

Challenges for Materials Modeling at the Atomic and Meso Scales

SAND2018-0867PE

Steve Plimpton
Sandia National Laboratories

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Presentation: SAND2015-9811PE



See you at the movies ...



CGI modeling advances by Pixar



Bug's Life (1998)
vegetation



Monsters, Inc (2001)
hair



Finding Nemo (2003)
water



Cars (2006)
painted surfaces



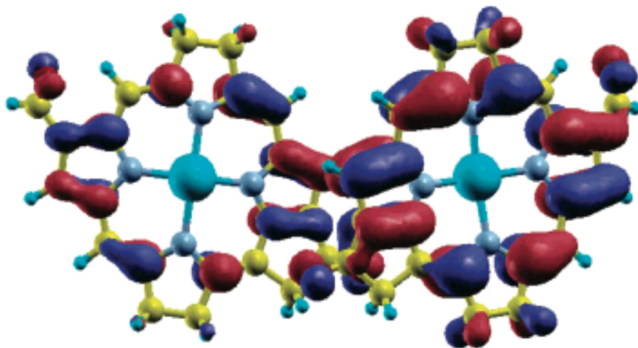
Ratatouille (2007)
food



Wall-E (2008)
rust & decay

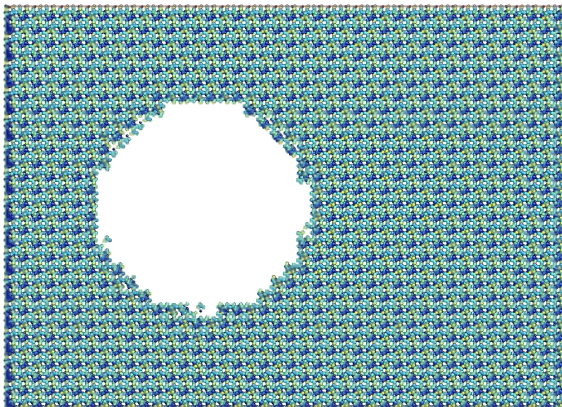
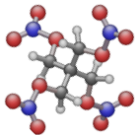
Quantum \Rightarrow MD \Rightarrow kMC \Rightarrow Continuum

- Quantum density functional theory (DFT) = ~ 100 atoms
 - **Schrodinger equation (PDE)** for electron density
 - $O(N^2)$ to $O(N^3)$ scaling with # of valence electrons



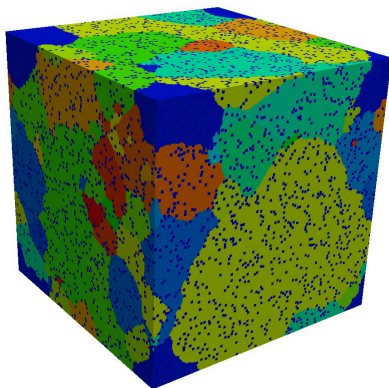
Quantum \Rightarrow MD \Rightarrow kMC \Rightarrow Continuum

- Classical molecular dynamics (MD) = $\sim 10^3$ to 10^9 atoms
 - atoms or coarse-grained particles, empirical forces
 - time-integrate **ODEs of Newtonian mechanics**
 - $O(N)$ scaling with # of particles



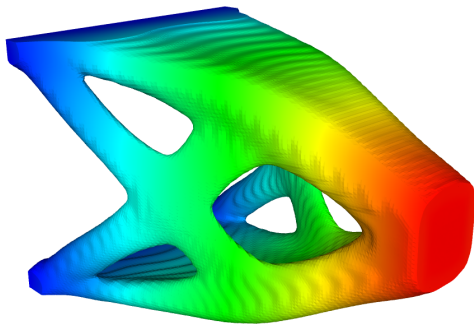
Quantum \Rightarrow MD \Rightarrow **kMC** \Rightarrow Continuum

- Kinetic Monte Carlo (kMC) = $\sim 10^6$ to 10^9 lattice sites
 - site = atom or meso-scale chunk of material
 - **Hamiltonian** to describe site-site interaction energies
 - $O(N)$ scaling with # of sites, due to local interactions



Quantum \Rightarrow MD \Rightarrow kMC \Rightarrow Continuum

- Continuum PDEs = $\sim 10^6$ to 10^9 grid cells
 - deformation stress/strain, Navier-Stokes, etc
 - discretize by **finite difference (FD)**, **finite elements (FE)**
 - $O(N)$ scaling with # of grid cells,
explicit or implicit (optimal multigrid, Krylov DD)



Recurrent challenges for 2 methods in the “middle”

- **Increase MD accuracy**
 - relative to quantum DFT = gold standard
- **Increase MD and kMC length & time scales**
 - via new models, new algorithms
 - aiming for continuum-scale validation & rigor

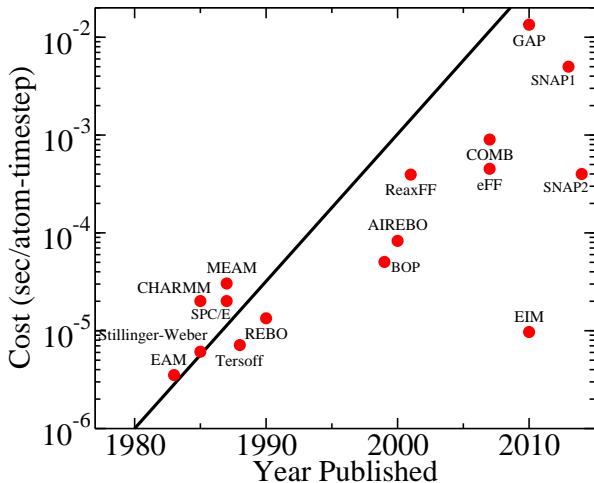
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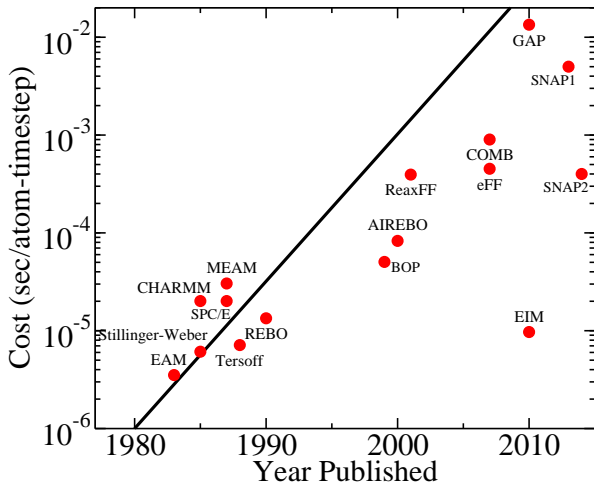
Remainder of talk: **3 examples**

- ① Quantum-accurate empirical potentials for MD
- ② Accelerated-time hyperdynamics algorithm for MD
- ③ Efficient and accurate algorithms for kMC

Moore's Law for interatomic potentials (force fields)



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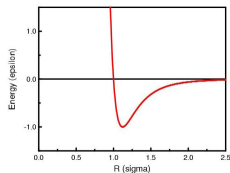
quantum DFT is 10^6 slower for 400 atoms, 10^9 for 40000, etc

Traditional interatomic potentials (force fields)

- For time-integration of N particles, just need ...
- Potential = energy of system, derivatives = forces

$$E_{total} = \Phi(\mathbf{R}_N) = \sum_{i,j} \phi_2(r_i, r_j) + \sum_{i,j,k} \phi_3(r_i, r_j, r_k) + \sum \phi_4() + \dots$$

- Truncate many-body interactions, distance cutoff $\Rightarrow O(N)$
- Lennard-Jones (2 params)
to ReaxFF (100s of params)



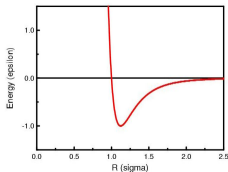
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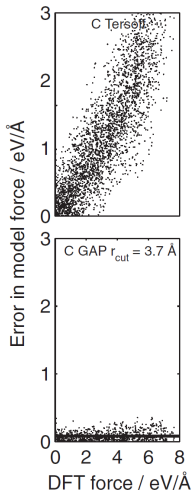
- Parameters fit to:
 - experimental data: density, elastic constants, melting temp, etc
 - quantum: bond stretch/stiffness, reaction barriers, etc
- **Big bottleneck** for materials modeling via classical MD

Quantum-accuracy with classical potentials?

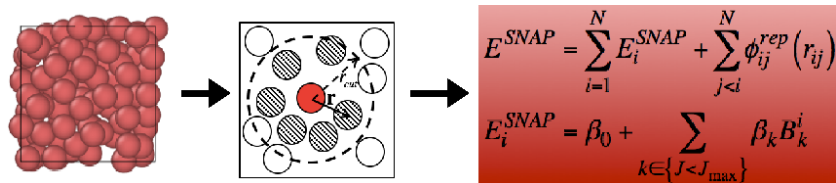
- **Traditional** potential
 - functional form based on physical insight
 - handful of params fit to specific QM calcs
- **Machine-learned** potential
 - generic descriptors span conformational space
 - fit via ML to large database of QM calcs

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- **GAP** = Gaussian approximation potential
 - Csányi & Bartók-Partay (U Cambridge)
 - *Phys Rev Lett*, 104, 136403 (2010)
 - Gaussian process =
high-dimensional interpolation method
- **SNAP** = spectral neighbor analysis potential
 - Aidan Thompson, Mitch Wood (Sandia)
 - *J Comp Phys*, 285, 316-330 (2015)
 - fit via simpler linear regression plus
genetic algorithm wrapper

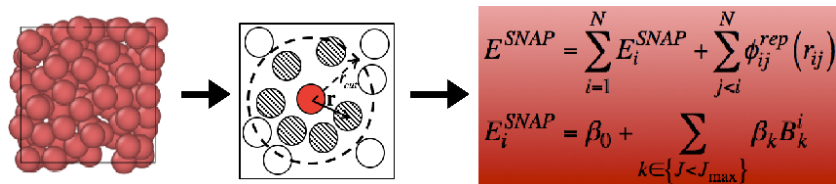


How SNAP potentials work



- Represent neighborhood via 4D hyperspherical harmonics
- $B_k^i = \text{descriptors}$ = bispectrum components for atom i

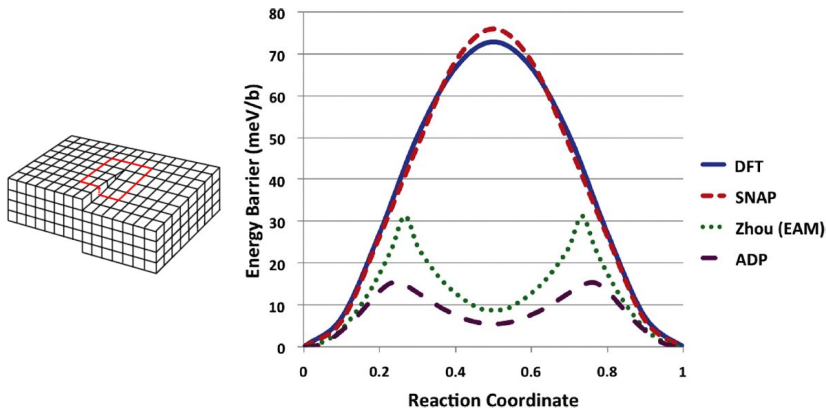
How SNAP potentials work



- Represent neighborhood via 4D hyperspherical harmonics
- $B_k^i =$ **descriptors** = bispectrum components for atom i
- Pre-compute **database of DFT results** for small systems
 - 1000s of wisely-chosen configurations (up to 100s of atoms)
- Each config gives gold-standard $F_i, E_{total}, \mathbf{W}_{ij}$
- Compute optimal β_k (unknowns) via least-squares
- Embed fitting in **DAKOTA** GA to optimize hyper-parameters
 - weights on QM configs, cutoff, # of basis functions
- Expensive, but still linear $O(N)$ cost in # of atoms
- SNAP reduces cost by $\sim 10x$ via symmetry exploitation

Success with SNAP potential for Tantalum

- Energy barrier for **screw dislocation migration** in bcc Ta
- *Thompson, et al, J Comp Phys, 285, 316-330 (2015)*



- Note: screw dislocations were **not** in QM database

Recent SNAP potential for W and W/He

	DFT ^a	EAM ^b	MEAM ^c	GAP ^d	SNAP ^e
a_0 (Å)	3.1803	3.165	3.164	3.1803	3.1806
C_{11} (GPa)	517	517	533	518	518
C_{12} (GPa)	198	200	205	198	196
C_{44} (GPa)	142	156	163	143	144

- Only match to sign of di-vacancy binding

	DFT ^a	EAM ^b	MEAM ^c	GAP ^d	SNAP ^e	SNAP ^f
$E_{W-Tetra}$	11.1	10.4	11.2	12.6	9.8	9.8
E_{W-Octa}	11.7	10.4	9.0	12.9	11.3	11.3
$E_{W-[110]d}$	9.8	10.1	8.9	11.6	9.2	9.2
$E_{W-[111]d}$	9.6	9.4	9.0	11.0	9.5	9.5
$E_{W-vac.}$	3.3	3.6	3.9	3.3	3.2	3.2
$E_{W-divac.}^g$	0.1	-0.4	-0.2	-0.3	0.1	0.1
$E_{He-Tetr}$	6.2	6.2	6.3	6.2	6.1	6.3
E_{He-Oct}	6.4	6.3	6.7	6.6	6.4	6.5
$E_{He-Subs}$	4.7	4.7	5.2	4.3	4.2	3.8
$E_{2He-Tetr}^h$	1.0	0.9	0.7	0.7	0.8	1.1

Wood & Thompson, "QM accurate MD potential for W and He", arXiv 1702.07042

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- Only match to sign of di-vacancy binding
- **Q:** why SNAP better than GAP?
- **A:** additional QM conformations, including multiple vacancies
- 3.8 \Rightarrow 4.9 for combined W/He potential

Complications

- How to insure a **sufficiently complete** database of quantum calculations?
- **Knobs** to turn when creating SNAP potential:
 - weighting of different quantum conformations
 - how many bispectrum components (20,30,more)
 - how big a cutoff \Rightarrow # of influencing neighbors
- Use DAKOTA optimization toolkit to automate knob tuning
 - iterate over fitting procedure many times
 - <https://dakota.sandia.gov>



Research challenges for quantum-accurate potentials

- 1 Can we answer **UQ**-style questions?
 - quantify errors induced by fitting & database lookup
 - how do errors depend on quantity/coverage of quantum data?
 - how do errors propagate to MD statistics:
barrier heights, diffusion coeffs, etc

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 - detect when interpolation of MD config is inaccurate
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 - re-fit to more quantum data incrementally

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- ④ **Holy grail**: for any new material, automatic quantum-accurate potentials with cost/scaling of classical MD

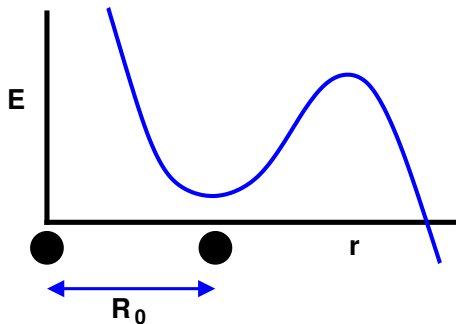
What is hyperdynamics (HD)

- **Accelerated time method** for MD
 - Voter, *J Chem Phys*, 106, 4665 (1997)
 - bias the PE surface to enable more rapid transitions
- **Bond-boost** formulation
 - Miron & Fichthorn, *J Chem Phys*, 119, 6210 (2003)
 - variant: apply bias to only one or few bonds
- **Local** hyperdynamics
 - Kim, Perez, Voter, *J Chem Phys* 139, 144110 (2013)
 - global: bias one bond in entire system at a time
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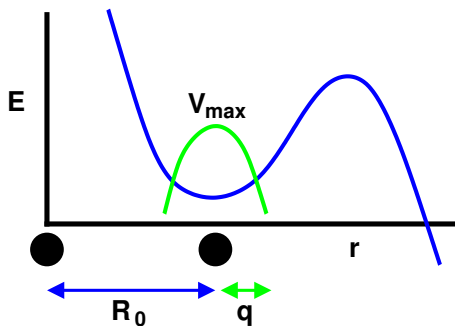
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- Key **caveat**:
 - applicable to solids with distinct energy basins, rare transitions from one basin to another
- Effective speed-up can be **orders of magnitude**
 - especially for high barriers and low temperatures
 - accelerating a single trajectory

Pictorial view of bond-boost hyperdynamics



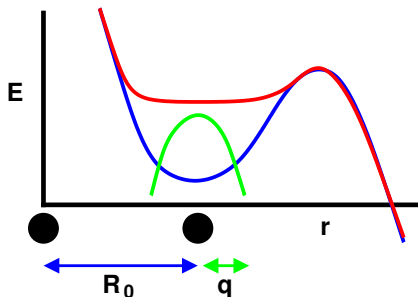
- Define (conceptual) **bonds** between all pairs of nearby atoms
- For example, ~ 12 nearest neighbors per atom in fcc lattice

Pictorial view of bond-boost hyperdynamics



- Bond strain: $\epsilon_{ij} = (R_{ij} - R_{oij})/R_{oij}$
- Add **bias potential** to two atoms in max-strain bond:
$$V_{ij} = V_{\max}[1 - (\epsilon_{ij}/q)^2], \quad |\epsilon_{ij}| < q, \quad \text{else } 0$$
- Bias may be added to different bond each timestep

Pictorial view of bond-boost hyperdynamics



- Shallow V_{ij} allows faster transition by I,J (and nearby) atoms
- Must choose V_{max} and q carefully:
 - if: zero bias at dividing surfaces
 - if: do not induce TST-violating correlated events
 - then: relative transition rates not altered
 - then: quantifiable **time boost factor** each timestep
 - then: resulting traj is time-accurate (unlike enhanced sampling)

Local hyperdynamics in parallel

Local HD **algorithm** loop:

- Run 100 steps of MD with local HD bias
 - bias all bonds which are max strain within D_{cut} region
 - adjust per-bond V_{max} to boost time uniformly everywhere
- Extra operations for HD:
 - **2nd neighbor list** out to D_{cut}
 - **double loops** over atoms and big neighbor list
 - **comm** to acquire bond-strain info for ghost atoms
- Quench to check if **event** has occurred
 - if yes: re-form bond list, preserving bond prefactors

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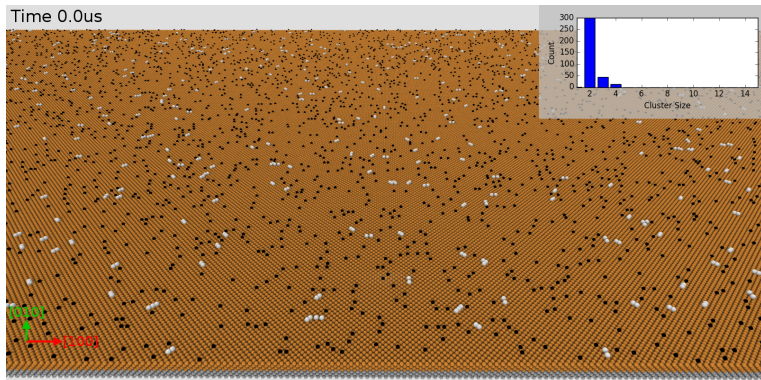
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Cost of HD versus regular MD:

- For cheap EAM, about 2x more expensive
 - half is quench & event search every 100 steps
 - half is comp/comm to find max-strain bonds
 - 2x shrinks for more expensive potentials
- Strong and weak scaling essentially same as MD

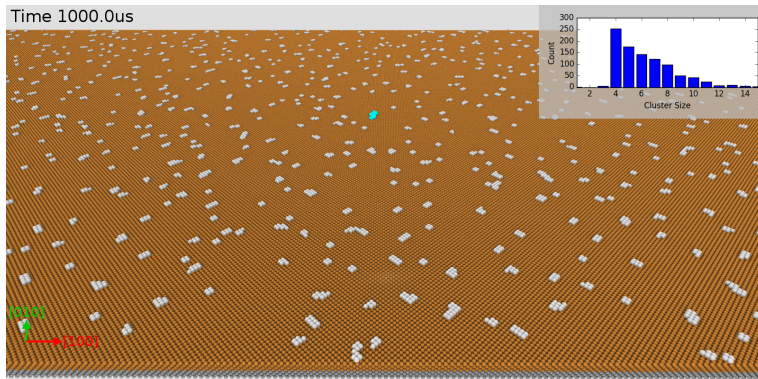
Pt surface diffusion model with EAM

- Pt (100) surface with 4% adatom coverage (random)
- Exchange barrier = 0.64 eV, hop barrier = 1.25 eV
- HD Vmax = 0.4 eV, T = 400K \Rightarrow **4000x boost**
- 1.2M atoms, 50M timesteps \Rightarrow **1 ms** of real time



Pt surface diffusion model with EAM

- 24 hrs on 128 Broadwell nodes (4096 cores, 300 atoms/core)
- Observed $\sim 400\text{K}$ diffusion events with 5900 adatoms

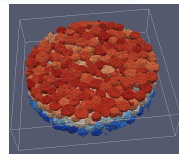
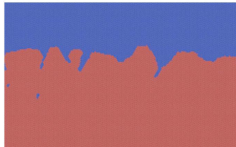
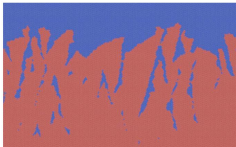
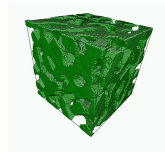
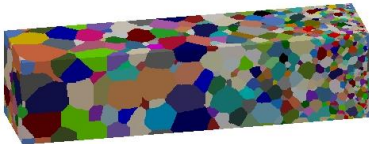


- Can use global/local HD with **any potential** in LAMMPS

Materials modeling via on-lattice kMC

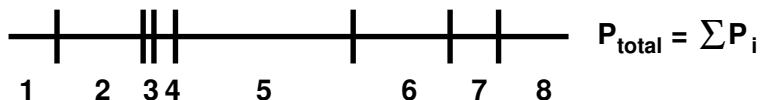
kMC = kinetic Monte Carlo

- Variety of models for time evolution of processed materials
- Length scale = atomic to mesoscale
- Time scale = microseconds to days
- Hamiltonian encodes physics of local interactions
- Time accurate (via event rates) versus Metropolis MC



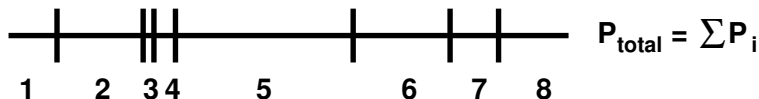
- **KMC algorithm:**

- select one of N events with correct relative probability
- $\Delta t = -\ln(RN)/P_{total}$
- update affected events



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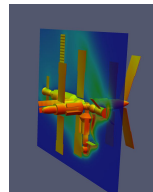
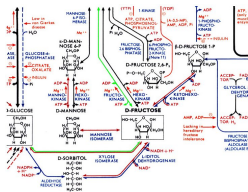
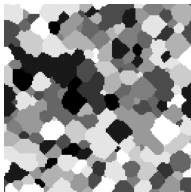
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- Serial algorithms are **exact**, but not parallel
- Parallel algorithms are **approximate**
 - deviate from exact event selection with “acceptable” error
 - acceptable to me, may not be acceptable to you
 - exploit **local** nature of many materials models

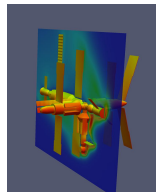
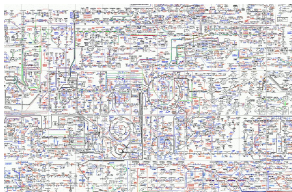
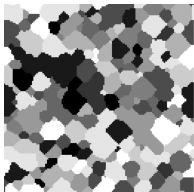
kMC algorithm arises in many contexts

- BKL algorithm for **Ising model spin updates**
 - *Bortz, Kalos, Lebowitz, J Comp Phys, 17, 10-18 (1975)*
 - event = flip one or a set of spins on lattice
- SSA for stochastic integration of coupled ODEs
 - *D Gillespie, J Chem Phys, 22, 403-434 (1976)*
 - event = which reaction occurs next
 - **biochemical reaction pathways**
- TC (time counter) algorithm for DSMC
 - *G Bird, Phys Fluids, 6, 1518 (1963)*
 - event = collision between 2 particles
 - **low density fluid flow**



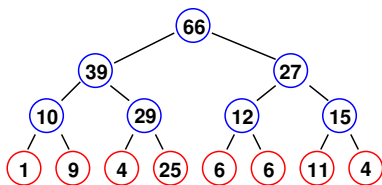
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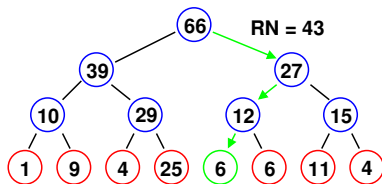
Exact linear and logarithmic kMC algorithms

- $O(N)$ **linear** algorithm is simple (Gillespie)
 - worked fine when N was small (early biochemical networks)
 - $O(N)$ to select from list, $O(1)$ to update
- $O(\log(N))$ **logarithmic** algorithm
 - Gibson & Bruck, *J Phys Chem A*, 104, 1876-89 (2000)
 - method-of-choice as network sizes grew
 - binary tree: leaves = events, branch nodes = summed probs



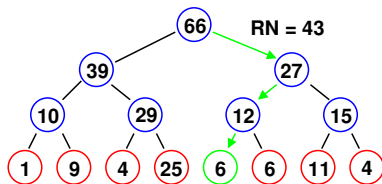
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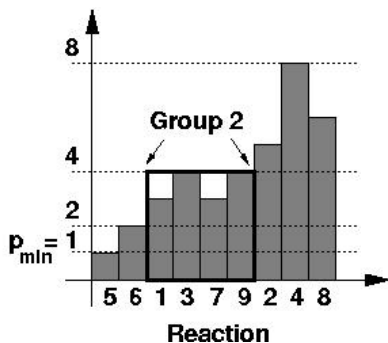
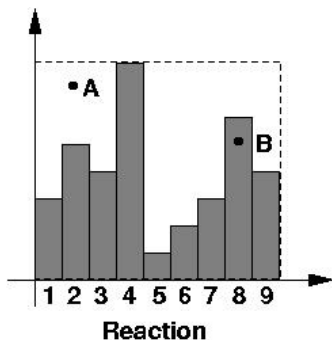
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- Is it possible to have $O(1)$ **constant-time** algorithm?

Exact constant-time kMC algorithm

- Devroye, *Non-uniform random variate generation* (1986)
- Based on **compostion/rejection** idea
- Applied to bio: *Slepoy et al, J Chem Phys 128, 205101* (2008)



- Group bounds increase in **powers of 2**
- Rejection coverage $> 50\% \Rightarrow < 2$ RN on average

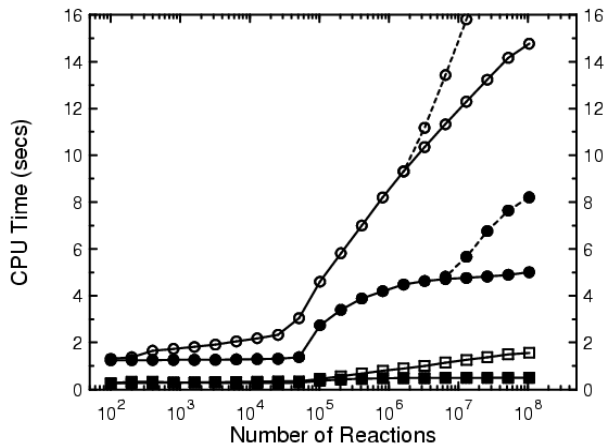
A few more details

- Constant-time requires $O(1)$ **operations** to:
 - find specific event within group (two-way pointers)
 - add/delete event to group (append to list, swap with end)
- **Condition #1:**
 - # of groups must be independent of N
 - bound ratio of max/min probabilities
- **Condition #2:**
 - # of affected-events per event does not grow with N

- Both typically satisfied for materials & bio network models

Performance of constant-time algorithm versus $\log(N)$ tree

- Network of cellular bio-chemistry reactions $A + B \xrightarrow{k} C + D$
- Biological cell = small well-mixed reaction volume

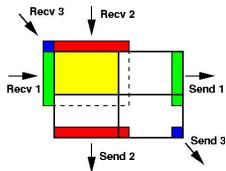
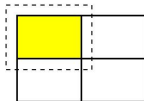
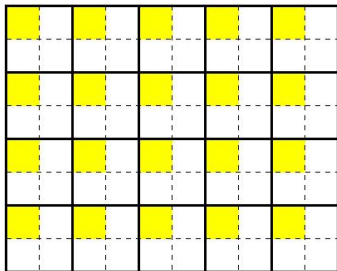


Parallel approximate kMC algorithm in SPPARKS

- Adapted from semi-rigorous synchronous sub-lattice idea
Shim & Amar, *Phys Rev B* 71, 125432 (2005)

Parallel approximate kMC algorithm in SPPARKS

- Adapted from semi-rigorous synchronous sub-lattice idea
Shim & Amar, *Phys Rev B* 71, 125432 (2005)
- Split domain into **sub-domains** and **sectors**: 4 in 2d, 8 in 3d
- Each processor works on same sector at same time
- kMC chooses site, sites can have multiple events
- Alternate kMC within sector, **comm of boundary sites**



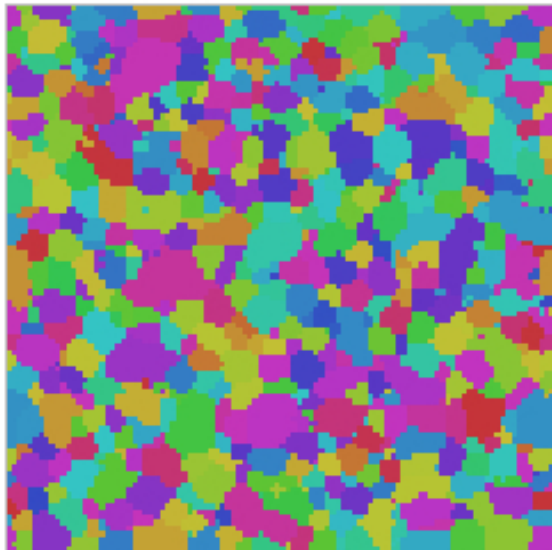
Sources of error

Approximate method for several reasons:

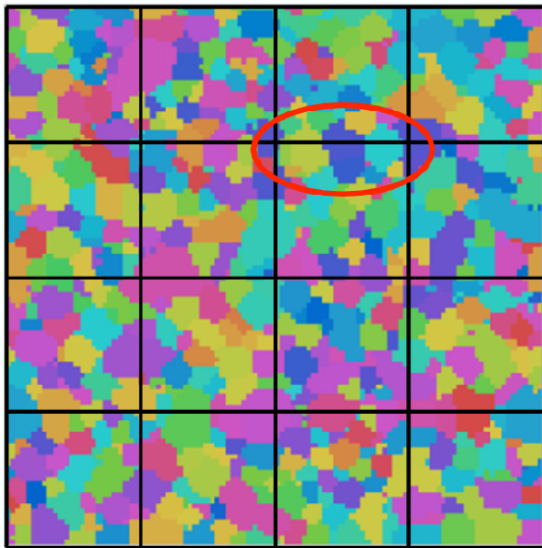
- Events occur simultaneously on different processors
- Order dependence induced by sector ordering
- Consecutive events in same sector are over-sampled
- Consecutive cross-sector events are under-sampled
- Boundary sites are older/younger than sector sites

Biggest issue: boundary sites are **frozen** during per-sector kMC

Can you find any bad grains?



Shish-kebab effect



Solution: adaptive heuristic using events/site metric

Basic trade-off:

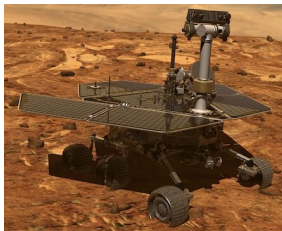
- Perform more events within a sector:
 - less communication \Rightarrow good parallel scalability
 - more sector boundary effects
- Perform less events within a sector:
 - more communication \Rightarrow poor parallel scalability
 - fewer sector boundary effects

Good compromise:

- User picks **nstop** = events per active site within sector
- $N_{stop} = 1$ is often a good rule-of-thumb
- **Adaptive** because active sites may vary greatly over time

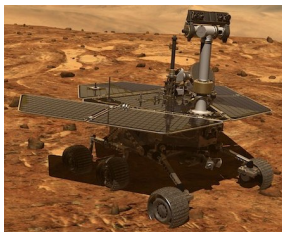
Materials processing for space applications

- John Mitchell & Veena Tikare for NASA, DOE/ONE
- Radioisotope thermal generators (**RTG**) for Mars rovers



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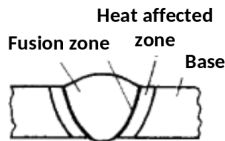
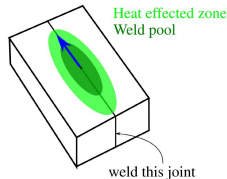
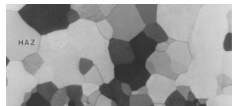
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- Decay heat \Rightarrow electrical power via thermoelectric effect
- Powers experiments, analysis (not spinning wheels)
- RTG **fuel pellet** = plutonia (PuO_2) in **Iridium container**
 - 3cm x 3cm cylinder, wrapped with 600 μ m thick Ir
 - Ir = refractory metal, melting pt near 2500° C
- Tungsten gas arc used to **weld container shut**

kMC model of welding process

- How a weld joins two pieces of metal?
 - metals are **polycrystalline**
 - arc spot melts the two pieces
 - recrystallizes to grain structure that spans the gap
 - good = small, equi-axial grains
- Arc melts a spot with 3d profile
- Nearby **heat-affected zone** where T drops off
- **Potts model** for grain growth
 - spin = crystal lattice orientation
 - grain = cluster of same spins
 - curvature-driven grain growth
 - add $T(x,t)$ -dependent mobility term



Model details

- kMC event = **spin flip** to neighbor site value
- Hamiltonian and event probability with **mobility prefactor**

$$H_i = \sum_{j=1}^N J(1 - \delta_{ij}), \quad \delta_{ij} = 1 \text{ if } s_i = s_j, \text{ else } 0$$

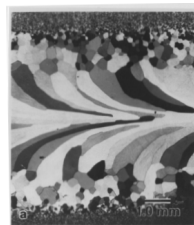
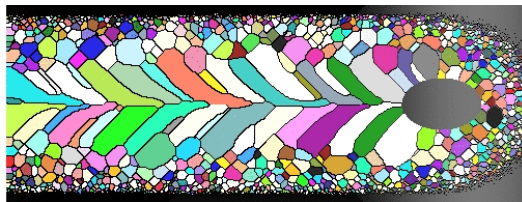
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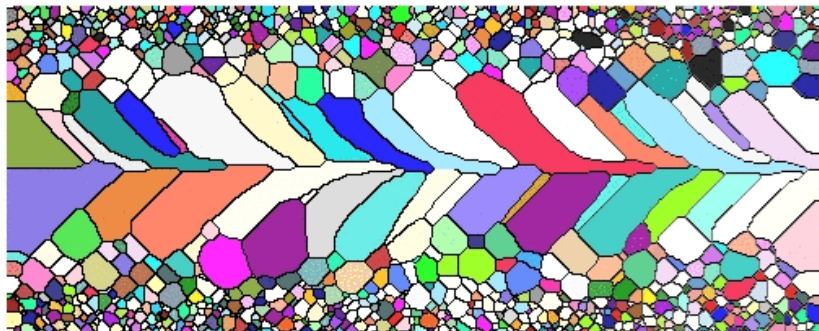
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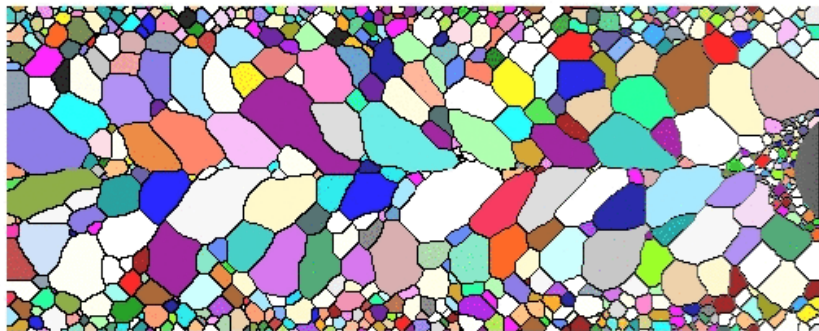
- **Banana shaped** grains!

Movie of arc spot motion

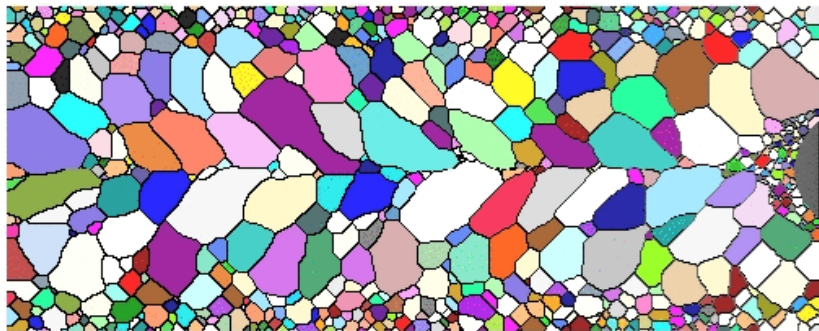
2d view of 3d lattice, tens of millions of lattice sites



Time-varying arc pulse \Rightarrow more equi-axial grains



Time-varying arc pulse \Rightarrow more equi-axial grains



- With $\sim 10^{10}$ sites \Rightarrow experimental length/time scales
 - 10 μm grain = 10x10x10 lattice sites
 - arc spot moving at ~ 1 cm/sec
 - dependence on speed, spot size/shape/time-variability

Research challenges for kMC modeling

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 - huge timescale advantage vs MD
 - μsec events vs fmsec timestepping
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 - irregular neighbors, no preferred direction, multi-atom moves
 - barrier heights via nudged-elastic band (NEB)
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- ③ **Coupled kMC/MD** algorithms (akin to MD/QM):
 - use MD to find kMC events
 - initially run mostly at tiny MD timescale (expensive)
 - until catalog all relevant events
 - then run at large kMC timescale (cheap)

Thanks and links

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- **Joint work** with many folks at Sandia:
 - LAMMPS: Aidan Thompson, Stan Moore, Mitch Wood, Axel Kohlmeyer (Temple U)
 - SPPARKS: Aidan Thompson, John Mitchell, Veena Tikare
- Open-source codes:
 - LAMMPS for MD: <http://lammps.sandia.gov>
 - SPPARKS for kMC: <http://spparks.sandia.gov>