tflops simulation of black holes in a galactic center on GRAPE-6

2003 Gordon Bell Prize, Special Achievement

Performance Evaluation and Tuning of GRAPE-6—Towards 40 ‘Real’ Tflop/s

Junichiro Makino, Hiroshi Daisaka, Eiichiro Kokubo, Toshiyuki Fukushige

2001 Gordon Bell Prize, Winner, Peak Performance

A 11.55 Tflops simulation of black holes in a galactic center on GRAPE-6

Junichiro Makino, Toshiyuki Fukushige

2000 Gordon Bell Prize, Winner, Peak Performance Category

A 1.349 Tflops simulation of black holes in a galactic center on GRAPE-6

Junichiro Makino, Toshiyuki Fukushige, Masaki Koga

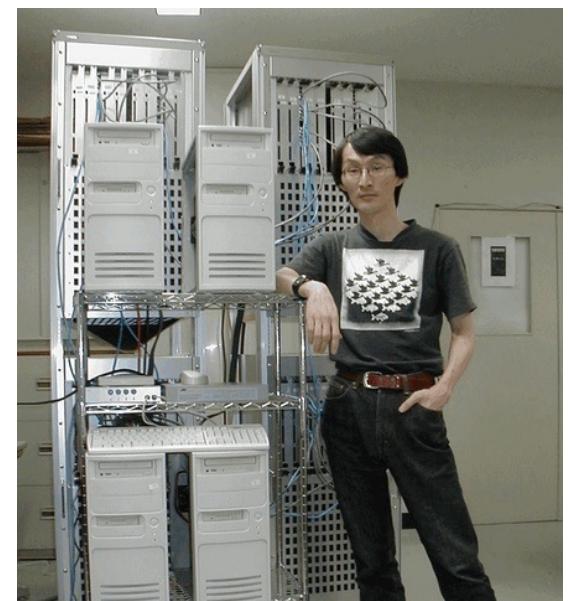
2000 Gordon Bell Prize, Winner, Peak Performance Category (tie with above)

1.34 Tflops Molecular Dynamic simulation for NaCl with a Special Purpose Computer: MDM (MD-GRAPE system)

Tetsu Narumi, Ryutaro Susukita, Takahiro Koishi, Kenji Yasuoka, Hideaki Furusawa, Atsushi Kawai, Toshikazu Ebisuzaki

*Gordon Bell Prize,
commonly
referred to as the
Nobel Prize of
Supercomputing
[Wikipedia].*

**J. Makino
& Grape 6
(2001)**



1999 Gordon Bell Prize, Price Performance, First Prize
Astrophysical N-body simulation
144 Glops / \$ 1 M on custom-built GRAPE-5 32-processor system

Atsushi Kawai, Toshiyuki Fukushige, and Junichiro Makino

1996 Gordon Bell Prize, Performance, Honorable Mention
Simulation of the motion of 780,000 stars
333 Gflops using the Grape-4 machine w/ 1,269 processors

Junichiro Makino, Toshiyuki Fukushige



1995 Gordon Bell Prize, First Place, Special Purpose Machines
Simulation of the Motion of 10,000 Stars
112 Gflops using the Grape-4 machine with 288 processors

Astrophysical N-body Simulations on GRAPE-4 Special-Purpose Computer
Junichiro Makino, Makoto Taiji



Green500 Rank	MFLOPS/W	Site*	Computer*	Total Power (kW)
1	1684.20	IBM Thomas J. Watson Research Center	NNSA/SC Blue Gene/Q Prototype	38.80
2+	1448.03	National Astronomical Observatory of Japan	GRAPE-DR accelerator Cluster, Infiniband	24.59
2	958.35	GSIC Center, Tokyo Institute of Technology	HP ProLiant SL390s G7 Xeon 6C X5670, Nvidia GPU, Linux/Windows	1243.80
3	933.06	NCSA	Hybrid Cluster Core i3 2.93Ghz Dual Core, NVIDIA C2050, Infiniband	36.00
4	828.67	RIKEN Advanced Institute for Computational Science	K computer, SPARC64 VIIIfx 2.0GHz, Tofu interconnect	57.96

Enabling Science by Hardware

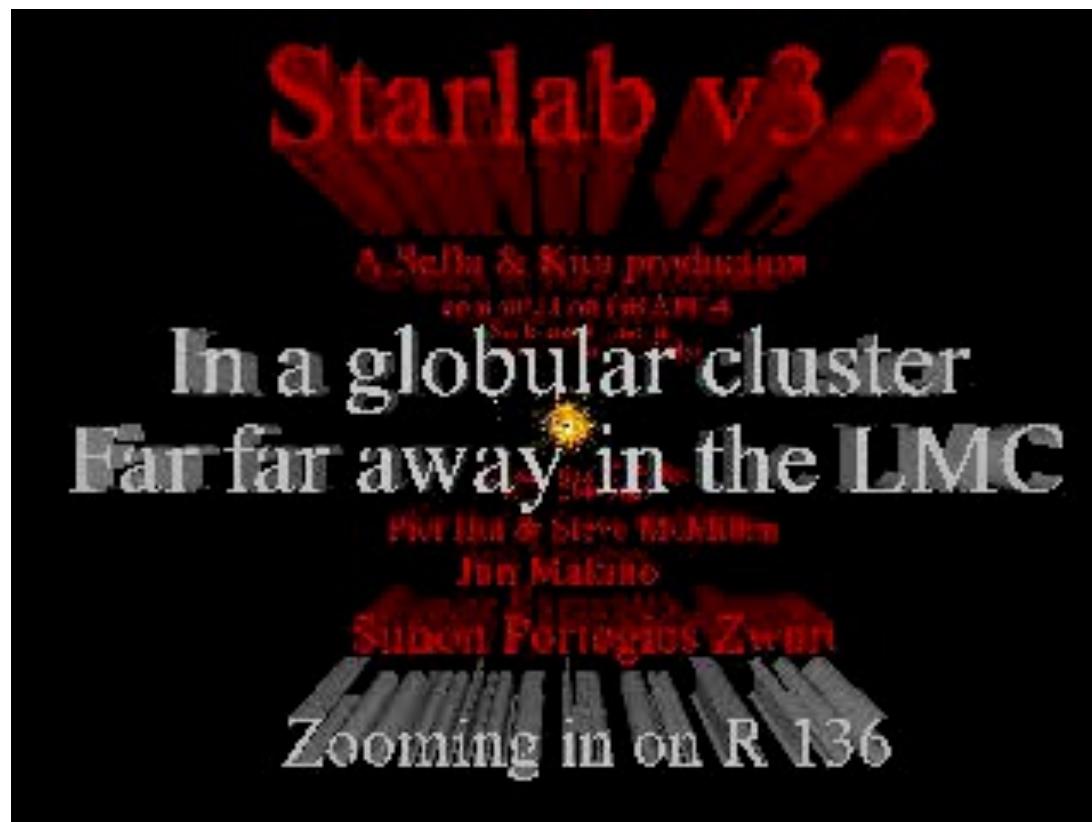
A special-purpose computer for gravitational many-body problems

Daiichiro Sugimoto^{*}, Yoshihiro Chikada[†], Junichiro Makino^{*}, Tomoyoshi Ito^{*}, Toshikazu Ebisuzaki^{*} & Masayuki Umemura[‡]

NATURE · VOL 345 · 3 MAY 1990

33

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In Univ. of Tokyo, computer science started as part of physics department (not math or CS)

Computer Physics Communications 60 (1990) 187–194

A special-purpose N -body machine GRAPE-1

Tomoyoshi Ito, Junichiro Makino, Toshikazu Ebisuzaki and Daiichiro Sugimoto
Department of Earth Science and Astronomy, College of Arts and Sciences, University of Tokyo, Tokyo 153, Japan

[CPC homepage](#)

Submit your first paper to CPC!

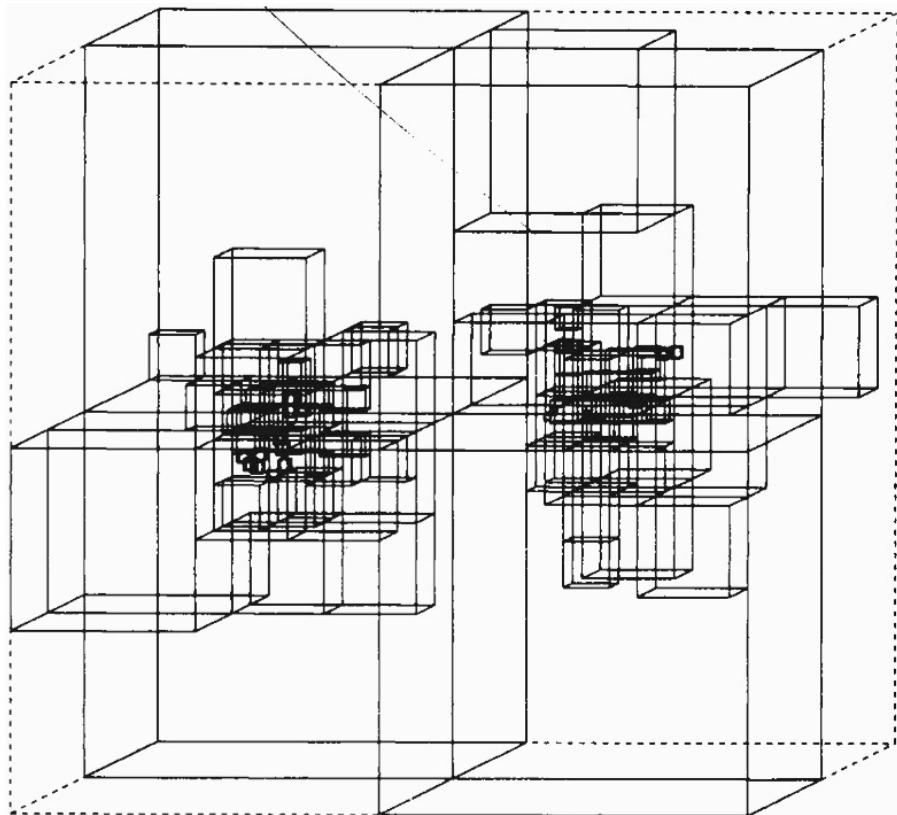
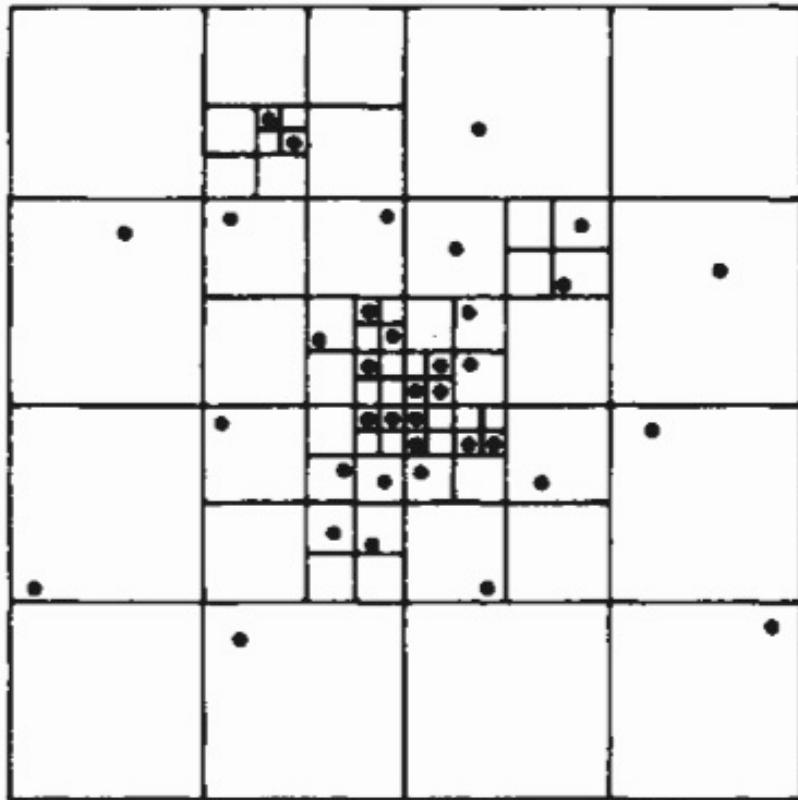
Enabling Science by Algorithm

NATURE

NATURE VOL. 324 4 DECEMBER 1986

A hierarchical $O(N \log N)$ force-calculation algorithm

Josh Barnes & Piet Hut



ACM Best Theses: Machine vs. Algorithm

DANNY HILLIS

Doctoral Dissertation Award
United States – 1985

CITATION

For his dissertation "The Connection Machine."



Watch: Hillis on Richard Feynman

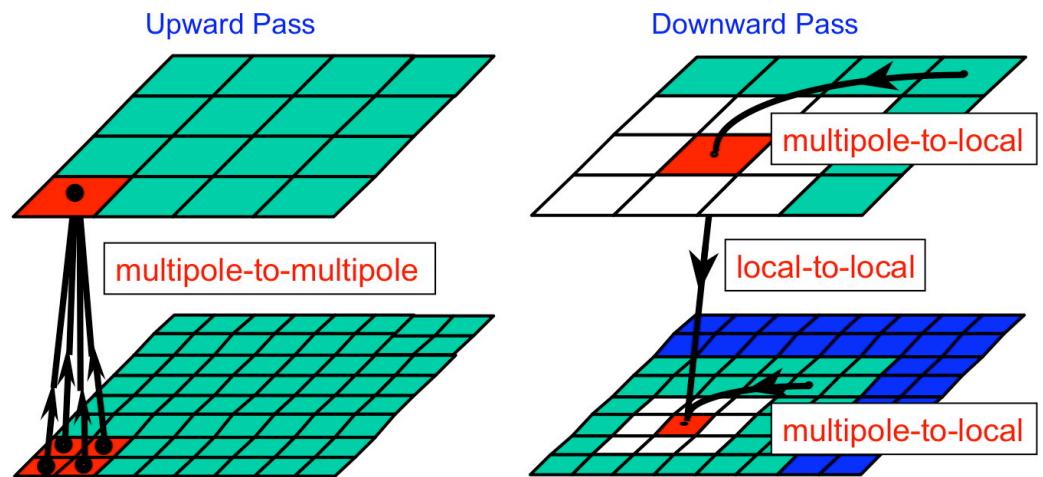
<http://longnow.org/essays/richard-feynman-connection-machine/>

LESLIE GREENGARD

Doctoral Dissertation Award
United States – 1987

CITATION

For his dissertation "The Rapid Evaluation of Potential Fields in Particle Systems."



See lecture notes at <https://aiichironakano.github.io/cs653.html>

A Small Step in Parallel MD

VOLUME 71, NUMBER 1

PHYSICAL REVIEW LETTERS

5 JULY 1993

Structural Correlations in Porous Silica: Molecular Dynamics Simulation on a Parallel Computer

Aiichiro Nakano, Lingsong Bi, Rajiv K. Kalia, and Priya Vashishta

*Concurrent Computing Laboratory for Materials Simulations, Department of Physics and Astronomy,
Department of Computer Science, Louisiana State University, Baton Rouge, Louisiana 70803-4001*

(Received 9 November 1992; revised manuscript received 2 April 1993)

Molecular dynamics simulations of porous silica in the density range $2.2\text{--}0.1 \text{ g/cm}^3$ are carried out on a 41 472 particle system using a multiple instruction multiple data computer. The internal surface area, pore surface-to-volume ratio, pore size distribution fractal dimension, correlation length, and mean particle size are determined as a function of the density. Structural transition between a condensed amorphous phase and a low-density porous phase is characterized by these quantities. Various dissimilar porous structures with different fractal dimensions are obtained by controlling the preparation schedule and temperature.

This work was supported by the U.S. Department of Energy, Office of Energy Research, Basic Energy Science, Materials Science Division, Grant No. DE-FG05-92ER45477. The computations were performed using the eight-node iPSC/860 in the Concurrent Computing Laboratory for Materials Simulations (CCLMS) at Louisiana State University. The facilities in the CCLMS were acquired with the Equipment Enhancement Grants awarded by the Louisiana Board of Regents through Louisiana



More *N*-body Simulations at SC

42 TFlops Hierarchical *N*-body Simulations on GPUs with Applications in both Astrophysics and Turbulence

Tsuyoshi Hamada
Department of Computer and Information Sciences
Nagasaki University
Nagasaki, Japan
hamada@cis.nagasaki-u.ac.jp

Tetsu Narumi
Department of Computer Science
University of Electro-Communications
Tokyo, Japan
narumi@cs.uec.ac.jp

Rio Yokota
Department of Mathematics
University of Bristol
Bristol, United Kingdom
rio.yokota@bristol.ac.uk

Kenji Yasuoka
Department of Mechanical Engineering
Keio University
Yokohama, Japan
yasuoka@mech.keio.ac.jp

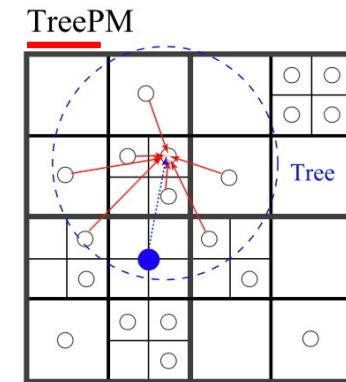
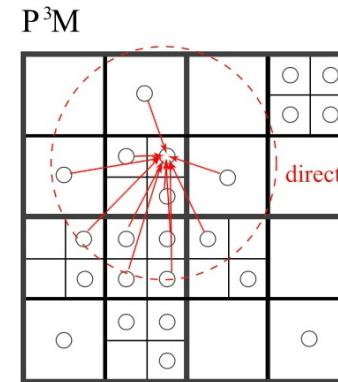
Keigo Nitadori
High-Performance Molecular Simulation Team
RIKEN Advanced Science Institute
Wako, Japan
keigo@riken.jp

Makoto Taiji
High-Performance Molecular Simulation Team
RIKEN Advanced Science Institute
Wako, Japan
taiji@riken.jp

2009 Gordon Bell Prize Price/Performance Category

Table 2: Price of the GPU cluster

Elements	Quantity	Price (JPY)	Price (\$)
GPUs	256	12,160,000	\$ 118,345
Host PCs	128	10,716,032	\$ 104,292
Network switch	4	644,800	\$ 6,275
Total		23,520,832	\$ 228,912



4.45 Pflops Astrophysical *N*-Body Simulation on K computer - The Gravitational Trillion-Body Problem

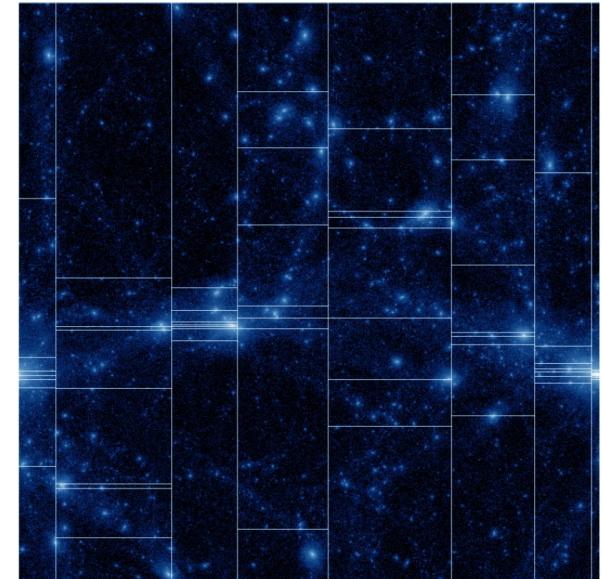
Tomoaki Ishiyama
Center for Computational Science
University of Tsukuba
ishiyma@ccs.tsukuba.ac.jp

Keigo Nitadori
Center for Computational Science
University of Tsukuba
keigo@ccs.tsukuba.ac.jp

Junichiro Makino
Graduate School of Science and Engineering
Tokyo Institute of Technology
makino@geo.titech.ac.jp

IEEE/ACM supercomputing, SC12

*Machine
&
algorithm!*

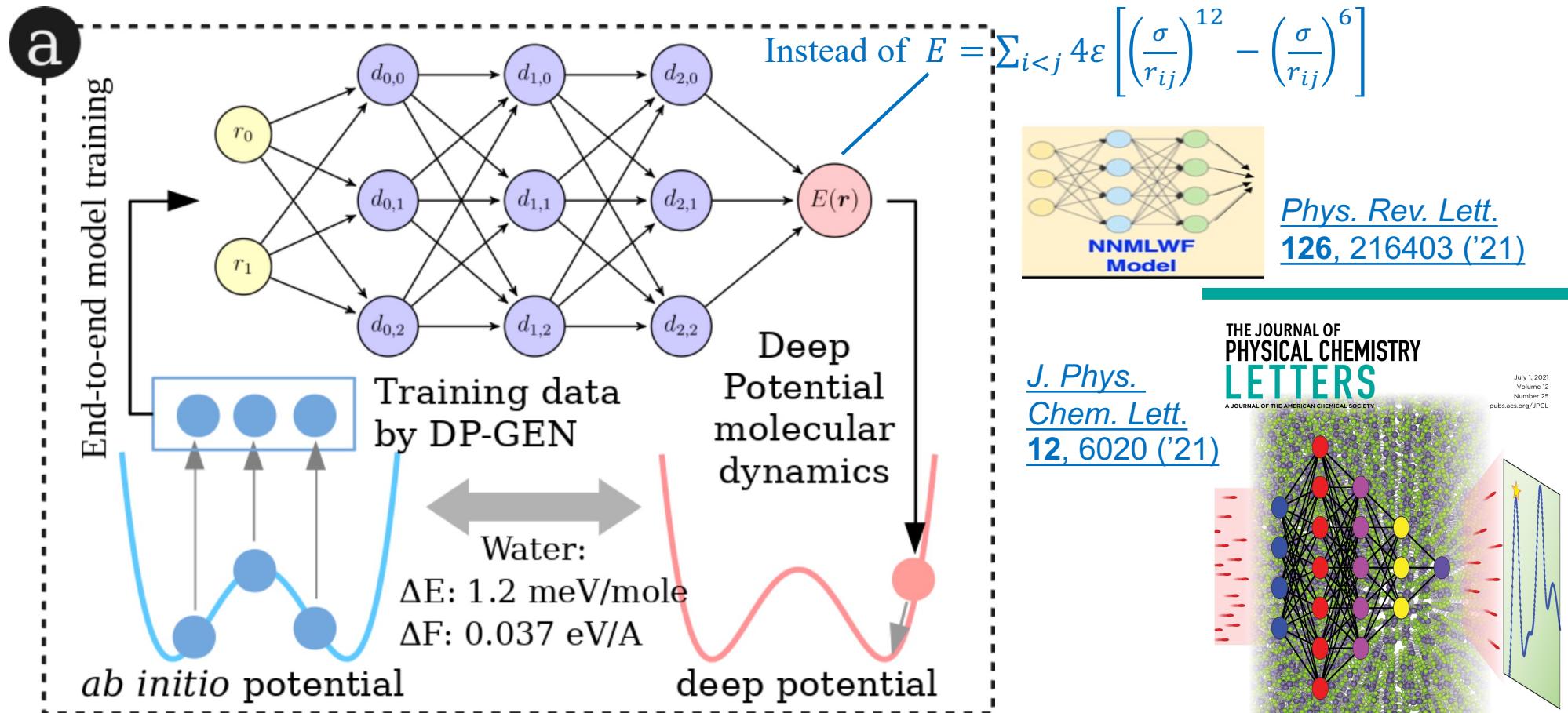


Now It's Deep MD

Pushing the limit of molecular dynamics with ab initio accuracy to 100 million atoms with machine learning

Weile Jia, Han Wang, Mohan Chen, Denghui Lu, Jiduan Liu, Lin Lin,
Roberto Car, Weinan E, Linfeng Zhang

Proc. Supercomputing, SC20, Gordon Bell prize



<https://aiichironakano.github.io/cs596/Jia-DeePMD-SC20.pdf>

Enabling Science by Online Game

nature

Vol 466 | 5 August 2010 | doi:10.1038/nature09304

LETTERS

Predicting protein structures with a multiplayer online game

Seth Cooper¹, Firas Khatib², Adrien Treuille^{1,3}, Janos Barbero¹, Jeehyung Lee³, Michael Beenen¹, Andrew Leaver-Fay²†, David Baker^{2,4}, Zoran Popović¹ & Foldit players

The image shows a screenshot of the Foldit game interface. On the left, there's a green header with the Foldit logo and the text "Solve Puzzles for Science". Below it is a large protein structure composed of green and blue sticks. A black callout box with white text says "Click to learn how you contribute to science by playing Foldit." To the right of the protein, there's a 3D view of the protein with numbered arrows pointing to specific residues or features: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, and 12. Above the protein, the text "Rank: 317 Score: 2534" is displayed, along with "Soloist Beginner Puzzle 8 (<150) Fruit Fly". To the right of the protein, there are two tables: "Soloist Competition" and "Group Competition". The "Soloist Competition" table lists players and their scores, with "Mike Crunching for Physics" at the top. The "Group Competition" table lists groups and their scores, with "Rice Biochemistry" at the top. At the bottom, there's a toolbar with icons for "Shake Sidechains", "Wiggle All", "Wiggle Backbone", "Wiggle Sidechains", "Freeze Protein", "Remove Bands", "Disable Bands", "Align Guide", "Reset Structures", "Reset Puzzle", "Help", "Glossary", and "Notifications".

#	Group Name	Score
1	Rice Biochemistry	9174
2	Team Commonwealth	9168
3	Team Canada	9160
4	Team Canada	9085
5	Firebird BioChem	9073
6	SETI Germany	9030
7	Bioinche	9001

#	Player Name	Current	Best
1	Mike Crunching for Physics	-	9242
2	weitzent	-	9222
3	ys719	-	9235
4	pharic	-	9211
5	kevin_karpilus	-	9196
6	JINXter	-	9195
7	abacuc	-	9181

Ising Machine



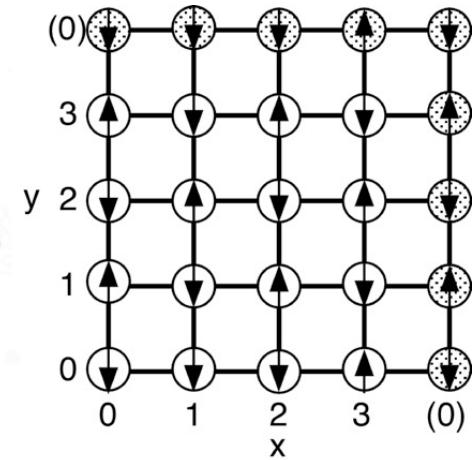
1bit の世界の専用計算機 —イジング・マシーン—

泰地 真弘人
(東京大学教養学部)
(1994年3月2日受理)

Ising Machine:
A Special Purpose Computer for 1-bit Worlds

TAIJI Makoto
(Received 3 March 1994)

$$V(s^N) = -J \sum_{(k,l)} s_k s_l - H \sum_k s_k, \quad s_k = \pm 1$$



<https://aiichironakano.github.io/phys516-lecture.html>

Abstract

This paper describes the development of special-purpose computer systems for Ising models, "Ising Machine" m-TIS 1 and 2. The first two sections explain Ising models and their Monte Carlo simulations. In section 3 and 4, I describe my motivation to build a special-purpose computer and the development of m-TIS 1. In section 5 and 6, the use of field-programmable gate arrays in a special-purpose computer is discussed. In the last two sections I discuss the potential abilities and future prospects of both Ising machine and a special-purpose computer in general. *J. Plasma Fusion Res.* **70**, 332 ('94)

cf. Original GRAPE was a 48-bit machine

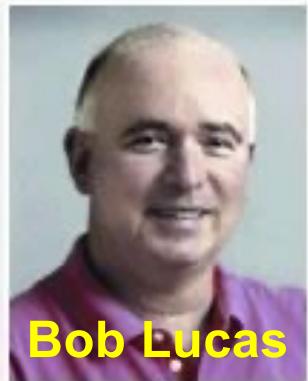
USC Quantum Computation Center

- D-Wave 2X system with 1,098-quantum bits (qubits)

Phase transitions in a programmable quantum spin glass simulator

R. Harris^{1*}, Y. Sato¹, A. J. Berkley¹, M. Reis¹, F. Altomare¹, M. H. Amin^{1,2}, K. Boothby¹, P. Bunyk¹, C. Deng¹, C. Enderud¹, S. Huang¹, E. Hoskinson¹, M. W. Johnson¹, E. Ladizinsky¹, N. Ladizinsky¹, T. Lanting¹, R. Li¹, T. Medina¹, R. Molavi^{1,3}, R. Neufeld¹, T. Oh¹, I. Pavlov¹, I. Perminov¹, G. Poulin-Lamarre¹, C. Rich¹, A. Smirnov¹, L. Swenson¹, N. Tsai¹, M. Volkmann¹, J. Whittaker¹, J. Yao¹

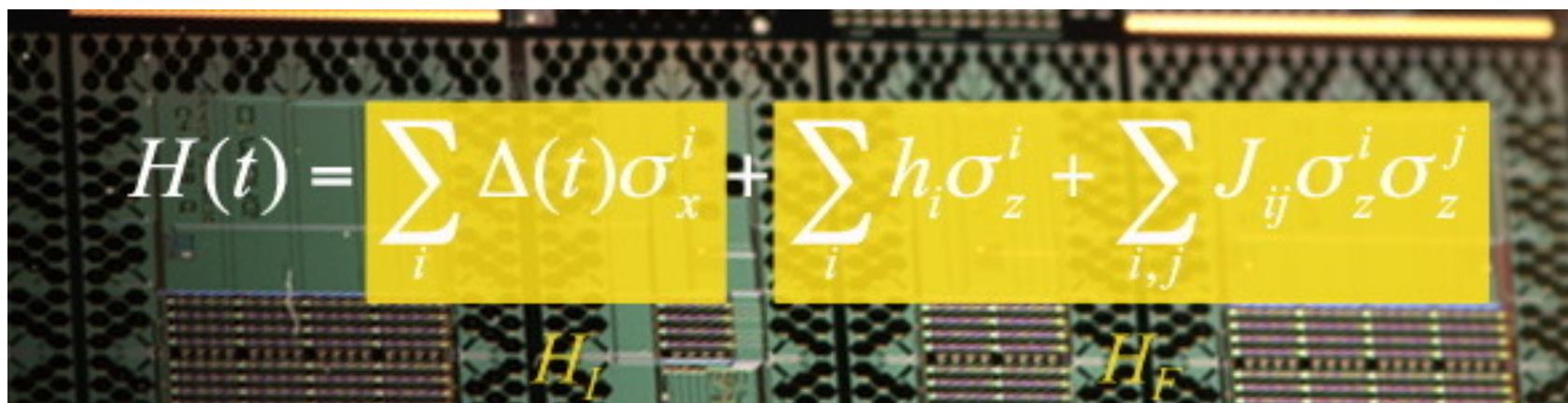
Harris *et al.*, *Science* **361**, 162–165 (2018) 13 July 2018



Bob Lucas

Daniel Lidar

- Adiabatic quantum optimization



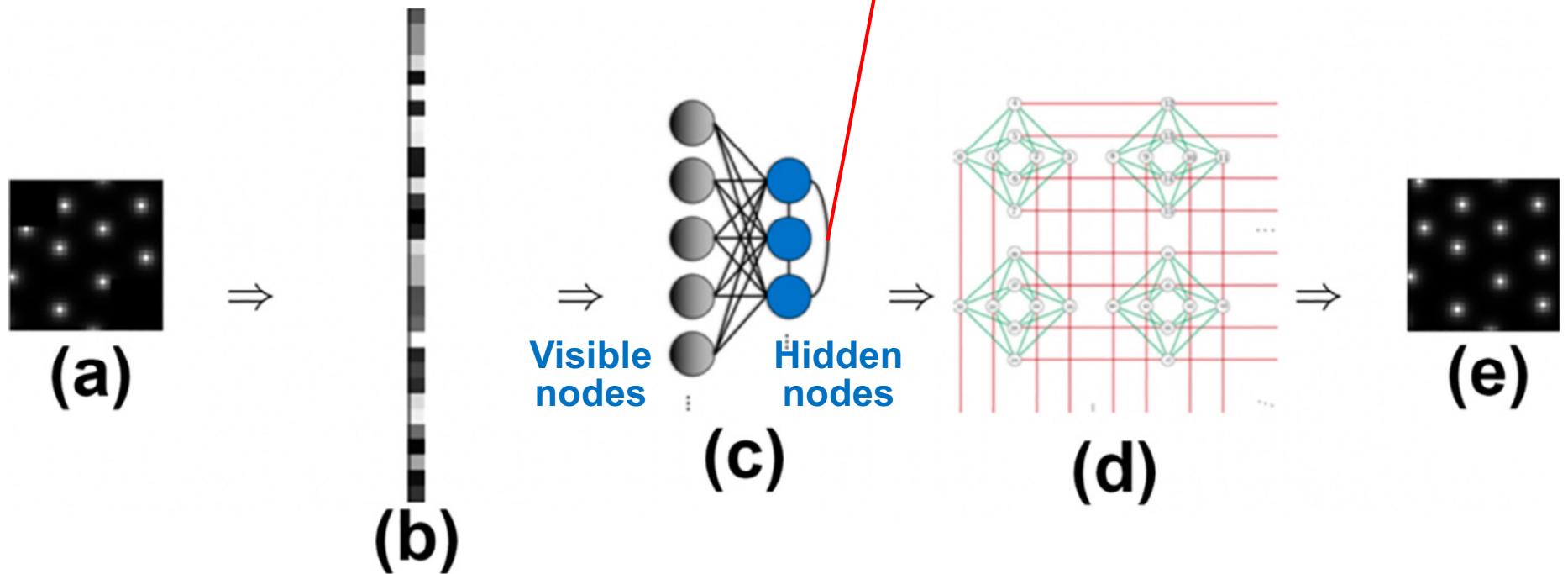
Machine Learning on D-Wave

Boltzmann machine modeling of layered MoS₂ synthesis on a quantum annealer

J. Liu, A. Mohan, R. K. Kalia, A. Nakano, K. Nomura, P. Vashishta, and K.T. Yao

Comput. Mater. Sci. **173**, 109429 ('20)

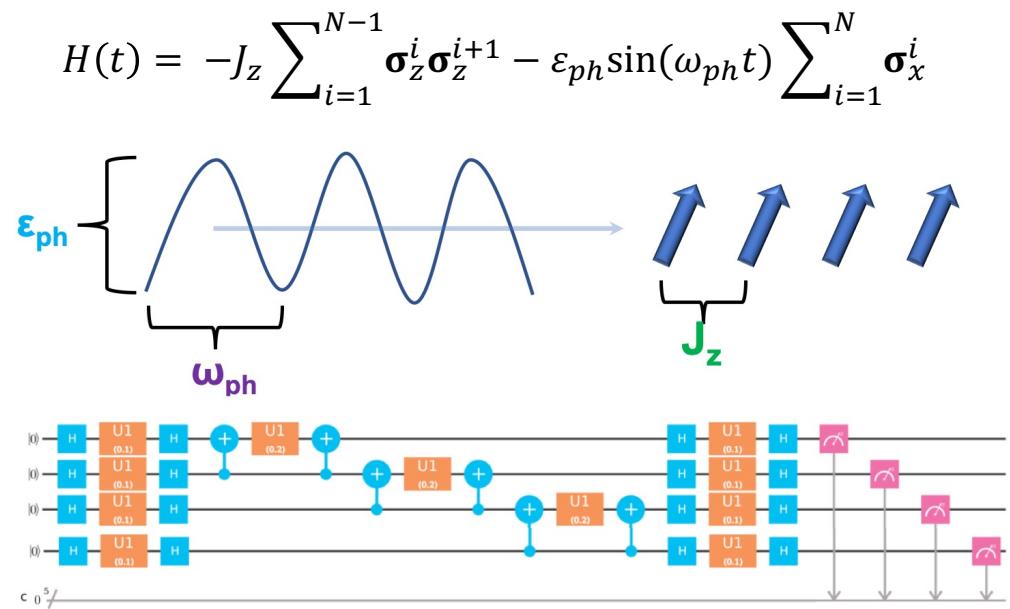
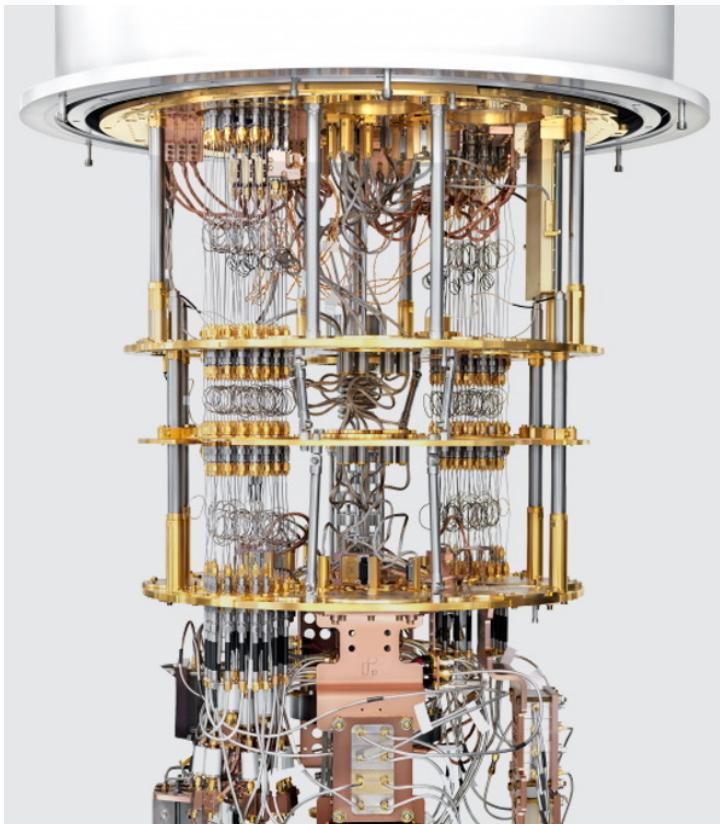
- Computing power of D-Wave allows unrestricted Boltzmann Machine to enhance machine learning performance



Final project by Ankith Mohan (MSCS) with Jeremy Liu (PhD-CS)

Quantum Computational Science

- Quantum computing for science: *Universal simulator of quantum many-body systems* [R. P. Feynman, [Int. J. Theo. Phys. 21, 467 \('82\)](#); S. Lloyd, [Science 273, 1073 \('96\)](#)]
- Successfully simulated quantum many-body dynamics on publicly-available IBM's Q16 Melbourne & Rigetti's Aspen quantum computers [L. Bassman *et al.*, [Phys. Rev. B 101, 184305 \('20\)](#)]
- AI-inspired domain-specific quantum compiler has reduced the circuit size by 30% below that by the vendor's native compiler [L. Bassman *et al.*, [Quant. Sci. Tech. 6, 014007 \('21\)](#)]



```
32 | ...#define the two non-commuting terms that comprise the Hamiltonian-
33 | ...Hz = PauliTerm("Z", 0, epsilon_0)-
34 | ...Hy = PauliTerm("Y", 0, epsilon_ph*np.sin(w_ph*t))-#
35 | ...#exponentiate the terms of the Hamiltonian for use in Trotter approx-
36 | ...exp_Hz = exponential_map(Hz)(delta_t/(2.0*hbar))-#
37 | ...exp_Hy = exponential_map(Hy)(delta_t/hbar)-
```