Large Scale Parallel Lattice Boltzmann Model of Dendritic Growth

Bohumir Jelinek Mohsen Eshraghi Sergio Felicelli

CAVS, Mississippi State University

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Why LBM-CA?

H. Yin et al. / Acta Materialia 59 (2011) 3124-3136



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When the fluid flow around solidifying dendrites is considered, lattice Boltzmann method is faster than alternatives



Lattice Boltzmann method



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Lattice-Boltzmann method (LBM) calculates time evolution of a quantity of interest governed by a partial differential equation subject to given initial and boundary conditions at regularly spaced nodes .



Lattice Boltzmann Method



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D2Q9 lattice

Each node has 9 distribution functions f_i representing portion of the mass density moving in the lattice direction e_i

$$\rho = \sum_{i=0}^{8} f_i, \quad \rho \boldsymbol{u} = \sum_{i=0}^{8} f_i \boldsymbol{e}_i$$





Lattice Boltzmann Method





 $f_i(\boldsymbol{r} + \boldsymbol{e}_i \Delta t, t + \Delta t) = f_i(\boldsymbol{r}, t) + \frac{1}{\tau_{\mathrm{u}}} \left(f_i^{\mathrm{eq}}(\boldsymbol{r}, t) - f_i(\boldsymbol{r}, t) \right)$





For each lattice direction e_i , *i*=0..8

$$f_i(\boldsymbol{r} + \boldsymbol{e}_i \Delta t, t + \Delta t) = f_i(\boldsymbol{r}, t) + \frac{1}{\tau_u} \left(f_i^{eq}(\boldsymbol{r}, t) - f_i(\boldsymbol{r}, t) \right)$$





For each lattice direction e_i , *i*=0..8

 $f_i(\boldsymbol{r} + \boldsymbol{e}_i \Delta t, t + \Delta t) = f_i(\boldsymbol{r}, t) + \frac{1}{\tau_u} \left(f_i^{eq}(\boldsymbol{r}, t) - f_i(\boldsymbol{r}, t) \right)$

Collision:

Adjusts the distribution function to approach equilibrium distribution



For each lattice direction e_i , *i*=0..8









Equilibrium distribution function







LBM parallelization

• • • • • • • • • • • • • • • • • • •	• • • • CPU 8	• • • • CPU 9 • • • •
• • • •	• • • •	• • • •
CPU 4	• • • • • • • • • • • • • • • • • • •	• • • • • • • • • •
• • • • •	 CPU 2 • • • • • • • • • 	• • • • • • • • • •

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Spatial domain decomposition











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LBM-CA solidification model C_I, u, T

Flow of solute between solidifying dendrites in a variable temperature field. Cooled at front and back boundaries, heated from left (inlet) and right (outlet) boundaries.





LBM-CA parallelization – dendrite growth



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For dendrite growth, information from neighboring nodes is needed to update local node value







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Populate ghost nodes after each local update



































Computational resources

Talon, MSU HPC²:

- 3072 cores, 12 cores/node (user limit 192 cores / job)
- Intel Xeon X5660 @2.8GHz (Westmere) processors
- 24 GByte/node memory
- Voltaire quad data-rate InfiniBand (40Gb/s)
- peak performance of over 34.4 TeraFLOPS

Kraken, NICS/ORNL:

- 112,896 cores, 12 cores/node (user limit cores / job)
- AMD Opteron (Istanbul) @2.6GHz (Istanbul) processors
- 16 GByte/node memory
- Cray SeaStar2+ router
- peak performance of 1.17 PetaFLOPS

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Generating an initial configuration for parallel scaling tests

Simulation domain:

- rectangular lattice, 8000x6000 grid points
- dimensions: 2.4 mm x 1.8 mm (0.3 µm/lattice distance)
- 3264 random dendrite nucleation sites
- constant cooling rate 100K/s across the whole domain
- forced melt flow through inlet (left) and outlet (right) boundaries
- almost 16 GB of memory = single node of Kraken
- 400k time steps
- took about 10 hours on 192 cores on Talon @ MSU

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Initial configuration







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Magnified portion of initial configuration



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Speed up

- Speed up (strong scaling) represents how much faster a task is solved utilizing multiple cores
- Speed up tests were performed by restarting simulation from the step when the dendrites were fairly grown in the incubation domain
- Incubation domain is "split" equally between varying number of cores, then executed for 587 time steps with a flow forced at the inlet (left) and outlet (right), and with a specified cooling flow rate at all boundaries



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Speed up - constant task, 1 core







Speed up - constant task, 2 cores







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Speed up - constant task, 4 cores







Speed up - constant task, 12 cores





Speed up - constant task, 12 cores





Speed up - constant task, 24 cores







Speed up - results



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strong scaling (speed up) near perfect up to 3072 cores

 Algorithm is memory bandwidth limited on multi-core architecture (low FLOP/byte ratio)



Scale up

- Scale up (weak scaling) tests checks if the algorithm can solve larger task when more cores are utilized without a significant performance penalty
- Scale up tests were initialized from the stage when the dendrites were fairly grown in the incubation domain
- Incubated domain was "duplicated" equally onto varying number of nodes, then executed for 587 time steps with a flow forced at the inlet (left) and outlet (right), and with a specified cooling flow rate at all boundaries









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Duplication of the incubation domain onto 4 nodes







Duplication of the incubation domain onto 4 nodes







Duplication of the incubation domain onto 16 nodes





Scale up - results



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Scale up - results

Demonstrated nearly perfect scale up

Largest domain:

- 41472 cores of Kraken
- over 165 billion grid nodes
- 11 millions of dendrites (only hundreds reported before)
- solute diffusion, melt convection, and heat transport
- dimensions 17.28 cm x 8.64 cm
- 587 time steps
- 40 minutes of simulation time

3D LBM-CA parallelization $-C_{I}$, u

3D Dendrite growth in undercooled AI-3wt%Cu melt



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3D columnar dendrites growing in undercooled melt of AI-3wt%Cu



Domain size 180x180x144 (µm)³ By Mohsen Eshraghi

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Conclusions

<u>2D:</u>

- Parallelized 2D lattice Boltzmann / cellular automaton model of dendritic growth
- Tested the strong and weak parallel scaling of LBM/CA model with dendrites at advanced growth stage
- Demonstrated nearly ideal speed up and scale up <u>3D:</u>
- Preliminary results exhibit similar speed up and scale up performance in 3D,
- measured tip growth velocity and solute concentration profiles

Effects of convection, to be presented by Mohsen
 Eshraghi - Frontiers in Solidif. Science, Wed. 5:40 PM

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