# **Solving Inverse Problems**

#### **Aiichiro Nakano**

Collaboratory for Advanced Computing & Simulations Department of Computer Science Department of Physics & Astronomy Department of Chemical Engineering & Materials Science Department of Biological Sciences University of Southern California

Email: anakano@usc.edu

Key concept: An ensemble (outer loop: desired property → solution structure) of forward solutions (inner loop:

given structure  $\rightarrow$  property)

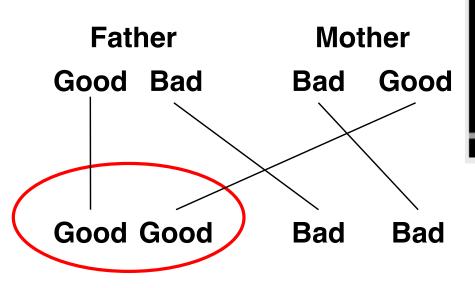


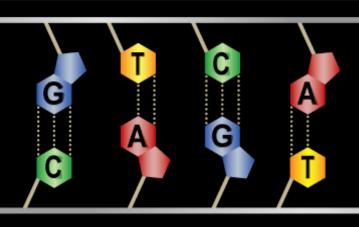
# **Genetic Algorithm**

**1D Ising model**  $\uparrow - \downarrow - \downarrow - \uparrow - \uparrow - \uparrow - \uparrow - \downarrow$ 

Gene = bit string = (10011110)

- Population in the solution space: Multiple chains, diversity
- **Selection: Elitist strategy = survival of the fittest**
- Crossover



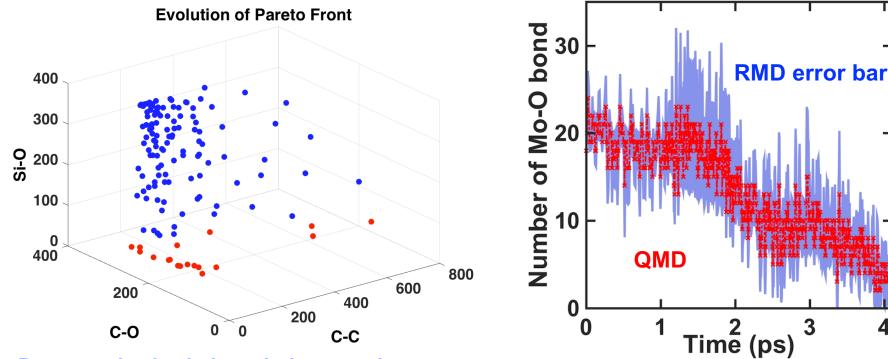


#### One Strand of DNA Is Like a Photographic Negative to the Other

An adenine (A) on one strand is always paired with a thymine (T) on the other strand, and a guanine (G) is always paired with a cytosine (C). If the sequence of nucleotides on one strand is known, the sequence of the other strand will be automatically known as well.

## **Pareto-Frontal Uncertainty Quantification**

- Train reactive force-field parameters by dynamically fitting reactive molecular dynamics (RMD) trajectories to quantum molecular dynamics (QMD) trajectories on-the-fly
- Pareto optimal front in multiobjective genetic algorithm (MOGA) provides an ensemble of force fields to enable uncertainty quantification (UQ)



- Pareto-optimal solutions during genetic training (RMD errors for three quantities-ofinterest)
- Converged Pareto-optimal front

A. Mishra et al., npj Comput. Mater. 4, 42 ('18)

# **Replica Exchange MC**

JOURNAL OF CHEMICAL PHYSICS

VOLUME 118, NUMBER 14

8 APRIL 2003

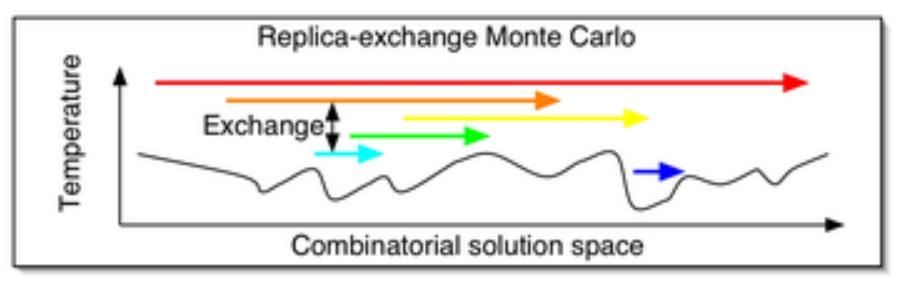
#### Replica-exchange multicanonical and multicanonical replica-exchange Monte Carlo simulations of peptides. I. Formulation and benchmark test

Ayori Mitsutake<sup>a)</sup> Department of Physics, Faculty of Science and Technology, Keio University, Yokohama, Kanagawa 223-8522, Japan

Yuji Sugita<sup>b)</sup> and Yuko Okamoto<sup>c)</sup> Department of Theoretical Studies, Institute for Molecular Science, Okazaki, Aichi 444-8585, Japan and Department of Functional Molecular Science, The Graduate University for Advanced Studies, Okazaki, Aichi 444-8585, Japan

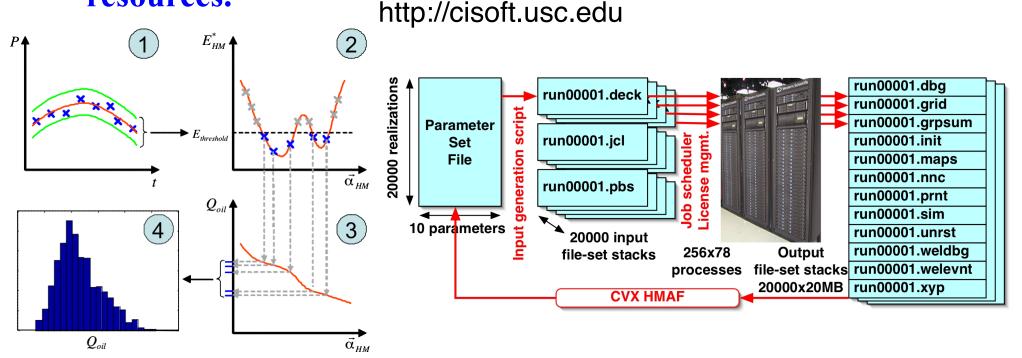
J. Chem. Phys. 118, 6664 ('03)

#### **Multiple Markov chains at different temperatures**



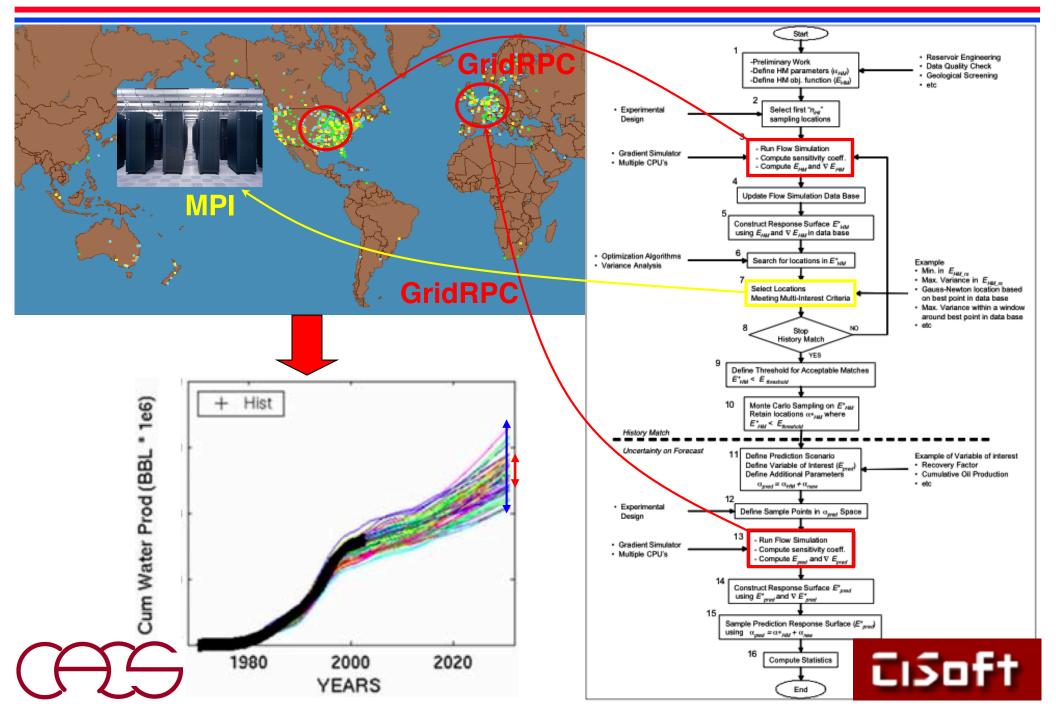
### **Parallel History Matching**

- Provide USC's parallel computing environment to demonstrate parallel execution of CVX's history match & associated forecast (HMAF) framework.
- History matching of a real field case (offshore Africa, North Sea & Gulf of Mexico) with 10,000-20,000 forward simulation runs on CACS high performance computing resources.



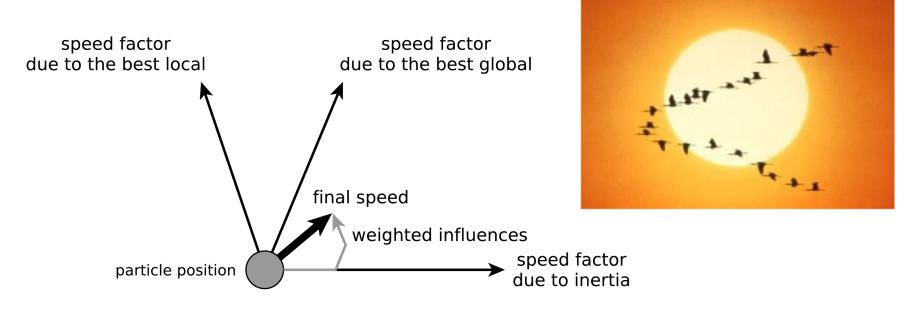
K. Nomura et al., J. Supercomputing 41, 109 ('07)

# **Opportunity: Overnight HMAF on a Grid**



#### **Particle Swarm Optimization**

An ensemble of interacting particles in the solution space explores the optimal solution: Each particle's movement is guided toward the best known positions in the search space, which are updated as better positions are found by other particles.



J. Kennedy & R. Eberhart, *IEEE Int'l Conf. Neural Networks* ('95) CALYPSO (particle-swarm structural prediction): <u>http://www.calypso.cn</u>

#### **Particle Swarm for Inverse Rendering**

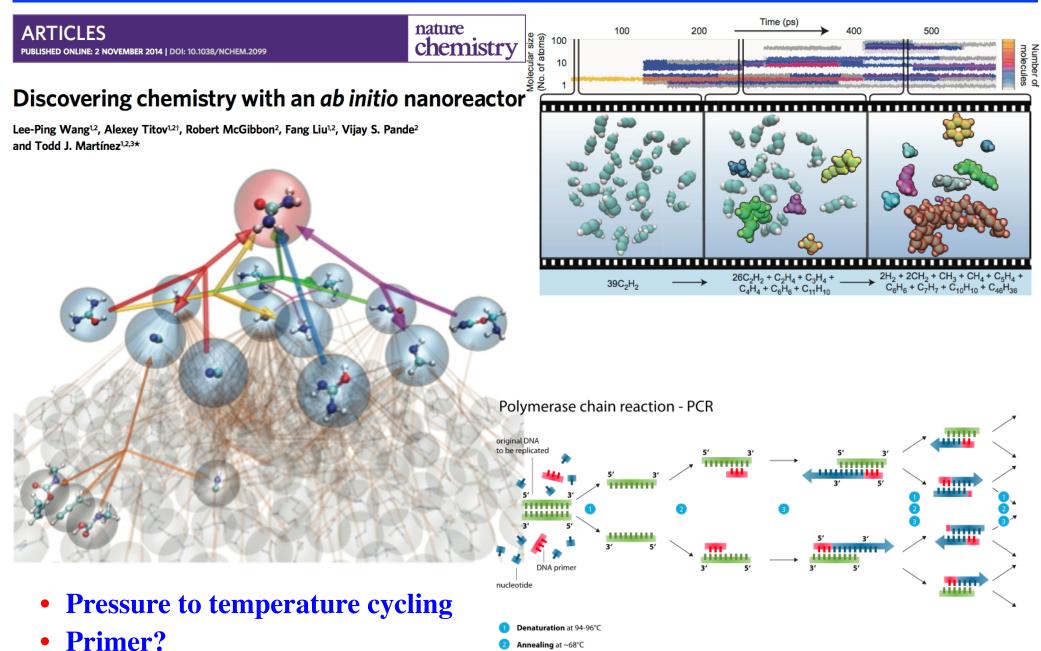


K. Nagano *et al.*, *J. Vis.* **20**, 195 ('17)

#### **Large Search-Space Exploration**

Stochastic Voyages into Uncharted Chemical Space Produce a Representative Library of All Possible Drug-Like Compounds Aaron M. Virshup,<sup>†,§</sup> Julia Contreras-García,<sup>†,§,#</sup> Peter Wipf,<sup>‡,§</sup> Weitao Yang,<sup>\*,†,§</sup> and David N. Beratan<sup>\*,†,§</sup> x Xx Initial library **Explore the set of 10<sup>60</sup>** molecules (< 500 Da) by a Breed new maximally diverse ensemble compounds Atom addition/removal/ modification Bond addition/removal/ modification Crossover Remove compounds outside target space Substructure filters Complexity limits Drug likeness Target properties Select maximally diverse subset Calculate chemical descriptors Maximin algorithm / J. Am. Chem. Soc. 2013, 135, 7296–7303 cell-based partitioning

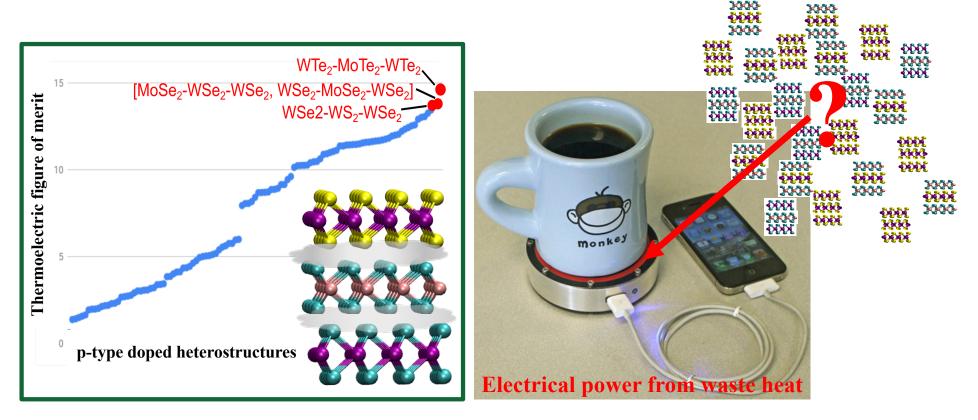
#### **Simulated PCR?**



3 Elongation at ca. 72 °C

## **Active Learning of Optimal Materials**

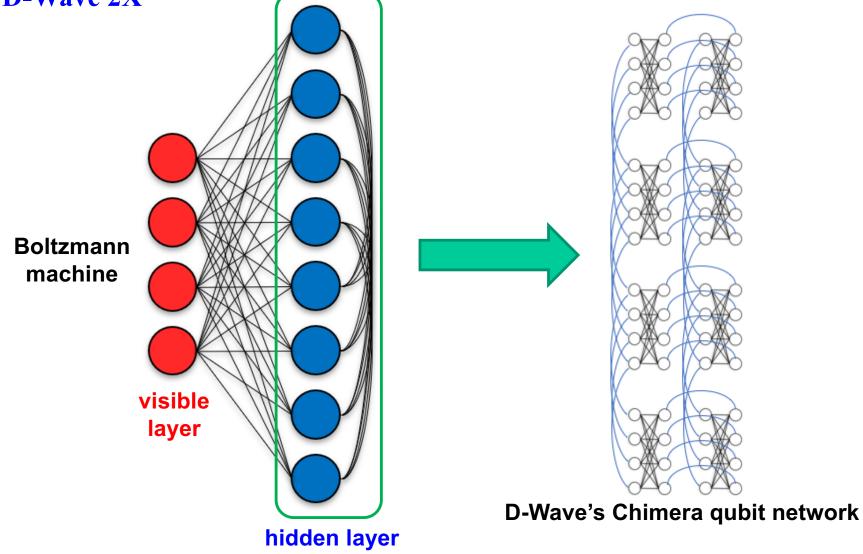
- Bayesian optimization balances exploitation & exploration to find a structure with the desired property with a minimal number of quantum-mechanical calculations
- Predicted three-layered transition-metal chalcogenide (TMDC) heterostacks with the largest thermoelectric figure-of-merit



L. Bassman et al., npj Comput. Mater. 4, 74 ('18)

# **Quantum-Classical Boltzmann Machine**

• Offload a hard machine-learning task to a 1,098-qubit quantum annealer, D-Wave 2X



J. Liu et al., Comput. Mater. Sci. 173, 109429 ('20)